



## Full wwPDB EM Validation Report ⓘ

Jan 27, 2022 – 03:35 am GMT

PDB ID : 7Q97  
EMDB ID : EMD-13867  
Title : Structure of the bacterial type VI secretion system effector RhsA.  
Authors : Guenther, P.; Quentin, D.; Ahmad, S.; Sachar, K.; Gatsogiannis, C.; Whitney, J.C.; Raunser, S.  
Deposited on : 2021-11-12  
Resolution : 3.30 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](mailto: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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.0.dev97  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.26

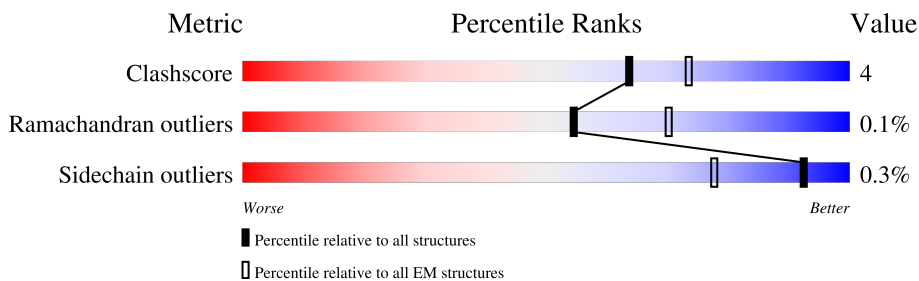
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.30 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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1426	
1	B	1426	

## 2 Entry composition i

There is only 1 type of molecule in this entry. The entry contains 32806 atoms, of which 15752 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 Rhs family protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	1047	16403	5311	7876	1575	1629	12	2	0
1	B	1047	16403	5311	7876	1575	1629	12	2	0

There are 148 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	MET	deletion	UNP Q4K3M9
A	?	-	SER	deletion	UNP Q4K3M9
A	?	-	ASP	deletion	UNP Q4K3M9
A	?	-	ALA	deletion	UNP Q4K3M9
A	?	-	LEU	deletion	UNP Q4K3M9
A	?	-	TRP	deletion	UNP Q4K3M9
A	?	-	ALA	deletion	UNP Q4K3M9
A	?	-	ALA	deletion	UNP Q4K3M9
A	?	-	ARG	deletion	UNP Q4K3M9
A	?	-	LEU	deletion	UNP Q4K3M9
A	?	-	GLY	deletion	UNP Q4K3M9
A	?	-	ASP	deletion	UNP Q4K3M9
A	?	-	GLY	deletion	UNP Q4K3M9
A	?	-	LEU	deletion	UNP Q4K3M9
A	?	-	GLU	deletion	UNP Q4K3M9
A	?	-	HIS	deletion	UNP Q4K3M9
A	?	-	THR	deletion	UNP Q4K3M9
A	?	-	SER	deletion	UNP Q4K3M9
A	?	-	MET	deletion	UNP Q4K3M9
A	?	-	MET	deletion	UNP Q4K3M9
A	?	-	ALA	deletion	UNP Q4K3M9
A	?	-	ASP	deletion	UNP Q4K3M9
A	?	-	ILE	deletion	UNP Q4K3M9
A	?	-	LEU	deletion	UNP Q4K3M9
A	?	-	GLY	deletion	UNP Q4K3M9
A	?	-	GLY	deletion	UNP Q4K3M9

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	VAL	deletion	UNP Q4K3M9
A	?	-	LEU	deletion	UNP Q4K3M9
A	?	-	GLU	deletion	UNP Q4K3M9
A	?	-	VAL	deletion	UNP Q4K3M9
A	?	-	ALA	deletion	UNP Q4K3M9
A	?	-	ALA	deletion	UNP Q4K3M9
A	?	-	ASN	deletion	UNP Q4K3M9
A	?	-	VAL	deletion	UNP Q4K3M9
A	?	-	ALA	deletion	UNP Q4K3M9
A	?	-	ILE	deletion	UNP Q4K3M9
A	?	-	GLY	deletion	UNP Q4K3M9
A	?	-	ALA	deletion	UNP Q4K3M9
A	?	-	LEU	deletion	UNP Q4K3M9
A	?	-	ALA	deletion	UNP Q4K3M9
A	?	-	THR	deletion	UNP Q4K3M9
A	?	-	MET	deletion	UNP Q4K3M9
A	?	-	ALA	deletion	UNP Q4K3M9
A	?	-	VAL	deletion	UNP Q4K3M9
A	?	-	ALA	deletion	UNP Q4K3M9
A	?	-	ALA	deletion	UNP Q4K3M9
A	?	-	ALA	deletion	UNP Q4K3M9
A	?	-	ALA	deletion	UNP Q4K3M9
A	?	-	GLY	deletion	UNP Q4K3M9
A	?	-	ILE	deletion	UNP Q4K3M9
A	?	-	THR	deletion	UNP Q4K3M9
A	?	-	VAL	deletion	UNP Q4K3M9
A	?	-	ALA	deletion	UNP Q4K3M9
A	?	-	THR	deletion	UNP Q4K3M9
A	?	-	GLY	deletion	UNP Q4K3M9
A	?	-	GLY	deletion	UNP Q4K3M9
A	?	-	LEU	deletion	UNP Q4K3M9
A	?	-	GLY	deletion	UNP Q4K3M9
A	?	-	ALA	deletion	UNP Q4K3M9
A	?	-	CYS	deletion	UNP Q4K3M9
A	?	-	VAL	deletion	UNP Q4K3M9
A	61	MET	LEU	conflict	UNP Q4K3M9
A	63	SER	-	insertion	UNP Q4K3M9
A	64	SER	LEU	conflict	UNP Q4K3M9
A	65	HIS	VAL	conflict	UNP Q4K3M9
A	66	HIS	VAL	conflict	UNP Q4K3M9
A	67	HIS	GLY	conflict	UNP Q4K3M9
A	68	HIS	VAL	conflict	UNP Q4K3M9

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	69	HIS	VAL	conflict	UNP Q4K3M9
A	70	HIS	VAL	conflict	UNP Q4K3M9
A	71	SER	GLY	conflict	UNP Q4K3M9
A	72	GLN	VAL	conflict	UNP Q4K3M9
A	73	ASP	VAL	conflict	UNP Q4K3M9
A	74	PRO	MET	conflict	UNP Q4K3M9
B	?	-	MET	deletion	UNP Q4K3M9
B	?	-	SER	deletion	UNP Q4K3M9
B	?	-	ASP	deletion	UNP Q4K3M9
B	?	-	ALA	deletion	UNP Q4K3M9
B	?	-	LEU	deletion	UNP Q4K3M9
B	?	-	TRP	deletion	UNP Q4K3M9
B	?	-	ALA	deletion	UNP Q4K3M9
B	?	-	ALA	deletion	UNP Q4K3M9
B	?	-	ARG	deletion	UNP Q4K3M9
B	?	-	LEU	deletion	UNP Q4K3M9
B	?	-	GLY	deletion	UNP Q4K3M9
B	?	-	ASP	deletion	UNP Q4K3M9
B	?	-	GLY	deletion	UNP Q4K3M9
B	?	-	LEU	deletion	UNP Q4K3M9
B	?	-	GLU	deletion	UNP Q4K3M9
B	?	-	HIS	deletion	UNP Q4K3M9
B	?	-	THR	deletion	UNP Q4K3M9
B	?	-	SER	deletion	UNP Q4K3M9
B	?	-	MET	deletion	UNP Q4K3M9
B	?	-	MET	deletion	UNP Q4K3M9
B	?	-	ALA	deletion	UNP Q4K3M9
B	?	-	ASP	deletion	UNP Q4K3M9
B	?	-	ILE	deletion	UNP Q4K3M9
B	?	-	LEU	deletion	UNP Q4K3M9
B	?	-	GLY	deletion	UNP Q4K3M9
B	?	-	GLY	deletion	UNP Q4K3M9
B	?	-	VAL	deletion	UNP Q4K3M9
B	?	-	LEU	deletion	UNP Q4K3M9
B	?	-	GLU	deletion	UNP Q4K3M9
B	?	-	VAL	deletion	UNP Q4K3M9
B	?	-	ALA	deletion	UNP Q4K3M9
B	?	-	ALA	deletion	UNP Q4K3M9
B	?	-	ASN	deletion	UNP Q4K3M9
B	?	-	VAL	deletion	UNP Q4K3M9
B	?	-	ALA	deletion	UNP Q4K3M9
B	?	-	ILE	deletion	UNP Q4K3M9

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	GLY	deletion	UNP Q4K3M9
B	?	-	ALA	deletion	UNP Q4K3M9
B	?	-	LEU	deletion	UNP Q4K3M9
B	?	-	ALA	deletion	UNP Q4K3M9
B	?	-	THR	deletion	UNP Q4K3M9
B	?	-	MET	deletion	UNP Q4K3M9
B	?	-	ALA	deletion	UNP Q4K3M9
B	?	-	VAL	deletion	UNP Q4K3M9
B	?	-	ALA	deletion	UNP Q4K3M9
B	?	-	ALA	deletion	UNP Q4K3M9
B	?	-	ALA	deletion	UNP Q4K3M9
B	?	-	ALA	deletion	UNP Q4K3M9
B	?	-	GLY	deletion	UNP Q4K3M9
B	?	-	ILE	deletion	UNP Q4K3M9
B	?	-	THR	deletion	UNP Q4K3M9
B	?	-	VAL	deletion	UNP Q4K3M9
B	?	-	ALA	deletion	UNP Q4K3M9
B	?	-	THR	deletion	UNP Q4K3M9
B	?	-	GLY	deletion	UNP Q4K3M9
B	?	-	GLY	deletion	UNP Q4K3M9
B	?	-	LEU	deletion	UNP Q4K3M9
B	?	-	GLY	deletion	UNP Q4K3M9
B	?	-	ALA	deletion	UNP Q4K3M9
B	?	-	CYS	deletion	UNP Q4K3M9
B	?	-	VAL	deletion	UNP Q4K3M9
B	61	MET	LEU	conflict	UNP Q4K3M9
B	63	SER	-	insertion	UNP Q4K3M9
B	64	SER	LEU	conflict	UNP Q4K3M9
B	65	HIS	VAL	conflict	UNP Q4K3M9
B	66	HIS	VAL	conflict	UNP Q4K3M9
B	67	HIS	GLY	conflict	UNP Q4K3M9
B	68	HIS	VAL	conflict	UNP Q4K3M9
B	69	HIS	VAL	conflict	UNP Q4K3M9
B	70	HIS	VAL	conflict	UNP Q4K3M9
B	71	SER	GLY	conflict	UNP Q4K3M9
B	72	GLN	VAL	conflict	UNP Q4K3M9
B	73	ASP	VAL	conflict	UNP Q4K3M9
B	74	PRO	MET	conflict	UNP Q4K3M9







I1087	T1022	H954	ALA	P751	T662	D599	R517	G438	VAL	ASP	LEU
Q1090	R1023	T955	GLN	T732	D663	M600	R518	D439	VAL	ASP	LEU
D1091	S1024	V956	ILE	R733	P664	L601	D522	R440	ARG	LEU	VAL
G1092	E1025	A957		F734	A665	M602	A623	N441	GLU	THR	THR
L1093	Y1026	G958		E735	G666	Q603	G524	D442	ILE	THR	CYS
Q1094	D1027	S959		T736	E667	T604	H525	M443	ARG	THR	LYS
G1095	L1028	L960		D737	S668	M605	I528	R444	SER	LYS	HIS
Q1096	C1029	R963		R738	R672	A606	E447	L447	THR	PRO	PRO
K1097	R1031	F964		R739	R673	F607	A533	E448	THR	PRO	PRO
E1098	L1032	D965		G740	D674	E608	T534	Y449	GLY	PRO	PRO
T1099	R1033	E966		N741	P675	D611	G535	D450	VAL	VAL	VAL
D1103	A1034	L967		V742	R676	E612	L536	A317	GLY	GLN	GLN
A1104	R1035	L970		K743	C679	R613	R537	D319	ALA	ALA	ALA
A1105	V902	L971		D747	I680	Q614	T543	D320	THR	THR	ALA
A1106	Q903	T972		A748	A681	L615	Q544	L321	VAL	VAL	ALA
M1107	R904	Q972		L749	E682	L616	F545	D322	VAL	VAL	GLY
L1108	L905	L975		G750	V683	S617	A646	F323	LEU	LEU	LYS
L1109	L906	P976		E751	D684	D620	A547	T324	VAL	VAL	VAL
D1110	L907	D977		H752	P685	F621	D547	L324	VAL	VAL	VAL
G1111	K908	K978		T753	L686	L622	Q549	L326	LYS	LYS	ILE
P1112	I909	R979		R754	G687	L622	R554	M329	GLY	GLY	ASP
K1113	T910	R979		D758	Q688	G623	R554	P330	GLY	GLN	GLN
A1114	D911	G844		C759	V689	G624	R554	F330	GLN	GLN	GLN
G1115	D912	M845		Q760	T690	R625	D588	I331	ALA	ALA	ALA
A1116	G913	R846		R762	Q691	A627	E559	E332	VAL	VAL	VAL
E1051	R914	L847		L768	R693	S629	Y685	K335	ARG	ARG	ARG
R1052	S915	S848		A769	H694	Y630	D685	R335	SER	SER	SER
H1053	Q916	E849		D770	D695	B631	S472	D341	ASP	ASP	ASP
L1054	Y917	E849		G771	A696	E632	T473	E342	ARG	ARG	ARG
D1057	T918	L863		R772	V700	T633	A571	R343	THR	THR	THR
D1058	Y919	D854		A773	V701	G634	Q572	R344	CYS	CYS	CYS
D1059	L920	G855		E774	E702	L636	I573	R344	ASP	ASP	ASP
S1060	P921	S856		E774	I703	L636	I573	R344	ALA	ALA	ALA
D1060	L922	A857		E774	I704	L636	Q575	R344	VAL	VAL	VAL
D1061	Q924	K858		E774	I704	L636	Q575	R344	VAL	VAL	VAL
V1063	L925	R859		E774	I704	L636	Q575	R344	VAL	VAL	VAL
A1066	L931	Y862		E774	I704	L636	Q575	R344	VAL	VAL	VAL
E1067	D932	D863		E774	I704	L636	Q575	R344	VAL	VAL	VAL
R1068	N933	L864		E774	I704	L636	Q575	R344	VAL	VAL	VAL
H1069	L934	L865		E774	I704	L636	Q575	R344	VAL	VAL	VAL
A1070	G935	N866		E774	I704	L636	Q575	R344	VAL	VAL	VAL
T1071	G935	E870		E774	I704	L636	Q575	R344	VAL	VAL	VAL
G1072	Q937	P875		E774	I704	L636	Q575	R344	VAL	VAL	VAL
Q1073	Q937	A876		E774	I704	L636	Q575	R344	VAL	VAL	VAL
H1074	L1009	R876		E774	I704	L636	Q575	R344	VAL	VAL	VAL
R1075	H1010	R877		E774	I704	L636	Q575	R344	VAL	VAL	VAL
Q1076	R1011	T877		E774	I704	L636	Q575	R344	VAL	VAL	VAL
R1147	L1011	T877		E774	I704	L636	Q575	R344	VAL	VAL	VAL
R1148	L1014	T877		E774	I704	L636	Q575	R344	VAL	VAL	VAL
G1149	R1015	T877		E774	I704	L636	Q575	R344	VAL	VAL	VAL
V1150	T1016	T877		E774	I704	L636	Q575	R344	VAL	VAL	VAL
Q1151	Q1017	T877		E774	I704	L636	Q575	R344	VAL	VAL	VAL
R1152	G1018	T877		E774	I704	L636	Q575	R344	VAL	VAL	VAL
D1156	R1019	T877		E774	I704	L636	Q575	R344	VAL	VAL	VAL
A1157	I1020	T877		E774	I704	L636	Q575	R344	VAL	VAL	VAL
E1158	S1021	T877		E774	I704	L636	Q575	R344	VAL	VAL	VAL



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	454740	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 ( $e^-/\text{\AA}^2$ )	61	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	105000	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor
Maximum map value	0.166	Depositor
Minimum map value	-0.093	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0331	Depositor
Map size (Å)	262.08002, 262.08002, 262.08002	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9100001, 0.9100001, 0.9100001	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	0.46	0/8737	0.59	0/11828
1	B	0.46	0/8737	0.59	0/11828
All	All	0.46	0/17474	0.59	0/23656

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8527	7876	8060	71	0
1	B	8527	7876	8060	73	0
All	All	17054	15752	16120	142	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 4.

All (142) 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:A:302:SER:OG	1:A:565:TYR:OH	1.94	0.86
1:B:302:SER:OG	1:B:565:TYR:OH	1.94	0.85

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1290:GLN:OE1	1:B:1293:ARG:NH1	2.11	0.84
1:A:1290:GLN:OE1	1:A:1293:ARG:NH1	2.11	0.82
1:A:441:ASN:OD1	1:A:676:ARG:NH2	2.17	0.77
1:B:441:ASN:OD1	1:B:676:ARG:NH2	2.17	0.77
1:A:398:GLU:OE1	1:A:398:GLU:N	2.20	0.74
1:A:902:VAL:HG12	1:A:903:GLY:H	1.53	0.74
1:B:1278:VAL:HG11	1:B:1281:ILE:HD11	1.70	0.74
1:B:398:GLU:N	1:B:398:GLU:OE1	2.20	0.73
1:B:902:VAL:HG12	1:B:903:GLY:H	1.53	0.73
1:A:1278:VAL:HG11	1:A:1281:ILE:HD11	1.69	0.73
1:B:483:GLU:OE1	1:B:491:ARG:NH1	2.24	0.71
1:A:993:GLN:OE1	1:A:995:ASN:ND2	2.24	0.71
1:B:575:GLN:N	1:B:575:GLN:OE1	2.24	0.71
1:A:483:GLU:OE1	1:A:491:ARG:NH1	2.24	0.70
1:A:575:GLN:N	1:A:575:GLN:OE1	2.24	0.70
1:B:993:GLN:OE1	1:B:995:ASN:ND2	2.24	0.70
1:B:899:ARG:NH1	1:B:903:GLY:O	2.24	0.70
1:A:899:ARG:NH1	1:A:903:GLY:O	2.24	0.69
1:B:1252:ASN:ND2	1:B:1341:PRO:O	2.25	0.69
1:A:1252:ASN:ND2	1:A:1341:PRO:O	2.25	0.69
1:A:558:ASP:OD2	1:A:801:ARG:NH2	2.31	0.64
1:A:596:GLU:OE2	1:A:598:THR:OG1	2.15	0.64
1:B:596:GLU:OE2	1:B:598:THR:OG1	2.15	0.64
1:A:1188:LYS:NZ	1:A:1300:ASP:OD2	2.31	0.64
1:B:833:ASN:CG	1:B:1118:LEU:HD13	2.19	0.63
1:B:1188:LYS:NZ	1:B:1300:ASP:OD2	2.31	0.63
1:A:737:ASP:OD1	1:A:741:ASN:N	2.32	0.62
1:B:737:ASP:OD1	1:B:741:ASN:N	2.32	0.62
1:A:833:ASN:CG	1:A:1118:LEU:HD13	2.19	0.62
1:B:558:ASP:OD2	1:B:801:ARG:NH2	2.31	0.62
1:A:448:GLU:OE2	1:A:459:ARG:NE	2.31	0.61
1:A:902:VAL:HG12	1:A:903:GLY:N	2.15	0.61
1:B:448:GLU:OE2	1:B:459:ARG:NE	2.31	0.61
1:A:534:THR:OG1	1:A:801:ARG:O	2.11	0.61
1:B:902:VAL:HG12	1:B:903:GLY:N	2.15	0.61
1:B:534:THR:OG1	1:B:801:ARG:O	2.11	0.60
1:B:1241:GLN:N	1:B:1241:GLN:OE1	2.36	0.59
1:A:1241:GLN:N	1:A:1241:GLN:OE1	2.36	0.59
1:A:794:THR:OG1	1:B:512:GLU:OE2	2.18	0.58
1:A:1103:ASP:OD1	1:A:1104:ALA:N	2.36	0.58
1:B:1092:GLY:O	1:B:1094:GLN:NE2	2.36	0.58

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1103:ASP:OD1	1:B:1104:ALA:N	2.36	0.58
1:B:378:GLN:N	1:B:378:GLN:OE1	2.38	0.57
1:A:378:GLN:OE1	1:A:378:GLN:N	2.38	0.57
1:A:1092:GLY:O	1:A:1094:GLN:NE2	2.36	0.57
1:A:842:ASP:OD1	1:A:846:ARG:N	2.36	0.57
1:A:522:ASP:OD1	1:A:523:ALA:N	2.36	0.56
1:A:833:ASN:OD1	1:A:1118:LEU:HD13	2.05	0.56
1:B:833:ASN:OD1	1:B:1118:LEU:HD13	2.05	0.56
1:B:533:ALA:O	1:B:781:ASN:ND2	2.39	0.56
1:A:902:VAL:CG1	1:A:903:GLY:H	2.19	0.56
1:A:631:ASP:OD1	1:A:632:GLU:N	2.36	0.56
1:A:533:ALA:O	1:A:781:ASN:ND2	2.39	0.55
1:B:322:ASP:OD1	1:B:335:ARG:NH1	2.40	0.55
1:B:902:VAL:CG1	1:B:903:GLY:H	2.19	0.55
1:A:322:ASP:OD1	1:A:335:ARG:NH1	2.40	0.54
1:A:512:GLU:OE2	1:B:794:THR:OG1	2.17	0.54
1:B:631:ASP:OD1	1:B:632:GLU:N	2.36	0.54
1:A:454:ARG:NH1	1:A:476:PRO:O	2.42	0.53
1:B:454:ARG:NH1	1:B:476:PRO:O	2.42	0.53
1:A:1075:ARG:O	1:A:1092:GLY:N	2.42	0.52
1:B:842:ASP:OD1	1:B:846:ARG:N	2.36	0.51
1:B:522:ASP:OD1	1:B:523:ALA:N	2.36	0.51
1:A:434:LEU:O	1:A:449:TYR:OH	2.19	0.50
1:A:1158:GLU:OE1	1:A:1160:ARG:NH2	2.45	0.50
1:B:1158:GLU:OE1	1:B:1160:ARG:NH2	2.45	0.50
1:B:1220:SER:HG	1:B:1234:ARG:HE	1.58	0.49
1:B:1167:GLN:OE1	1:B:1172:GLU:HG2	2.12	0.49
1:A:1167:GLN:OE1	1:A:1172:GLU:HG2	2.12	0.49
1:A:270:LYS:HB3	1:A:270:LYS:NZ	2.28	0.49
1:B:1075:ARG:O	1:B:1092:GLY:N	2.42	0.49
1:B:434:LEU:O	1:B:449:TYR:OH	2.19	0.48
1:B:270:LYS:NZ	1:B:270:LYS:HB3	2.28	0.48
1:A:320:ASP:OD1	1:A:517:ARG:NH1	2.47	0.48
1:B:1057:ASP:OD1	1:B:1058:ASP:N	2.41	0.48
1:B:819:ASP:OD1	1:B:820:TYR:N	2.47	0.48
1:B:772:ARG:NH2	1:B:1029:CYS:SG	2.87	0.48
1:A:772:ARG:NH2	1:A:1029:CYS:SG	2.87	0.47
1:B:1107:ASN:ND2	1:B:1122:ASN:OD1	2.40	0.47
1:A:1053:HIS:C	1:A:1054:LEU:HD12	2.34	0.47
1:A:819:ASP:OD1	1:A:820:TYR:N	2.47	0.47
1:A:1104:ALA:O	1:A:1105:ALA:HB3	2.14	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1231:PRO:O	1:B:1249:ASN:ND2	2.48	0.47
1:B:1053:HIS:C	1:B:1054:LEU:HD12	2.34	0.47
1:A:543:THR:HG22	1:A:544:GLN:N	2.31	0.46
1:B:800:ASN:OD1	1:B:804:GLN:N	2.48	0.46
1:B:679:CYS:O	1:B:694:HIS:NE2	2.48	0.46
1:A:800:ASN:OD1	1:A:804:GLN:N	2.48	0.46
1:A:676:ARG:NH2	1:A:696:ALA:O	2.44	0.46
1:A:679:CYS:O	1:A:694:HIS:NE2	2.48	0.46
1:B:543:THR:HG22	1:B:544:GLN:N	2.30	0.46
1:A:1231:PRO:O	1:A:1249:ASN:ND2	2.48	0.46
1:B:320:ASP:OD1	1:B:517:ARG:NH1	2.47	0.46
1:A:376:ASP:OD1	1:A:380:ARG:N	2.48	0.46
1:A:1057:ASP:OD1	1:A:1058:ASP:N	2.41	0.46
1:A:1166:ASN:OD1	1:A:1167:GLN:N	2.49	0.46
1:B:376:ASP:OD1	1:B:380:ARG:N	2.48	0.46
1:B:1104:ALA:O	1:B:1105:ALA:HB3	2.14	0.46
1:A:810:ASP:OD1	1:A:810:ASP:N	2.48	0.45
1:B:700:VAL:O	1:B:715:TRP:NE1	2.45	0.45
1:B:1166:ASN:OD1	1:B:1167:GLN:N	2.49	0.45
1:B:810:ASP:N	1:B:810:ASP:OD1	2.48	0.45
1:A:620:ASP:N	1:A:620:ASP:OD1	2.48	0.45
1:B:620:ASP:N	1:B:620:ASP:OD1	2.48	0.45
1:A:468:GLU:OE1	1:A:491:ARG:NH2	2.44	0.45
1:A:700:VAL:O	1:A:715:TRP:NE1	2.45	0.44
1:B:902:VAL:CG1	1:B:903:GLY:N	2.79	0.44
1:B:1093:LEU:HD12	1:B:1093:LEU:N	2.32	0.44
1:A:292:THR:O	1:A:296:THR:HG23	2.18	0.44
1:A:1093:LEU:HD12	1:A:1093:LEU:N	2.33	0.44
1:B:292:THR:O	1:B:296:THR:HG23	2.18	0.44
1:A:686:LEU:HD11	1:A:947:LEU:HD13	2.00	0.43
1:B:474:LEU:H	1:B:474:LEU:HD12	1.83	0.43
1:A:474:LEU:H	1:A:474:LEU:HD12	1.83	0.43
1:A:947:LEU:HD12	1:A:947:LEU:N	2.33	0.43
1:B:676:ARG:NH2	1:B:696:ALA:O	2.44	0.43
1:B:1212:GLN:OE1	1:B:1214:GLN:NE2	2.52	0.43
1:B:447:LEU:HD12	1:B:447:LEU:N	2.34	0.43
1:A:447:LEU:HD12	1:A:447:LEU:N	2.34	0.42
1:A:1273:VAL:HG23	1:A:1274:TRP:N	2.34	0.42
1:B:947:LEU:N	1:B:947:LEU:HD12	2.33	0.42
1:A:902:VAL:CG1	1:A:903:GLY:N	2.79	0.42
1:A:1212:GLN:OE1	1:A:1214:GLN:NE2	2.52	0.42

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1273:VAL:HG23	1:B:1274:TRP:N	2.34	0.42
1:A:1073:GLN:OE1	1:A:1073:GLN:N	2.38	0.42
1:B:1129:ASP:OD1	1:B:1129:ASP:N	2.50	0.42
1:B:468:GLU:OE1	1:B:491:ARG:NH2	2.44	0.41
1:B:932:ASP:N	1:B:932:ASP:OD1	2.53	0.41
1:B:686:LEU:HD11	1:B:947:LEU:HD13	2.00	0.41
1:A:920:ASP:HB2	1:A:924:GLN:HG2	2.01	0.41
1:B:847:LEU:O	1:B:862:TYR:OH	2.32	0.41
1:B:1276:ASN:ND2	1:B:1293:ARG:HB3	2.35	0.41
1:A:1276:ASN:ND2	1:A:1293:ARG:HB3	2.34	0.41
1:B:920:ASP:HB2	1:B:924:GLN:HG2	2.01	0.41
1:A:561:ASP:OD1	1:A:562:SER:N	2.54	0.40
1:A:486:TYR:OH	1:A:492:GLU:OE1	2.25	0.40
1:A:1107:ASN:ND2	1:A:1122:ASN:OD1	2.40	0.40
1:A:450:ASP:OD1	1:A:451:SER:N	2.53	0.40
1:B:1054:LEU:HD12	1:B:1054:LEU:N	2.36	0.40
1:B:1164:VAL:HB	1:B:1175:VAL:CG2	2.52	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	1029/1426 (72%)	992 (96%)	36 (4%)	1 (0%)	51   81
1	B	1029/1426 (72%)	992 (96%)	36 (4%)	1 (0%)	51   81
All	All	2058/2852 (72%)	1984 (96%)	72 (4%)	2 (0%)	54   81

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1284	PRO

Continued on next page...



*Continued from previous page...*

Mol	Chain	Res	Type
1	B	1284	PRO

### 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	890/1178 (76%)	887 (100%)	3 (0%)	92	96
1	B	890/1178 (76%)	887 (100%)	3 (0%)	92	96
All	All	1780/2356 (76%)	1774 (100%)	6 (0%)	92	96

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

Mol	Chain	Res	Type
1	A	758	ASP
1	A	810	ASP
1	A	1322	THR
1	B	758	ASP
1	B	810	ASP
1	B	1322	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1010	HIS
1	A	1196	ASN
1	A	1214	GLN
1	A	1276	ASN
1	B	1010	HIS
1	B	1196	ASN
1	B	1214	GLN
1	B	1276	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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

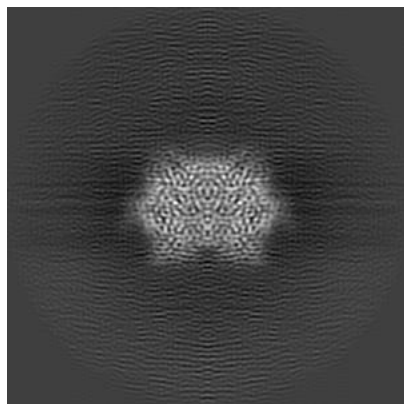
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13867. These allow visual inspection of the internal detail of the map and identification of artifacts.

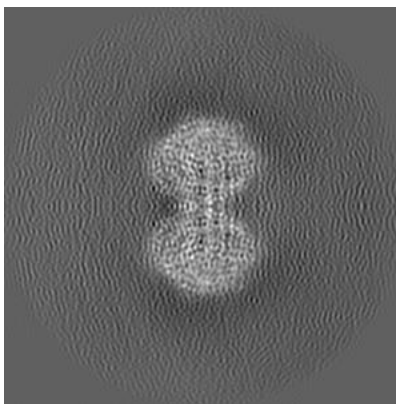
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

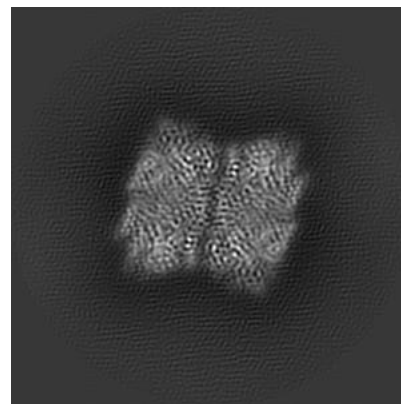
#### 6.1.1 Primary map



X

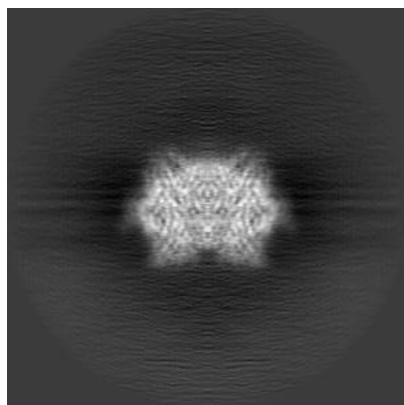


Y

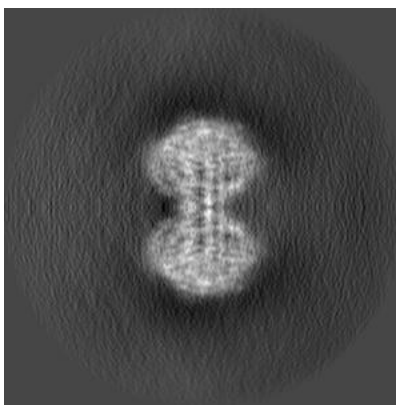


Z

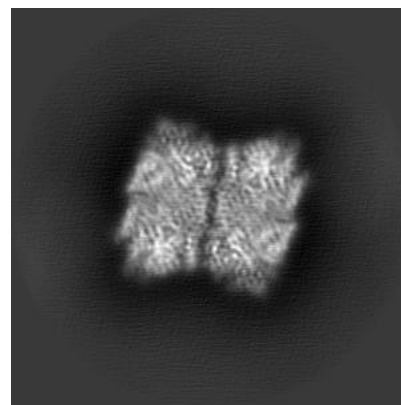
#### 6.1.2 Raw map



X



Y



Z

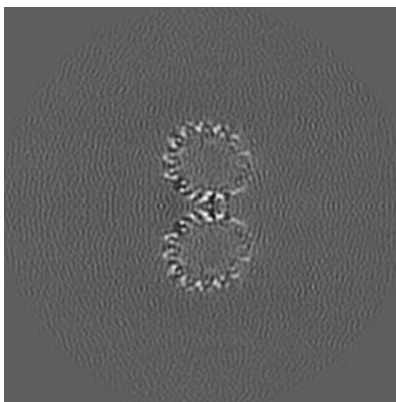
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

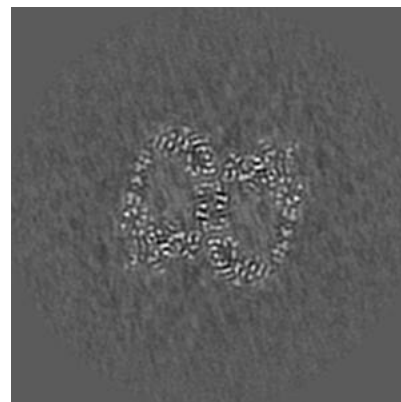
### 6.2.1 Primary map



X Index: 144

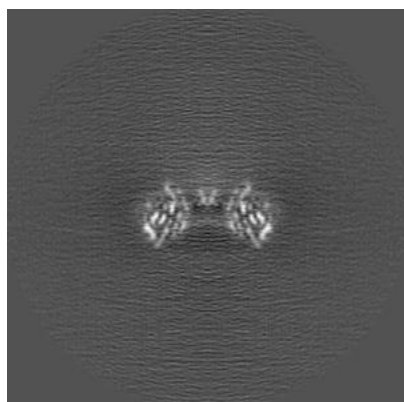


Y Index: 144

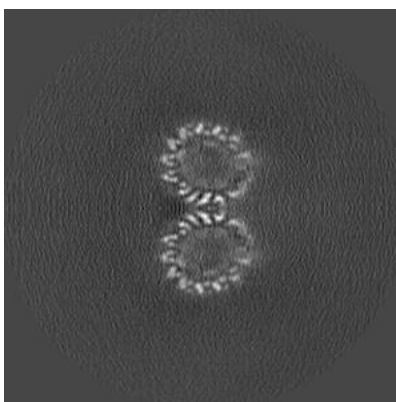


Z Index: 144

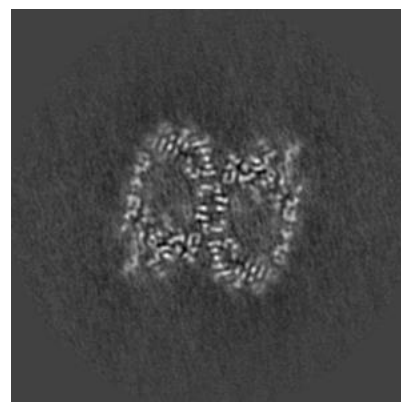
### 6.2.2 Raw map



X Index: 144



Y Index: 144

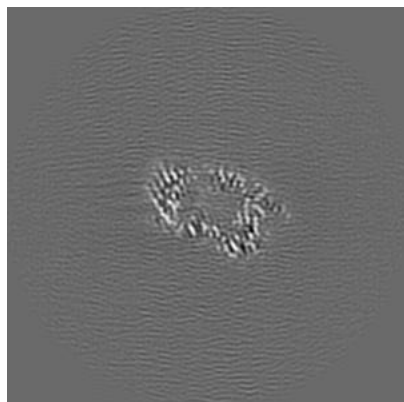


Z Index: 144

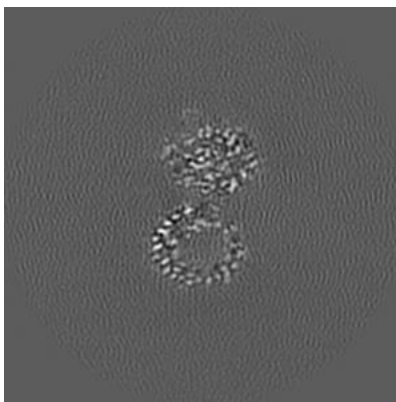
The images above show central slices of the map in three orthogonal directions.

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

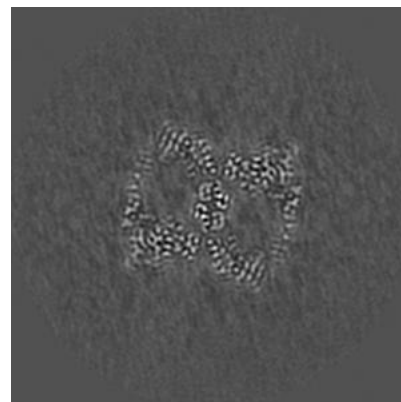
### 6.3.1 Primary map



X Index: 128

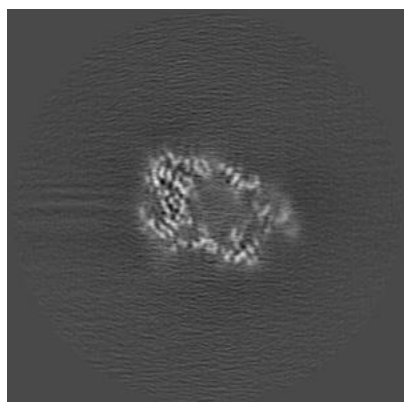


Y Index: 167

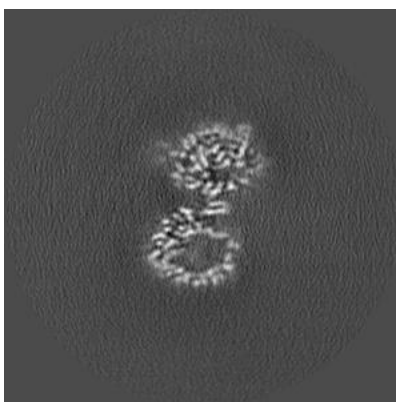


Z Index: 146

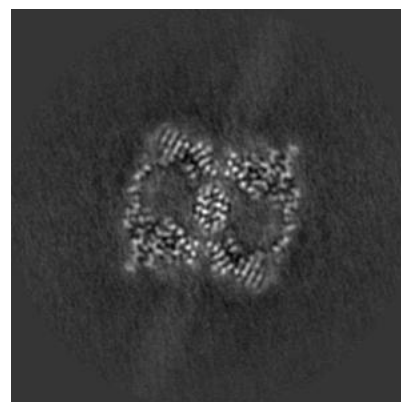
### 6.3.2 Raw map



X Index: 107



Y Index: 173

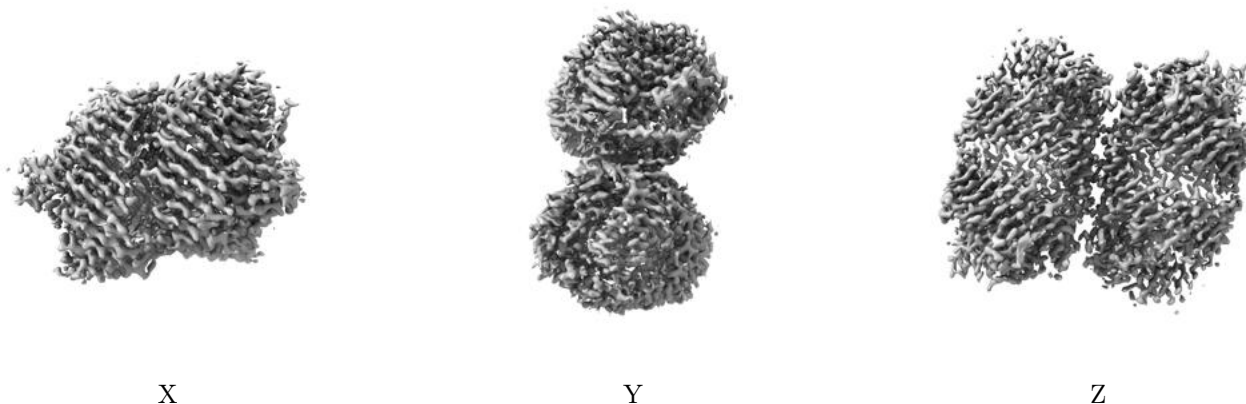


Z Index: 147

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

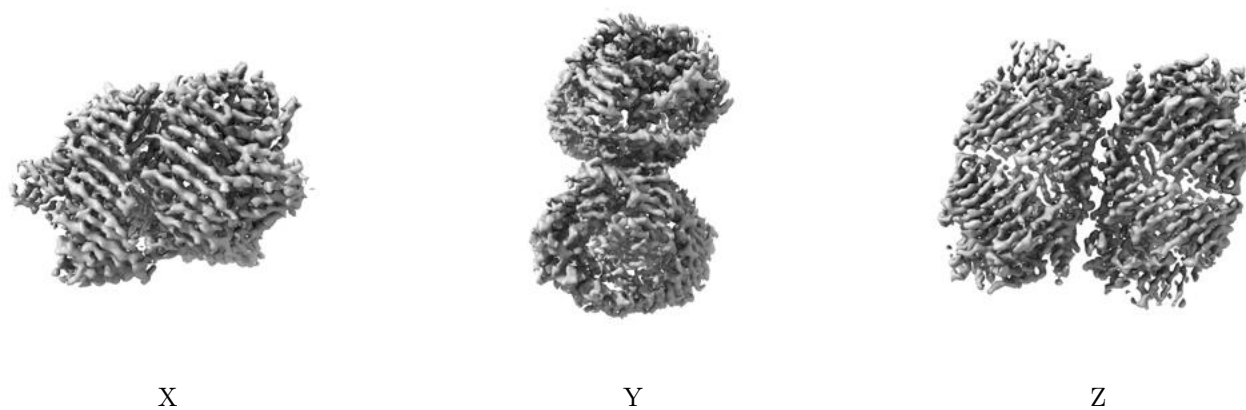
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0331. 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.

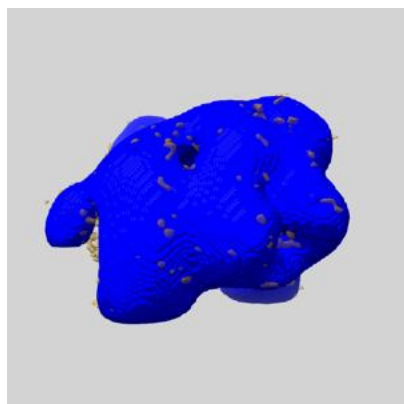
## 6.5 Mask visualisation [i](#)

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

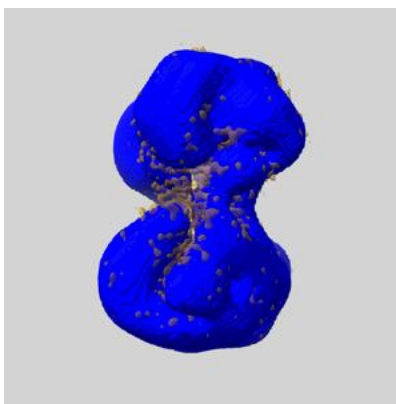
A mask typically either:

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

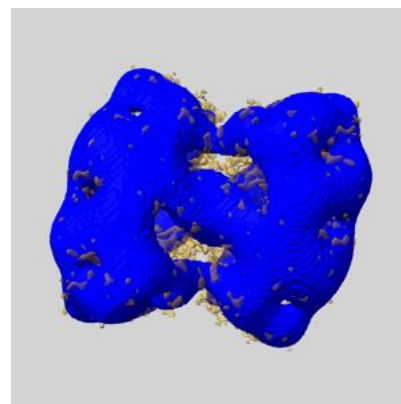
### 6.5.1 emd\_13867\_msk\_1.map [i](#)



X



Y



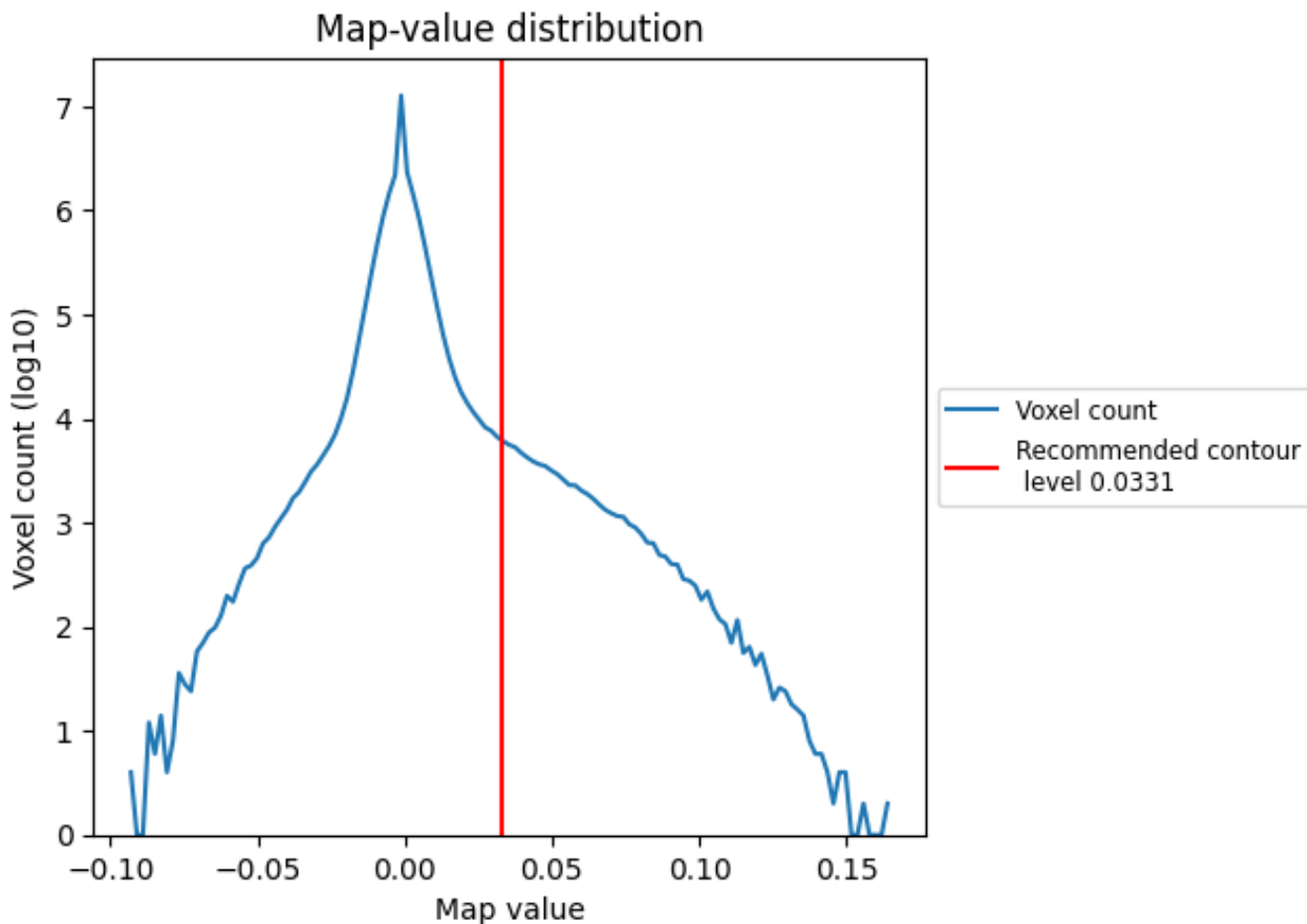
Z



## 7 Map analysis [i](#)

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

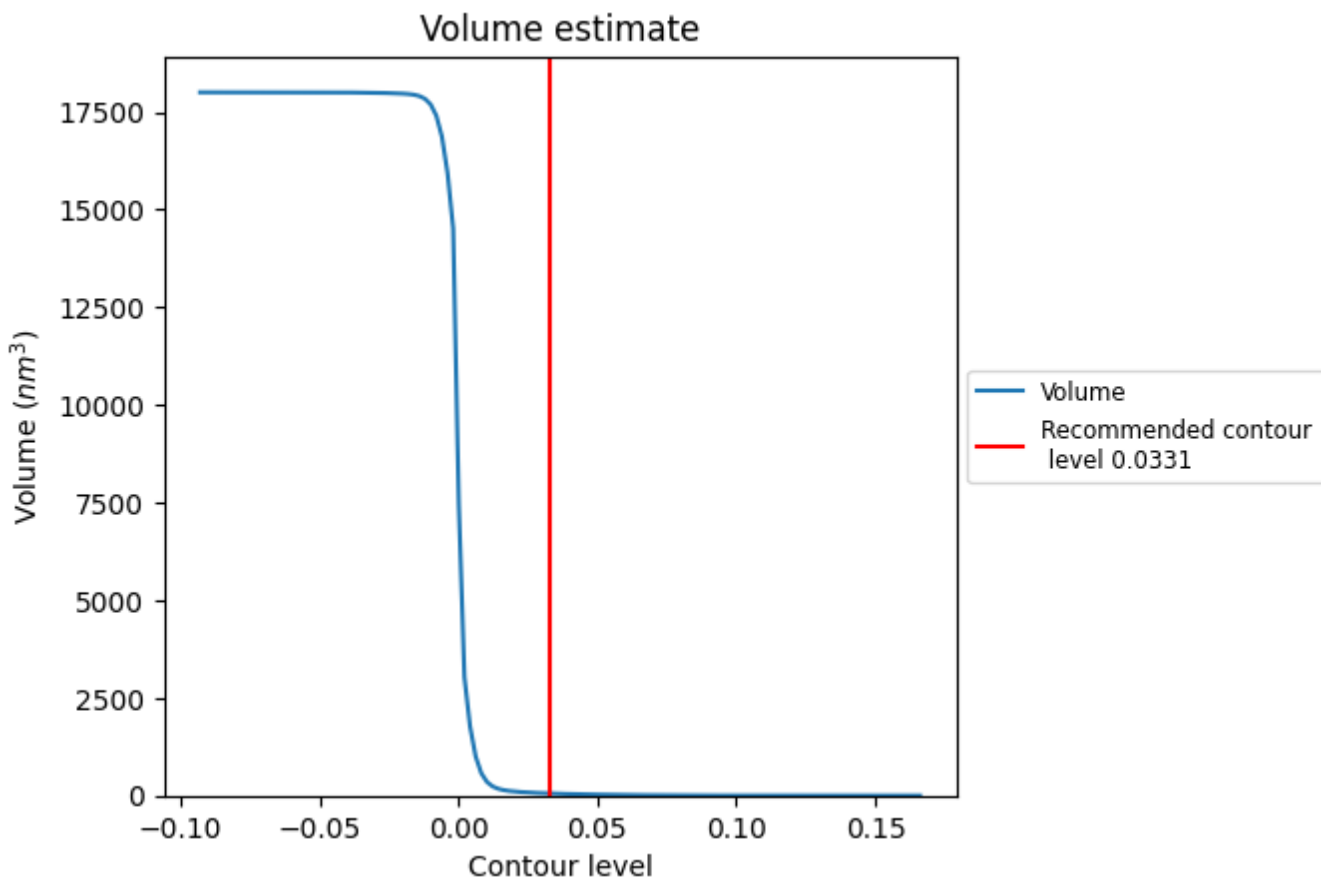
### 7.1 Map-value distribution [i](#)



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.



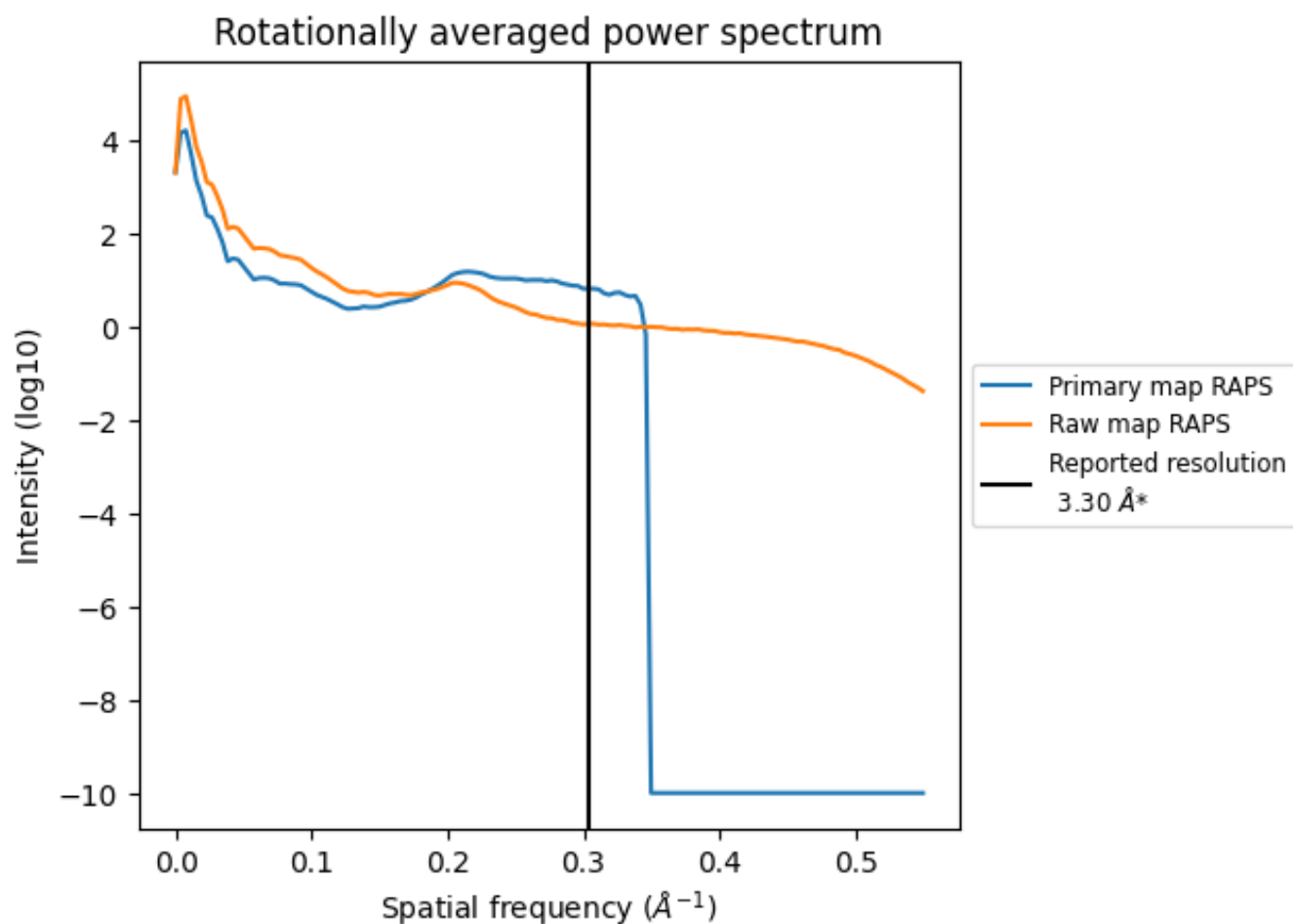
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 54 nm<sup>3</sup>; this corresponds to an approximate mass of 49 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 [\(i\)](#)

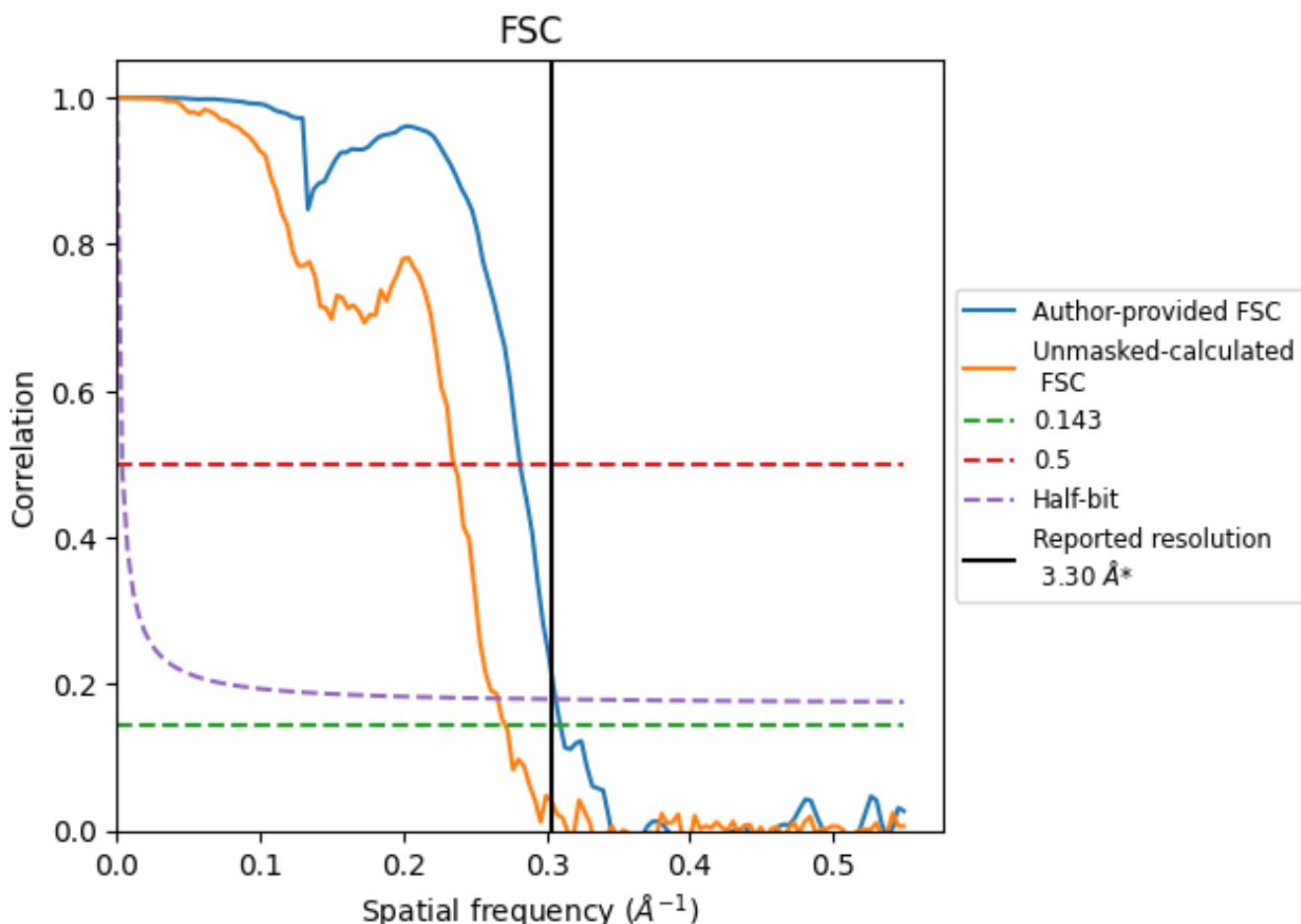


\*Reported resolution corresponds to spatial frequency of 0.303 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.303  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

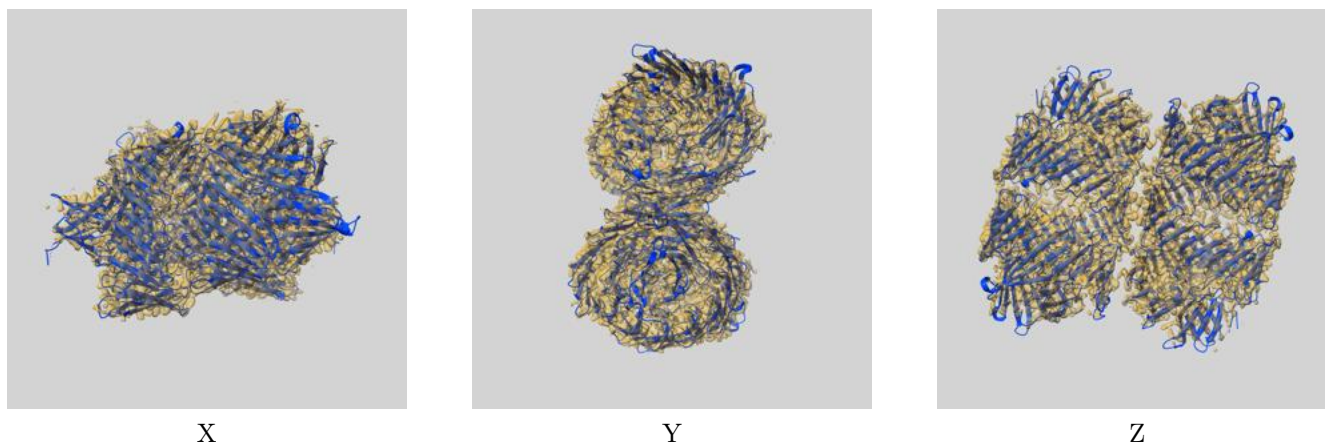
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.23	3.55	3.26
Unmasked-calculated*	3.69	4.25	3.76

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.69 differs from the reported value 3.3 by more than 10 %

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

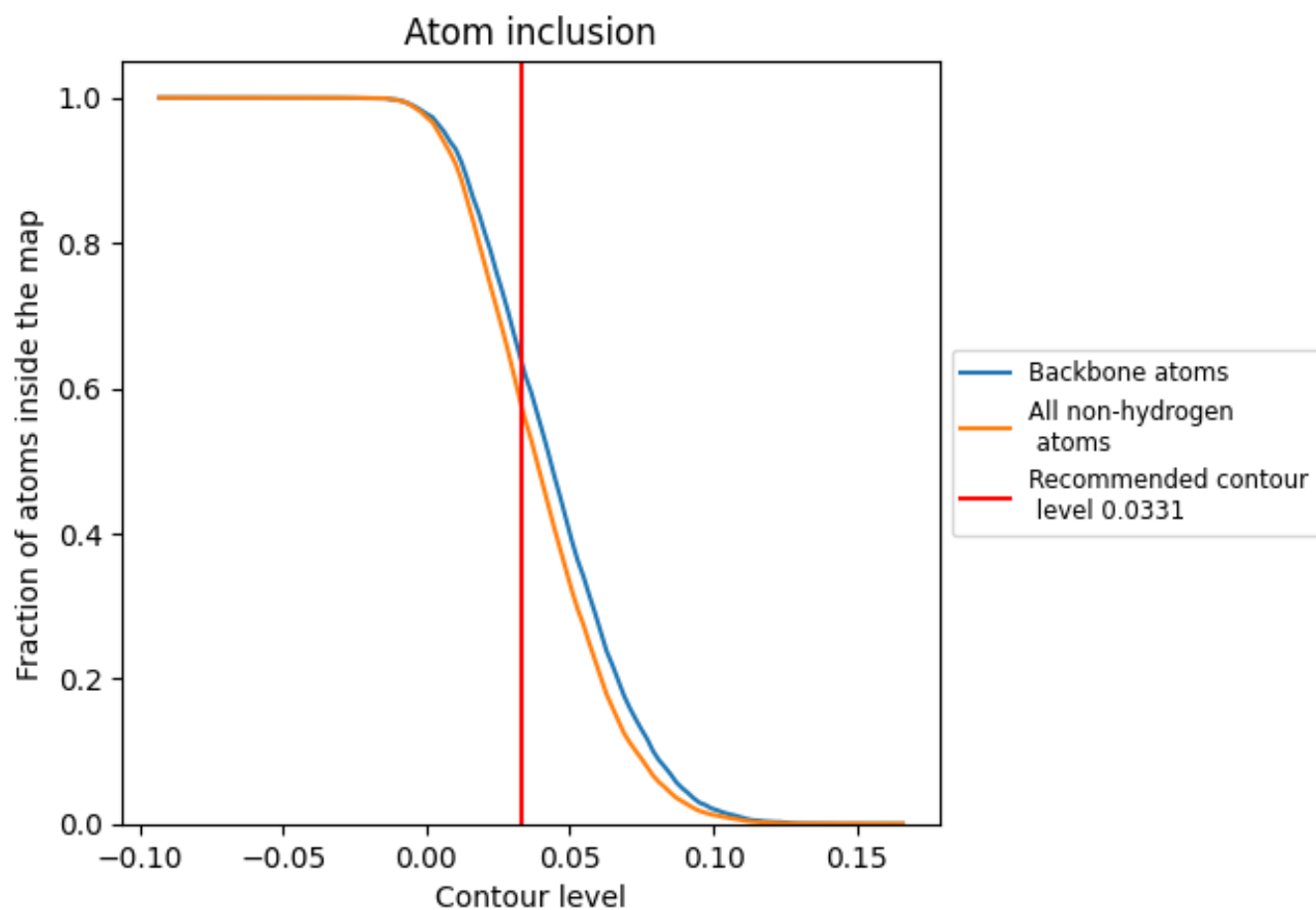
This section contains information regarding the fit between EMDB map EMD-13867 and PDB model 7Q97. Per-residue inclusion information can be found in section 3 on page 7.

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



The images above show the 3D surface view of the map at the recommended contour level 0.0331 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 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 58% of all non-hydrogen atoms, are inside the map.