Full wwPDB EM Validation Report

Jun 17, 2025 – 12:20 PM JST

PDB ID	:	7VKU / pdb_00007vku
EMDB ID	:	EMD-32019
Title	:	Cryo-EM structure of SAM-Tom40 intermediate complex
Authors	:	Takeda, H.; Tsutsumi, A.; Kikkawa, M.; Endo, T.
Deposited on	:	2021-10-01
Resolution	:	3.20 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:

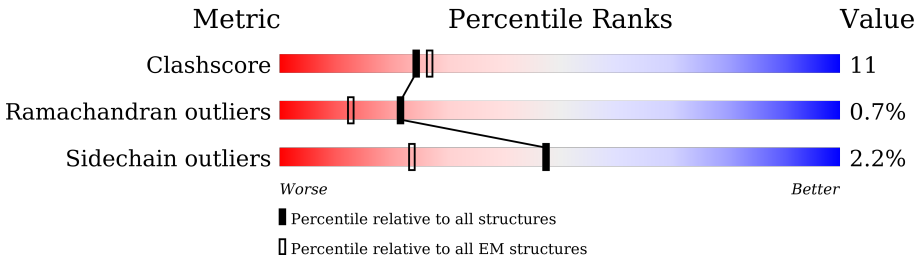
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.44

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 <=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	484	12% 71% 14% 14%
2	B	329	80% 13% 7%
3	C	327	68% 14% 16%
4	X	387	13% 24% 14% 60%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9219 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Sorting assembly machinery 50 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	418	3314	2122	573	606	13	0	0

- Molecule 2 is a protein called Sorting assembly machinery 35 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	306	2460	1574	412	460	14	0	0

- Molecule 3 is a protein called Sorting assembly machinery 37 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	275	2227	1420	378	421	8	0	0

- Molecule 4 is a protein called Mitochondrial import receptor subunit TOM40.

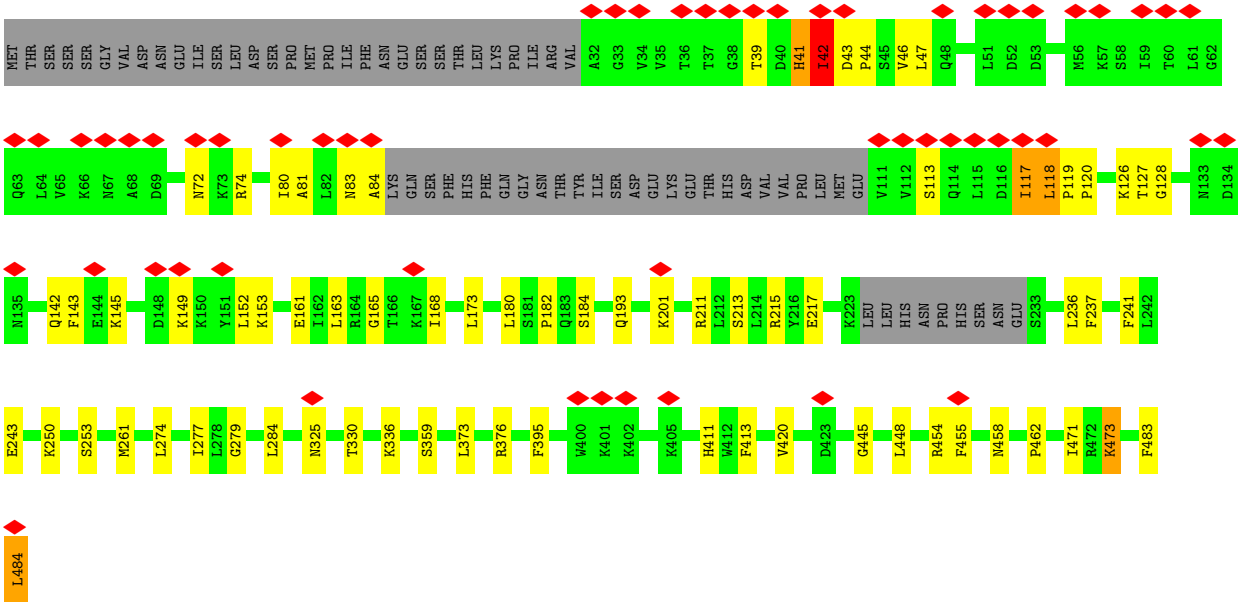
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	X	155	1218	786	202	226	4	0	0

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.

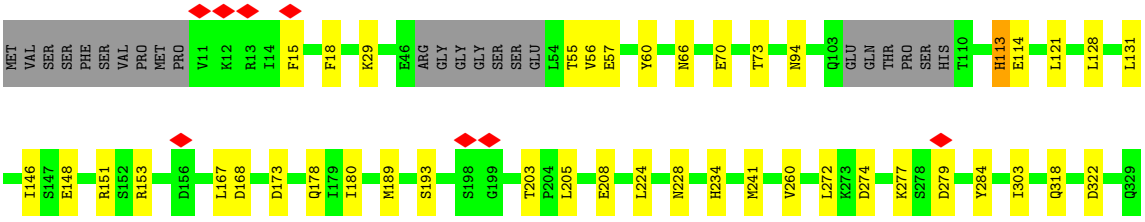
• Molecule 1: Sorting assembly machinery 50 kDa subunit

Chain A:



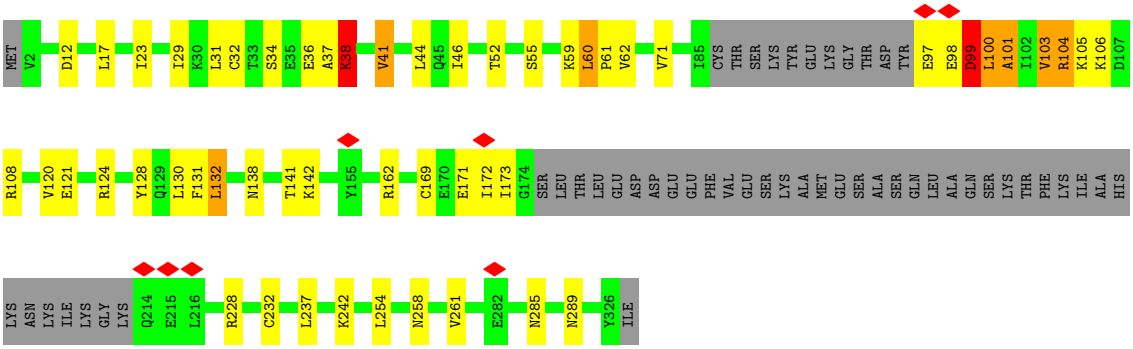
• Molecule 2: Sorting assembly machinery 35 kDa subunit

Chain B:

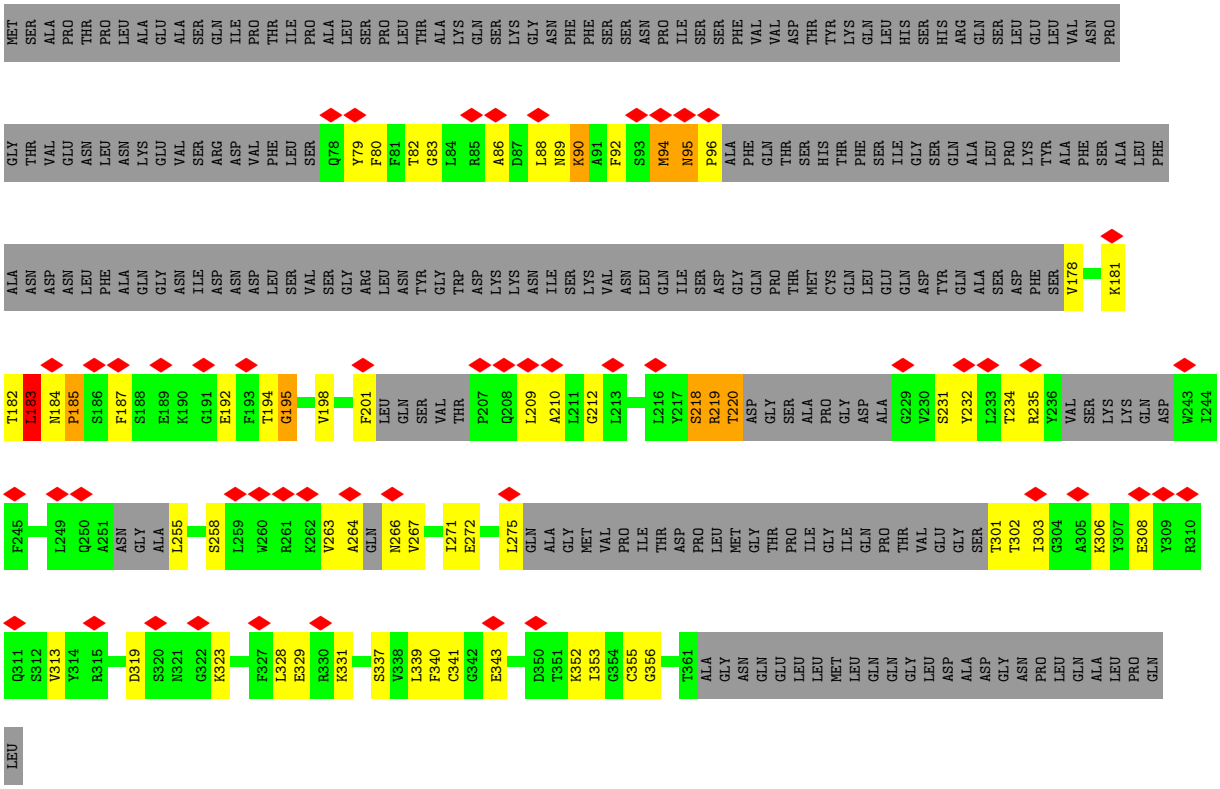


• Molecule 3: Sorting assembly machinery 37 kDa subunit

Chain C:



• Molecule 4: Mitochondrial import receptor subunit TOM40



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	23542	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 ($e^-/Å^2$)	48	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.422	Depositor
Minimum map value	-0.202	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	249.0, 249.0, 249.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.245, 1.245, 1.245	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	0.45	0/3393	0.74	0/4587
2	B	0.53	0/2501	0.63	3/3382 (0.1%)
3	C	0.66	5/2264 (0.2%)	0.74	8/3056 (0.3%)
4	X	0.48	1/1237 (0.1%)	0.91	3/1662 (0.2%)
All	All	0.53	6/9395 (0.1%)	0.74	14/12687 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
2	B	0	2
3	C	0	1
All	All	0	5

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	100	LEU	CA-C	-8.36	1.41	1.52
3	C	38	LYS	CA-C	-6.78	1.43	1.52
4	X	183	LEU	CA-C	-6.42	1.44	1.53
3	C	100	LEU	C-O	-5.76	1.16	1.24
3	C	101	ALA	C-O	-5.45	1.16	1.23
3	C	99	ASP	C-O	-5.41	1.17	1.24

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	38	LYS	N-CA-C	-12.65	98.35	114.04
4	X	195	GLY	N-CA-C	8.21	127.52	110.69
4	X	183	LEU	N-CA-C	-7.73	92.16	107.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	X	178	VAL	N-CA-CB	6.59	122.70	111.50
3	C	59	LYS	CA-C-N	-6.52	115.63	122.28
3	C	59	LYS	C-N-CA	-6.52	115.63	122.28
3	C	242	LYS	N-CA-C	-6.12	106.79	114.56
3	C	99	ASP	CA-C-N	5.74	132.50	121.54
3	C	99	ASP	C-N-CA	5.74	132.50	121.54
3	C	99	ASP	N-CA-C	5.68	122.90	110.80
2	B	18	PHE	N-CA-C	5.32	121.57	109.81
3	C	41	VAL	N-CA-C	-5.27	108.70	113.71
2	B	113	HIS	CA-C-N	5.06	131.21	121.54
2	B	113	HIS	C-N-CA	5.06	131.21	121.54

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	152	LEU	Peptide
1	A	153	LYS	Peptide
2	B	113	HIS	Peptide
2	B	128	LEU	Peptide
3	C	60	LEU	Peptide

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	3314	0	3305	67	0
2	B	2460	0	2505	29	0
3	C	2227	0	2241	37	0
4	X	1218	0	1212	72	0
All	All	9219	0	9263	194	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 11.

All (194) 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)
4:X:95:ASN:HB3	4:X:96:PRO:CD	1.55	1.35
4:X:79:TYR:HE1	4:X:235:ARG:NH2	1.25	1.32
4:X:302:THR:HG22	4:X:319:ASP:CA	1.71	1.20
4:X:79:TYR:CE1	4:X:235:ARG:NH2	2.06	1.20
4:X:302:THR:HG22	4:X:319:ASP:CB	1.72	1.18
4:X:302:THR:HG22	4:X:319:ASP:HA	1.25	1.16
4:X:95:ASN:CB	4:X:96:PRO:CD	2.25	1.14
4:X:264:ALA:C	4:X:266:ASN:N	2.07	1.13
3:C:104:ARG:HD3	3:C:106:LYS:HZ3	1.14	1.12
1:A:454:ARG:HD3	1:A:483:PHE:CE1	1.87	1.09
4:X:302:THR:CG2	4:X:319:ASP:HB2	1.89	1.03
4:X:263:VAL:O	4:X:267:VAL:O	1.76	1.02
4:X:95:ASN:CB	4:X:96:PRO:HD3	1.89	1.00
4:X:302:THR:CG2	4:X:319:ASP:CB	2.41	0.97
3:C:104:ARG:HD3	3:C:106:LYS:NZ	1.82	0.95
1:A:473:LYS:HE2	2:B:15:PHE:CE2	2.02	0.94
1:A:41:HIS:CE1	1:A:119:PRO:HD3	2.02	0.94
4:X:95:ASN:HB3	4:X:96:PRO:HD3	0.95	0.93
4:X:185:PRO:HG2	4:X:194:THR:HG22	1.47	0.93
4:X:302:THR:HG21	4:X:319:ASP:HB2	1.53	0.88
1:A:42:ILE:O	1:A:149:LYS:HE2	1.74	0.86
4:X:185:PRO:HG2	4:X:194:THR:O	1.77	0.85
4:X:92:PHE:CZ	4:X:341:CYS:SG	2.69	0.84
3:C:104:ARG:CD	3:C:106:LYS:HZ3	1.90	0.84
3:C:38:LYS:HB2	3:C:38:LYS:NZ	1.93	0.84
1:A:454:ARG:HB3	1:A:483:PHE:CZ	2.13	0.83
4:X:95:ASN:CB	4:X:96:PRO:HD2	2.11	0.81
4:X:187:PHE:HD2	4:X:192:GLU:H	1.27	0.80
1:A:336:LYS:HD2	1:A:484:LEU:HG	1.64	0.80
4:X:302:THR:CG2	4:X:319:ASP:HA	2.10	0.77
3:C:128:TYR:CD1	3:C:132:LEU:HD12	2.20	0.77
3:C:98:GLU:N	3:C:98:GLU:OE2	2.16	0.76
4:X:187:PHE:CD2	4:X:192:GLU:N	2.52	0.76
1:A:454:ARG:HD3	1:A:483:PHE:CD1	2.24	0.72
3:C:38:LYS:HB2	3:C:38:LYS:HZ3	1.53	0.71
4:X:92:PHE:CE1	4:X:341:CYS:SG	2.83	0.70
1:A:484:LEU:C	1:A:484:LEU:HD22	2.17	0.69
4:X:302:THR:CG2	4:X:319:ASP:CA	2.60	0.69
1:A:484:LEU:C	1:A:484:LEU:HD13	2.17	0.69
1:A:454:ARG:CD	1:A:483:PHE:CE1	2.72	0.69
1:A:454:ARG:HB3	1:A:483:PHE:HZ	1.59	0.68
3:C:31:LEU:HD22	3:C:99:ASP:HB2	1.74	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:X:183:LEU:C	4:X:183:LEU:HD22	2.20	0.66
4:X:82:THR:HG21	4:X:272:GLU:CD	2.20	0.66
4:X:95:ASN:HB2	4:X:96:PRO:HD2	1.78	0.66
4:X:187:PHE:CE2	4:X:192:GLU:N	2.61	0.65
3:C:103:VAL:HG11	3:C:108:ARG:HA	1.79	0.64
3:C:32:CYS:HB3	3:C:37:ALA:O	1.96	0.64
4:X:302:THR:HG22	4:X:319:ASP:CG	2.23	0.63
1:A:41:HIS:HE1	1:A:119:PRO:HD3	1.60	0.63
1:A:473:LYS:O	1:A:473:LYS:HG2	1.96	0.63
1:A:41:HIS:CG	1:A:119:PRO:HB3	2.35	0.62
1:A:72:ASN:ND2	1:A:84:ALA:O	2.31	0.62
1:A:81:ALA:HB2	1:A:117:ILE:HG13	1.81	0.62
1:A:473:LYS:HE2	2:B:15:PHE:CD2	2.35	0.62
3:C:104:ARG:HG3	3:C:104:ARG:HH11	1.65	0.62
3:C:128:TYR:HD1	3:C:132:LEU:HD12	1.65	0.61
4:X:94:MET:SD	4:X:94:MET:N	2.70	0.61
1:A:39:THR:HG21	1:A:47:LEU:HD22	1.83	0.61
2:B:153:ARG:NH2	2:B:284:TYR:OH	2.33	0.60
1:A:274:LEU:HD23	2:B:208:GLU:HB2	1.84	0.60
1:A:448:LEU:HB3	1:A:455:PHE:HB2	1.83	0.60
3:C:104:ARG:HH11	3:C:104:ARG:CG	2.16	0.59
3:C:120:VAL:HG23	3:C:121:GLU:HG2	1.84	0.58
1:A:215:ARG:NH1	1:A:217:GLU:OE2	2.36	0.58
4:X:308:GLU:HA	4:X:313:VAL:HG13	1.85	0.58
4:X:194:THR:HG22	4:X:194:THR:O	2.03	0.58
1:A:236:LEU:HD12	1:A:284:LEU:HD13	1.86	0.57
2:B:66:ASN:ND2	2:B:193:SER:O	2.37	0.57
1:A:376:ARG:O	2:B:29:LYS:NZ	2.38	0.57
1:A:165:GLY:HA3	1:A:168:ILE:HG22	1.86	0.57
3:C:128:TYR:CE1	3:C:132:LEU:HD12	2.40	0.56
1:A:454:ARG:HB3	1:A:483:PHE:CE1	2.40	0.56
1:A:41:HIS:CE1	1:A:119:PRO:CD	2.83	0.56
1:A:83:ASN:HB2	1:A:118:LEU:HD13	1.88	0.56
4:X:210:ALA:HB3	4:X:235:ARG:HB2	1.88	0.55
2:B:178:GLN:NE2	2:B:303:ILE:O	2.40	0.55
4:X:181:LYS:HB3	4:X:198:VAL:HB	1.88	0.55
4:X:209:LEU:HD21	4:X:234:THR:HG23	1.89	0.55
3:C:169:CYS:HB3	3:C:173:ILE:HD12	1.87	0.55
4:X:185:PRO:CG	4:X:194:THR:O	2.53	0.54
4:X:255:LEU:N	4:X:275:LEU:O	2.40	0.54
1:A:41:HIS:ND1	1:A:119:PRO:HB3	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:X:328:LEU:HB2	4:X:340:PHE:HB3	1.89	0.54
4:X:79:TYR:CD1	4:X:235:ARG:NH2	2.70	0.53
4:X:201:PHE:HB3	4:X:212:GLY:HA2	1.91	0.53
1:A:201:LYS:HG2	1:A:253:SER:HA	1.90	0.53
1:A:42:ILE:O	1:A:149:LYS:CE	2.52	0.52
1:A:473:LYS:HE2	2:B:15:PHE:CZ	2.44	0.52
4:X:231:SER:OG	4:X:232:TYR:N	2.42	0.52
3:C:17:LEU:HA	3:C:23:ILE:HD11	1.92	0.52
4:X:264:ALA:CB	4:X:266:ASN:N	2.73	0.52
4:X:271:ILE:HG13	4:X:303:ILE:HG22	1.91	0.52
1:A:484:LEU:HD22	1:A:484:LEU:O	2.09	0.51
3:C:254:LEU:O	3:C:258:ASN:ND2	2.43	0.51
3:C:97:GLU:OE1	3:C:101:ALA:HA	2.09	0.51
4:X:92:PHE:HE1	4:X:341:CYS:HB3	1.75	0.51
4:X:329:GLU:HG2	4:X:339:LEU:HG	1.91	0.51
2:B:148:GLU:OE2	2:B:151:ARG:NH2	2.45	0.50
2:B:260:VAL:HG21	3:C:71:VAL:HG13	1.92	0.50
4:X:79:TYR:HE1	4:X:235:ARG:HH22	0.57	0.50
3:C:131:PHE:HB3	3:C:162:ARG:HG2	1.92	0.50
2:B:279:ASP:N	2:B:279:ASP:OD1	2.43	0.50
1:A:462:PRO:HG3	1:A:471:ILE:HG23	1.93	0.50
4:X:195:GLY:O	4:X:218:SER:HA	2.11	0.50
4:X:306:LYS:HZ3	4:X:308:GLU:HB3	1.78	0.49
1:A:143:PHE:HD2	1:A:145:LYS:HB2	1.78	0.49
3:C:285:ASN:O	3:C:289:ASN:ND2	2.46	0.49
1:A:473:LYS:CE	2:B:15:PHE:CE2	2.88	0.49
4:X:302:THR:CG2	4:X:319:ASP:CG	2.84	0.48
3:C:172:ILE:HG23	3:C:173:ILE:HG13	1.95	0.48
2:B:318:GLN:NE2	2:B:322:ASP:OD1	2.47	0.48
4:X:319:ASP:HB3	4:X:323:LYS:HB3	1.94	0.48
3:C:52:THR:O	3:C:55:SER:OG	2.24	0.48
1:A:445:GLY:HA3	1:A:458:ASN:HA	1.96	0.48
4:X:302:THR:HG22	4:X:319:ASP:OD1	2.14	0.47
1:A:39:THR:HG22	1:A:42:ILE:HD11	1.95	0.47
1:A:80:ILE:HG22	1:A:117:ILE:HD11	1.95	0.47
2:B:56:VAL:HG13	2:B:57:GLU:HG2	1.95	0.47
2:B:180:ILE:HD11	2:B:224:LEU:HD23	1.97	0.47
3:C:104:ARG:CG	3:C:104:ARG:NH1	2.75	0.47
4:X:187:PHE:HD2	4:X:192:GLU:N	1.98	0.47
2:B:167:LEU:HD21	2:B:272:LEU:HD11	1.97	0.47
3:C:38:LYS:HB2	3:C:38:LYS:HZ2	1.75	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:189:MET:O	2:B:193:SER:OG	2.28	0.46
2:B:173:ASP:OD2	2:B:234:HIS:NE2	2.40	0.46
4:X:183:LEU:C	4:X:183:LEU:CD2	2.84	0.46
1:A:39:THR:CG2	1:A:42:ILE:HD11	2.46	0.46
2:B:131:LEU:HB2	2:B:146:ILE:HD11	1.98	0.45
1:A:454:ARG:CB	1:A:483:PHE:CZ	2.93	0.45
4:X:264:ALA:HB1	4:X:266:ASN:N	2.31	0.45
4:X:210:ALA:O	4:X:235:ARG:N	2.47	0.45
3:C:29:ILE:HD12	3:C:46:ILE:HD11	1.99	0.45
1:A:454:ARG:CB	1:A:483:PHE:CE1	3.00	0.45
1:A:173:LEU:HD13	1:A:193:GLN:HE22	1.82	0.45
1:A:325:ASN:OD1	1:A:325:ASN:N	2.48	0.45
1:A:484:LEU:C	1:A:484:LEU:CD1	2.86	0.45
1:A:168:ILE:CD1	4:X:94:MET:CE	2.95	0.45
4:X:182:THR:CG2	4:X:184:ASN:HB2	2.47	0.45
1:A:117:ILE:O	1:A:117:ILE:HG23	2.16	0.44
1:A:217:GLU:HB3	1:A:237:PHE:HB3	1.98	0.44
3:C:130:LEU:HD11	3:C:261:VAL:HG11	1.99	0.44
4:X:258:SER:HA	4:X:272:GLU:HA	1.99	0.44
1:A:261:MET:HE3	1:A:261:MET:HB3	1.86	0.44
1:A:113:SER:O	1:A:113:SER:OG	2.32	0.44
2:B:60:TYR:OH	2:B:94:ASN:ND2	2.50	0.44
2:B:241:MET:HB3	2:B:241:MET:HE2	1.81	0.44
4:X:343:GLU:HB3	4:X:352:LYS:HB3	1.99	0.44
1:A:168:ILE:HD13	4:X:94:MET:CE	2.47	0.44
1:A:127:THR:OG1	1:A:128:GLY:N	2.51	0.44
3:C:228:ARG:NH2	3:C:232:CYS:SG	2.91	0.43
2:B:29:LYS:HA	2:B:29:LYS:HD3	1.75	0.43
3:C:60:LEU:HD12	3:C:62:VAL:HG23	2.00	0.43
1:A:126:LYS:HB3	1:A:142:GLN:HG3	2.00	0.43
1:A:411:HIS:CE1	1:A:413:PHE:HB3	2.54	0.43
4:X:86:ALA:N	4:X:89:ASN:OD1	2.41	0.43
2:B:203:THR:HG22	2:B:205:LEU:H	1.82	0.43
4:X:94:MET:SD	4:X:94:MET:C	3.01	0.43
4:X:219:ARG:HE	4:X:220:THR:H	1.65	0.43
1:A:163:LEU:HD11	4:X:94:MET:HG3	2.00	0.43
3:C:104:ARG:CD	3:C:106:LYS:NZ	2.63	0.43
4:X:302:THR:CG2	4:X:319:ASP:OD1	2.67	0.43
3:C:130:LEU:O	3:C:141:THR:HG21	2.18	0.43
1:A:43:ASP:HB3	1:A:46:VAL:HG12	2.01	0.42
1:A:43:ASP:HA	1:A:44:PRO:HD3	1.91	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:55:THR:OG1	2:B:56:VAL:N	2.52	0.42
4:X:264:ALA:C	4:X:266:ASN:CA	2.89	0.42
1:A:330:THR:HB	1:A:395:PHE:HB2	2.01	0.42
1:A:359:SER:HB2	1:A:373:LEU:HB2	2.02	0.42
2:B:70:GLU:OE1	2:B:73:THR:OG1	2.30	0.42
2:B:274:ASP:O	2:B:277:LYS:NZ	2.52	0.42
3:C:44:LEU:HD23	3:C:44:LEU:HA	1.88	0.42
4:X:201:PHE:HB3	4:X:212:GLY:CA	2.50	0.42
1:A:211:ARG:NH2	1:A:243:GLU:OE2	2.53	0.42
1:A:243:GLU:HB3	1:A:277:ILE:HG22	2.00	0.41
2:B:168:ASP:O	2:B:228:ASN:ND2	2.53	0.41
4:X:331:LYS:HD2	4:X:337:SER:HB3	2.01	0.41
4:X:355:CYS:SG	4:X:356:GLY:N	2.93	0.41
3:C:124:ARG:NH1	3:C:171:GLU:OE2	2.53	0.41
1:A:211:ARG:HB2	1:A:243:GLU:HG3	2.02	0.41
3:C:34:SER:HB3	3:C:37:ALA:HB3	2.02	0.41
3:C:138:ASN:HA	3:C:142:LYS:HD2	2.02	0.41
4:X:255:LEU:HD11	4:X:275:LEU:HD12	2.03	0.41
1:A:161:GLU:HB3	1:A:173:LEU:HB3	2.03	0.41
1:A:180:LEU:HB2	1:A:184:SER:HB2	2.03	0.41
1:A:241:PHE:CE2	1:A:279:GLY:HA3	2.56	0.41
1:A:250:LYS:HA	2:B:121:LEU:HB3	2.03	0.41
4:X:86:ALA:HA	4:X:90:LYS:HB2	2.03	0.41
4:X:88:LEU:O	4:X:92:PHE:CE2	2.73	0.40
3:C:237:LEU:HD23	3:C:237:LEU:HA	1.94	0.40
2:B:277:LYS:HE2	2:B:277:LYS:HB2	1.96	0.40
1:A:74:ARG:NH1	1:A:182:PRO:O	2.54	0.40
4:X:80:PHE:HD2	4:X:83:GLY:H	1.68	0.40
1:A:213:SER:HA	1:A:241:PHE:HA	2.04	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	412/484 (85%)	359 (87%)	51 (12%)	2 (0%)	25 60
2	B	300/329 (91%)	275 (92%)	24 (8%)	1 (0%)	37 69
3	C	269/327 (82%)	247 (92%)	19 (7%)	3 (1%)	12 44
4	X	139/387 (36%)	118 (85%)	19 (14%)	2 (1%)	9 40
All	All	1120/1527 (73%)	999 (89%)	113 (10%)	8 (1%)	21 54

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	120	PRO
4	X	95	ASN
2	B	114	GLU
3	C	12	ASP
3	C	99	ASP
4	X	185	PRO
3	C	61	PRO
1	A	42	ILE

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	369/433 (85%)	362 (98%)	7 (2%)	52 76
2	B	280/300 (93%)	280 (100%)	0	100 100
3	C	253/299 (85%)	245 (97%)	8 (3%)	34 65
4	X	131/327 (40%)	123 (94%)	8 (6%)	15 47
All	All	1033/1359 (76%)	1010 (98%)	23 (2%)	47 73

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	HIS
1	A	42	ILE
1	A	117	ILE

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Mol	Chain	Res	Type
1	A	118	LEU
1	A	420	VAL
1	A	473	LYS
1	A	484	LEU
3	C	36	GLU
3	C	38	LYS
3	C	41	VAL
3	C	100	LEU
3	C	103	VAL
3	C	104	ARG
3	C	105	LYS
3	C	132	LEU
4	X	90	LYS
4	X	94	MET
4	X	183	LEU
4	X	218	SER
4	X	219	ARG
4	X	220	THR
4	X	301	THR
4	X	353	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	ASN
1	A	78	HIS
1	A	130	ASN
1	A	135	ASN
1	A	175	ASN
1	A	187	ASN
1	A	207	GLN
1	A	254	GLN
1	A	280	HIS
1	A	303	ASN
1	A	411	HIS
1	A	421	ASN
2	B	94	ASN
2	B	178	GLN
2	B	321	GLN
2	B	326	ASN
4	X	95	ASN
4	X	349	ASN

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Mol	Chain	Res	Type
4	X	358	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

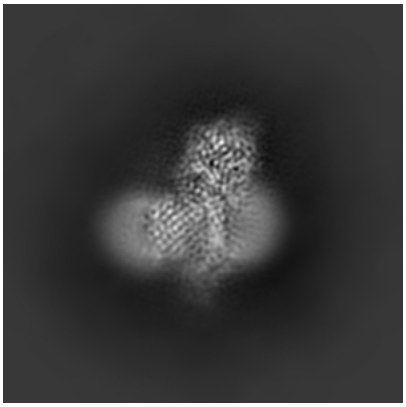
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-32019. These allow visual inspection of the internal detail of the map and identification of artifacts.

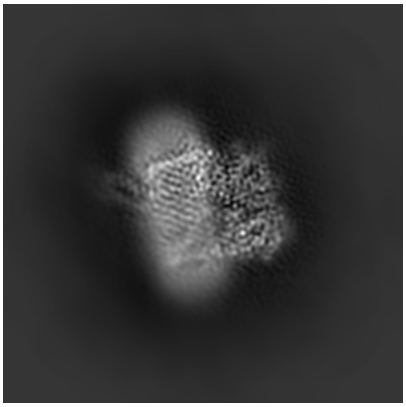
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

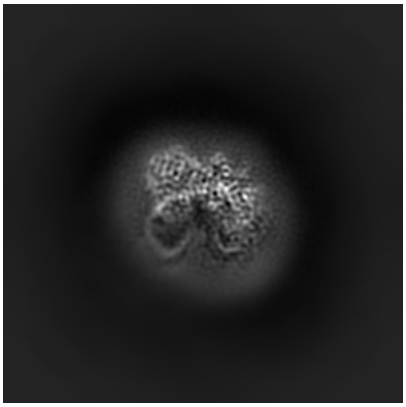
6.1.1 Primary map



X



Y

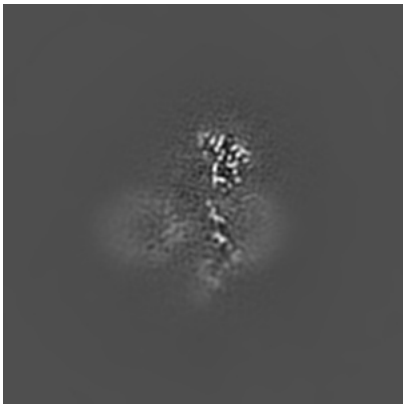


Z

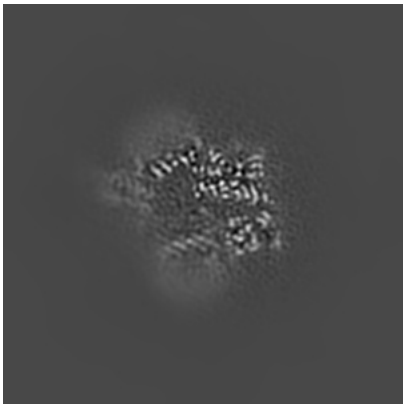
The images above show the map projected in three orthogonal directions.

6.2 Central slices

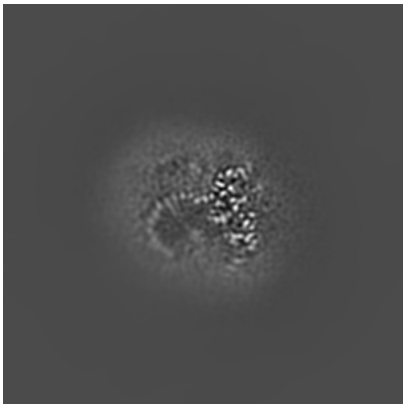
6.2.1 Primary map



X Index: 100



Y Index: 100

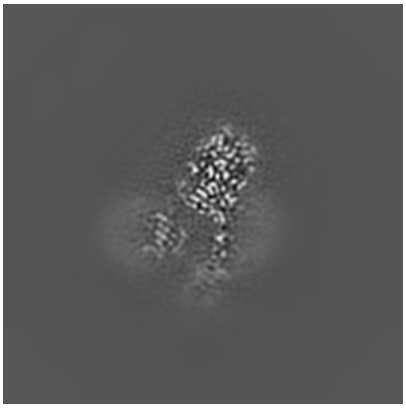


Z Index: 100

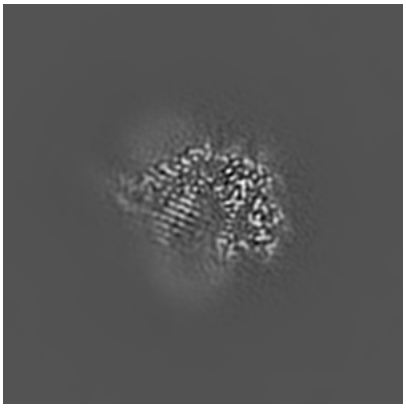
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

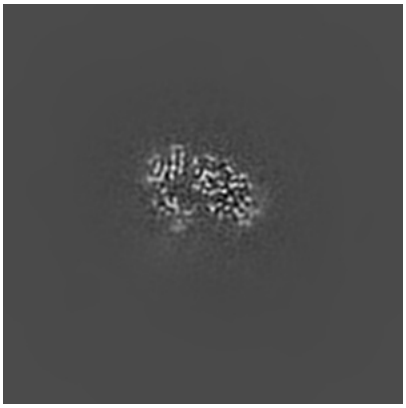
6.3.1 Primary map



X Index: 108



Y Index: 106

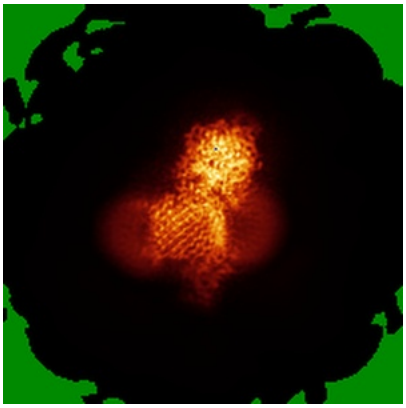


Z Index: 119

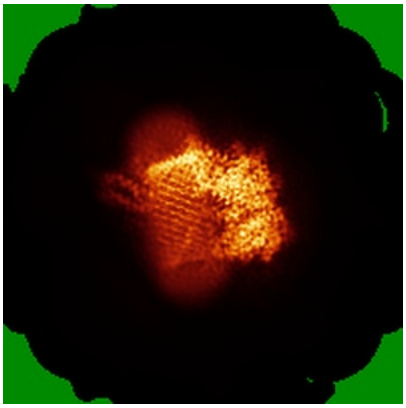
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

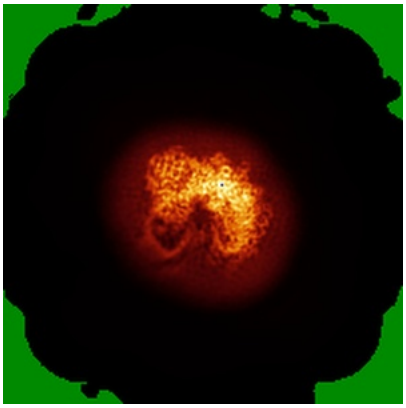
6.4.1 Primary map



X



Y

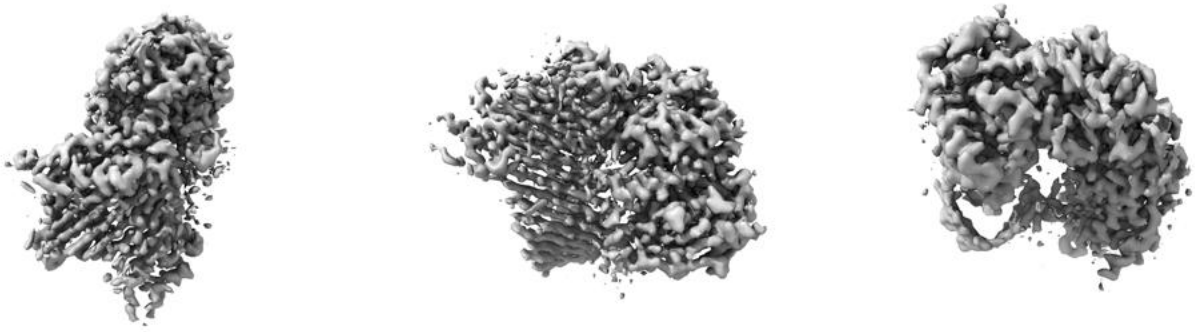


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

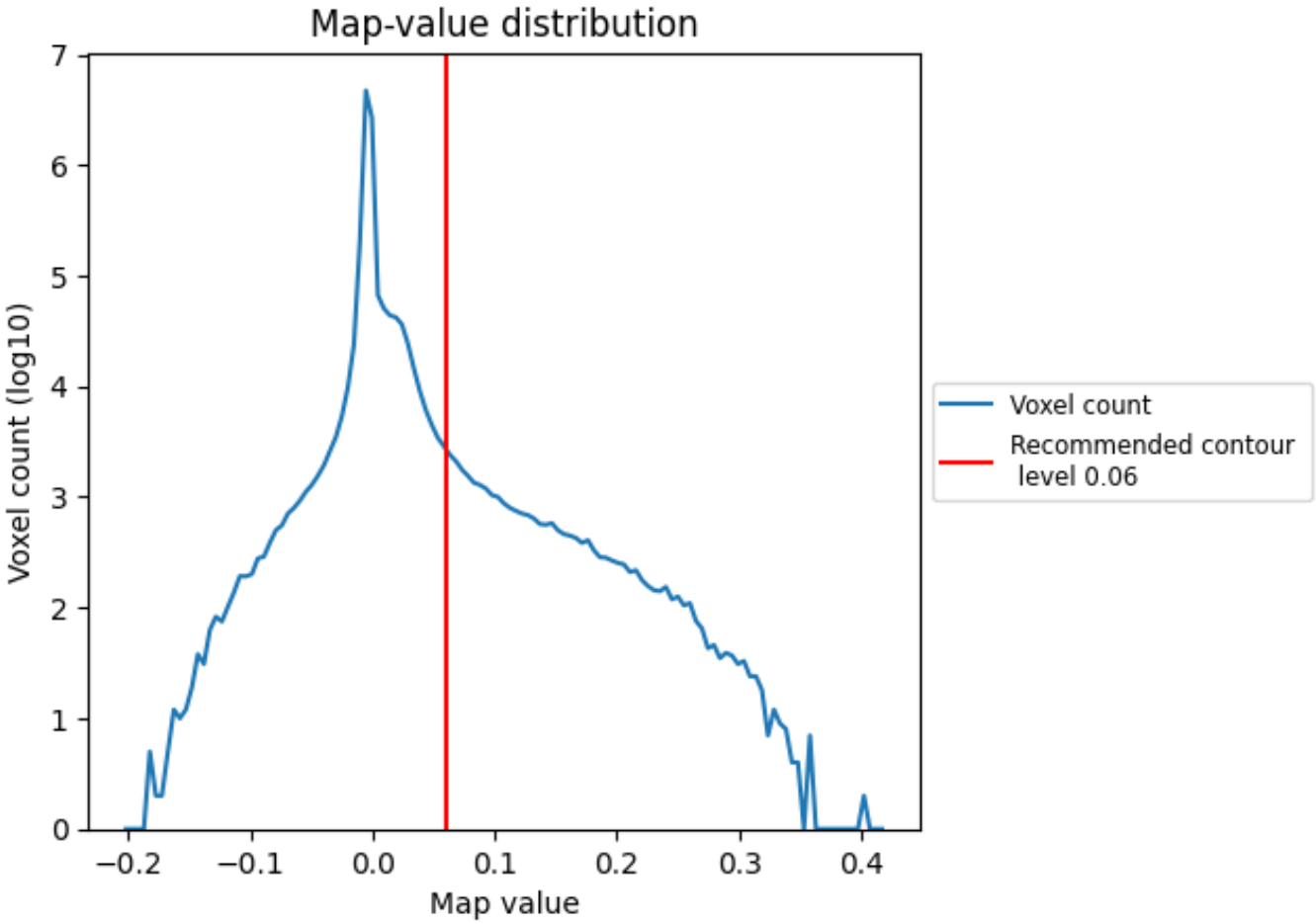
6.6 Mask visualisation (i)

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

7 Map analysis

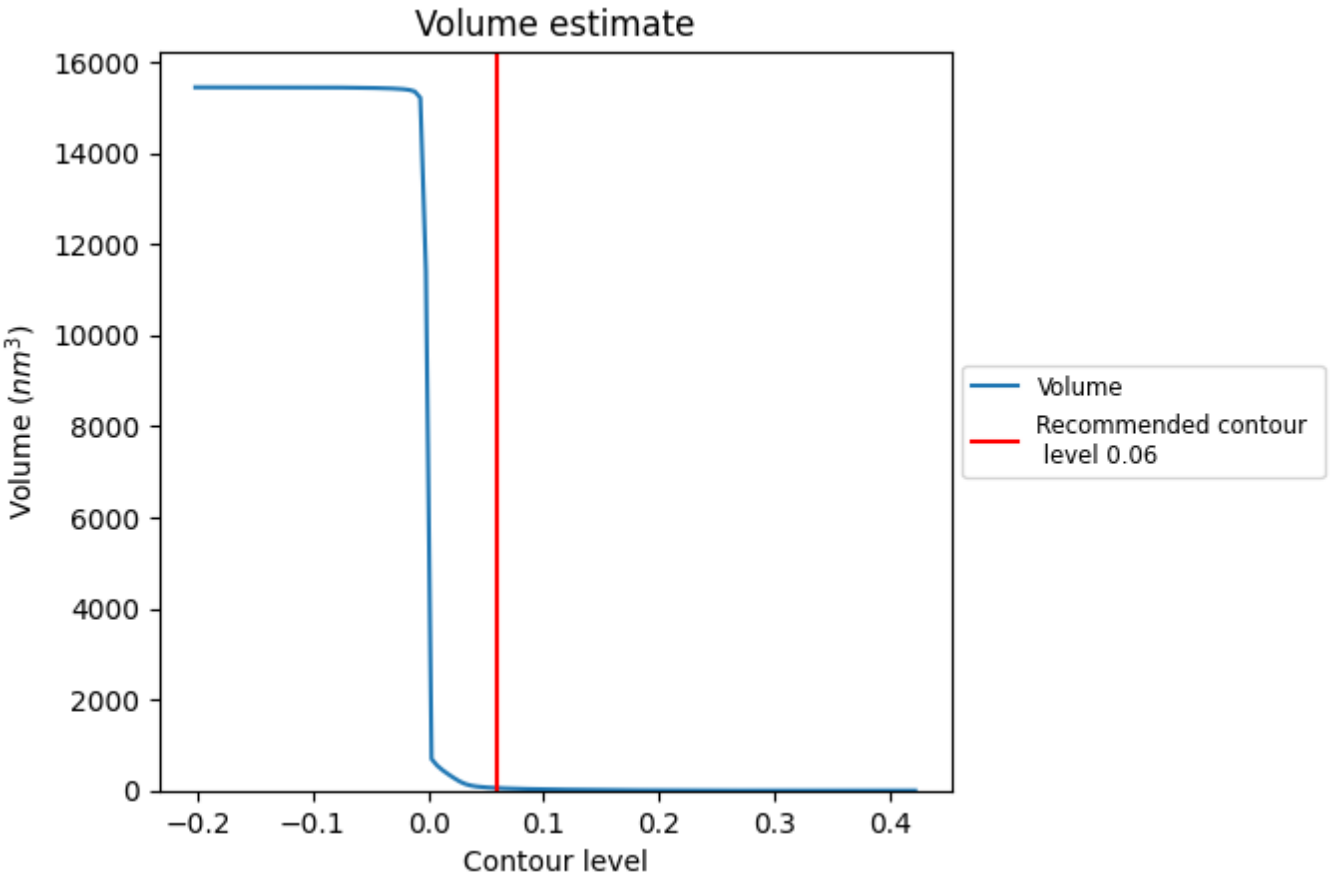
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

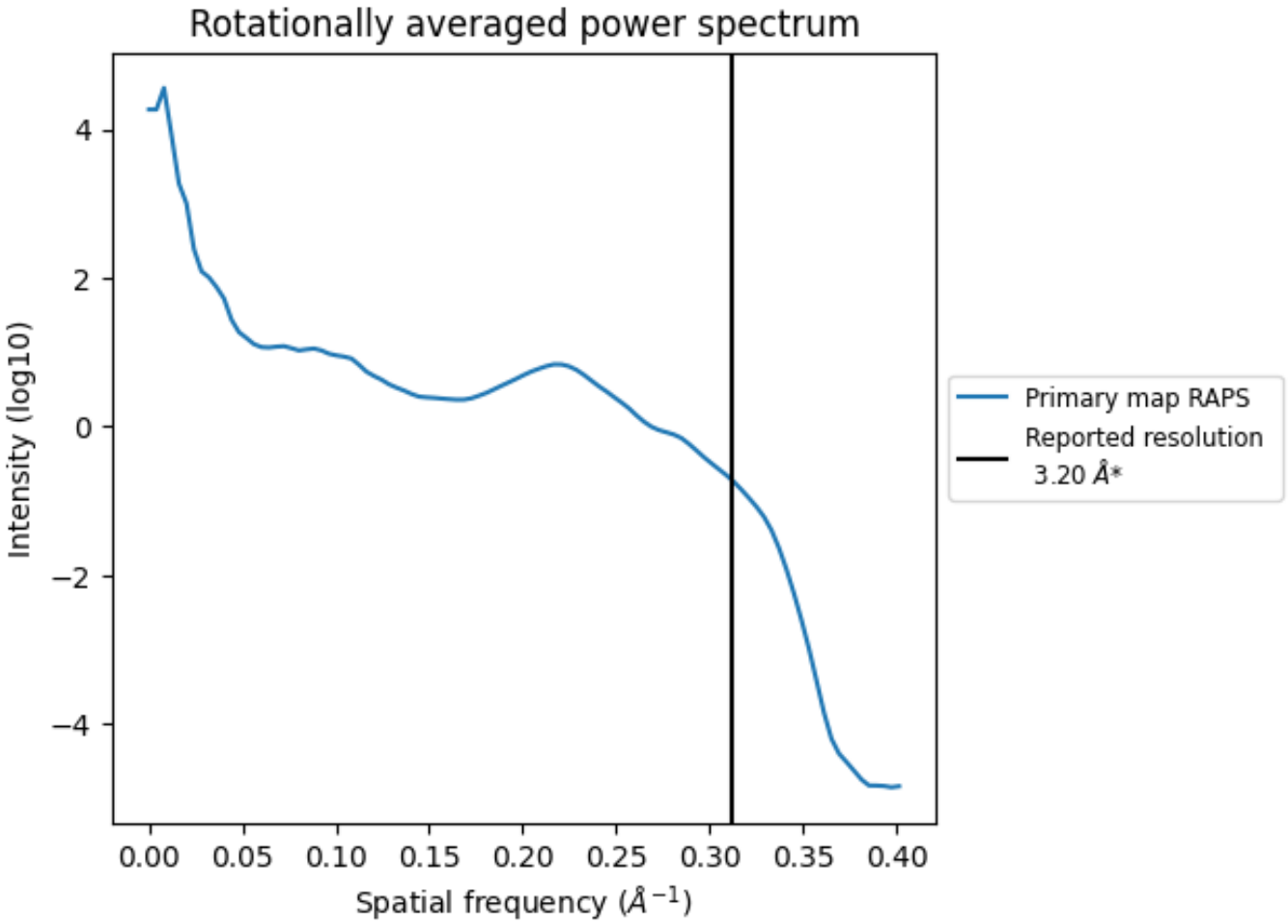
7.2 Volume estimate



The volume at the recommended contour level is 55 nm^3; 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)

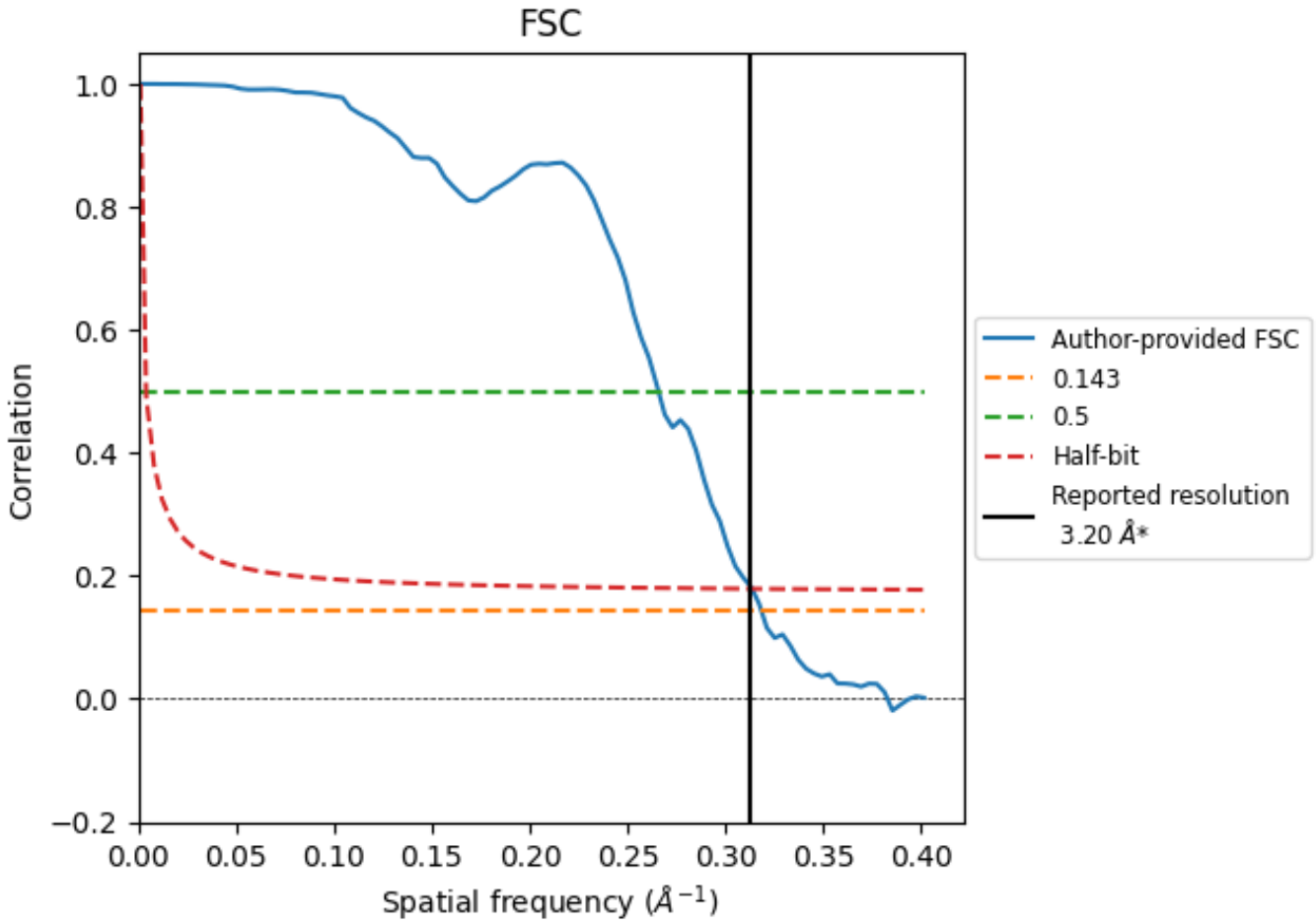


*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8.2 Resolution estimates (i)

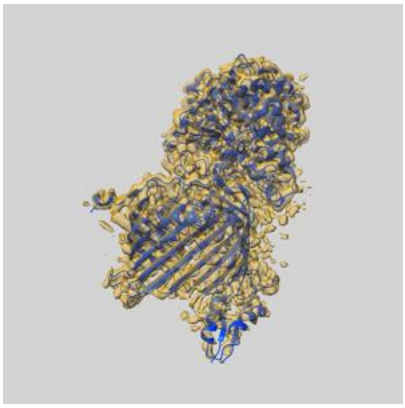
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.14	3.76	3.19
Unmasked-calculated*	-	-	-

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

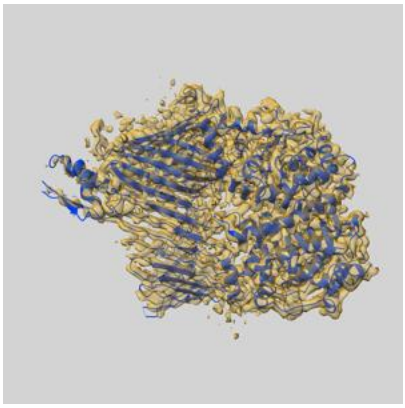
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-32019 and PDB model 7VKU. Per-residue inclusion information can be found in section 3 on page 4.

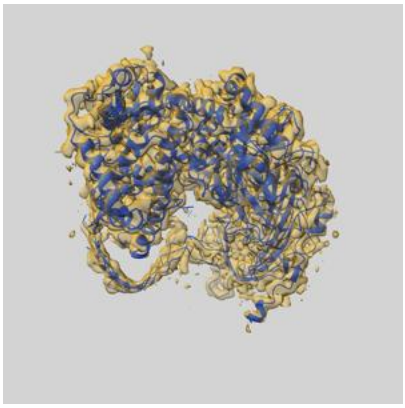
9.1 Map-model overlay



X



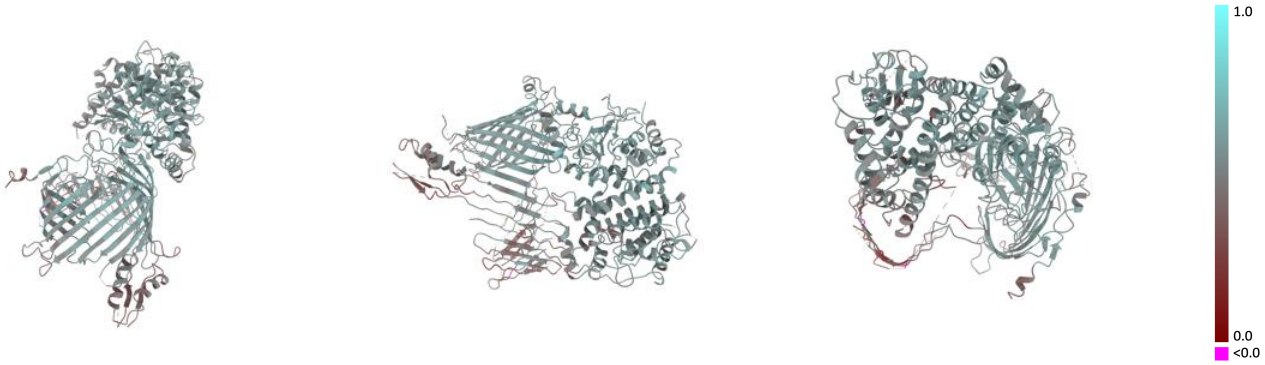
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06 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.

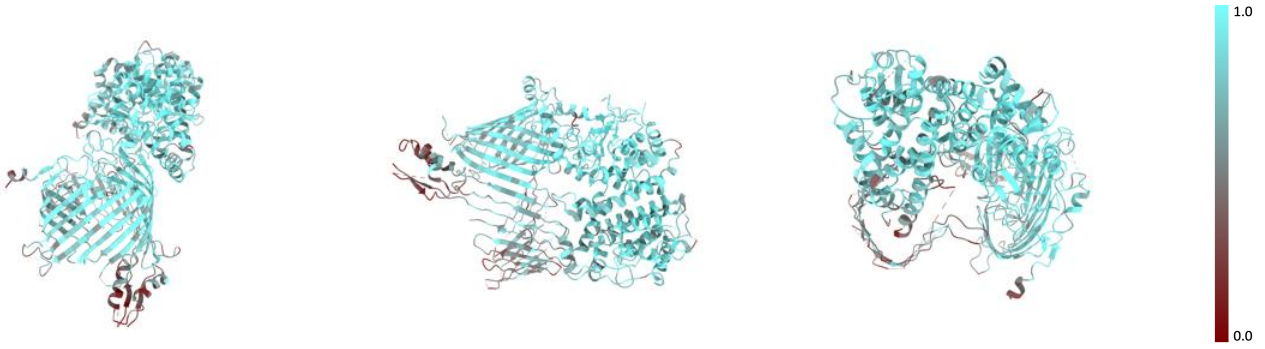
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

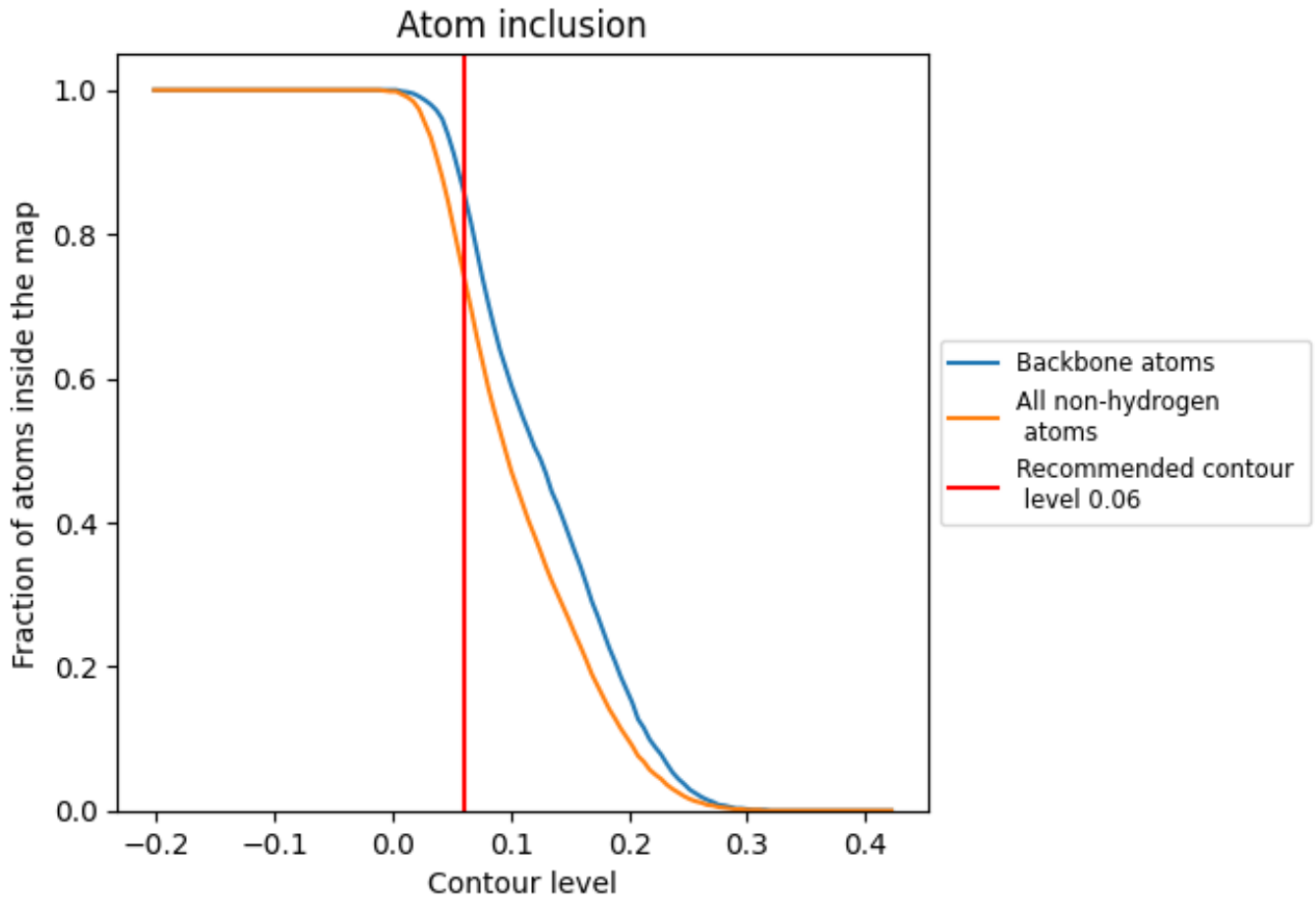
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.06).

9.4 Atom inclusion (i)



At the recommended contour level, 86% of all backbone atoms, 74% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7440	0.5090
A	0.7220	0.5140
B	0.8580	0.5570
C	0.7960	0.5240
X	0.4750	0.3720