



Full wwPDB EM Validation Report ⓘ

Mar 14, 2026 – 06:25 AM UTC

PDB ID : 6SZ9 / pdb_00006sz9
EMDB ID : EMD-10350
Title : Type IV Coupling Complex (T4CC) from *L. pneumophila*.
Authors : Mace, K.; Meir, A.; Lukyanova, N.; Waksman, G.
Deposited on : 2019-10-02
Resolution : 3.70 Å (reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

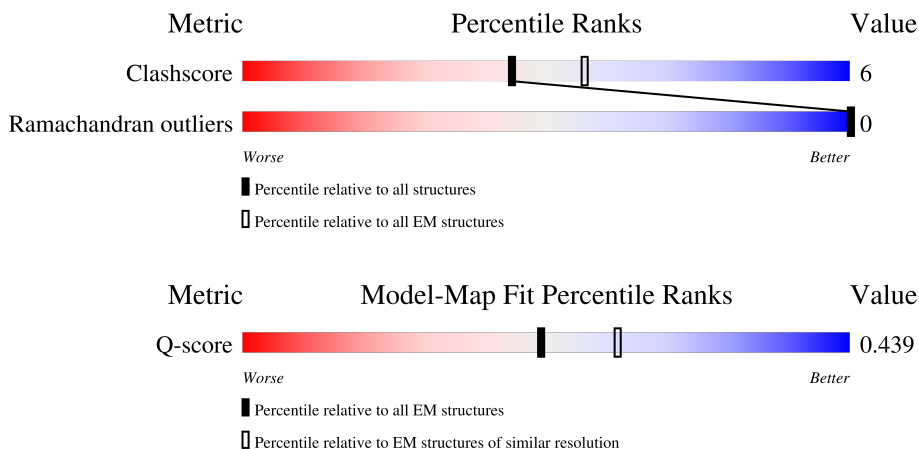
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	783	13% 51% 10% 40%
2	B	380	60% 8% 32%
3	C	208	9% 80% 17%
4	D	294	20% 79% 17%
5	E	230	11% 28% 68%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10233 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 IcmO (DotL).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	473	Total	C	N	O	S	0	0
			3665	2345	619	684	17		

- Molecule 2 is a protein called IcmP (DotM).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	259	Total	C	N	O	S	0	0
			2085	1326	367	377	15		

- Molecule 3 is a protein called IcmJ (DotN).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	202	Total	C	N	O	S	0	0
			1615	1024	277	304	10		

- Molecule 4 is a protein called DotZ.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	283	Total	C	N	O	S	0	0
			2284	1452	389	441	2		

- Molecule 5 is a protein called DotY.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	73	Total	C	N	O	S	0	0
			583	373	96	110	4		

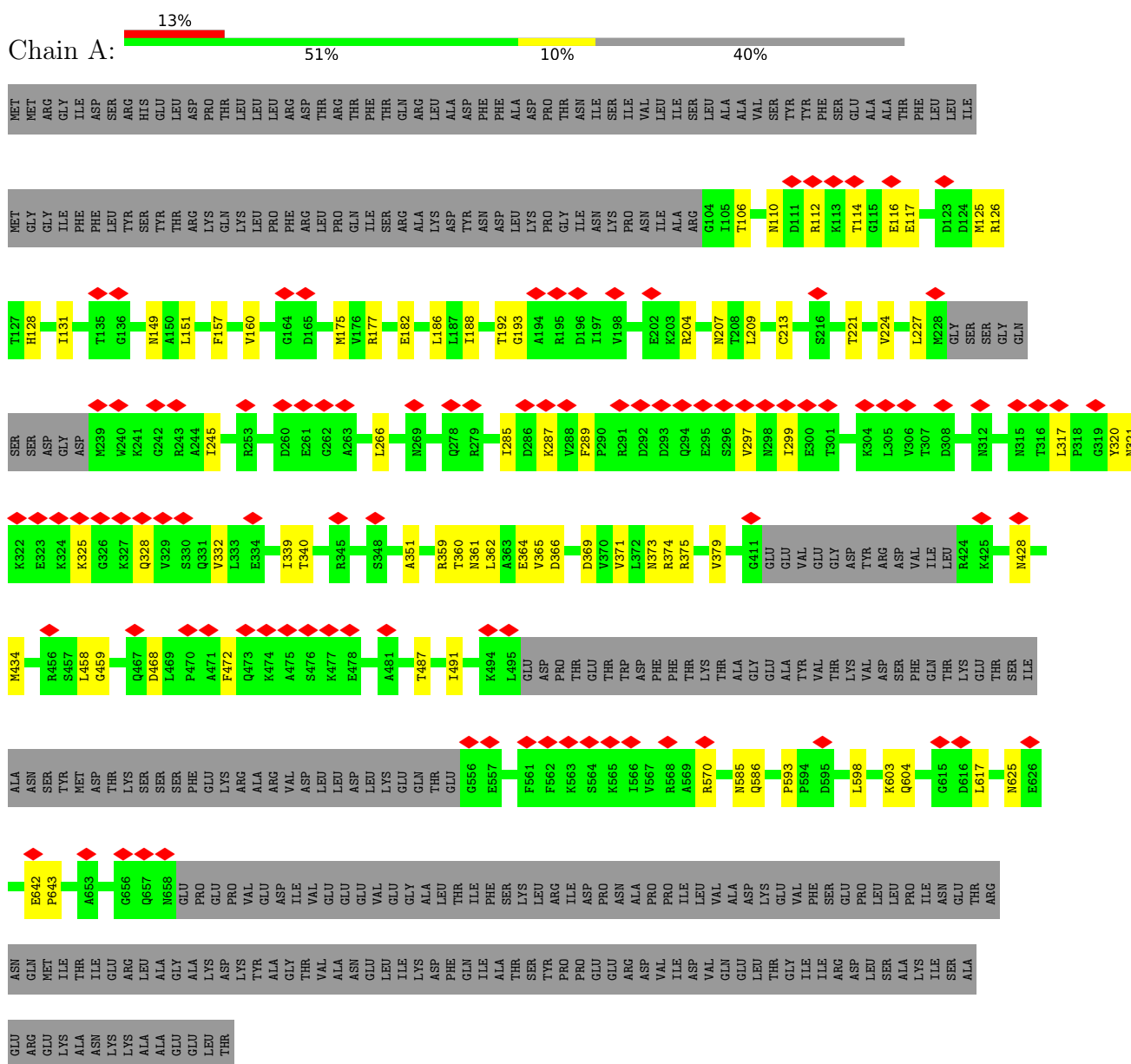
- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
6	C	1	Total 1	Zn 1	0

3 Residue-property plots

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: IcmO (DotL)



• Molecule 2: IcmP (DotM)



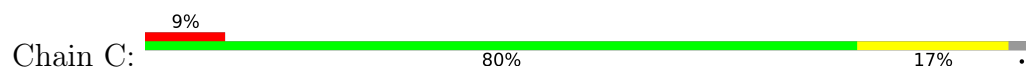
MET
 TYR
 ILE
 GLU
 MET
 MET
 ALA
 GLN
 GLN
 GLN
 GLN
 GLN
 SER
 GLY
 SER
 ASP
 ASP
 SER
 MET
 MET
 ALA
 PRO
 VAL
 VAL
 TRP
 ILE
 ASP
 VAL
 ILE
 ILE
 LEU
 LEU
 PHE
 PHE
 ILE
 THR
 THR
 ALA
 THR
 THR
 PHE
 VAL
 GLY
 TRP
 ALA
 MET
 LEU
 ALA
 HIS
 GLN
 TYR
 ILE
 VAL
 CYS
 VAL
 SER
 PHE
 PHE
 VAL
 PHE
 THR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

TYR
 R122
 K123
 T124
 Y125
 K128
 R131
 Y145
 K146
 E147
 D148
 S151
 K156
 P158
 W159
 D183
 M191
 D199
 A200
 R201
 R202
 T205
 D213
 E216
 L225
 N234
 D253
 G254
 K255
 F256
 D257
 Y268
 H281
 L288
 Y300
 P302
 R314
 L320

N321
 T327
 E342
 K345
 E346
 R347
 V351
 I354
 D355
 A357
 I358
 R359
 P372
 R373
 Q374
 R375
 E376
 P380

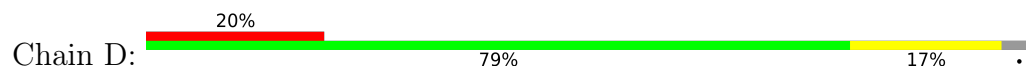
• Molecule 3: IcmJ (DotN)



MET
 ALA
 ASP
 ASN
 GLN
 GLN
 R7
 L10
 R20
 R25
 D28
 E29
 R30
 F31
 K32
 S33
 Y34
 C46
 Q47
 F48
 C49
 G50
 L55
 D58
 D63
 G64
 D65
 N68
 N69
 R70
 V75
 I76
 A77
 C78
 C79
 F85
 S89
 Q108
 M124
 Y128
 R137
 S138
 R142

S143
 Q144
 I145
 I146
 E147
 G151
 E152
 Q162
 L163
 D166
 N170
 S171
 E172
 E173
 I174
 L178
 L184
 F191
 R192
 K193
 W196
 L203
 D208

• Molecule 4: DotZ



MET
 ASP
 GLU
 ILE
 LYS
 ASP
 ASP
 LEU
 S11
 Q12
 W13
 L14
 T21
 R24
 R28
 S32
 L33
 P34
 Q35
 D36
 E37
 E40
 A41
 Y49
 Q54
 I55
 P56
 L57
 K58
 N59
 A76
 L80
 I81
 D82
 E88
 S89
 S90
 K91
 E92
 P93
 D94
 Q96
 G97
 R101
 E102

D106
 L111
 D126
 N127
 L128
 K146
 L147
 E148
 L151
 S152
 N155
 S156
 L157
 Y158
 K159
 N160
 N162
 S163
 K164
 I165
 K166
 K167
 N168
 A169
 K172
 I55
 K176
 A177
 F178
 I179
 H180
 C181
 D182
 K185
 D186
 Q187
 K190
 N191
 Q194
 K198
 Q201
 T202
 L203
 A204
 V205
 S206
 V207

E210
 L211
 K212
 I215
 L216
 T217
 N218
 L219
 E227
 T237
 D238
 R239
 T240
 N241
 R251
 V257
 I258
 I262
 I265
 P269
 K272
 I273
 K54
 D274
 Q277
 D278
 A279
 I280
 N281
 R282
 Y286
 R289
 E293
 ARG

• Molecule 5: DotY



MET
 PRO
 TYR
 LYS
 T5
 D10
 L13
 R32
 F33
 E34
 L37
 T38
 K41
 L42
 L43
 P44
 P45
 C46
 N47
 P48
 F51
 K52
 I53
 K54
 E55
 Q58
 F59
 Y60
 K61
 F62
 K63
 L64
 L65
 S66
 S67
 A68
 Q69
 Q74
 F75
 E76
 F77
 THR
 SER
 ASP
 TYR
 GLN
 ASN
 THR
 GLN
 GLU
 ASN
 LYS

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

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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	219593	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 ($e^-/\text{\AA}^2$)	54	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	42.540	Depositor
Minimum map value	-29.188	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.841	Depositor
Recommended contour level	7	Depositor
Map size (Å)	313.5, 313.5, 313.5	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	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	0.20	0/3727	0.48	0/5031
2	B	0.22	0/2132	0.47	0/2883
3	C	0.28	0/1646	0.50	0/2213
4	D	0.23	0/2318	0.52	0/3131
5	E	0.16	0/592	0.40	0/796
All	All	0.22	0/10415	0.48	0/14054

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	3665	0	3720	48	0
2	B	2085	0	2098	22	0
3	C	1615	0	1578	38	0
4	D	2284	0	2327	34	0
5	E	583	0	599	6	0
6	C	1	0	0	0	0
All	All	10233	0	10322	132	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 6.

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:10:LEU:HG	3:C:48:PHE:HD2	1.52	0.74
3:C:79:CYS:SG	3:C:191:PHE:CE1	2.86	0.68
1:A:126:ARG:HE	1:A:459:GLY:HA2	1.61	0.64
3:C:10:LEU:HG	3:C:48:PHE:CD2	2.32	0.64
3:C:48:PHE:CZ	3:C:85:PHE:CE2	2.87	0.61
3:C:79:CYS:SG	3:C:191:PHE:HE1	2.23	0.60
3:C:79:CYS:HG	3:C:191:PHE:HE1	1.41	0.60
3:C:48:PHE:CZ	3:C:85:PHE:HE2	2.20	0.60
3:C:108:GLN:HE22	3:C:184:LEU:H	1.50	0.59
1:A:369:ASP:OD1	1:A:373:ASN:ND2	2.37	0.58
1:A:106:THR:OG1	1:A:149:ASN:ND2	2.36	0.58
4:D:76:ALA:HB2	4:D:258:ILE:HG12	1.86	0.57
4:D:187:GLN:HA	4:D:191:ASN:HD21	1.70	0.57
3:C:208:ASP:O	4:D:54:GLN:NE2	2.38	0.56
1:A:227:LEU:HD22	1:A:245:ILE:HD11	1.86	0.56
1:A:213:CYS:SG	1:A:361:ASN:ND2	2.79	0.56
2:B:158:PRO:O	2:B:314:ARG:NH1	2.41	0.54
2:B:347:ARG:NH2	3:C:166:ASP:OD2	2.41	0.54
1:A:375:ARG:NH2	2:B:321:ASN:O	2.41	0.54
2:B:345:MET:SD	2:B:347:ARG:NH1	2.81	0.53
1:A:186:LEU:HD22	1:A:365:VAL:HB	1.91	0.53
1:A:617:LEU:HD12	3:C:178:LEU:HD13	1.90	0.53
3:C:79:CYS:SG	3:C:191:PHE:CZ	2.97	0.53
1:A:468:ASP:O	1:A:472:PHE:N	2.40	0.53
4:D:34:PRO:HB3	4:D:37:GLU:HB2	1.91	0.52
1:A:371:VAL:O	1:A:374:ARG:NH2	2.42	0.52
2:B:201:LYS:HG2	2:B:354:ILE:HD11	1.92	0.52
4:D:251:ARG:NH2	4:D:289:ARG:O	2.43	0.52
2:B:183:ASP:OD1	2:B:183:ASP:N	2.41	0.52
2:B:356:GLU:OE1	2:B:359:ARG:NH2	2.43	0.51
3:C:58:ASP:N	3:C:58:ASP:OD1	2.40	0.51
1:A:177:ARG:NH2	1:A:182:GLU:OE1	2.42	0.51
2:B:131:ARG:HG2	2:B:145:VAL:HG23	1.91	0.51
2:B:199:ASP:OD1	2:B:202:ARG:NH2	2.43	0.51
2:B:351:VAL:HG11	3:C:162:GLN:HG2	1.92	0.51
2:B:372:PRO:HA	2:B:375:MET:HB3	1.91	0.51
4:D:82:ASP:OD1	5:E:32:ARG:NH1	2.44	0.51
1:A:593:PRO:HG2	1:A:598:LEU:HD11	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:THR:OG1	1:A:116:GLU:OE1	2.29	0.50
1:A:207:ASN:ND2	1:A:364:GLU:OE1	2.44	0.50
3:C:162:GLN:O	3:C:166:ASP:HB2	2.12	0.50
1:A:604:GLN:HB3	3:C:163:LEU:HD11	1.94	0.50
1:A:625:ASN:ND2	3:C:138:SER:OG	2.45	0.50
4:D:186:ASP:O	4:D:191:ASN:ND2	2.44	0.50
1:A:128:HIS:HB2	1:A:487:THR:HG22	1.93	0.50
4:D:37:GLU:HA	4:D:40:GLU:HG2	1.93	0.50
4:D:237:THR:O	4:D:241:ASN:ND2	2.45	0.50
4:D:274:ASP:N	4:D:274:ASP:OD1	2.42	0.50
1:A:351:ALA:O	1:A:359:ARG:NH1	2.44	0.49
4:D:128:LEU:HD13	4:D:239:ARG:HD2	1.95	0.49
2:B:281:HIS:ND1	2:B:342:GLU:OE2	2.41	0.49
3:C:48:PHE:CD1	3:C:77:ALA:HB2	2.48	0.49
3:C:128:TYR:HE2	4:D:24:ARG:HD3	1.78	0.49
1:A:362:LEU:HB3	2:B:327:THR:HG22	1.94	0.48
1:A:289:PHE:HB3	1:A:297:VAL:HB	1.94	0.48
1:A:285:ILE:O	1:A:287:LYS:NZ	2.46	0.48
1:A:321:ASN:HD22	1:A:328:GLN:HB3	1.78	0.48
3:C:69:ASN:OD1	3:C:69:ASN:N	2.47	0.48
1:A:325:LYS:HG3	1:A:328:GLN:HE21	1.78	0.47
2:B:213:ASP:OD1	2:B:213:ASP:N	2.46	0.47
3:C:46:CYS:O	3:C:50:GLY:HA2	2.14	0.47
4:D:165:ILE:HG12	4:D:203:LEU:HD11	1.96	0.47
3:C:171:SER:HB2	3:C:174:ILE:HG22	1.97	0.47
2:B:234:ASN:HD22	2:B:268:TYR:HD1	1.61	0.47
3:C:55:LEU:O	3:C:198:TRP:NE1	2.39	0.47
5:E:60:VAL:O	5:E:64:LEU:HB2	2.15	0.46
4:D:37:GLU:O	4:D:41:ALA:HB2	2.15	0.46
1:A:112:ARG:HG2	1:A:570:ARG:HG3	1.96	0.46
1:A:131:ILE:HG13	1:A:491:ILE:HB	1.97	0.46
2:B:191:MET:HA	2:B:375:MET:HE2	1.98	0.46
4:D:146:LYS:HA	4:D:146:LYS:HD3	1.73	0.46
3:C:142:ARG:HD3	3:C:145:ILE:HD12	1.97	0.45
4:D:272:LYS:HE3	4:D:272:LYS:HB2	1.78	0.45
1:A:175:MET:HE3	1:A:175:MET:HB2	1.68	0.45
4:D:126:ASP:OD2	5:E:76:ARG:NH2	2.49	0.45
1:A:289:PHE:HB2	1:A:299:ILE:HD11	1.98	0.45
4:D:262:ILE:HA	4:D:265:ILE:HG22	1.99	0.45
1:A:317:LEU:HD11	1:A:320:TYR:HD1	1.81	0.44
3:C:89:SER:O	3:C:89:SER:OG	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:585:ASN:N	1:A:585:ASN:OD1	2.48	0.44
1:A:125:MET:HE2	1:A:434:MET:HE2	1.98	0.44
3:C:79:CYS:HG	3:C:191:PHE:HZ	1.50	0.44
1:A:151:LEU:HD22	1:A:157:PHE:HE2	1.82	0.44
1:A:339:ILE:HG13	1:A:340:THR:HG23	1.99	0.44
4:D:49:TYR:HD1	4:D:179:ILE:HD11	1.82	0.44
4:D:28:ARG:HA	4:D:28:ARG:HD2	1.87	0.44
4:D:95:SER:OG	4:D:96:GLN:N	2.50	0.43
1:A:177:ARG:NH1	2:B:159:TRP:O	2.50	0.43
1:A:221:THR:HA	1:A:224:VAL:HG12	2.00	0.43
3:C:47:GLN:HG3	3:C:75:VAL:CG2	2.48	0.43
3:C:124:ASN:OD1	4:D:21:THR:OG1	2.32	0.43
2:B:225:LEU:HD13	2:B:320:LEU:HD11	2.00	0.43
4:D:56:PRO:HA	4:D:59:ASN:HD22	1.83	0.43
1:A:192:THR:OG1	1:A:193:GLY:N	2.52	0.43
3:C:193:LYS:NZ	4:D:286:TYR:O	2.42	0.43
3:C:48:PHE:CZ	3:C:85:PHE:CZ	3.06	0.43
4:D:158:TYR:HA	4:D:161:THR:HG23	2.01	0.43
4:D:80:LEU:HA	4:D:80:LEU:HD23	1.81	0.42
3:C:147:GLU:HG2	3:C:152:GLU:HA	2.02	0.42
4:D:215:ILE:O	4:D:219:LEU:HB2	2.19	0.42
4:D:277:GLN:HA	4:D:280:ILE:HG22	2.00	0.42
1:A:110:ASN:HA	1:A:117:GLU:HA	2.01	0.42
3:C:10:LEU:CD2	3:C:48:PHE:CD2	3.02	0.42
5:E:44:PRO:HA	5:E:47:ASN:HB2	2.02	0.42
1:A:428:ASN:N	1:A:428:ASN:OD1	2.50	0.42
3:C:203:LEU:HD22	4:D:57:LEU:HD22	2.01	0.42
4:D:91:LYS:HB2	4:D:97:GLY:HA3	2.01	0.42
1:A:204:ARG:NH1	1:A:586:GLN:OE1	2.53	0.42
1:A:360:THR:OG1	1:A:361:ASN:N	2.53	0.42
3:C:10:LEU:HD11	3:C:48:PHE:HB3	2.02	0.42
4:D:278:ASP:OD2	4:D:282:ARG:NH1	2.52	0.42
3:C:25:ARG:HD3	3:C:25:ARG:HA	1.89	0.42
1:A:160:VAL:HA	1:A:379:VAL:HG13	2.01	0.42
1:A:188:ILE:HD13	1:A:209:LEU:HD13	2.02	0.42
1:A:317:LEU:HB2	1:A:332:VAL:HG21	2.02	0.42
1:A:374:ARG:NH1	1:A:458:LEU:O	2.38	0.41
3:C:48:PHE:CE2	3:C:85:PHE:CZ	3.09	0.41
5:E:54:LYS:HA	5:E:54:LYS:HD2	1.78	0.41
4:D:111:LEU:HD13	4:D:257:VAL:HG11	2.02	0.41
4:D:237:THR:HG22	4:D:241:ASN:HD21	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:366:ASP:N	1:A:366:ASP:OD1	2.54	0.41
2:B:288:ILE:HG22	2:B:320:LEU:HD21	2.02	0.41
2:B:358:ILE:H	2:B:358:ILE:HG12	1.67	0.41
1:A:642:GLU:HA	1:A:643:PRO:HD3	1.93	0.40
2:B:300:VAL:HG22	2:B:302:PRO:HD3	2.03	0.40
5:E:37:LEU:HD23	5:E:37:LEU:HA	1.90	0.40
1:A:177:ARG:HA	1:A:177:ARG:HD2	1.94	0.40
1:A:266:LEU:HD12	1:A:266:LEU:HA	1.88	0.40
4:D:14:LEU:HD12	4:D:14:LEU:HA	1.95	0.40
1:A:603:LYS:HD3	1:A:603:LYS:HA	1.95	0.40
3:C:48:PHE:CE1	3:C:77:ALA:HB2	2.56	0.40
2:B:205:THR:HG22	3:C:20:ARG:HG2	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	465/783 (59%)	448 (96%)	17 (4%)	0	100	100
2	B	257/380 (68%)	251 (98%)	6 (2%)	0	100	100
3	C	200/208 (96%)	194 (97%)	6 (3%)	0	100	100
4	D	281/294 (96%)	271 (96%)	10 (4%)	0	100	100
5	E	71/230 (31%)	69 (97%)	2 (3%)	0	100	100
All	All	1274/1895 (67%)	1233 (97%)	41 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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 [i](#)

There are no chain breaks in this entry.

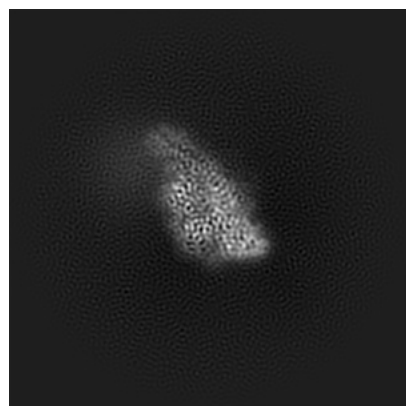
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10350. These allow visual inspection of the internal detail of the map and identification of artifacts.

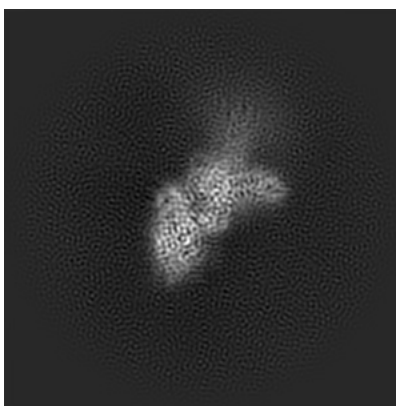
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

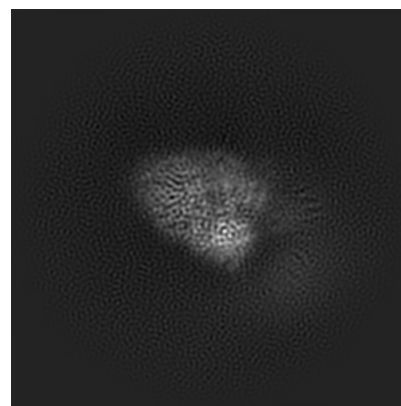
6.1.1 Primary map



X

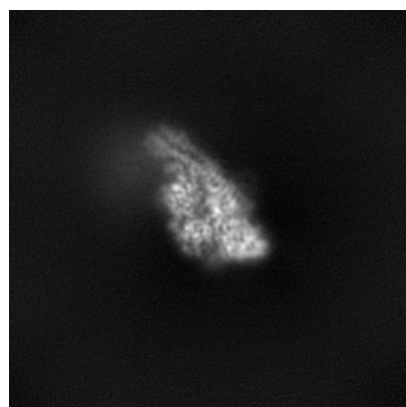


Y

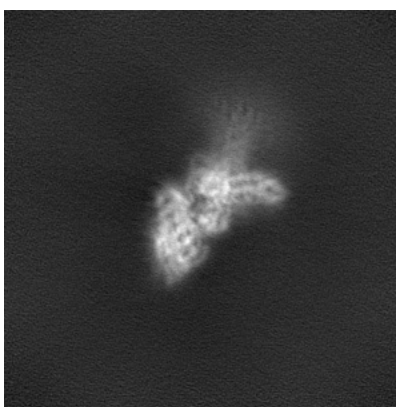


Z

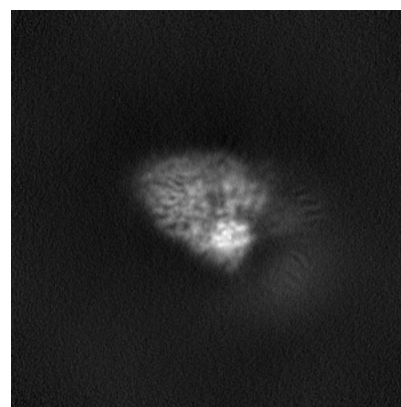
6.1.2 Raw map



X



Y

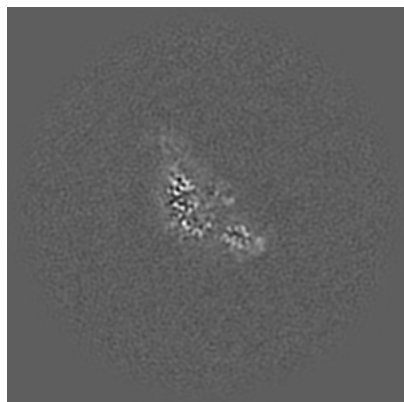


Z

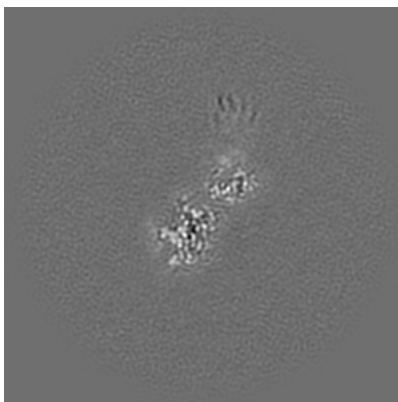
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

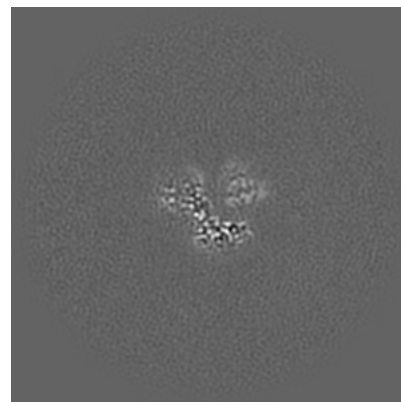
6.2.1 Primary map



X Index: 150



Y Index: 150



Z Index: 150

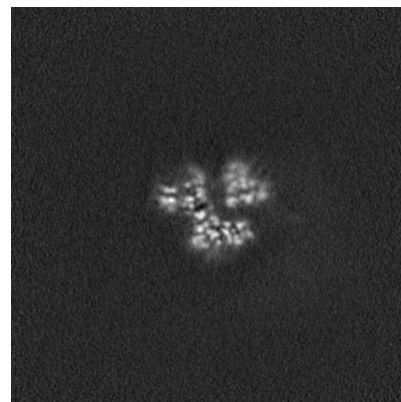
6.2.2 Raw map



X Index: 150



Y Index: 150

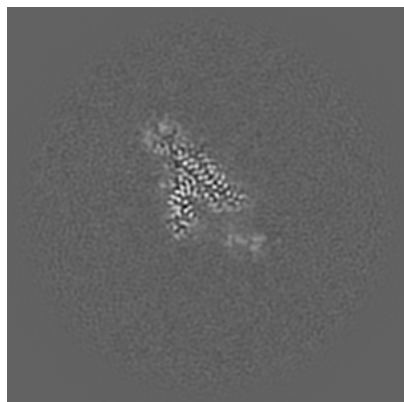


Z Index: 150

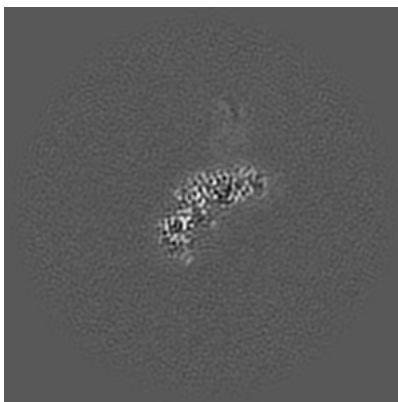
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

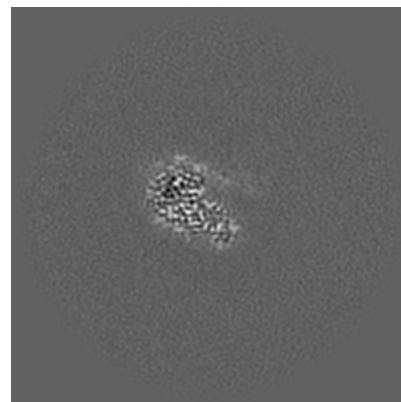
6.3.1 Primary map



X Index: 164

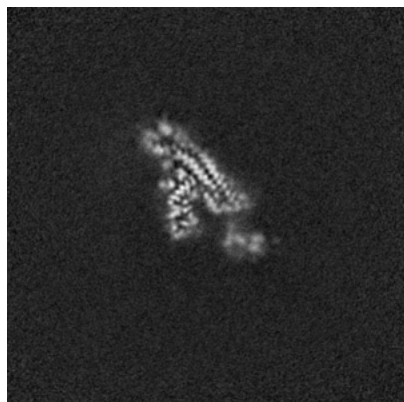


Y Index: 137

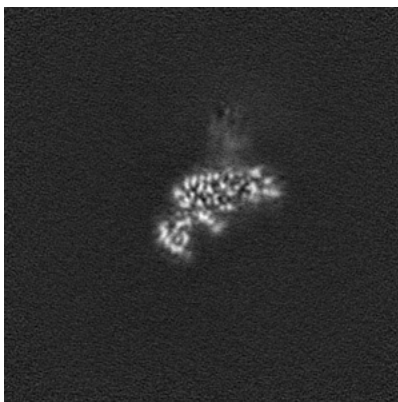


Z Index: 136

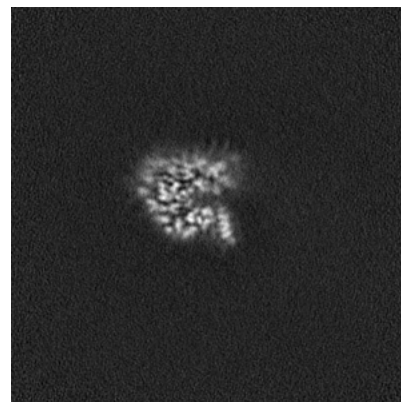
6.3.2 Raw map



X Index: 164



Y Index: 133

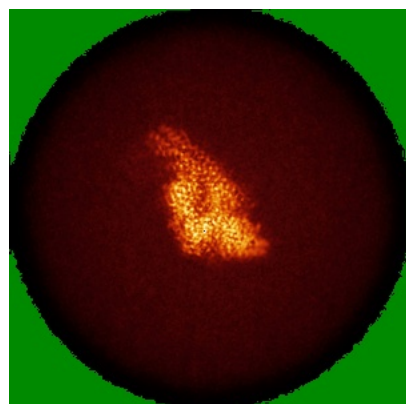


Z Index: 130

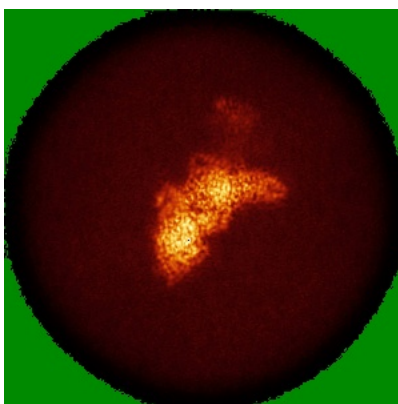
The images above show the largest variance slices of the map in three orthogonal directions.

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

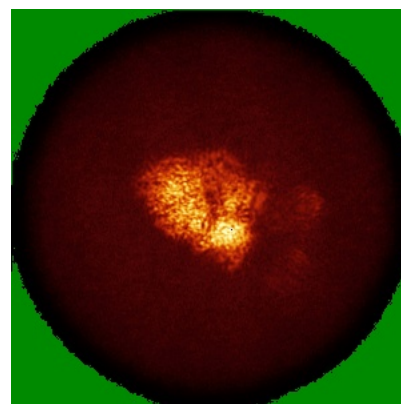
6.4.1 Primary map



X



Y

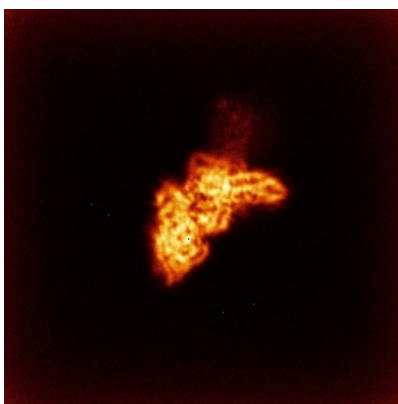


Z

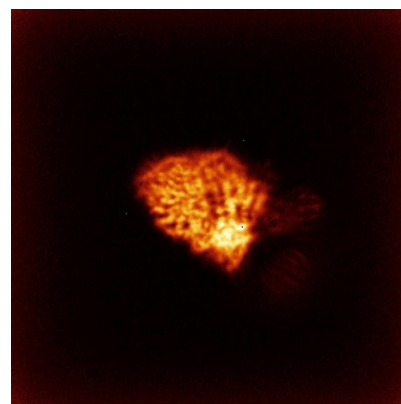
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 7.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

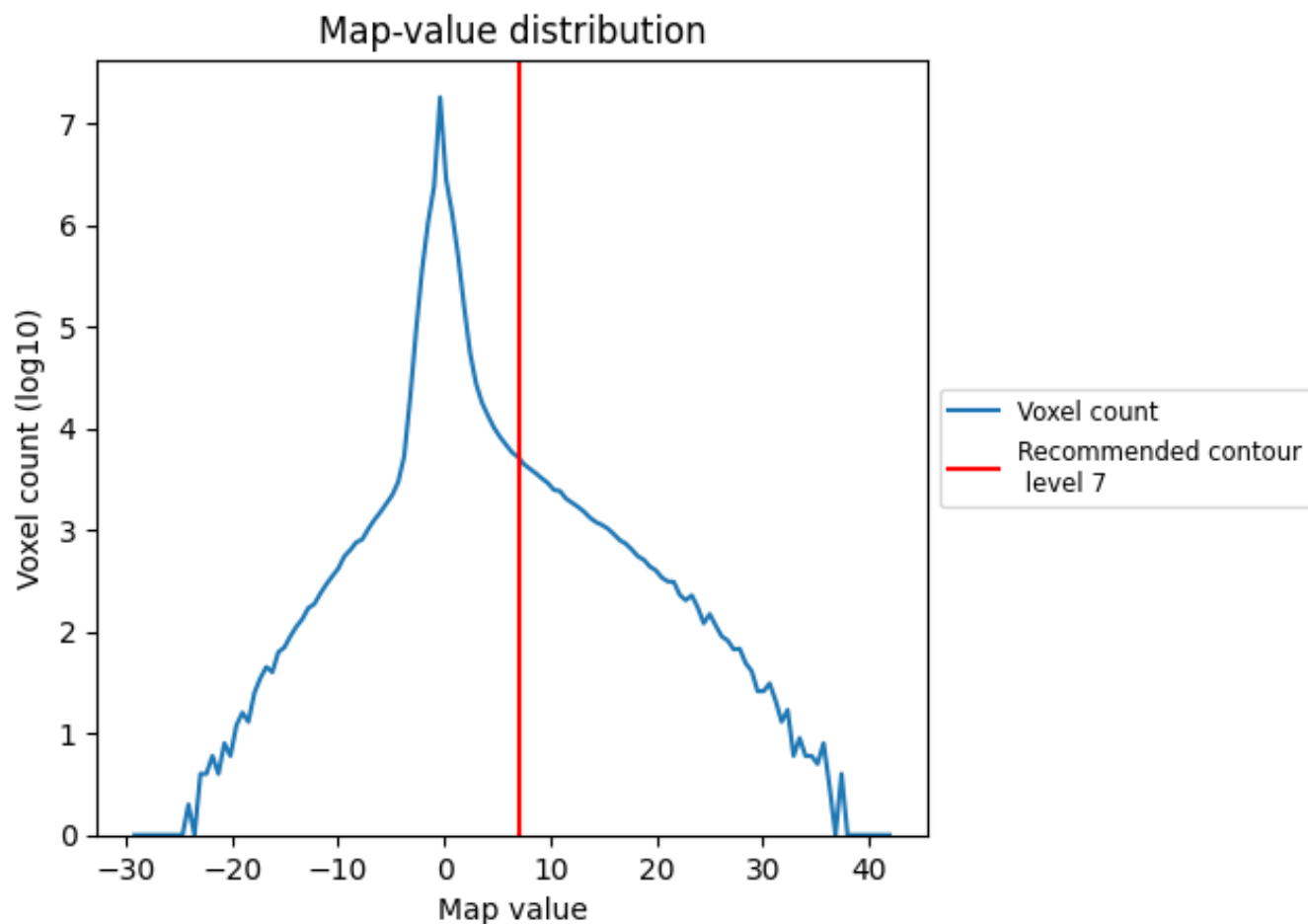
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

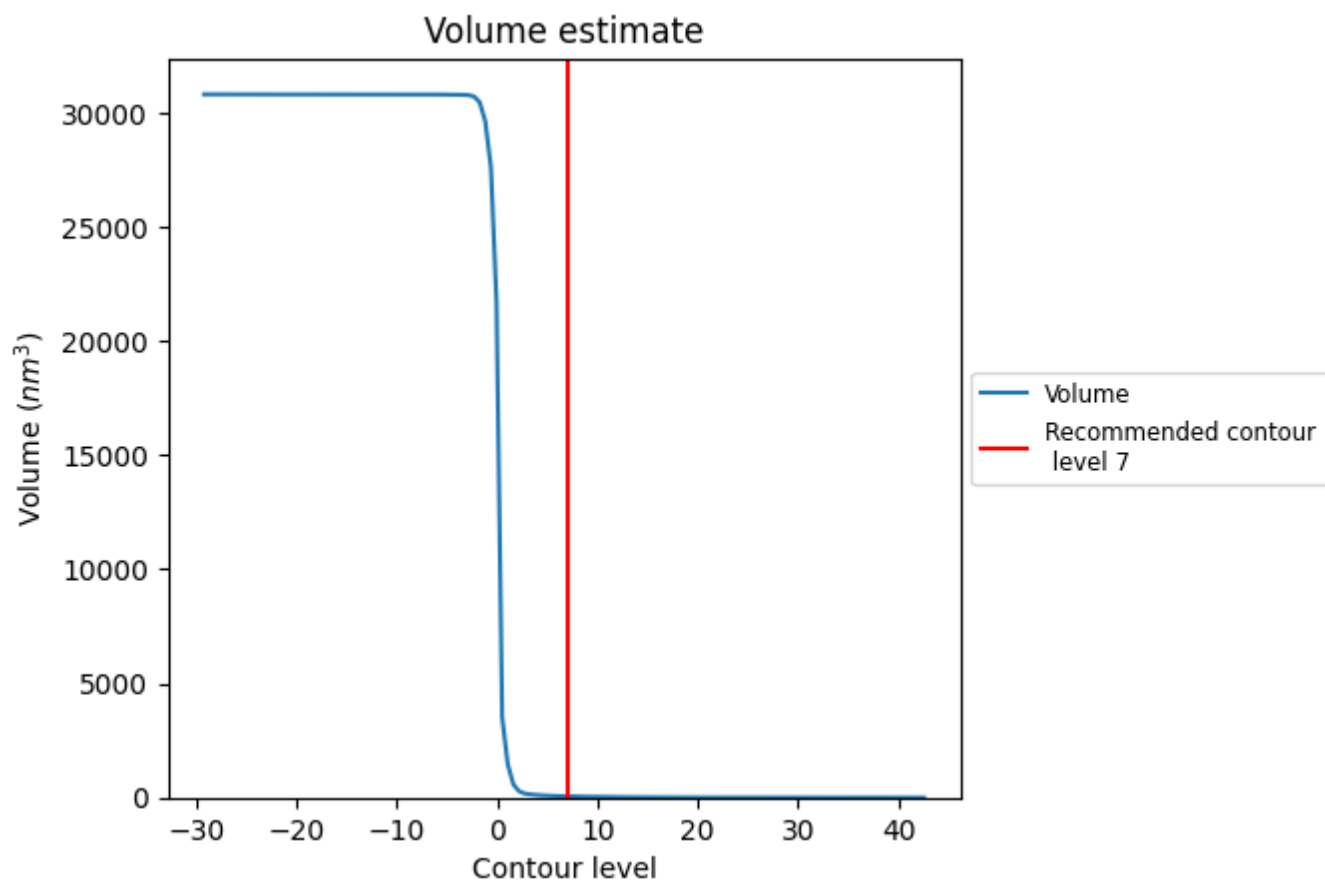
This section contains the results of statistical analysis of the map.

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.

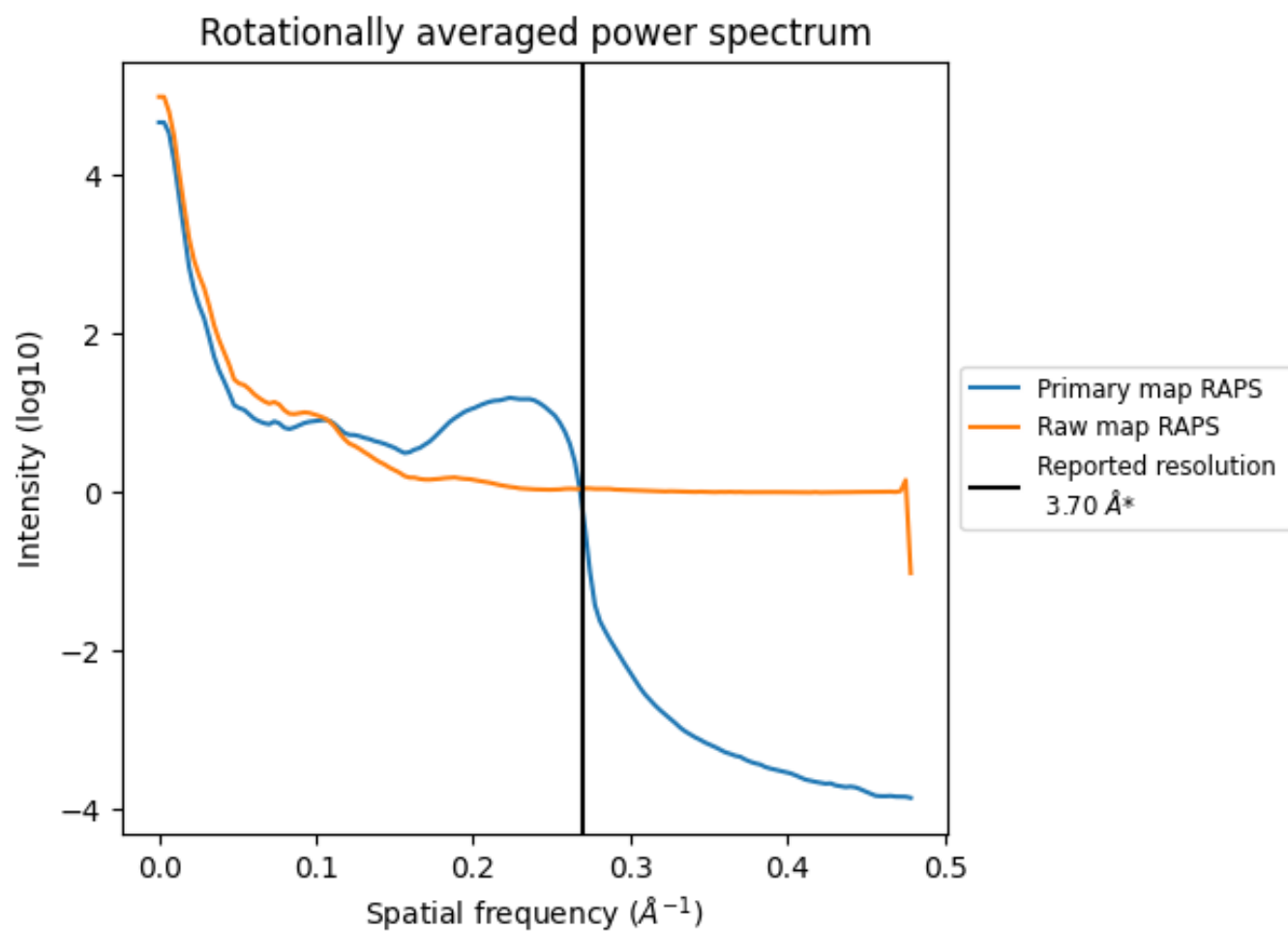
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 54 nm^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 ⓘ

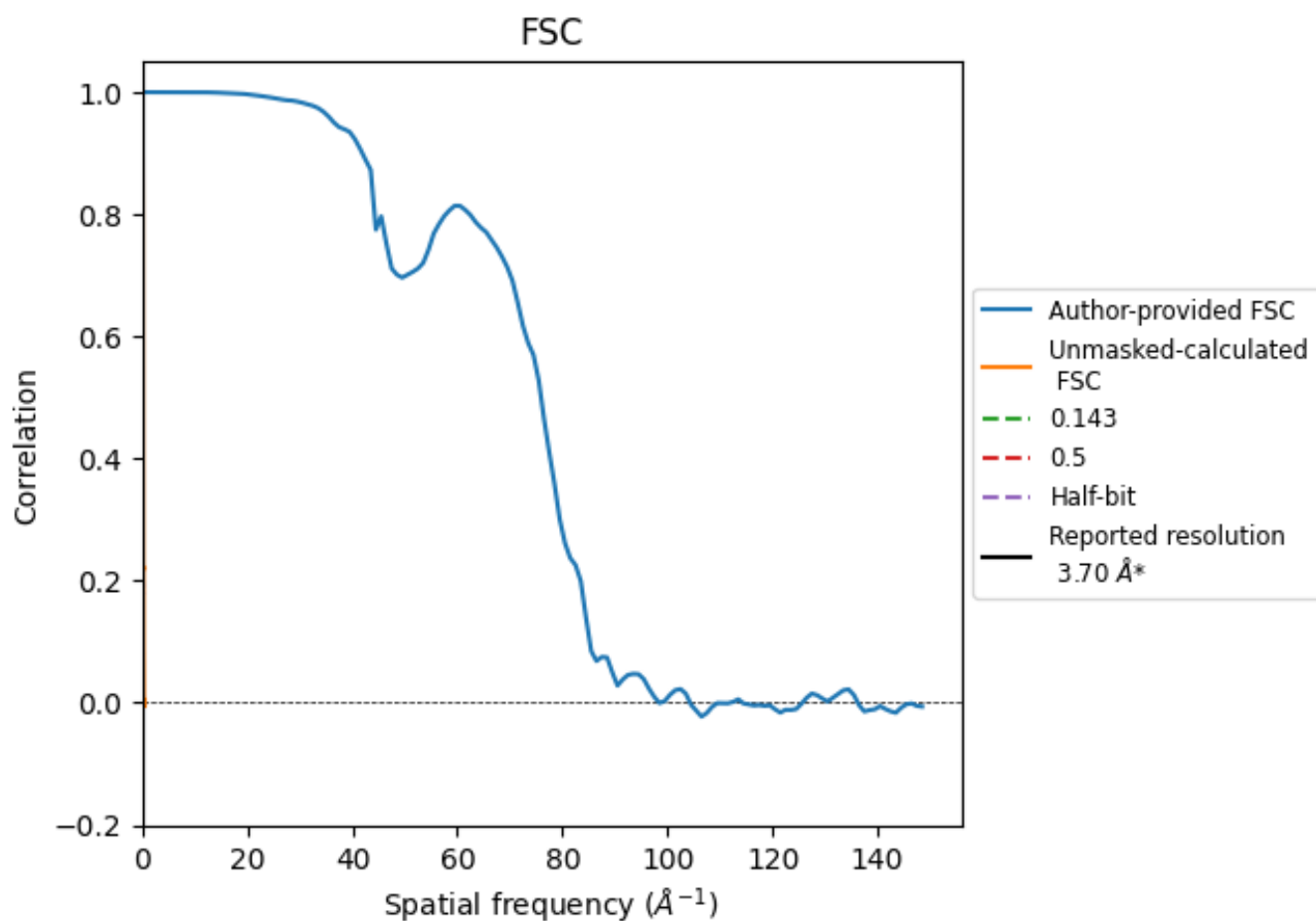


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	0.01	0.01	0.01
Unmasked-calculated*	4.72	7.42	4.88

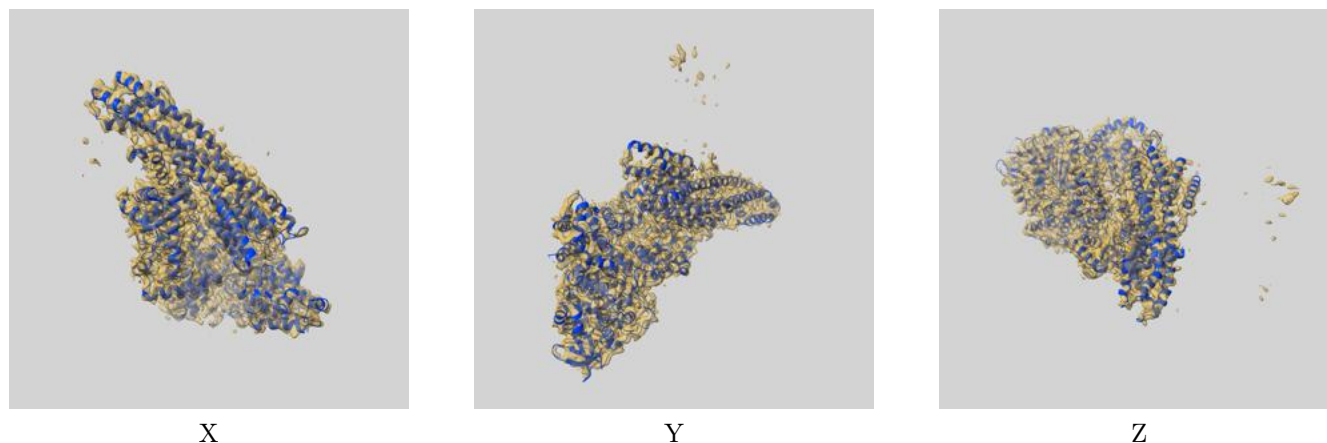
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 0.01 differs from the reported value 3.7 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.72 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

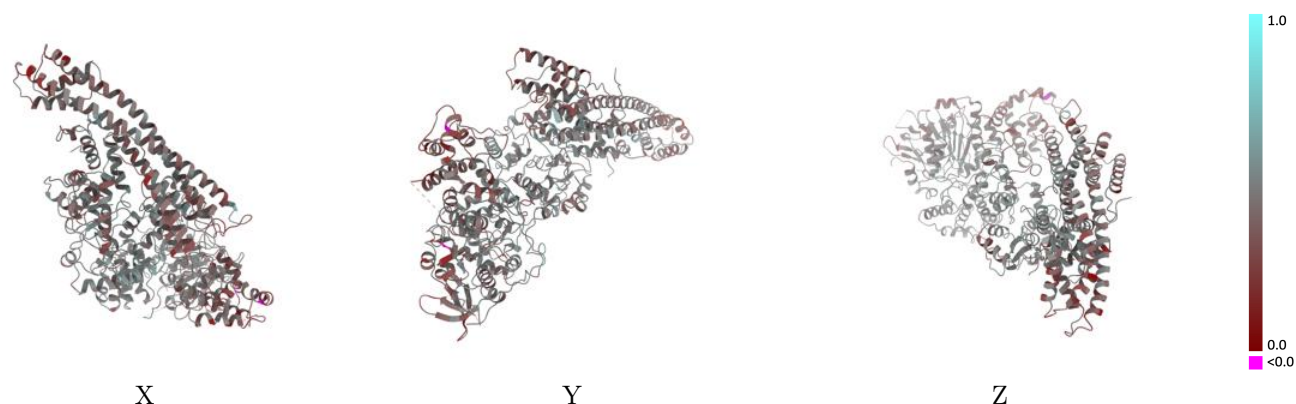
This section contains information regarding the fit between EMDB map EMD-10350 and PDB model 6SZ9. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



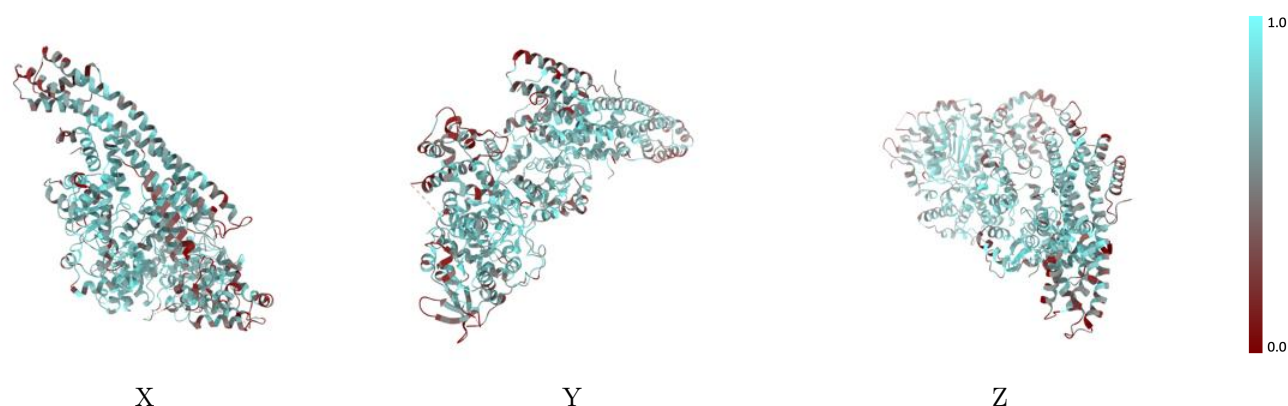
The images above show the 3D surface view of the map at the recommended contour level 7.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



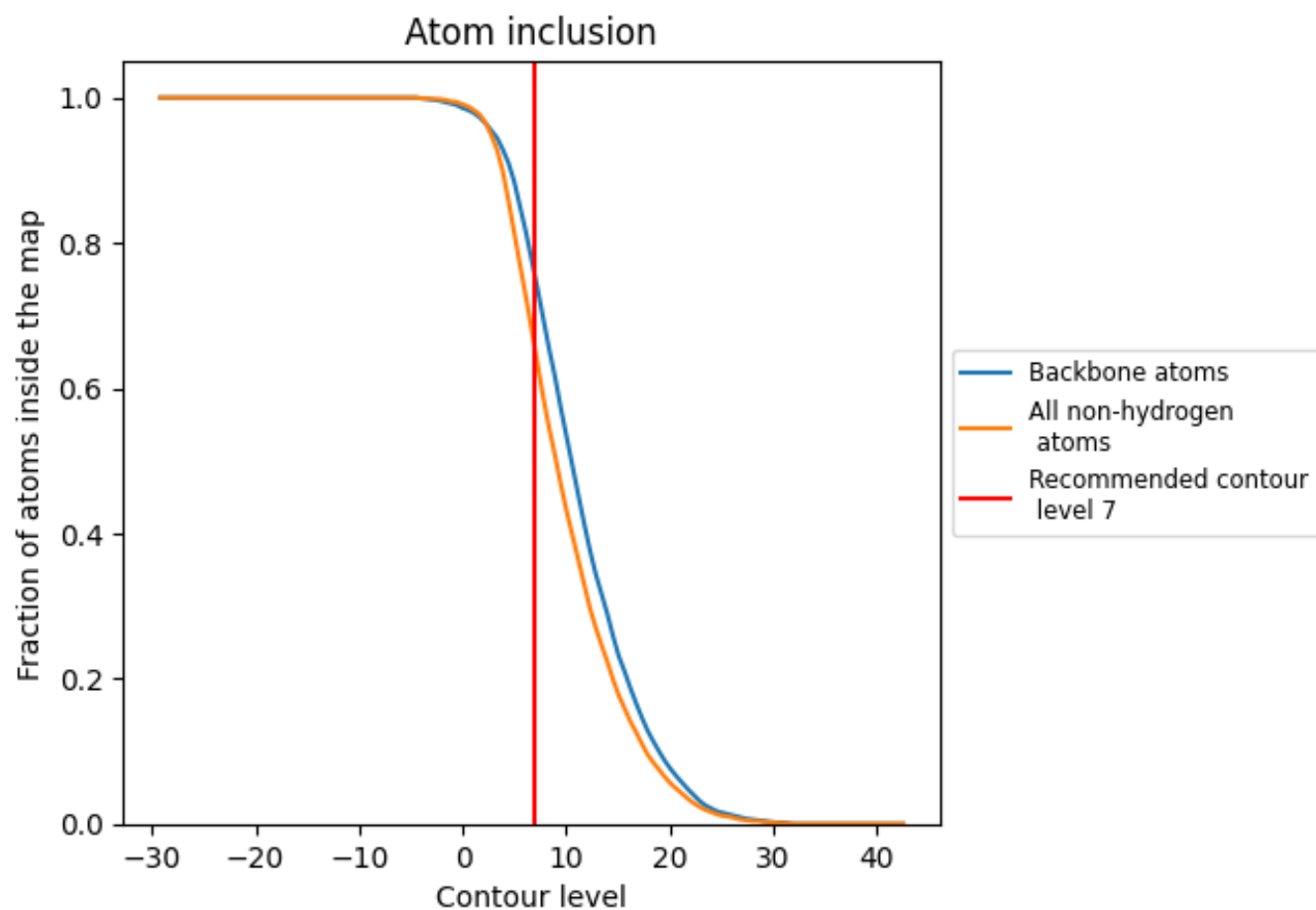
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (7).

9.4 Atom inclusion ⓘ



At the recommended contour level, 75% of all backbone atoms, 65% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6520	0.4390
A	0.6200	0.4220
B	0.7300	0.4770
C	0.7410	0.4690
D	0.6070	0.4190
E	0.5140	0.4020

