Full wwPDB EM Validation Report ⓘ

Nov 14, 2022 – 02:12 AM EST

PDB ID	:	7KAS
EMDB ID	:	EMD-22782
Title	:	Cryo-EM structure of the Sec complex from S. cerevisiae, Sec63 FN3 mutant, class with Sec62
Authors	:	Itskanov, S.; Park, E.
Deposited on	:	2020-10-01
Resolution	:	3.90 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:

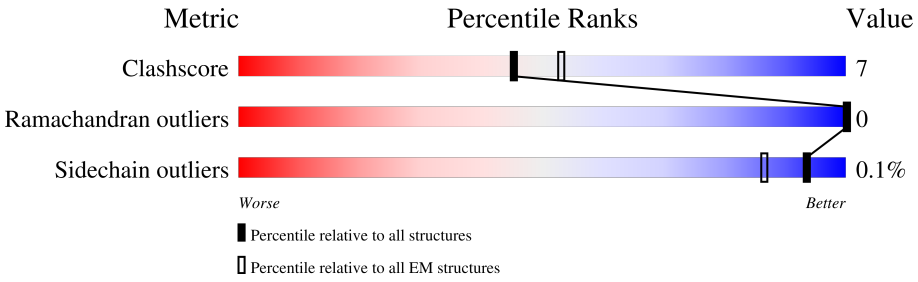
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	480	16% 71% 19% 10%
2	C	80	60% 9% 31%
3	B	82	34% 5% 61%
4	D	676	5% 61% 11% 28%
5	E	206	57% 10% 33%
6	F	193	78% 21%
7	G	56	91% 100%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 10616 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 Protein transport protein SEC61.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	430	3268	2161	523	570	14	0	0

- Molecule 2 is a protein called Protein transport protein SSS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	55	435	294	71	69	1	0	0

- Molecule 3 is a protein called Protein transport protein SBH1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	B	32	229	157	38	34	0	0

- Molecule 4 is a protein called Protein translocation protein SEC63.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	484	3804	2479	647	664	14	0	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-13	GLY	-	expression tag	UNP P14906
D	-12	GLY	-	expression tag	UNP P14906
D	-11	SER	-	expression tag	UNP P14906
D	-10	GLY	-	expression tag	UNP P14906
D	-9	GLY	-	expression tag	UNP P14906
D	-8	SER	-	expression tag	UNP P14906
D	-7	GLY	-	expression tag	UNP P14906
D	-6	GLY	-	expression tag	UNP P14906
D	-5	SER	-	expression tag	UNP P14906

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-4	GLY	-	expression tag	UNP P14906
D	-3	GLY	-	expression tag	UNP P14906
D	-2	SER	-	expression tag	UNP P14906
D	-1	GLY	-	expression tag	UNP P14906
D	0	GLY	-	expression tag	UNP P14906
D	1	SER	-	expression tag	UNP P14906
D	440	ARG	GLU	engineered mutation	UNP P14906
D	?	-	ASN	deletion	UNP P14906
D	?	-	GLN	deletion	UNP P14906
D	?	-	VAL	deletion	UNP P14906
D	?	-	THR	deletion	UNP P14906
D	?	-	PRO	deletion	UNP P14906
D	?	-	SER	deletion	UNP P14906
D	?	-	SER	deletion	UNP P14906
D	?	-	THR	deletion	UNP P14906
D	481	SER	PHE	engineered mutation	UNP P14906
D	664	GLY	-	expression tag	UNP P14906
D	665	GLU	-	expression tag	UNP P14906
D	666	ASN	-	expression tag	UNP P14906
D	667	LEU	-	expression tag	UNP P14906
D	668	TYR	-	expression tag	UNP P14906
D	669	PHE	-	expression tag	UNP P14906
D	670	GLN	-	expression tag	UNP P14906

- Molecule 5 is a protein called Translocation protein SEC66.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	138	Total	C	N	O	S	0	0
			1129	722	200	202	5		

- Molecule 6 is a protein called Translocation protein SEC72.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	190	Total	C	N	O	S	0	0
			1471	934	256	274	7		

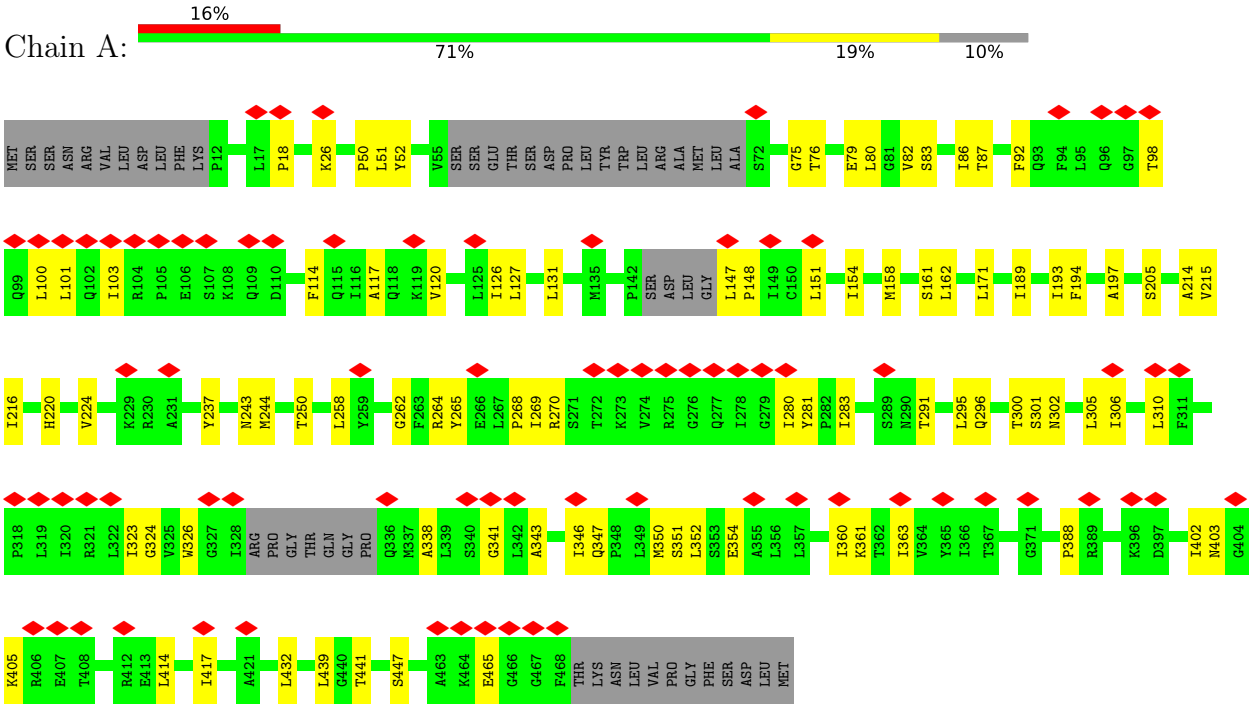
- Molecule 7 is a protein called Protein transport protein SEC62.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	G	56	Total	C	N	O	0	0
			280	168	56	56		

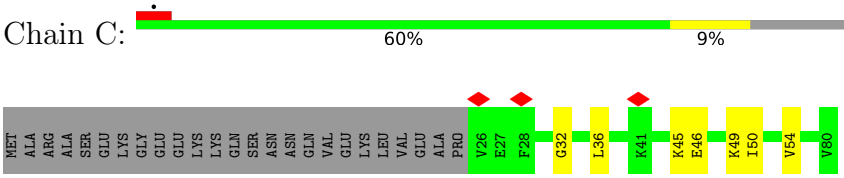
3 Residue-property plots (i)

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.

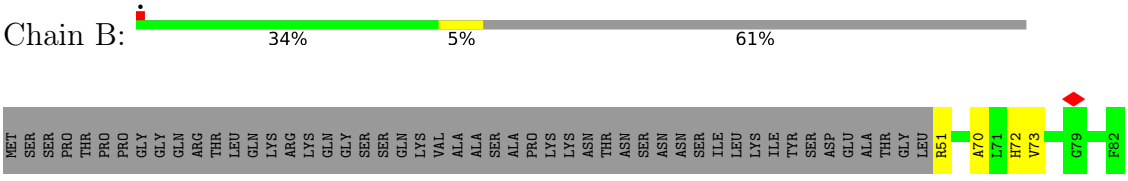
• Molecule 1: Protein transport protein SEC61



• Molecule 2: Protein transport protein SSS1

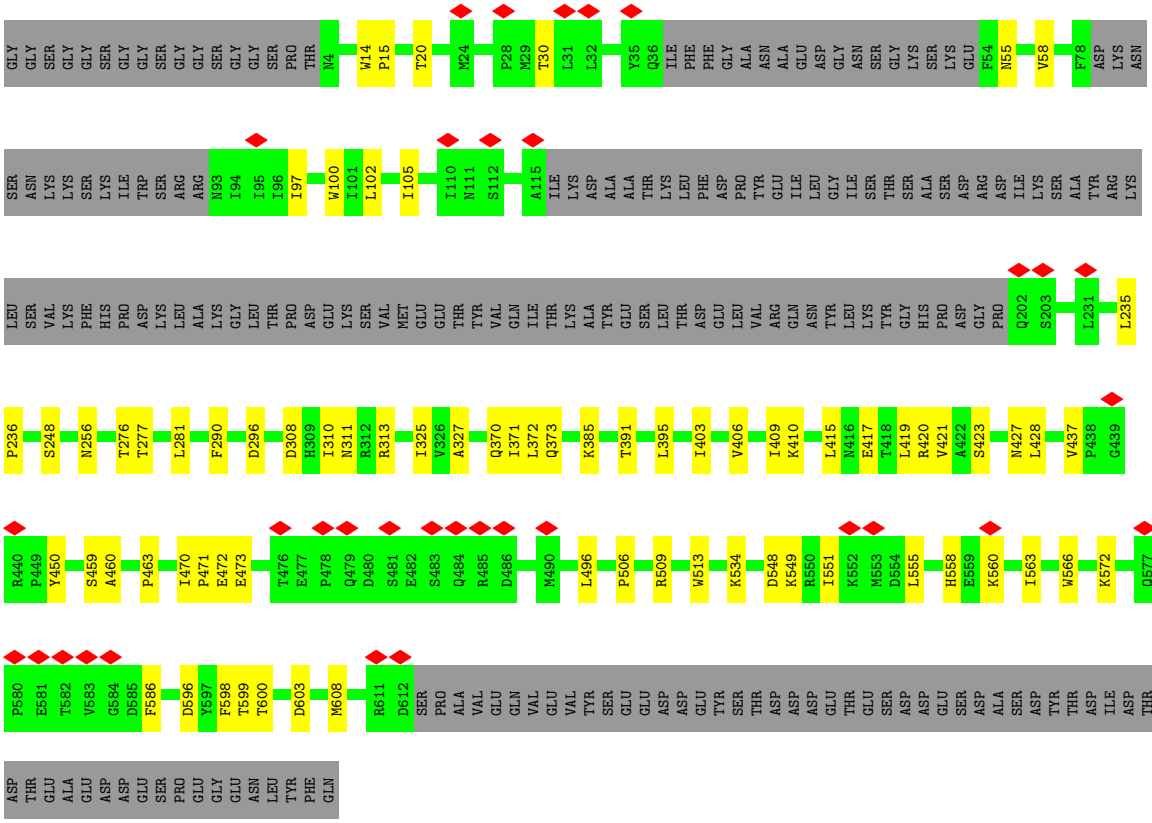


• Molecule 3: Protein transport protein SBH1



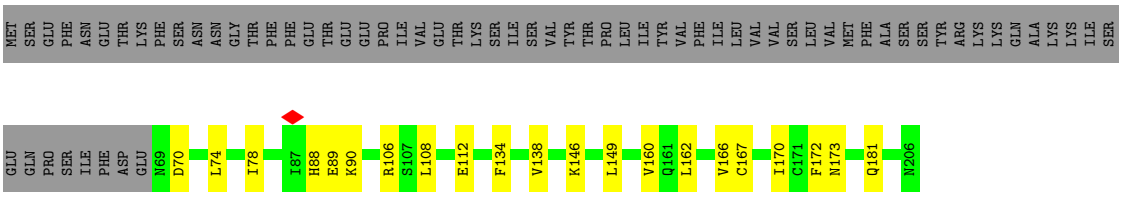
• Molecule 4: Protein translocation protein SEC63

Chain D:



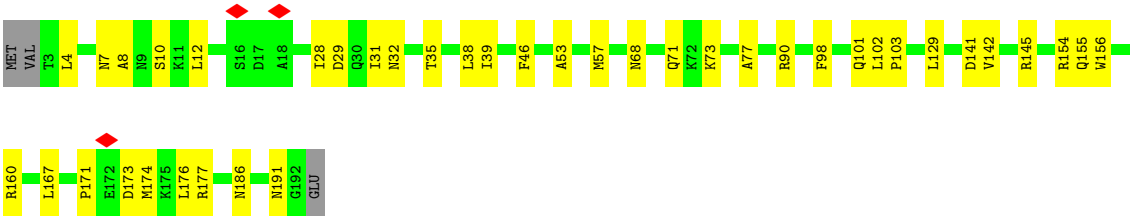
• Molecule 5: Translocation protein SEC66

Chain E:



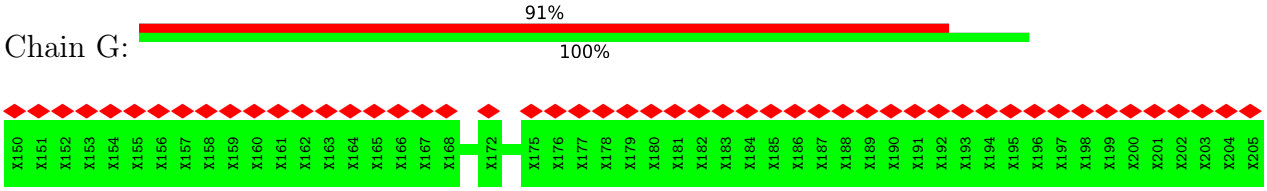
• Molecule 6: Translocation protein SEC72

Chain F:



• Molecule 7: Protein transport protein SEC62

Chain G:


91%
100%
X150 X151 X152 X153 X154 X155 X156 X157 X158 X159 X160 X161 X162 X163 X164 X165 X166 X167 X168 X172 X175 X176 X177 X178 X179 X180 X181 X182 X183 X184 X185 X186 X187 X188 X189 X190 X191 X192 X193 X194 X195 X196 X197 X198 X199 X200 X201 X202 X203 X204 X205

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	119420	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 ($e^-/Å^2$)	49.1	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	42017	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.724	Depositor
Minimum map value	-0.695	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.052	Depositor
Recommended contour level	0.375	Depositor
Map size (Å)	304.64, 304.64, 304.64	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.19, 1.19, 1.19	Depositor

5 Model quality

5.1 Standard geometry

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	0.27	0/3334	0.43	0/4527
2	C	0.32	0/443	0.40	0/596
3	B	0.32	0/233	0.39	0/318
4	D	0.29	0/3893	0.44	0/5288
5	E	0.29	0/1147	0.41	0/1540
6	F	0.26	0/1491	0.43	0/2018
All	All	0.28	0/10541	0.43	0/14287

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

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	3268	0	3391	56	0
2	C	435	0	481	4	0
3	B	229	0	243	4	0
4	D	3804	0	3850	46	0
5	E	1129	0	1145	18	0
6	F	1471	0	1512	31	0
7	G	280	0	59	0	0
All	All	10616	0	10681	143	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 7.

All (143) 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)
5:E:90:LYS:HD2	6:F:39:ILE:HD13	1.67	0.74
5:E:70:ASP:HB3	5:E:106:ARG:HH22	1.54	0.70
4:D:55:ASN:ND2	4:D:496:LEU:O	2.25	0.69
1:A:326:TRP:HA	1:A:338:ALA:HA	1.76	0.67
1:A:310:LEU:HD11	1:A:323:ILE:HD11	1.77	0.66
4:D:371:ILE:HD11	4:D:395:LEU:HD13	1.79	0.65
6:F:171:PRO:O	6:F:177:ARG:NH1	2.29	0.65
4:D:281:LEU:HD11	4:D:310:ILE:HD12	1.78	0.64
5:E:181:GLN:HE22	6:F:90:ARG:HH12	1.45	0.63
1:A:237:TYR:O	1:A:243:ASN:ND2	2.27	0.61
6:F:154:ARG:O	6:F:155:GLN:NE2	2.33	0.61
1:A:265:TYR:HB3	1:A:283:ILE:HB	1.82	0.61
4:D:463:PRO:HG3	4:D:549:LYS:HA	1.82	0.61
4:D:403:ILE:HG21	4:D:419:LEU:HD21	1.83	0.60
6:F:35:THR:O	6:F:39:ILE:HG12	2.02	0.60
4:D:311:ASN:HD22	4:D:313:ARG:HH22	1.50	0.59
1:A:26:LYS:NZ	1:A:465:GLU:OE1	2.35	0.59
1:A:324:GLY:HA2	1:A:341:GLY:HA3	1.84	0.59
4:D:102:LEU:HA	4:D:105:ILE:HD12	1.85	0.59
5:E:134:PHE:O	5:E:138:VAL:HG23	2.02	0.59
1:A:18:PRO:HA	3:B:51:ARG:HE	1.66	0.58
6:F:28:ILE:O	6:F:32:ASN:ND2	2.37	0.58
6:F:7:ASN:OD1	6:F:8:ALA:N	2.34	0.57
1:A:75:GLY:N	1:A:79:GLU:OE2	2.36	0.57
1:A:414:LEU:HA	1:A:417:ILE:HG22	1.85	0.57
4:D:427:ASN:HD22	4:D:600:THR:H	1.53	0.57
6:F:141:ASP:O	6:F:145:ARG:NH2	2.37	0.57
5:E:173:ASN:ND2	6:F:101:GLN:OE1	2.33	0.57
4:D:509:ARG:NH1	4:D:596:ASP:OD1	2.37	0.57
5:E:78:ILE:HD11	6:F:4:LEU:HD11	1.85	0.56
1:A:98:THR:HG23	1:A:100:LEU:HD13	1.86	0.56
4:D:370:GLN:NE2	4:D:598:PHE:O	2.37	0.56
1:A:343:ALA:HA	1:A:346:ILE:HG12	1.88	0.56
6:F:12:LEU:HD23	6:F:32:ASN:HB3	1.88	0.56
1:A:83:SER:HA	1:A:86:ILE:HD12	1.87	0.56
4:D:548:ASP:OD1	4:D:549:LYS:N	2.39	0.56
4:D:427:ASN:ND2	4:D:599:THR:OG1	2.39	0.56
4:D:603:ASP:HB2	6:F:160:ARG:HH12	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:SER:O	1:A:87:THR:HG23	2.06	0.55
4:D:296:ASP:OD1	4:D:296:ASP:N	2.35	0.55
6:F:102:LEU:HB3	6:F:103:PRO:HD3	1.90	0.54
4:D:248:SER:O	4:D:256:ASN:ND2	2.41	0.54
5:E:149:LEU:HD11	5:E:160:VAL:HG13	1.89	0.54
4:D:308:ASP:OD1	4:D:313:ARG:NH1	2.34	0.54
1:A:117:ALA:HA	1:A:120:VAL:HG12	1.89	0.53
1:A:265:TYR:O	1:A:283:ILE:N	2.36	0.53
4:D:276:THR:HG22	4:D:277:THR:H	1.73	0.53
1:A:52:TYR:HA	3:B:72:HIS:HE2	1.75	0.52
4:D:385:LYS:HZ1	4:D:406:VAL:HA	1.74	0.52
4:D:30:THR:HG21	4:D:100:TRP:HE1	1.75	0.52
2:C:46:GLU:O	2:C:50:ILE:HG12	2.10	0.51
4:D:450:TYR:HE2	4:D:572:LYS:HD3	1.74	0.51
6:F:129:LEU:HD22	6:F:142:VAL:HG13	1.92	0.51
4:D:417:GLU:O	4:D:421:VAL:HG23	2.11	0.51
6:F:173:ASP:OD1	6:F:174:MET:N	2.44	0.51
6:F:68:ASN:HB2	6:F:77:ALA:HB2	1.93	0.50
4:D:496:LEU:HD23	4:D:534:LYS:HG2	1.94	0.50
1:A:360:ILE:HG13	1:A:361:LYS:N	2.27	0.49
1:A:268:PRO:HA	1:A:280:ILE:HD13	1.94	0.49
1:A:296:GLN:O	1:A:300:THR:HG23	2.12	0.49
4:D:558:HIS:CD2	4:D:560:LYS:H	2.30	0.49
1:A:82:VAL:O	1:A:86:ILE:HG13	2.12	0.49
2:C:32:GLY:O	2:C:36:LEU:HG	2.13	0.49
6:F:71:GLN:OE1	6:F:73:LYS:HB2	2.13	0.48
4:D:97:ILE:H	4:D:97:ILE:HD12	1.78	0.48
4:D:470:ILE:HG22	4:D:472:GLU:H	1.79	0.48
1:A:197:ALA:O	1:A:214:ALA:N	2.33	0.48
6:F:156:TRP:CD1	6:F:186:ASN:HB3	2.49	0.48
1:A:302:ASN:O	1:A:306:ILE:HG12	2.13	0.48
1:A:50:PRO:HA	1:A:76:THR:HA	1.94	0.48
1:A:51:LEU:O	3:B:72:HIS:NE2	2.45	0.48
1:A:270:ARG:HE	1:A:403:ASN:HA	1.78	0.47
4:D:370:GLN:OE1	4:D:391:THR:OG1	2.16	0.47
1:A:82:VAL:HG23	1:A:86:ILE:HD11	1.97	0.47
1:A:291:THR:O	1:A:295:LEU:HG	2.15	0.47
4:D:423:SER:O	4:D:423:SER:OG	2.29	0.47
4:D:391:THR:HG21	6:F:191:ASN:HA	1.97	0.46
5:E:108:LEU:O	5:E:112:GLU:HG2	2.15	0.46
5:E:88:HIS:CD2	5:E:89:GLU:H	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:74:LEU:O	5:E:78:ILE:HG12	2.15	0.46
5:E:90:LYS:HD3	6:F:38:LEU:HB3	1.97	0.46
5:E:166:VAL:HG21	6:F:46:PHE:HE1	1.80	0.46
2:C:45:LYS:O	2:C:49:LYS:NZ	2.49	0.46
1:A:262:GLY:O	1:A:264:ARG:NH1	2.49	0.46
1:A:351:SER:OG	1:A:352:LEU:N	2.49	0.45
6:F:167:LEU:HG	6:F:176:LEU:HB3	1.98	0.45
1:A:126:ILE:HD13	1:A:161:SER:OG	2.16	0.45
1:A:301:SER:O	1:A:305:LEU:HG	2.15	0.45
6:F:29:ASP:HA	6:F:32:ASN:HD22	1.81	0.45
1:A:258:LEU:HD11	2:C:54:VAL:HG21	1.98	0.45
4:D:58:VAL:HB	4:D:420:ARG:NH2	2.32	0.45
5:E:146:LYS:HA	5:E:146:LYS:HD2	1.86	0.45
4:D:327:ALA:HB2	4:D:506:PRO:HG2	1.99	0.44
5:E:167:CYS:HA	5:E:170:ILE:HG12	1.99	0.44
1:A:189:ILE:HG12	1:A:447:SER:HB3	1.98	0.44
1:A:250:THR:HB	1:A:441:THR:HB	1.99	0.44
1:A:402:ILE:HB	1:A:405:LYS:HB3	1.99	0.44
6:F:53:ALA:O	6:F:57:MET:HG2	2.17	0.44
1:A:439:LEU:HD23	1:A:439:LEU:HA	1.87	0.44
4:D:235:LEU:HB3	4:D:236:PRO:HD3	1.99	0.44
5:E:70:ASP:N	5:E:70:ASP:OD1	2.49	0.44
4:D:409:ILE:HD11	4:D:415:LEU:HD13	2.00	0.43
4:D:14:TRP:CG	4:D:15:PRO:HD3	2.53	0.43
1:A:220:HIS:O	1:A:224:VAL:HG12	2.18	0.43
1:A:216:ILE:HD13	4:D:20:THR:HG21	2.01	0.43
4:D:428:LEU:HD11	4:D:513:TRP:CZ3	2.53	0.43
4:D:551:ILE:HB	4:D:555:LEU:HD11	1.99	0.43
1:A:101:LEU:HD22	1:A:103:ILE:HG13	2.01	0.42
1:A:193:ILE:HD13	1:A:193:ILE:HA	1.89	0.42
1:A:92:PHE:HB3	1:A:114:PHE:CZ	2.55	0.42
1:A:432:LEU:HD23	1:A:432:LEU:HA	1.84	0.42
1:A:171:LEU:HD23	1:A:171:LEU:HA	1.93	0.42
3:B:70:ALA:HA	3:B:73:VAL:HG12	2.01	0.42
1:A:205:SER:O	1:A:205:SER:OG	2.33	0.42
6:F:38:LEU:HD23	6:F:38:LEU:HA	1.91	0.42
1:A:269:ILE:HG13	1:A:281:TYR:HB2	2.02	0.42
6:F:31:ILE:O	6:F:35:THR:HG22	2.20	0.42
4:D:290:PHE:CD1	4:D:325:ILE:HG22	2.55	0.42
6:F:10:SER:O	6:F:12:LEU:HD12	2.19	0.42
1:A:343:ALA:O	1:A:347:GLN:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:215:VAL:HA	1:A:244:MET:HE1	2.01	0.41
4:D:586:PHE:HB2	4:D:608:MET:HG3	2.00	0.41
1:A:360:ILE:HA	1:A:363:ILE:HG22	2.02	0.41
4:D:409:ILE:HG13	4:D:410:LYS:N	2.34	0.41
5:E:162:LEU:HD21	6:F:46:PHE:O	2.20	0.41
1:A:80:LEU:HD22	1:A:126:ILE:HG23	2.02	0.41
4:D:373:GLN:OE1	4:D:598:PHE:HB2	2.20	0.41
6:F:129:LEU:HD23	6:F:129:LEU:HA	1.90	0.41
1:A:388:PRO:HB3	1:A:414:LEU:HB3	2.03	0.41
5:E:172:PHE:HB3	6:F:98:PHE:CE2	2.55	0.41
1:A:147:LEU:HB3	1:A:148:PRO:HD3	2.02	0.41
4:D:372:LEU:HD23	4:D:372:LEU:HA	1.92	0.41
1:A:151:LEU:O	1:A:154:ILE:HG22	2.21	0.41
4:D:459:SER:OG	4:D:460:ALA:N	2.53	0.41
4:D:471:PRO:HB2	4:D:473:GLU:HG2	2.03	0.41
1:A:162:LEU:HA	1:A:162:LEU:HD12	1.86	0.41
4:D:558:HIS:HD2	4:D:560:LYS:H	1.67	0.41
1:A:350:MET:HB2	1:A:354:GLU:OE2	2.21	0.40
4:D:437:VAL:HG13	4:D:437:VAL:O	2.20	0.40
4:D:563:ILE:HD12	4:D:566:TRP:CD1	2.56	0.40
5:E:181:GLN:NE2	6:F:90:ARG:HH22	2.19	0.40
1:A:131:LEU:HD12	1:A:131:LEU:HA	1.92	0.40
1:A:127:LEU:HA	1:A:158:MET:HE1	2.02	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	422/480 (88%)	407 (96%)	15 (4%)	0	100	100
2	C	53/80 (66%)	52 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	B	30/82 (37%)	30 (100%)	0	0	100	100
4	D	476/676 (70%)	449 (94%)	27 (6%)	0	100	100
5	E	136/206 (66%)	133 (98%)	3 (2%)	0	100	100
6	F	188/193 (97%)	183 (97%)	5 (3%)	0	100	100
All	All	1305/1717 (76%)	1254 (96%)	51 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	343/406 (84%)	342 (100%)	1 (0%)	92	95
2	C	46/67 (69%)	46 (100%)	0	100	100
3	B	23/69 (33%)	23 (100%)	0	100	100
4	D	414/603 (69%)	414 (100%)	0	100	100
5	E	120/191 (63%)	120 (100%)	0	100	100
6	F	157/165 (95%)	157 (100%)	0	100	100
All	All	1103/1501 (74%)	1102 (100%)	1 (0%)	93	97

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	194	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	403	ASN
4	D	307	GLN
4	D	311	ASN

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Mol	Chain	Res	Type
4	D	424	HIS
4	D	427	ASN
4	D	539	ASN
4	D	558	HIS
5	E	88	HIS
5	E	181	GLN
6	F	32	ASN
6	F	68	ASN
6	F	155	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 monosaccharides 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.

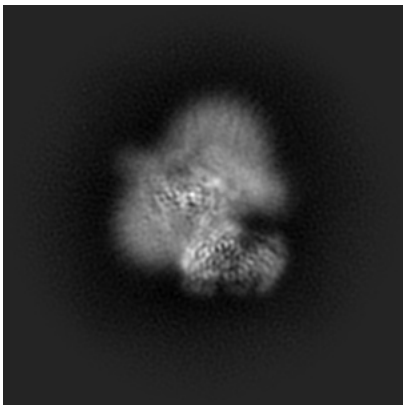
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-22782. These allow visual inspection of the internal detail of the map and identification of artifacts.

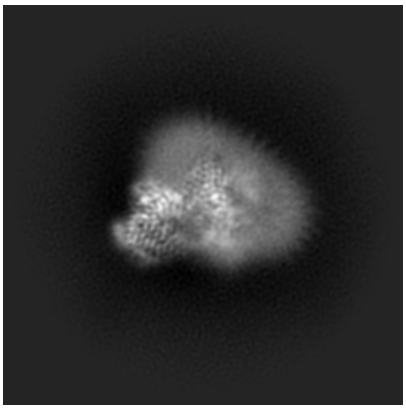
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

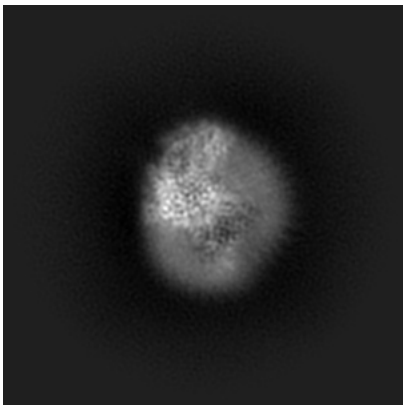
6.1.1 Primary map



X

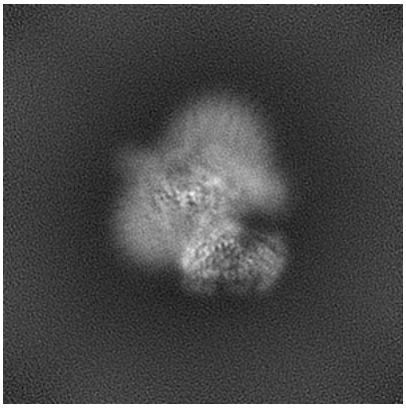


Y

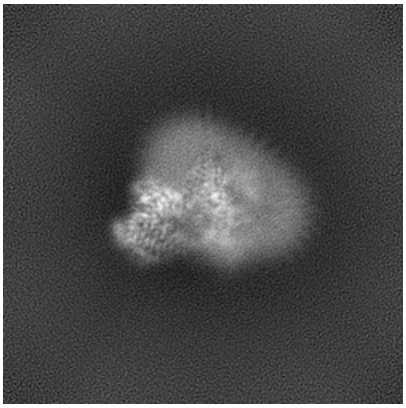


Z

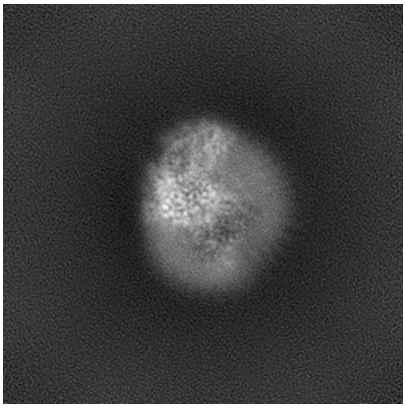
6.1.2 Raw map



X



Y

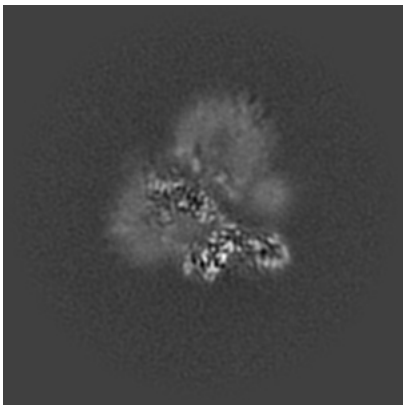


Z

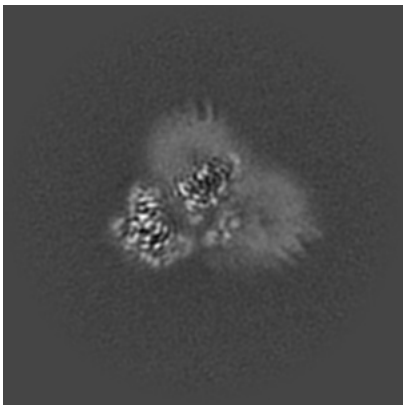
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

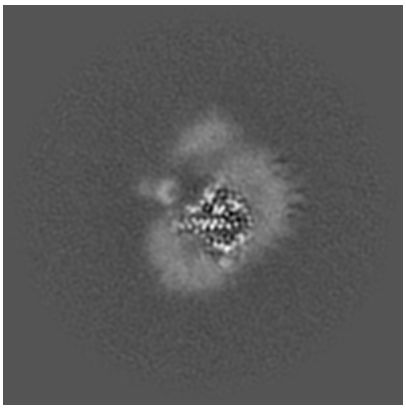
6.2.1 Primary map



X Index: 128

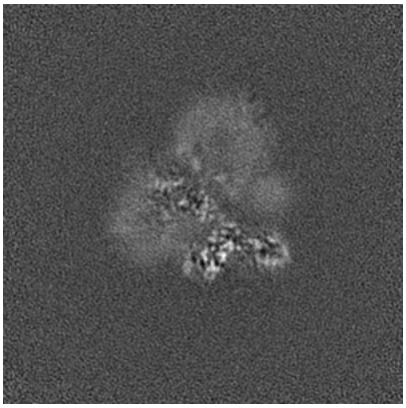


Y Index: 128

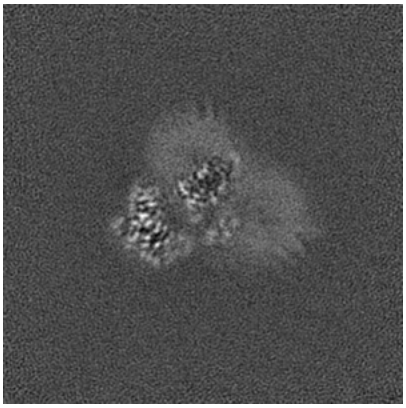


Z Index: 128

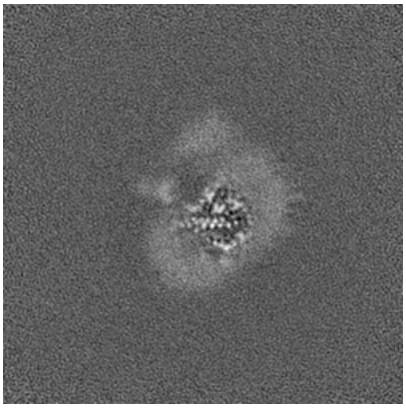
6.2.2 Raw map



X Index: 128



Y Index: 128

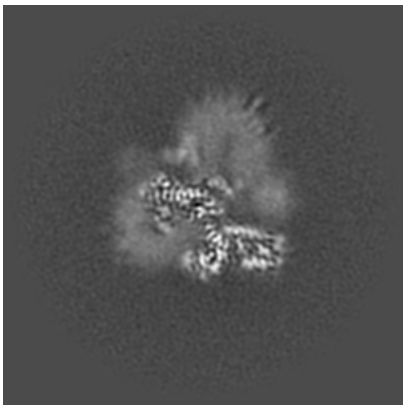


Z Index: 128

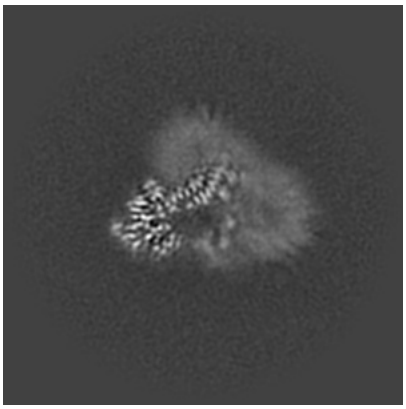
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

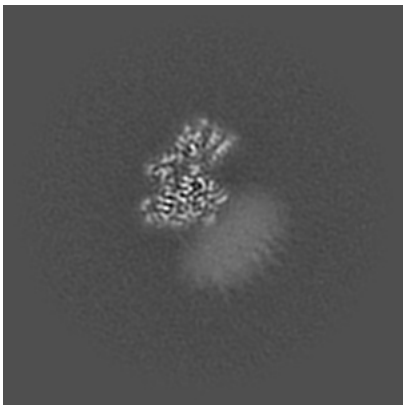
6.3.1 Primary map



X Index: 132

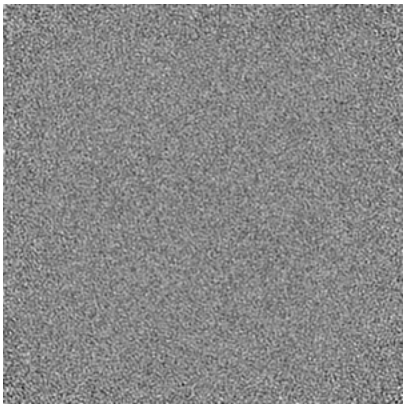


Y Index: 133

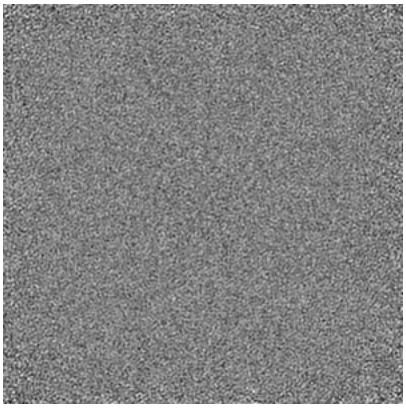


Z Index: 96

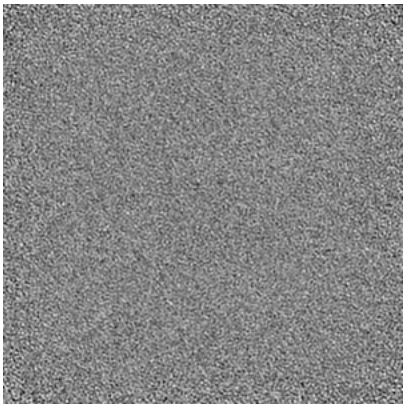
6.3.2 Raw map



X Index: 0



Y Index: 0



Z Index: 0

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

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.375. 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

X Y Z

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.

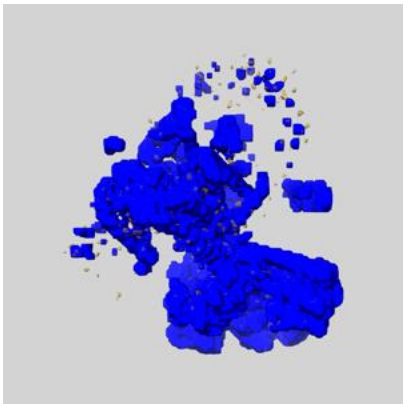
6.5 Mask visualisation (i)

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

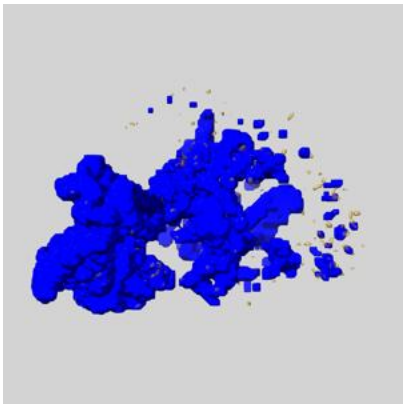
A mask typically either:

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

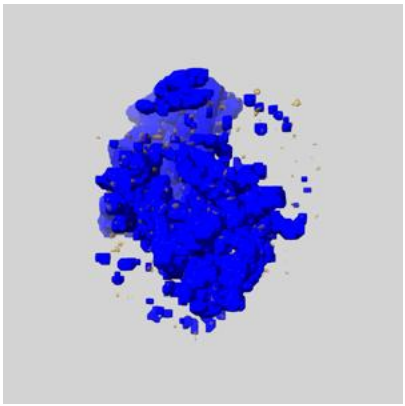
6.5.1 emd_22782_msk_1.map (i)



X



Y

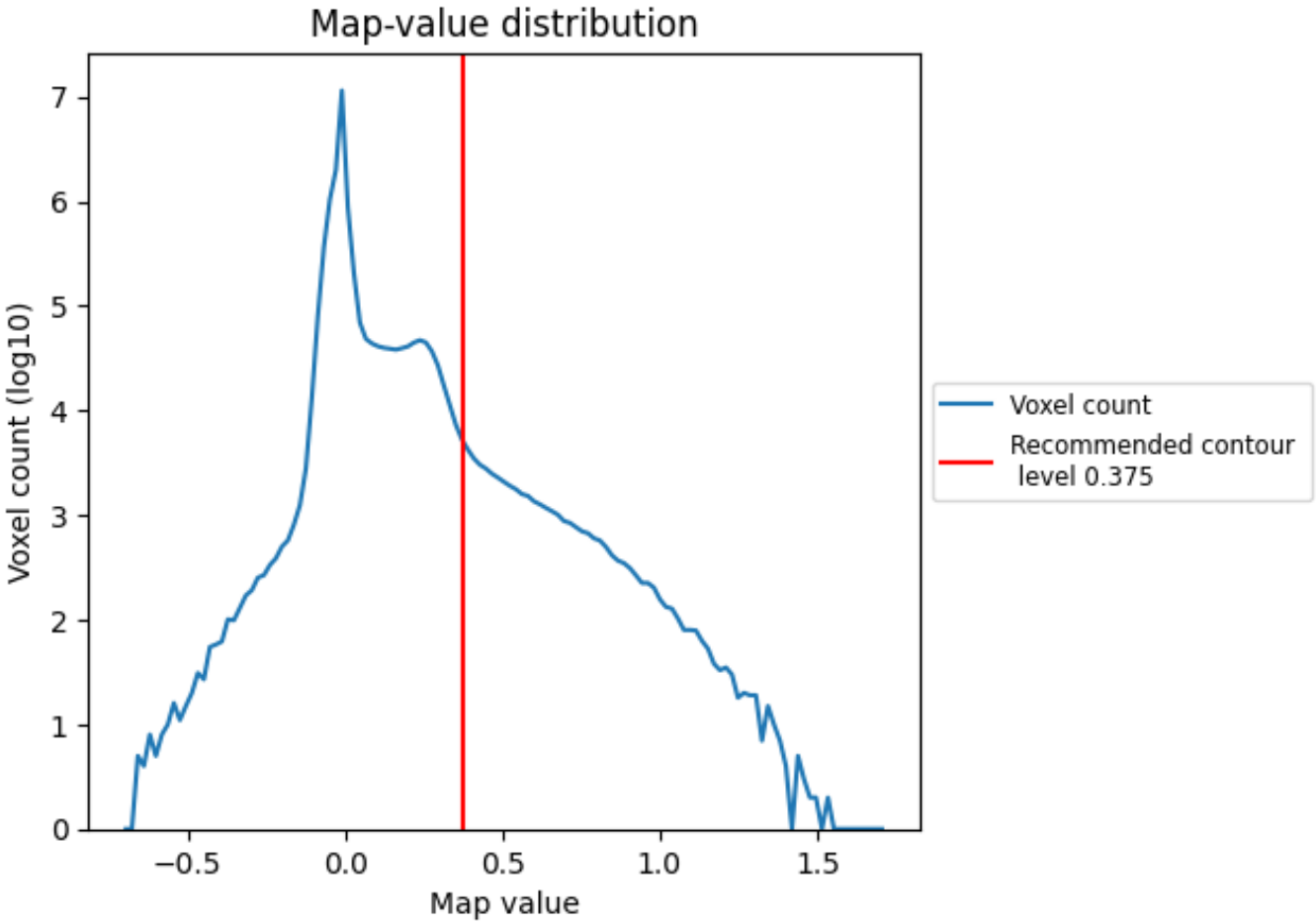


Z

7 Map analysis

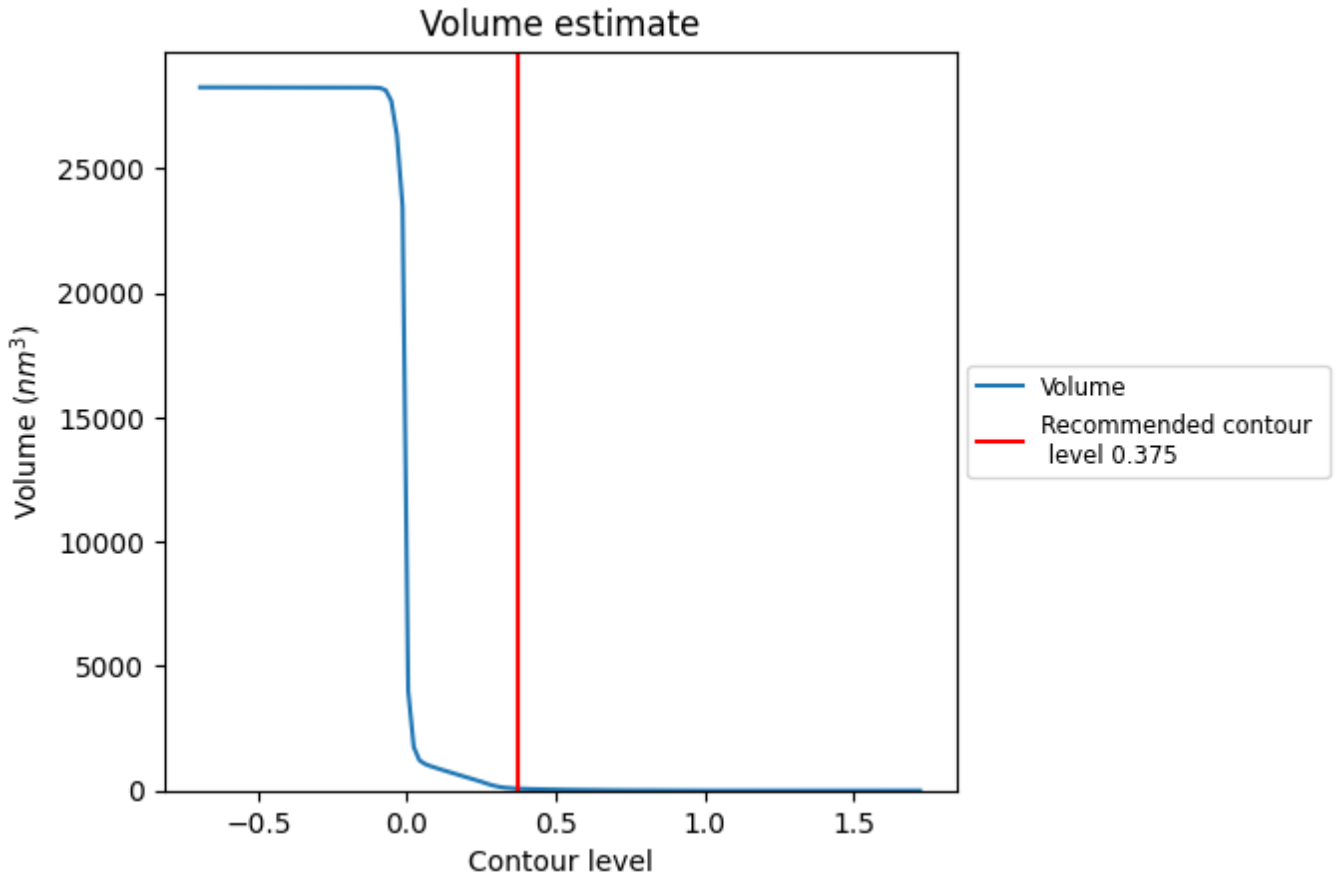
This section contains the results of statistical analysis of the map.

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.

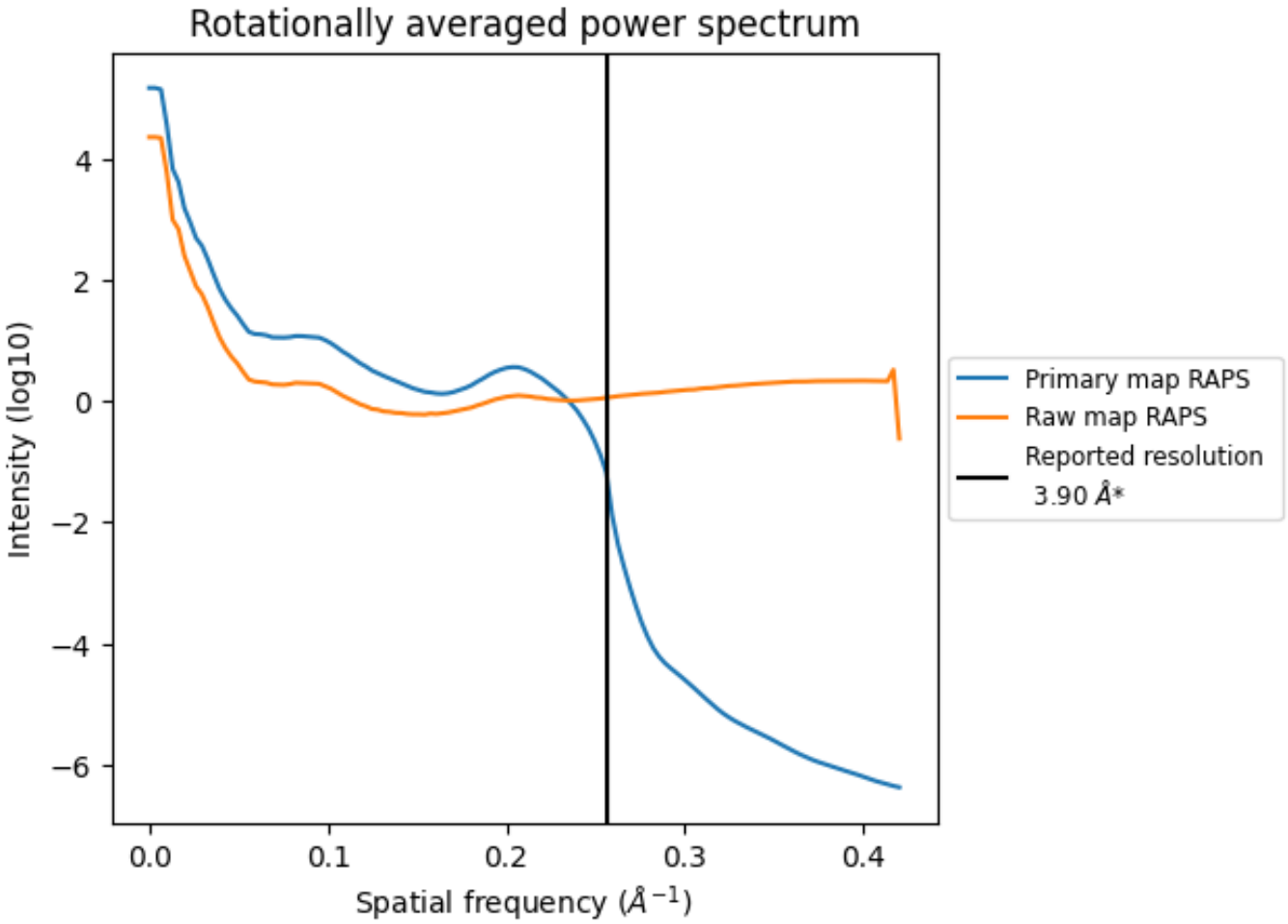
7.2 Volume estimate



The volume at the recommended contour level is 79 nm^3; this corresponds to an approximate mass of 71 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

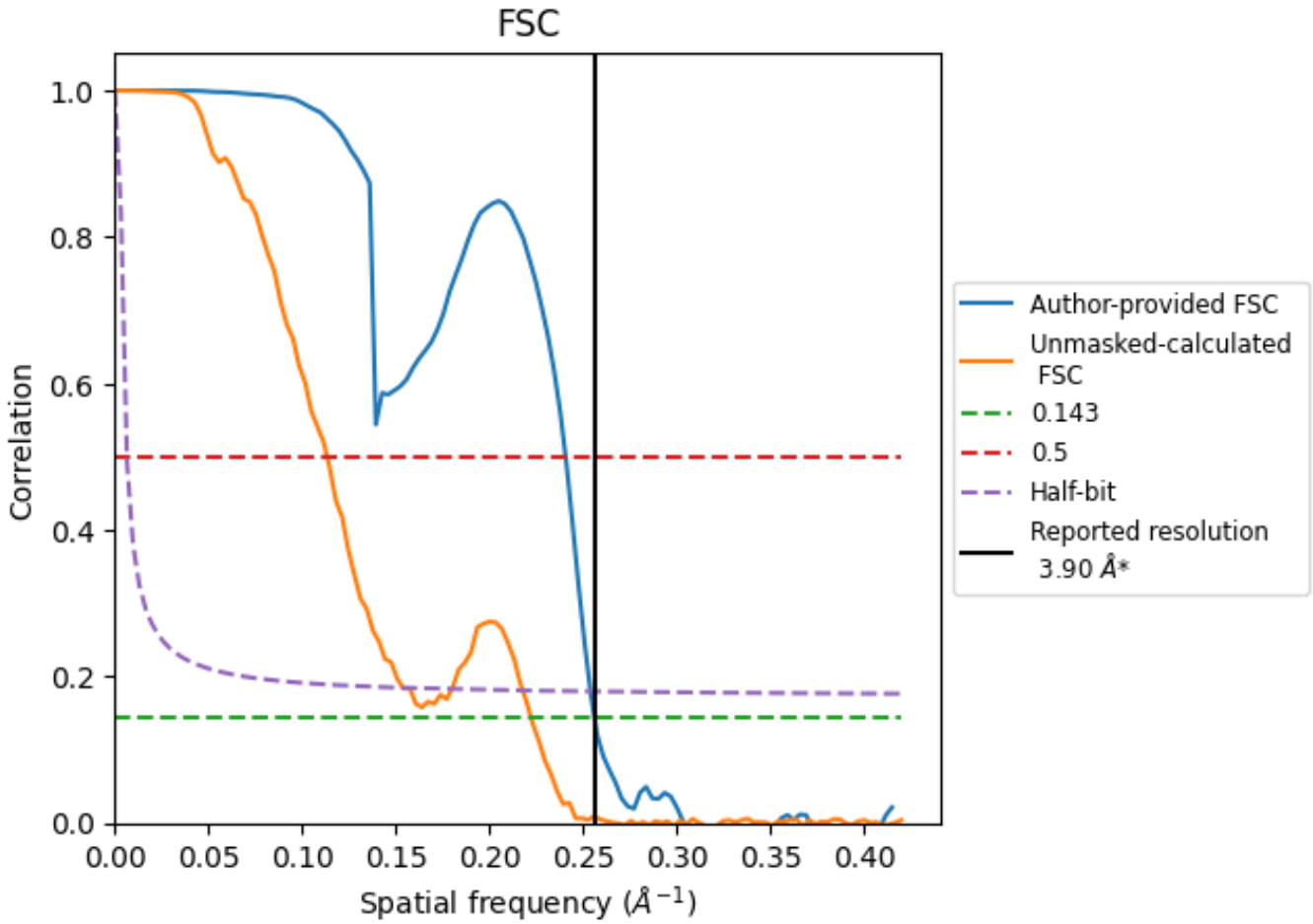


*Reported resolution corresponds to spatial frequency of 0.256 $Å^{-1}$

8 Fourier-Shell correlation

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 0.256 Å^{-1}

8.2 Resolution estimates (i)

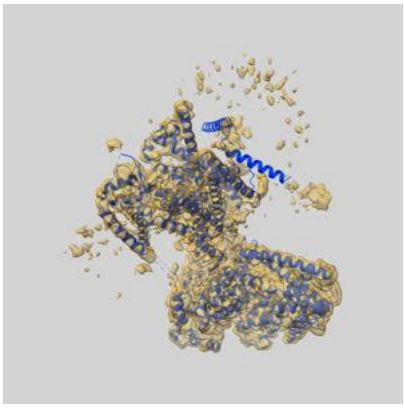
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.90	4.15	3.93
Unmasked-calculated*	4.50	8.82	6.49

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.50 differs from the reported value 3.9 by more than 10 %

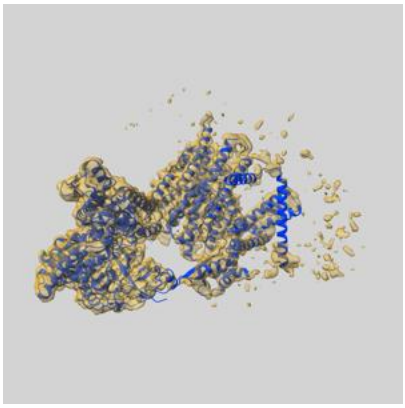
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-22782 and PDB model 7KAS. Per-residue inclusion information can be found in section 3 on page 5.

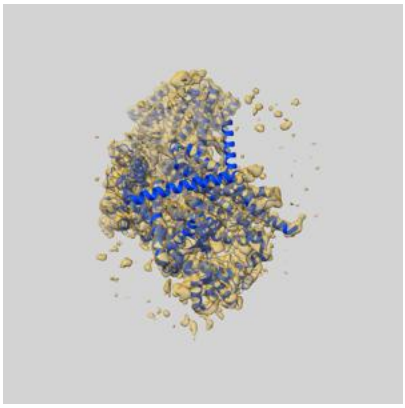
9.1 Map-model overlay



X



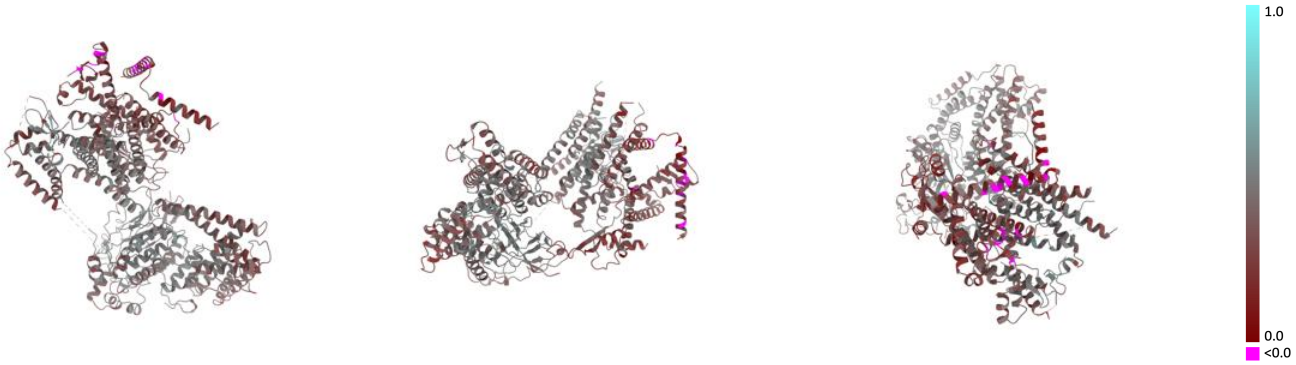
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.375 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.

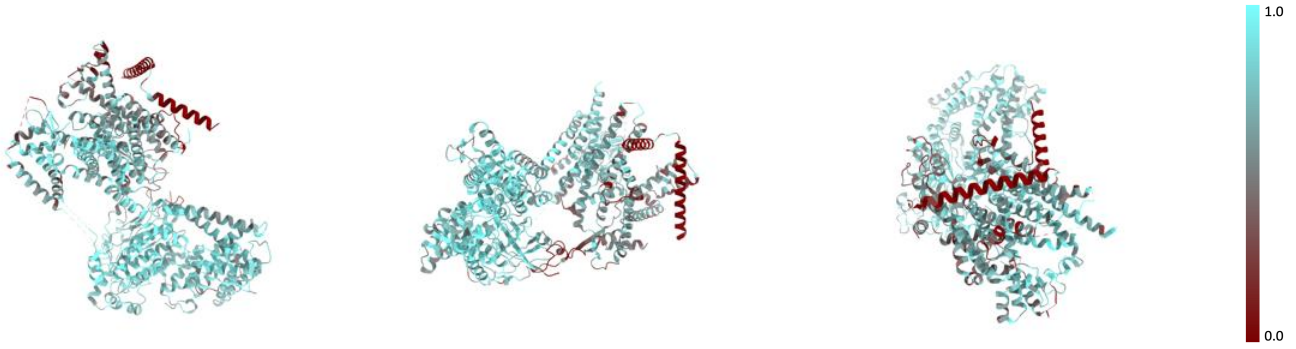
9.2 Q-score mapped to coordinate model (i)



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.

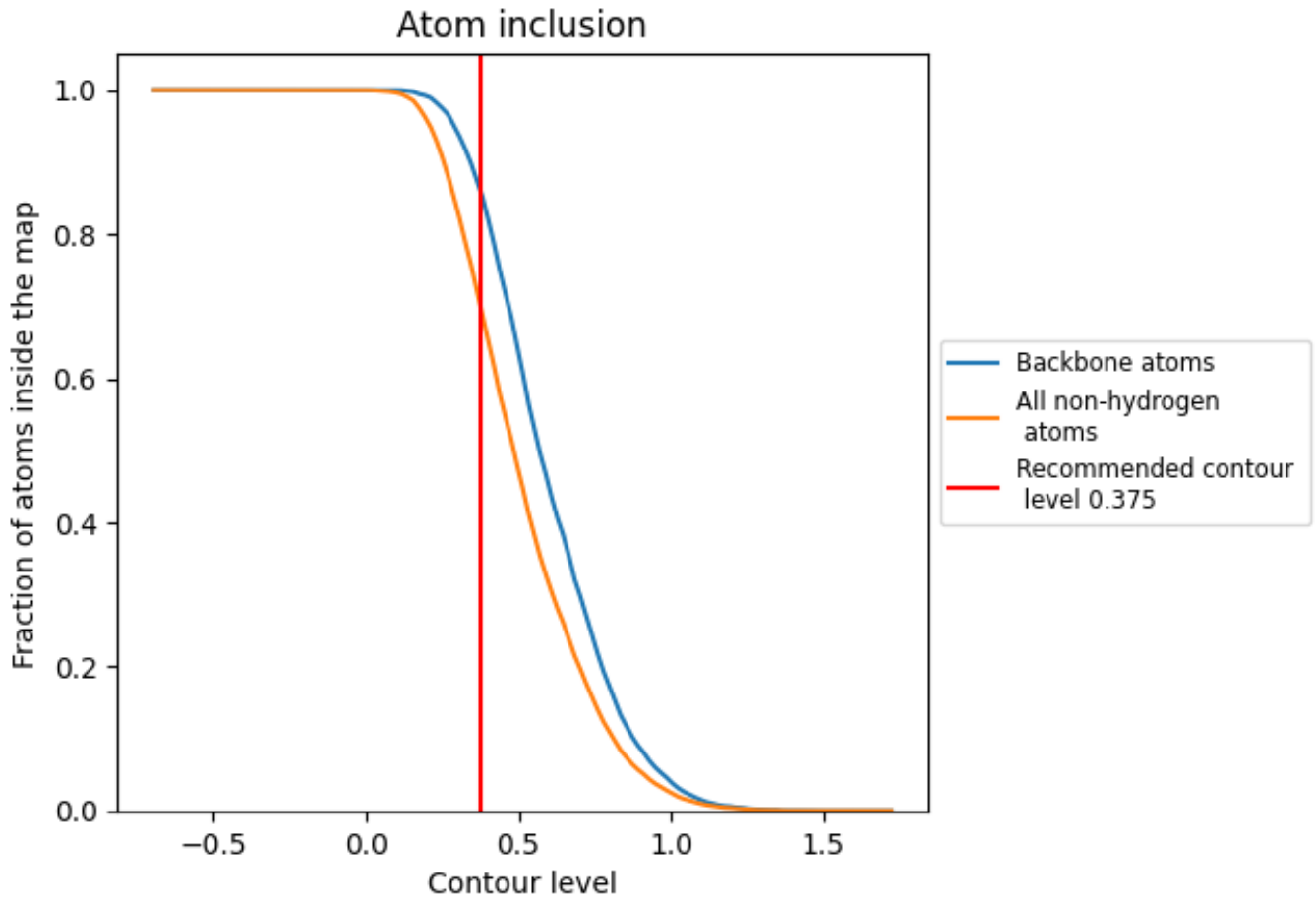
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.375).

9.4 Atom inclusion (i)



At the recommended contour level, 86% of all backbone atoms, 70% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.375) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7008	0.3900
A	0.6035	0.3400
B	0.7401	0.4260
C	0.6776	0.3700
D	0.7772	0.4370
E	0.7618	0.4010
F	0.7950	0.4070
G	0.0750	0.1900