Full wwPDB EM Validation Report ⓘ

Nov 19, 2022 – 10:49 pm GMT

PDB ID	:	6FCZ
EMDB ID	:	EMD-4232
Title	:	Model of gC1q-Fc complex based on 7A EM map
Authors	:	Ugurlar, D.; Howes, S.C.; de Kreuk, B.J.K.; de Jong, R.N.; Beurskens, F.J.; Koster, A.J.; Parren, P.W.H.I.; Sharp, T.H.; Gros, P.; Koning, R.I.
Deposited on	:	2017-12-21
Resolution	:	10.00 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:

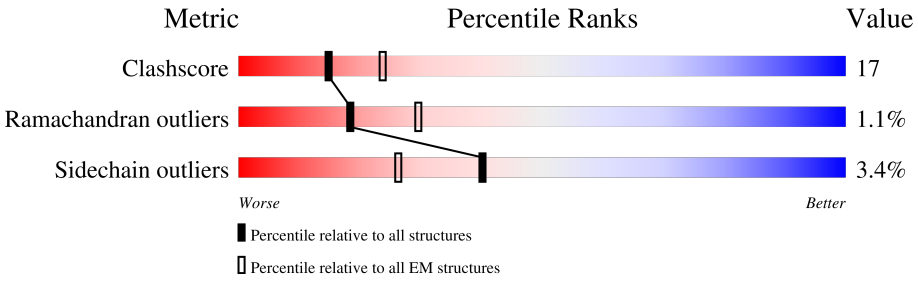
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 10.00 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	133	74% 83% 17%
2	B	132	80% 79% 18% ·
3	C	129	91% 84% 16%
4	H	216	50% 55% 40% · ·
4	K	216	40% 72% 24% · ·

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6710 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 Complement C1q subcomponent subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	133	Total	C	N	O	S	0	0
			1052	671	181	195	5		

- Molecule 2 is a protein called Complement C1q subcomponent subunit B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	132	Total	C	N	O	S	0	0
			1053	665	186	195	7		

- Molecule 3 is a protein called Complement C1q subcomponent subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	129	Total	C	N	O	S	0	0
			1010	649	169	188	4		

- Molecule 4 is a protein called Immunoglobulin gamma-1 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	216	Total	C	N	O	S	0	0
			1721	1096	289	330	6		
4	K	210	Total	C	N	O	S	0	0
			1676	1067	282	321	6		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		AltConf
5	A	75	Total	O	0
			75	75	
5	B	43	Total	O	0
			43	43	
5	C	76	Total	O	0
			76	76	

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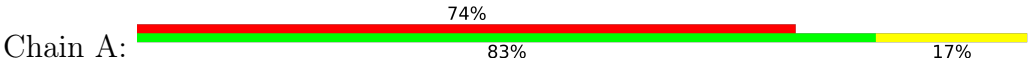
Mol	Chain	Residues	Atoms	AltConf
5	H	2	Total O 2 2	0
5	K	2	Total O 2 2	0

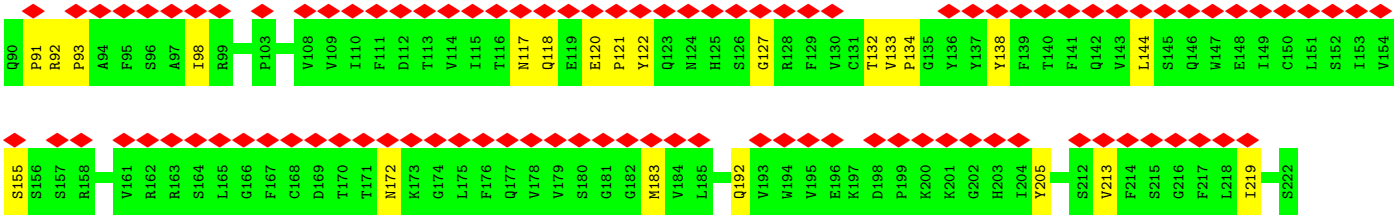
3 Residue-property plots (i)

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: Complement C1q subcomponent subunit A

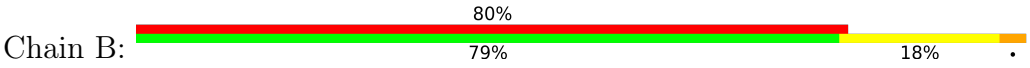
Chain A:

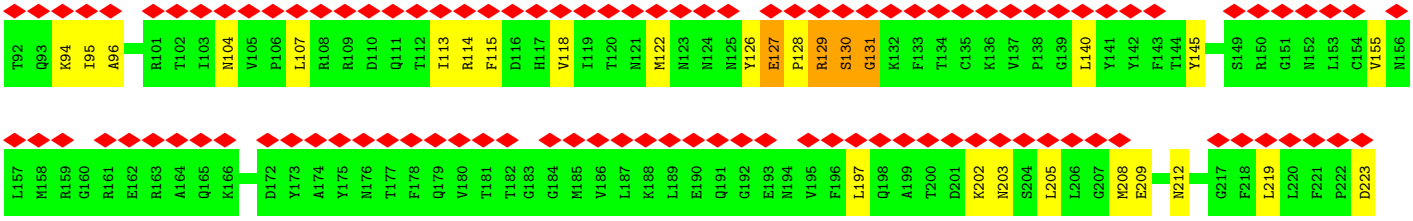




• Molecule 2: Complement C1q subcomponent subunit B

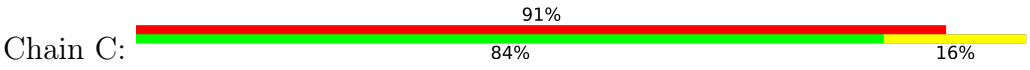
Chain B:

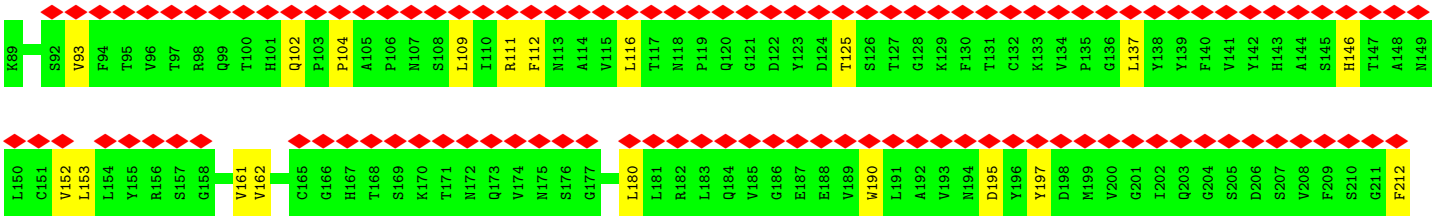




• Molecule 3: Complement C1q subcomponent subunit C

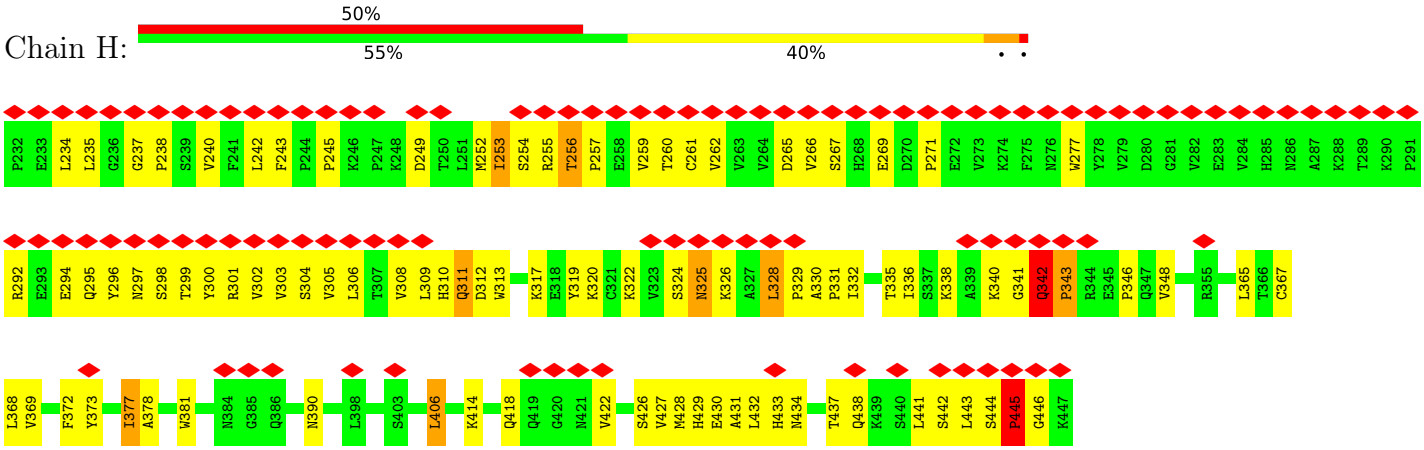
Chain C:





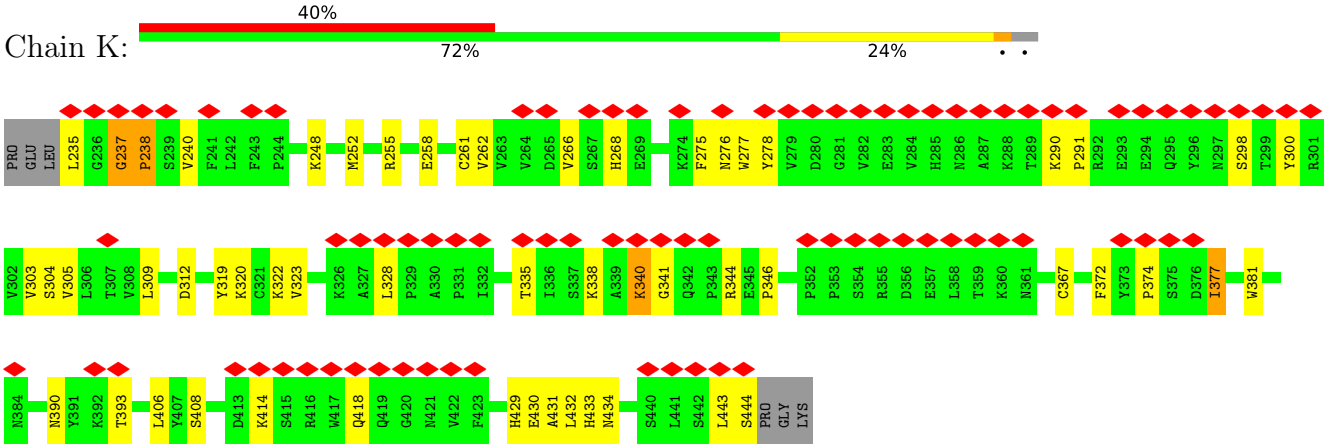
• Molecule 4: Immunoglobulin gamma-1 heavy chain

Chain H:



• Molecule 4: Immunoglobulin gamma-1 heavy chain

Chain K:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	79120	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	9.468	Depositor
Minimum map value	-2.345	Depositor
Average map value	0.030	Depositor
Map value standard deviation	0.545	Depositor
Recommended contour level	2.54	Depositor
Map size (Å)	509.37598, 509.37598, 509.37598	wwPDB
Map dimensions	224, 224, 224	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.274, 2.274, 2.274	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	0.49	0/1080	0.76	0/1463
2	B	0.44	0/1074	0.71	0/1448
3	C	0.51	0/1037	0.77	0/1412
4	H	0.49	1/1769 (0.1%)	0.91	4/2408 (0.2%)
4	K	0.64	2/1722 (0.1%)	1.31	7/2346 (0.3%)
All	All	0.53	3/6682 (0.0%)	0.97	11/9077 (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
4	H	0	1
4	K	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	K	237	GLY	C-N	17.76	1.68	1.34
4	H	342	GLN	C-N	13.03	1.59	1.34
4	K	340	LYS	C-N	7.13	1.45	1.33

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	K	340	LYS	O-C-N	-39.97	55.25	123.20
4	K	237	GLY	C-N-CD	-23.35	69.22	120.60
4	H	342	GLN	CA-C-N	-20.25	60.41	117.10
4	K	237	GLY	O-C-N	-18.03	86.83	121.10
4	H	342	GLN	O-C-N	17.93	155.18	121.10
4	K	340	LYS	CA-C-N	14.02	144.23	116.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	H	342	GLN	C-N-CD	13.73	157.24	128.40
4	H	342	GLN	C-N-CA	-13.18	66.64	122.00
4	K	237	GLY	CA-C-N	12.87	153.12	117.10
4	K	340	LYS	C-N-CA	8.83	140.84	122.30
4	K	237	GLY	C-N-CA	7.81	154.79	122.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	H	342	GLN	Mainchain
4	K	340	LYS	Mainchain

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	1052	0	1015	17	0
2	B	1053	0	1033	41	0
3	C	1010	0	979	30	0
4	H	1721	0	1693	105	0
4	K	1676	0	1645	52	0
5	A	75	0	0	0	0
5	B	43	0	0	3	0
5	C	76	0	0	4	0
5	H	2	0	0	5	0
5	K	2	0	0	0	0
All	All	6710	0	6365	215	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 17.

All (215) 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:K:237:GLY:C	4:K:238:PRO:CD	1.80	1.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:237:GLY:C	4:K:238:PRO:N	1.68	1.47
3:C:195:ASP:OD2	4:H:331:PRO:CB	1.81	1.28
4:H:234:LEU:HA	5:H:502:HOH:O	1.11	1.25
3:C:195:ASP:OD1	4:H:322:LYS:NZ	1.74	1.18
2:B:114:ARG:CG	2:B:130:SER:O	1.94	1.16
4:H:341:GLY:O	4:H:343:PRO:N	1.79	1.11
2:B:114:ARG:NE	2:B:129:ARG:O	1.85	1.10
5:B:304:HOH:O	4:H:330:ALA:HB2	0.93	1.10
4:H:377:ILE:HD11	4:H:427:VAL:HG13	1.38	1.05
4:K:248:LYS:HE2	4:K:252:MET:HE1	1.09	1.04
3:C:195:ASP:OD2	4:H:331:PRO:CG	2.05	1.04
2:B:114:ARG:HG2	2:B:130:SER:O	1.60	1.01
4:K:237:GLY:C	4:K:238:PRO:HD2	1.79	1.01
4:H:341:GLY:O	4:H:343:PRO:CD	2.10	1.00
4:H:234:LEU:HD12	5:H:502:HOH:O	1.63	0.96
2:B:114:ARG:HG3	2:B:130:SER:O	1.65	0.96
4:H:346:PRO:HB3	4:H:372:PHE:HB3	1.49	0.94
4:H:328:LEU:HD23	4:H:329:PRO:HD2	1.49	0.94
3:C:195:ASP:OD2	4:H:331:PRO:HG3	1.68	0.92
3:C:195:ASP:OD2	4:H:331:PRO:HB3	1.70	0.92
4:K:237:GLY:O	4:K:238:PRO:N	2.02	0.91
2:B:129:ARG:HG2	4:K:268:HIS:ND1	1.86	0.91
4:H:234:LEU:CA	5:H:502:HOH:O	1.77	0.90
4:K:237:GLY:C	4:K:238:PRO:HD3	1.91	0.89
4:K:248:LYS:CE	4:K:252:MET:HE1	2.00	0.88
4:H:252:MET:CE	4:H:428:MET:SD	2.62	0.86
2:B:113:ILE:HD12	2:B:197:LEU:CB	2.04	0.86
2:B:113:ILE:HD12	2:B:197:LEU:HB2	1.56	0.85
4:H:320:LYS:HG2	4:H:335:THR:HG22	1.58	0.84
3:C:195:ASP:OD2	4:H:331:PRO:HB2	1.75	0.84
2:B:129:ARG:HG2	4:K:268:HIS:CE1	2.13	0.82
3:C:195:ASP:CG	4:H:331:PRO:HG3	2.00	0.82
2:B:113:ILE:CG2	2:B:115:PHE:CE1	2.63	0.81
2:B:113:ILE:HG21	2:B:115:PHE:CE1	2.14	0.81
2:B:114:ARG:NH2	4:K:298:SER:HB3	1.96	0.80
4:K:262:VAL:HG22	4:K:303:VAL:HG22	1.64	0.80
4:H:429:HIS:CD2	4:H:431:ALA:H	2.00	0.79
4:H:377:ILE:HD13	4:H:378:ALA:N	1.98	0.79
4:K:237:GLY:CA	4:K:238:PRO:CD	2.61	0.79
2:B:114:ARG:HH22	4:K:298:SER:HB3	1.49	0.76
2:B:130:SER:OG	2:B:131:GLY:N	2.17	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:377:ILE:HD12	4:K:429:HIS:HB2	1.68	0.75
2:B:129:ARG:CG	4:K:268:HIS:CE1	2.70	0.74
4:H:338:LYS:NZ	4:H:430:GLU:OE1	2.20	0.74
4:K:276:ASN:HB2	4:K:322:LYS:HB3	1.70	0.72
2:B:104:ASN:OD1	4:H:234:LEU:HG	1.89	0.72
4:H:234:LEU:C	5:H:502:HOH:O	2.10	0.72
5:C:302:HOH:O	4:H:331:PRO:HG2	1.91	0.69
2:B:113:ILE:HD12	2:B:197:LEU:HB3	1.76	0.68
4:K:346:PRO:HB3	4:K:372:PHE:HB3	1.75	0.68
3:C:195:ASP:OD1	4:H:322:LYS:CE	2.41	0.68
4:H:341:GLY:O	4:H:343:PRO:HD3	1.93	0.68
2:B:126:TYR:O	2:B:128:PRO:HD3	1.95	0.67
3:C:195:ASP:OD2	4:H:322:LYS:HE3	1.95	0.67
4:H:252:MET:HE3	4:H:428:MET:SD	2.33	0.67
3:C:195:ASP:OD2	4:H:322:LYS:CE	2.44	0.66
4:K:248:LYS:HD3	4:K:255:ARG:NH2	2.12	0.64
2:B:113:ILE:HG22	2:B:115:PHE:CE1	2.32	0.64
4:H:252:MET:HE1	4:H:428:MET:SD	2.37	0.63
4:H:311:GLN:H	4:H:311:GLN:CD	2.01	0.63
4:H:243:PHE:HE1	4:H:262:VAL:HG12	1.65	0.62
4:K:237:GLY:CA	4:K:238:PRO:HD2	2.27	0.62
3:C:217:ASP:OXT	3:C:217:ASP:OD1	2.16	0.62
4:H:367:CYS:HB2	4:H:381:TRP:CZ2	2.35	0.62
1:A:183:MET:CE	3:C:116:LEU:HD13	2.29	0.62
4:H:292:ARG:HG2	4:H:302:VAL:HG22	1.80	0.61
2:B:127:GLU:OE2	2:B:128:PRO:HD2	2.01	0.61
4:K:309:LEU:HD12	4:K:312:ASP:OD2	2.01	0.61
4:H:242:LEU:HD12	4:H:260:THR:O	2.00	0.61
4:K:261:CYS:HB2	4:K:277:TRP:CH2	2.36	0.61
1:A:98:ILE:HG22	1:A:213:VAL:HG22	1.83	0.60
4:K:429:HIS:CD2	4:K:431:ALA:H	2.19	0.60
4:H:245:PRO:HD3	4:H:259:VAL:HG22	1.83	0.60
4:H:341:GLY:HA3	4:H:373:TYR:HE2	1.67	0.60
4:K:320:LYS:HB2	4:K:335:THR:HG22	1.84	0.60
4:H:309:LEU:HB2	4:H:312:ASP:OD2	2.01	0.59
4:H:266:VAL:HB	4:H:300:TYR:HB2	1.83	0.59
4:H:340:LYS:HA	4:H:340:LYS:HE2	1.84	0.59
4:H:377:ILE:HD11	4:H:427:VAL:CG1	2.25	0.59
3:C:93:VAL:HG23	3:C:212:PHE:HB3	1.86	0.58
2:B:94:LYS:NZ	3:C:217:ASP:HB3	2.19	0.58
2:B:114:ARG:CD	2:B:129:ARG:O	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:312:ASP:O	4:H:317:LYS:HB2	2.04	0.57
4:K:248:LYS:HE2	4:K:252:MET:CE	2.05	0.57
2:B:126:TYR:OH	2:B:131:GLY:HA2	2.04	0.57
4:H:328:LEU:HD22	4:H:330:ALA:O	2.05	0.57
3:C:195:ASP:CG	4:H:322:LYS:CE	2.73	0.57
4:H:310:HIS:HB2	4:H:311:GLN:OE1	2.05	0.56
4:H:338:LYS:CE	4:H:430:GLU:OE1	2.52	0.56
5:B:304:HOH:O	4:H:330:ALA:CB	1.78	0.56
4:K:237:GLY:CA	4:K:238:PRO:HD3	2.32	0.56
3:C:102:GLN:HG3	5:C:327:HOH:O	2.04	0.55
4:H:257:PRO:HD3	4:H:310:HIS:CE1	2.41	0.55
1:A:183:MET:HE3	3:C:116:LEU:HD13	1.88	0.55
4:H:341:GLY:O	4:H:343:PRO:CG	2.55	0.55
5:B:333:HOH:O	4:H:332:ILE:HD11	2.05	0.54
4:H:377:ILE:HD13	4:H:378:ALA:H	1.71	0.54
4:H:328:LEU:HD23	4:H:329:PRO:CD	2.31	0.54
4:H:320:LYS:CG	4:H:335:THR:HG22	2.34	0.54
4:H:320:LYS:HE2	4:H:335:THR:HG21	1.89	0.54
4:H:238:PRO:HG2	4:H:328:LEU:HD12	1.90	0.54
4:K:377:ILE:CD1	4:K:429:HIS:HB2	2.38	0.53
1:A:183:MET:HE3	3:C:116:LEU:CD1	2.39	0.53
4:H:267:SER:HB2	4:H:269:GLU:OE1	2.08	0.53
2:B:114:ARG:HG3	2:B:130:SER:C	2.28	0.53
4:H:406:LEU:HD12	4:H:406:LEU:C	2.29	0.53
2:B:94:LYS:HZ1	3:C:217:ASP:HB3	1.74	0.53
4:H:242:LEU:HD23	4:H:336:ILE:HB	1.91	0.52
2:B:107:LEU:HB2	2:B:203:ASN:HB2	1.92	0.51
4:K:338:LYS:HD2	4:K:430:GLU:OE1	2.10	0.51
4:H:377:ILE:HD13	4:H:378:ALA:C	2.30	0.51
1:A:120:GLU:N	1:A:121:PRO:HD3	2.26	0.50
1:A:92:ARG:N	1:A:93:PRO:HD3	2.26	0.50
2:B:114:ARG:CZ	2:B:129:ARG:O	2.54	0.50
3:C:195:ASP:CB	4:H:331:PRO:HG3	2.41	0.50
4:H:320:LYS:HG2	4:H:335:THR:CG2	2.38	0.50
4:H:252:MET:SD	4:H:428:MET:SD	3.10	0.50
4:H:253:ILE:HD13	4:H:253:ILE:O	2.12	0.50
4:K:266:VAL:HB	4:K:300:TYR:HB2	1.93	0.50
1:A:118:GLN:HG2	2:B:140:LEU:HD11	1.93	0.50
4:H:253:ILE:HD13	4:H:253:ILE:C	2.32	0.50
2:B:122:MET:SD	3:C:137:LEU:HD13	2.52	0.49
4:H:433:HIS:O	4:H:434:ASN:HB2	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:245:PRO:HD2	4:H:313:TRP:CH2	2.47	0.49
1:A:91:PRO:HB3	1:A:133:VAL:HG21	1.95	0.49
4:H:325:ASN:HD22	4:H:326:LYS:H	1.60	0.49
4:H:341:GLY:HA3	4:H:373:TYR:CE2	2.47	0.49
3:C:146:HIS:HE1	5:C:362:HOH:O	1.96	0.49
4:H:305:VAL:HG23	4:H:305:VAL:O	2.12	0.49
4:H:368:LEU:HD12	4:H:369:VAL:N	2.28	0.49
4:H:262:VAL:HG23	4:H:303:VAL:HG22	1.95	0.48
5:C:302:HOH:O	4:H:331:PRO:CG	2.55	0.48
4:K:320:LYS:CB	4:K:335:THR:HG22	2.42	0.48
1:A:183:MET:HE1	3:C:116:LEU:HD13	1.96	0.48
4:H:378:ALA:HB3	4:H:428:MET:HB2	1.95	0.47
4:H:235:LEU:N	5:H:502:HOH:O	2.42	0.47
4:H:295:GLN:NE2	4:H:301:ARG:HB2	2.29	0.47
4:K:238:PRO:HD2	4:K:328:LEU:CD2	2.44	0.47
4:H:235:LEU:C	4:H:237:GLY:H	2.18	0.47
2:B:145:TYR:CZ	2:B:155:VAL:HG11	2.50	0.47
4:H:444:SER:O	4:H:445:PRO:C	2.53	0.47
4:K:346:PRO:HG2	4:K:432:LEU:HD21	1.97	0.47
2:B:202:LYS:HD2	2:B:202:LYS:N	2.29	0.47
3:C:112:PHE:O	3:C:125:THR:HG22	2.15	0.46
4:K:278:TYR:CD2	4:K:320:LYS:HD2	2.50	0.46
1:A:117:ASN:OD1	1:A:121:PRO:HD2	2.15	0.46
4:H:320:LYS:HE2	4:H:335:THR:CG2	2.45	0.46
4:K:238:PRO:HD2	4:K:328:LEU:HD21	1.98	0.46
4:H:297:ASN:O	4:H:298:SER:HB3	2.15	0.46
4:K:237:GLY:HA3	4:K:328:LEU:HD23	1.97	0.46
2:B:113:ILE:HG21	2:B:115:PHE:CZ	2.49	0.46
4:H:317:LYS:HB3	4:H:319:TYR:CE1	2.51	0.46
4:H:341:GLY:C	4:H:343:PRO:CD	2.75	0.46
4:K:235:LEU:C	4:K:237:GLY:H	2.18	0.46
1:A:144:LEU:HD23	1:A:205:TYR:CD2	2.51	0.45
4:K:443:LEU:HG	4:K:444:SER:N	2.30	0.45
4:H:346:PRO:HG2	4:H:432:LEU:HD21	1.98	0.45
4:H:319:TYR:O	4:H:335:THR:HA	2.16	0.45
4:K:290:LYS:HE3	4:K:305:VAL:CG2	2.47	0.45
4:K:367:CYS:HB2	4:K:381:TRP:CZ2	2.52	0.45
4:K:406:LEU:HD12	4:K:406:LEU:C	2.37	0.45
2:B:205:LEU:C	2:B:205:LEU:HD23	2.37	0.44
4:H:260:THR:HG23	4:H:303:VAL:CG1	2.48	0.44
4:K:414:LYS:O	4:K:418:GLN:HG2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:129:ARG:HG3	4:K:268:HIS:CE1	2.50	0.44
4:K:429:HIS:HD2	4:K:431:ALA:H	1.66	0.44
4:H:243:PHE:HE1	4:H:262:VAL:CG1	2.30	0.44
4:H:306:LEU:O	4:H:308:VAL:HG13	2.18	0.43
4:H:418:GLN:HA	4:H:443:LEU:HD22	1.99	0.43
4:K:374:PRO:O	4:K:429:HIS:HE1	2.02	0.43
1:A:91:PRO:C	1:A:93:PRO:HD3	2.39	0.43
4:K:443:LEU:O	4:K:444:SER:HB3	2.18	0.43
1:A:138:TYR:HB2	1:A:219:ILE:HD11	2.01	0.43
4:K:290:LYS:HB3	4:K:291:PRO:HD2	1.99	0.43
4:H:414:LYS:O	4:H:418:GLN:HG3	2.19	0.43
4:H:343:PRO:HA	4:H:373:TYR:O	2.19	0.43
4:H:338:LYS:HE3	4:H:430:GLU:OE1	2.19	0.42
4:H:324:SER:OG	4:H:331:PRO:HB3	2.19	0.42
3:C:161:VAL:HG12	3:C:162:VAL:HG13	2.00	0.42
4:H:271:PRO:HB3	4:H:300:TYR:CE2	2.55	0.42
4:K:393:THR:HA	4:K:408:SER:HA	2.02	0.42
1:A:155:SER:HA	1:A:192:GLN:O	2.20	0.42
2:B:95:ILE:HD12	2:B:219:LEU:HD22	2.00	0.42
3:C:104:PRO:HD2	3:C:197:TYR:O	2.20	0.42
4:K:433:HIS:O	4:K:434:ASN:HB2	2.19	0.42
4:K:290:LYS:HE3	4:K:305:VAL:HG21	2.01	0.42
4:H:277:TRP:HZ2	4:H:304:SER:HG	1.64	0.42
4:H:295:GLN:HB2	4:H:299:THR:OG1	2.19	0.42
4:H:311:GLN:OE1	4:H:311:GLN:N	2.40	0.42
2:B:114:ARG:HA	2:B:130:SER:O	2.19	0.41
1:A:118:GLN:CB	2:B:140:LEU:HD11	2.50	0.41
4:K:240:VAL:HG22	4:K:323:VAL:HG21	2.02	0.41
4:H:256:THR:HA	4:H:257:PRO:HD3	1.83	0.41
1:A:122:TYR:OH	1:A:127:GLY:HA2	2.20	0.41
2:B:104:ASN:OD1	4:H:234:LEU:CG	2.66	0.41
4:H:325:ASN:HD22	4:H:326:LYS:N	2.18	0.41
4:H:365:LEU:HD13	4:H:441:LEU:HD23	2.01	0.41
3:C:109:LEU:HD12	3:C:190:TRP:CD1	2.55	0.41
4:H:240:VAL:HB	4:H:332:ILE:HG21	2.02	0.41
4:K:278:TYR:HB2	4:K:320:LYS:HB3	2.03	0.41
4:H:265:ASP:HA	4:H:299:THR:CG2	2.51	0.41
3:C:152:VAL:C	3:C:153:LEU:HD12	2.41	0.41
1:A:132:THR:O	1:A:134:PRO:HD3	2.22	0.40
4:K:319:TYR:O	4:K:335:THR:HA	2.21	0.40
4:H:253:ILE:O	4:H:255:ARG:N	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:422:VAL:HG22	4:H:442:SER:HB3	2.03	0.40
2:B:208:MET:O	2:B:212:ASN:ND2	2.54	0.40
3:C:153:LEU:HD12	3:C:153:LEU:N	2.36	0.40
2:B:113:ILE:HG22	2:B:115:PHE:CD1	2.56	0.40
2:B:114:ARG:CG	2:B:129:ARG:O	2.70	0.40
4:H:348:VAL:HG21	4:H:437:THR:CG2	2.51	0.40
4:K:275:PHE:CD2	4:K:304:SER:HB2	2.57	0.40
2:B:96:ALA:HB1	3:C:180:LEU:HD13	2.02	0.40
4:H:261:CYS:HB2	4:H:277:TRP:CH2	2.56	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	131/133 (98%)	124 (95%)	7 (5%)	0	100 100
2	B	130/132 (98%)	121 (93%)	7 (5%)	2 (2%)	10 46
3	C	127/129 (98%)	124 (98%)	3 (2%)	0	100 100
4	H	214/216 (99%)	193 (90%)	16 (8%)	5 (2%)	6 34
4	K	208/216 (96%)	198 (95%)	8 (4%)	2 (1%)	15 55
All	All	810/826 (98%)	760 (94%)	41 (5%)	9 (1%)	18 52

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	H	342	GLN
4	H	445	PRO
4	K	238	PRO
4	K	341	GLY
4	H	446	GLY

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Mol	Chain	Res	Type
2	B	131	GLY
2	B	130	SER
4	H	254	SER
4	H	343	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	117/117 (100%)	116 (99%)	1 (1%)	78	87
2	B	115/115 (100%)	110 (96%)	5 (4%)	29	53
3	C	113/113 (100%)	112 (99%)	1 (1%)	78	87
4	H	200/200 (100%)	186 (93%)	14 (7%)	15	40
4	K	195/200 (98%)	191 (98%)	4 (2%)	53	72
All	All	740/745 (99%)	715 (97%)	25 (3%)	40	60

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	172	ASN
2	B	118	VAL
2	B	127	GLU
2	B	129	ARG
2	B	209	GLU
2	B	223	ASP
3	C	111	ARG
4	H	249	ASP
4	H	253	ILE
4	H	256	THR
4	H	294	GLU
4	H	296	TYR
4	H	311	GLN
4	H	325	ASN
4	H	328	LEU

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Mol	Chain	Res	Type
4	H	377	ILE
4	H	390	ASN
4	H	406	LEU
4	H	426	SER
4	H	438	GLN
4	H	445	PRO
4	K	258	GLU
4	K	344	ARG
4	K	377	ILE
4	K	390	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	ASN
1	A	186	GLN
1	A	189	GLN
3	C	146	HIS
4	H	295	GLN
4	H	310	HIS
4	H	325	ASN
4	H	347	GLN
4	H	361	ASN
4	H	390	ASN
4	H	421	ASN
4	H	429	HIS
4	H	435	HIS
4	K	347	GLN
4	K	390	ASN
4	K	419	GLN
4	K	421	ASN
4	K	429	HIS
4	K	434	ASN
4	K	435	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	K	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	237:GLY	C	238:PRO	N	1.68

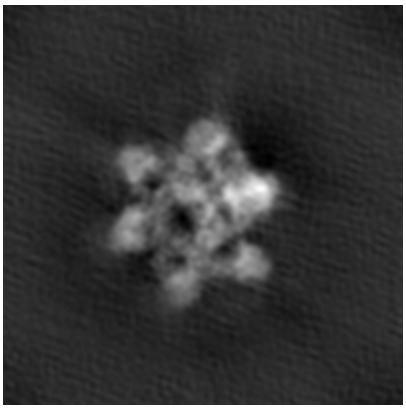
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-4232. These allow visual inspection of the internal detail of the map and identification of artifacts.

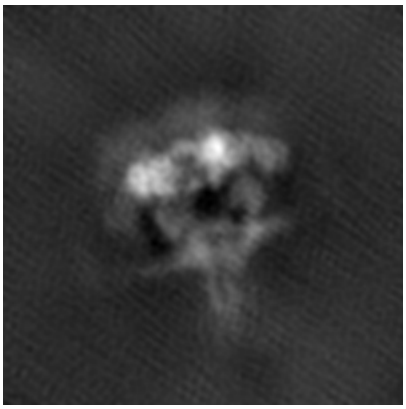
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

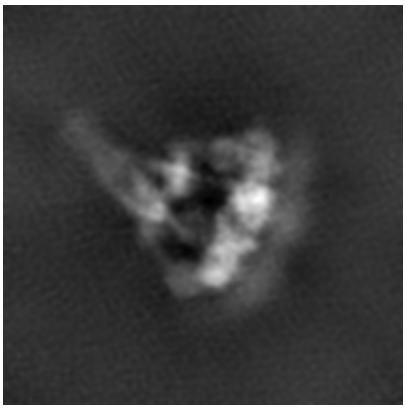
6.1.1 Primary map



X

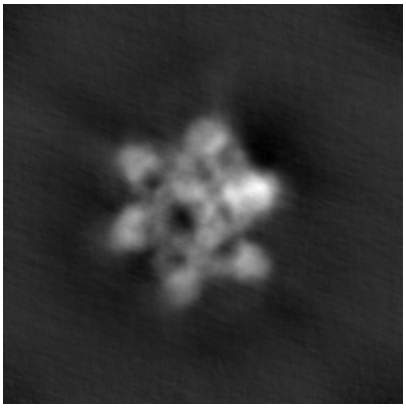


Y

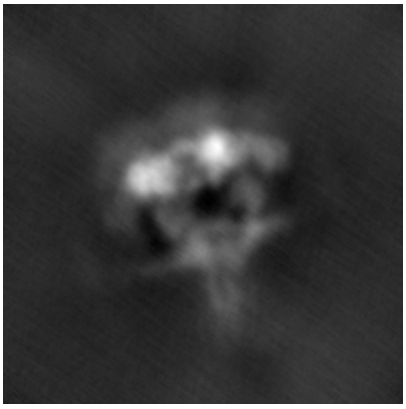


Z

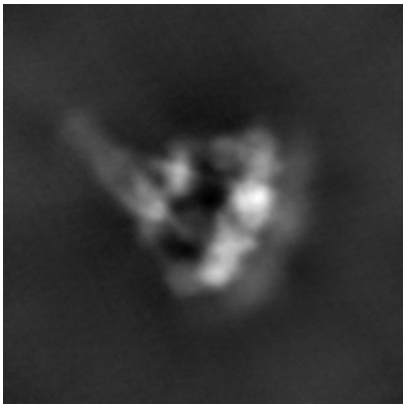
6.1.2 Raw map



X



Y

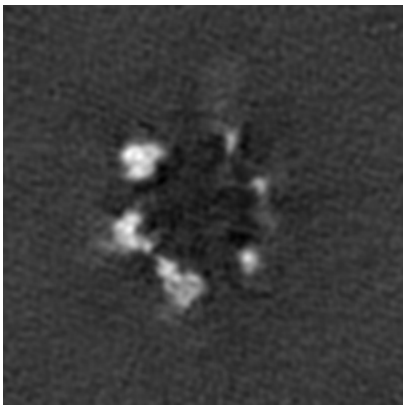


Z

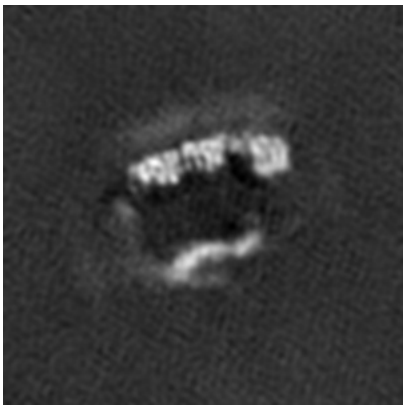
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

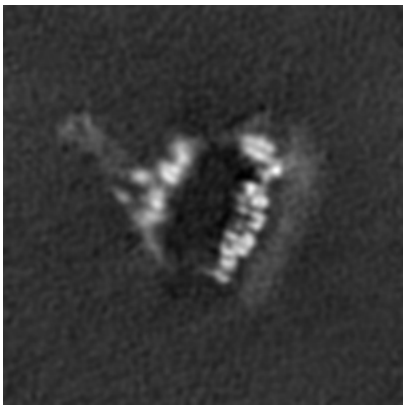
6.2.1 Primary map



X Index: 112

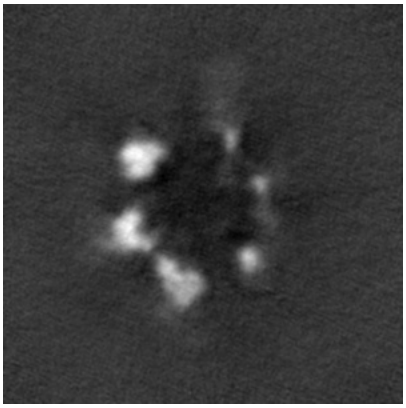


Y Index: 112

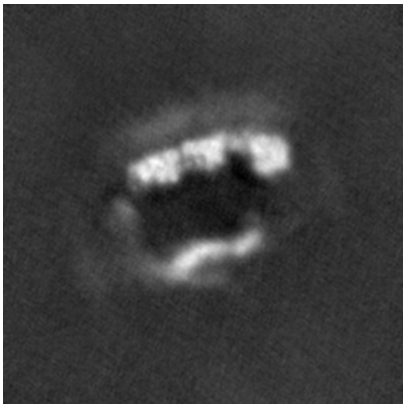


Z Index: 112

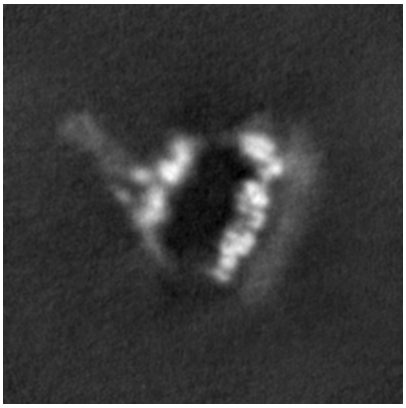
6.2.2 Raw map



X Index: 112



Y Index: 112

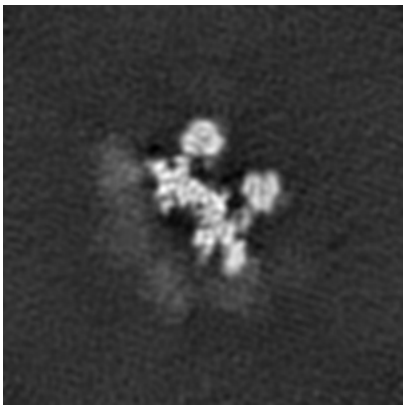


Z Index: 112

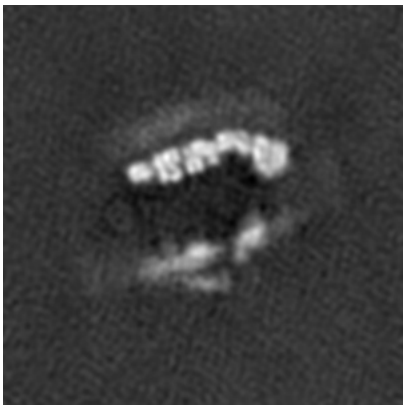
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

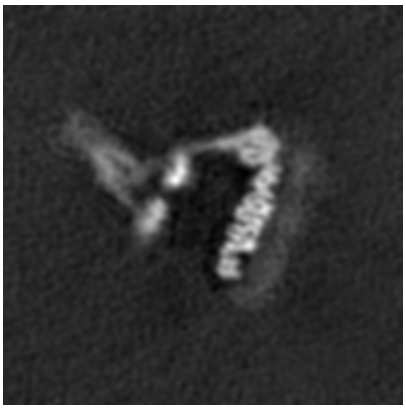
6.3.1 Primary map



X Index: 139

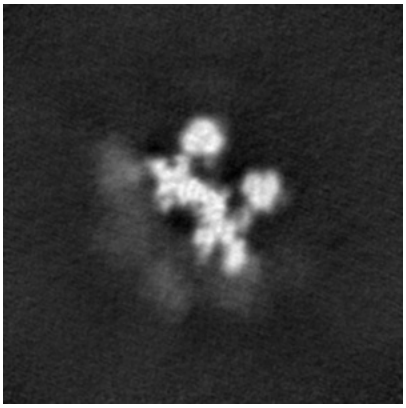


Y Index: 115

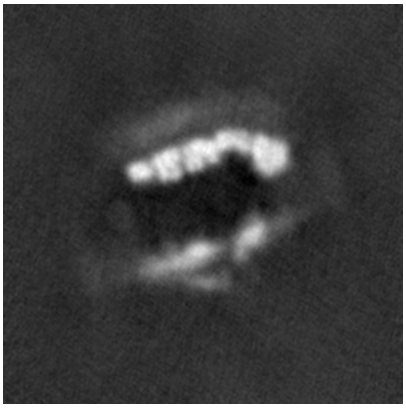


Z Index: 119

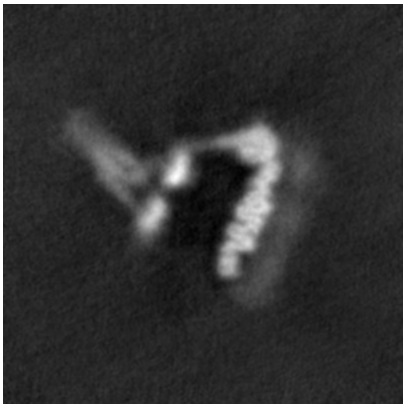
6.3.2 Raw map



X Index: 139



Y Index: 115

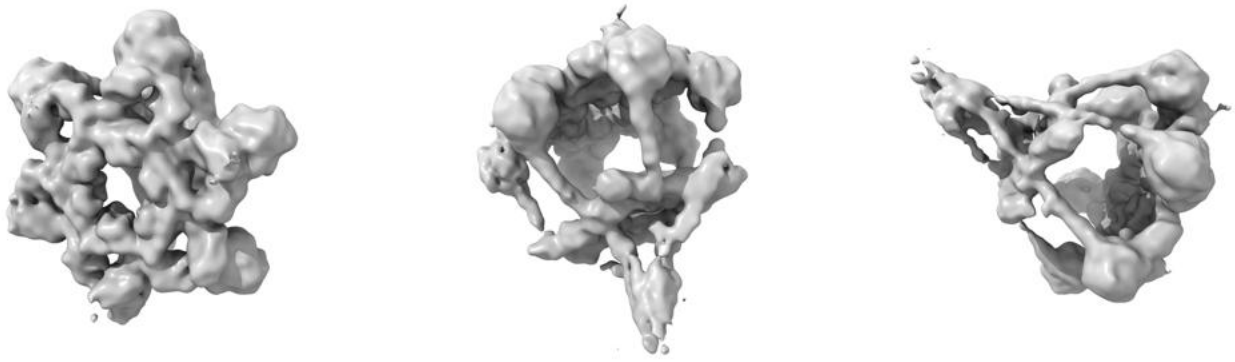


Z Index: 118

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 2.54. 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.

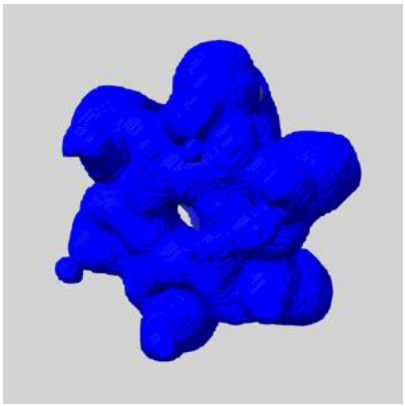
6.5 Mask visualisation (i)

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

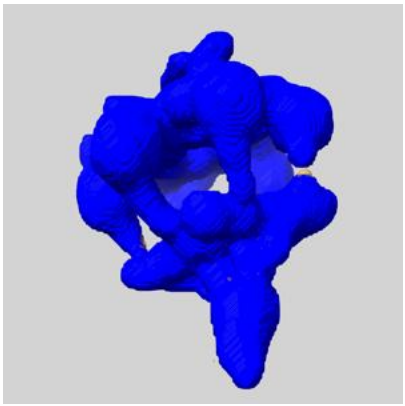
A mask typically either:

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

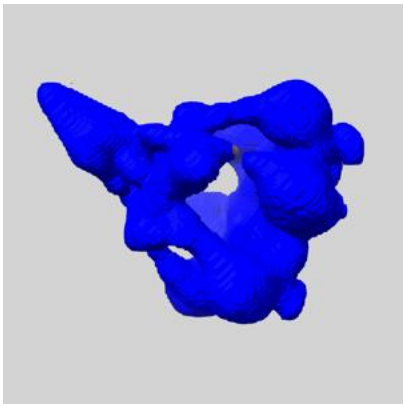
6.5.1 emd_4232_msk_1.map (i)



X



Y

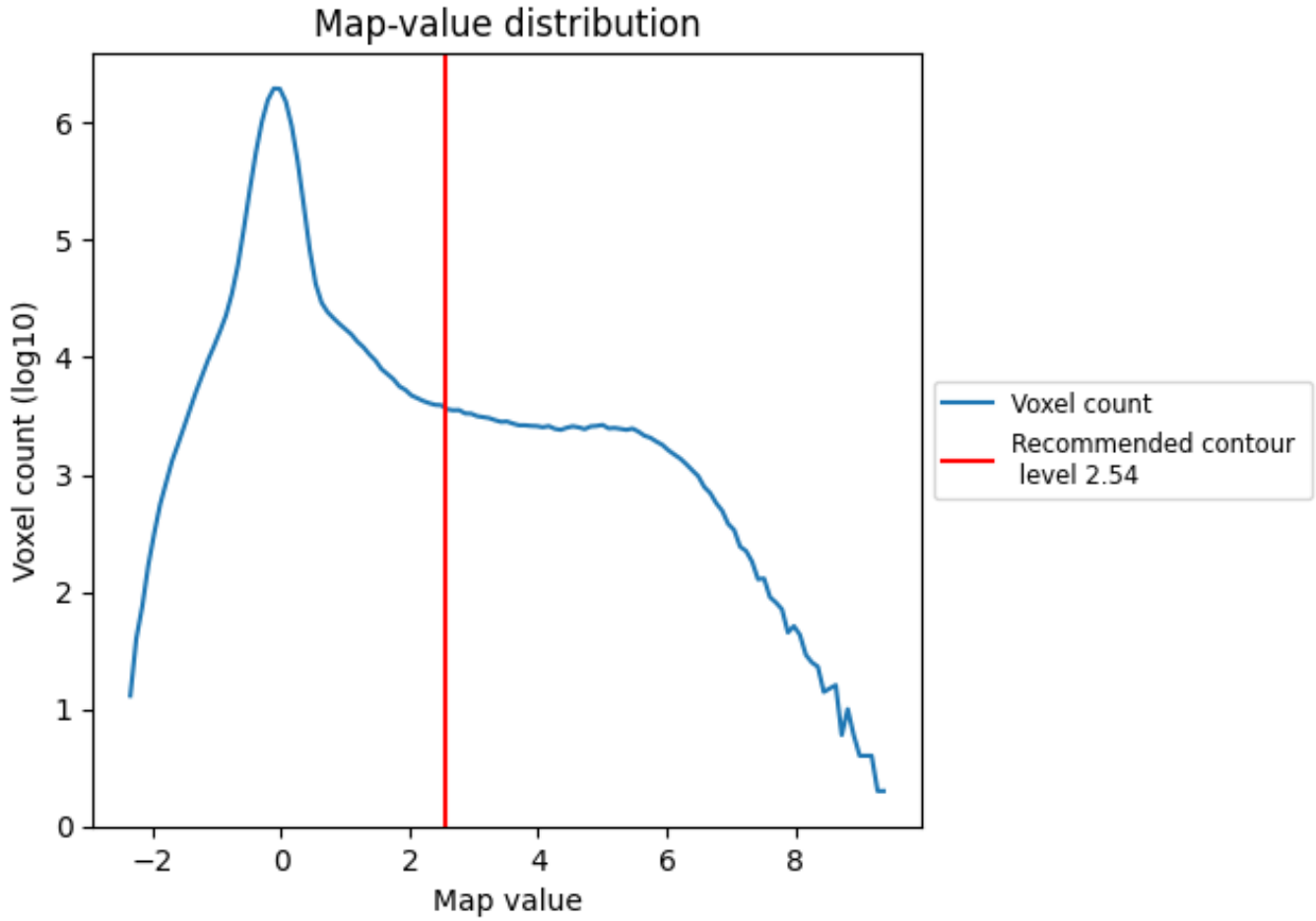


Z

7 Map analysis

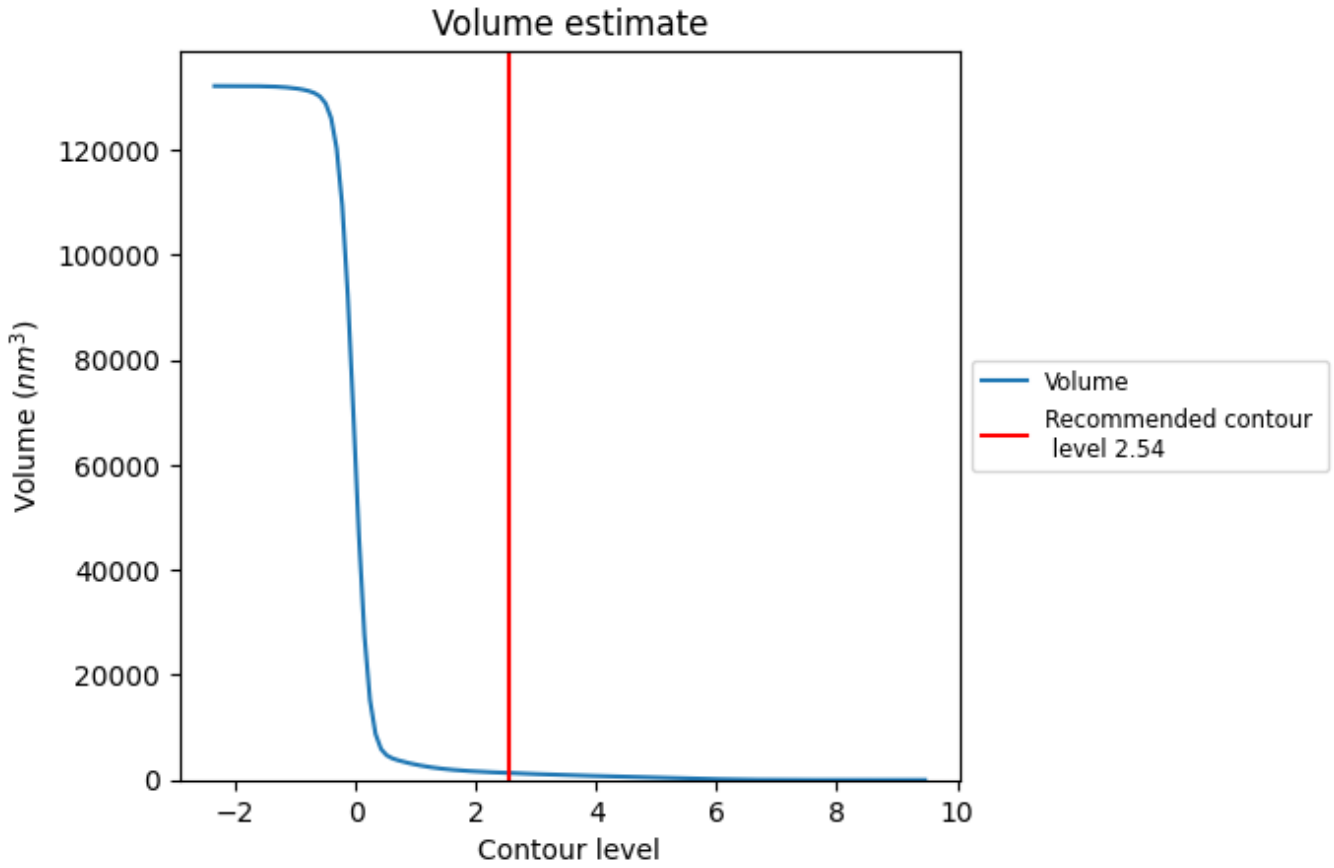
This section contains the results of statistical analysis of the map.

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.

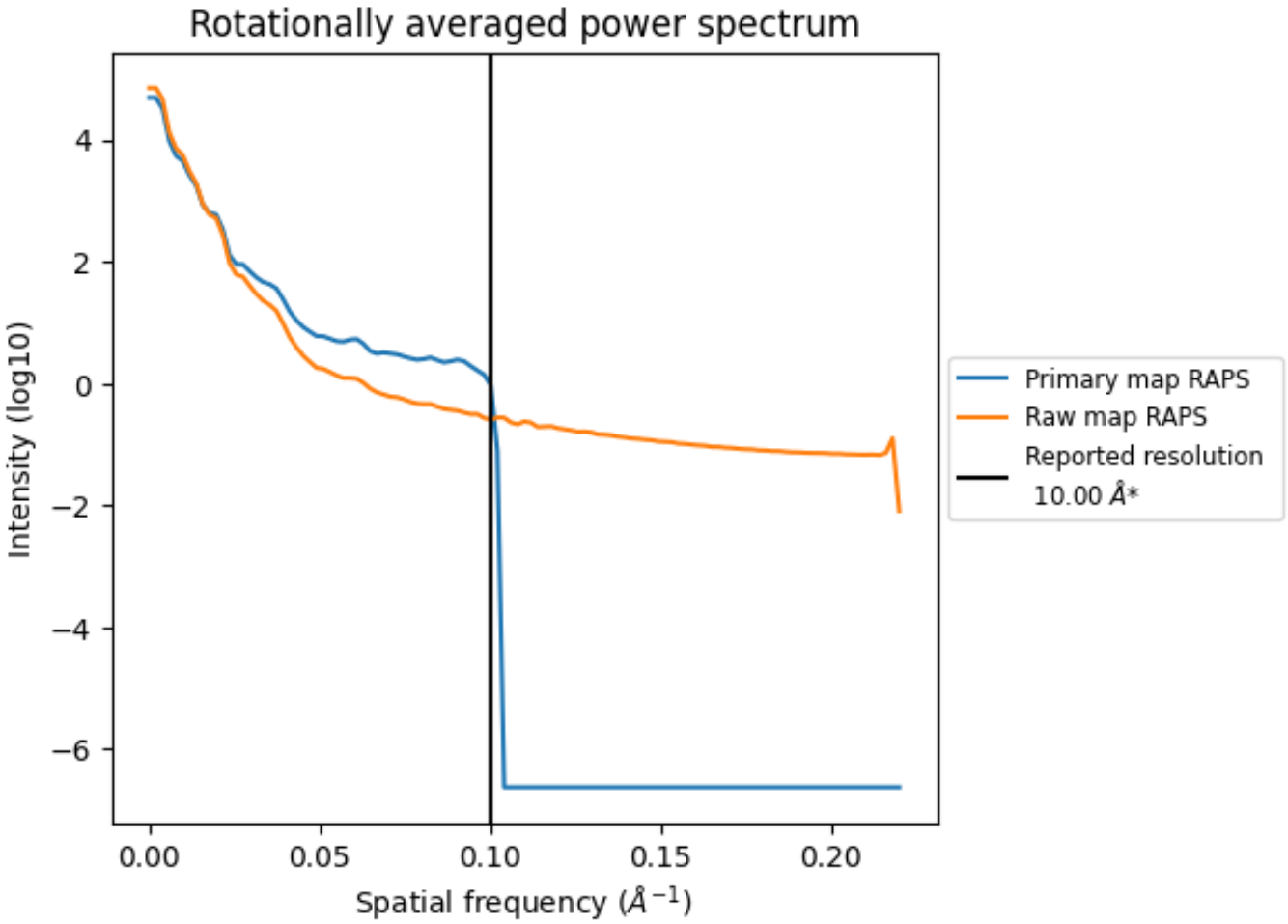
7.2 Volume estimate



The volume at the recommended contour level is 1330 nm^3; this corresponds to an approximate mass of 1201 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)

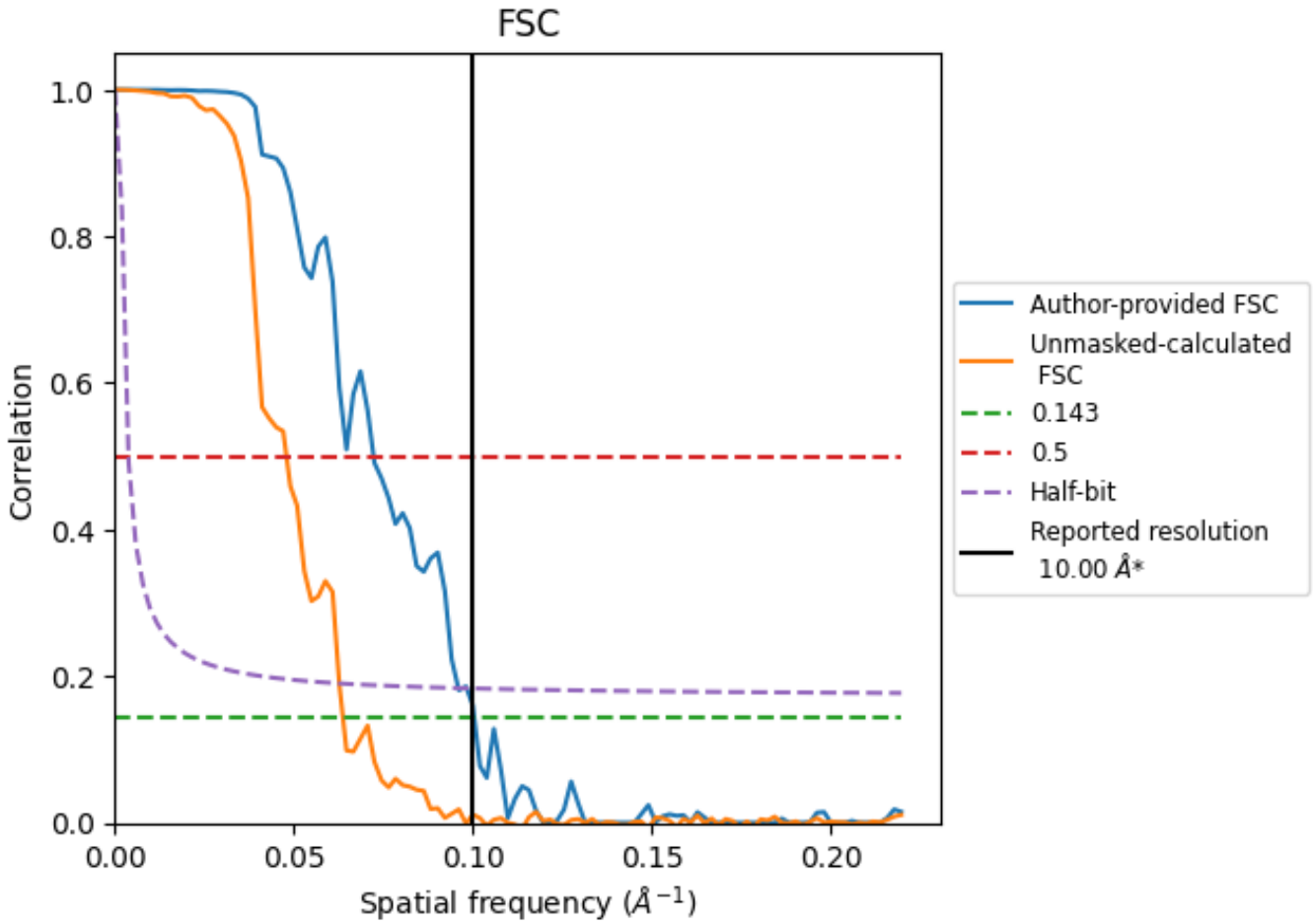


*Reported resolution corresponds to spatial frequency of 0.100 Å^{-1}

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 0.100 Å^{-1}

8.2 Resolution estimates (i)

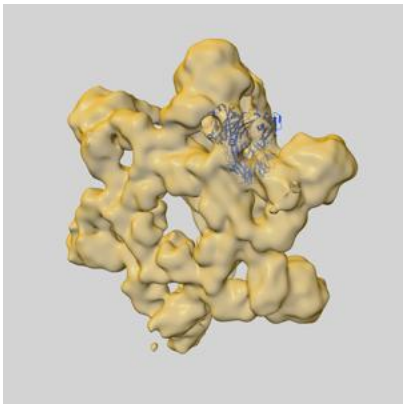
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	10.00	-	-
Author-provided FSC curve	9.95	13.81	10.41
Unmasked-calculated*	15.67	20.83	15.92

*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 15.67 differs from the reported value 10.0 by more than 10 %

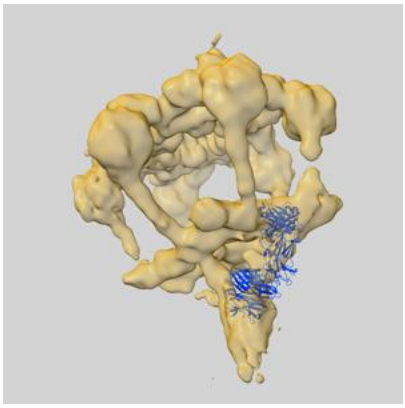
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-4232 and PDB model 6FCZ. Per-residue inclusion information can be found in section 3 on page 5.

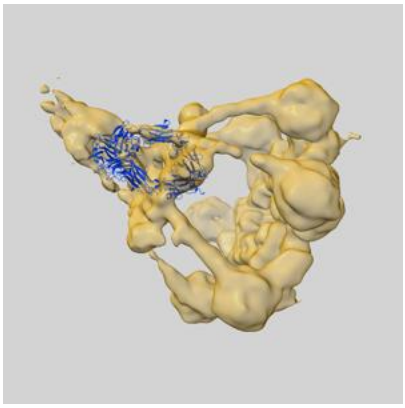
9.1 Map-model overlay



X



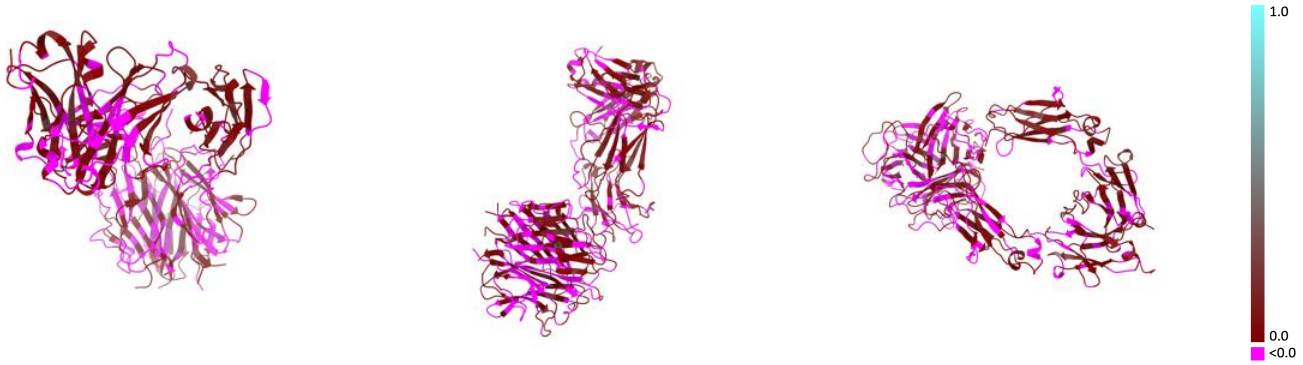
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.54 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.

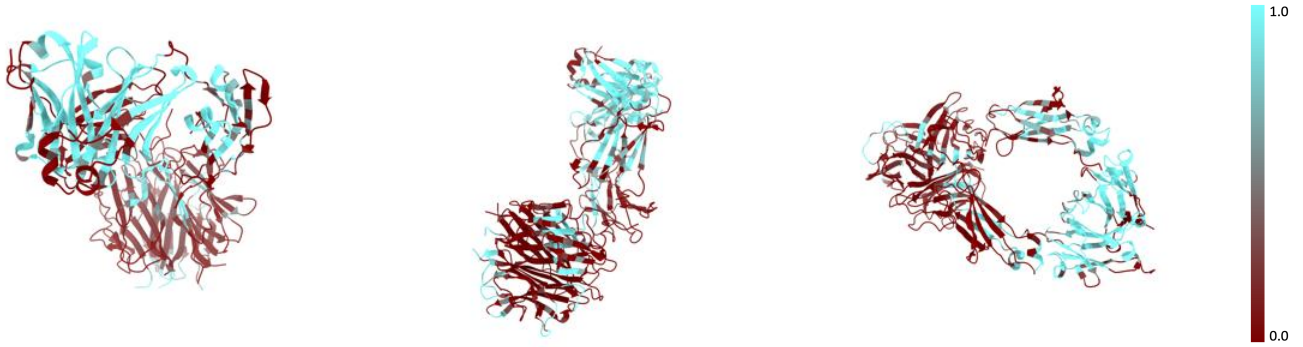
9.2 Q-score mapped to coordinate model



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.

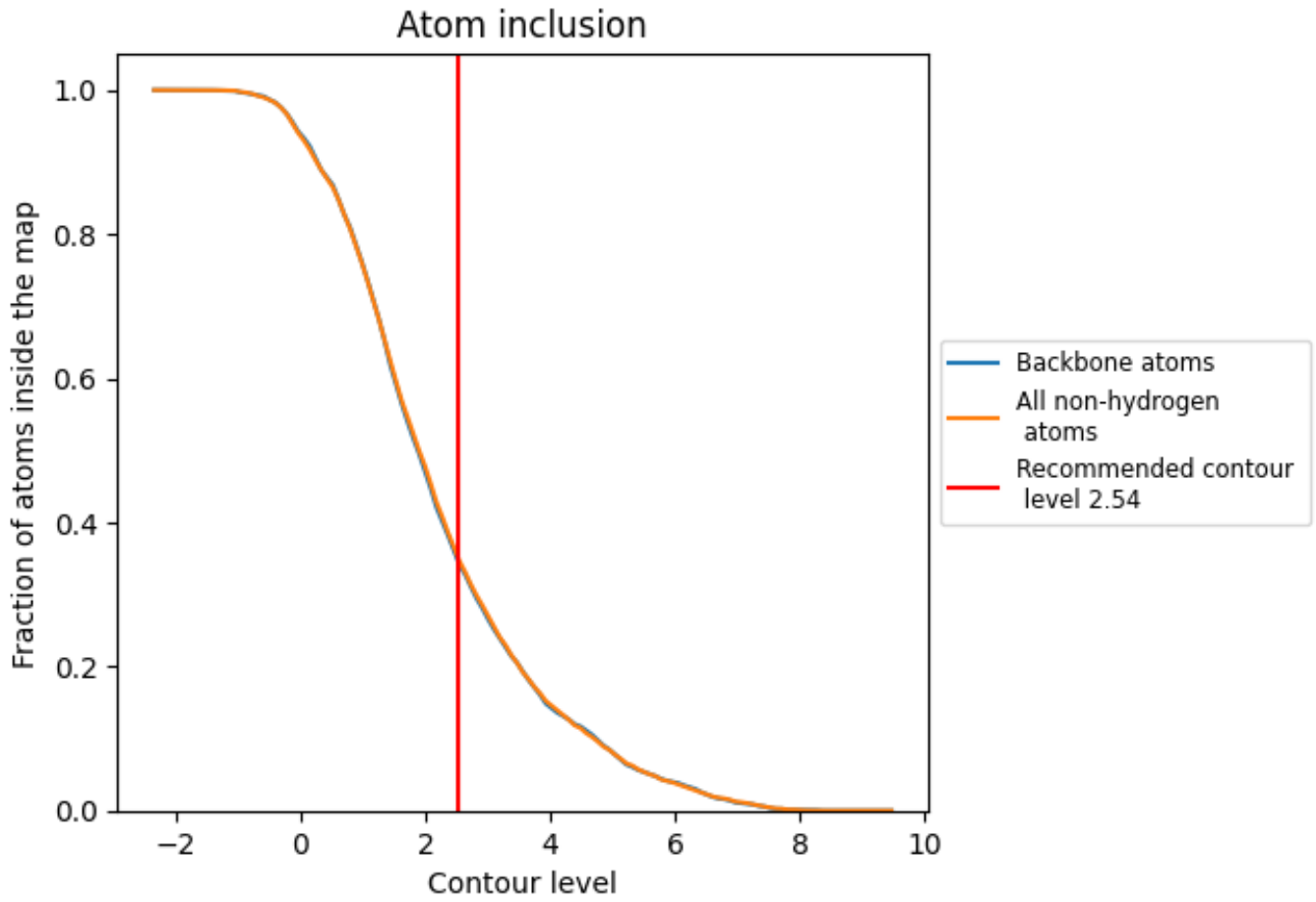
9.3 Atom inclusion mapped to coordinate model



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 (2.54).

9.4 Atom inclusion (i)



At the recommended contour level, 34% of all backbone atoms, 35% 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 (2.54) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3483	0.0130
A	0.2289	-0.0100
B	0.1788	0.0030
C	0.0895	-0.0080
H	0.4876	0.0250
K	0.5433	0.0340