Full wwPDB EM Validation Report

Dec 31, 2023 – 06:17 AM EST

PDB ID	:	8G5I
EMDB ID	:	EMD-29745
Title	:	Cryo-EM structure of the Mismatch Sensing Complex (I) of Human Mitochondrial DNA Polymerase Gamma
Authors	:	Nayak, A.R.; Buchel, G.; Herbine, K.H.; Sarfallah, A.; Sokolova, V.O.; Zamudio-Ochoa, A.; Temiakov, D.
Deposited on	:	2023-02-13
Resolution	:	2.75 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 (i) 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 (i)) were used in the production of this report:

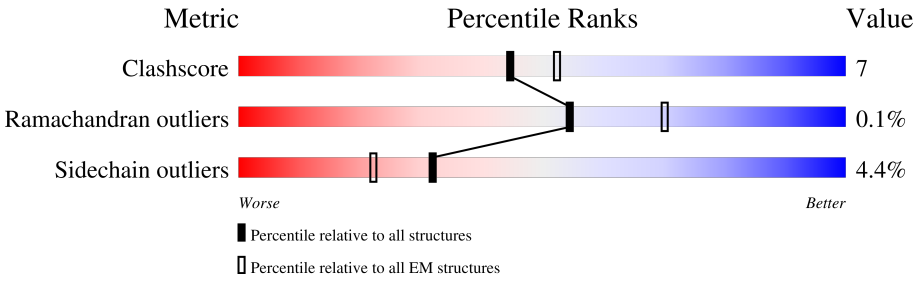
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.75 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	1239	7% 63% 12% 24%
2	B	485	65% 11% 23%
2	C	485	62% 11% 26%
3	P	20	75% 5% 10% 10%
4	T	26	15% 62% 12% 27%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14084 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 DNA polymerase subunit gamma-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	941	Total	C	N	O	S	0	0
			7430	4726	1293	1362	49		

- Molecule 2 is a protein called DNA polymerase subunit gamma-2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	372	Total	C	N	O	S	0	0
			2986	1911	529	530	16		
2	C	358	Total	C	N	O	S	0	0
			2890	1855	509	511	15		

- Molecule 3 is a DNA chain called Mismatched Primer DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	P	18	Total	C	N	O	P	1	0
			392	185	79	109	19		

- Molecule 4 is a DNA chain called Template DNA.

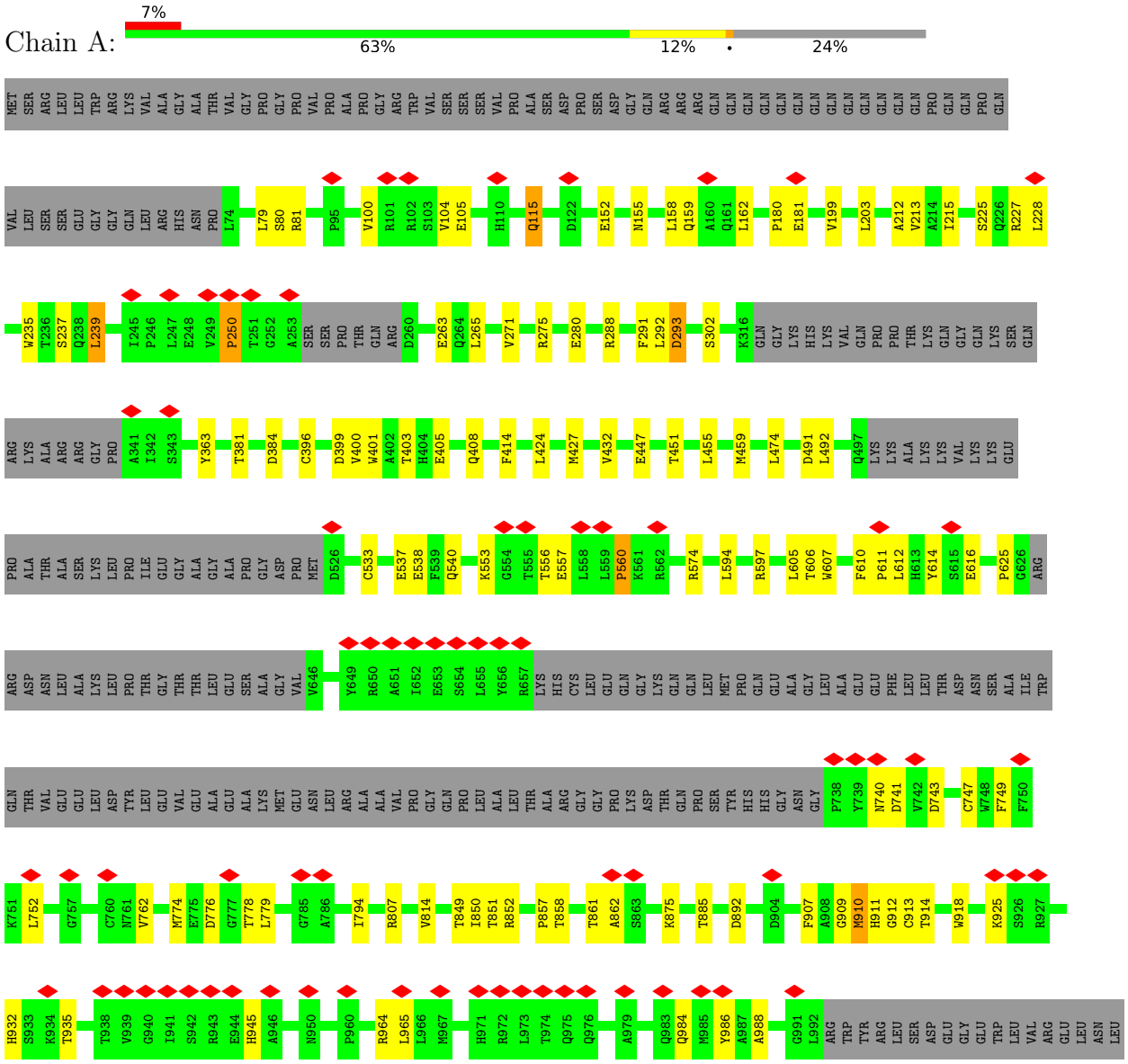
Mol	Chain	Residues	Atoms					AltConf	Trace
4	T	19	Total	C	N	O	P	0	0
			386	182	70	115	19		

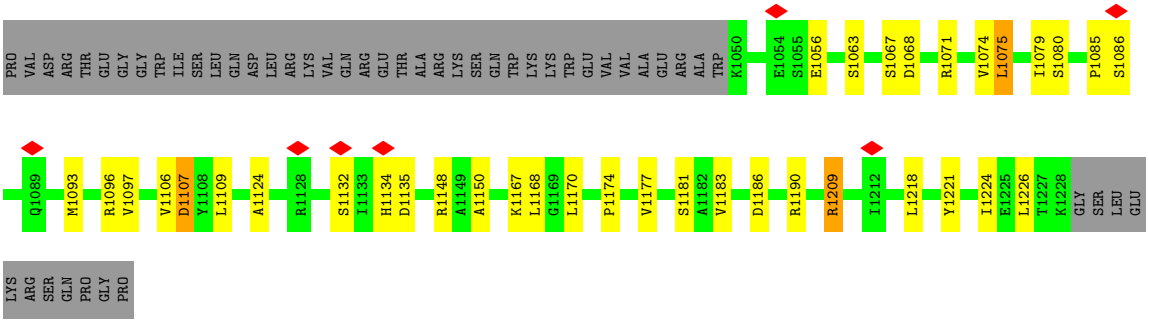
3 Residue-property plots (i)

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: DNA polymerase subunit gamma-1

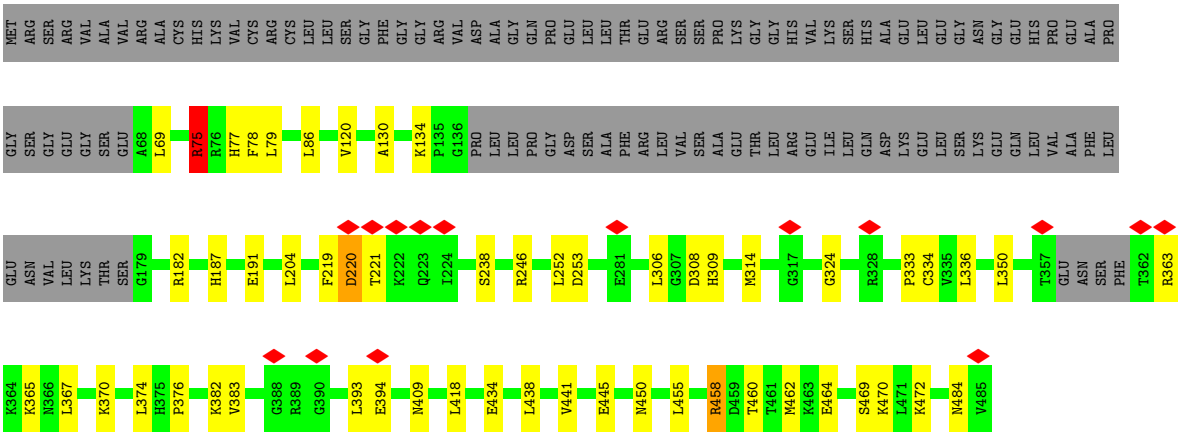
Chain A:





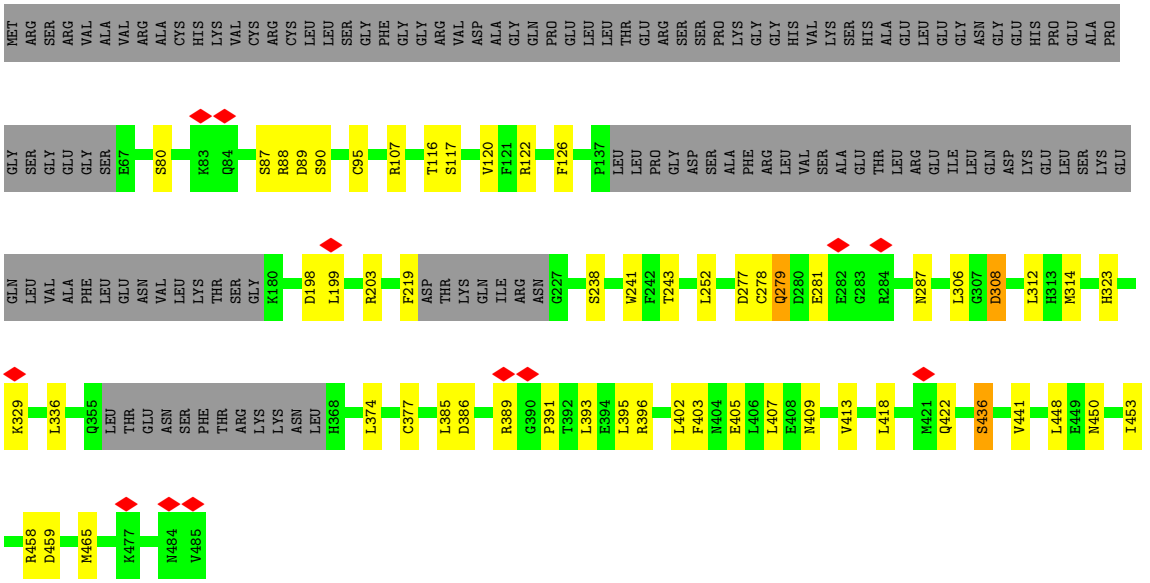
• Molecule 2: DNA polymerase subunit gamma-2, mitochondrial

Chain B:



• Molecule 2: DNA polymerase subunit gamma-2, mitochondrial

Chain C:

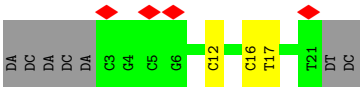


• Molecule 3: Mismatched Primer DNA

Chain P:

• Molecule 4: Template DNA

Chain T:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	816448	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 ($e^-/Å^2$)	70	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	18000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.476	Depositor
Minimum map value	-0.274	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	264.32, 264.32, 264.32	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82600003, 0.82600003, 0.82600003	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	0.28	0/7621	0.59	3/10350 (0.0%)
2	B	0.27	0/3060	0.56	0/4138
2	C	0.27	0/2963	0.57	1/4006 (0.0%)
3	P	1.12	3/442 (0.7%)	1.61	4/678 (0.6%)
4	T	0.54	0/431	0.88	0/662
All	All	0.34	3/14517 (0.0%)	0.65	8/19834 (0.0%)

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

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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	27[A]	DA	P-OP2	13.42	1.71	1.49
3	P	27[B]	DA	P-OP2	13.42	1.71	1.49
3	P	26	DG	O3'-P	-6.93	1.52	1.61

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	P	27[A]	DA	O5'-P-OP2	-20.78	85.76	110.70
3	P	27[B]	DA	O5'-P-OP2	-20.78	85.76	110.70
3	P	27[A]	DA	OP1-P-OP2	13.64	140.06	119.60
3	P	27[B]	DA	OP1-P-OP2	13.64	140.06	119.60
1	A	560	PRO	N-CA-CB	6.82	111.48	103.30
1	A	250	PRO	N-CA-CB	6.50	111.10	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	625	PRO	N-CA-CB	5.93	110.42	103.30
2	C	198	ASP	CB-CG-OD1	5.27	123.05	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	852	ARG	Sidechain
2	B	363	ARG	Sidechain
2	B	75	ARG	Sidechain

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	7430	0	7235	112	0
2	B	2986	0	2959	40	0
2	C	2890	0	2873	36	0
3	P	392	0	213	3	0
4	T	386	0	213	8	0
All	All	14084	0	13493	187	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 (187) 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)
2:B:134:LYS:HE2	2:B:187:HIS:CD2	1.66	1.29
2:C:241:TRP:CD1	2:C:243:THR:CG2	2.33	1.12
2:C:241:TRP:NE1	2:C:243:THR:CG2	2.19	1.04
2:B:134:LYS:CE	2:B:187:HIS:CD2	2.44	1.01
2:C:241:TRP:CD1	2:C:243:THR:HG23	1.99	0.97
1:A:807:ARG:HH11	1:A:858:THR:HG22	1.35	0.93
1:A:597:ARG:HE	4:T:12:DC:H4'	1.34	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:241:TRP:CD1	2:C:243:THR:HG21	2.05	0.89
2:B:134:LYS:HE2	2:B:187:HIS:CG	2.07	0.88
2:C:241:TRP:NE1	2:C:243:THR:HG21	1.93	0.82
1:A:553:LYS:O	1:A:553:LYS:NZ	2.12	0.81
1:A:81:ARG:NE	1:A:912:GLY:HA3	1.96	0.81
2:B:134:LYS:CE	2:B:187:HIS:HD2	1.93	0.81
2:C:396:ARG:HH12	2:C:418:LEU:HB3	1.46	0.80
1:A:414:PHE:HZ	1:A:427:MET:SD	2.05	0.79
1:A:280:GLU:N	1:A:280:GLU:OE1	2.15	0.79
2:C:385:LEU:HD21	2:C:402:LEU:HD23	1.65	0.78
2:C:396:ARG:NH1	2:C:418:LEU:HB3	1.98	0.77
2:C:241:TRP:NE1	2:C:243:THR:HG22	1.99	0.77
1:A:414:PHE:CZ	1:A:427:MET:SD	2.78	0.77
1:A:81:ARG:CG	1:A:918:TRP:HZ3	2.00	0.74
2:B:445:GLU:N	2:B:445:GLU:OE2	2.19	0.74
2:C:241:TRP:HE1	2:C:243:THR:CG2	1.97	0.74
1:A:807:ARG:NH1	1:A:858:THR:HG22	2.02	0.73
1:A:81:ARG:CZ	1:A:912:GLY:N	2.51	0.73
1:A:81:ARG:HG2	1:A:918:TRP:HZ3	1.53	0.73
1:A:491:ASP:OD1	1:A:574:ARG:NH2	2.22	0.72
1:A:162:LEU:HD11	1:A:215:ILE:HD11	1.73	0.71
2:C:90:SER:OG	2:C:95:CYS:O	2.09	0.71
1:A:984:GLN:NE2	1:A:986:TYR:O	2.24	0.71
1:A:81:ARG:CZ	1:A:912:GLY:H	2.03	0.71
2:C:441:VAL:HG13	2:C:453:ILE:HD12	1.74	0.70
2:B:409:ASN:HD21	2:B:472:LYS:HE2	1.56	0.69
2:B:252:LEU:HA	2:B:336:LEU:HD11	1.74	0.69
2:C:277:ASP:OD1	2:C:287:ASN:ND2	2.24	0.69
1:A:857:PRO:O	1:A:861:THR:OG1	2.11	0.69
1:A:399:ASP:O	1:A:403:THR:HG23	1.93	0.69
1:A:1074:VAL:HG12	1:A:1075:LEU:HD23	1.76	0.67
1:A:597:ARG:HD2	4:T:12:DC:H5"	1.76	0.67
2:B:130:ALA:O	2:B:182:ARG:NH1	2.27	0.66
1:A:597:ARG:CD	4:T:12:DC:H5"	2.25	0.66
2:C:241:TRP:HE1	2:C:243:THR:HG21	1.58	0.66
1:A:597:ARG:HE	4:T:12:DC:C4'	2.09	0.66
1:A:81:ARG:CG	1:A:918:TRP:CZ3	2.78	0.66
2:B:120:VAL:HG13	2:C:407:LEU:HD12	1.79	0.64
1:A:807:ARG:HH11	1:A:858:THR:CG2	2.09	0.64
2:B:438:LEU:O	2:B:458:ARG:N	2.31	0.64
1:A:115:GLN:N	1:A:115:GLN:OE1	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:474:LEU:HD23	2:B:462:MET:HE1	1.79	0.64
1:A:1067:SER:OG	1:A:1071:ARG:HD2	1.99	0.63
1:A:199:VAL:HG12	1:A:212:ALA:HB2	1.80	0.63
1:A:225:SER:O	1:A:227:ARG:NH1	2.32	0.63
1:A:858:THR:O	1:A:862:ALA:HB2	1.98	0.63
2:C:396:ARG:HH12	2:C:418:LEU:CB	2.12	0.63
1:A:474:LEU:HD23	2:B:462:MET:CE	2.29	0.62
2:C:393:LEU:O	2:C:393:LEU:HD13	1.98	0.62
1:A:1135:ASP:OD2	3:P:27[A]:DA:H2"	1.99	0.62
1:A:213:VAL:HG23	1:A:400:VAL:HG21	1.82	0.61
1:A:1093:MET:SD	1:A:1096:ARG:NH2	2.73	0.61
2:B:365:LYS:HE3	2:B:367:LEU:HB2	1.83	0.60
1:A:265:LEU:HD21	1:A:292:LEU:HD11	1.83	0.60
1:A:1124:ALA:O	1:A:1148:ARG:NH2	2.34	0.60
1:A:597:ARG:NE	4:T:12:DC:H4'	2.12	0.59
1:A:909:GLY:O	1:A:1170:LEU:HD13	2.03	0.58
1:A:401:TRP:NE1	1:A:405:GLU:OE2	2.35	0.58
2:C:117:SER:O	2:C:122:ARG:NH2	2.36	0.58
2:B:204:LEU:HD21	2:B:333:PRO:HB3	1.85	0.58
2:B:134:LYS:HE3	2:B:187:HIS:HD2	1.69	0.57
1:A:263:GLU:OE2	1:A:288:ARG:NH2	2.37	0.57
1:A:885:THR:OG1	1:A:1186:ASP:O	2.12	0.57
1:A:81:ARG:HD3	1:A:918:TRP:CZ3	2.39	0.57
1:A:774:MET:HB2	1:A:779:LEU:HD13	1.85	0.57
2:B:75:ARG:CZ	2:B:75:ARG:CB	2.82	0.56
1:A:474:LEU:HD21	1:A:492:LEU:HD21	1.88	0.56
2:C:279:GLN:O	2:C:279:GLN:HG3	2.06	0.56
1:A:862:ALA:HB3	1:A:875:LYS:HE3	1.87	0.55
1:A:265:LEU:HD21	1:A:292:LEU:CD1	2.36	0.55
1:A:611:PRO:C	1:A:612:LEU:HD12	2.27	0.55
2:B:393:LEU:HD13	2:B:394:GLU:H	1.72	0.55
2:B:370:LYS:NZ	2:B:434:GLU:OE2	2.39	0.54
1:A:79:LEU:O	1:A:80:SER:OG	2.22	0.54
1:A:381:THR:N	1:A:384:ASP:OD2	2.40	0.54
1:A:81:ARG:HG2	1:A:918:TRP:CZ3	2.39	0.54
1:A:850:ILE:HD12	1:A:851:THR:N	2.23	0.54
1:A:81:ARG:HH22	1:A:910:MET:HB3	1.73	0.53
2:B:469:SER:O	2:B:470:LYS:HG2	2.09	0.53
2:B:350:LEU:HD23	2:B:374:LEU:HD11	1.89	0.53
1:A:239:LEU:HD13	1:A:239:LEU:O	2.08	0.53
2:B:86:LEU:HD12	2:B:86:LEU:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:308:ASP:N	2:C:308:ASP:OD1	2.41	0.52
1:A:199:VAL:HG12	1:A:212:ALA:CB	2.38	0.52
3:P:26:DG:C2	3:P:27[B]:DA:N6	2.77	0.52
1:A:597:ARG:HD3	1:A:614:TYR:CE1	2.43	0.52
4:T:16:DC:H2'	4:T:17:DT:C6	2.44	0.52
1:A:302:SER:HG	1:A:363:TYR:HH	1.55	0.52
1:A:988:ALA:N	1:A:1056:GLU:OE2	2.43	0.52
2:C:441:VAL:CG1	2:C:453:ILE:HD12	2.40	0.52
1:A:553:LYS:NZ	1:A:557:GLU:OE2	2.34	0.52
1:A:459:MET:SD	1:A:594:LEU:HD23	2.50	0.51
2:C:403:PHE:CE1	2:C:413:VAL:HG13	2.45	0.51
1:A:432:VAL:HG12	1:A:432:VAL:O	2.10	0.51
1:A:81:ARG:NH2	1:A:912:GLY:H	2.07	0.51
1:A:851:THR:O	1:A:1106:VAL:HG21	2.11	0.51
1:A:945:HIS:CD2	1:A:965:LEU:HD12	2.45	0.51
1:A:597:ARG:HE	4:T:12:DC:C5'	2.23	0.50
2:B:306:LEU:O	2:B:309:HIS:ND1	2.45	0.50
1:A:100:VAL:O	1:A:104:VAL:HG23	2.12	0.50
1:A:162:LEU:CD1	1:A:215:ILE:HD11	2.41	0.50
2:B:75:ARG:CZ	2:B:75:ARG:HB2	2.42	0.50
1:A:849:THR:HG22	1:A:851:THR:H	1.77	0.49
1:A:762:VAL:HG22	3:P:22:DG:OP1	2.12	0.49
2:B:460:THR:O	2:B:462:MET:N	2.45	0.49
2:B:69:LEU:HD13	2:B:69:LEU:O	2.13	0.49
1:A:275:ARG:HD3	1:A:291:PHE:CD1	2.46	0.49
2:C:436:SER:O	2:C:436:SER:OG	2.28	0.49
1:A:271:VAL:N	1:A:293:ASP:OD2	2.47	0.48
1:A:1174:PRO:HG2	1:A:1177:VAL:HG22	1.94	0.48
1:A:945:HIS:NE2	1:A:965:LEU:HD12	2.27	0.48
4:T:17:DT:OP2	4:T:17:DT:H73	2.13	0.48
1:A:743:ASP:N	1:A:743:ASP:OD1	2.44	0.48
1:A:1167:LYS:C	1:A:1168:LEU:HD12	2.34	0.48
1:A:1079:ILE:HG23	1:A:1080:SER:H	1.78	0.47
1:A:81:ARG:CZ	1:A:912:GLY:HA3	2.45	0.47
1:A:913:CYS:SG	1:A:914:THR:N	2.89	0.46
1:A:81:ARG:CZ	1:A:912:GLY:CA	2.93	0.46
1:A:807:ARG:HB3	1:A:858:THR:CG2	2.46	0.46
2:B:393:LEU:HD13	2:B:394:GLU:N	2.31	0.46
1:A:1109:LEU:HD12	1:A:1109:LEU:O	2.16	0.46
1:A:1190:ARG:NH2	1:A:1209:ARG:O	2.49	0.46
2:B:409:ASN:ND2	2:B:472:LYS:HE2	2.26	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:441:VAL:HG22	2:B:455:LEU:CD1	2.46	0.46
2:C:386:ASP:OD1	2:C:422:GLN:NE2	2.48	0.46
2:B:77:HIS:NE2	2:B:434:GLU:OE1	2.35	0.45
1:A:556:THR:OG1	1:A:557:GLU:N	2.48	0.45
2:B:220:ASP:O	2:B:221:THR:OG1	2.23	0.45
1:A:100:VAL:HG12	1:A:104:VAL:HG23	1.99	0.45
1:A:850:ILE:HD12	1:A:851:THR:HG23	1.99	0.45
1:A:1085:PRO:O	1:A:1086:SER:OG	2.29	0.45
1:A:932:HIS:O	1:A:935:THR:OG1	2.34	0.45
2:C:450:ASN:OD1	2:C:450:ASN:N	2.49	0.45
1:A:451:THR:HG22	1:A:455:LEU:HD23	1.99	0.45
1:A:911:HIS:CD2	1:A:1170:LEU:HD12	2.51	0.45
2:C:252:LEU:HB2	2:C:336:LEU:HD11	1.99	0.45
1:A:1224:ILE:HD12	1:A:1224:ILE:H	1.81	0.45
1:A:228:LEU:HD12	1:A:228:LEU:H	1.81	0.44
1:A:537:GLU:OE2	1:A:540:GLN:NE2	2.51	0.44
2:B:204:LEU:HD11	2:B:333:PRO:HB3	1.99	0.44
1:A:302:SER:OG	1:A:363:TYR:OH	2.25	0.44
2:B:220:ASP:N	2:B:220:ASP:OD1	2.50	0.44
2:B:204:LEU:HD23	2:B:324:GLY:HA3	2.00	0.44
1:A:81:ARG:CD	1:A:918:TRP:CZ3	3.01	0.44
1:A:81:ARG:CD	1:A:918:TRP:HZ3	2.30	0.44
1:A:1075:LEU:HD21	1:A:1107:ASP:OD1	2.18	0.44
1:A:1093:MET:O	1:A:1097:VAL:HG13	2.18	0.44
2:C:465:MET:HA	2:C:465:MET:HE2	2.00	0.43
1:A:81:ARG:HD3	1:A:918:TRP:CE3	2.53	0.43
1:A:158:LEU:O	1:A:408:GLN:NE2	2.51	0.43
1:A:776:ASP:OD1	1:A:778:THR:HG22	2.18	0.43
1:A:1079:ILE:HG23	1:A:1080:SER:N	2.33	0.43
2:B:382:LYS:O	2:B:438:LEU:N	2.49	0.43
1:A:1150:ALA:HB1	1:A:1183:VAL:HG11	1.99	0.43
2:B:418:LEU:HD13	2:C:203:ARG:HH22	1.84	0.43
1:A:81:ARG:NH1	1:A:912:GLY:N	2.66	0.43
2:B:376:PRO:HA	2:B:438:LEU:HD21	2.00	0.43
2:C:116:THR:HA	2:C:120:VAL:HG22	2.01	0.43
2:B:191:GLU:HG3	2:B:314:MET:HE1	1.99	0.43
2:C:405:GLU:O	2:C:409:ASN:ND2	2.50	0.42
2:C:374:LEU:O	2:C:458:ARG:NH2	2.50	0.42
1:A:605:LEU:HD13	1:A:610:PHE:HA	2.00	0.42
1:A:225:SER:O	1:A:225:SER:OG	2.37	0.42
2:C:87:SER:OG	2:C:88:ARG:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:126:PHE:CD2	2:C:199:LEU:HD23	2.55	0.42
1:A:225:SER:OG	1:A:227:ARG:NH1	2.53	0.42
2:B:383:VAL:CG2	2:B:441:VAL:HG23	2.50	0.42
2:B:464:GLU:HA	2:B:464:GLU:OE2	2.19	0.42
1:A:455:LEU:O	1:A:794:ILE:HD11	2.20	0.41
2:B:469:SER:O	2:B:470:LYS:CG	2.68	0.41
2:C:395:LEU:HD21	2:C:448:LEU:HD21	2.02	0.41
1:A:606:THR:HG22	1:A:779:LEU:HG	2.02	0.41
1:A:155:ASN:O	1:A:159:GLN:NE2	2.53	0.41
1:A:432:VAL:O	1:A:432:VAL:CG1	2.69	0.41
1:A:607:TRP:N	1:A:778:THR:O	2.44	0.41
1:A:180:PRO:O	1:A:181:GLU:HG2	2.20	0.41
1:A:892:ASP:OD2	1:A:1181:SER:OG	2.24	0.41
2:C:279:GLN:O	2:C:279:GLN:CG	2.69	0.41
2:C:389:ARG:O	2:C:391:PRO:HD3	2.20	0.41
1:A:237:SER:O	1:A:814:VAL:HG13	2.20	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	927/1239 (75%)	854 (92%)	71 (8%)	2 (0%)	47 69
2	B	366/485 (76%)	342 (93%)	24 (7%)	0	100 100
2	C	350/485 (72%)	334 (95%)	16 (5%)	0	100 100
All	All	1643/2209 (74%)	1530 (93%)	111 (7%)	2 (0%)	54 75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	250	PRO

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Mol	Chain	Res	Type
1	A	560	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	782/1044 (75%)	750 (96%)	32 (4%)	30 50
2	B	325/426 (76%)	312 (96%)	13 (4%)	31 51
2	C	317/426 (74%)	300 (95%)	17 (5%)	22 38
All	All	1424/1896 (75%)	1362 (96%)	62 (4%)	32 47

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	105	GLU
1	A	115	GLN
1	A	152	GLU
1	A	203	LEU
1	A	235	TRP
1	A	239	LEU
1	A	293	ASP
1	A	396	CYS
1	A	424	LEU
1	A	447	GLU
1	A	533	CYS
1	A	538	GLU
1	A	616	GLU
1	A	740	ASN
1	A	741	ASP
1	A	747	CYS
1	A	749	PHE
1	A	752	LEU
1	A	907	PHE
1	A	910	MET
1	A	925	LYS

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Mol	Chain	Res	Type
1	A	964	ARG
1	A	1063	SER
1	A	1068	ASP
1	A	1075	LEU
1	A	1107	ASP
1	A	1132	SER
1	A	1134	HIS
1	A	1209	ARG
1	A	1218	LEU
1	A	1221	TYR
1	A	1226	LEU
2	B	75	ARG
2	B	78	PHE
2	B	79	LEU
2	B	219	PHE
2	B	220	ASP
2	B	238	SER
2	B	246	ARG
2	B	253	ASP
2	B	308	ASP
2	B	334	CYS
2	B	450	ASN
2	B	458	ARG
2	B	484	ASN
2	C	80	SER
2	C	89	ASP
2	C	107	ARG
2	C	219	PHE
2	C	238	SER
2	C	278	CYS
2	C	279	GLN
2	C	281	GLU
2	C	306	LEU
2	C	308	ASP
2	C	312	LEU
2	C	314	MET
2	C	323	HIS
2	C	329	LYS
2	C	377	CYS
2	C	436	SER
2	C	459	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	GLN
1	A	138	HIS
1	A	144	GLN
1	A	493	GLN
1	A	811	GLN
1	A	975	GLN
1	A	1157	ASN
2	B	187	HIS
2	B	355	GLN
2	C	309	HIS
2	C	313	HIS

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.

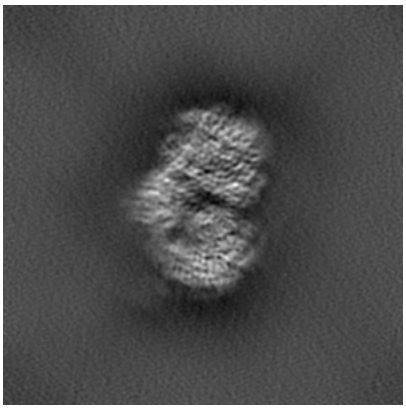
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-29745. These allow visual inspection of the internal detail of the map and identification of artifacts.

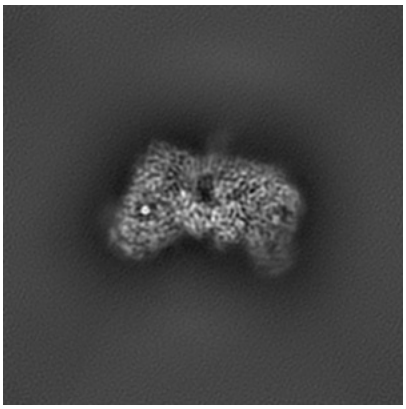
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

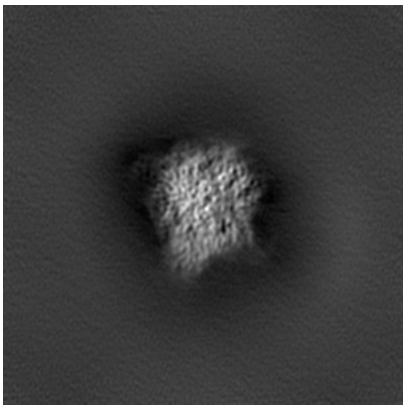
6.1.1 Primary map



X

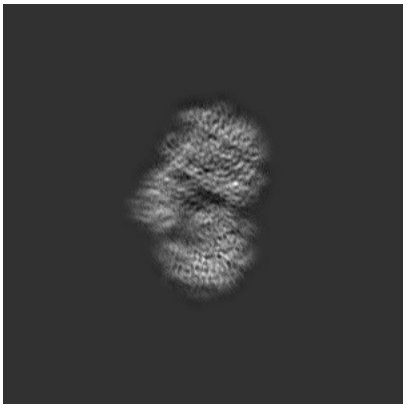


Y

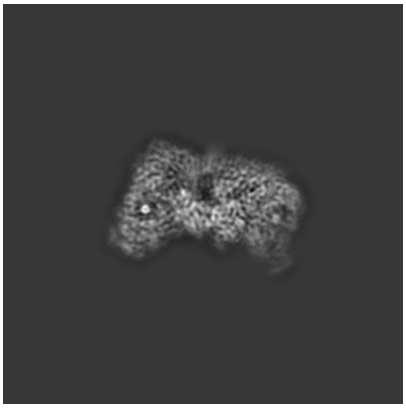


Z

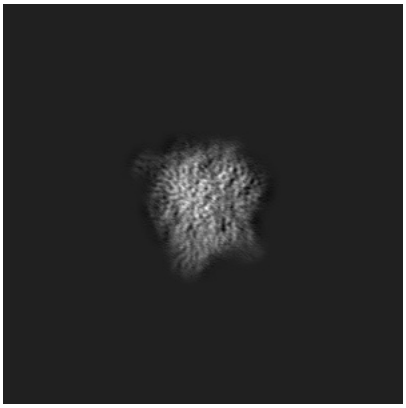
6.1.2 Raw map



X



Y

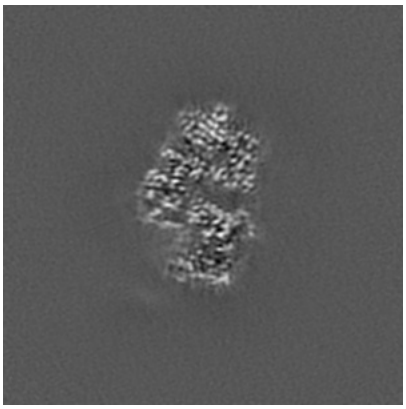


Z

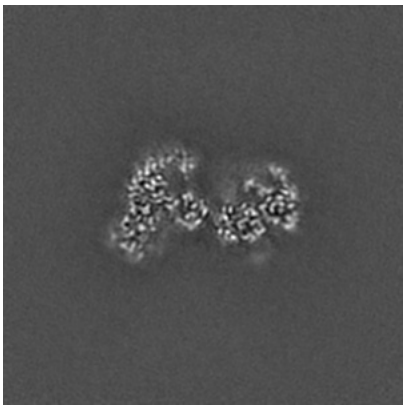
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

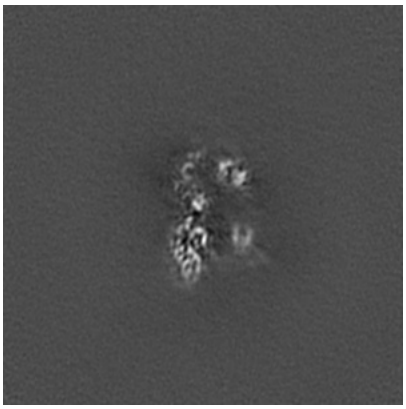
6.2.1 Primary map



X Index: 160



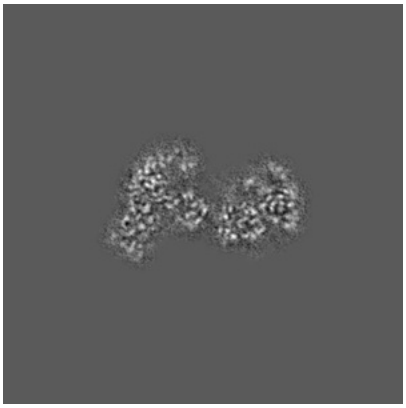
Y Index: 160



Z Index: 160

6.2.2 Raw map

X Index: 160



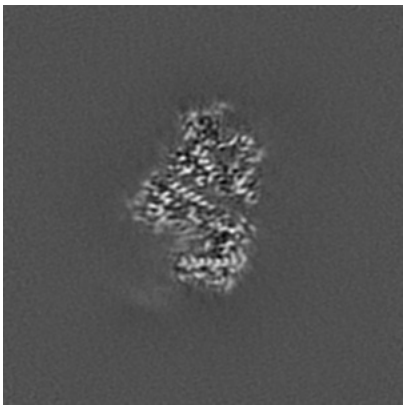
Y Index: 160

Z Index: 160

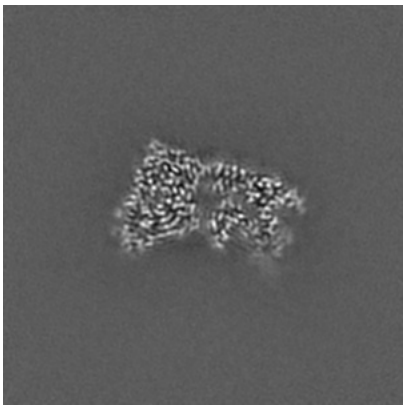
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

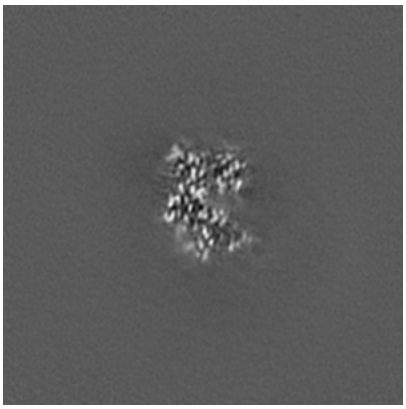
6.3.1 Primary map



X Index: 154



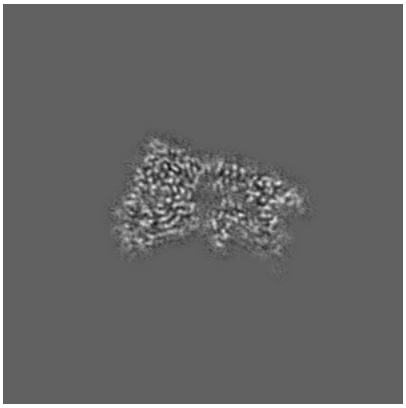
Y Index: 178



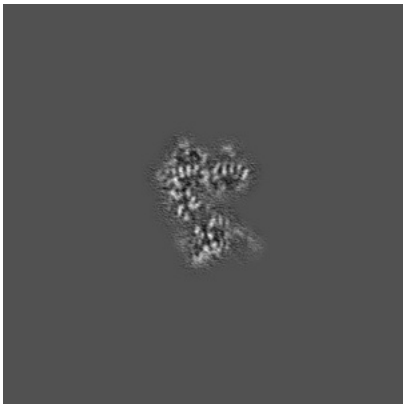
Z Index: 184

6.3.2 Raw map

X Index: 154



Y Index: 178

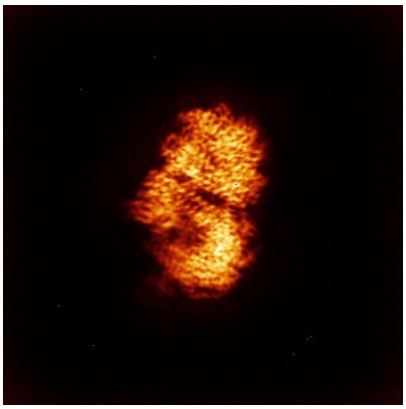


Z Index: 176

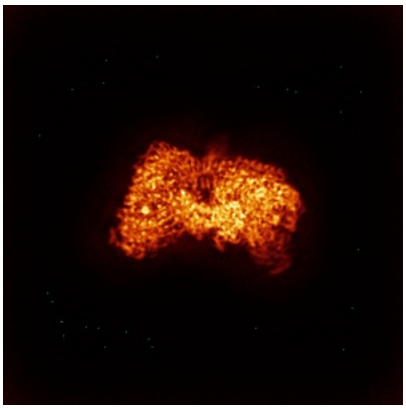
The images above show the largest variance slices of the map in three orthogonal directions.

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

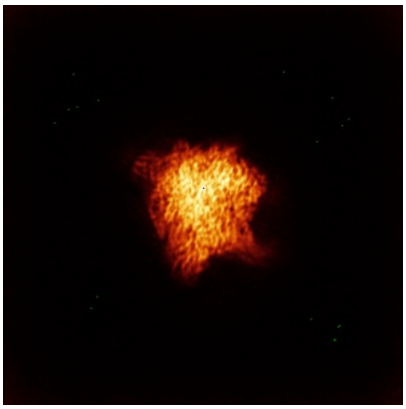
6.4.1 Primary map



X

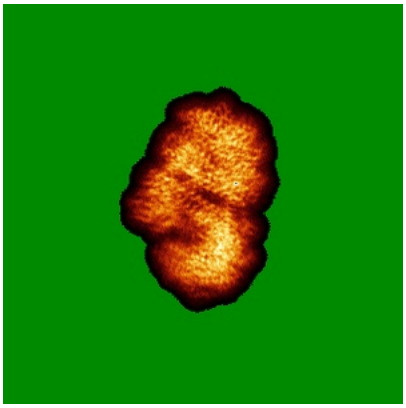


Y

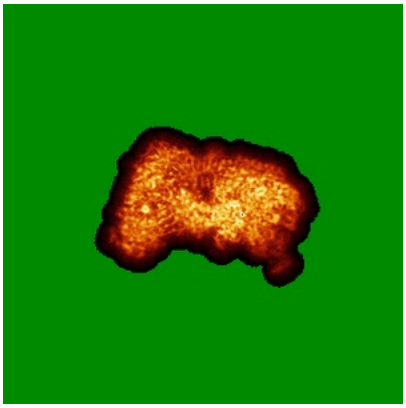


Z

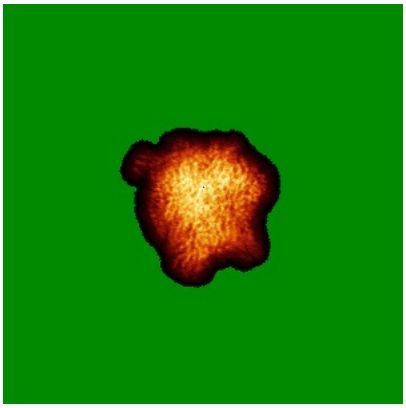
6.4.2 Raw map



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

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 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.

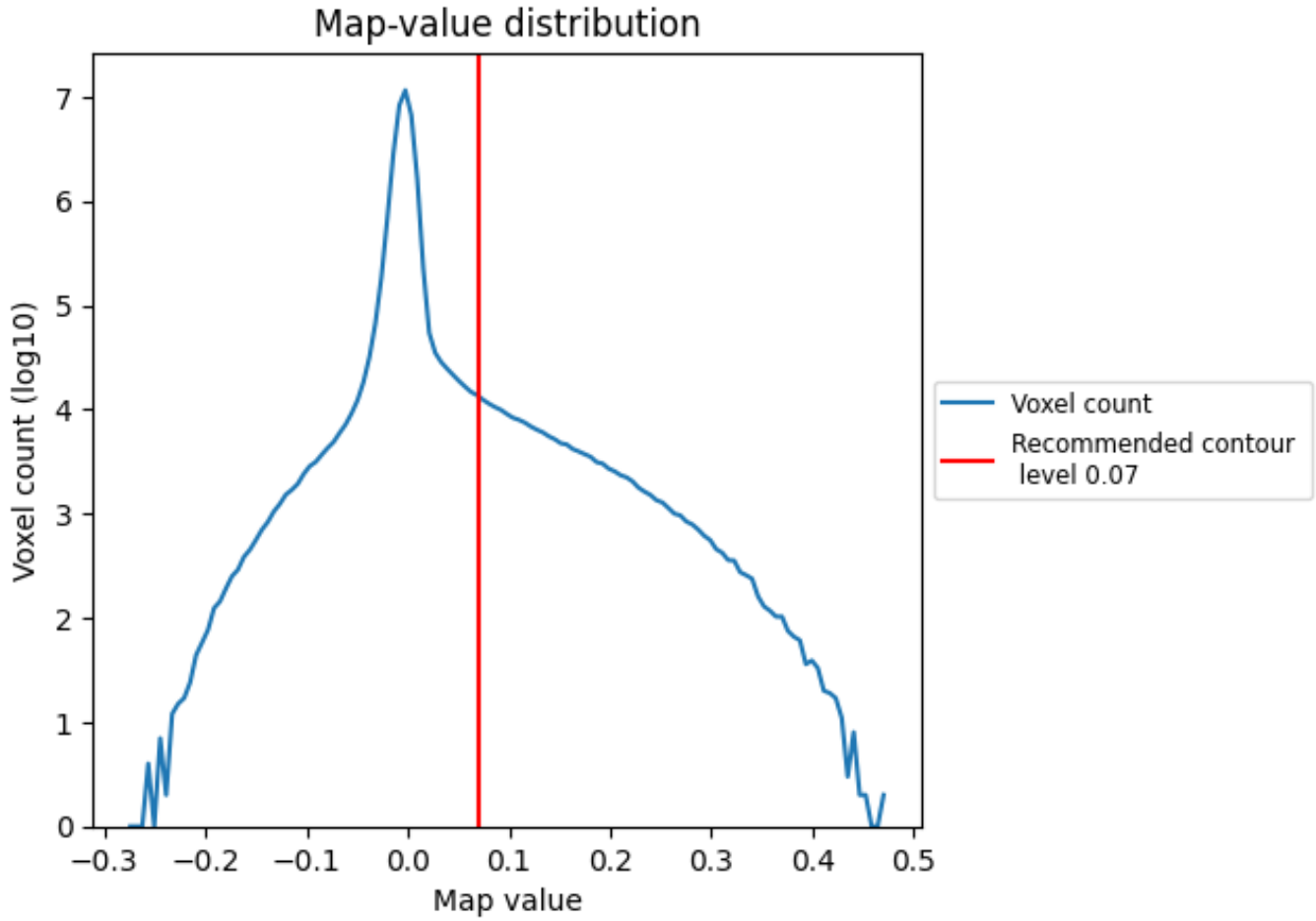
6.6 Mask visualisation (i)

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

7 Map analysis

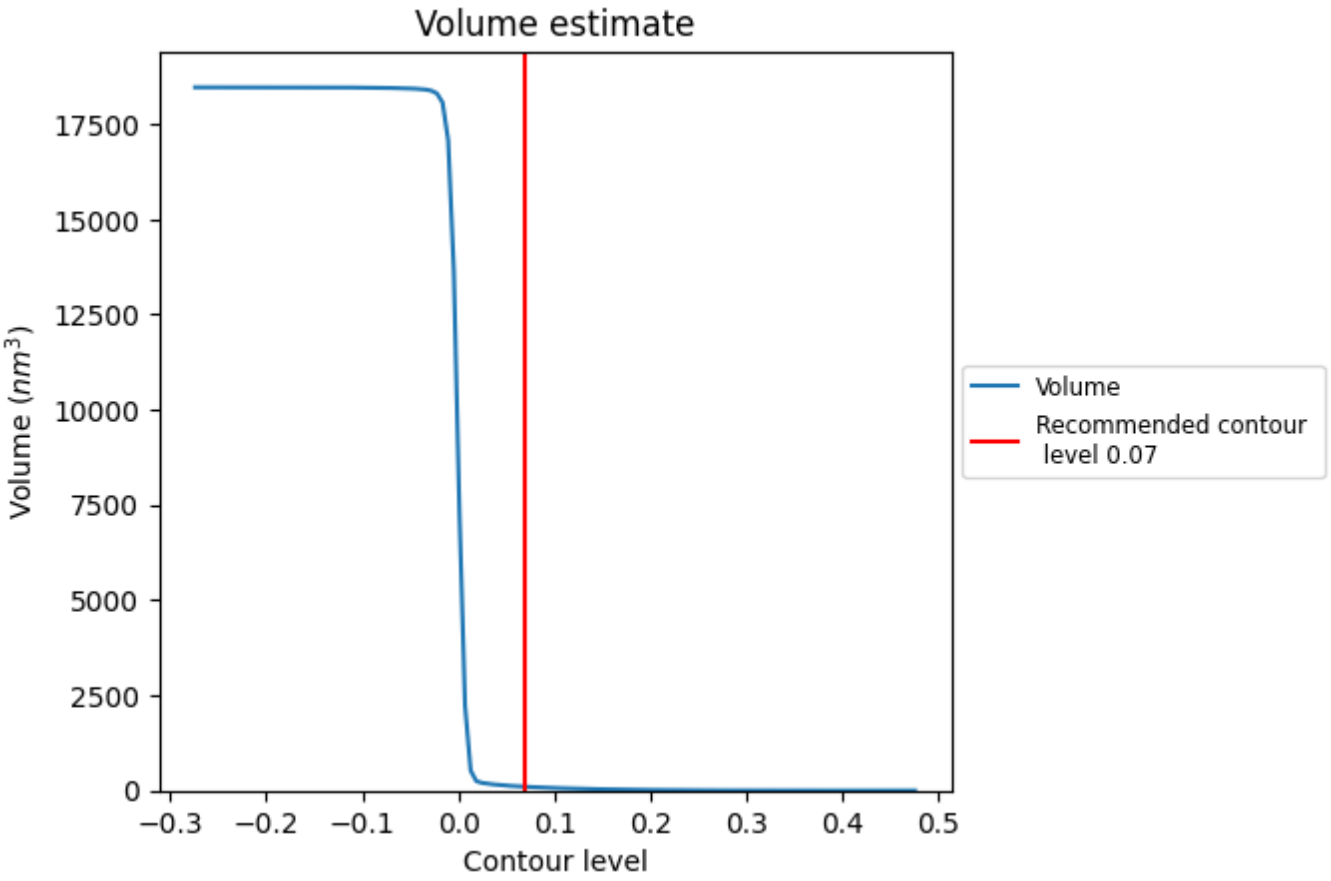
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

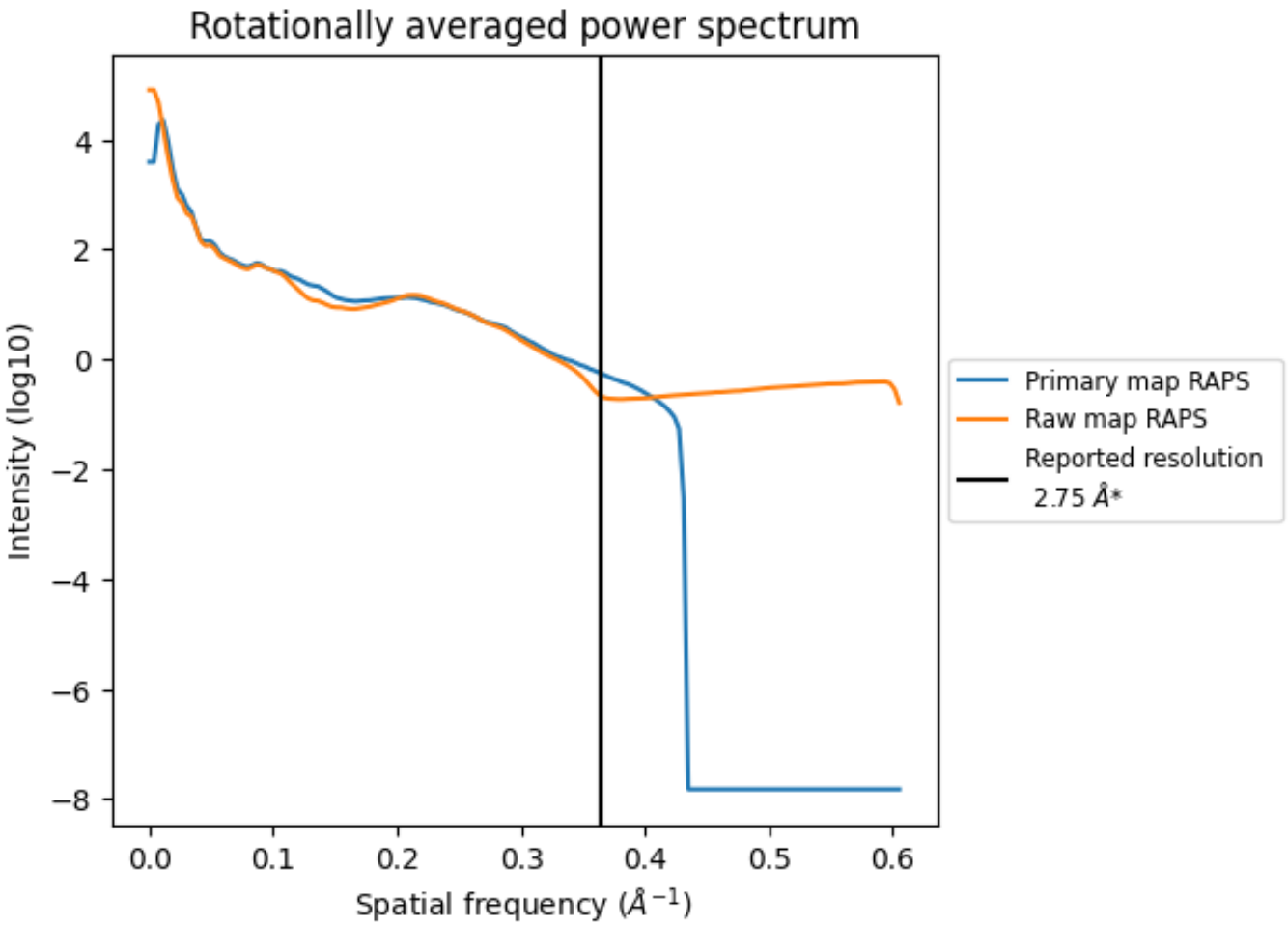
7.2 Volume estimate



The volume at the recommended contour level is 100 nm^3; this corresponds to an approximate mass of 90 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)

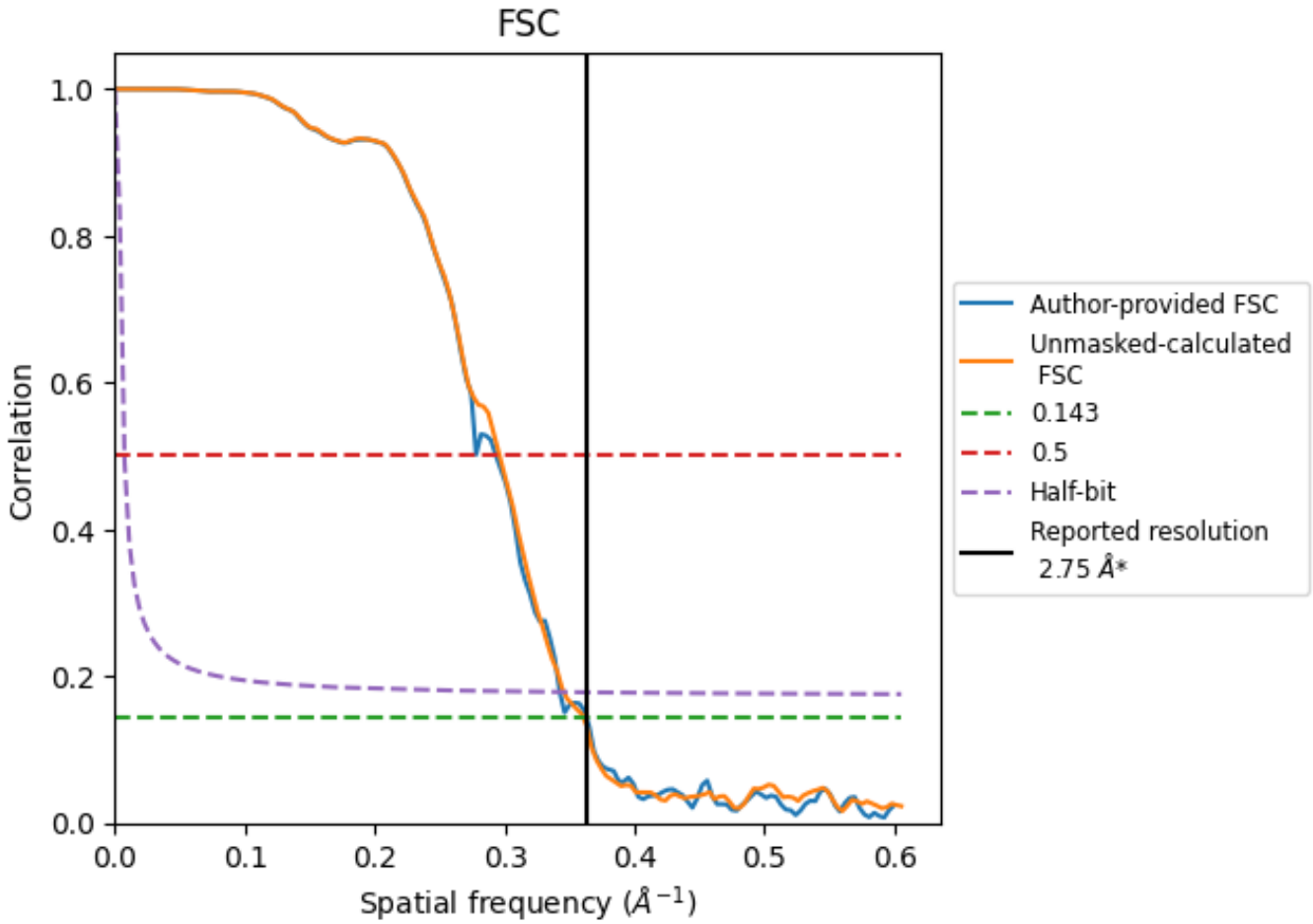


*Reported resolution corresponds to spatial frequency of 0.364 Å^{-1}

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 0.364 Å^{-1}

8.2 Resolution estimates (i)

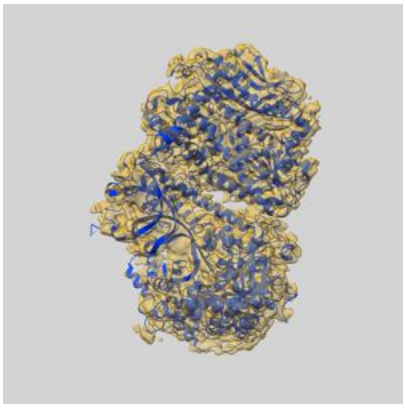
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.75	-	-
Author-provided FSC curve	2.75	3.41	2.92
Unmasked-calculated*	2.77	3.37	2.89

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

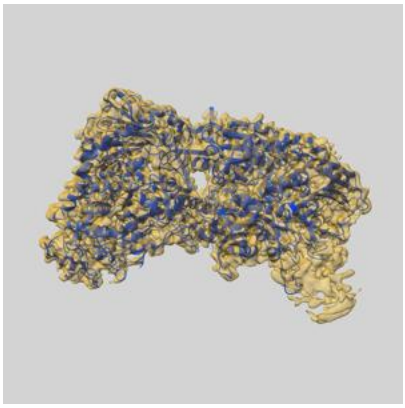
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-29745 and PDB model 8G5I. Per-residue inclusion information can be found in section 3 on page 4.

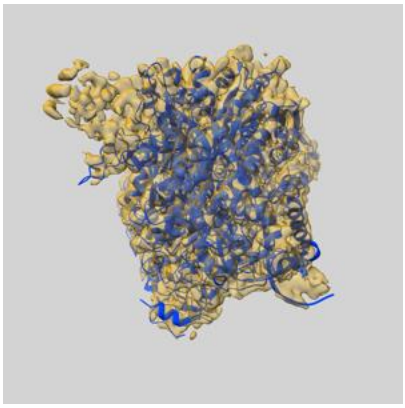
9.1 Map-model overlay



X



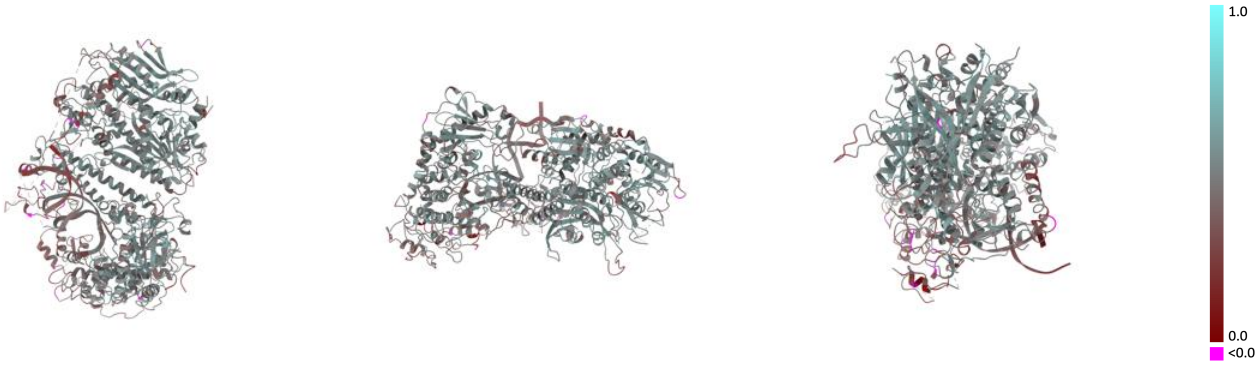
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.07 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.

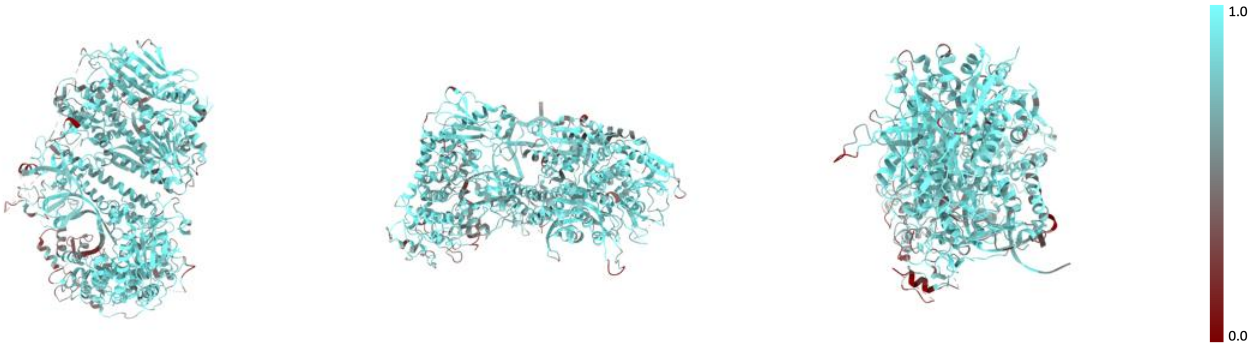
9.2 Q-score mapped to coordinate model



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.

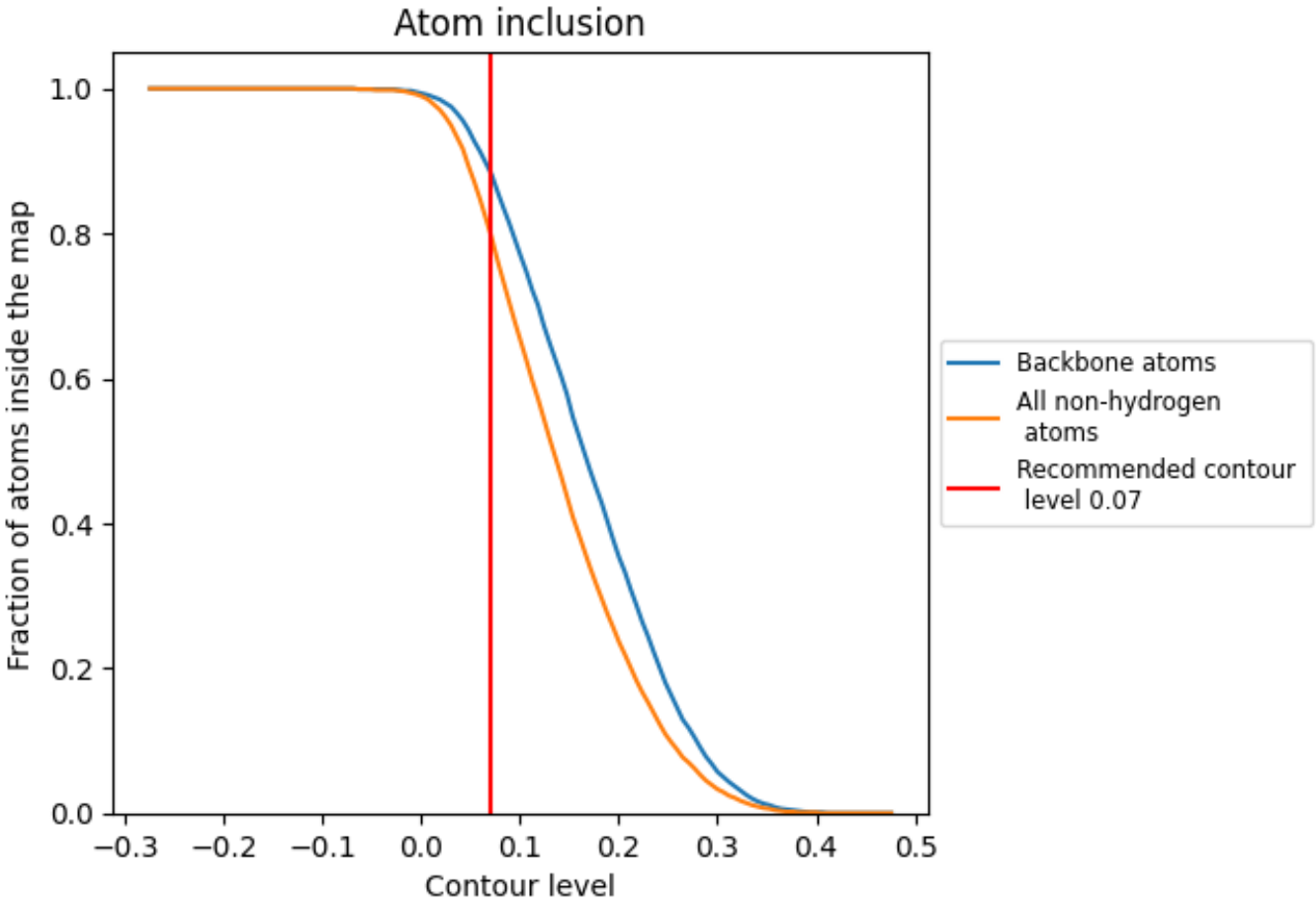
9.3 Atom inclusion mapped to coordinate model



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 (0.07).

9.4 Atom inclusion (i)



At the recommended contour level, 89% of all backbone atoms, 80% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8010	0.4700
A	0.7790	0.4490
B	0.8330	0.5050
C	0.8470	0.5100
P	0.7580	0.3750
T	0.6840	0.3770