



Full wwPDB EM Validation Report ⓘ

May 27, 2026 – 12:27 PM JST

PDB ID : 22BJ / pdb_000022bj
EMDB ID : EMD-68152
Title : KCNQ2/3 heterotetramer with 3:1 stoichiometry
Authors : Lu, F.; Fan, X.; Huang, J.
Deposited on : 2026-01-05
Resolution : 2.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

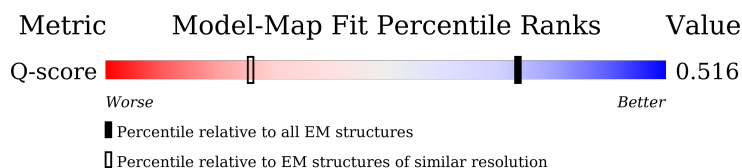
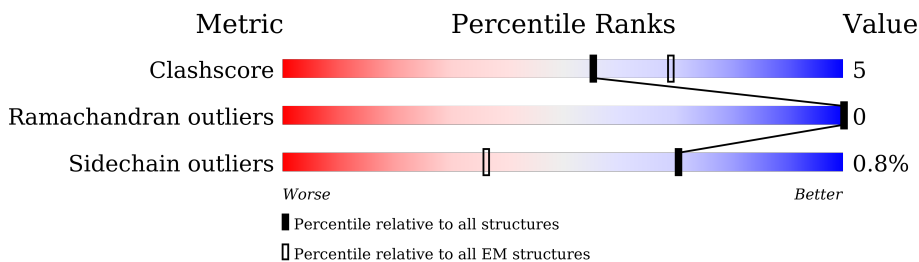
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5628 (1.90 - 2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	872	
1	B	872	
1	C	872	
2	D	872	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8084 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 Potassium voltage-gated channel subfamily KQT member 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	248	Total	C	N	O	S	0	0
			2016	1339	339	329	9		
1	B	248	Total	C	N	O	S	0	0
			2016	1339	339	329	9		
1	C	249	Total	C	N	O	S	0	0
			2027	1345	343	330	9		

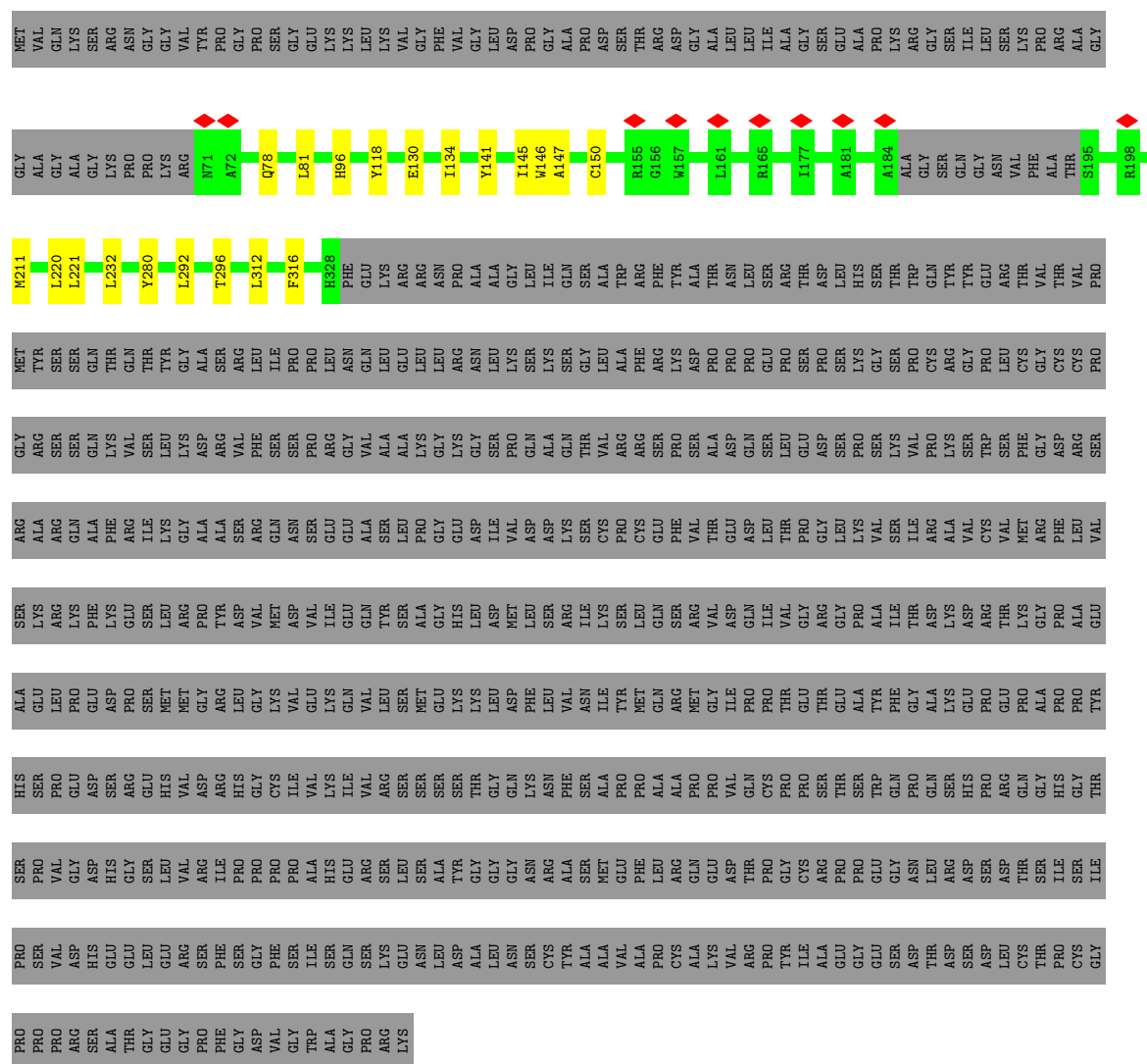
- Molecule 2 is a protein called Potassium voltage-gated channel subfamily KQT member 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	251	Total	C	N	O	S	0	0
			2021	1341	337	333	10		

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

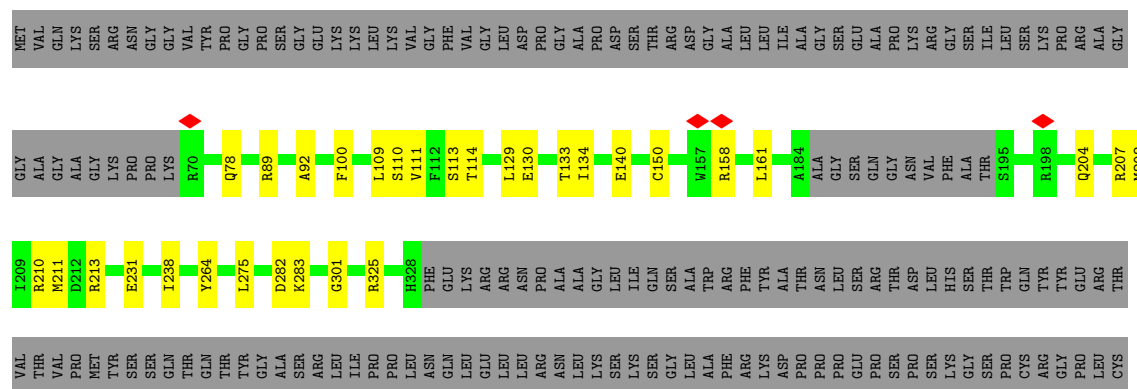
Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	K	0
			1	1	
3	C	3	Total	K	0
			3	3	

Chain B:  26% 72%



- Molecule 1: Potassium voltage-gated channel subfamily KQT member 2

Chain C:  25% 71%



[illegible]

- Molecule 2: Potassium voltage-gated channel subfamily KQT member 3



MET	THR	PHE	ILE	ALA	ARG	R236	A122	ALA	MET
GLY	THR	THR	GLU	ILE	ILE	L249	L123	ASP	GLY
LYS	GLY	LEU	LEU	GLU	LEU	L250	L124	LYS	LYS
LEU	PRO	LYS	SER	SER	VAL	K259	L128	GLY	ALA
ASP	PRO	ALA	SER	PRO	ALA	E260	V129	THR	ARG
PHE	SER	ALA	SER	SER	THR	F269	F130	LEU	ARG
LEU	THR	ILE	ILE	LYS	TRP	V282	I131	LEU	ALA
VAL	PRO	ARG	GLU	PRO	PHE	E283	I132	GLY	ALA
ASP	LYS	ALA	PRO	PRO	THR	E296	G135	GLY	ALA
MET	HIS	VAL	PRO	LYS	GLU	M296	A140	GLY	ALA
HIS	LYS	ARG	VAL	PRO	SER	E288	T144	GLY	GLY
MET	LYS	ILE	VAL	VAL	VAL	VAL	L157	GLN	GLY
GLN	SER	LEU	LEU	LYS	PHE	ASP	E160	ARG	GLY
HIS	GLN	GLN	GLU	GLU	PHE	ALA	I174	GLY	GLY
GLY	THR	THR	THR	GLU	PHE	GLN	F165	THR	GLY
THR	GLY	LYS	ARG	ARG	ARG	GLY	R174	PRO	GLY
GLY	VAL	PHE	THR	THR	LYS	GLU	G180	GLN	GLY
VAL	PRO	PHE	THR	ALA	GLN	E295	A178	ARG	GLY
THR	GLN	GLU	PHE	ALA	LEU	M296	G179	ALA	ALA
GLU	THR	THR	MET	ARG	GLU	D321	C181	LEU	ASN
TYR	GLN	SER	LEU	LYS	ALA	K325	C182	PRO	ALA
PRO	PRO	ARG	ALA	ALA	SER	T326	C182	LYS	ALA
THR	ASN	PRO	TYR	TYR	SER	W327	R183	THR	GLY
LYS	GLU	ASP	ALA	PHE	GLN	E328	G184	PRO	GLY
GLY	PRO	VAL	THR	TRP	LYS	G329	Y184	ASP	GLY
THR	SER	VAL	ASP	TRP	LEU	R330	K185	LEU	ALA
SER	VAL	VAL	ASP	GLN	GLY	R364	R188	SER	ALA
PRO	ALA	ARG	SER	SER	LEU	H367	K192	ARG	ALA
ALA	ARG	ILE	GLU	GLU	ASP	PHE	R195	VAL	ALA
GLU	PRO	GLU	ASP	GLU	THR	GLU	V210	LYS	VAL
ALA	SER	GLN	ASP	ASP	VAL	TYR	P211	GLU	GLY
GLU	THR	THR	GLY	GLY	ARG	LYS	V212	ASN	GLY
LYS	SER	ALA	THR	THR	LEU	ARG	VAL	ASN	ARG
GLY	ILE	GLY	GLY	GLY	SER	SER	ALA	ALA	LYS
ASP	GLU	HIS	ASP	ASP	ASN	LYS	ALA	ALA	VAL
ASN	ASN	LEU	LEU	PRO	PRO	PRO	VAL	ALA	GLY
ARG	ARG	ASP	ASP	MET	ALA	ALA	P211	LEU	ALA
TYR	SER	MET	MET	GLY	GLY	GLY	V212	PRO	PRO
SER	MET	LEU	LEU	GLY	SER	GLU	VAL	GLY	ALA
ASP	MET	SER	SER	ASP	ASN	ASN	ALA	ASN	PRO
LEU	GLY	ARG	ARG	ARG	THR	LEU	VAL	THR	THR
LYS	LYS	PHE	ILE	GLY	ILE	ILE	VAL	GLY	GLY
THR	THR	PHE	LYS	TYR	GLY	GLN	ASN	GLN	GLN
ILE	ILE	VAL	THR	GLY	LYS	ALA	THR	GLY	THR
LYS	VAL	VAL	GLN	ASN	LEU	ASN	ASN	GLY	VAL
CYS	VAL	VAL	GLN	ASP	PHE	ASP	ASN	THR	THR
ASN	GLU	GLU	THR	PHE	THR	TYR	V221	LEU	ALA
TYR	SER	GLN	ILE	ILE	PRO	PRO	L222	ALA	ALA
GLU	VAL	ASP	GLU	ILE	LEU	ALA	A223	LEU	GLY
THR	GLN	MET	ASP	THR	ASN	THR	R117	ALA	GLY
TYR	ASP	THR	THR	MET	ASP	ASN	P113	ALA	GLY

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

ILE

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	664977	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.591	Depositor
Minimum map value	-1.025	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	262.08, 262.08, 262.08	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93599993, 0.93599993, 0.93599993	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section:
K

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	0.10	0/2071	0.25	0/2805
1	B	0.11	0/2071	0.24	0/2805
1	C	0.11	0/2082	0.23	0/2819
2	D	0.21	0/2070	0.33	0/2801
All	All	0.14	0/8294	0.27	0/11230

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
1	C	0	1
2	D	0	4
All	All	0	6

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	210	ARG	Sidechain
1	C	213	ARG	Sidechain
2	D	105	ARG	Sidechain
2	D	106	ARG	Sidechain
2	D	227	ARG	Sidechain
2	D	230	ARG	Sidechain

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	2016	0	2053	23	0
1	B	2016	0	2053	16	0
1	C	2027	0	2066	20	0
2	D	2021	0	2101	38	0
3	A	1	0	0	0	0
3	C	3	0	0	0	0
All	All	8084	0	8273	82	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 5.

All (82) 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:D:192:LYS:CE	2:D:195:ARG:HE	1.50	1.22
2:D:192:LYS:HE2	2:D:195:ARG:HE	1.06	1.09
2:D:192:LYS:HE2	2:D:195:ARG:NE	1.75	1.01
1:B:118:TYR:HH	2:D:327:TRP:CD1	1.89	0.90
2:D:192:LYS:HE3	2:D:195:ARG:HE	1.36	0.90
2:D:192:LYS:CE	2:D:195:ARG:NE	2.32	0.86
2:D:192:LYS:HE2	2:D:195:ARG:HH21	1.56	0.71
2:D:192:LYS:HE2	2:D:195:ARG:CZ	2.20	0.70
2:D:192:LYS:HE2	2:D:195:ARG:NH2	2.08	0.69
1:C:100:PHE:HE1	1:C:208:MET:HE3	1.60	0.66
1:B:78:GLN:HG2	1:B:150:CYS:HB3	1.76	0.66
1:A:155:ARG:HE	1:A:156:GLY:H	1.48	0.62
1:A:220:LEU:HD22	2:D:259:LYS:HE3	1.81	0.61
2:D:325:LYS:HA	2:D:330:ARG:HH11	1.65	0.60
1:C:133:THR:HG21	1:C:204:GLN:HE22	1.65	0.60
1:A:204:GLN:OE1	1:A:207:ARG:NH1	2.35	0.59
2:D:157:LEU:HD13	2:D:226:LEU:HG	1.85	0.58
1:A:230:LYS:HE3	1:B:220:LEU:HD12	1.85	0.57
2:D:140:ALA:HB1	2:D:229:LEU:HD13	1.88	0.56
2:D:192:LYS:HE3	2:D:195:ARG:NE	2.08	0.56
1:C:158:ARG:HD3	1:C:161:LEU:HD21	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:ARG:H	1:A:92:ALA:HB3	1.72	0.55
1:B:96:HIS:HB3	1:B:211:MET:HE3	1.89	0.54
1:B:118:TYR:HH	2:D:327:TRP:CG	2.26	0.53
1:A:274:THR:OG1	1:B:280:TYR:OH	2.21	0.53
1:A:207:ARG:HA	1:A:210:ARG:HD3	1.90	0.53
2:D:160:GLU:OE2	2:D:236:ARG:NH2	2.34	0.52
2:D:131:LEU:O	2:D:135:GLY:N	2.42	0.51
1:C:110:SER:O	1:C:113:SER:OG	2.30	0.50
1:C:140:GLU:OE2	1:C:210:ARG:NH2	2.45	0.49
2:D:283:GLU:OE2	2:D:329:GLY:HA3	2.13	0.49
1:C:208:MET:HA	1:C:211:MET:HE2	1.95	0.49
1:C:282:ASP:OD1	1:C:283:LYS:N	2.47	0.48
1:A:220:LEU:HD21	2:D:260:GLU:HG3	1.96	0.48
1:A:196:ALA:HA	1:A:198:ARG:HH11	1.78	0.48
1:C:78:GLN:HB3	1:C:150:CYS:HB3	1.96	0.48
1:B:78:GLN:HG3	1:B:147:ALA:HA	1.96	0.47
1:C:89:ARG:H	1:C:92:ALA:HB3	1.80	0.47
2:D:106:ARG:O	2:D:109:THR:OG1	2.33	0.47
2:D:212:VAL:HG12	2:D:226:LEU:HD22	1.97	0.47
1:C:109:LEU:HD12	1:C:129:LEU:HD12	1.96	0.46
1:C:111:VAL:O	1:C:114:THR:HG22	2.16	0.46
1:A:141:TYR:CE2	1:A:173:ILE:HD11	2.51	0.46
2:D:116:GLU:OE2	2:D:174:ARG:NH1	2.48	0.46
1:A:109:LEU:HD12	1:A:129:LEU:HD12	1.98	0.46
1:A:307:LEU:HD21	1:B:316:PHE:HE2	1.81	0.46
2:D:160:GLU:CD	2:D:236:ARG:HH22	2.19	0.46
1:B:81:LEU:HD12	1:B:146:TRP:HZ3	1.81	0.45
2:D:103:LYS:O	2:D:107:ILE:HG12	2.15	0.45
1:A:110:SER:HA	1:A:126:LEU:HD11	1.98	0.45
1:A:238:ILE:HD13	1:B:221:LEU:HD22	1.98	0.44
1:C:264:TYR:HB2	2:D:144:THR:HG21	1.98	0.44
1:B:292:LEU:O	1:B:296:THR:HG23	2.18	0.44
1:C:158:ARG:O	1:C:161:LEU:HG	2.18	0.44
1:B:232:LEU:HD11	1:B:312:LEU:HD21	1.98	0.43
1:A:171:ILE:HD13	1:A:174:MET:HE2	2.00	0.43
2:D:108:GLN:HA	2:D:111:ILE:HD12	2.00	0.43
1:C:231:GLU:N	1:C:231:GLU:OE1	2.51	0.42
1:C:238:ILE:HD13	2:D:250:LEU:HD22	2.00	0.42
1:A:116:LYS:HA	1:A:119:GLU:HG2	2.01	0.42
1:B:130:GLU:O	1:B:134:ILE:HD12	2.19	0.42
1:B:141:TYR:O	1:B:145:ILE:HG12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:PHE:HE1	1:A:210:ARG:HH22	1.68	0.42
1:A:208:MET:HE1	2:D:269:PHE:HE2	1.84	0.42
2:D:109:THR:HA	2:D:180:CYS:SG	2.60	0.42
2:D:128:LEU:O	2:D:132:ILE:HG12	2.20	0.42
1:A:275:LEU:HD22	1:A:301:GLY:HA3	2.02	0.42
2:D:112:TYR:CE2	2:D:181:CYS:HB3	2.55	0.42
2:D:130:PHE:HD2	2:D:131:LEU:HD12	1.84	0.41
1:C:325:ARG:HH22	2:D:364:ARG:HH22	1.68	0.41
2:D:282:VAL:HG23	2:D:283:GLU:HG3	2.00	0.41
1:A:155:ARG:HE	1:A:156:GLY:N	2.16	0.41
1:C:231:GLU:HG3	2:D:249:LEU:HD21	2.02	0.41
1:C:130:GLU:O	1:C:134:ILE:HG12	2.21	0.41
1:A:231:GLU:HG3	1:B:220:LEU:HD21	2.02	0.41
1:C:204:GLN:OE1	1:C:207:ARG:NH1	2.53	0.41
2:D:192:LYS:CE	2:D:195:ARG:HH21	2.31	0.41
2:D:103:LYS:HA	2:D:106:ARG:HB3	2.02	0.41
1:A:81:LEU:HA	1:A:84:VAL:HG12	2.03	0.41
1:A:234:THR:HG21	1:B:220:LEU:HD22	2.02	0.40
1:C:275:LEU:HD22	1:C:301:GLY:HA3	2.03	0.40
2:D:321:ASP:OD1	2:D:321:ASP:N	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	244/872 (28%)	244 (100%)	0	0	100	100
1	B	244/872 (28%)	243 (100%)	1 (0%)	0	100	100
1	C	245/872 (28%)	244 (100%)	1 (0%)	0	100	100
2	D	245/872 (28%)	240 (98%)	5 (2%)	0	100	100
All	All	978/3488 (28%)	971 (99%)	7 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	207/728 (28%)	207 (100%)	0	100	100
1	B	207/728 (28%)	207 (100%)	0	100	100
1	C	208/728 (29%)	208 (100%)	0	100	100
2	D	209/725 (29%)	202 (97%)	7 (3%)	33	55
All	All	831/2909 (29%)	824 (99%)	7 (1%)	70	86

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	103	LYS
2	D	104	TYR
2	D	106	ARG
2	D	226	LEU
2	D	227	ARG
2	D	230	ARG
2	D	330	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	328	HIS
1	B	328	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

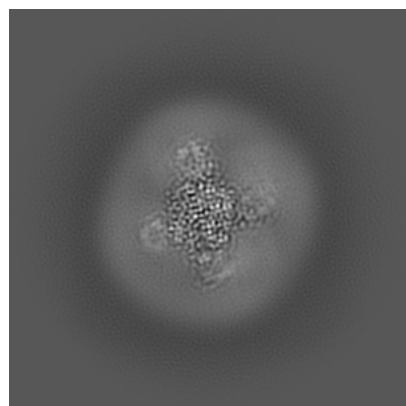
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-68152. These allow visual inspection of the internal detail of the map and identification of artifacts.

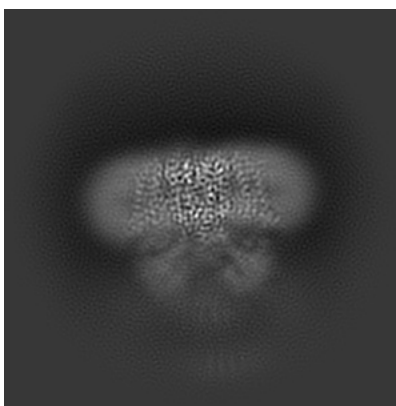
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

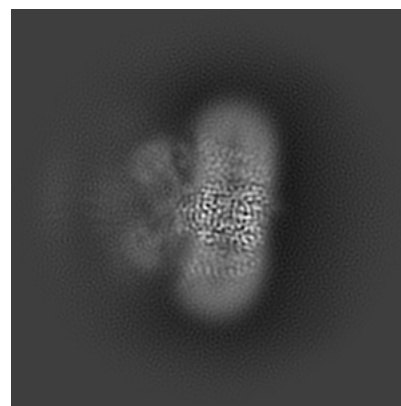
6.1.1 Primary map



X

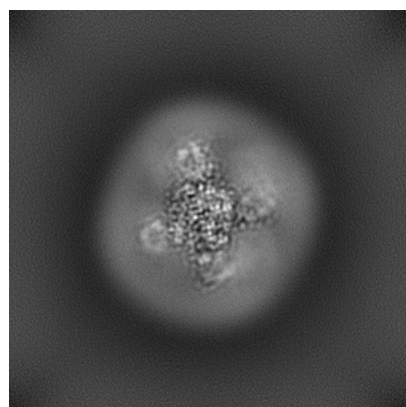


Y

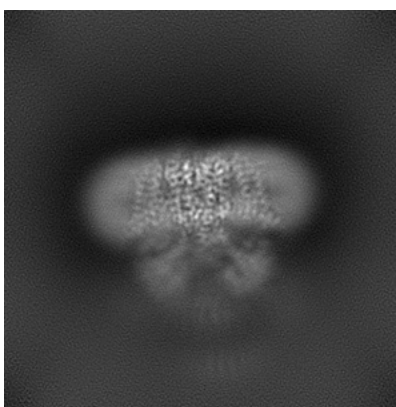


Z

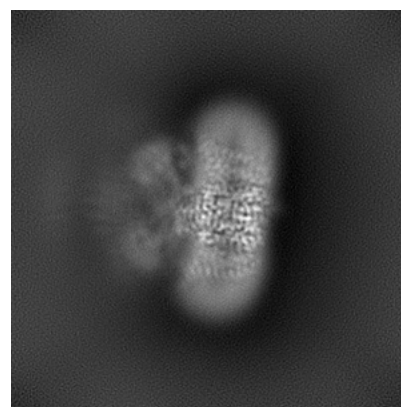
6.1.2 Raw map



X



Y

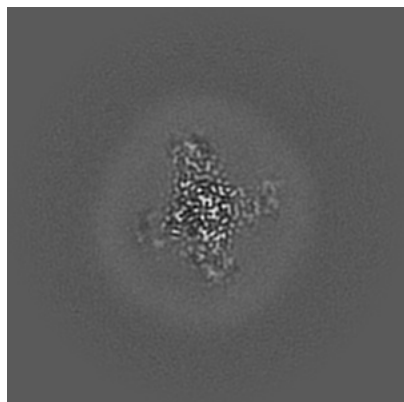


Z

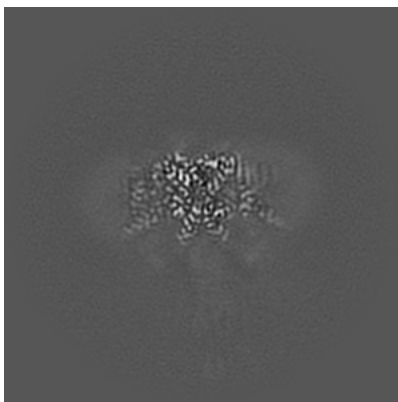
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

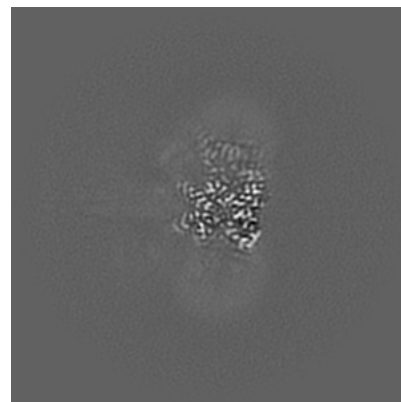
6.2.1 Primary map



X Index: 140

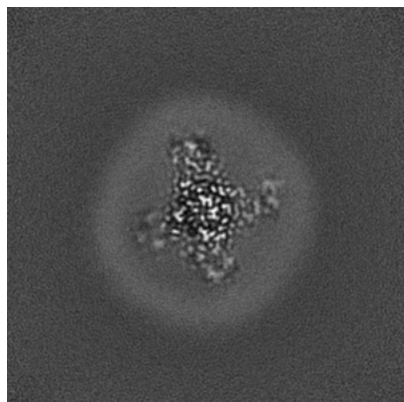


Y Index: 140

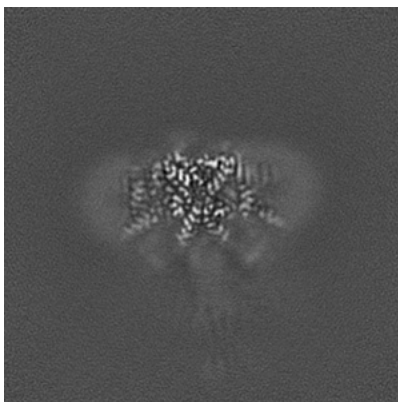


Z Index: 140

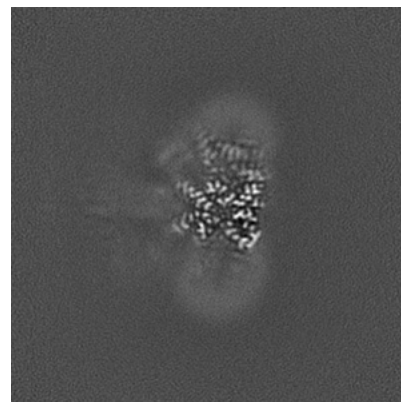
6.2.2 Raw map



X Index: 140



Y Index: 140

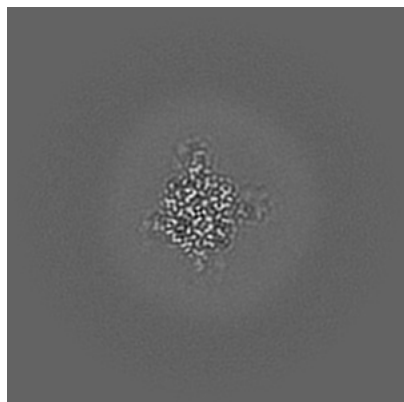


Z Index: 140

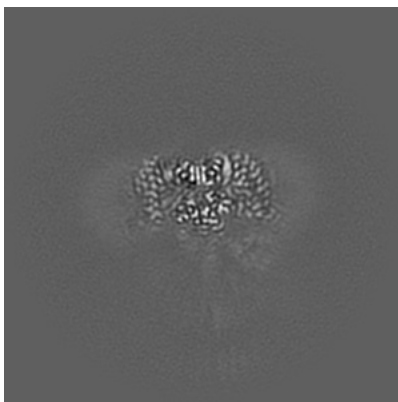
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

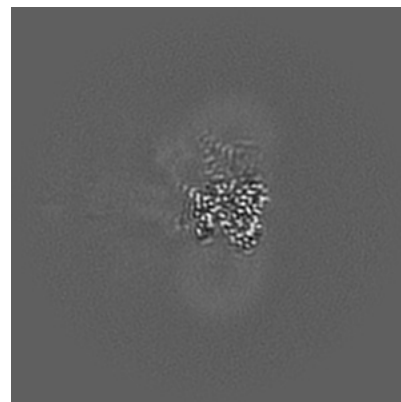
6.3.1 Primary map



X Index: 165

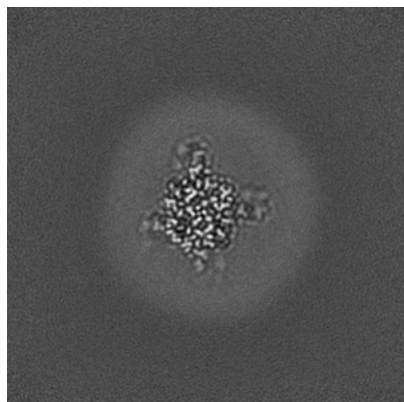


Y Index: 134

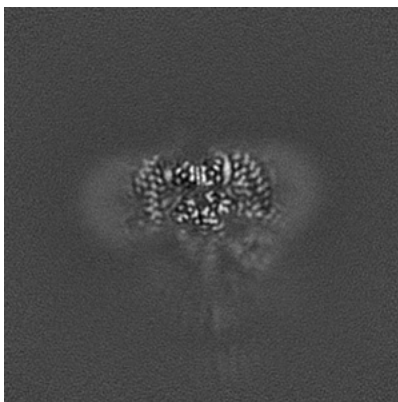


Z Index: 142

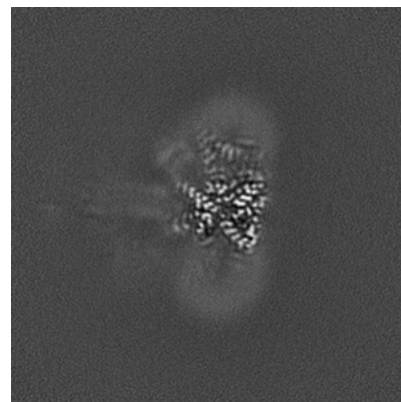
6.3.2 Raw map



X Index: 165



Y Index: 134

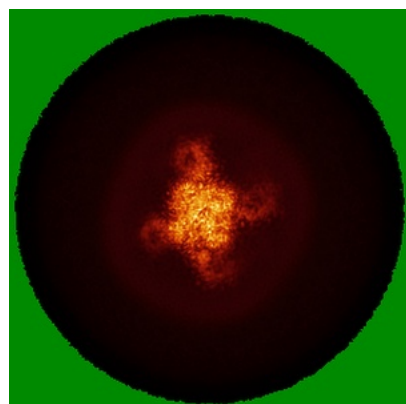


Z Index: 141

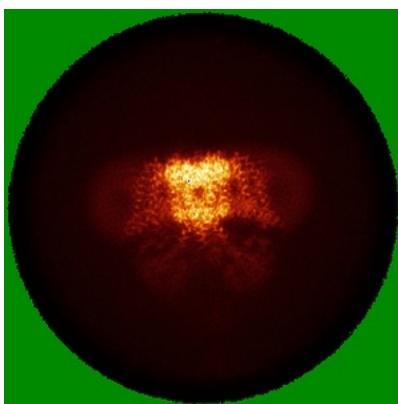
The images above show the largest variance slices of the map in three orthogonal directions.

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

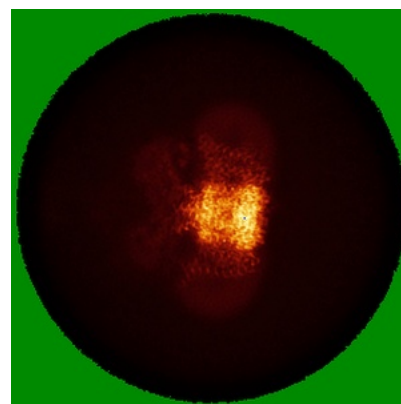
6.4.1 Primary map



X

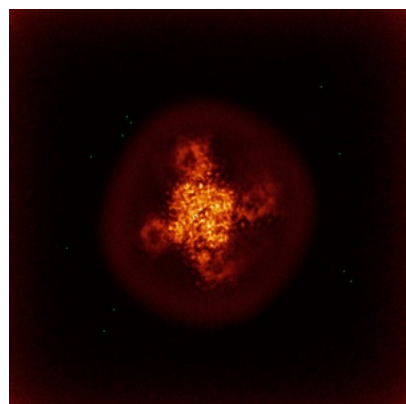


Y

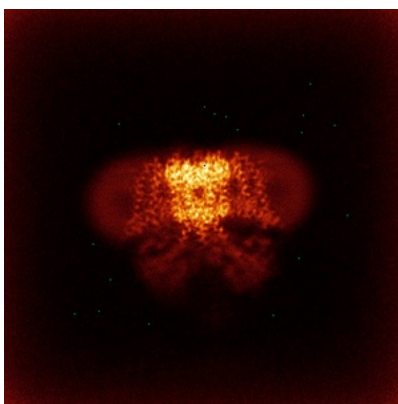


Z

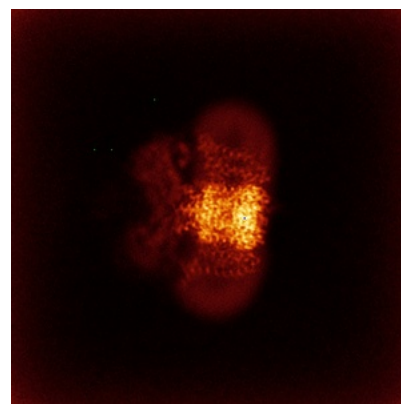
6.4.2 Raw map



X



Y

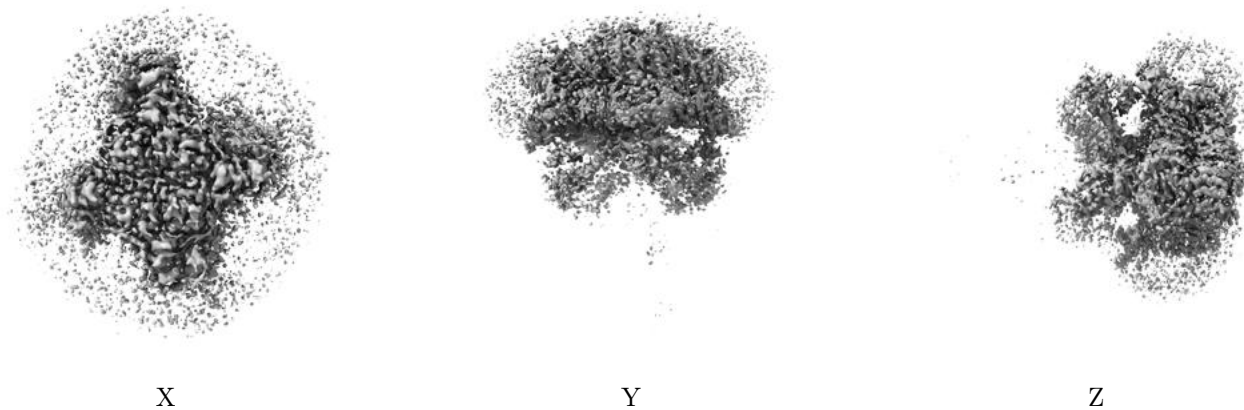


Z

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

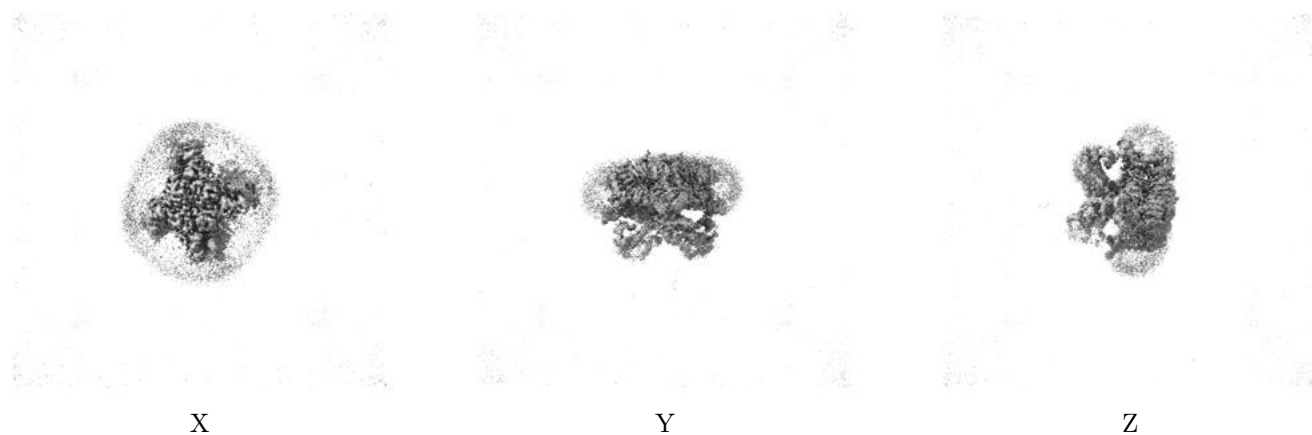
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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



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.

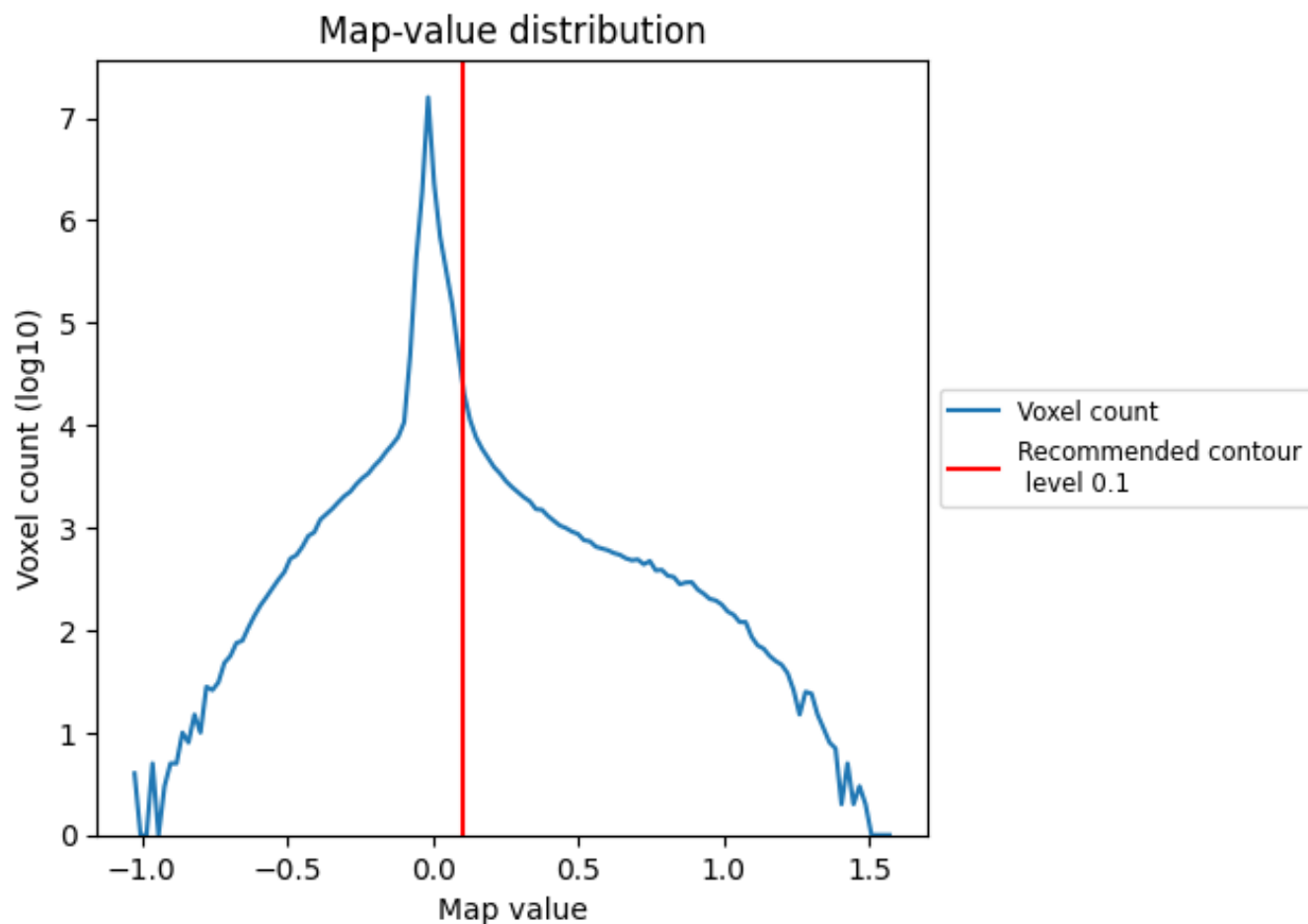
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

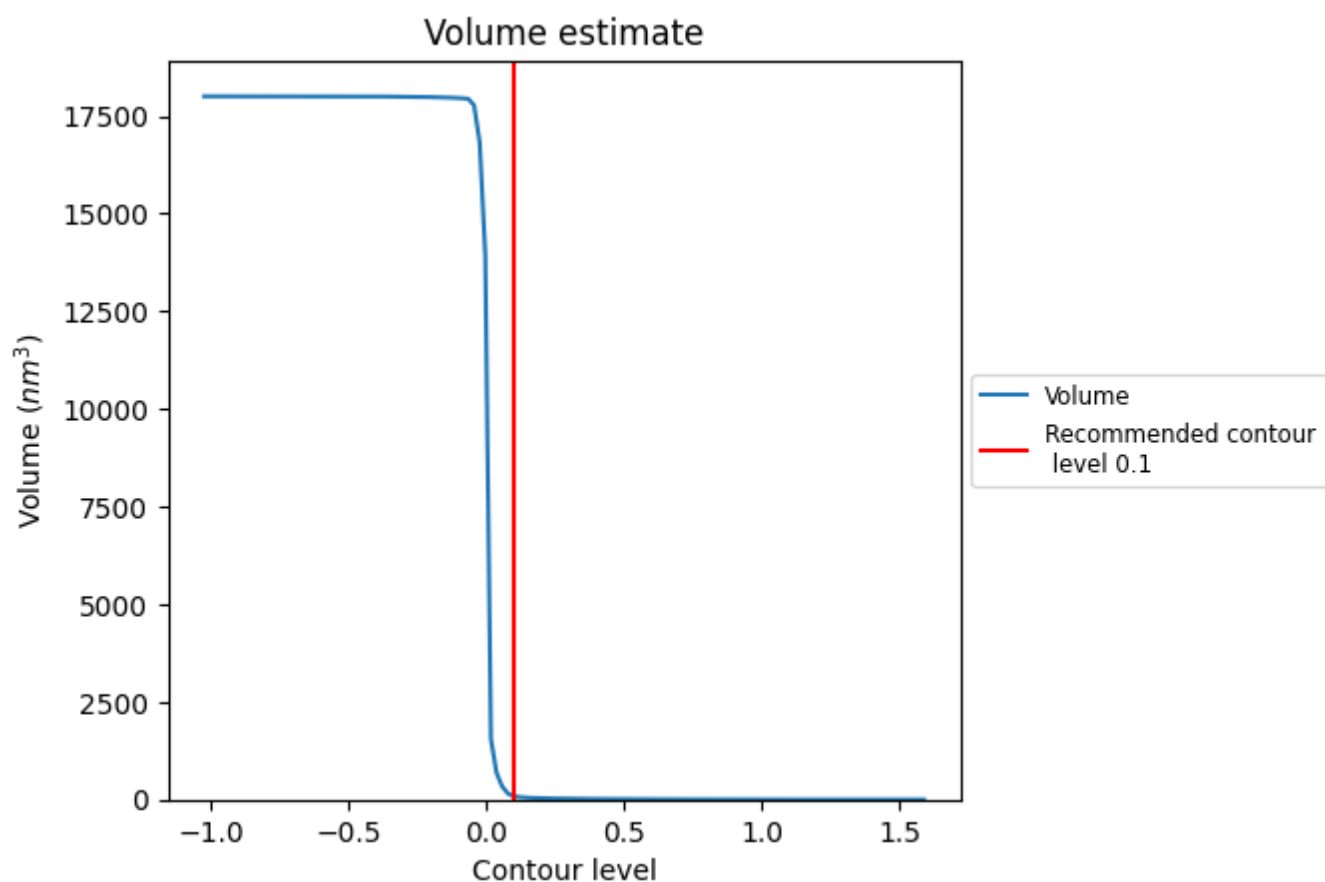
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

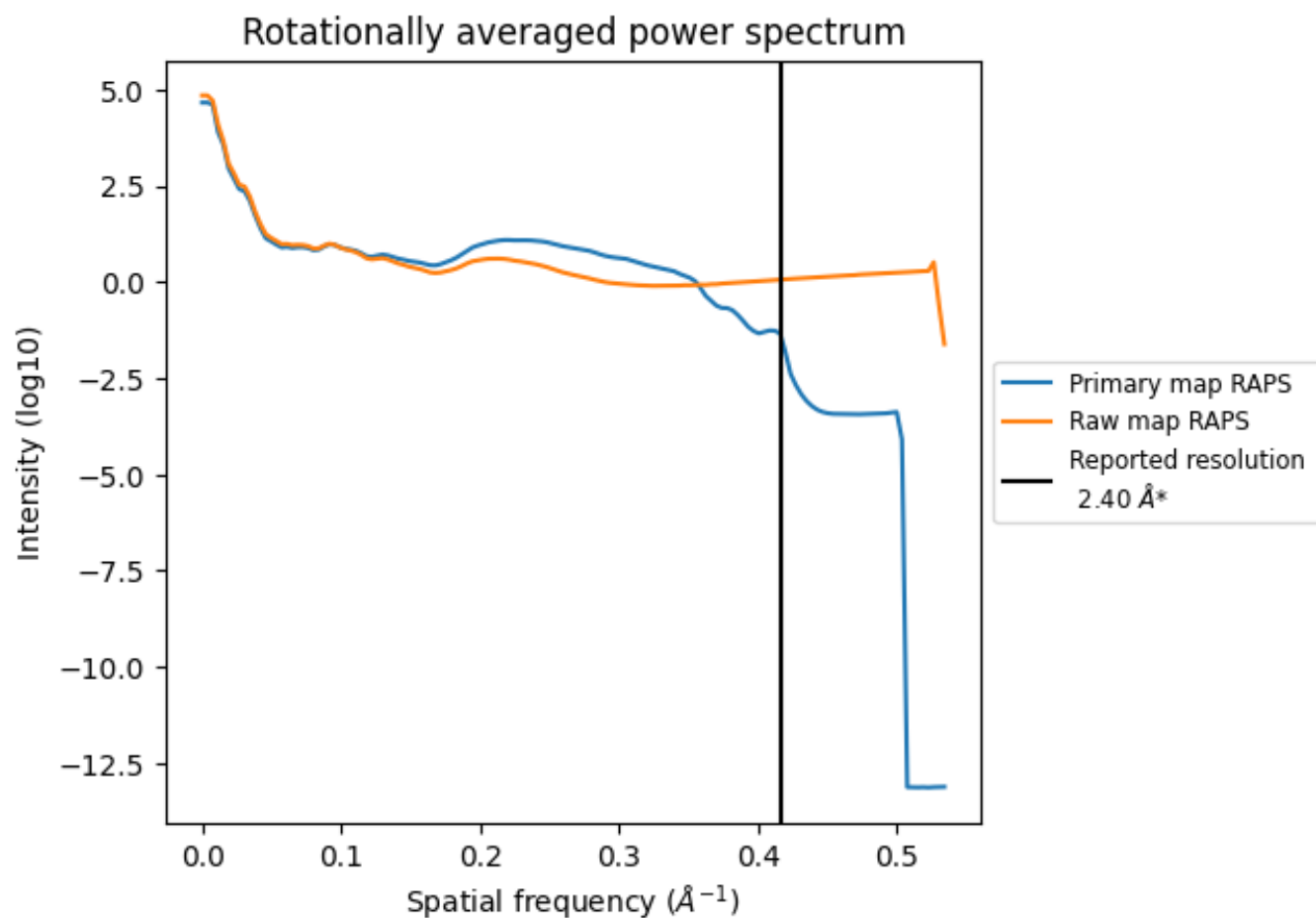
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 86 nm^3 ; this corresponds to an approximate mass of 78 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

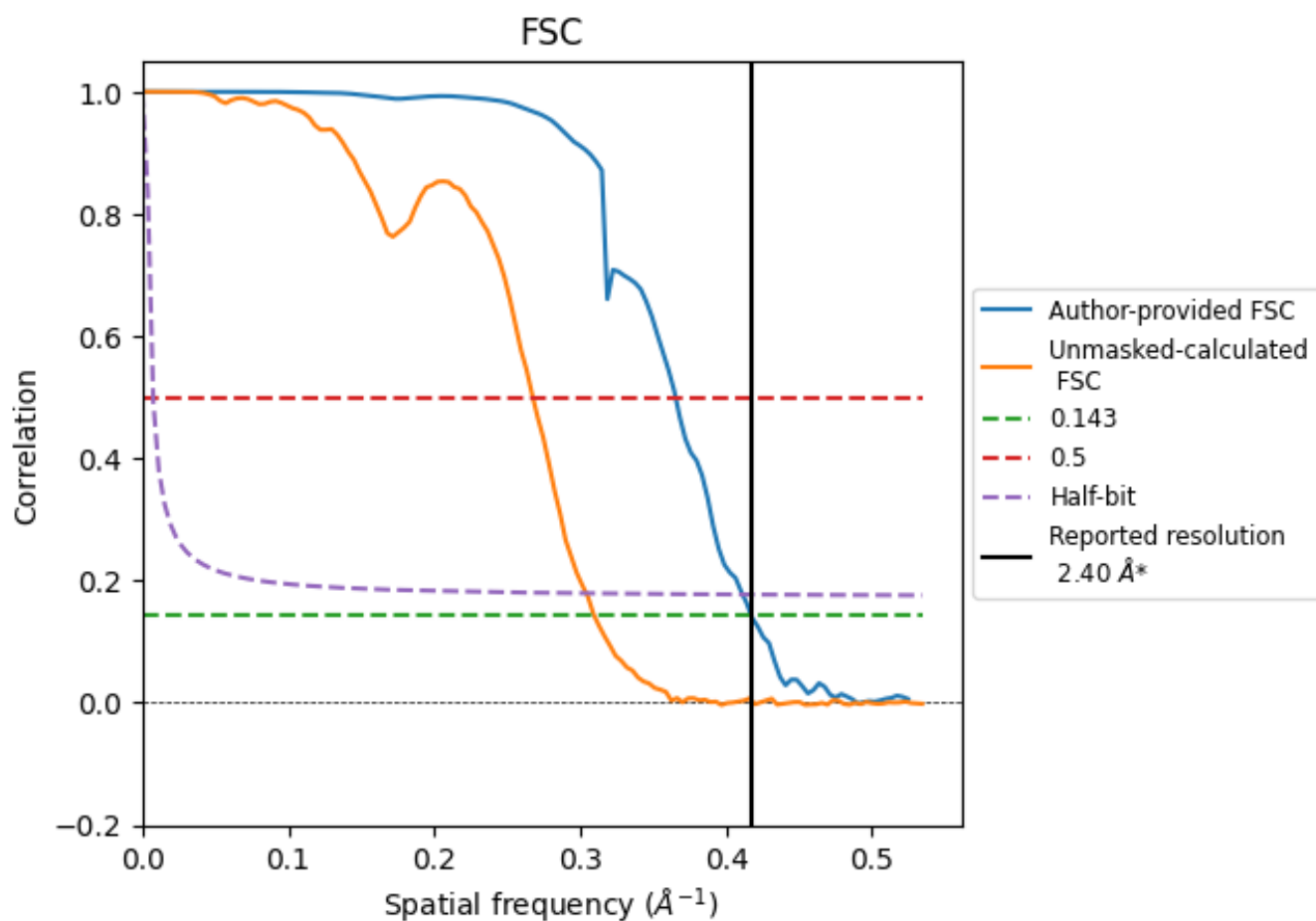


*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.417 \AA^{-1}

8.2 Resolution estimates [i](#)

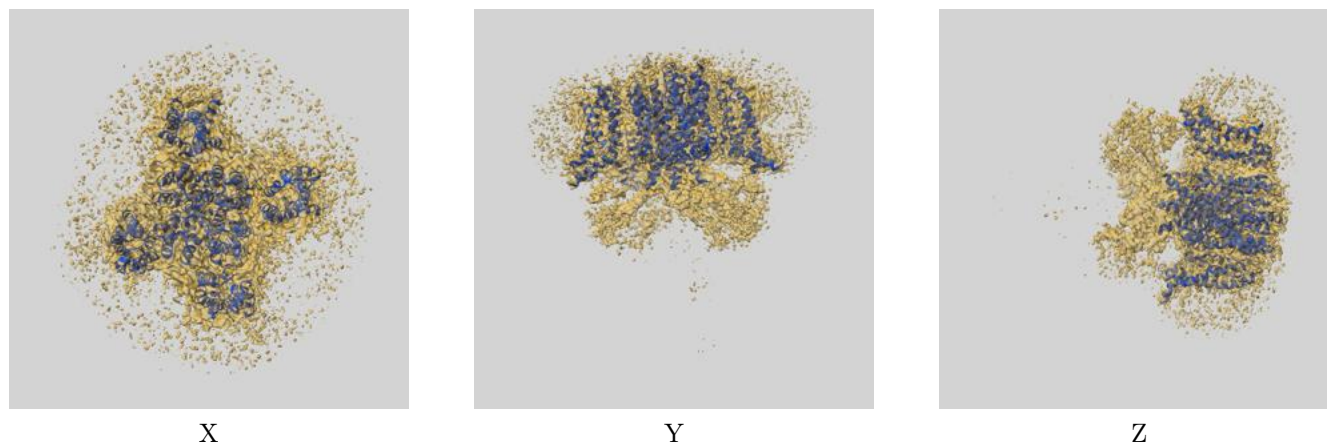
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.40	2.74	2.43
Unmasked-calculated*	3.23	3.74	3.29

*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 3.23 differs from the reported value 2.4 by more than 10 %

9 Map-model fit [i](#)

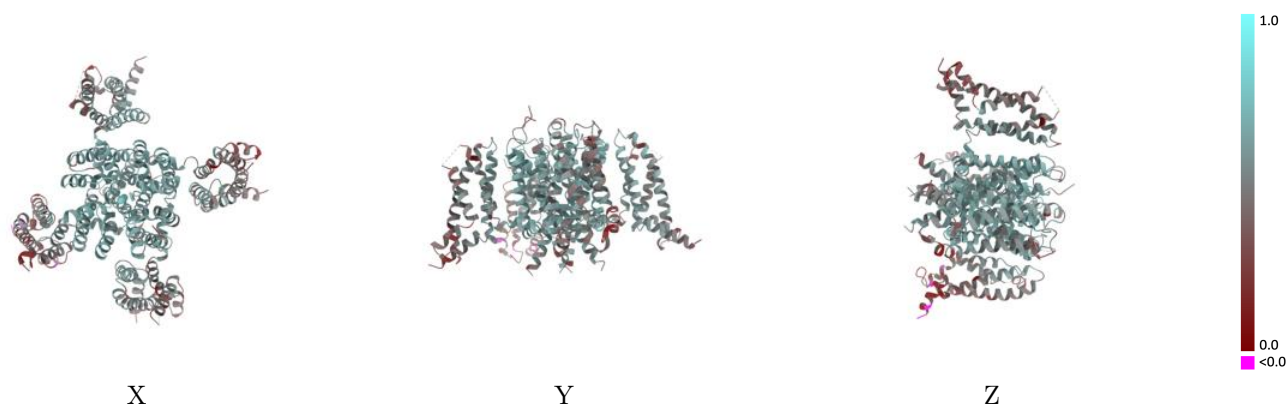
This section contains information regarding the fit between EMDB map EMD-68152 and PDB model 22BJ. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



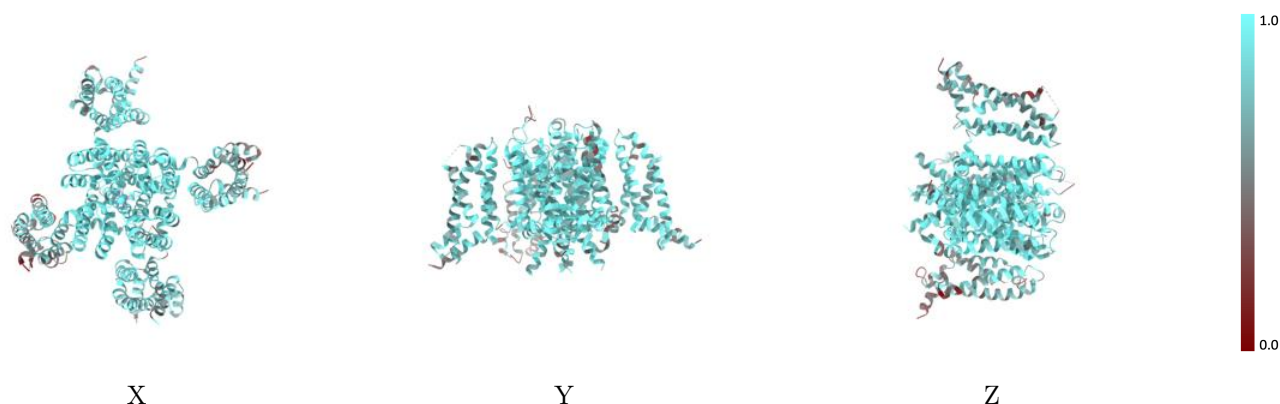
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



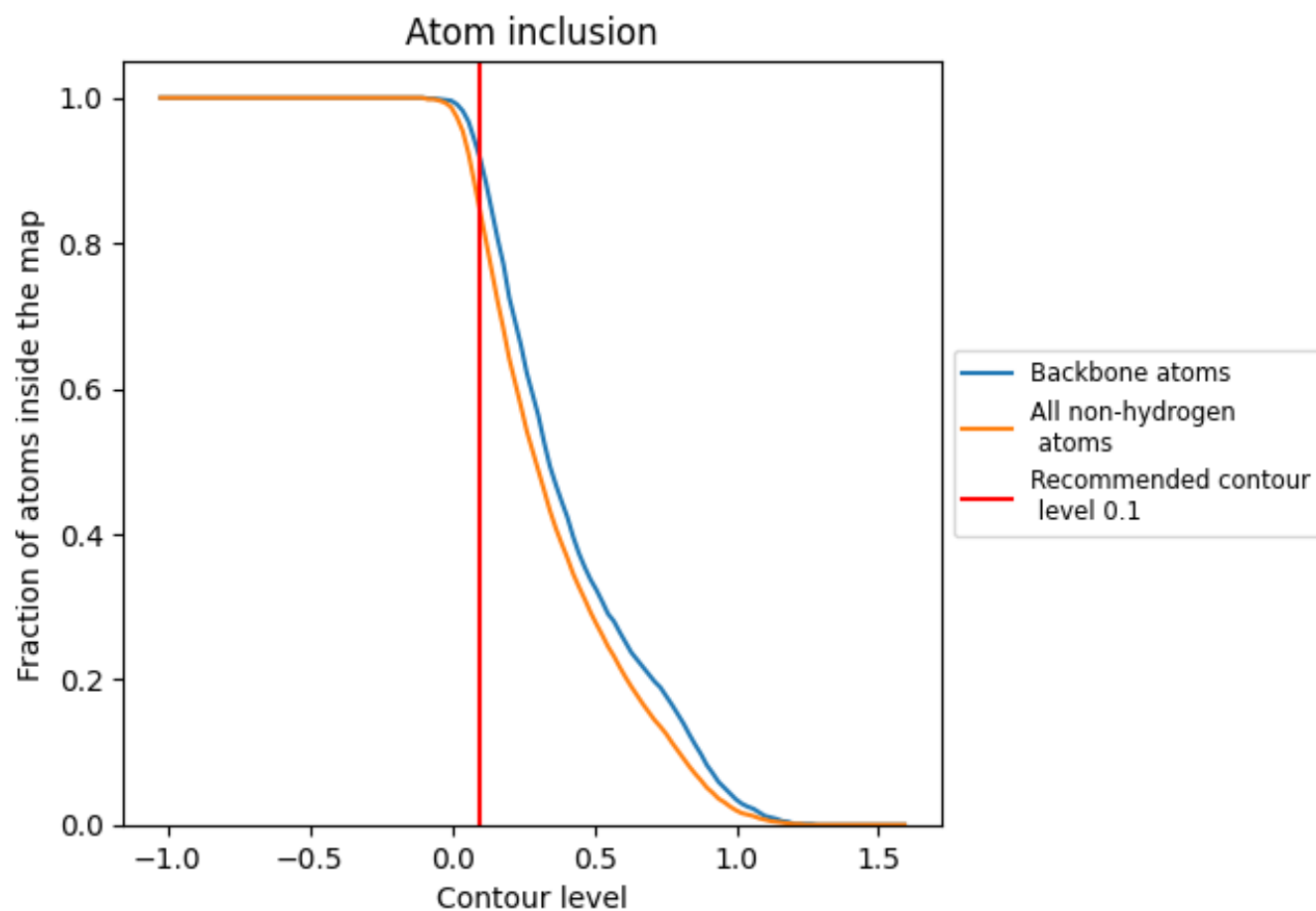
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 84% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8410	<div></div> 0.5160
A	<div></div> 0.8710	<div></div> 0.5340
B	<div></div> 0.8410	<div></div> 0.5190
C	<div></div> 0.8930	<div></div> 0.5490
D	<div></div> 0.7580	<div></div> 0.4630

