



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 06:38 PM UTC

PDB ID : 6S1K / pdb_00006s1k
EMDB ID : EMD-10050
Title : E. coli Core Signaling Unit, carrying QQQQ receptor mutation
Authors : Cassidy, C.K.
Deposited on : 2019-06-18
Resolution : 8.38 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:

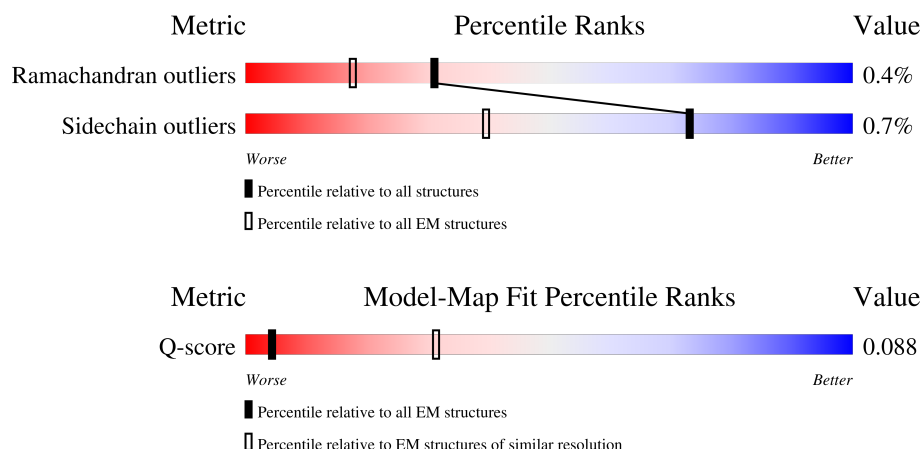
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 8.38 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.



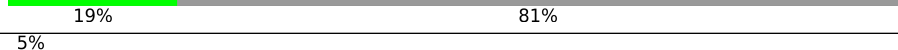
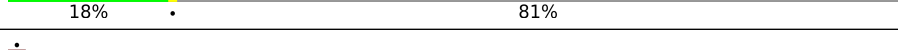
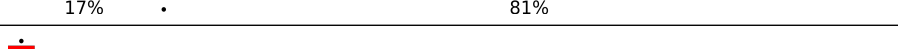
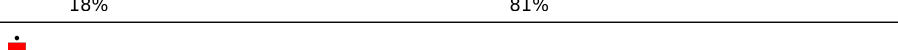
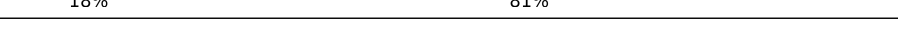
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	298 (7.90 - 8.90)

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	654	29% 57% 41%
1	B	654	30% 56% 41%
2	C	167	56% 82% 5% 13%
2	D	167	53% 83% 13%
3	E	551	18% 81%

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Mol	Chain	Length	Quality of chain
3	F	551	 18%81%
3	G	551	 18%81%
3	H	551	 18%81%
3	I	551	 18%81%
3	J	551	 18%81%
3	K	551	 18%81%
3	L	551	 19%81%
3	M	551	 5%18%81%
3	N	551	 17%81%
3	O	551	 18%81%
3	P	551	 18%81%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 16884 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 Chemotaxis protein CheA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	383	Total	C	N	O	S	0	0
			2909	1818	519	559	13		
1	B	383	Total	C	N	O	S	0	0
			2909	1818	519	559	13		

- Molecule 2 is a protein called CheW.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	145	Total	C	N	O	S	0	0
			1117	715	183	217	2		
2	D	145	Total	C	N	O	S	0	0
			1117	715	183	217	2		

- Molecule 3 is a protein called Methyl-accepting chemotaxis protein I.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	102	Total	C	N	O	S	0	0
			736	449	134	152	1		
3	F	102	Total	C	N	O	S	0	0
			736	449	134	152	1		
3	G	102	Total	C	N	O	S	0	0
			736	449	134	152	1		
3	H	102	Total	C	N	O	S	0	0
			736	449	134	152	1		
3	I	102	Total	C	N	O	S	0	0
			736	449	134	152	1		
3	J	102	Total	C	N	O	S	0	0
			736	449	134	152	1		
3	K	102	Total	C	N	O	S	0	0
			736	449	134	152	1		
3	L	102	Total	C	N	O	S	0	0
			736	449	134	152	1		
3	M	102	Total	C	N	O	S	0	0
			736	449	134	152	1		

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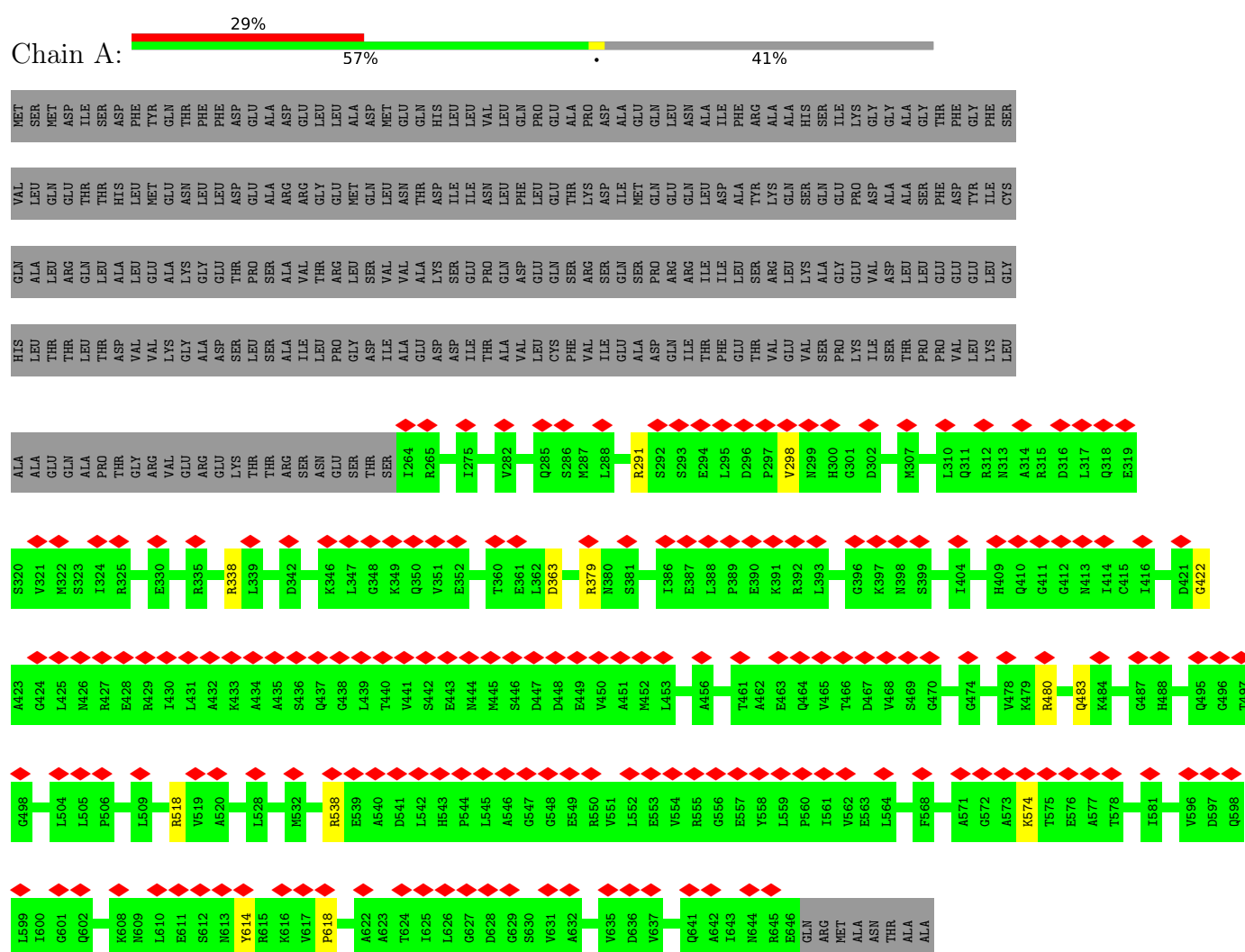
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Mol	Chain	Residues	Atoms					AltConf	Trace
3	N	102	Total	C	N	O	S	0	0
			736	449	134	152	1		
3	O	102	Total	C	N	O	S	0	0
			736	449	134	152	1		
3	P	102	Total	C	N	O	S	0	0
			736	449	134	152	1		

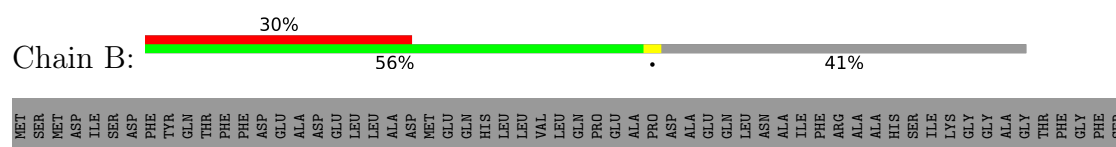
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Chemotaxis protein CheA



• Molecule 1: Chemotaxis protein CheA





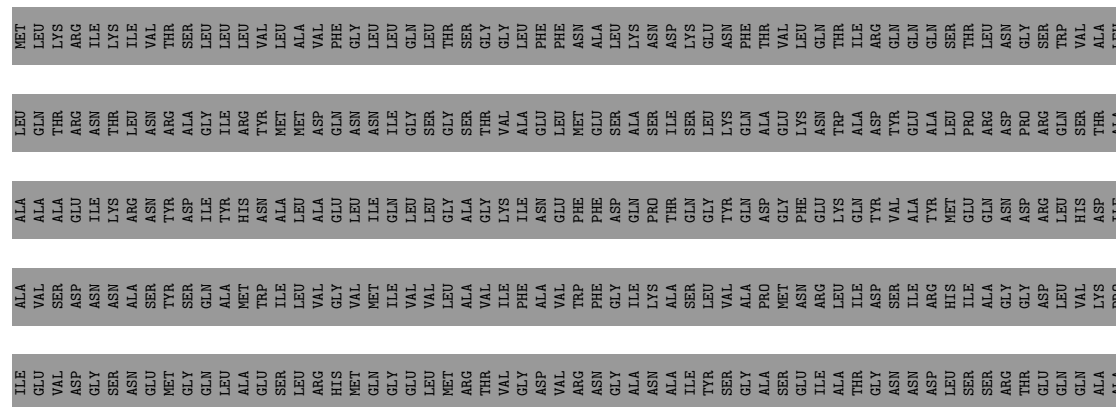
• Molecule 3: Methyl-accepting chemotaxis protein I

Chain E: 18% 81%

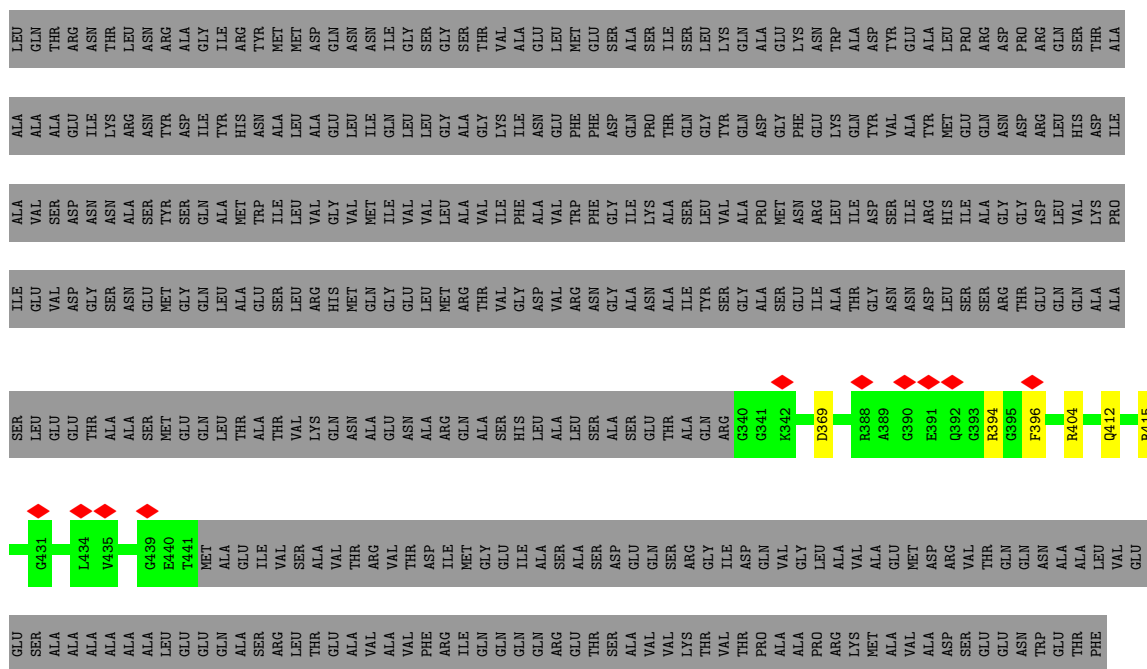


• Molecule 3: Methyl-accepting chemotaxis protein I

Chain F: 18% 81%







- Molecule 3: Methyl-accepting chemotaxis protein I



- Molecule 3: Methyl-accepting chemotaxis protein I



GLU	GLN	ALA	SER	ILE	ALA	ALA	LEU	LEU	MET
GLN	ALA	ILE	GLU	GLU	VAL	VAL	GLN	GLN	LEU
ALA	ILE	ALA	GLU	ASP	GLY	ASP	ASP	THR	THR
SER	SER	VAL	THR	THR	GLY	ASN	ASN	ARG	ARG
ARG	SER	SER	ALA	SER	SER	ASN	LYS	THR	LYS
LEU	THR	VAL	ALA	ASN	GLU	ALA	ARG	ILE	ILE
THR	GLU	THR	SER	GLU	GLU	SER	ASN	THR	VAL
ALA	ALA	ARG	MET	MET	MET	TYR	TYR	ARG	ASN
VAL	VAL	VAL	GLU	GLY	GLY	LEU	ASP	ALA	SER
ALA	ALA	THR	GLN	GLN	GLN	GLN	ILE	GLY	LEU
ALA	ASP	THR	LEU	LEU	ALA	ALA	TYR	ILE	LEU
PHE	ILE	ILE	THR	ALA	ALA	MET	HIS	ARG	LEU
ARG	ARG	MET	ALA	GLU	TRP	ASN	ASN	THR	VAL
ILE	GLY	GLY	THR	SER	ILE	ILE	ALA	MET	LEU
GLN	GLU	GLU	VAL	LEU	LEU	VAL	LEU	ASP	ALA
GLN	GLN	ILE	LYS	ARG	VAL	VAL	ALA	ASP	VAL
GLN	ALA	SER	GLN	HIS	GLY	GLY	GLU	GLN	PHE
GLN	SER	SER	ASN	MET	VAL	VAL	LEU	ASN	GLY
ARG	ARG	ALA	ALA	GLN	ILE	ILE	GLN	ILE	LEU
GLU	GLU	SER	GLU	GLU	VAL	VAL	GLY	THR	GLY
THR	THR	ASP	ASN	GLU	VAL	VAL	LYS	VAL	GLY
SER	SER	GLU	ALA	LEU	GLY	GLY	LEU	ALA	LEU
ALA	ALA	GLN	ARG	MET	LEU	LEU	GLY	SER	LEU
VAL	VAL	SER	GLN	THR	ALA	ALA	ALA	SER	THR
VAL	VAL	ARG	ALA	THR	VAL	VAL	PHE	GLU	GLY
LYS	LYS	GLY	SER	VAL	ILE	ILE	GLN	ALA	LEU
THR	THR	ILE	HIS	GLY	ASP	ALA	ASN	ALA	PHE
VAL	VAL	ASP	LEU	GLY	VAL	VAL	GLU	GLU	PHE
THR	THR	GLN	ALA	VAL	VAL	VAL	THR	MET	ASN
PRO	PRO	VAL	LEU	ARG	TRP	PHE	GLU	ALA	GLY
ALA	ALA	GLY	SER	ASN	PHE	PHE	SER	LEU	LYS
PRO	PRO	LEU	ALA	ALA	GLY	ILE	GLN	ALA	ASN
ARG	ARG	VAL	SER	ALA	ILE	LYS	PRO	SER	ASN
LYS	LYS	ALA	GLU	ASN	LYS	PRO	GLN	ILE	ASN
MET	MET	GLU	ALA	ILE	SER	ALA	GLN	ASP	LYS
ALA	ALA	MET	GLN	TYR	LEU	LEU	GLY	LEU	GLU
VAL	VAL	ASP	ARG	SER	VAL	VAL	TYR	LYS	ASN
ALA	ARG	VAL	ALA	GLY	ALA	ALA	GLN	ALA	PHE
ASP	ASP	THR	G340	GLY	ALA	PRO	ASP	ALA	THR
SER	SER	THR	G341	SER	ALA	MET	GLY	GLU	VAL
GLU	GLU	GLN	K342	GLU	ASN	PHE	LEU	LYS	VAL
GLU	GLU	GLN	V343	ILE	ARG	ARG	ASN	ASN	GLN
ASN	ASN	ASN	V344	ALA	LEU	LEU	LYS	TRP	THR
TRP	TRP	ALA		THR	ILE	ILE	GLN	ALA	ILE
GLU	GLU	ALA		GLY	ASP	ASP	TYR	ASP	ARG
THR	THR	LEU		ASN	SER	SER	VAL	GLU	GLN
PHE	PHE	VAL		ASN	ILE	ILE	TYR	ALA	GLN
		VAL	E391	ASN	ARG	HIS	GLU	ARG	SER
		GLU	Q392	ASP	ASP	ILE	GLN	GLN	LEU
		SER	G393	SER	ILE	ILE	GLU	ARG	THR
		ALA	R394	ARG	ALA	ALA	GLN	ASN	LEU
		ALA	G395	THR	GLY	GLY	ASP	ASP	GLY
		ALA	F396	THR	ASP	ASP	LEU	SER	SER
		ALA		GLN	LEU	LEU	GLN	TRP	VAL
		ALA		GLN	VAL	VAL	LEU	SER	ALA
		ALA	R409	GLN	VAL	VAL	HIS	THR	ALA
		LEU		GLN	LYS	LYS	ASP	ALA	LEU
		GLU	S432	GLU	PRO	PRO	ILE	THR	LEU
			T441						

4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of subtomograms used	91636	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.3	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	14.403	Depositor
Minimum map value	-7.622	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.175	Depositor
Recommended contour level	2.15	Depositor
Map size (Å)	627.50397, 627.50397, 627.50397	wwPDB
Map dimensions	204, 204, 204	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	3.0759997, 3.0759997, 3.0759997	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.89	0/2939	1.45	2/3975 (0.1%)
1	B	0.88	0/2939	1.45	9/3975 (0.2%)
2	C	0.87	0/1130	1.34	4/1537 (0.3%)
2	D	0.87	0/1130	1.33	1/1537 (0.1%)
3	E	0.89	0/737	1.67	1/994 (0.1%)
3	F	0.88	0/737	1.68	2/994 (0.2%)
3	G	0.88	0/737	1.67	3/994 (0.3%)
3	H	0.89	0/737	1.63	1/994 (0.1%)
3	I	0.88	0/737	1.65	0/994
3	J	0.88	0/737	1.62	1/994 (0.1%)
3	K	0.88	0/737	1.67	2/994 (0.2%)
3	L	0.89	0/737	1.65	0/994
3	M	0.89	0/737	1.67	0/994
3	N	0.89	0/737	1.67	2/994 (0.2%)
3	O	0.89	0/737	1.67	0/994
3	P	0.90	0/737	1.66	1/994 (0.1%)
All	All	0.88	0/16982	1.55	29/22952 (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
1	A	0	6
1	B	0	5
3	F	0	2
3	G	0	1
3	H	0	1
3	I	0	1
3	J	0	2
3	M	0	2
3	N	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	O	0	1
3	P	0	1
All	All	0	25

There are no bond length outliers.

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	369	ASP	CA-CB-CG	7.65	120.25	112.60
3	N	396	PHE	CA-CB-CG	6.51	120.31	113.80
3	H	396	PHE	CA-CB-CG	6.34	120.14	113.80
2	C	32	ASP	CA-CB-CG	6.14	118.74	112.60
3	E	369	ASP	CA-CB-CG	6.05	118.65	112.60
3	K	369	ASP	CA-CB-CG	5.89	118.49	112.60
1	B	471	ARG	CA-C-N	5.87	126.84	120.44
1	B	471	ARG	C-N-CA	5.87	126.84	120.44
3	F	363	ASP	CA-CB-CG	5.81	118.41	112.60
3	G	368	ILE	CA-C-N	5.77	128.02	120.28
3	G	368	ILE	C-N-CA	5.77	128.02	120.28
3	P	396	PHE	CA-CB-CG	5.75	119.55	113.80
1	B	384	HIS	N-CA-C	5.51	117.28	111.28
2	D	32	ASP	CA-CB-CG	5.46	118.06	112.60
2	C	103	ASP	CA-CB-CG	5.45	118.05	112.60
2	C	78	VAL	CA-C-N	5.41	128.39	120.71
2	C	78	VAL	C-N-CA	5.41	128.39	120.71
1	B	472	GLY	N-CA-C	5.40	118.27	112.33
1	B	363	ASP	CA-CB-CG	5.37	117.97	112.60
1	B	329	MET	CA-C-N	5.36	127.72	120.38
1	B	329	MET	C-N-CA	5.36	127.72	120.38
3	K	429	ASP	CA-CB-CG	5.33	117.94	112.60
3	J	373	PHE	CA-CB-CG	5.29	119.09	113.80
1	A	363	ASP	CA-CB-CG	5.15	117.75	112.60
1	B	400	VAL	CA-C-N	5.14	125.22	120.34
1	B	400	VAL	C-N-CA	5.14	125.22	120.34
3	N	369	ASP	CA-CB-CG	5.11	117.71	112.60
1	A	298	VAL	N-CA-C	5.07	115.29	110.42
3	F	396	PHE	CA-CB-CG	5.00	118.80	113.80

There are no chirality outliers.

All (25) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	338	ARG	Sidechain
1	A	379	ARG	Sidechain
1	A	480	ARG	Sidechain
1	A	518	ARG	Sidechain
1	A	538	ARG	Sidechain
1	A	614	TYR	Sidechain
1	B	338	ARG	Sidechain
1	B	379	ARG	Sidechain
1	B	480	ARG	Sidechain
1	B	538	ARG	Sidechain
1	B	614	TYR	Sidechain
3	F	394	ARG	Sidechain
3	F	409	ARG	Sidechain
3	G	415	ARG	Sidechain
3	H	404	ARG	Sidechain
3	I	415	ARG	Sidechain
3	J	404	ARG	Sidechain
3	J	415	ARG	Sidechain
3	M	352	ARG	Sidechain
3	M	404	ARG	Sidechain
3	N	394	ARG	Sidechain
3	N	404	ARG	Sidechain
3	N	415	ARG	Sidechain
3	O	415	ARG	Sidechain
3	P	409	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	2909	0	3009	0	0
1	B	2909	0	3009	0	0
2	C	1117	0	1152	0	0
2	D	1117	0	1152	0	0
3	E	736	0	750	0	0
3	F	736	0	750	0	0
3	G	736	0	750	0	0
3	H	736	0	750	0	0
3	I	736	0	750	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	J	736	0	750	0	0
3	K	736	0	750	0	0
3	L	736	0	750	0	0
3	M	736	0	750	0	0
3	N	736	0	750	0	0
3	O	736	0	750	0	0
3	P	736	0	750	0	0
All	All	16884	0	17322	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

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	381/654 (58%)	368 (97%)	10 (3%)	3 (1%)	16	54
1	B	381/654 (58%)	372 (98%)	7 (2%)	2 (0%)	24	63
2	C	143/167 (86%)	135 (94%)	6 (4%)	2 (1%)	9	40
2	D	143/167 (86%)	135 (94%)	6 (4%)	2 (1%)	9	40
3	E	100/551 (18%)	100 (100%)	0	0	100	100
3	F	100/551 (18%)	100 (100%)	0	0	100	100
3	G	100/551 (18%)	100 (100%)	0	0	100	100
3	H	100/551 (18%)	100 (100%)	0	0	100	100
3	I	100/551 (18%)	100 (100%)	0	0	100	100
3	J	100/551 (18%)	100 (100%)	0	0	100	100
3	K	100/551 (18%)	100 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	L	100/551 (18%)	100 (100%)	0	0	100	100
3	M	100/551 (18%)	100 (100%)	0	0	100	100
3	N	100/551 (18%)	100 (100%)	0	0	100	100
3	O	100/551 (18%)	100 (100%)	0	0	100	100
3	P	100/551 (18%)	100 (100%)	0	0	100	100
All	All	2248/8254 (27%)	2210 (98%)	29 (1%)	9 (0%)	31	67

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	81	ASP
2	D	81	ASP
1	A	618	PRO
1	B	579	GLN
1	B	618	PRO
2	D	121	GLU
1	A	574	LYS
1	A	422	GLY
2	C	124	VAL

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	321/552 (58%)	319 (99%)	2 (1%)	78	83
1	B	321/552 (58%)	320 (100%)	1 (0%)	86	86
2	C	126/143 (88%)	123 (98%)	3 (2%)	43	64
2	D	126/143 (88%)	123 (98%)	3 (2%)	43	64
3	E	77/438 (18%)	77 (100%)	0	100	100
3	F	77/438 (18%)	76 (99%)	1 (1%)	61	74
3	G	77/438 (18%)	77 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	H	77/438 (18%)	77 (100%)	0	100	100
3	I	77/438 (18%)	76 (99%)	1 (1%)	61	74
3	J	77/438 (18%)	77 (100%)	0	100	100
3	K	77/438 (18%)	77 (100%)	0	100	100
3	L	77/438 (18%)	77 (100%)	0	100	100
3	M	77/438 (18%)	76 (99%)	1 (1%)	61	74
3	N	77/438 (18%)	76 (99%)	1 (1%)	61	74
3	O	77/438 (18%)	77 (100%)	0	100	100
3	P	77/438 (18%)	77 (100%)	0	100	100
All	All	1818/6646 (27%)	1805 (99%)	13 (1%)	73	81

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	291	ARG
1	A	483	GLN
1	B	483	GLN
2	C	96	ARG
2	C	115	GLN
2	C	126	LEU
2	D	96	ARG
2	D	115	GLN
2	D	126	LEU
3	F	408	GLN
3	I	349	GLN
3	M	365	ILE
3	N	412	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 [i](#)

There are no oligosaccharides 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](#)

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10050. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

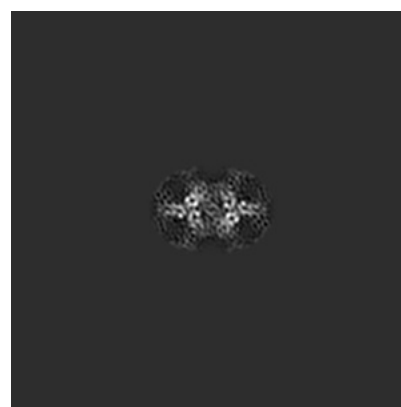
6.1.1 Primary map



X



Y



Z

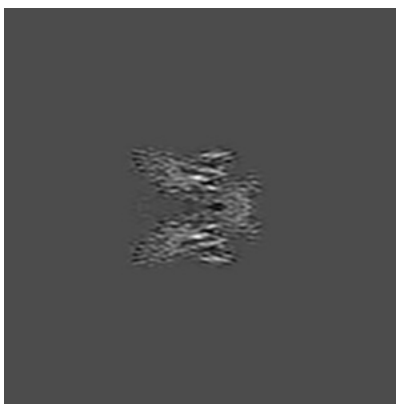
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 102



Y Index: 102



Z Index: 102

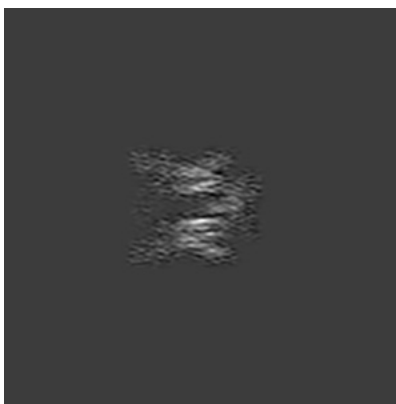
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

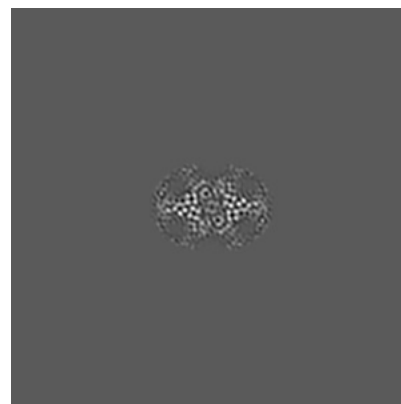
6.3.1 Primary map



X Index: 110



Y Index: 100

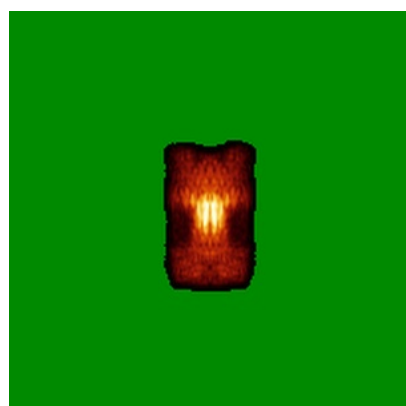


Z Index: 105

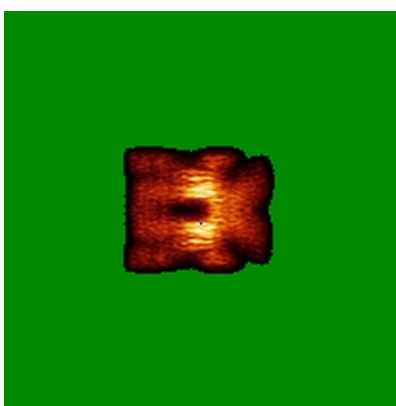
The images above show the largest variance slices of the map in three orthogonal directions.

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

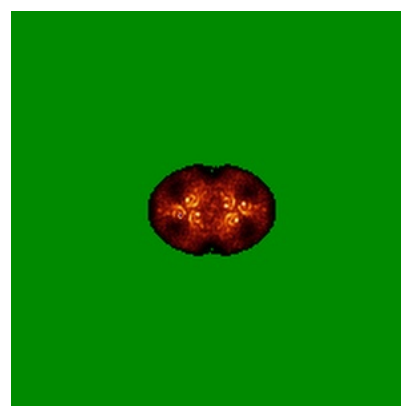
6.4.1 Primary map



X



Y

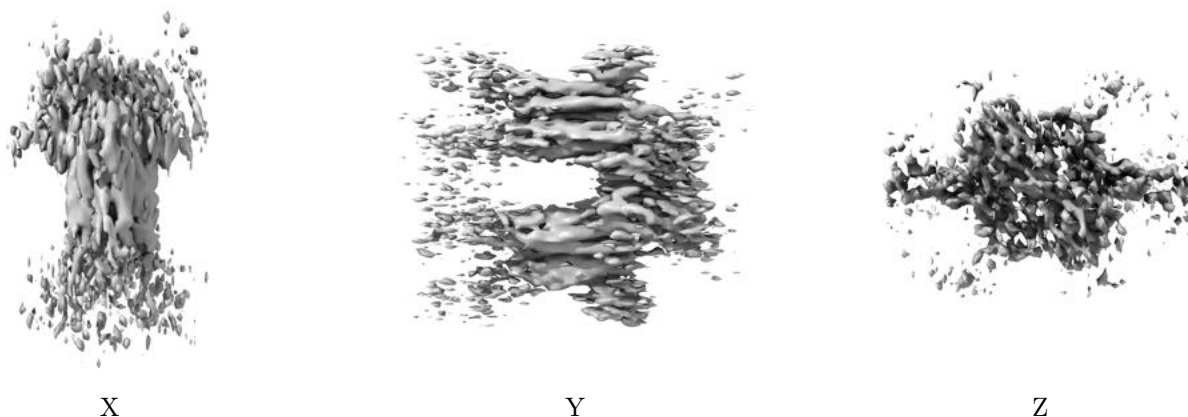


Z

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 2.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

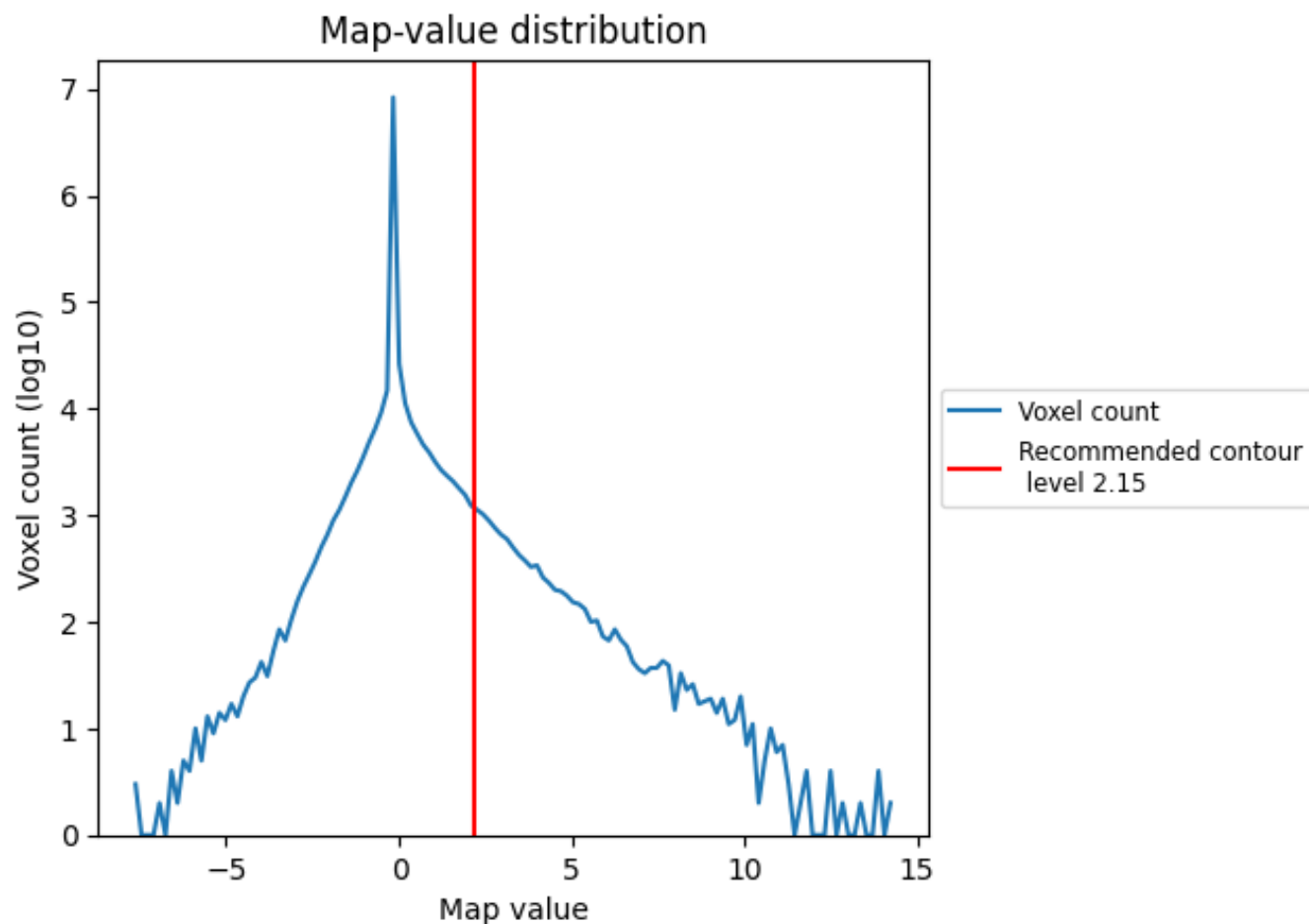
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

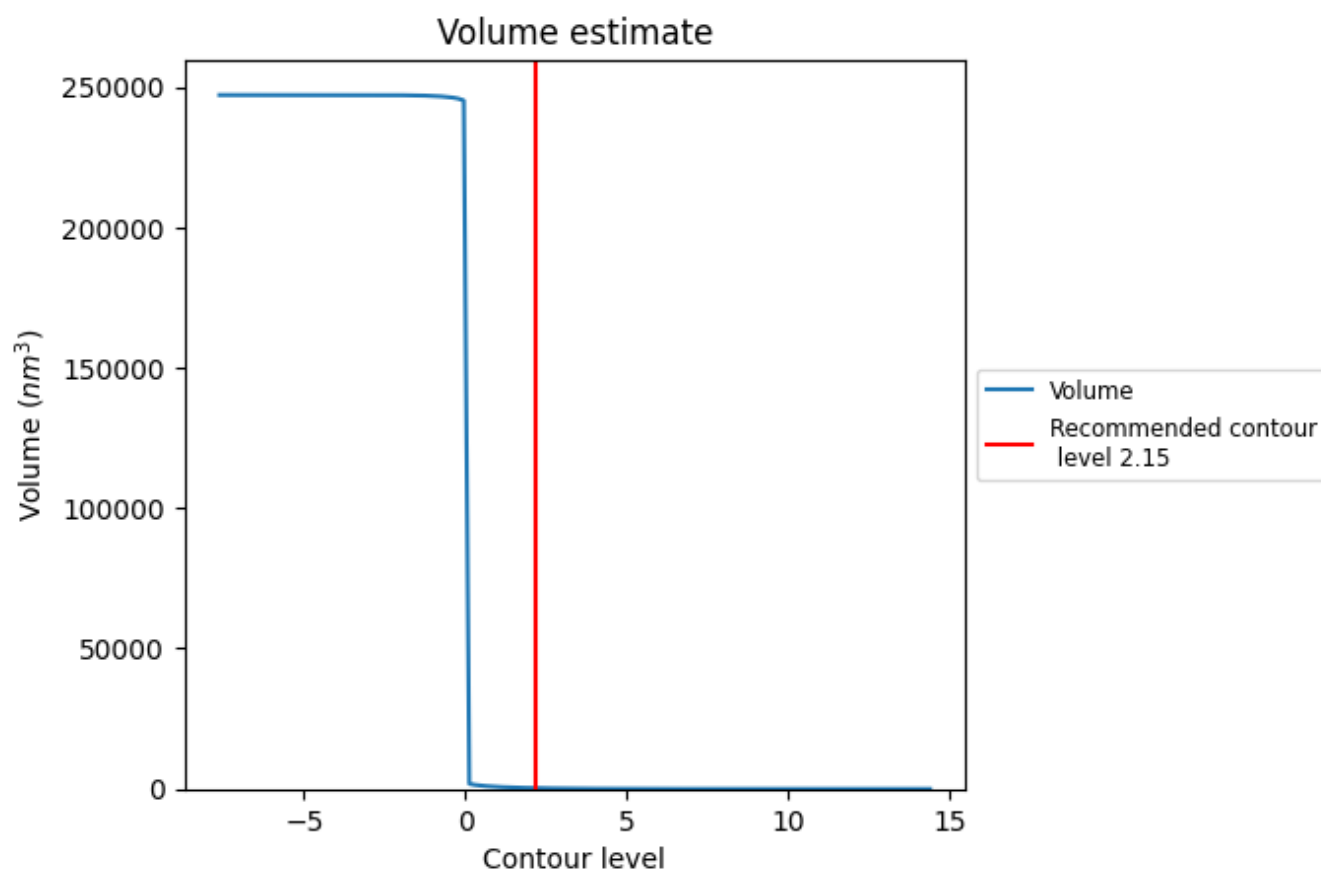
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

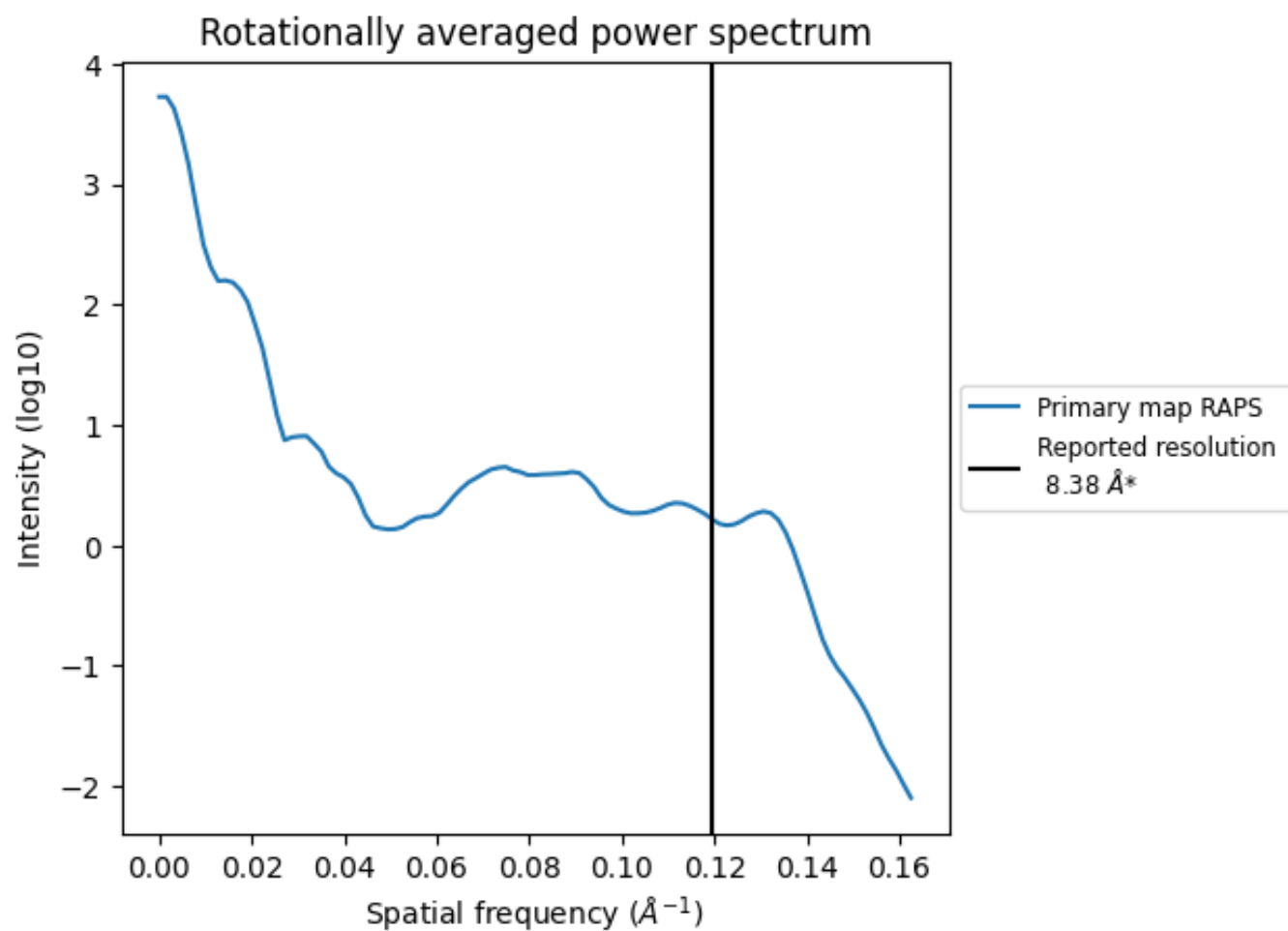
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 305 nm^3 ; this corresponds to an approximate mass of 275 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 0.119 $\text{\AA}^{-1}$

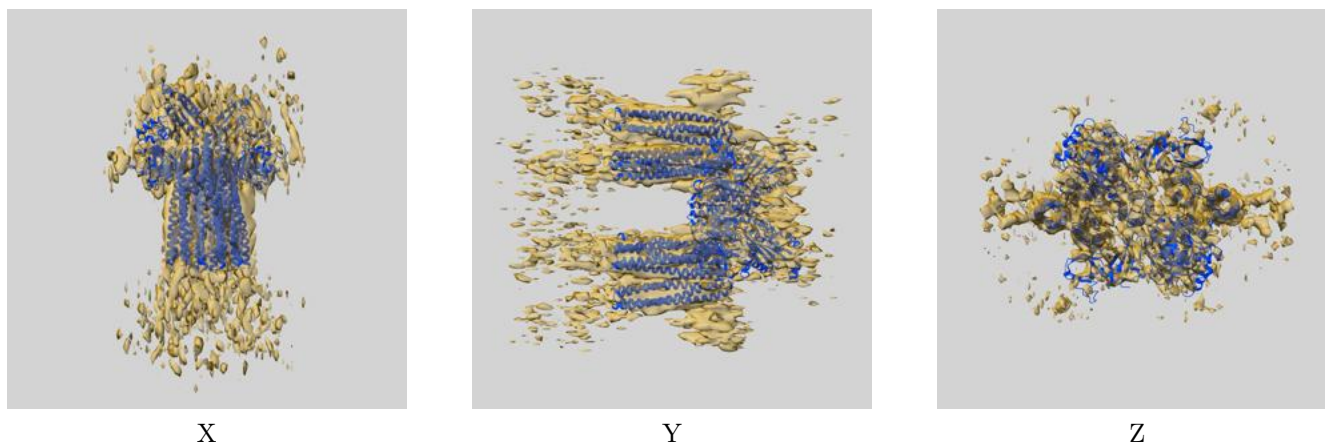
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

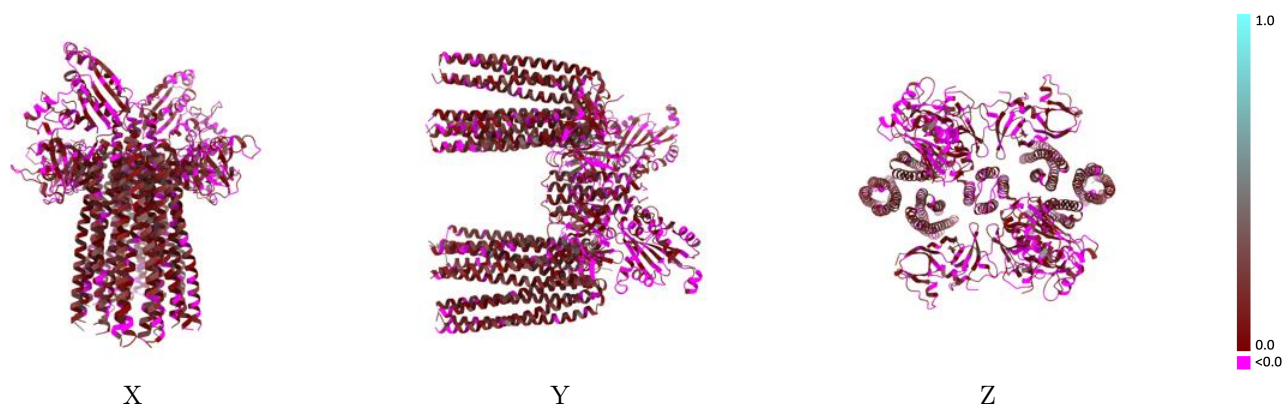
This section contains information regarding the fit between EMDB map EMD-10050 and PDB model 6S1K. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



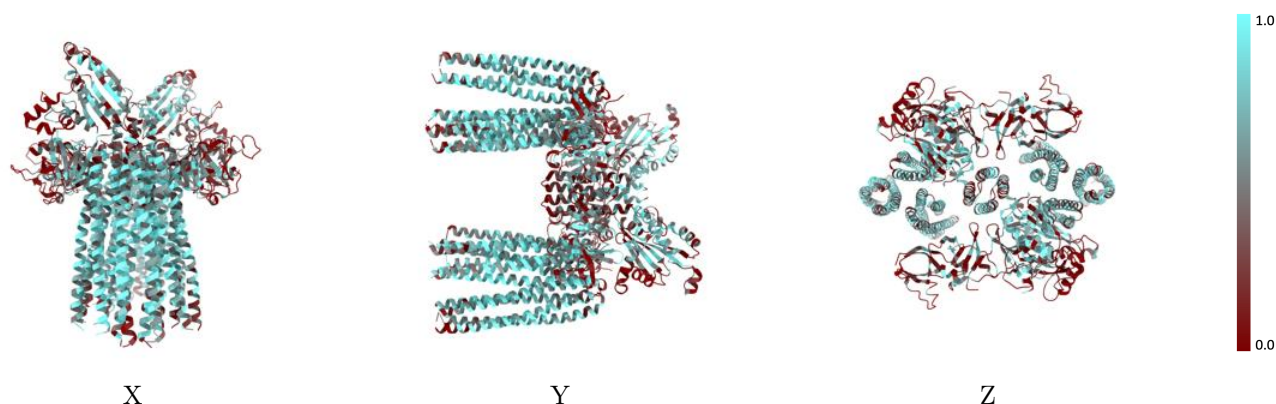
The images above show the 3D surface view of the map at the recommended contour level 2.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



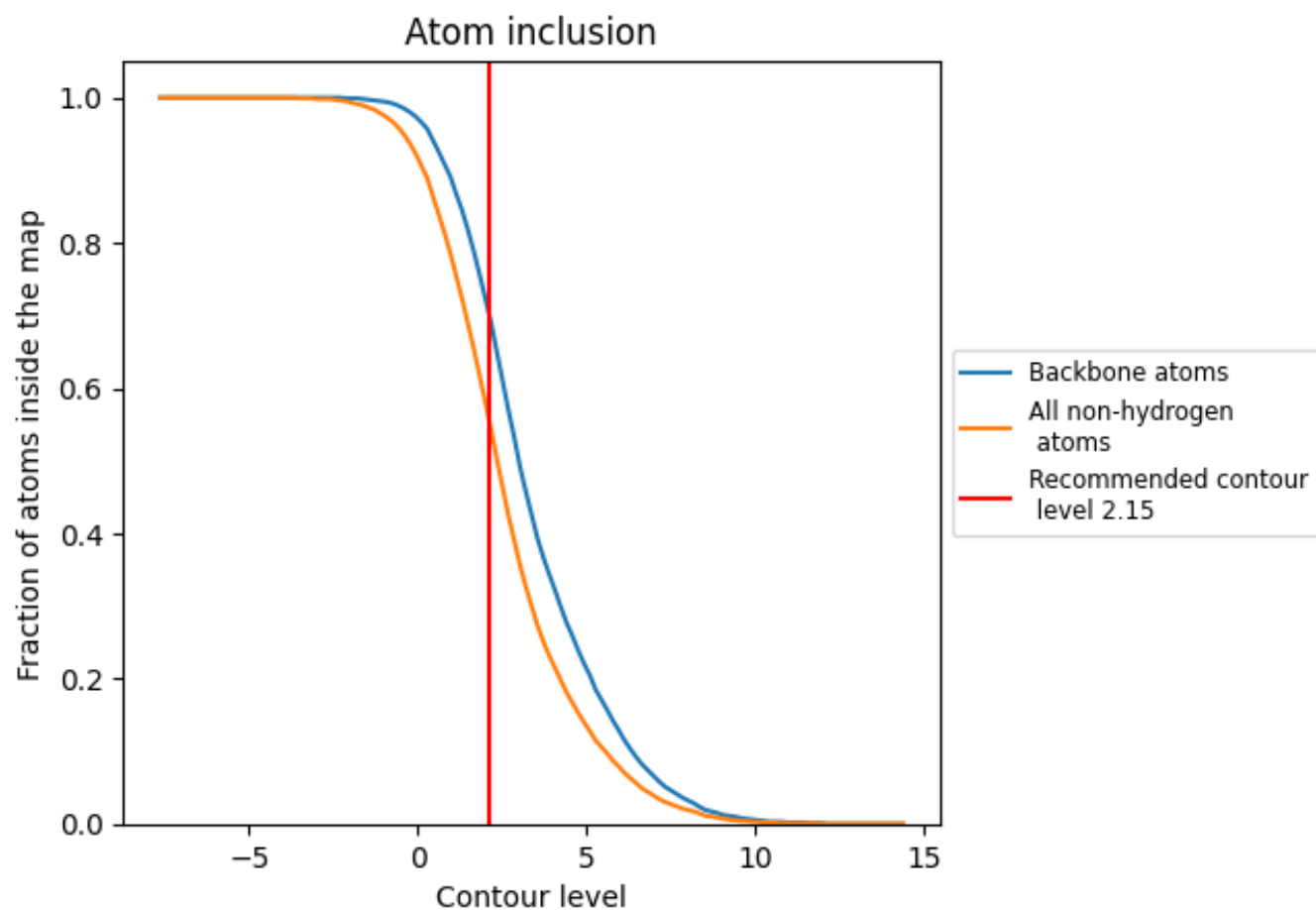
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 55% 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 (2.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5500	 0.0880
A	 0.4200	 0.0390
B	 0.4140	 0.0380
C	 0.3040	 0.0660
D	 0.3050	 0.0480
E	 0.6880	 0.1330
F	 0.7570	 0.1300
G	 0.6330	 0.1230
H	 0.7670	 0.1270
I	 0.6630	 0.1200
J	 0.7110	 0.1200
K	 0.6800	 0.1340
L	 0.7680	 0.1470
M	 0.6130	 0.1220
N	 0.7460	 0.1350
O	 0.6600	 0.1160
P	 0.7140	 0.1240

