



Full wwPDB EM Validation Report ⓘ

Mar 17, 2026 – 12:05 PM UTC

PDB ID : 7Z7N / pdb_00007z7n
EMDB ID : EMD-14534
Title : Mot1E1434Q:TBP:DNA - substrate recognition state
Authors : Woike, S.; Eustermann, S.; Jung, J.; Wenzl, S.J.; Hagemann, G.; Bartho, J.D.;
Lammens, K.; Butryn, A.; Herzog, F.; Hopfner, K.-P.
Deposited on : 2022-03-16
Resolution : 5.10 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:

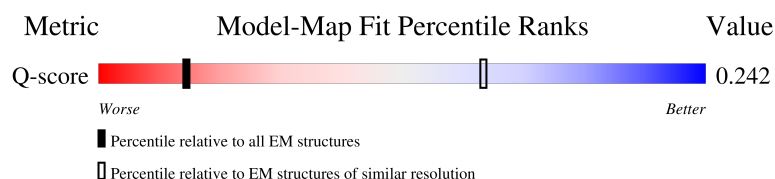
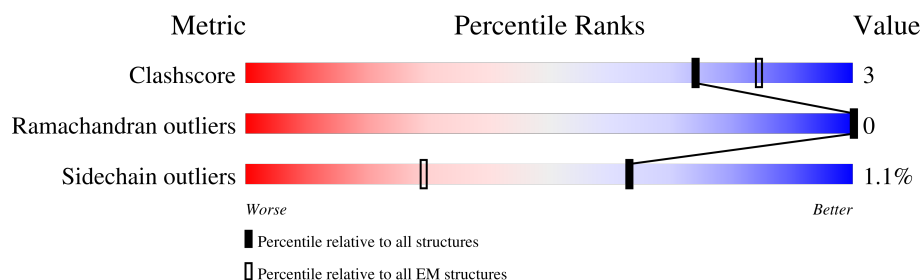
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 5.10 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	844 (4.60 - 5.60)

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	36	
2	B	36	
3	D	276	
4	E	1897	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 25969 atoms, of which 12825 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 DNA chain called DNA (36-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	36	Total	C	H	N	O	P	0	0
			1144	348	400	147	213	36		

- Molecule 2 is a DNA chain called DNA (36-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	36	Total	C	H	N	O	P	0	0
			1135	345	403	132	219	36		

- Molecule 3 is a protein called Putative tata-box binding protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	D	178	Total	C	H	N	O	S	0	0
			2907	919	1490	245	247	6		

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-20	MET	-	initiating methionine	UNP G0SAL6
D	-19	GLY	-	expression tag	UNP G0SAL6
D	-18	SER	-	expression tag	UNP G0SAL6
D	-17	SER	-	expression tag	UNP G0SAL6
D	-16	HIS	-	expression tag	UNP G0SAL6
D	-15	HIS	-	expression tag	UNP G0SAL6
D	-14	HIS	-	expression tag	UNP G0SAL6
D	-13	HIS	-	expression tag	UNP G0SAL6
D	-12	HIS	-	expression tag	UNP G0SAL6
D	-11	HIS	-	expression tag	UNP G0SAL6
D	-10	SER	-	expression tag	UNP G0SAL6
D	-9	SER	-	expression tag	UNP G0SAL6
D	-8	GLY	-	expression tag	UNP G0SAL6
D	-7	GLU	-	expression tag	UNP G0SAL6
D	-6	ASN	-	expression tag	UNP G0SAL6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-5	LEU	-	expression tag	UNP G0SAL6
D	-4	TYR	-	expression tag	UNP G0SAL6
D	-3	PHE	-	expression tag	UNP G0SAL6
D	-2	GLN	-	expression tag	UNP G0SAL6
D	-1	GLY	-	expression tag	UNP G0SAL6
D	0	HIS	-	expression tag	UNP G0SAL6

- Molecule 4 is a protein called Helicase-like protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	E	1306	Total	C	H	N	O	S	0	0
			20783	6520	10532	1807	1872	52		

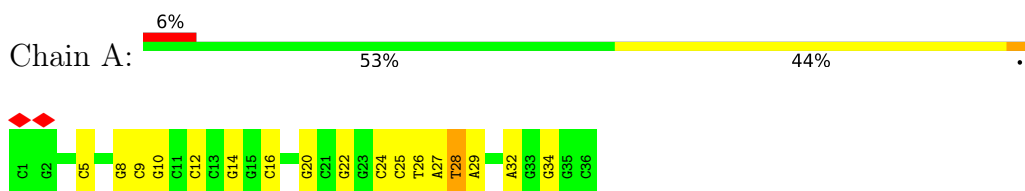
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	1434	GLN	GLU	engineered mutation	UNP G0S6C0
E	1887	ALA	-	expression tag	UNP G0S6C0
E	1888	ALA	-	expression tag	UNP G0S6C0
E	1889	ALA	-	expression tag	UNP G0S6C0
E	1890	TRP	-	expression tag	UNP G0S6C0
E	1891	SER	-	expression tag	UNP G0S6C0
E	1892	HIS	-	expression tag	UNP G0S6C0
E	1893	PRO	-	expression tag	UNP G0S6C0
E	1894	GLN	-	expression tag	UNP G0S6C0
E	1895	PHE	-	expression tag	UNP G0S6C0
E	1896	GLU	-	expression tag	UNP G0S6C0
E	1897	LYS	-	expression tag	UNP G0S6C0

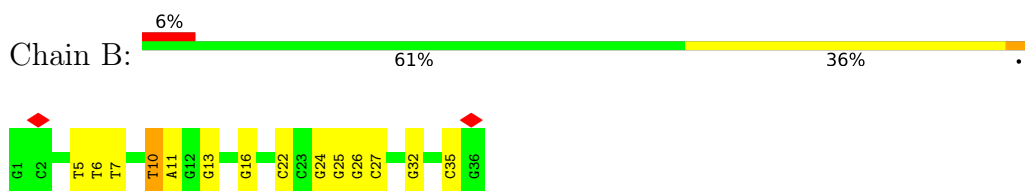
3 Residue-property plots

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.

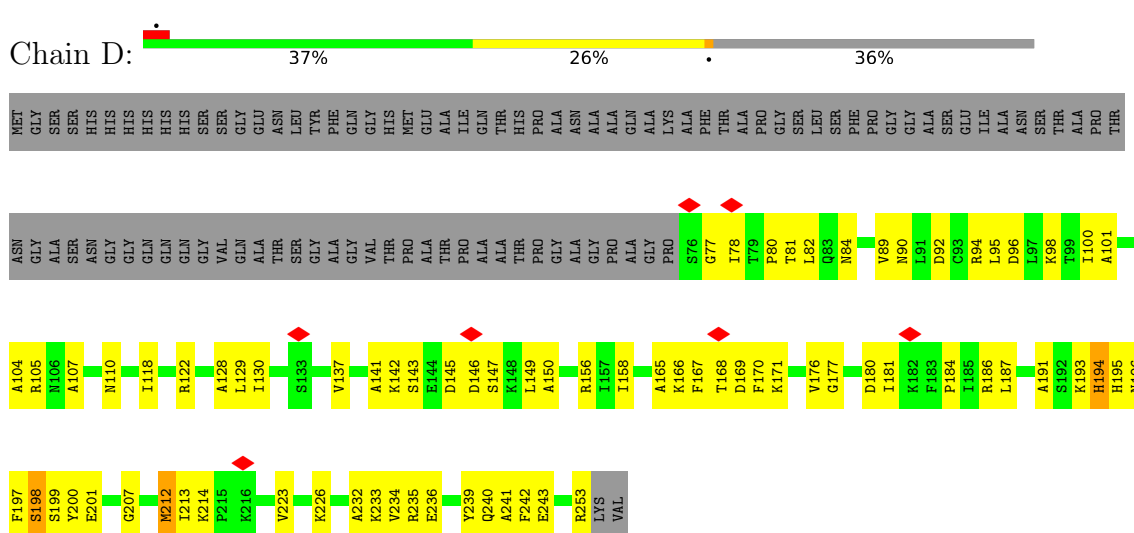
- Molecule 1: DNA (36-MER)



- Molecule 2: DNA (36-MER)



- Molecule 3: Putative tata-box binding protein



- Molecule 4: Helicase-like protein





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

LEU
TRP
ASP
ASN
ALA
GLN
TYR
GLU
GLU
SER
PHE
ASP
LEU
ASP
GLY
PHE
LEU
LYS
THR
MET
GLN
ALA
ALA
ALA
TRP
SER
HIS
PRO
GLN
PHE
GLU
LYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	44000	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 ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.056	Depositor
Minimum map value	-0.471	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.036	Depositor
Recommended contour level	0.219	Depositor
Map size (Å)	296.52002, 296.52002, 296.52002	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	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	0.72	0/836	1.27	1/1289 (0.1%)
2	B	0.72	0/818	1.33	2/1259 (0.2%)
3	D	2.31	36/1444 (2.5%)	2.41	118/1945 (6.1%)
4	E	0.79	23/10441 (0.2%)	0.87	95/14151 (0.7%)
All	All	1.06	59/13539 (0.4%)	1.19	216/18644 (1.2%)

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	17
2	B	0	13
All	All	0	30

All (59) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	1371	HIS	CE1-NE2	-8.80	1.23	1.32
4	E	1436	HIS	CE1-NE2	-8.76	1.23	1.32
3	D	195	HIS	ND1-CE1	-8.71	1.23	1.32
3	D	194	HIS	CE1-NE2	-8.66	1.23	1.32
4	E	1371	HIS	ND1-CE1	-8.47	1.24	1.32
4	E	1371	HIS	CD2-NE2	-8.13	1.28	1.37
3	D	194	HIS	CD2-NE2	-8.05	1.28	1.37
4	E	1436	HIS	CD2-NE2	-8.02	1.29	1.37
3	D	207	GLY	N-CA	-7.79	1.38	1.45
3	D	122	ARG	CZ-NH2	-7.58	1.23	1.33
4	E	1451	ARG	CZ-NH2	-7.54	1.23	1.33
3	D	253	ARG	CZ-NH2	-7.52	1.23	1.33
4	E	1502	ARG	CZ-NH2	-7.52	1.23	1.33
3	D	186	ARG	CZ-NH2	-7.50	1.23	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	129	ARG	CZ-NH2	-7.42	1.23	1.33
3	D	105	ARG	CZ-NH2	-7.39	1.23	1.33
3	D	235	ARG	CZ-NH2	-7.37	1.23	1.33
3	D	94	ARG	CZ-NH2	-7.35	1.23	1.33
3	D	253	ARG	CZ-NH1	-6.93	1.23	1.32
3	D	186	ARG	CZ-NH1	-6.89	1.23	1.32
4	E	129	ARG	CZ-NH1	-6.84	1.23	1.32
4	E	1502	ARG	CZ-NH1	-6.80	1.23	1.32
4	E	1451	ARG	CZ-NH1	-6.80	1.23	1.32
3	D	177	GLY	N-CA	-6.80	1.37	1.44
3	D	122	ARG	CZ-NH1	-6.80	1.23	1.32
3	D	235	ARG	CZ-NH1	-6.79	1.23	1.32
4	E	1495	ALA	CA-CB	-6.78	1.42	1.53
3	D	105	ARG	CZ-NH1	-6.78	1.23	1.32
3	D	94	ARG	CZ-NH1	-6.77	1.23	1.32
3	D	101	ALA	CA-CB	-6.67	1.43	1.53
3	D	241	ALA	CA-CB	-6.63	1.43	1.53
3	D	191	ALA	CA-CB	-6.62	1.43	1.53
4	E	1393	ALA	CA-CB	-6.62	1.43	1.53
4	E	1499	ALA	CA-CB	-6.59	1.43	1.53
3	D	150	ALA	CA-CB	-6.55	1.43	1.53
4	E	1448	ALA	CA-CB	-6.54	1.43	1.53
3	D	165	ALA	CA-CB	-6.30	1.43	1.53
3	D	141	ALA	CA-CB	-6.30	1.42	1.53
4	E	1496	LYS	N-CA	-6.27	1.41	1.46
3	D	232	ALA	CA-CB	-6.25	1.43	1.53
4	E	1506	ALA	CA-CB	-6.11	1.43	1.53
4	E	1370	GLY	N-CA	-6.07	1.38	1.45
4	E	1514	GLY	N-CA	-6.05	1.38	1.45
3	D	226	LYS	C-O	-6.04	1.16	1.24
3	D	107	ALA	CA-CB	-6.03	1.43	1.54
3	D	128	ALA	CA-CB	-5.65	1.43	1.53
3	D	105	ARG	CD-NE	-5.32	1.38	1.46
3	D	201	GLU	CA-CB	-5.31	1.47	1.53
3	D	186	ARG	CD-NE	-5.29	1.38	1.46
3	D	122	ARG	CD-NE	-5.29	1.38	1.46
3	D	253	ARG	CD-NE	-5.28	1.38	1.46
3	D	177	GLY	CA-C	-5.26	1.47	1.52
3	D	94	ARG	CD-NE	-5.21	1.39	1.46
4	E	1364	CYS	N-CA	-5.17	1.41	1.46
3	D	184	PRO	CA-CB	-5.09	1.46	1.53
3	D	235	ARG	CD-NE	-5.06	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	129	ARG	CD-NE	-5.05	1.39	1.46
4	E	1451	ARG	CD-NE	-5.02	1.39	1.46
4	E	1502	ARG	CD-NE	-5.01	1.39	1.46

All (216) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	176	VAL	CA-C-N	9.45	129.71	121.58
3	D	176	VAL	C-N-CA	9.45	129.71	121.58
3	D	137	VAL	CA-C-N	8.20	133.36	123.19
3	D	137	VAL	C-N-CA	8.20	133.36	123.19
3	D	226	LYS	CA-C-N	8.16	133.83	123.14
3	D	226	LYS	C-N-CA	8.16	133.83	123.14
4	E	1494	PHE	CA-CB-CG	7.61	121.41	113.80
4	E	1371	HIS	CA-CB-CG	7.59	121.39	113.80
4	E	1476	PHE	CA-CB-CG	7.23	121.03	113.80
3	D	194	HIS	CA-CB-CG	7.16	120.96	113.80
2	B	10	DT	C4'-C3'-O3'	7.12	120.68	110.00
4	E	1389	VAL	CA-C-N	7.09	135.31	121.41
4	E	1389	VAL	C-N-CA	7.09	135.31	121.41
3	D	92	ASP	CA-CB-CG	6.96	119.56	112.60
3	D	110	ASN	CA-CB-CG	6.95	119.55	112.60
3	D	197	PHE	CA-CB-CG	6.84	120.64	113.80
4	E	387	ASP	CA-CB-CG	6.84	119.44	112.60
3	D	180	ASP	CA-CB-CG	6.69	119.29	112.60
3	D	170	PHE	CA-CB-CG	6.65	120.45	113.80
4	E	1468	ASN	CA-CB-CG	6.63	119.23	112.60
3	D	129	LEU	CA-C-N	6.60	131.79	123.14
3	D	129	LEU	C-N-CA	6.60	131.79	123.14
4	E	1478	PHE	CA-CB-CG	6.58	120.38	113.80
3	D	96	ASP	CA-CB-CG	6.57	119.17	112.60
4	E	1433	ASP	CA-CB-CG	6.57	119.17	112.60
3	D	167	PHE	CA-CB-CG	6.53	120.33	113.80
3	D	212	MET	CA-C-N	6.50	130.37	122.63
3	D	212	MET	C-N-CA	6.50	130.37	122.63
4	E	1467	ASN	CA-CB-CG	6.47	119.07	112.60
3	D	146	ASP	CA-CB-CG	6.44	119.04	112.60
4	E	1492	ASP	CA-CB-CG	6.43	119.03	112.60
3	D	80	PRO	CA-C-N	6.41	131.30	122.77
3	D	80	PRO	C-N-CA	6.41	131.30	122.77
4	E	1408	VAL	CA-C-N	6.40	131.00	122.93
4	E	1408	VAL	C-N-CA	6.40	131.00	122.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	1493	ARG	CA-C-N	6.39	130.05	122.44
4	E	1493	ARG	C-N-CA	6.39	130.05	122.44
3	D	90	ASN	CA-CB-CG	6.30	118.90	112.60
4	E	1420	ASP	CA-CB-CG	6.28	118.88	112.60
3	D	235	ARG	CD-NE-CZ	6.25	133.15	124.40
3	D	207	GLY	CA-C-N	6.24	130.95	122.84
3	D	207	GLY	C-N-CA	6.24	130.95	122.84
4	E	1502	ARG	CD-NE-CZ	6.20	133.08	124.40
4	E	1407	ILE	CA-C-N	6.18	131.32	123.10
4	E	1407	ILE	C-N-CA	6.18	131.32	123.10
3	D	200	TYR	CA-C-N	6.17	130.62	123.15
3	D	200	TYR	C-N-CA	6.17	130.62	123.15
4	E	129	ARG	CD-NE-CZ	6.17	133.04	124.40
4	E	1362	ILE	CA-C-N	6.17	131.22	123.14
4	E	1362	ILE	C-N-CA	6.17	131.22	123.14
3	D	169	ASP	CA-CB-CG	6.15	118.75	112.60
4	E	1361	LEU	CA-C-N	6.14	131.03	123.10
4	E	1361	LEU	C-N-CA	6.14	131.03	123.10
3	D	89	VAL	CA-C-N	6.14	131.83	123.11
3	D	89	VAL	C-N-CA	6.14	131.83	123.11
4	E	1433	ASP	CA-C-N	6.14	131.26	123.03
4	E	1433	ASP	C-N-CA	6.14	131.26	123.03
4	E	1451	ARG	CD-NE-CZ	6.12	132.96	124.40
4	E	1420	ASP	CA-C-N	6.08	130.65	121.65
4	E	1420	ASP	C-N-CA	6.08	130.65	121.65
4	E	1360	SER	CA-C-N	6.08	131.57	123.00
4	E	1360	SER	C-N-CA	6.08	131.57	123.00
3	D	242	PHE	CA-CB-CG	6.04	119.84	113.80
4	E	1418	ASP	CA-CB-CG	6.02	118.62	112.60
3	D	184	PRO	CA-C-N	6.00	130.58	122.90
3	D	184	PRO	C-N-CA	6.00	130.58	122.90
4	E	1477	ASP	CA-CB-CG	5.89	118.49	112.60
4	E	1498	ILE	N-CA-CB	5.85	116.76	110.62
4	E	1431	VAL	CA-C-N	5.81	130.14	122.42
4	E	1431	VAL	C-N-CA	5.81	130.14	122.42
4	E	1518	ILE	N-CA-CB	5.77	117.30	110.55
4	E	390	SER	N-CA-CB	5.69	118.37	110.17
4	E	1458	LEU	CA-C-N	5.69	130.67	123.10
4	E	1458	LEU	C-N-CA	5.69	130.67	123.10
3	D	171	LYS	CA-C-N	5.67	130.88	122.99
3	D	171	LYS	C-N-CA	5.67	130.88	122.99
3	D	239	TYR	CA-C-N	5.64	127.78	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	239	TYR	C-N-CA	5.64	127.78	120.44
3	D	242	PHE	N-CA-CB	5.64	118.41	110.12
3	D	104	ALA	CA-C-N	5.64	131.00	121.14
3	D	104	ALA	C-N-CA	5.64	131.00	121.14
4	E	1507	SER	CA-C-N	5.63	131.34	122.11
4	E	1507	SER	C-N-CA	5.63	131.34	122.11
4	E	386	THR	CA-C-N	5.59	130.86	122.47
4	E	386	THR	C-N-CA	5.59	130.86	122.47
3	D	199	SER	CA-C-N	5.59	131.23	123.07
3	D	199	SER	C-N-CA	5.59	131.23	123.07
4	E	1503	TYR	CA-C-N	5.58	127.76	120.28
4	E	1503	TYR	C-N-CA	5.58	127.76	120.28
4	E	1459	ILE	CA-C-N	5.58	130.86	123.05
4	E	1459	ILE	C-N-CA	5.58	130.86	123.05
4	E	1430	CYS	CA-C-N	5.58	130.45	123.14
4	E	1430	CYS	C-N-CA	5.58	130.45	123.14
4	E	129	ARG	CG-CD-NE	5.57	124.26	112.00
4	E	129	ARG	CA-CB-CG	5.55	125.21	114.10
3	D	105	ARG	CA-CB-CG	5.55	125.20	114.10
3	D	233	LYS	CA-C-N	5.53	130.76	122.58
3	D	233	LYS	C-N-CA	5.53	130.76	122.58
3	D	122	ARG	CA-C-N	5.52	130.91	123.46
3	D	122	ARG	C-N-CA	5.52	130.91	123.46
4	E	1477	ASP	N-CA-CB	5.52	118.01	110.01
3	D	94	ARG	N-CA-CB	5.51	118.39	110.06
4	E	128	LEU	CA-C-N	5.50	128.66	120.90
4	E	128	LEU	C-N-CA	5.50	128.66	120.90
4	E	1365	PRO	N-CA-CB	5.46	106.25	103.19
4	E	1415	CYS	N-CA-CB	5.45	117.92	110.01
4	E	1510	GLU	CA-C-N	5.42	127.49	120.44
4	E	1510	GLU	C-N-CA	5.42	127.49	120.44
4	E	1473	TRP	N-CA-CB	5.41	117.85	110.01
3	D	158	ILE	N-CA-CB	5.40	116.51	110.51
4	E	1447	LEU	CA-C-N	5.36	127.73	120.44
4	E	1447	LEU	C-N-CA	5.36	127.73	120.44
3	D	77	GLY	CA-C-N	5.36	127.68	120.50
3	D	77	GLY	C-N-CA	5.36	127.68	120.50
3	D	156	ARG	CA-C-N	5.35	127.30	120.56
3	D	156	ARG	C-N-CA	5.35	127.30	120.56
3	D	118	ILE	CA-C-N	5.34	131.56	122.37
3	D	118	ILE	C-N-CA	5.34	131.56	122.37
3	D	195	HIS	CE1-NE2-CD2	-5.34	103.66	109.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	142	LYS	CA-CB-CG	5.32	124.74	114.10
4	E	1465	ILE	CA-C-N	5.32	130.01	122.24
4	E	1465	ILE	C-N-CA	5.32	130.01	122.24
4	E	1371	HIS	ND1-CG-CD2	-5.32	100.78	106.10
3	D	78	ILE	CA-C-N	5.31	128.03	120.49
3	D	78	ILE	C-N-CA	5.31	128.03	120.49
3	D	146	ASP	CA-C-N	5.30	127.33	120.44
3	D	146	ASP	C-N-CA	5.30	127.33	120.44
3	D	141	ALA	CA-C-N	5.29	129.68	120.68
3	D	141	ALA	C-N-CA	5.29	129.68	120.68
3	D	168	THR	CA-C-N	5.28	130.86	122.62
3	D	168	THR	C-N-CA	5.28	130.86	122.62
3	D	180	ASP	CA-C-N	5.28	131.02	122.68
3	D	180	ASP	C-N-CA	5.28	131.02	122.68
3	D	186	ARG	CA-C-N	5.27	127.34	120.28
3	D	186	ARG	C-N-CA	5.27	127.34	120.28
4	E	1491	LEU	CA-C-N	5.27	127.34	120.28
4	E	1491	LEU	C-N-CA	5.27	127.34	120.28
3	D	195	HIS	ND1-CG-CD2	-5.26	100.84	106.10
3	D	243	GLU	CA-C-N	5.25	127.75	120.29
3	D	243	GLU	C-N-CA	5.25	127.75	120.29
3	D	181	ILE	CA-C-N	5.25	127.58	120.65
3	D	181	ILE	C-N-CA	5.25	127.58	120.65
4	E	1498	ILE	CA-C-N	5.24	127.31	120.28
4	E	1498	ILE	C-N-CA	5.24	127.31	120.28
3	D	145	ASP	CA-C-N	5.24	127.25	120.44
3	D	145	ASP	C-N-CA	5.24	127.25	120.44
3	D	143	SER	CA-C-N	5.24	127.25	120.44
3	D	143	SER	C-N-CA	5.24	127.25	120.44
3	D	82	LEU	N-CA-CB	5.23	117.66	109.97
3	D	196	ASN	CA-C-N	5.23	129.98	121.98
3	D	196	ASN	C-N-CA	5.23	129.98	121.98
3	D	94	ARG	CD-NE-CZ	5.22	131.71	124.40
3	D	96	ASP	CA-C-N	5.22	127.28	120.28
3	D	96	ASP	C-N-CA	5.22	127.28	120.28
3	D	195	HIS	CG-CD2-NE2	5.22	112.42	107.20
1	A	28	DT	O4'-C1'-N1	5.21	116.22	108.40
4	E	1517	ALA	CA-C-N	5.20	127.11	120.56
4	E	1517	ALA	C-N-CA	5.20	127.11	120.56
3	D	149	LEU	CA-C-N	5.19	127.19	120.44
3	D	149	LEU	C-N-CA	5.19	127.19	120.44
4	E	1368	LEU	CA-C-N	5.18	127.17	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	1368	LEU	C-N-CA	5.18	127.17	120.44
3	D	240	GLN	CA-C-N	5.18	127.17	120.44
3	D	240	GLN	C-N-CA	5.18	127.17	120.44
4	E	1497	PRO	CA-C-N	5.16	127.53	120.77
4	E	1497	PRO	C-N-CA	5.16	127.53	120.77
4	E	1470	LEU	CA-C-N	5.16	127.70	120.28
4	E	1470	LEU	C-N-CA	5.16	127.70	120.28
3	D	98	LYS	N-CA-CB	5.15	117.69	110.12
3	D	166	LYS	CA-C-N	5.13	130.47	122.26
3	D	166	LYS	C-N-CA	5.13	130.47	122.26
4	E	1467	ASN	CA-C-N	5.13	130.01	122.77
4	E	1467	ASN	C-N-CA	5.13	130.01	122.77
4	E	1474	SER	N-CA-CB	5.13	117.45	110.01
4	E	16	SER	CA-C-N	5.11	130.59	122.62
4	E	16	SER	C-N-CA	5.11	130.59	122.62
4	E	1494	PHE	CA-C-N	5.11	127.40	120.65
4	E	1494	PHE	C-N-CA	5.11	127.40	120.65
3	D	198	SER	CA-C-N	5.10	130.90	122.33
3	D	198	SER	C-N-CA	5.10	130.90	122.33
3	D	84	ASN	CA-C-N	5.10	130.08	122.99
3	D	84	ASN	C-N-CA	5.10	130.08	122.99
3	D	100	ILE	CA-C-N	5.10	127.06	120.44
3	D	100	ILE	C-N-CA	5.10	127.06	120.44
3	D	234	VAL	CA-C-N	5.09	127.62	120.28
3	D	234	VAL	C-N-CA	5.09	127.62	120.28
3	D	81	THR	CA-C-N	5.09	128.10	120.87
3	D	81	THR	C-N-CA	5.09	128.10	120.87
3	D	95	LEU	CA-C-N	5.09	130.49	122.34
3	D	95	LEU	C-N-CA	5.09	130.49	122.34
4	E	15	GLY	CA-C-N	5.09	127.61	120.28
4	E	15	GLY	C-N-CA	5.09	127.61	120.28
3	D	193	LYS	CA-C-N	5.08	130.74	123.17
3	D	193	LYS	C-N-CA	5.08	130.74	123.17
3	D	236	GLU	CA-C-N	5.08	127.05	120.44
3	D	236	GLU	C-N-CA	5.08	127.05	120.44
3	D	90	ASN	CA-C-N	5.07	129.30	120.68
3	D	90	ASN	C-N-CA	5.07	129.30	120.68
3	D	187	LEU	CA-C-N	5.07	127.03	120.44
3	D	187	LEU	C-N-CA	5.07	127.03	120.44
3	D	239	TYR	CA-CB-CG	5.07	123.03	113.90
4	E	1477	ASP	CA-C-N	5.06	127.06	120.28
4	E	1477	ASP	C-N-CA	5.06	127.06	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	35	DC	O5'-C5'-C4'	5.05	118.38	110.80
3	D	147	SER	N-CA-CB	5.05	117.33	110.01
3	D	169	ASP	CA-C-N	5.04	129.86	122.39
3	D	169	ASP	C-N-CA	5.04	129.86	122.39
4	E	1432	LEU	CA-C-N	5.04	127.30	120.44
4	E	1432	LEU	C-N-CA	5.04	127.30	120.44
3	D	213	ILE	CA-C-N	5.04	130.56	123.30
3	D	213	ILE	C-N-CA	5.04	130.56	123.30
4	E	1478	PHE	N-CA-CB	5.04	117.53	110.12
4	E	1370	GLY	CA-C-N	5.04	127.34	120.54
4	E	1370	GLY	C-N-CA	5.04	127.34	120.54
4	E	1468	ASN	CA-C-N	5.01	128.90	120.29
4	E	1468	ASN	C-N-CA	5.01	128.90	120.29

There are no chirality outliers.

All (30) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	10	DG	Sidechain
1	A	12	DC	Sidechain
1	A	14	DG	Sidechain
1	A	16	DC	Sidechain
1	A	20	DG	Sidechain
1	A	22	DG	Sidechain
1	A	24	DC	Sidechain
1	A	25	DC	Sidechain
1	A	26	DT	Sidechain
1	A	27	DA	Sidechain
1	A	28	DT	Sidechain
1	A	29	DA	Sidechain
1	A	32	DA	Sidechain
1	A	34	DG	Sidechain
1	A	5	DC	Sidechain
1	A	8	DG	Sidechain
1	A	9	DC	Sidechain
2	B	10	DT	Sidechain
2	B	11	DA	Sidechain
2	B	13	DG	Sidechain
2	B	16	DG	Sidechain
2	B	22	DC	Sidechain
2	B	24	DG	Sidechain
2	B	25	DG	Sidechain

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Mol	Chain	Res	Type	Group
2	B	26	DG	Sidechain
2	B	27	DC	Sidechain
2	B	32	DG	Sidechain
2	B	5	DT	Sidechain
2	B	6	DT	Sidechain
2	B	7	DT	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	744	400	400	0	0
2	B	732	403	403	0	0
3	D	1417	1490	1489	3	0
4	E	10251	10532	10526	80	0
All	All	13144	12825	12818	83	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 3.

All (83) 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:E:1226:MET:O	4:E:1234:ARG:NH2	1.68	1.26
4:E:1227:SER:OG	4:E:1315:HIS:HB3	1.32	1.22
4:E:1227:SER:OG	4:E:1315:HIS:CB	2.22	0.87
4:E:1226:MET:HE2	4:E:1480:MET:SD	2.17	0.85
4:E:606:GLY:N	4:E:650:GLU:OE1	2.24	0.71
4:E:942:CYS:SG	4:E:980:THR:OG1	2.48	0.71
4:E:830:ARG:NH1	4:E:870:GLY:O	2.26	0.68
4:E:1226:MET:O	4:E:1234:ARG:CZ	2.42	0.67
4:E:1226:MET:CE	4:E:1480:MET:SD	2.83	0.67
4:E:541:LEU:HB3	4:E:547:VAL:HG21	1.77	0.66
4:E:1251:GLU:N	4:E:1251:GLU:OE1	2.28	0.66
4:E:13:GLU:OE2	4:E:52:HIS:NE2	2.30	0.64
4:E:1398:MET:O	4:E:1398:MET:HG3	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:1339:ASP:OD2	4:E:1429:TYR:OH	2.14	0.60
4:E:664:HIS:O	4:E:752:ARG:NH1	2.36	0.58
4:E:1228:ASP:N	4:E:1228:ASP:OD1	2.37	0.57
4:E:1225:ARG:HH11	4:E:1225:ARG:HG2	1.69	0.56
4:E:1017:GLU:N	4:E:1017:GLU:OE1	2.38	0.56
3:D:223:VAL:HG22	3:D:223:VAL:O	2.06	0.55
4:E:352:ARG:NH1	4:E:361:ASN:OD1	2.39	0.55
4:E:1227:SER:HG	4:E:1315:HIS:HB3	1.63	0.54
4:E:1204:ILE:HG21	4:E:1243:THR:HG23	1.89	0.54
4:E:1170:VAL:O	4:E:1174:THR:HG23	2.09	0.53
4:E:1336:VAL:HG12	4:E:1429:TYR:CD2	2.42	0.53
4:E:1235:LEU:O	4:E:1238:THR:OG1	2.21	0.52
4:E:844:GLN:NE2	4:E:848:ASN:OD1	2.42	0.52
4:E:392:THR:O	4:E:394:VAL:HG13	2.09	0.52
4:E:1154:ARG:NH2	4:E:1194:GLN:OE1	2.41	0.52
4:E:1535:GLU:N	4:E:1535:GLU:OE1	2.41	0.52
4:E:675:MET:HE3	4:E:735:MET:O	2.10	0.51
4:E:1077:GLU:N	4:E:1077:GLU:OE1	2.43	0.50
4:E:1257:PRO:CB	4:E:1260:LEU:HD22	2.42	0.50
4:E:472:VAL:HG23	4:E:512:LEU:HD21	1.94	0.50
4:E:839:VAL:HG22	4:E:921:VAL:HG22	1.93	0.50
4:E:1040:HIS:O	4:E:1042:ASP:N	2.45	0.49
4:E:1257:PRO:HB2	4:E:1260:LEU:HD22	1.94	0.49
4:E:19:LEU:HD21	4:E:1519:GLU:CG	2.43	0.49
4:E:656:GLU:OE1	4:E:656:GLU:N	2.46	0.49
4:E:418:HIS:ND1	4:E:467:MET:SD	2.86	0.48
4:E:970:ASN:OD1	4:E:972:GLU:N	2.46	0.48
4:E:1174:THR:HG22	4:E:1264:LEU:HD11	1.95	0.48
4:E:662:ALA:O	4:E:752:ARG:NH2	2.46	0.48
4:E:1081:THR:O	4:E:1084:THR:OG1	2.27	0.47
4:E:1097:ASP:OD1	4:E:1098:LEU:N	2.48	0.47
4:E:970:ASN:OD1	4:E:973:LEU:N	2.40	0.47
4:E:517:TRP:O	4:E:569:ARG:NH1	2.47	0.47
4:E:1354:GLU:N	4:E:1354:GLU:OE1	2.48	0.46
4:E:1225:ARG:NE	4:E:1225:ARG:HA	2.31	0.46
4:E:167:GLU:OE1	4:E:167:GLU:N	2.49	0.46
4:E:792:ALA:HA	4:E:795:MET:HE2	1.97	0.46
3:D:212:MET:SD	3:D:214:LYS:N	2.89	0.46
4:E:840:ARG:NE	4:E:865:ALA:O	2.48	0.46
4:E:1388:TYR:HD1	4:E:1388:TYR:O	1.99	0.45
4:E:541:LEU:HD22	4:E:547:VAL:CG2	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:880:SER:N	4:E:883:ASN:OD1	2.48	0.45
4:E:1329:THR:HG23	4:E:1372:TRP:CZ2	2.51	0.45
4:E:1521:LEU:O	4:E:1525:VAL:HG22	2.17	0.44
4:E:1345:GLU:OE1	4:E:1349:ARG:NE	2.46	0.44
4:E:113:GLU:OE1	4:E:113:GLU:N	2.50	0.44
4:E:1225:ARG:HG2	4:E:1225:ARG:NH1	2.33	0.43
4:E:1226:MET:SD	4:E:1226:MET:C	3.02	0.43
4:E:1007:PHE:O	4:E:1010:VAL:HG23	2.20	0.42
4:E:15:GLY:O	4:E:21:ARG:NH1	2.53	0.42
4:E:517:TRP:CD2	4:E:566:LEU:HD21	2.55	0.42
4:E:1465:ILE:HD12	4:E:1468:ASN:O	2.19	0.42
4:E:459:ASP:OD1	4:E:460:LEU:N	2.52	0.42
4:E:1204:ILE:HG21	4:E:1243:THR:CG2	2.50	0.42
4:E:1209:ASP:OD1	4:E:1209:ASP:N	2.53	0.42
4:E:386:THR:HG21	4:E:388:TYR:CZ	2.54	0.41
4:E:1226:MET:O	4:E:1226:MET:SD	2.79	0.41
4:E:1227:SER:OG	4:E:1315:HIS:CG	2.74	0.41
4:E:792:ALA:O	4:E:796:VAL:HG23	2.20	0.41
4:E:858:GLN:OE1	4:E:859:GLY:N	2.52	0.41
4:E:553:VAL:O	4:E:557:GLN:NE2	2.49	0.41
4:E:1316:LEU:O	4:E:1317:HIS:ND1	2.54	0.41
4:E:1017:GLU:HB2	4:E:1020:ILE:HD12	2.04	0.40
4:E:1319:ILE:HG23	4:E:1459:ILE:O	2.21	0.40
4:E:481:ASP:OD1	4:E:482:ILE:N	2.54	0.40
4:E:1296:GLU:OE1	4:E:1296:GLU:N	2.49	0.40
4:E:1135:VAL:O	4:E:1139:VAL:HG23	2.21	0.40
3:D:194:HIS:O	3:D:198:SER:N	2.55	0.40
4:E:1118:SER:HA	4:E:1121:ARG:HG2	2.04	0.40
4:E:1209:ASP:HA	4:E:1247:LEU:HD22	2.04	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	
3	D	176/276 (64%)	170 (97%)	6 (3%)	0	100	100
4	E	1296/1897 (68%)	1243 (96%)	53 (4%)	0	100	100
All	All	1472/2173 (68%)	1413 (96%)	59 (4%)	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	
3	D	154/219 (70%)	153 (99%)	1 (1%)	78	82
4	E	1114/1620 (69%)	1101 (99%)	13 (1%)	63	74
All	All	1268/1839 (69%)	1254 (99%)	14 (1%)	63	74

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	130	ILE
4	E	380	LEU
4	E	516	VAL
4	E	528	SER
4	E	530	SER
4	E	534	ILE
4	E	654	HIS
4	E	1067	LEU
4	E	1082	LEU
4	E	1226	MET
4	E	1228	ASP
4	E	1363	ILE
4	E	1389	VAL
4	E	1418	ASP

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

5.3.3 RNA [i](#)

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](#)

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.

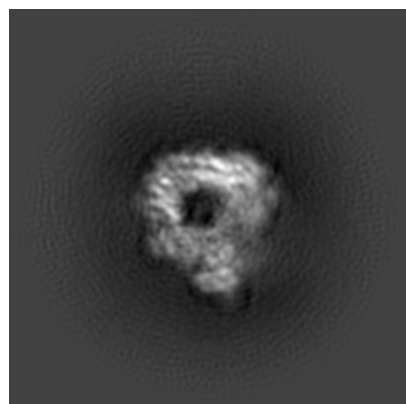
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14534. These allow visual inspection of the internal detail of the map and identification of artifacts.

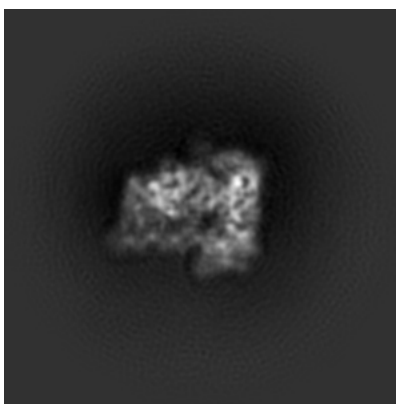
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

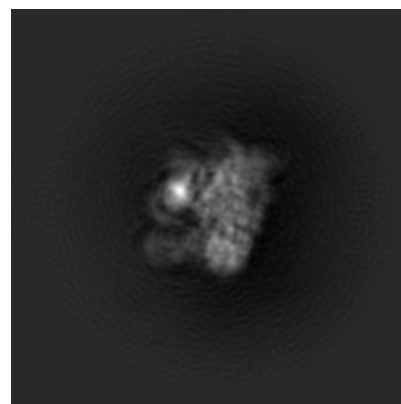
6.1.1 Primary map



X

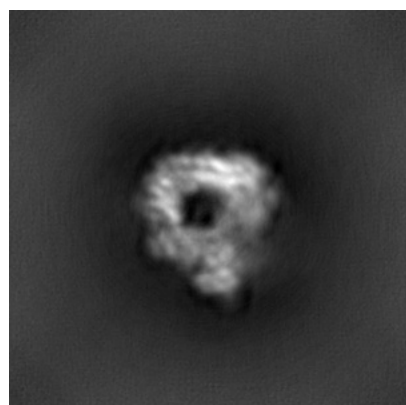


Y

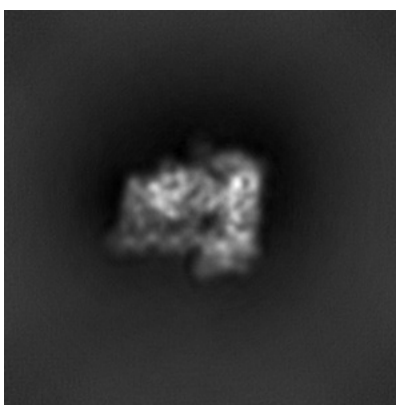


Z

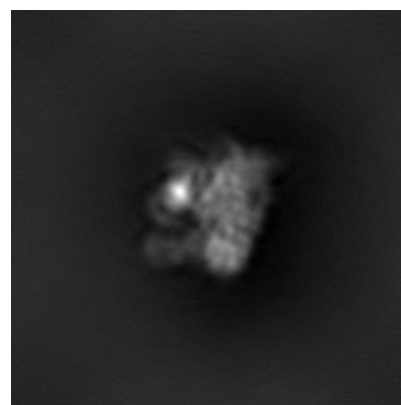
6.1.2 Raw map



X



Y

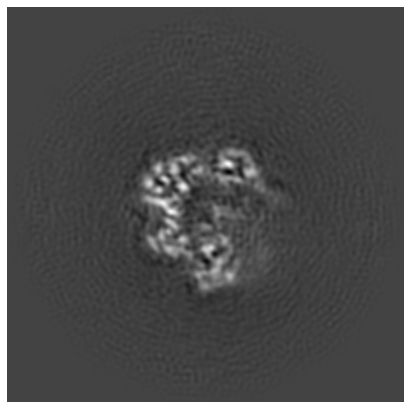


Z

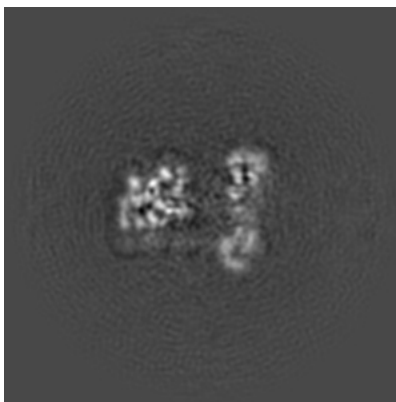
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

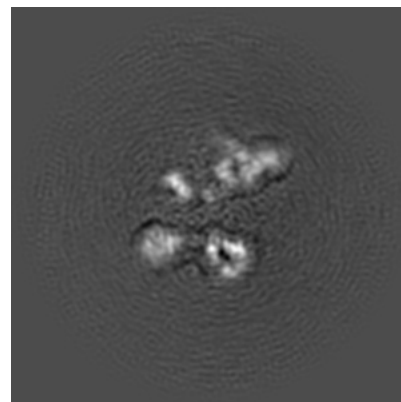
6.2.1 Primary map



X Index: 140

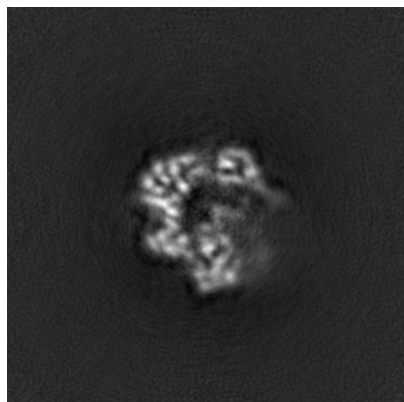


Y Index: 140

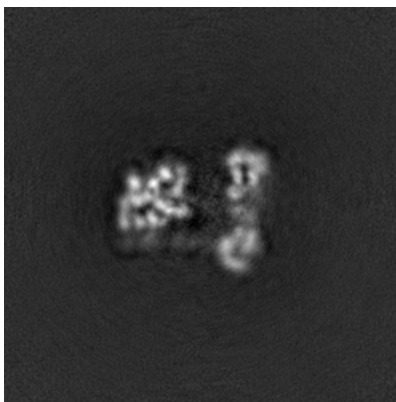


Z Index: 140

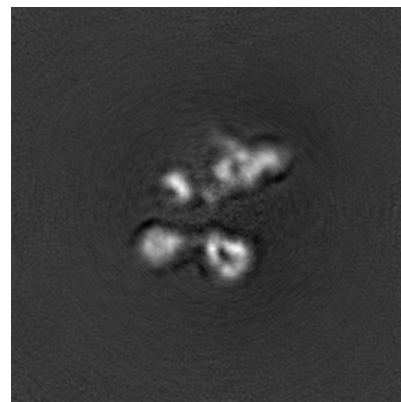
6.2.2 Raw map



X Index: 140



Y Index: 140

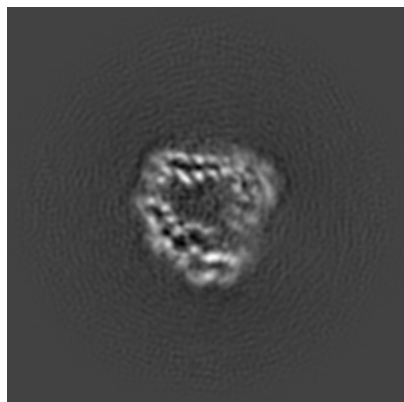


Z Index: 140

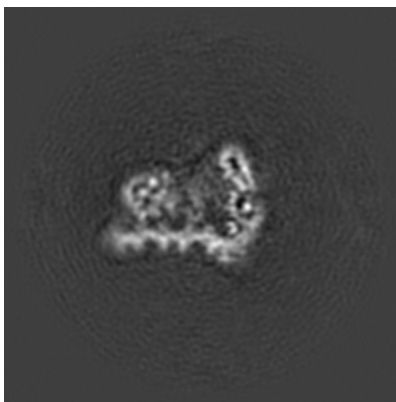
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

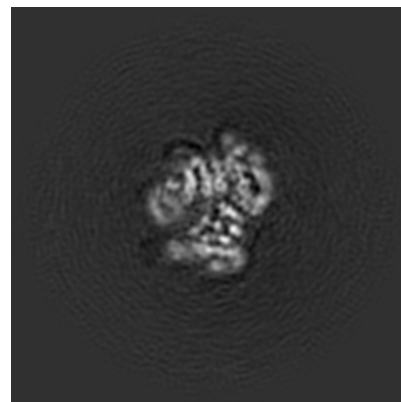
6.3.1 Primary map



X Index: 156

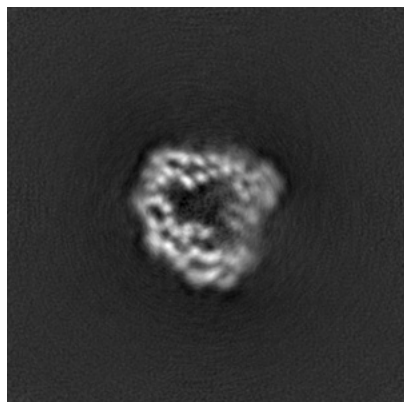


Y Index: 153

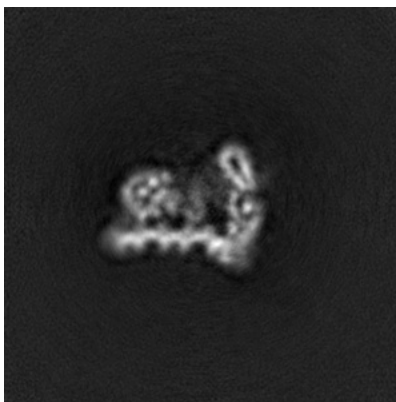


Z Index: 160

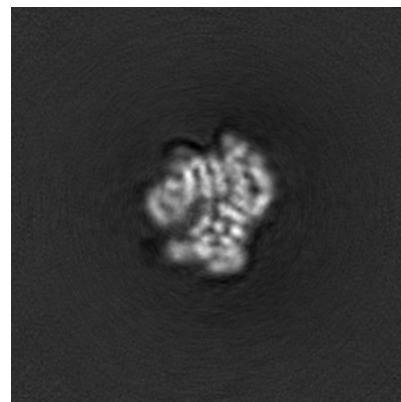
6.3.2 Raw map



X Index: 154



Y Index: 152

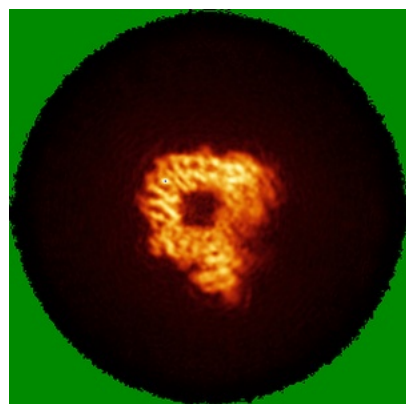


Z Index: 161

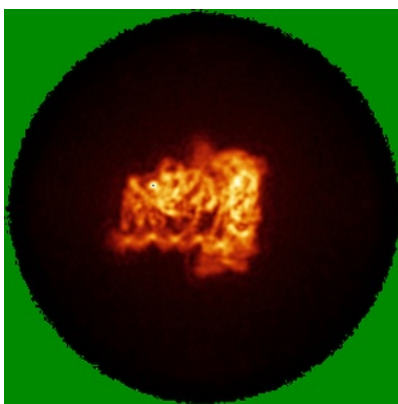
The images above show the largest variance slices of the map in three orthogonal directions.

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

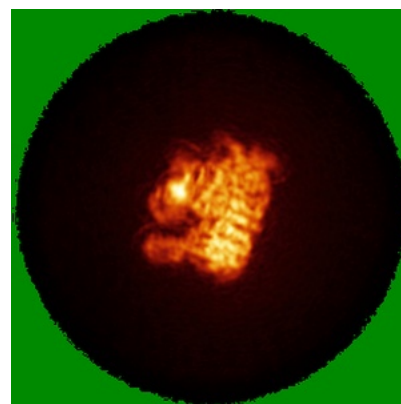
6.4.1 Primary map



X



Y

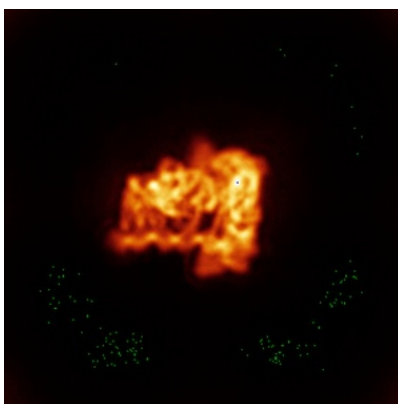


Z

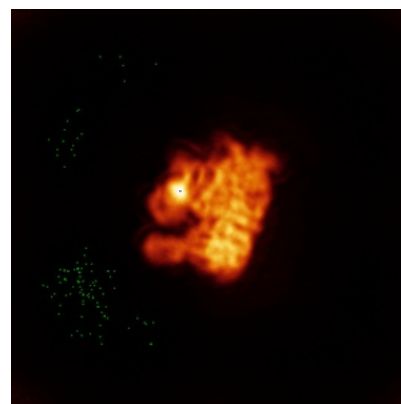
6.4.2 Raw map



X



Y

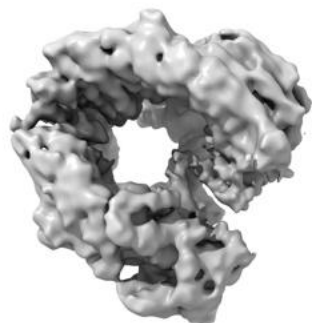


Z

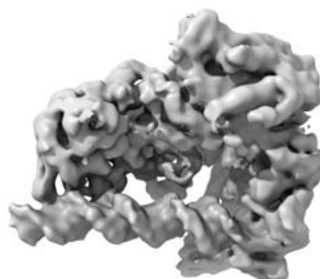
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

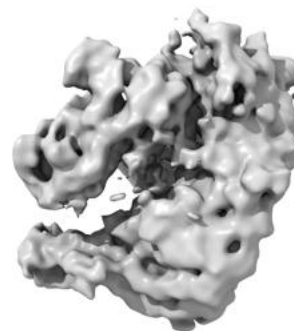
6.5.1 Primary map



X



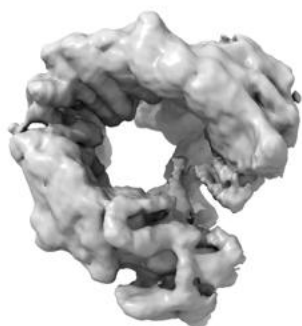
Y



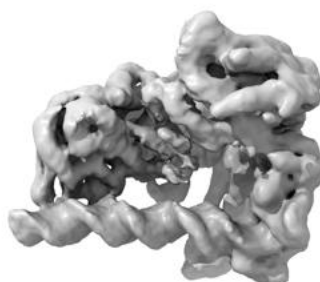
Z

The images above show the 3D surface view of the map at the recommended contour level 0.219. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

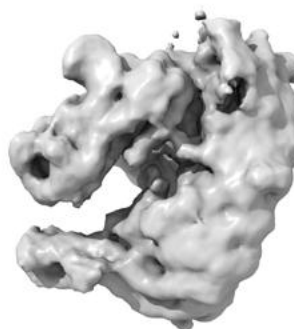
6.5.2 Raw map



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.

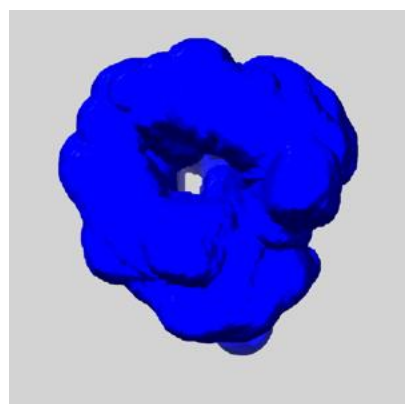
6.6 Mask visualisation [i](#)

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

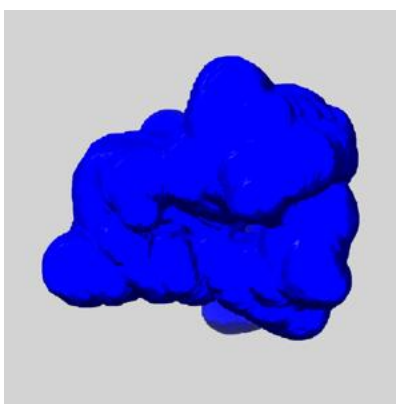
A mask typically either:

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

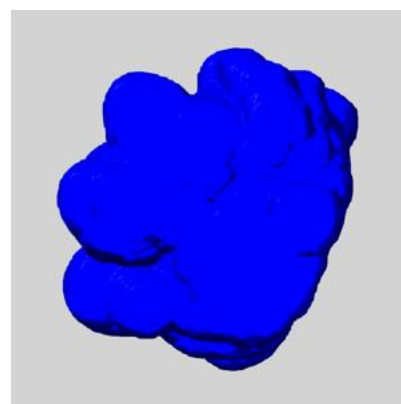
6.6.1 emd_14534_msk_1.map [i](#)



X



Y

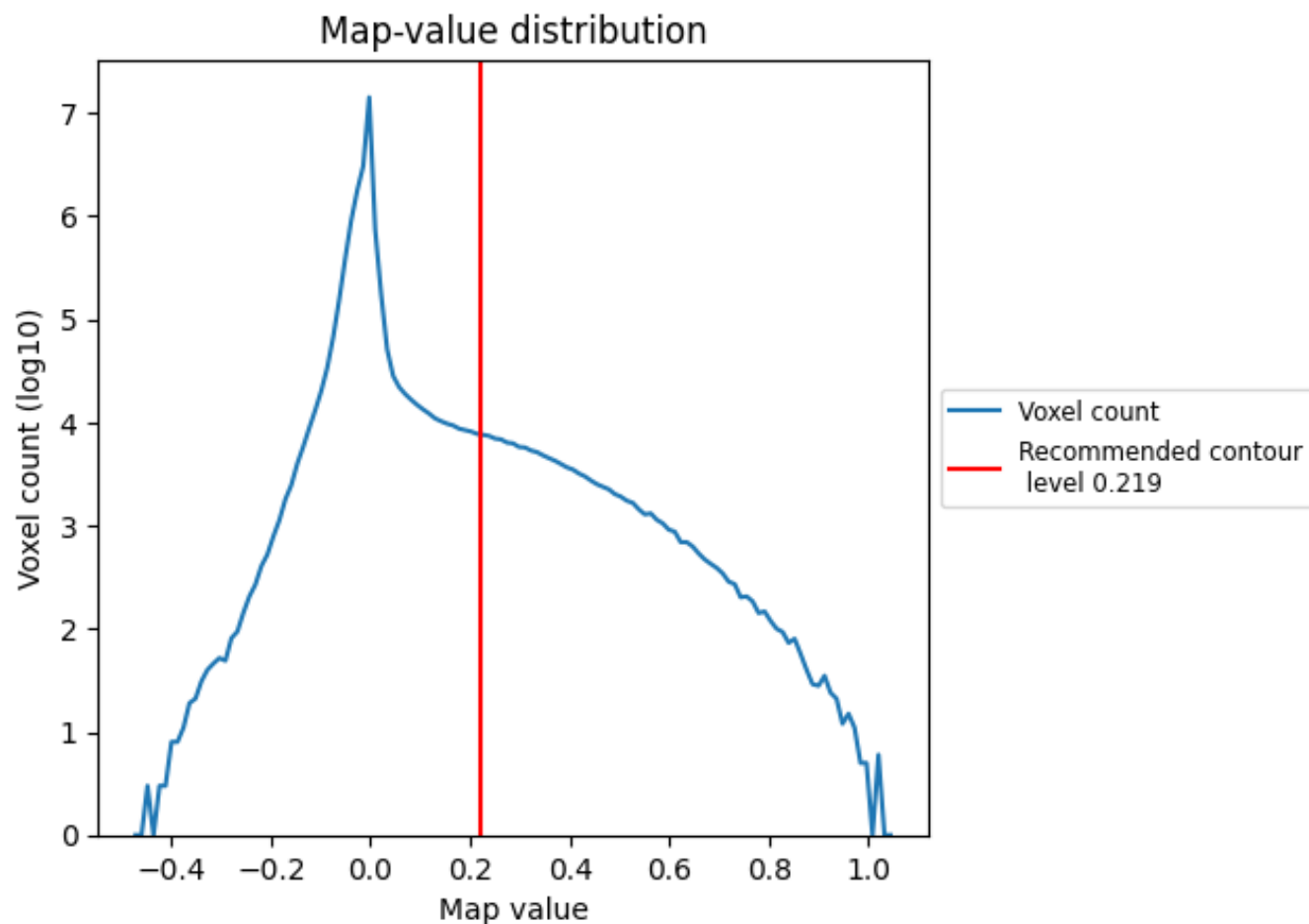


Z

7 Map analysis [i](#)

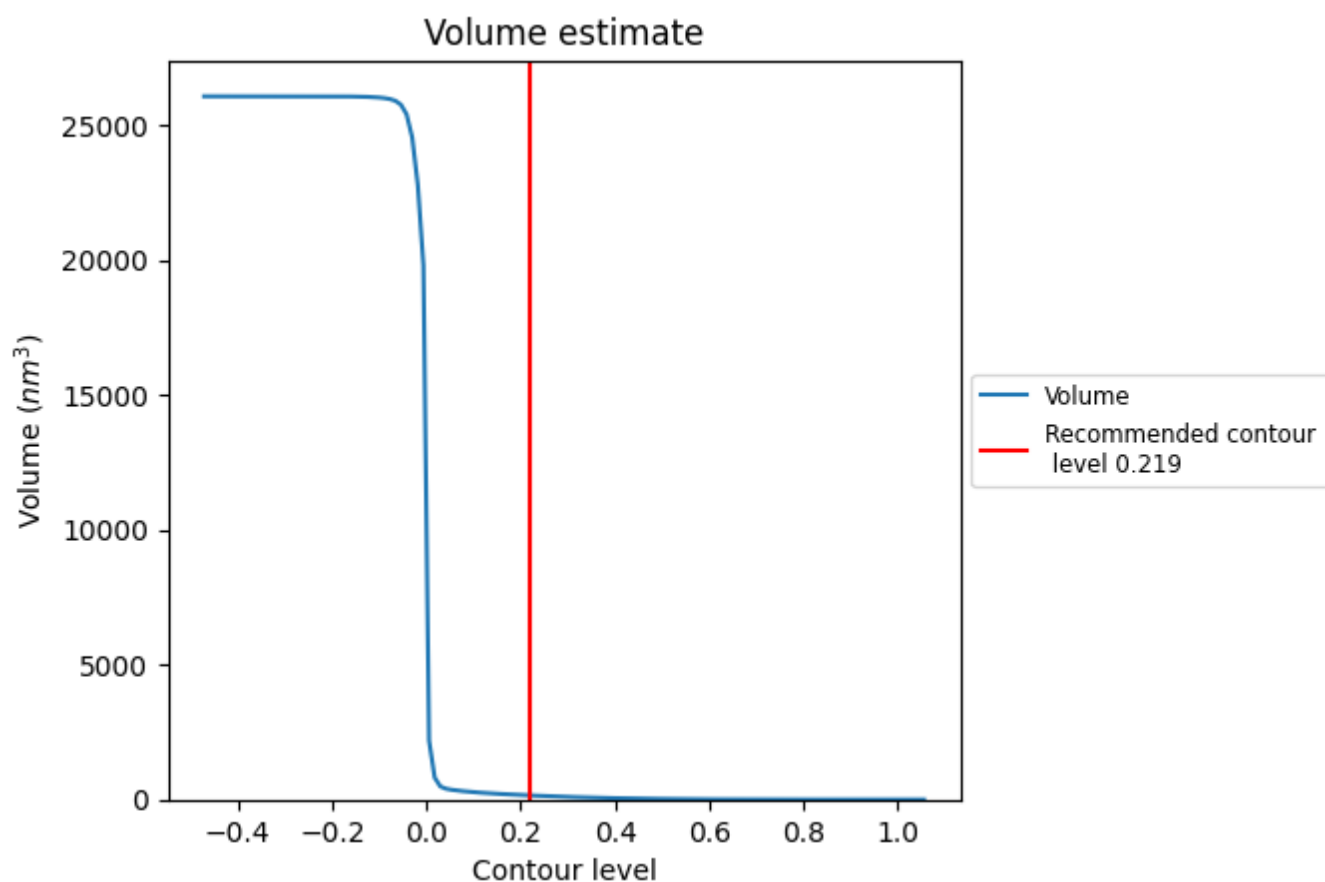
This section contains the results of statistical analysis of the map.

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.

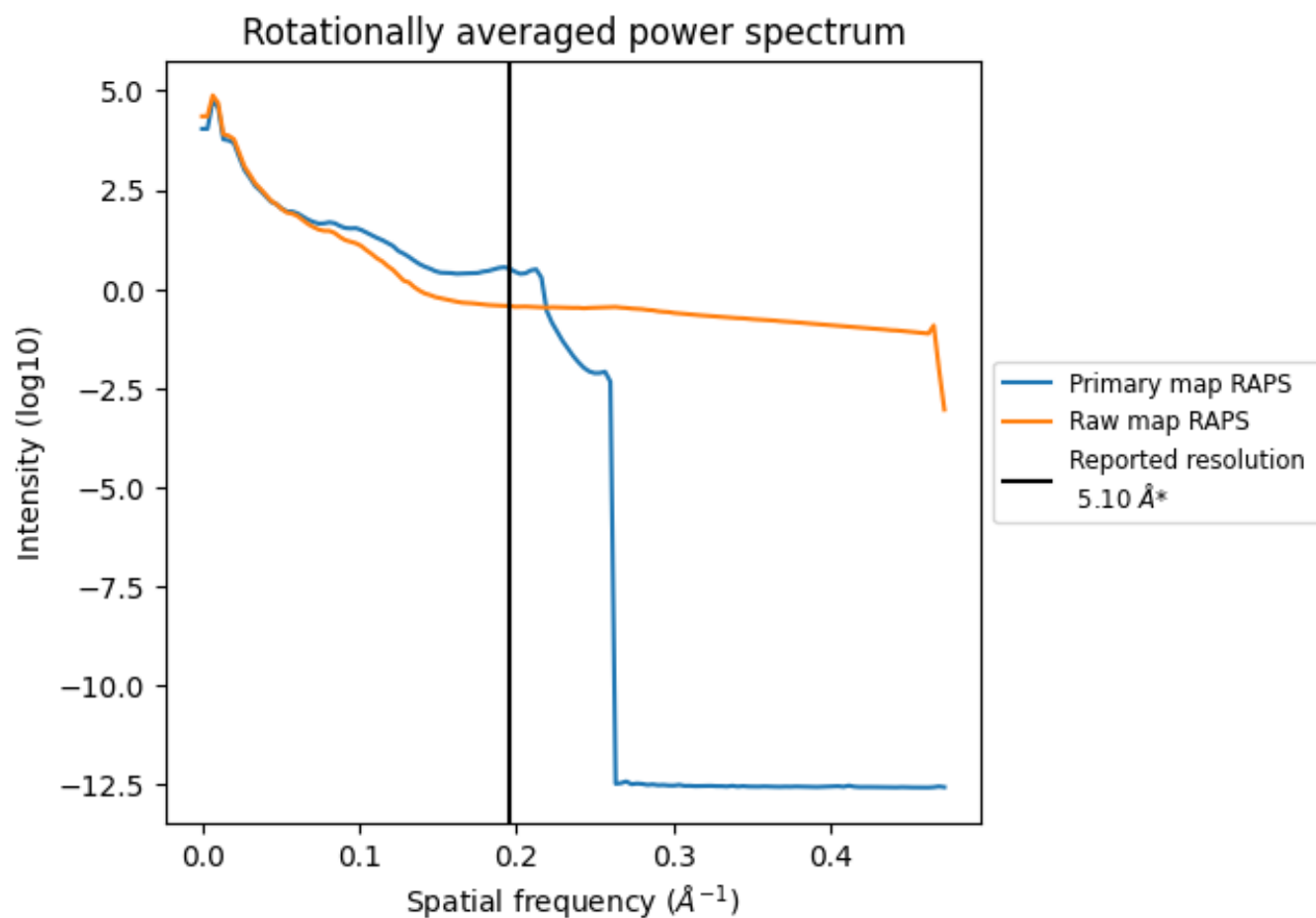
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 155 nm^3 ; this corresponds to an approximate mass of 140 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 ⓘ

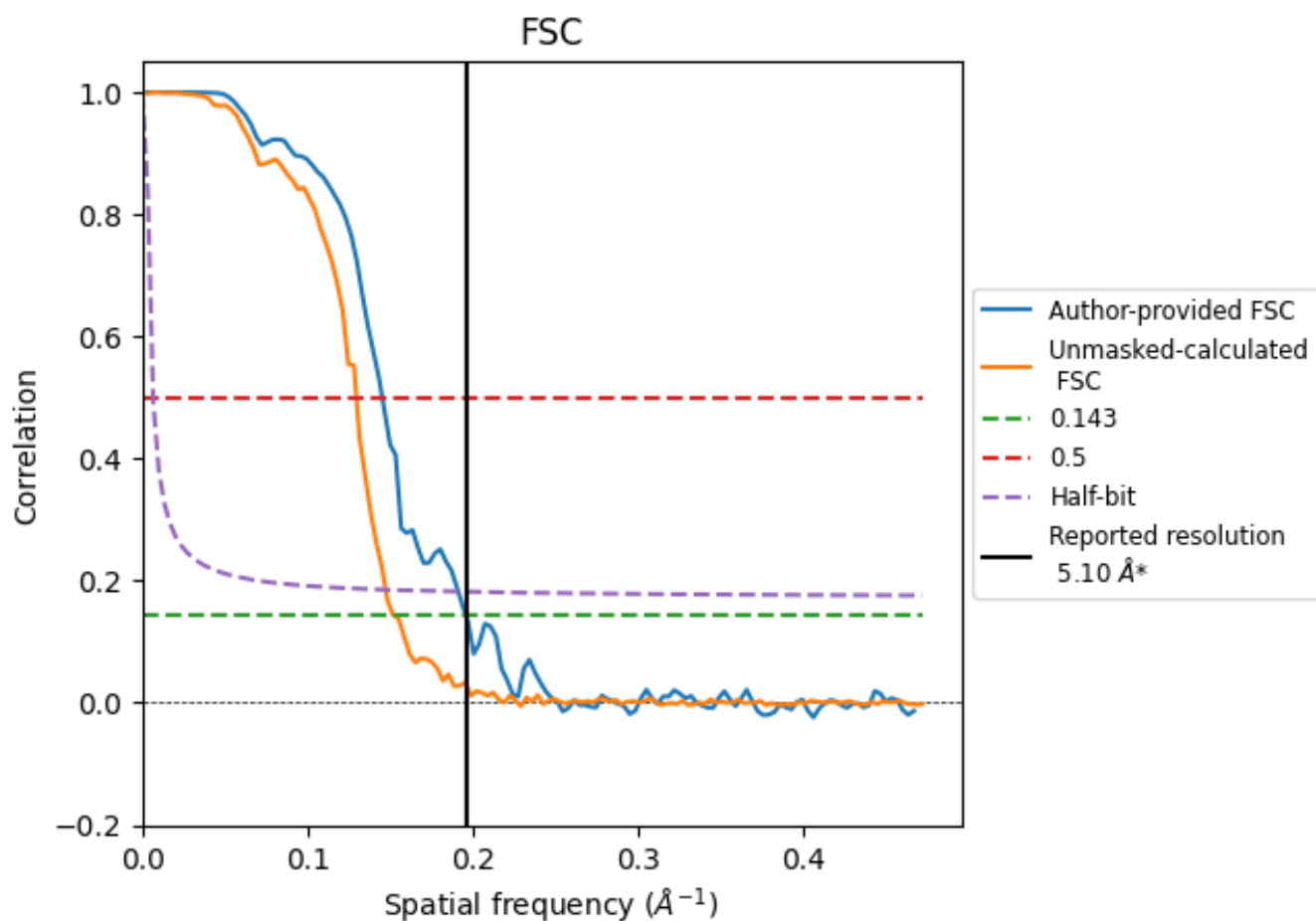


*Reported resolution corresponds to spatial frequency of 0.196 Å⁻¹

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 0.196 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

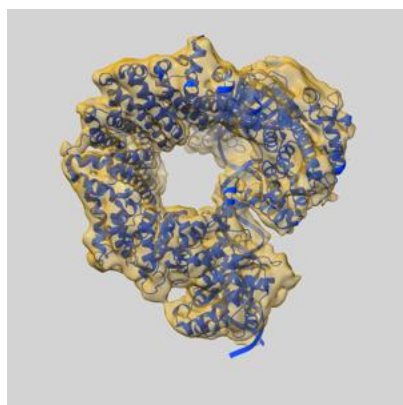
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.10	-	-
Author-provided FSC curve	5.10	6.88	5.22
Unmasked-calculated*	6.57	7.71	6.78

*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 6.57 differs from the reported value 5.1 by more than 10 %

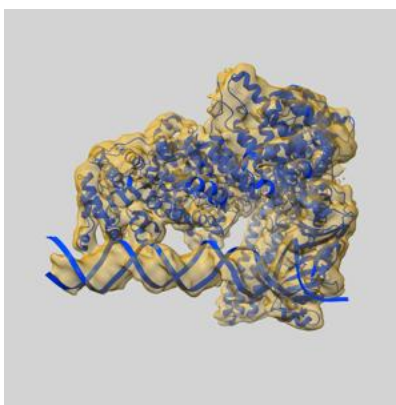
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14534 and PDB model 7Z7N. Per-residue inclusion information can be found in section [3](#) on page [5](#).

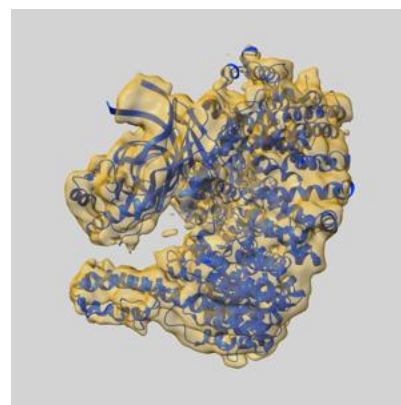
9.1 Map-model overlay [i](#)



X



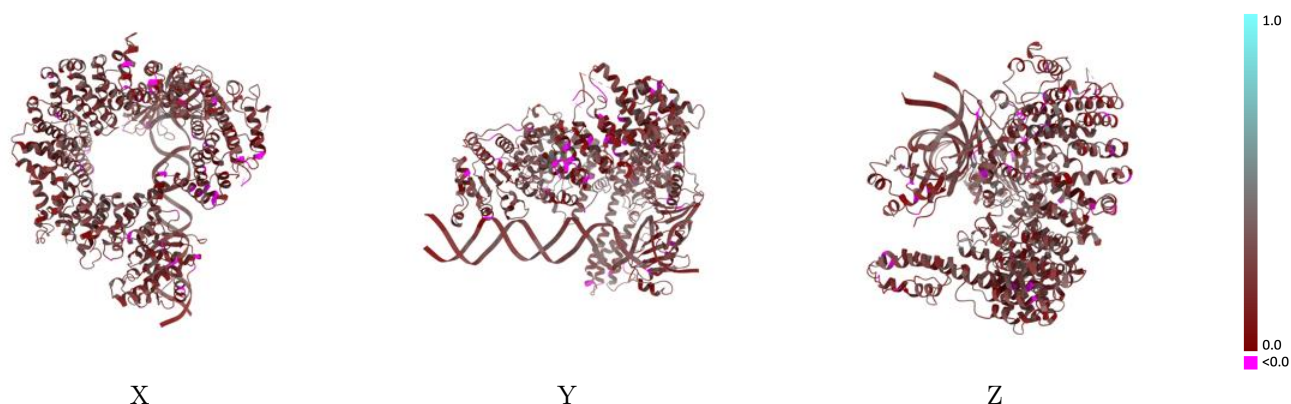
Y



Z

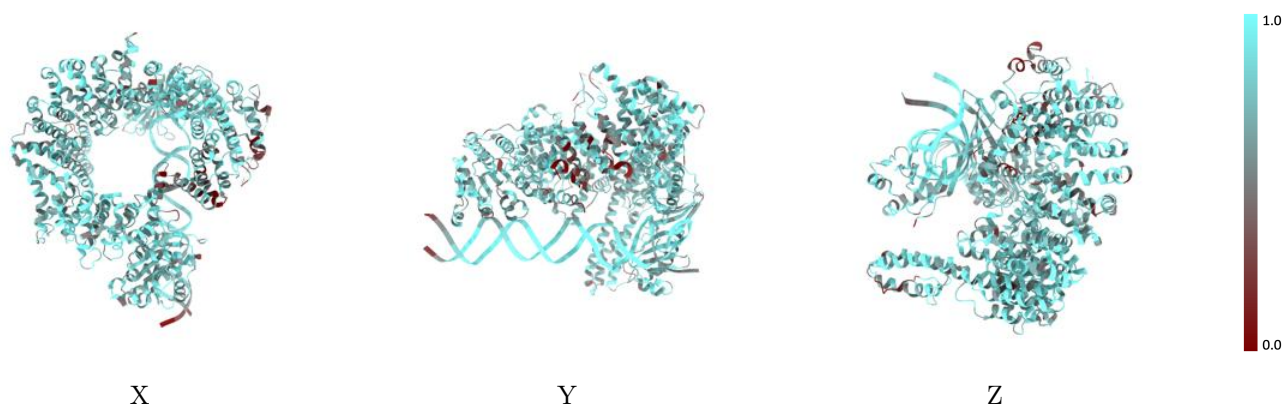
The images above show the 3D surface view of the map at the recommended contour level 0.219 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



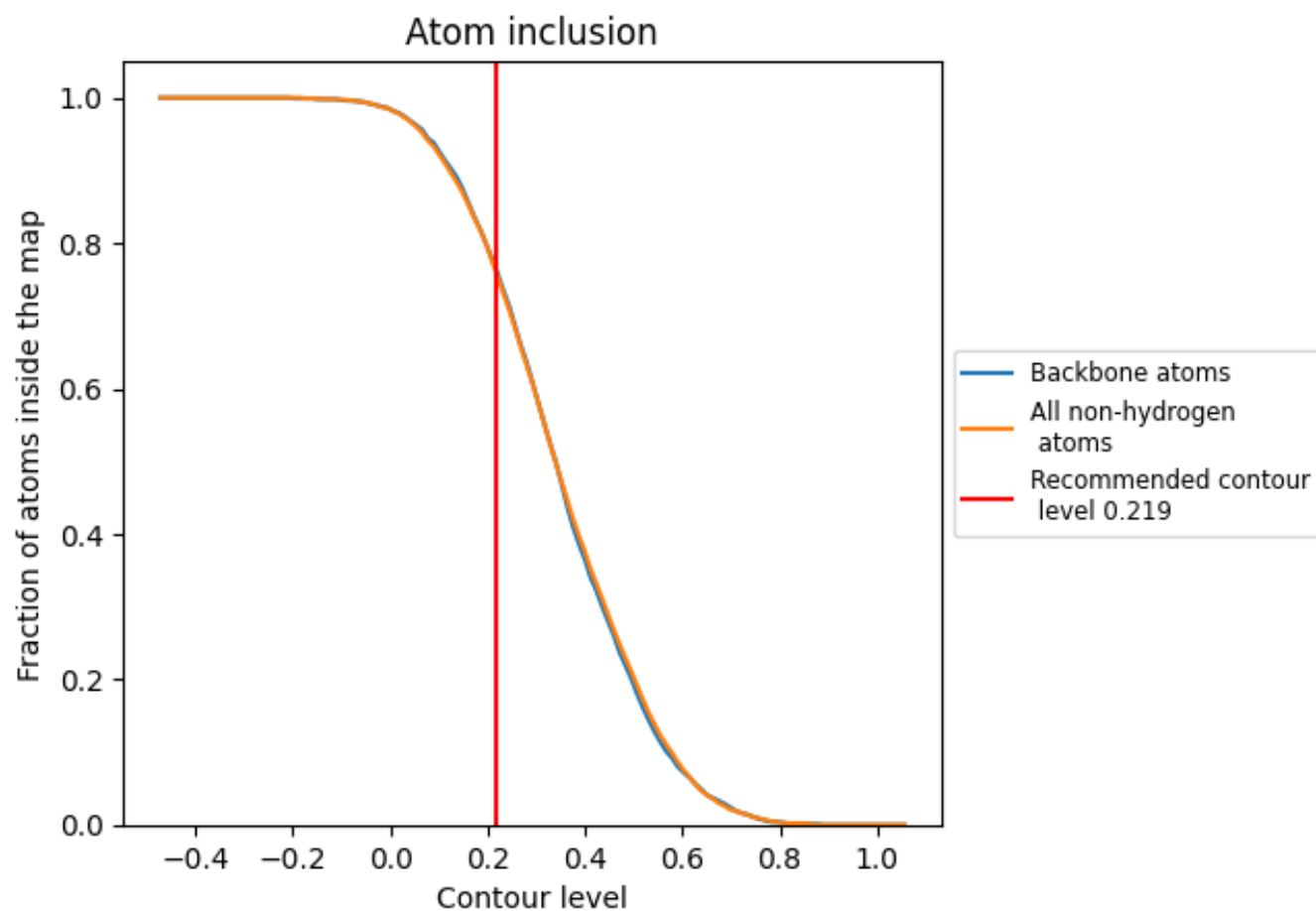
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.219).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 76% 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 (0.219) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7570	0.2420
A	0.8660	0.2710
B	0.8180	0.2560
D	0.7630	0.2440
E	0.7570	0.2380

