



Full wwPDB EM Validation Report ⓘ

Mar 24, 2026 – 12:56 PM UTC

PDB ID : 9E1X / pdb_00009e1x
EMDB ID : EMD-47424
Title : Snf2h bound nucleosome complex - ClassD1
Authors : Malik, D.; Deshmukh, A.A.; Bilokapic, S.; Halic, M.
Deposited on : 2024-10-21
Resolution : 3.40 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:

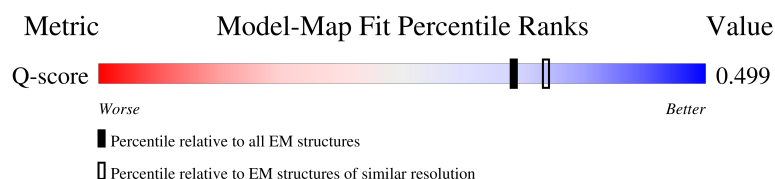
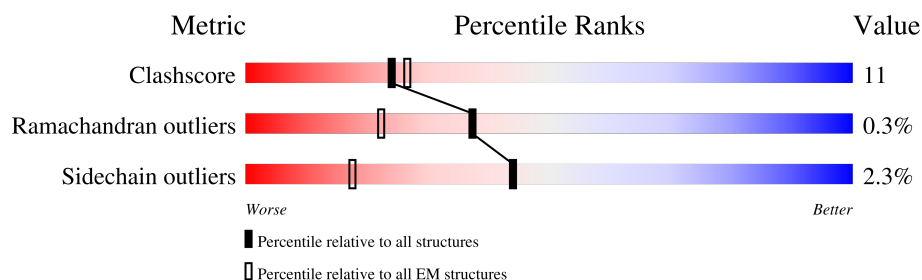
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	136	
1	E	136	
2	B	103	
2	F	103	

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Mol	Chain	Length	Quality of chain
3	C	130	76%8%16%
3	G	130	74%10%16%
4	D	126	62%13%•24%
4	H	126	66%9%•24%
5	I	151	42%56%•
6	J	152	49%49%••
7	W	1052	13%25%16%•58%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 15885 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 Histone H3.2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	97	Total	C	N	O	S	0	0
			799	505	153	138	3		
1	E	96	Total	C	N	O	S	0	0
			790	499	151	137	3		

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	85	Total	C	N	O	S	0	0
			679	428	135	115	1		
2	F	80	Total	C	N	O	S	0	0
			641	405	125	110	1		

- Molecule 3 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	109	Total	C	N	O	0	0
			837	526	165	146		
3	G	109	Total	C	N	O	0	0
			837	526	165	146		

- Molecule 4 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	96	Total	C	N	O	S	0	0
			746	469	134	141	2		
4	H	96	Total	C	N	O	S	0	0
			756	475	138	141	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	29	THR	SER	engineered mutation	UNP P02281

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Chain	Residue	Modelled	Actual	Comment	Reference
H	29	THR	SER	engineered mutation	UNP P02281

- Molecule 5 is a DNA chain called DNA (149-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	149	Total	C	N	O	P	0	0
			3072	1453	578	892	149		

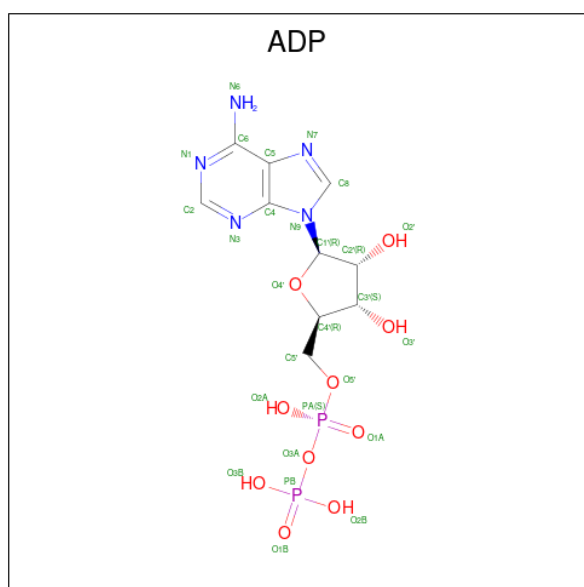
- Molecule 6 is a DNA chain called DNA (150-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	150	Total	C	N	O	P	0	0
			3056	1451	553	902	150		

- Molecule 7 is a protein called SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	W	443	Total	C	N	O	S	0	0
			3645	2334	639	649	23		

- Molecule 8 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).

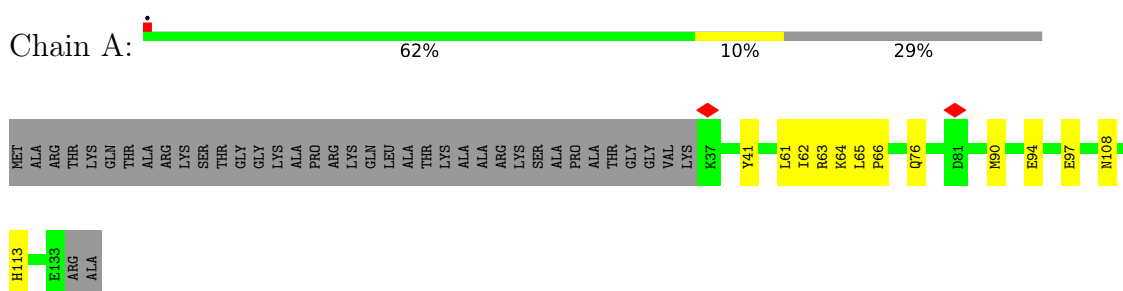


Mol	Chain	Residues	Atoms					AltConf
8	W	1	Total	C	N	O	P	0
			27	10	5	10	2	

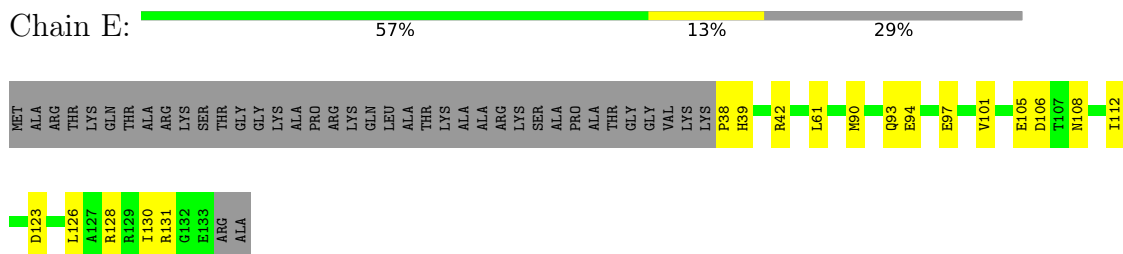
3 Residue-property plots [i](#)

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

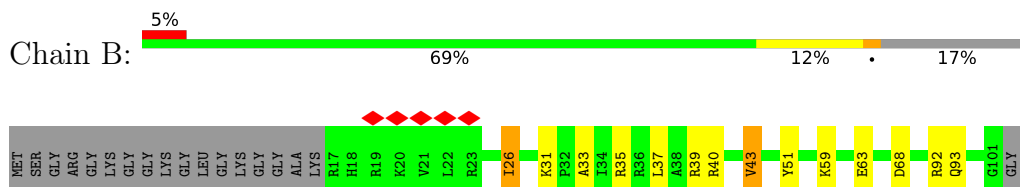
- Molecule 1: Histone H3.2



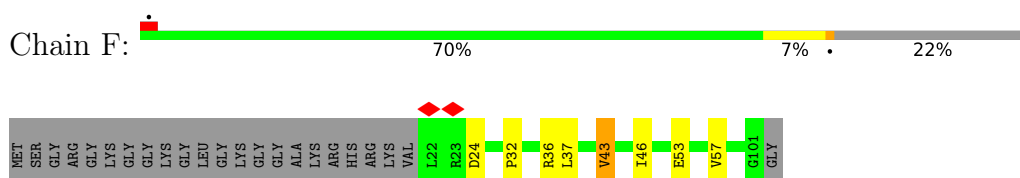
- Molecule 1: Histone H3.2



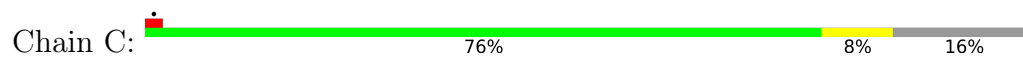
- Molecule 2: Histone H4



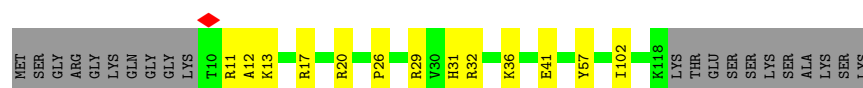
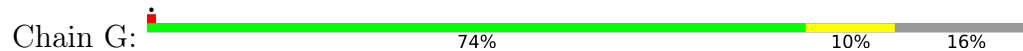
- Molecule 2: Histone H4



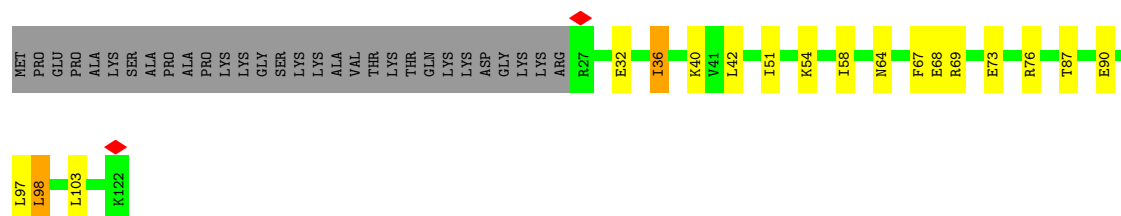
- Molecule 3: Histone H2A



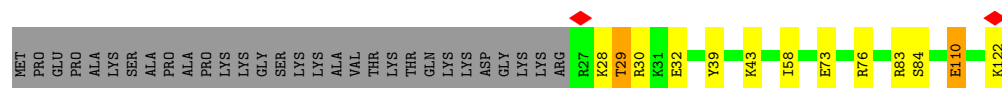
• Molecule 3: Histone H2A



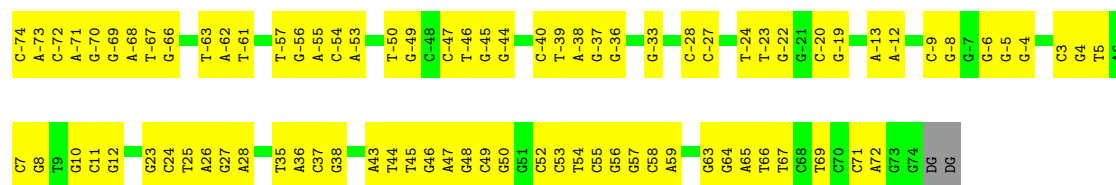
• Molecule 4: Histone H2B 1.1



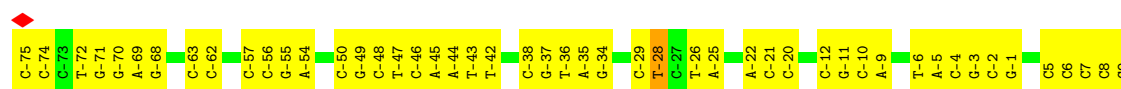
• Molecule 4: Histone H2B 1.1

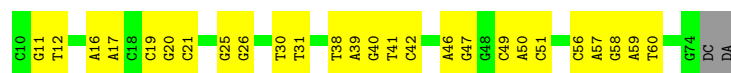


• Molecule 5: DNA (149-MER)

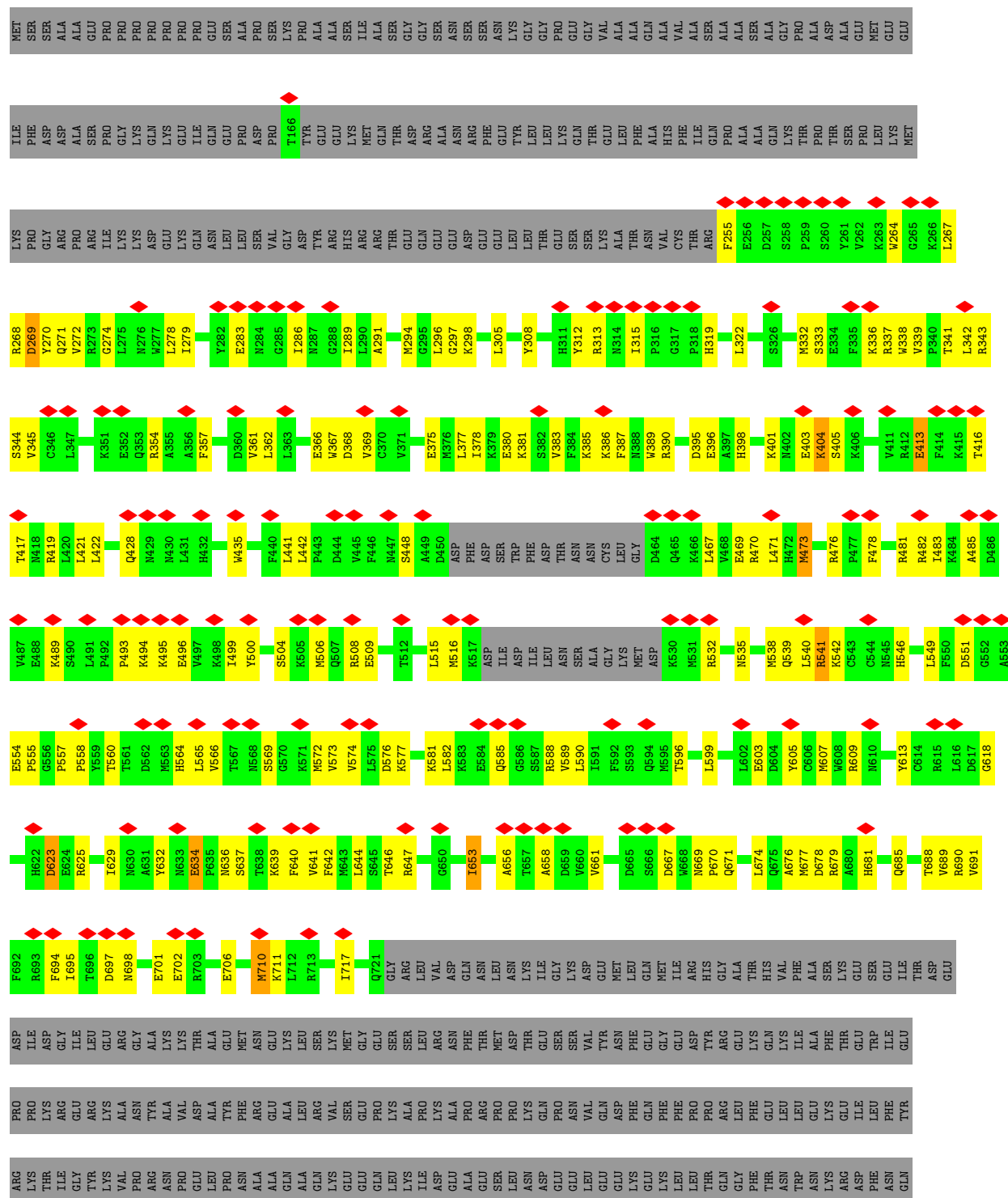


• Molecule 6: DNA (150-MER)





- Molecule 7: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family A member 5



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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	9200	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	27.073	Depositor
Minimum map value	-0.291	Depositor
Average map value	-0.019	Depositor
Map value standard deviation	0.258	Depositor
Recommended contour level	4	Depositor
Map size (Å)	497.0, 497.0, 497.0	wwPDB
Map dimensions	497, 497, 497	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.18	0/811	0.28	0/1088
1	E	0.17	0/802	0.27	0/1076
2	B	0.23	0/687	0.28	0/921
2	F	0.18	0/648	0.30	0/868
3	C	0.16	0/847	0.28	0/1144
3	G	0.16	0/847	0.28	0/1144
4	D	0.15	0/757	0.26	0/1018
4	H	0.17	0/767	0.29	0/1029
5	I	0.26	0/3450	0.42	0/5327
6	J	0.27	0/3423	0.40	2/5276 (0.0%)
7	W	0.16	0/3721	0.40	0/5024
All	All	0.21	0/16760	0.37	2/23915 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	-28	DT	C2'-C3'-O3'	-5.79	102.81	111.50
6	J	-69	DA	C2'-C3'-O3'	-5.11	103.84	111.50

There are no chirality outliers.

There are no planarity outliers.

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	799	0	838	11	0
1	E	790	0	826	14	0
2	B	679	0	717	12	0
2	F	641	0	684	8	0
3	C	837	0	891	9	0
3	G	837	0	891	13	0
4	D	746	0	764	13	0
4	H	756	0	786	13	0
5	I	3072	0	1671	75	0
6	J	3056	0	1684	60	0
7	W	3645	0	3716	129	0
8	W	27	0	12	1	0
All	All	15885	0	13480	313	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 11.

All (313) 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)
7:W:623:ASP:OD1	7:W:623:ASP:N	2.15	0.80
7:W:435:TRP:NE1	7:W:448:SER:O	2.20	0.75
7:W:289:ILE:HG13	7:W:441:LEU:HD11	1.71	0.72
7:W:398:HIS:HA	7:W:401:LYS:HB3	1.74	0.70
2:F:36:ARG:NH2	5:I:-13:DA:OP1	2.25	0.70
7:W:688:THR:O	7:W:690:ARG:NH1	2.25	0.69
6:J:-22:DA:H2''	6:J:-21:DC:H5''	1.75	0.68
7:W:332:MET:SD	7:W:336:LYS:NZ	2.64	0.68
7:W:361:VAL:HG12	7:W:367:TRP:HD1	1.58	0.67
1:E:61:LEU:O	2:F:36:ARG:NH1	2.28	0.67
5:I:23:DG:H5''	7:W:647:ARG:HH22	1.60	0.67
7:W:560:THR:O	7:W:564:HIS:NE2	2.22	0.66
7:W:678:ASP:HA	7:W:681:HIS:HB3	1.76	0.66
7:W:588:ARG:HB3	7:W:658:ALA:HA	1.77	0.65
7:W:385:LYS:NZ	7:W:413:GLU:OE2	2.29	0.65
7:W:362:LEU:HA	7:W:367:TRP:HE1	1.62	0.64
7:W:647:ARG:HH21	7:W:667:ASP:HB2	1.62	0.64
5:I:-55:DA:H2''	5:I:-54:DC:C5	2.33	0.64
7:W:632:TYR:HA	7:W:639:LYS:HD2	1.78	0.63
5:I:65:DA:H1'	5:I:66:DT:OP2	1.97	0.63
7:W:315:ILE:O	7:W:390:ARG:NH1	2.30	0.63
5:I:-47:DC:H2''	5:I:-46:DT:C5	2.33	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:308:TYR:OH	7:W:313:ARG:NH1	2.32	0.62
7:W:566:VAL:HA	7:W:572:MET:HG3	1.80	0.62
1:E:108:ASN:HB2	2:F:43:VAL:HG12	1.80	0.62
3:G:13:LYS:NZ	6:J:46:DA:OP1	2.33	0.62
5:I:23:DG:P	7:W:669:ASN:ND2	2.73	0.61
1:E:42:ARG:NH1	5:I:72:DA:OP1	2.34	0.61
6:J:30:DT:H2'	6:J:31:DT:H71	1.82	0.61
5:I:47:DA:H2''	5:I:48:DG:C8	2.36	0.61
7:W:291:ALA:HB3	7:W:481:ARG:HB2	1.84	0.60
7:W:428:GLN:HE22	7:W:671:GLN:HB2	1.67	0.59
3:G:102:ILE:HG23	4:H:58:ILE:HD13	1.83	0.59
6:J:-4:DC:H2''	6:J:-3:DG:C8	2.37	0.59
7:W:538:MET:O	7:W:538:MET:HG3	2.02	0.59
5:I:11:DC:H2'	5:I:12:DG:C8	2.38	0.59
7:W:343:ARG:NH1	7:W:366:GLU:O	2.33	0.59
7:W:538:MET:HE1	7:W:541:ARG:HH11	1.66	0.59
5:I:-6:DG:H2''	5:I:-5:DG:C8	2.38	0.59
7:W:354:ARG:NH1	7:W:380:GLU:OE2	2.36	0.59
5:I:66:DT:H2''	5:I:67:DT:OP1	2.03	0.58
1:E:61:LEU:HD12	2:F:37:LEU:HD23	1.86	0.58
5:I:58:DC:H2''	5:I:59:DA:C8	2.39	0.58
7:W:588:ARG:HH22	7:W:637:SER:HB2	1.69	0.58
5:I:-57:DT:H2''	5:I:-56:DG:C8	2.39	0.57
5:I:-63:DT:H2''	5:I:-62:DA:H8	1.70	0.57
5:I:-24:DT:H2'	5:I:-23:DT:H71	1.87	0.57
5:I:53:DC:H2'	5:I:54:DT:C6	2.39	0.57
5:I:35:DT:H2''	5:I:36:DA:C8	2.40	0.56
3:G:17:ARG:HH12	3:G:31:HIS:HD2	1.52	0.56
1:A:61:LEU:HD12	2:B:37:LEU:HD23	1.87	0.56
3:C:32:ARG:NH2	4:D:32:GLU:OE2	2.32	0.56
3:G:11:ARG:HG2	3:G:12:ALA:H	1.69	0.56
6:J:25:DG:H2''	6:J:26:DG:C8	2.40	0.56
7:W:542:LYS:HB2	7:W:549:LEU:HD12	1.87	0.56
2:B:68:ASP:OD2	2:B:93:GLN:NE2	2.38	0.56
7:W:656:ALA:O	7:W:685:GLN:NE2	2.39	0.56
5:I:26:DA:H2''	5:I:27:DG:C8	2.41	0.56
5:I:-37:DG:H2''	5:I:-36:DG:C8	2.41	0.56
5:I:23:DG:P	7:W:669:ASN:HD21	2.28	0.56
7:W:268:ARG:HB2	7:W:270:TYR:CE2	2.40	0.55
6:J:-57:DC:H2''	6:J:-56:DC:C5	2.40	0.55
7:W:396:GLU:N	7:W:422:LEU:O	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:49:DC:H2''	5:I:50:DG:C8	2.41	0.55
6:J:56:DC:H2''	6:J:57:DA:C8	2.42	0.55
7:W:286:ILE:HG23	7:W:442:LEU:HD11	1.89	0.55
5:I:-54:DC:H2''	5:I:-53:DA:C8	2.42	0.55
3:G:26:PRO:HB2	3:G:29:ARG:HB3	1.88	0.55
6:J:6:DC:H2''	6:J:7:DC:C6	2.42	0.54
7:W:267:LEU:HD13	7:W:271:GLN:HB2	1.89	0.54
7:W:569:SER:HB3	7:W:572:MET:HB3	1.89	0.54
5:I:23:DG:OP2	7:W:669:ASN:ND2	2.32	0.54
1:A:61:LEU:HD11	2:B:40:ARG:HE	1.71	0.54
5:I:3:DC:H2''	5:I:4:DG:C8	2.42	0.54
5:I:-72:DC:H2''	5:I:-71:DA:C8	2.43	0.54
7:W:670:PRO:HG3	7:W:711:LYS:HB2	1.89	0.54
7:W:554:GLU:HG2	7:W:555:PRO:HD2	1.90	0.53
3:C:78:ILE:HB	4:D:51:ILE:HG13	1.89	0.53
6:J:-56:DC:H2''	6:J:-55:DG:C8	2.44	0.53
7:W:361:VAL:HG12	7:W:367:TRP:CD1	2.42	0.53
3:C:13:LYS:NZ	5:I:47:DA:O5'	2.41	0.53
3:C:14:ALA:HB1	6:J:-44:DA:H4'	1.89	0.53
3:G:32:ARG:NH2	4:H:32:GLU:OE2	2.29	0.53
5:I:65:DA:H2''	5:I:66:DT:OP1	2.06	0.53
5:I:-63:DT:H2''	5:I:-62:DA:C8	2.43	0.53
7:W:395:ASP:HA	7:W:422:LEU:HB2	1.91	0.53
4:D:69:ARG:HB3	4:D:98:LEU:HD21	1.90	0.53
6:J:16:DA:H2''	6:J:17:DA:C8	2.43	0.53
6:J:-6:DT:H2''	6:J:-5:DA:C8	2.44	0.53
6:J:-29:DC:H1'	6:J:-28:DT:H5'	1.91	0.53
7:W:403:GLU:O	7:W:404:LYS:NZ	2.30	0.53
5:I:55:DC:H2''	5:I:56:DG:C8	2.44	0.52
7:W:298:LYS:HB3	7:W:422:LEU:HD23	1.91	0.52
6:J:-36:DT:H2''	6:J:-35:DA:C8	2.45	0.52
3:G:41:GLU:HG2	4:H:84:SER:HB2	1.92	0.52
6:J:38:DT:H2''	6:J:39:DA:C8	2.44	0.52
6:J:-43:DT:H2''	6:J:-42:DT:H5''	1.91	0.52
1:A:64:LYS:HG2	1:A:90:MET:HE1	1.92	0.52
3:C:30:VAL:HG13	4:D:67:PHE:HE2	1.74	0.52
4:D:87:THR:OG1	4:D:90:GLU:OE1	2.25	0.52
6:J:-26:DT:H2''	6:J:-25:DA:C8	2.45	0.52
5:I:-69:DG:H2''	5:I:-68:DA:C8	2.45	0.52
5:I:48:DG:H2''	5:I:49:DC:H5''	1.92	0.52
7:W:319:HIS:HD1	7:W:369:VAL:HG22	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:582:LEU:HD13	7:W:589:VAL:HG21	1.92	0.52
7:W:483:ILE:HG22	7:W:485:ALA:H	1.75	0.51
7:W:646:THR:HG23	7:W:676:ALA:HB2	1.91	0.51
7:W:717:ILE:O	7:W:717:ILE:HG22	2.11	0.51
4:D:73:GLU:OE1	4:D:76:ARG:NH2	2.38	0.51
6:J:8:DC:H2''	6:J:9:DG:C8	2.45	0.51
3:G:20:ARG:HH11	4:H:122:LYS:HB3	1.76	0.51
7:W:390:ARG:O	7:W:417:THR:OG1	2.22	0.51
7:W:640:PHE:HD2	7:W:641:VAL:HG23	1.76	0.51
3:G:17:ARG:HH12	3:G:31:HIS:CD2	2.29	0.50
4:H:83:ARG:HH22	5:I:-33:DG:P	2.33	0.50
5:I:23:DG:H2''	5:I:24:DC:C6	2.46	0.50
6:J:-26:DT:H2''	6:J:-25:DA:H8	1.76	0.50
5:I:-28:DC:H2''	5:I:-27:DC:C6	2.46	0.50
7:W:319:HIS:ND1	7:W:368:ASP:O	2.45	0.50
7:W:476:ARG:NE	7:W:476:ARG:O	2.45	0.50
5:I:23:DG:OP1	7:W:669:ASN:ND2	2.45	0.50
7:W:701:GLU:N	7:W:701:GLU:OE1	2.45	0.50
4:H:39:TYR:OH	5:I:-53:DA:O5'	2.30	0.50
7:W:473:MET:SD	7:W:473:MET:N	2.85	0.49
4:H:28:LYS:NZ	6:J:50:DA:H3'	2.27	0.49
6:J:-12:DC:H2''	6:J:-11:DG:H8	1.77	0.49
7:W:336:LYS:NZ	7:W:344:SER:OG	2.34	0.49
7:W:538:MET:SD	7:W:541:ARG:HD3	2.51	0.49
2:B:35:ARG:O	2:B:39:ARG:HG2	2.13	0.49
7:W:499:ILE:HG21	7:W:574:VAL:HG11	1.94	0.49
6:J:-47:DT:H2''	6:J:-46:DC:C5	2.48	0.49
7:W:269:ASP:HA	7:W:272:VAL:HG22	1.95	0.49
7:W:535:ASN:O	7:W:539:GLN:HG2	2.13	0.49
5:I:36:DA:H2''	5:I:37:DC:C5	2.47	0.49
3:G:57:TYR:HB2	4:H:110:GLU:CD	2.38	0.48
4:H:29:THR:OG1	4:H:30:ARG:N	2.44	0.48
5:I:-40:DC:H2'	5:I:-39:DT:H71	1.95	0.48
2:B:92:ARG:NH1	4:D:97:LEU:HB3	2.28	0.48
5:I:-62:DA:H2'	5:I:-61:DT:C6	2.49	0.48
7:W:576:ASP:OD1	7:W:609:ARG:NH1	2.46	0.48
7:W:576:ASP:OD1	7:W:605:TYR:OH	2.27	0.48
3:C:104:GLN:OE1	4:D:54:LYS:NZ	2.47	0.48
5:I:27:DG:H2''	5:I:28:DA:C8	2.48	0.48
6:J:-46:DC:H2''	6:J:-45:DA:C8	2.49	0.48
6:J:5:DC:H2''	6:J:6:DC:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:605:TYR:OH	7:W:609:ARG:NH1	2.46	0.48
5:I:-9:DC:H2''	5:I:-8:DG:C8	2.49	0.48
5:I:66:DT:H2'	5:I:67:DT:C6	2.49	0.48
6:J:-63:DC:H2''	6:J:-62:DC:H5''	1.95	0.48
7:W:697:ASP:OD2	7:W:698:ASN:ND2	2.45	0.48
6:J:-38:DC:H2''	6:J:-37:DG:C8	2.49	0.47
6:J:-10:DC:H2''	6:J:-9:DA:C8	2.48	0.47
3:C:102:ILE:HG23	4:D:58:ILE:HD13	1.96	0.47
5:I:52:DC:H2'	5:I:53:DC:C6	2.49	0.47
5:I:36:DA:H2''	5:I:37:DC:C6	2.49	0.47
6:J:56:DC:H2''	6:J:57:DA:N7	2.28	0.47
7:W:557:PRO:N	7:W:558:PRO:HD2	2.29	0.47
7:W:566:VAL:HG22	7:W:572:MET:HE3	1.96	0.47
7:W:590:LEU:HD23	7:W:642:PHE:HB3	1.96	0.47
5:I:-13:DA:H2''	5:I:-12:DA:C8	2.49	0.47
5:I:-5:DG:H2''	5:I:-4:DG:C8	2.50	0.47
7:W:573:VAL:O	7:W:577:LYS:HG2	2.13	0.47
7:W:322:LEU:HD21	7:W:377:LEU:HD22	1.95	0.47
7:W:674:LEU:HA	7:W:677:MET:HG3	1.97	0.47
1:E:39:HIS:HD2	6:J:-68:DG:H5''	1.80	0.47
5:I:56:DG:H2''	5:I:57:DG:N7	2.30	0.47
7:W:383:VAL:O	7:W:386:LYS:NZ	2.48	0.47
7:W:634:GLU:OE1	7:W:636:ASN:N	2.45	0.47
5:I:27:DG:C8	5:I:27:DG:H5'	2.50	0.47
6:J:49:DC:H2''	6:J:50:DA:C8	2.49	0.47
5:I:-45:DG:H1'	5:I:-44:DG:C8	2.50	0.47
6:J:59:DA:H2'	6:J:60:DT:H71	1.95	0.47
7:W:489:LYS:HE2	7:W:489:LYS:HB2	1.78	0.47
5:I:63:DG:H2''	5:I:64:DG:H8	1.79	0.46
6:J:-45:DA:H2''	6:J:-44:DA:H8	1.79	0.46
3:C:16:THR:O	3:C:19:SER:OG	2.30	0.46
7:W:506:MET:HE3	7:W:506:MET:HB3	1.67	0.46
6:J:11:DG:H1'	6:J:12:DT:H5'	1.98	0.46
4:D:64:ASN:O	4:D:68:GLU:HG2	2.15	0.46
1:A:41:TYR:HD1	5:I:10:DG:OP1	1.99	0.46
1:E:106:ASP:OD2	1:E:131:ARG:NH2	2.48	0.46
4:H:43:LYS:HA	4:H:43:LYS:HD3	1.77	0.46
2:B:31:LYS:HD3	2:B:51:TYR:CG	2.51	0.46
5:I:-67:DT:H2''	5:I:-66:DG:C8	2.51	0.46
5:I:-67:DT:H2''	5:I:-66:DG:H8	1.80	0.46
6:J:-44:DA:H2'	6:J:-43:DT:H71	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:493:PRO:O	7:W:688:THR:OG1	2.34	0.45
7:W:640:PHE:CD2	7:W:641:VAL:HG23	2.52	0.45
1:A:63:ARG:HB2	1:A:66:PRO:HD2	1.98	0.45
5:I:7:DC:H2''	5:I:8:DG:C8	2.51	0.45
7:W:389:TRP:HB2	7:W:416:THR:HG22	1.98	0.45
7:W:538:MET:HE1	7:W:541:ARG:NH1	2.32	0.45
6:J:-50:DC:H5'	6:J:-50:DC:C6	2.52	0.45
6:J:41:DT:H1'	6:J:42:DC:H5'	1.98	0.45
5:I:37:DC:H2''	5:I:38:DG:C8	2.51	0.45
7:W:339:VAL:HG12	7:W:342:LEU:H	1.82	0.45
5:I:26:DA:H2''	5:I:27:DG:H8	1.80	0.45
6:J:58:DG:H2''	6:J:59:DA:C8	2.52	0.45
1:E:101:VAL:O	1:E:105:GLU:HG3	2.16	0.44
7:W:268:ARG:HB2	7:W:270:TYR:HE2	1.81	0.44
7:W:279:ILE:O	7:W:283:GLU:HG2	2.17	0.44
7:W:644:LEU:HD21	7:W:679:ARG:HH11	1.81	0.44
2:F:53:GLU:O	2:F:57:VAL:HG23	2.18	0.44
6:J:-71:DG:H2''	6:J:-70:DG:C8	2.52	0.44
7:W:494:LYS:HD2	7:W:689:VAL:HG23	1.99	0.44
7:W:717:ILE:O	7:W:717:ILE:CG2	2.66	0.44
7:W:516:MET:HE2	7:W:516:MET:HB2	1.94	0.44
7:W:618:GLY:HA2	7:W:625:ARG:HH21	1.83	0.44
5:I:-70:DG:H2''	5:I:-69:DG:C8	2.53	0.44
5:I:-23:DT:H2''	5:I:-22:DG:H8	1.82	0.44
4:H:73:GLU:OE1	4:H:76:ARG:NH2	2.50	0.44
5:I:-74:DC:H2''	5:I:-73:DA:C8	2.53	0.44
6:J:46:DA:H2''	6:J:47:DG:N7	2.33	0.44
7:W:286:ILE:HD13	7:W:478:PHE:HE1	1.82	0.44
6:J:-48:DC:H2''	6:J:-47:DT:C5	2.53	0.44
7:W:588:ARG:NH1	7:W:639:LYS:O	2.51	0.44
1:A:108:ASN:HB2	2:B:43:VAL:HG12	2.00	0.44
5:I:69:DT:H5'	5:I:69:DT:C6	2.53	0.44
6:J:-45:DA:H2''	6:J:-44:DA:C8	2.53	0.44
7:W:504:SER:O	7:W:508:ARG:HG2	2.17	0.44
5:I:43:DA:H2'	5:I:44:DT:H71	1.99	0.44
7:W:274:GLY:N	7:W:482:ARG:HH22	2.16	0.44
7:W:607:MET:HE3	7:W:607:MET:HB3	1.88	0.44
1:E:38:PRO:HB2	1:E:39:HIS:H	1.64	0.43
7:W:264:TRP:O	7:W:264:TRP:CG	2.71	0.43
7:W:296:LEU:HD12	7:W:296:LEU:HA	1.71	0.43
1:A:61:LEU:HD21	2:B:40:ARG:HH21	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:28:LYS:NZ	6:J:51:DC:OP2	2.42	0.43
5:I:-54:DC:H2''	5:I:-53:DA:H8	1.82	0.43
5:I:-50:DT:H2''	5:I:-49:DG:C8	2.53	0.43
5:I:4:DG:H4'	5:I:5:DT:OP1	2.18	0.43
6:J:19:DC:H2''	6:J:20:DG:H8	1.83	0.43
7:W:581:LYS:O	7:W:585:GLN:HG3	2.18	0.43
7:W:596:THR:HA	7:W:599:LEU:HD12	2.00	0.43
7:W:661:VAL:O	7:W:691:VAL:HA	2.18	0.43
2:F:43:VAL:HG21	2:F:46:ILE:HD11	1.99	0.43
3:G:13:LYS:HD2	3:G:13:LYS:HA	1.79	0.43
6:J:-12:DC:H2''	6:J:-11:DG:C8	2.53	0.43
1:E:93:GLN:O	1:E:97:GLU:HG2	2.19	0.43
3:G:20:ARG:HD3	4:H:122:LYS:HB3	2.00	0.43
1:E:39:HIS:CD2	6:J:-68:DG:H5''	2.53	0.43
2:F:32:PRO:O	2:F:36:ARG:HG3	2.18	0.43
6:J:-21:DC:OP1	7:W:596:THR:N	2.52	0.43
7:W:495:LYS:HE3	7:W:690:ARG:HD2	2.00	0.43
6:J:-47:DT:H2''	6:J:-46:DC:C6	2.54	0.43
7:W:319:HIS:HB2	7:W:369:VAL:HA	1.99	0.43
7:W:636:ASN:N	7:W:636:ASN:OD1	2.51	0.43
5:I:-57:DT:H2''	5:I:-56:DG:N7	2.34	0.43
5:I:-38:DA:H2''	5:I:-37:DG:C8	2.53	0.43
6:J:-34:DG:C8	6:J:-34:DG:H5'	2.53	0.43
7:W:333:SER:O	7:W:337:ARG:HB2	2.19	0.43
7:W:499:ILE:O	7:W:695:ILE:N	2.45	0.43
1:A:90:MET:O	1:A:94:GLU:HG2	2.19	0.43
6:J:-75:DC:H2''	6:J:-74:DC:C5	2.53	0.42
6:J:-55:DG:H2''	6:J:-54:DA:H8	1.84	0.42
7:W:629:ILE:HD12	7:W:653:ILE:HG23	2.01	0.42
5:I:-72:DC:H2''	5:I:-71:DA:H8	1.84	0.42
5:I:23:DG:C5	5:I:24:DC:C4	3.06	0.42
2:B:59:LYS:O	2:B:63:GLU:HG3	2.19	0.42
5:I:52:DC:H2'	5:I:53:DC:H6	1.84	0.42
6:J:20:DG:H2''	6:J:21:DC:H5'	2.00	0.42
7:W:312:TYR:O	7:W:313:ARG:C	2.62	0.42
7:W:419:ARG:NH2	7:W:441:LEU:O	2.35	0.42
4:D:36:ILE:O	4:D:40:LYS:HG3	2.20	0.42
6:J:-5:DA:H2''	6:J:-4:DC:C6	2.54	0.42
6:J:-55:DG:H2''	6:J:-54:DA:C8	2.53	0.42
7:W:470:ARG:HG3	7:W:471:LEU:N	2.34	0.42
7:W:494:LYS:NZ	7:W:677:MET:O	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:ILE:HG22	2:B:33:ALA:HB1	2.00	0.42
7:W:289:ILE:HG12	7:W:421:LEU:HD12	2.01	0.42
7:W:540:LEU:O	7:W:541:ARG:C	2.61	0.42
7:W:618:GLY:HA2	7:W:625:ARG:NH2	2.34	0.42
7:W:603:GLU:HG3	7:W:613:TYR:CZ	2.55	0.42
3:G:36:LYS:HE2	3:G:36:LYS:HB3	1.95	0.42
6:J:58:DG:H2''	6:J:59:DA:H8	1.85	0.42
7:W:255:PHE:O	7:W:272:VAL:HB	2.20	0.42
7:W:551:ASP:OD1	7:W:551:ASP:N	2.46	0.42
5:I:46:DG:H2''	5:I:47:DA:N7	2.35	0.42
7:W:387:PHE:HB2	7:W:389:TRP:CH2	2.54	0.42
3:C:63:LEU:HD13	4:D:42:LEU:HB2	2.02	0.42
7:W:278:LEU:HD13	7:W:305:LEU:HD22	2.02	0.42
6:J:-72:DT:H2''	6:J:-71:DG:C8	2.55	0.41
6:J:-21:DC:C2	6:J:-20:DC:C5	3.07	0.41
7:W:345:VAL:HB	7:W:357:PHE:HZ	1.84	0.41
7:W:381:LYS:O	7:W:385:LYS:HG3	2.20	0.41
7:W:565:LEU:HD23	7:W:565:LEU:HA	1.92	0.41
7:W:375:GLU:O	7:W:378:ILE:HG22	2.20	0.41
7:W:603:GLU:HG3	7:W:613:TYR:CE1	2.55	0.41
1:E:126:LEU:O	1:E:130:ILE:HG12	2.20	0.41
1:E:128:ARG:NH1	2:F:57:VAL:HG22	2.35	0.41
7:W:499:ILE:HD12	7:W:694:PHE:CE1	2.56	0.41
2:B:92:ARG:HH12	4:D:97:LEU:HB3	1.86	0.41
1:E:90:MET:O	1:E:94:GLU:HG2	2.20	0.41
7:W:500:TYR:HE2	7:W:695:ILE:HD12	1.85	0.41
7:W:506:MET:O	7:W:509:GLU:HG3	2.20	0.41
6:J:-2:DC:H2''	6:J:-1:DG:H8	1.86	0.41
7:W:386:LYS:HE2	7:W:386:LYS:HB2	1.87	0.41
7:W:577:LYS:HA	7:W:577:LYS:HD3	1.79	0.41
7:W:710:MET:N	7:W:710:MET:SD	2.94	0.41
1:A:113:HIS:NE2	1:E:123:ASP:OD1	2.54	0.41
5:I:50:DG:C2	6:J:-49:DG:N2	2.89	0.41
1:A:76:GLN:HB2	7:W:532:ARG:HH21	1.86	0.40
5:I:-20:DC:H2''	5:I:-19:DG:C8	2.56	0.40
5:I:45:DT:H2''	5:I:46:DG:C8	2.56	0.40
6:J:46:DA:H2''	6:J:47:DG:C8	2.56	0.40
7:W:702:GLU:O	7:W:706:GLU:HG3	2.21	0.40
6:J:39:DA:H2''	6:J:40:DG:H8	1.86	0.40
5:I:24:DC:H2'	5:I:25:DT:O4'	2.21	0.40
7:W:467:LEU:O	7:W:469:GLU:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:634:GLU:HB3	7:W:637:SER:OG	2.21	0.40
2:B:26:ILE:HD13	2:B:26:ILE:HA	1.82	0.40
7:W:297:GLY:HA2	8:W:1201:ADP:PB	2.61	0.40
5:I:71:DC:H2"	5:I:72:DA:C8	2.57	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	95/136 (70%)	92 (97%)	3 (3%)	0	100	100
1	E	94/136 (69%)	89 (95%)	5 (5%)	0	100	100
2	B	83/103 (81%)	78 (94%)	5 (6%)	0	100	100
2	F	78/103 (76%)	75 (96%)	3 (4%)	0	100	100
3	C	107/130 (82%)	106 (99%)	1 (1%)	0	100	100
3	G	107/130 (82%)	102 (95%)	5 (5%)	0	100	100
4	D	94/126 (75%)	92 (98%)	2 (2%)	0	100	100
4	H	94/126 (75%)	92 (98%)	2 (2%)	0	100	100
7	W	436/1052 (41%)	407 (93%)	25 (6%)	4 (1%)	14	42
All	All	1188/2042 (58%)	1133 (95%)	51 (4%)	4 (0%)	37	65

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	W	294	MET
7	W	405	SER
7	W	541	ARG
7	W	653	ILE

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	85/111 (77%)	83 (98%)	2 (2%)	43	62
1	E	84/111 (76%)	83 (99%)	1 (1%)	63	72
2	B	69/79 (87%)	67 (97%)	2 (3%)	37	60
2	F	66/79 (84%)	64 (97%)	2 (3%)	36	59
3	C	85/102 (83%)	85 (100%)	0	100	100
3	G	85/102 (83%)	85 (100%)	0	100	100
4	D	80/106 (76%)	77 (96%)	3 (4%)	29	54
4	H	82/106 (77%)	80 (98%)	2 (2%)	43	62
7	W	408/939 (44%)	396 (97%)	12 (3%)	37	60
All	All	1044/1735 (60%)	1020 (98%)	24 (2%)	44	63

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	LEU
1	A	97	GLU
2	B	26	ILE
2	B	43	VAL
4	D	36	ILE
4	D	98	LEU
4	D	103	LEU
1	E	112	ILE
2	F	24	ASP
2	F	43	VAL
4	H	29	THR
4	H	110	GLU
7	W	269	ASP
7	W	338	TRP
7	W	341	THR
7	W	404	LYS
7	W	413	GLU
7	W	473	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	W	496	GLU
7	W	515	LEU
7	W	546	HIS
7	W	623	ASP
7	W	634	GLU
7	W	710	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
4	D	81	ASN
4	D	92	GLN
1	E	108	ASN
3	G	31	HIS
4	H	60	ASN
7	W	301	GLN
7	W	428	GLN
7	W	610	ASN
7	W	669	ASN

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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	ADP	W	1201	-	28,29,29	1.43	5 (17%)	43,45,45	1.83	9 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	ADP	W	1201	-	-	3/16/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	W	1201	ADP	C5-C4	4.69	1.47	1.39
8	W	1201	ADP	C5-C6	2.77	1.48	1.41
8	W	1201	ADP	C8-N7	2.39	1.36	1.31
8	W	1201	ADP	C5-N7	-2.29	1.34	1.39
8	W	1201	ADP	PA-O3A	2.05	1.61	1.59

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	W	1201	ADP	C5-C4-N3	-5.80	118.73	126.72
8	W	1201	ADP	N3-C4-N9	4.56	134.93	127.17
8	W	1201	ADP	C2-N3-C4	3.71	120.88	111.83
8	W	1201	ADP	C4-C5-N7	-3.46	106.63	110.58
8	W	1201	ADP	N3-C2-N1	-3.22	123.70	128.58
8	W	1201	ADP	C4-N9-C8	2.61	108.48	105.74
8	W	1201	ADP	C5-N7-C8	2.54	107.44	103.45
8	W	1201	ADP	C3'-C2'-C1'	2.40	106.01	101.46
8	W	1201	ADP	C6-C5-N7	2.13	136.19	132.09

There are no chirality outliers.

All (3) torsion outliers are listed below:

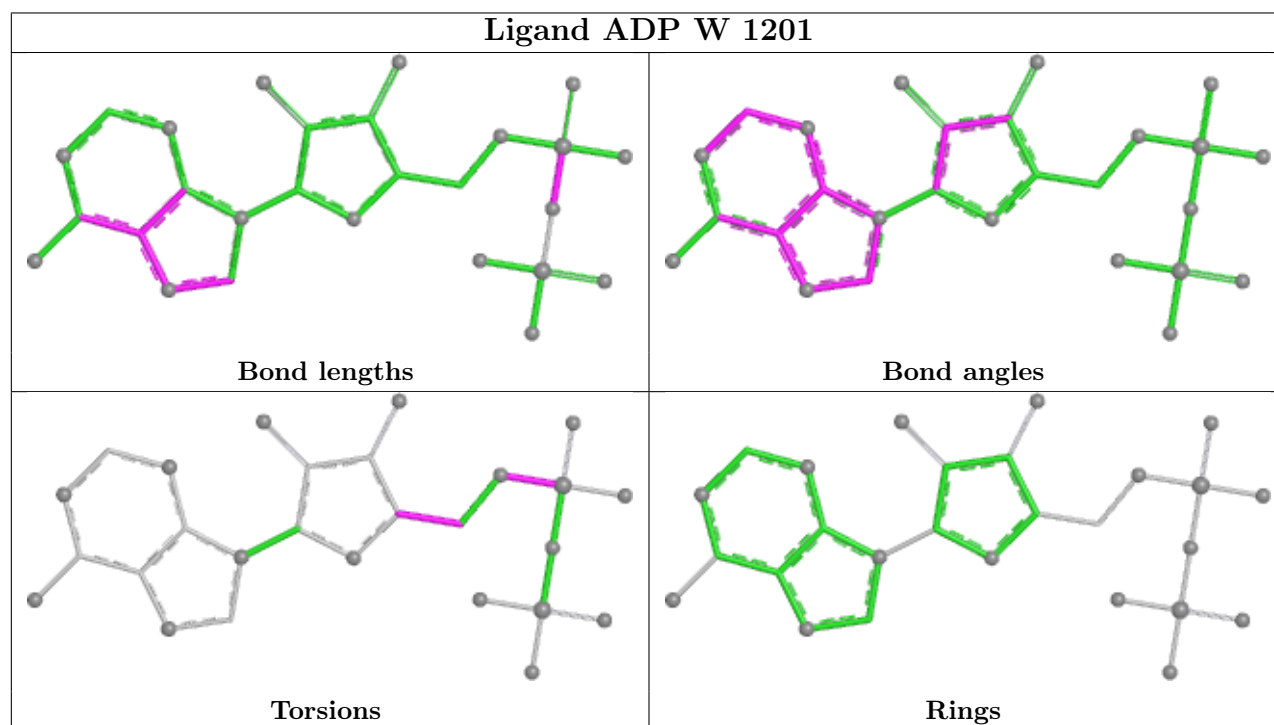
Mol	Chain	Res	Type	Atoms
8	W	1201	ADP	O4'-C4'-C5'-O5'
8	W	1201	ADP	C3'-C4'-C5'-O5'
8	W	1201	ADP	C5'-O5'-PA-O1A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	W	1201	ADP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

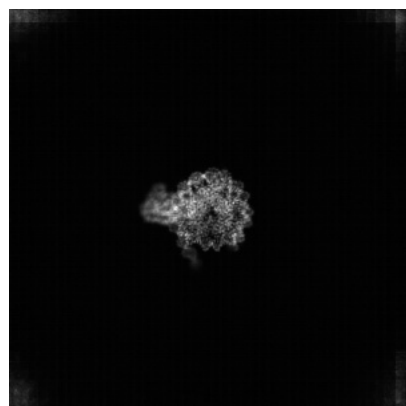
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47424. These allow visual inspection of the internal detail of the map and identification of artifacts.

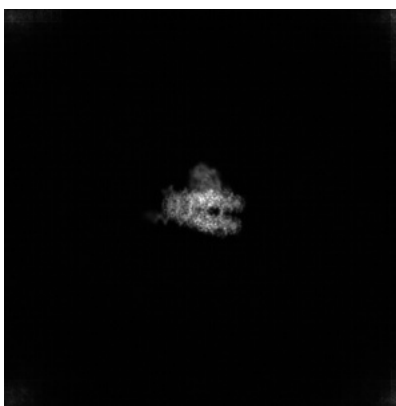
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

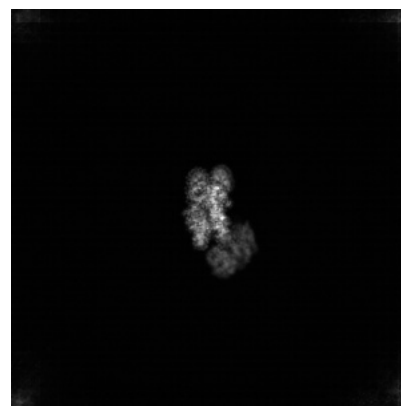
6.1.1 Primary map



X

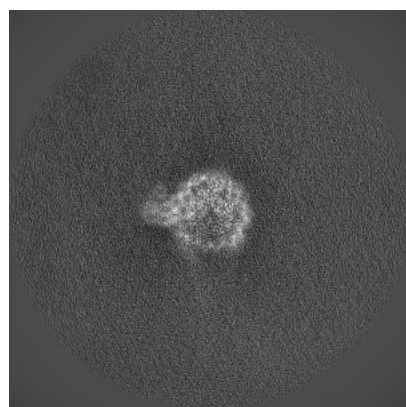


Y

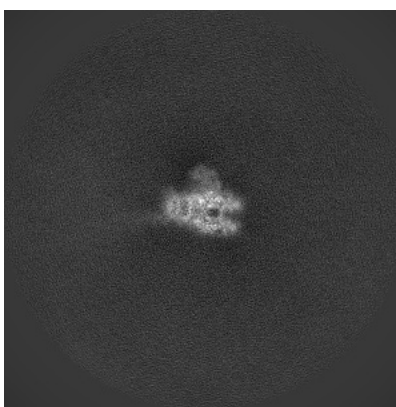


Z

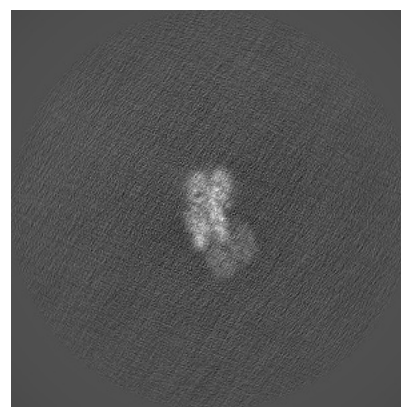
6.1.2 Raw map



X



Y

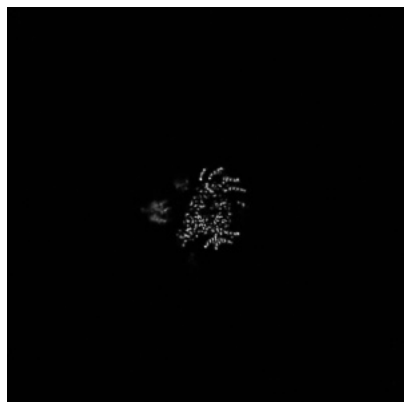


Z

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

6.2 Central slices [i](#)

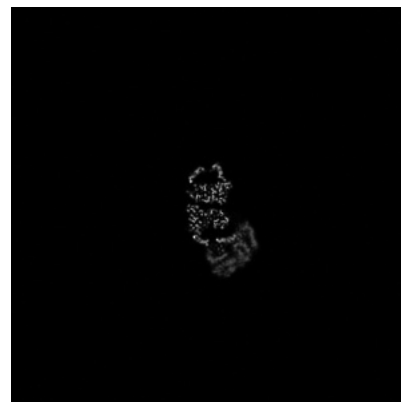
6.2.1 Primary map



X Index: 248

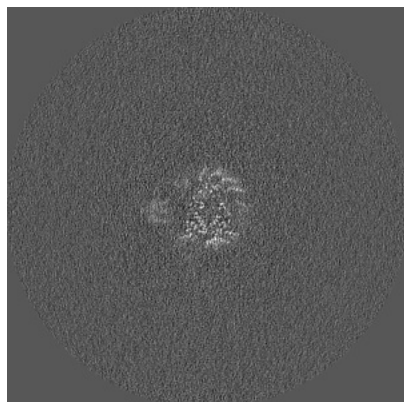


Y Index: 248

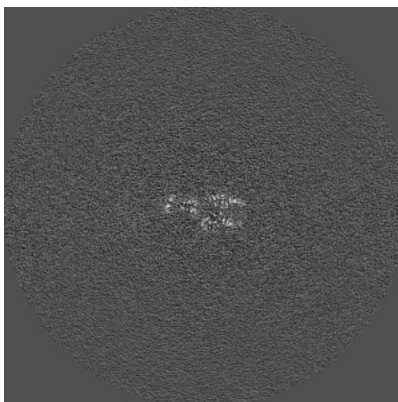


Z Index: 248

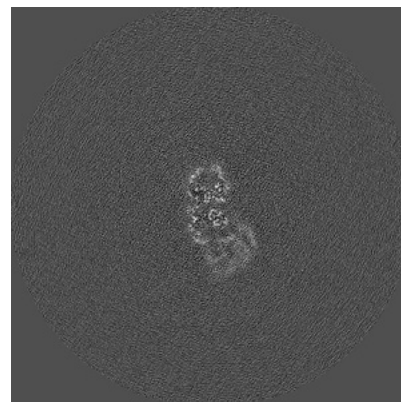
6.2.2 Raw map



X Index: 192



Y Index: 192

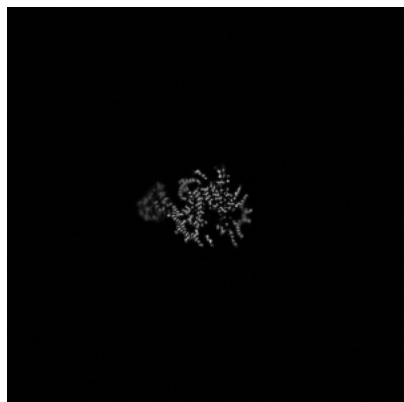


Z Index: 192

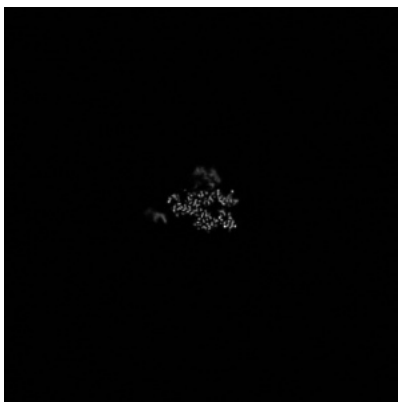
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

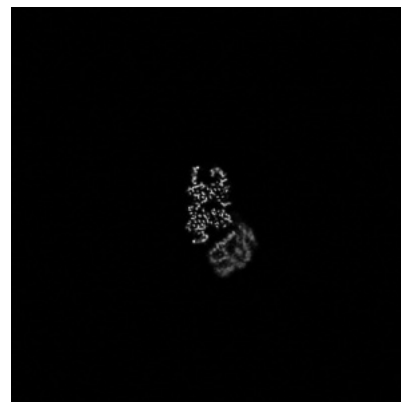
6.3.1 Primary map



X Index: 262

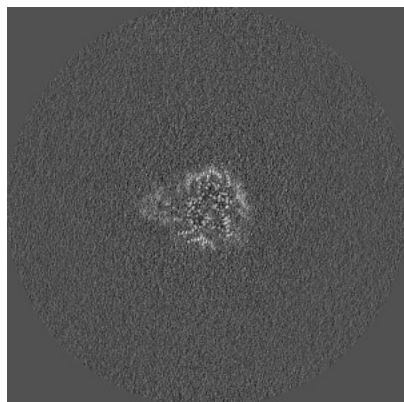


Y Index: 225

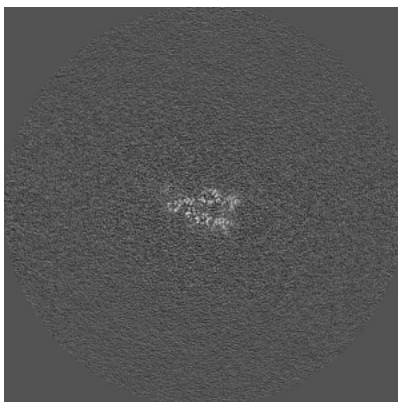


Z Index: 252

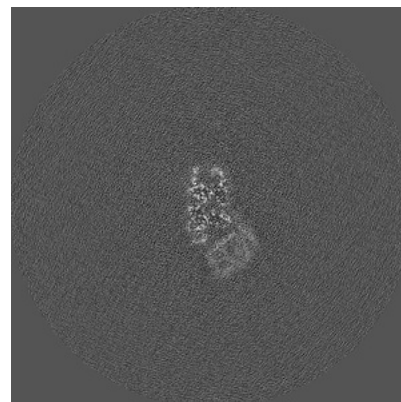
6.3.2 Raw map



X Index: 197



Y Index: 211

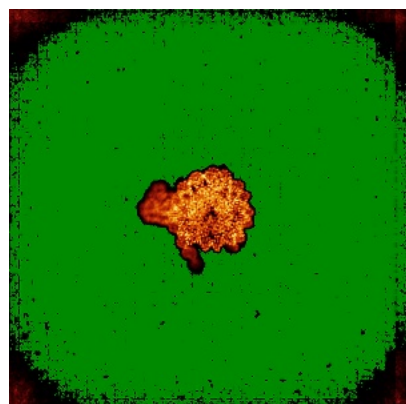


Z Index: 194

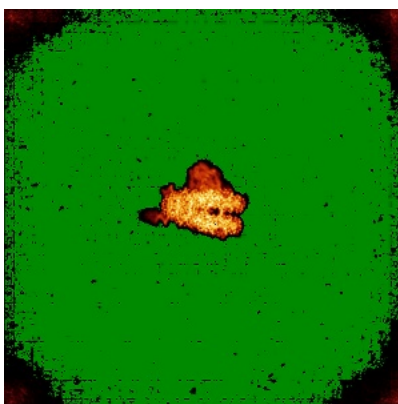
The images above show the largest variance slices of the map in three orthogonal directions.

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

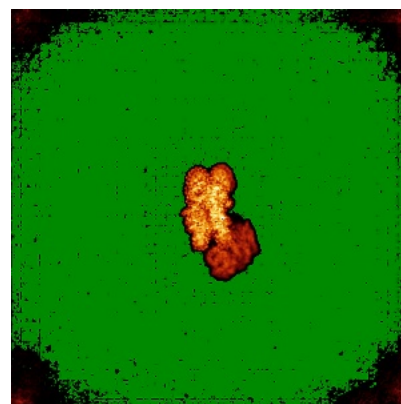
6.4.1 Primary map



X

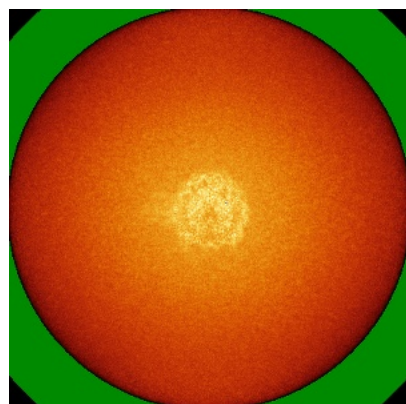


Y

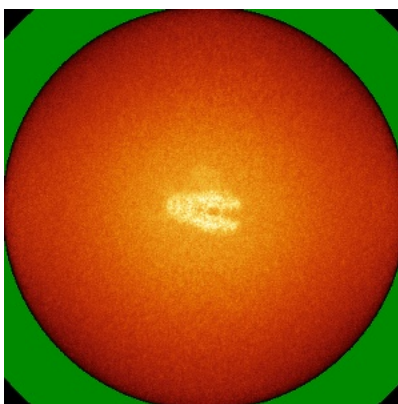


Z

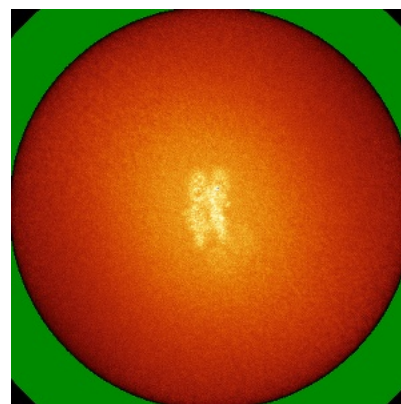
6.4.2 Raw map



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.

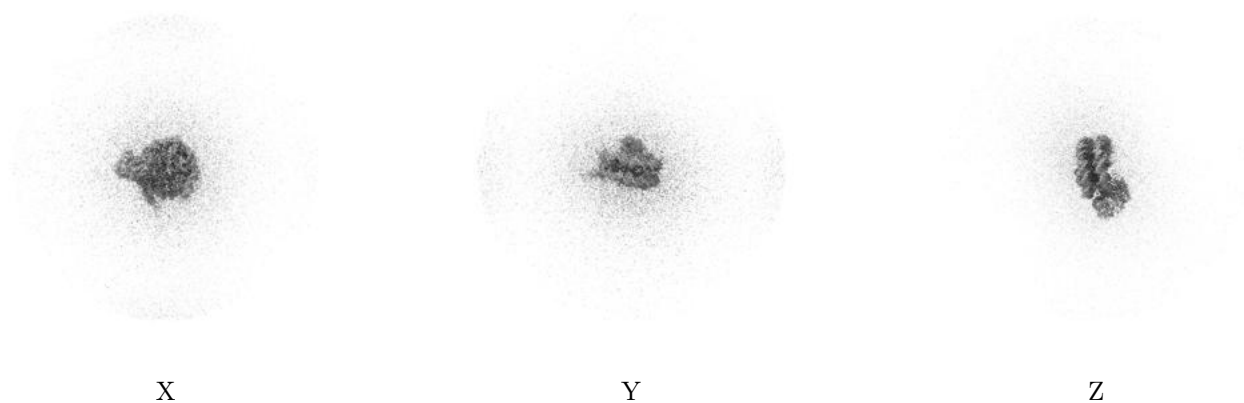
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.0. 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.

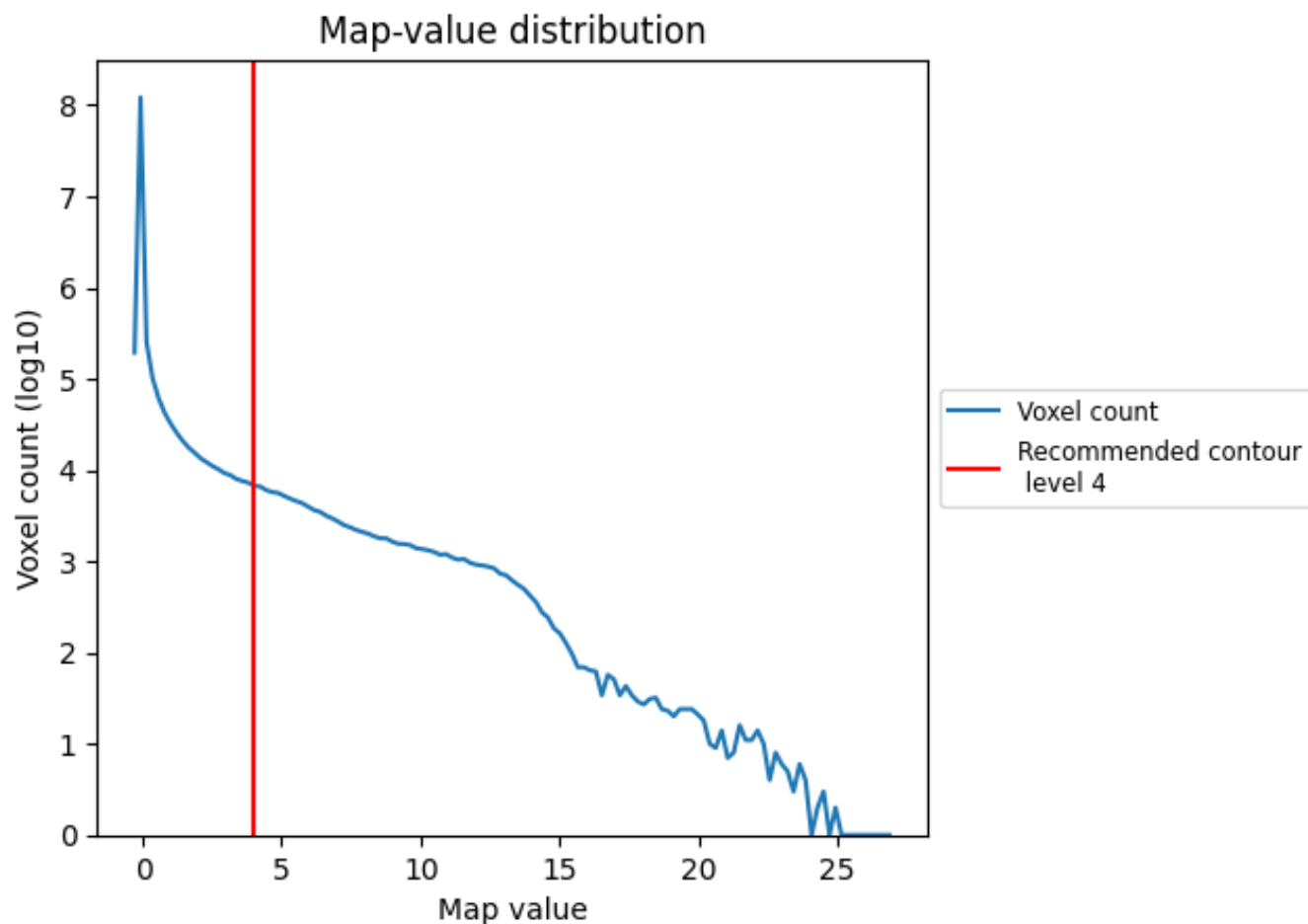
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

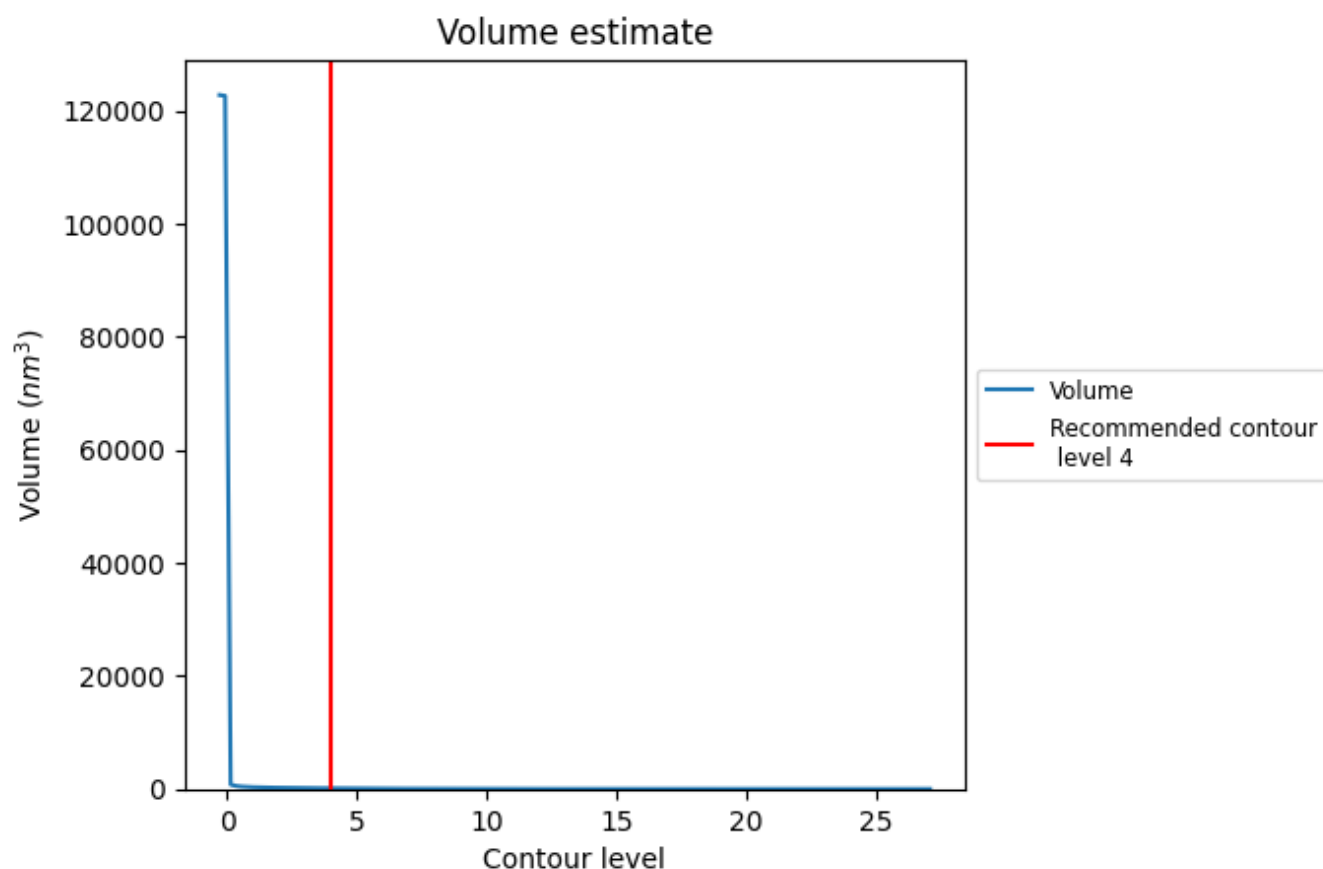
This section contains the results of statistical analysis of the map.

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.

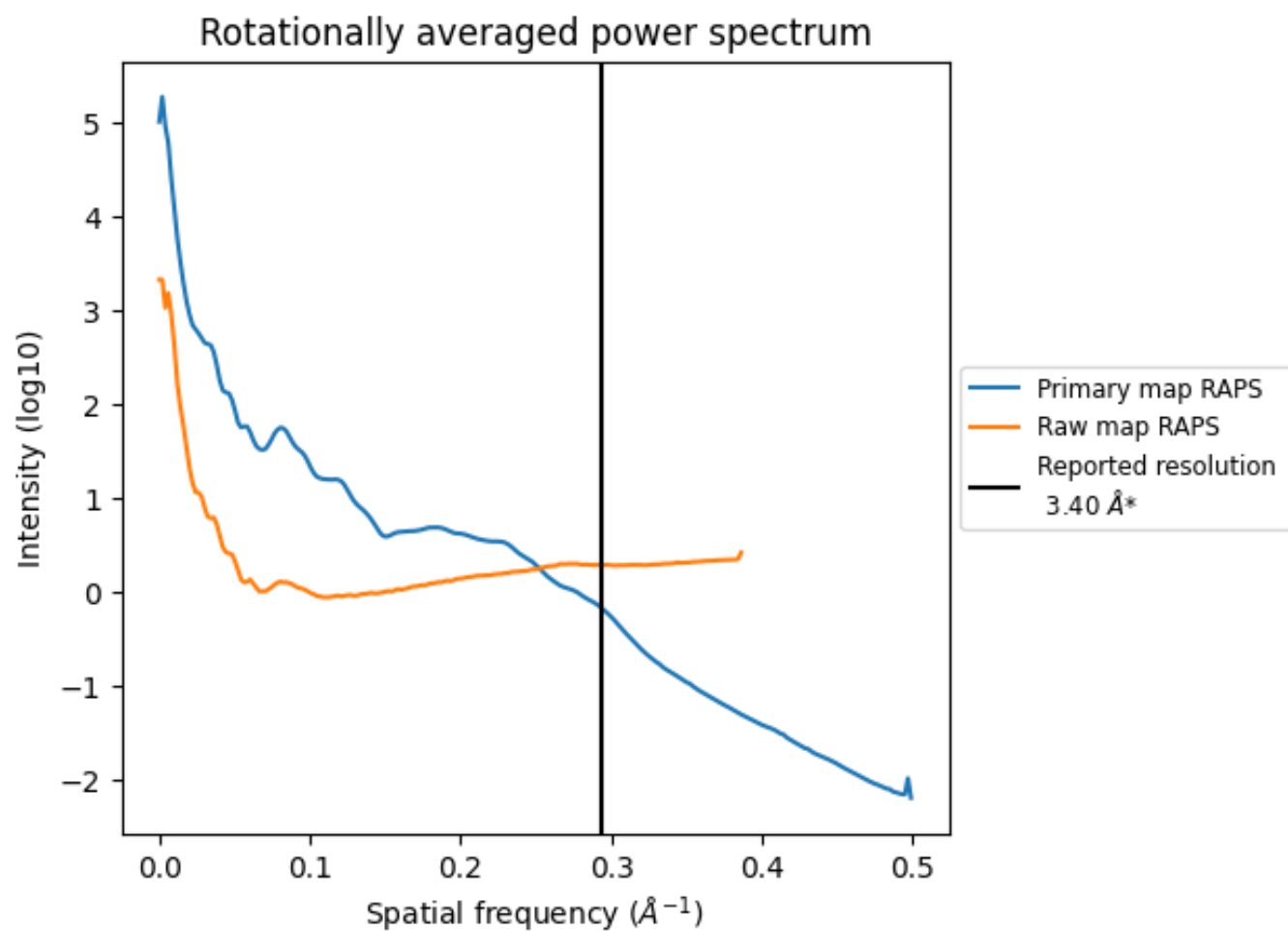
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 114 nm^3 ; this corresponds to an approximate mass of 103 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 ⓘ

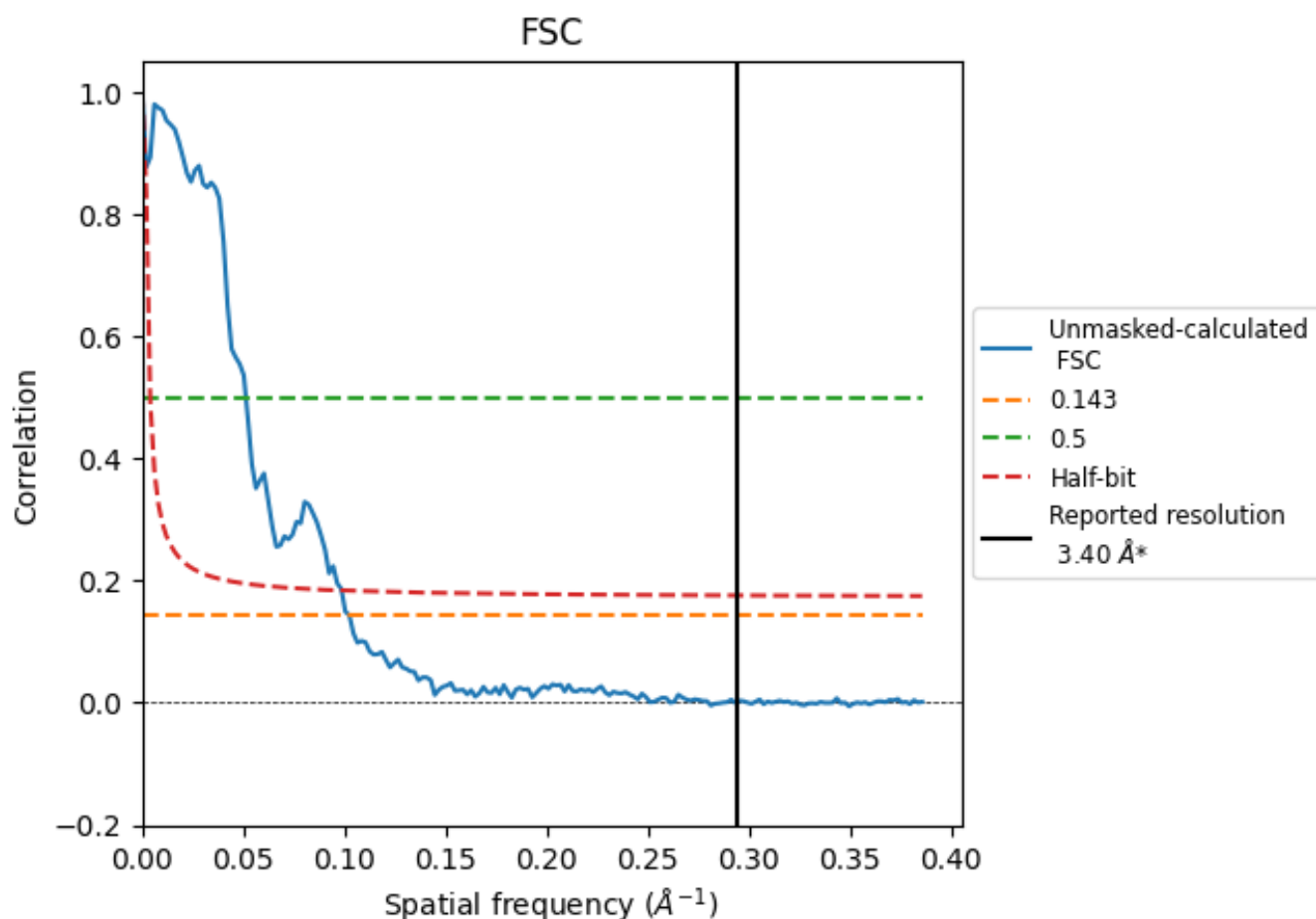


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

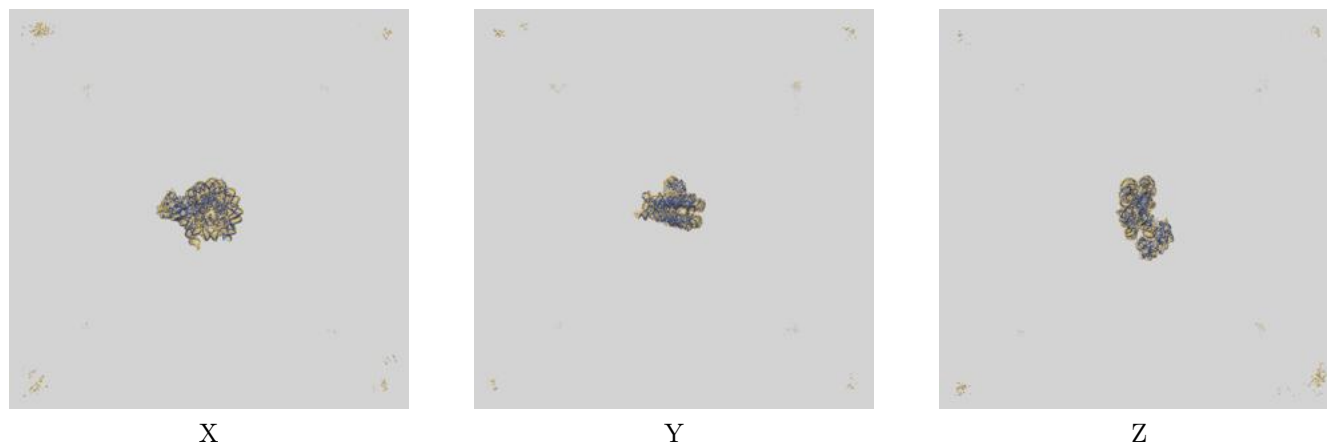
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	9.77	19.53	10.15

*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 9.77 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

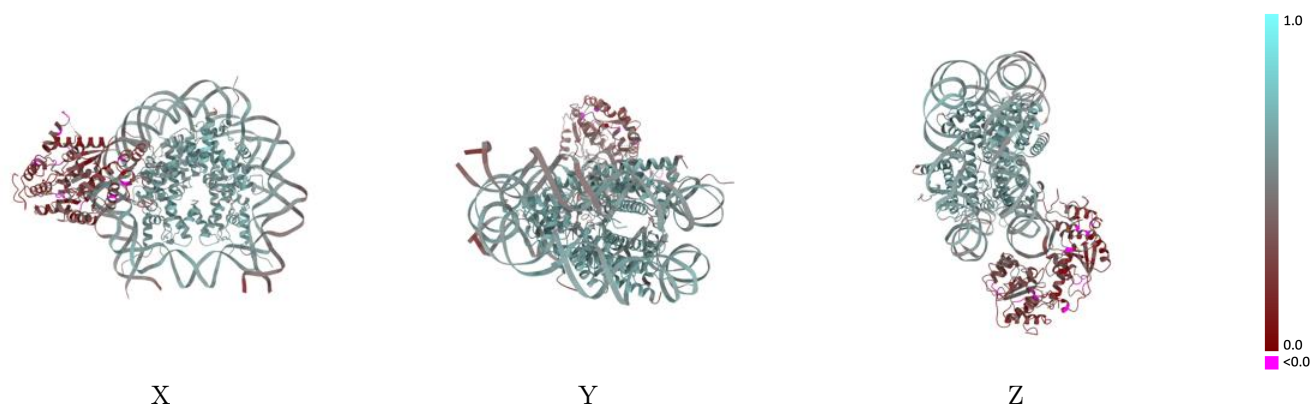
This section contains information regarding the fit between EMDB map EMD-47424 and PDB model 9E1X. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



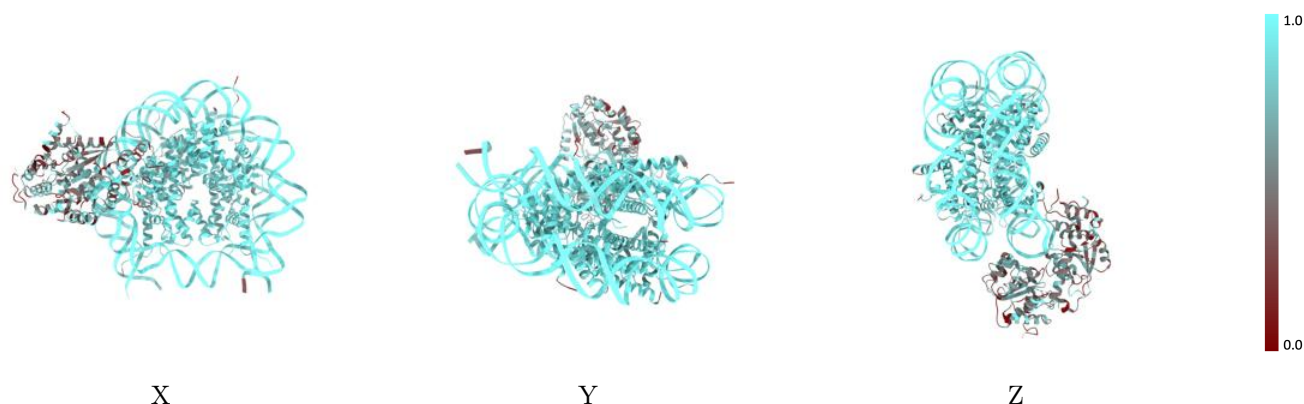
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



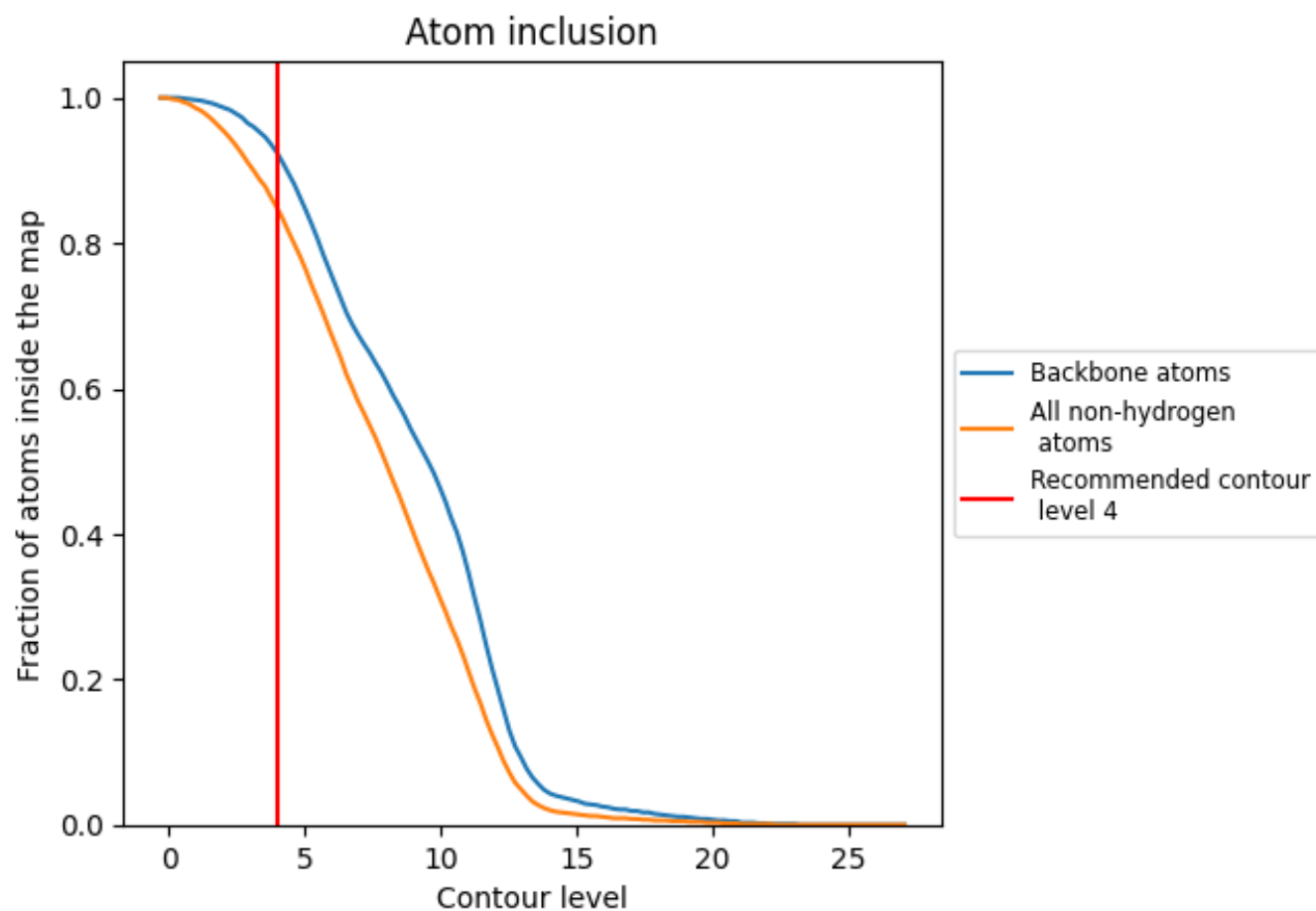
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 85% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8480	0.4990
A	0.9250	0.6120
B	0.8990	0.5900
C	0.9200	0.6110
D	0.9330	0.6190
E	0.9490	0.6200
F	0.9400	0.6260
G	0.9270	0.6170
H	0.9230	0.6030
I	0.9580	0.5370
J	0.9550	0.5340
W	0.5340	0.2510

1.0

0.0

<0.0