



# Full wwPDB EM Validation Report ⓘ

May 13, 2025 – 05:38 AM EDT

PDB ID : 9E1V / pdb\_00009e1v  
EMDB ID : EMD-47422  
Title : Snf2h bound nucleosome complex - ClassC2  
Authors : Malik, D.; Deshmukh, A.A.; Bilokapic, S.; Halic, M.  
Deposited on : 2024-10-21  
Resolution : 3.10 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev118  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0rc1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

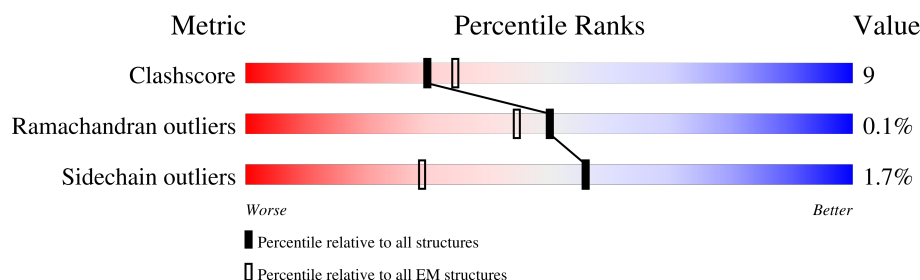
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.10 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	
3	C	130	
3	G	130	
4	D	126	
4	H	126	

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Mol	Chain	Length	Quality of chain
5	I	151	<div><div></div><div>40%</div><div>60%</div></div>
6	J	152	<div><div></div><div>55%</div><div>45%</div></div>
7	W	1052	<div><div>5%</div><div>28%</div><div>13%</div><div>58%</div></div>

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 15959 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 type 1.

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		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	99	ARG	GLY	conflict	UNP P06897
C	123	SER	ALA	conflict	UNP P06897
G	99	ARG	GLY	conflict	UNP P06897
G	123	SER	ALA	conflict	UNP P06897

- 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
H	29	THR	SER	engineered mutation	UNP P02281

- Molecule 5 is a DNA chain called DNA (151-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	151	Total	C	N	O	P	0	0
			3113	1472	586	904	151		

- Molecule 6 is a DNA chain called DNA (152-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	152	Total	C	N	O	P	0	0
			3096	1470	561	913	152		

- 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	442	Total	C	N	O	S	0	0
			3638	2330	638	647	23		

- Molecule 8 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).

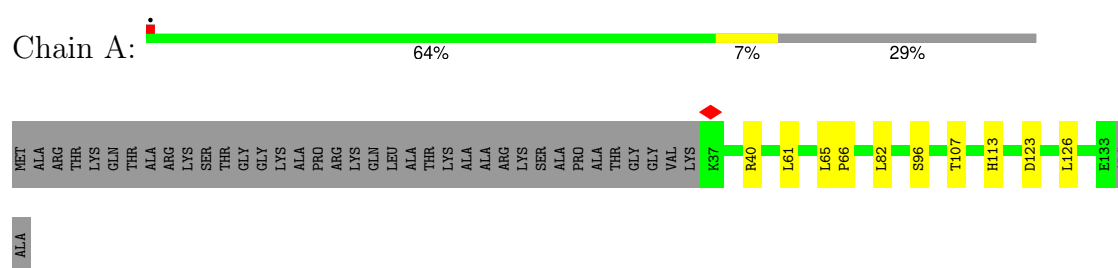


Mol	Chain	Residues	Atoms					AltConf
8	W	1	Total	C	N	O	P	0
			27	10	5	10	2	

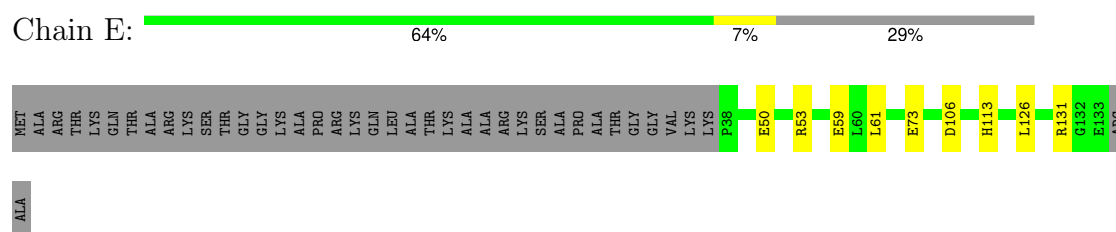
### 3 Residue-property plots [i](#)

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.

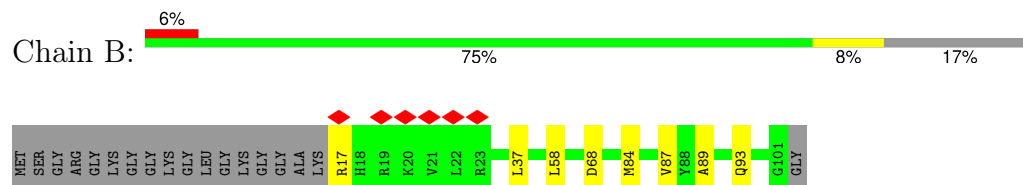
- Molecule 1: Histone H3.2



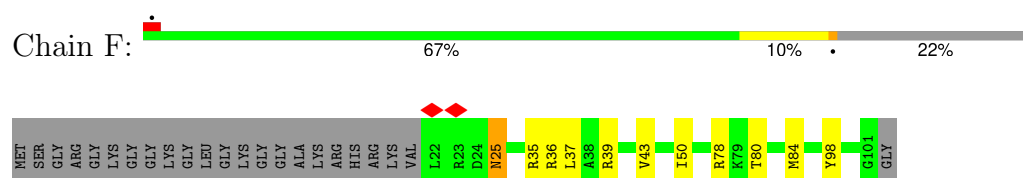
- Molecule 1: Histone H3.2



- Molecule 2: Histone H4



- Molecule 2: Histone H4

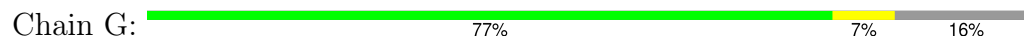


- Molecule 3: Histone H2A type 1

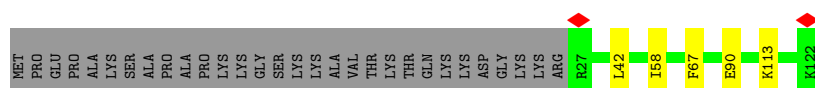




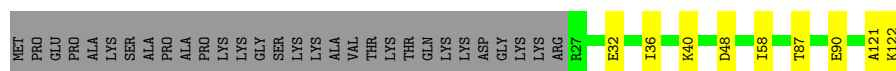
• Molecule 3: Histone H2A type 1



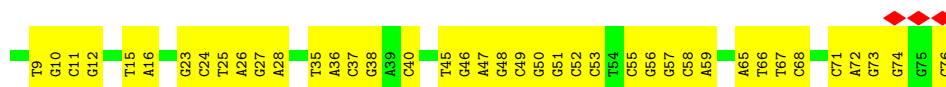
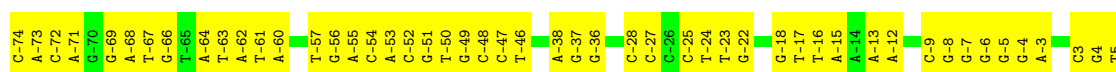
• Molecule 4: Histone H2B 1.1



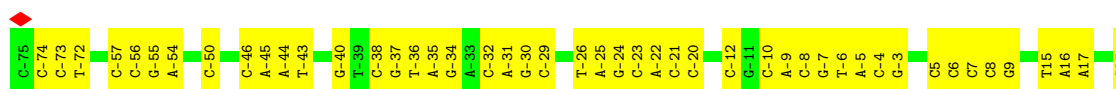
• Molecule 4: Histone H2B 1.1



• Molecule 5: DNA (151-MER)



• Molecule 6: DNA (152-MER)



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





MET	ILE	LYS	R186	E293	R389	F463	I568	ASP	GLN	THR	ILE	TRP	THR
SER	PHE	PRO	L191	K294	L393	D464	A569	GLU	SER	GLU	GLU	GLU	GLU
ALA	ASP	GLY	I192	K298	R394	E467	T570	MET	SER	GLU	ASP	ARG	GLU
ALA	ALA	PRO		K299	R395		A571	LEU	VAL	GLU	ASN	CYS	GLU
GLU	SER	ARG		F300	I396		V574	ASN	TYR	GLU	ASP	GLU	GLU
PRO	PRO	ILE			K397	P470		ILE	PHE	LEU	GLU	LEU	GLU
PRO	GLY	LYS			R303	P471		ARG	GLN	GLU	LYS	GLN	LEU
PRO	LYS	LYS			Y304	Y472		HIS	PHE	ILE	LYS	ILE	ILE
PRO	GLN	ASP			D399	T473		GLY	GLU	GLY	GLY	GLY	GLY
PRO	LYS	GLU			L305	T474		ALA	PRO	ASP	ALA	ILE	ILE
PRO	GLU	G201			Y306	D475		ALA	TYR	GLU	GLU	GLY	GLY
PRO	ILE	L202			I307	M476		THR	ARG	THR	PRO	LYS	LYS
GLU	GLN	L203				H477		HIS	GLU	GLU	GLU	ILE	ILE
SER	GLN	ASN			H311			VAL	VAL	VAL	ARG	GLY	GLY
PRO	LEU	LEU			K314	S403		PHE	PHE	GLY	GLY	GLY	GLY
ALA	PRO	LEU			R315	L404		ALA	GLN	GLU	GLN	GLN	GLN
PRO	ASP	SER			E316	P405		LEU	LYS	LEU	LEU	LEU	LEU
PRO	PRO	VAL			K317	P406		LYS	ILE	ASP	ASP	ASP	ASP
LYS	THR	GLY			T212	K407		ALA	PHE	GLU	LYS	LYS	LYS
PRO	TYR	ASP			T216	K408		SER	ALA	THR	GLY	ARG	GLY
ALA	GLU	TYR			G220			ILE	THR	GLU	ARG	GLY	GLY
ALA	GLU	ARG			K223	L412		GLU	GLU	GLU	GLY	GLY	GLY
SER	THR	THR			H224	L416		ASP	ARG	GLU	ILE	ILE	ILE
GLY	ASP	GLN			Y225	Q420		ILE	LYS	PRO	LYS	ILE	ILE
SER	ALA	ALA			R226	R421		ALA	ALA	GLU	GLY	ALA	ALA
ASN	ALA	GLU			M227			ALA	TYR	ASN	ALA	ALA	ALA
SER	ARG	GLU			T228			LYS	VAL	ASN	ALA	GLN	GLN
SER	ARG	ASP						THR	ASP	GLU	ALA	ALA	ALA
ASN	PHE	GLU			H232	R426		LEU	LEU	LEU	GLU	GLU	GLU
LYS	TYR	GLU			M233	L427		ALA	ALA	ALA	LEU	LEU	LEU
GLY	GLY	LEU			L235	L428		THR	ARG	GLU	GLU	GLU	GLU
PRO	GLN	GLY			L255	M429		THR	LYS	ASN	ALA	ALA	ALA
GLU	THR	GLN			R256	K430		ALA	GLY	GLY	GLU	GLU	GLU
VAL	ILE	LYS			L260	A362		ASN	LYS	MET	LYS	LYS	LYS
ALA	PHE	ALA			I261	D363		THR	ALA	ASP	GLY	GLY	GLY
ALA	GLN	ASN			K264	ASP		GLY	GLY	GLY	GLY	GLY	GLY
VAL	HIS	VAL				PHE		ASN	THR	ASP	GLY	GLY	GLY
VAL	PHE	ILE			R267	ASN		GLY	ASN	GLY	GLY	GLY	GLY
ALA	PRO	PRO			V271	CYS		ASP	CYS	ASP	GLY	GLY	GLY
ALA	ALA	ALA			F168	LEU		LEU	LEU	K443	GLY	GLY	GLY
SER	ALA	SER			E169	GLY		GLY	GLY	M444	ARG	ARG	ARG
ALA	GLN	ALA			D170	D377		LEU	LEU	R445	LEU	LEU	LEU
LYS	LYS	GLY			S171	V274		VAL	VAL	P555	VAL	VAL	VAL
PRO	THR	PRO			P172	L275		ASP	ASP	M556	ASP	ASP	ASP
ASP	THR	ASP			S173	L276		GLN	GLN	L447	LYS	LYS	LYS
ALA	SER	ALA				E279		ASN	ASN	M448	ALA	ALA	ALA
GLU	PRO	GLU			K179	W290		LEU	LEU	T449	GLU	GLU	GLU
MET	LYS	LYS			R181	E382		ASN	ASN	L450	LEU	LEU	LEU
GLU	MET	GLU			D182	R383		THR	THR	M451	GLY	GLY	GLY
					Y183	L384		LYS	LYS	Q452	LYS	LYS	LYS
						H385		GLY	GLY	L453	ILE	ILE	ILE
						M386		LYS	LYS	R454	GLY	GLY	GLY
										K455	LYS	LYS	LYS
										P460			
										Y461			
										L462			

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	30000	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	33.808	Depositor
Minimum map value	-0.676	Depositor
Average map value	-0.022	Depositor
Map value standard deviation	0.288	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	0.16	0/811	0.27	0/1088
1	E	0.16	0/802	0.27	0/1076
2	B	0.15	0/687	0.30	0/921
2	F	0.16	0/648	0.29	0/868
3	C	0.14	0/847	0.23	0/1144
3	G	0.14	0/847	0.29	0/1144
4	D	0.13	0/757	0.24	0/1018
4	H	0.14	0/767	0.25	0/1029
5	I	0.25	0/3496	0.43	0/5398
6	J	0.25	0/3468	0.40	0/5345
7	W	0.15	0/3715	0.34	0/5017
All	All	0.20	0/16845	0.35	0/24048

There are no bond length outliers.

There are no bond angle outliers.

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	8	0
1	E	790	0	826	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	679	0	717	7	0
2	F	641	0	684	9	0
3	C	837	0	891	8	0
3	G	837	0	891	5	0
4	D	746	0	764	4	0
4	H	756	0	786	7	0
5	I	3113	0	1693	79	0
6	J	3096	0	1706	59	0
7	W	3638	0	3710	94	0
8	W	27	0	12	0	0
All	All	15959	0	13518	261	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 9.

All (261) 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:619:GLU:O	7:W:623:MET:HG3	1.61	1.01
5:I:24:DC:H42	6:J:-24:DG:H1	1.17	0.91
5:I:40:DC:H42	6:J:-40:DG:H1	1.32	0.77
5:I:52:DC:H2''	5:I:53:DC:H5''	1.69	0.75
2:B:17:ARG:HD3	7:W:467:GLU:HG2	1.69	0.73
7:W:609:THR:HG1	7:W:612:THR:HG1	1.36	0.73
5:I:24:DC:H2''	5:I:25:DT:O4'	1.92	0.70
7:W:426:ARG:O	7:W:426:ARG:NH1	2.25	0.69
6:J:68:DT:H2''	6:J:69:DC:H5''	1.75	0.69
7:W:386:MET:SD	7:W:389:ARG:NH1	2.64	0.68
7:W:495:LEU:O	7:W:498:GLN:C	2.36	0.68
7:W:235:LEU:HD11	7:W:290:LEU:HD22	1.73	0.68
7:W:200:ASN:ND2	7:W:354:LEU:O	2.23	0.68
5:I:24:DC:N4	6:J:-24:DG:H1	1.91	0.67
7:W:199:ILE:HG23	7:W:355:LEU:HD11	1.77	0.67
7:W:260:LEU:HD21	7:W:293:GLU:HG3	1.77	0.66
6:J:-22:DA:H2''	6:J:-21:DC:H5''	1.77	0.66
5:I:15:DT:H2''	5:I:16:DA:C8	2.31	0.65
5:I:23:DG:OP1	7:W:582:ASN:ND2	2.22	0.65
6:J:-23:DC:O2	7:W:451:MET:HE3	1.96	0.65
6:J:30:DT:H2'	6:J:31:DT:H71	1.79	0.64
7:W:629:SER:O	7:W:633:GLN:HG3	1.98	0.64
5:I:66:DT:H2'	5:I:67:DT:C6	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:546:ASN:ND2	7:W:567:ASN:O	2.28	0.64
7:W:202:ILE:HG13	7:W:354:LEU:HD11	1.80	0.63
7:W:455:LYS:HB2	7:W:462:LEU:HD12	1.78	0.63
7:W:569:ALA:O	7:W:598:GLN:NE2	2.31	0.63
1:E:61:LEU:O	2:F:36:ARG:NH1	2.32	0.63
7:W:342:ASN:N	7:W:346:GLU:OE2	2.28	0.63
1:A:40:ARG:NH2	5:I:9:DT:O2	2.32	0.62
2:F:36:ARG:NH2	5:I:-13:DA:OP1	2.33	0.62
7:W:416:LEU:HB2	7:W:421:ARG:HD3	1.80	0.61
5:I:47:DA:H2''	5:I:48:DG:N7	2.16	0.61
7:W:591:ASP:HA	7:W:594:HIS:HB3	1.83	0.61
6:J:-6:DT:H2''	6:J:-5:DA:C8	2.35	0.61
5:I:-25:DC:H2''	5:I:-24:DT:H72	1.83	0.60
7:W:211:LYS:HB3	7:W:335:LEU:HD23	1.84	0.60
7:W:256:ARG:HD2	7:W:280:TRP:HA	1.84	0.60
6:J:35:DC:H2''	6:J:36:DC:C5	2.38	0.59
1:A:61:LEU:HD12	2:B:37:LEU:HD23	1.85	0.59
5:I:26:DA:H2''	5:I:27:DG:C8	2.38	0.59
6:J:49:DC:H2''	6:J:50:DA:C8	2.37	0.59
7:W:501:ARG:NH2	7:W:545:TYR:O	2.35	0.59
7:W:513:ASP:OD1	7:W:528:ARG:NH1	2.36	0.58
5:I:-18:DG:H1'	5:I:-17:DT:H5'	1.85	0.58
5:I:3:DC:H2''	5:I:4:DG:C8	2.39	0.58
7:W:501:ARG:NH1	7:W:552:LYS:O	2.37	0.58
5:I:-57:DT:H2''	5:I:-56:DG:C8	2.39	0.58
7:W:220:GLY:O	7:W:224:HIS:ND1	2.28	0.58
4:H:87:THR:OG1	4:H:90:GLU:OE1	2.22	0.57
5:I:-47:DC:H2''	5:I:-46:DT:C5	2.39	0.57
5:I:-55:DA:H2''	5:I:-54:DC:C5	2.40	0.56
1:E:106:ASP:OD2	1:E:131:ARG:NH1	2.39	0.56
5:I:55:DC:H2''	5:I:56:DG:C8	2.41	0.56
6:J:-30:DG:H1'	6:J:-29:DC:H5'	1.86	0.56
7:W:232:HIS:CD2	7:W:303:ARG:HB2	2.41	0.56
5:I:-72:DC:H2''	5:I:-71:DA:C8	2.41	0.56
6:J:-25:DA:H2''	6:J:-24:DG:H8	1.71	0.56
5:I:-64:DA:H2'	5:I:-63:DT:H71	1.86	0.55
5:I:12:DG:H1	6:J:-12:DC:H42	1.53	0.55
6:J:8:DC:H2''	6:J:9:DG:C8	2.41	0.55
5:I:-16:DT:H2''	5:I:-15:DA:C8	2.41	0.55
5:I:26:DA:H2''	5:I:27:DG:H8	1.69	0.55
3:C:16:THR:HA	6:J:-44:DA:H5''	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:311:HIS:O	7:W:314:LYS:NZ	2.32	0.55
5:I:-69:DG:H2''	5:I:-68:DA:C8	2.43	0.54
7:W:495:LEU:O	7:W:498:GLN:O	2.25	0.54
6:J:-4:DC:H2''	6:J:-3:DG:C8	2.43	0.54
7:W:294:LYS:O	7:W:298:LYS:HB2	2.07	0.54
7:W:590:MET:HE3	7:W:604:VAL:HG21	1.88	0.54
5:I:-67:DT:H2''	5:I:-66:DG:C8	2.43	0.54
5:I:-62:DA:H2'	5:I:-61:DT:H71	1.89	0.53
5:I:-6:DG:H2''	5:I:-5:DG:C8	2.43	0.53
7:W:566:ILE:O	7:W:595:ARG:NH1	2.41	0.53
3:C:10:THR:OG1	3:C:11:ARG:N	2.42	0.53
2:F:84:MET:HA	2:F:84:MET:HE2	1.90	0.53
5:I:74:DG:C8	5:I:76:DC:H5'	2.44	0.53
5:I:27:DG:H2''	5:I:28:DA:C8	2.43	0.53
6:J:-46:DC:H2''	6:J:-45:DA:C8	2.44	0.53
6:J:38:DT:H2''	6:J:39:DA:C8	2.43	0.53
3:G:102:ILE:HG23	4:H:58:ILE:HD13	1.90	0.53
6:J:71:DT:H2''	6:J:72:DG:C8	2.44	0.53
3:C:102:ILE:HG23	4:D:58:ILE:HD13	1.89	0.53
6:J:73:DT:H2''	6:J:74:DG:C8	2.44	0.52
5:I:-54:DC:H2''	5:I:-53:DA:C8	2.44	0.52
7:W:271:VAL:HG22	7:W:276:LEU:HG	1.92	0.52
7:W:279:GLU:N	7:W:279:GLU:OE1	2.42	0.52
6:J:35:DC:H2''	6:J:36:DC:C6	2.45	0.52
7:W:512:LEU:HD22	7:W:556:MET:HB3	1.91	0.52
5:I:-71:DA:C8	5:I:-71:DA:H5'	2.45	0.52
7:W:256:ARG:NH1	7:W:279:GLU:O	2.43	0.52
5:I:-63:DT:H2''	5:I:-62:DA:H5''	1.92	0.52
6:J:51:DC:H2''	6:J:52:DG:H5''	1.92	0.52
7:W:450:LEU:O	7:W:454:ARG:HG3	2.09	0.51
3:C:73:ASN:ND2	3:C:73:ASN:O	2.42	0.51
1:E:50:GLU:HA	1:E:53:ARG:HG2	1.91	0.51
7:W:561:ALA:O	7:W:592:ARG:NH2	2.43	0.51
7:W:361:SER:OG	7:W:362:ALA:N	2.41	0.51
7:W:207:MET:HG3	7:W:564:LEU:HD12	1.92	0.51
5:I:45:DT:H2''	5:I:46:DG:C8	2.45	0.51
7:W:233:MET:HE3	7:W:305:LEU:HD13	1.92	0.51
6:J:-21:DC:H2''	6:J:-20:DC:H5'	1.93	0.50
7:W:525:GLU:OE2	7:W:552:LYS:NZ	2.44	0.50
5:I:50:DG:H2''	5:I:51:DG:C8	2.46	0.50
7:W:420:GLN:HG2	7:W:460:PRO:HD3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:-36:DT:H2''	6:J:-35:DA:C8	2.47	0.50
3:G:26:PRO:HB2	3:G:29:ARG:HB3	1.94	0.50
6:J:-73:DC:H2''	6:J:-72:DT:H71	1.93	0.50
6:J:-35:DA:H2''	6:J:-34:DG:C8	2.47	0.49
6:J:-26:DT:H2''	6:J:-25:DA:H8	1.76	0.49
3:C:30:VAL:HG13	4:D:67:PHE:HE2	1.77	0.49
5:I:72:DA:C6	5:I:73:DG:C6	3.01	0.49
6:J:-57:DC:H2''	6:J:-56:DC:C5	2.47	0.49
7:W:223:LYS:HG3	7:W:255:LEU:HD13	1.94	0.49
7:W:316:GLU:O	7:W:317:LYS:HG2	2.12	0.49
6:J:15:DT:H2''	6:J:16:DA:C8	2.46	0.49
5:I:36:DA:H2''	5:I:37:DC:C5	2.48	0.49
6:J:25:DG:H2''	6:J:26:DG:N7	2.28	0.49
7:W:408:LYS:HD3	7:W:601:THR:HG23	1.93	0.49
5:I:-38:DA:H5'	5:I:-38:DA:C8	2.48	0.49
5:I:-28:DC:H2''	5:I:-27:DC:C6	2.48	0.49
5:I:11:DC:H2''	5:I:12:DG:C8	2.48	0.49
5:I:57:DG:H2''	5:I:58:DC:C5	2.48	0.49
1:E:61:LEU:HD12	2:F:37:LEU:HD23	1.94	0.49
5:I:-67:DT:H2''	5:I:-66:DG:H8	1.78	0.49
6:J:62:DT:H2''	6:J:63:DA:C8	2.47	0.49
6:J:25:DG:H2''	6:J:26:DG:C8	2.48	0.48
2:B:68:ASP:OD2	2:B:93:GLN:NE2	2.46	0.48
5:I:-9:DC:H2''	5:I:-8:DG:C8	2.49	0.48
6:J:-44:DA:H2'	6:J:-43:DT:H71	1.96	0.48
5:I:46:DG:H2''	5:I:47:DA:C8	2.49	0.48
5:I:25:DT:H2''	5:I:26:DA:O4'	2.13	0.48
6:J:-74:DC:H2''	6:J:-73:DC:C6	2.49	0.48
6:J:-10:DC:H2''	6:J:-9:DA:C8	2.48	0.48
2:B:17:ARG:NH1	7:W:472:TYR:HB3	2.28	0.48
5:I:4:DG:H2''	5:I:5:DT:H72	1.96	0.48
6:J:-23:DC:C2	6:J:-22:DA:N7	2.82	0.48
7:W:380:LEU:O	7:W:382:GLU:N	2.46	0.47
5:I:-48:DC:H2''	5:I:-47:DC:C6	2.48	0.47
7:W:574:VAL:HB	7:W:604:VAL:HG22	1.97	0.47
7:W:191:LEU:HD11	7:W:203:LEU:HD11	1.95	0.47
5:I:-37:DG:H2''	5:I:-36:DG:C8	2.49	0.47
7:W:584:GLN:NE2	7:W:628:ASP:OD1	2.23	0.47
7:W:204:ALA:HB3	7:W:394:ARG:HB2	1.95	0.47
5:I:-50:DT:H2''	5:I:-49:DG:C8	2.49	0.47
5:I:-7:DG:H2''	5:I:-6:DG:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:628:ASP:O	7:W:632:ILE:HB	2.15	0.47
6:J:-35:DA:H2''	6:J:-34:DG:H8	1.80	0.47
7:W:183:TYR:O	7:W:186:ARG:HG2	2.15	0.47
7:W:212:THR:O	7:W:216:ILE:HG12	2.15	0.46
7:W:385:HIS:CE1	7:W:634:GLN:HG2	2.50	0.46
6:J:-8:DC:H2''	6:J:-7:DG:C8	2.50	0.46
7:W:286:SER:OG	7:W:289:MET:HG2	2.15	0.46
7:W:393:LEU:HD21	7:W:395:ARG:HH12	1.79	0.46
7:W:540:ASP:OD2	7:W:540:ASP:N	2.46	0.46
5:I:71:DC:H2''	5:I:72:DA:C8	2.51	0.46
7:W:490:LYS:O	7:W:494:LYS:HG2	2.16	0.46
1:A:82:LEU:HD23	1:A:82:LEU:HA	1.82	0.46
6:J:59:DA:H2'	6:J:60:DT:H71	1.96	0.46
6:J:6:DC:H2''	6:J:7:DC:C6	2.50	0.46
6:J:16:DA:H2''	6:J:17:DA:C8	2.51	0.46
7:W:470:PRO:N	7:W:471:PRO:HD2	2.30	0.46
5:I:4:DG:H4'	5:I:5:DT:OP1	2.16	0.46
5:I:25:DT:H2''	5:I:26:DA:C8	2.51	0.46
6:J:5:DC:H2''	6:J:6:DC:C5	2.51	0.46
7:W:450:LEU:HD21	7:W:581:TRP:HH2	1.80	0.46
7:W:426:ARG:HH12	7:W:430:LYS:HB2	1.81	0.46
5:I:65:DA:C8	5:I:66:DT:H72	2.51	0.46
5:I:-69:DG:H2''	5:I:-68:DA:H8	1.79	0.45
5:I:-52:DC:H2''	5:I:-51:DG:C8	2.51	0.45
7:W:448:ASN:O	7:W:452:GLN:HG2	2.16	0.45
2:F:78:ARG:NH1	2:F:80:THR:O	2.49	0.45
6:J:-26:DT:H2''	6:J:-25:DA:C8	2.51	0.45
7:W:171:SER:HB3	7:W:179:LYS:HD2	1.98	0.45
1:E:73:GLU:OE1	2:F:25:ASN:ND2	2.39	0.45
5:I:36:DA:H2''	5:I:37:DC:C6	2.52	0.45
5:I:47:DA:H2''	5:I:48:DG:C8	2.51	0.45
7:W:501:ARG:HB3	7:W:571:ALA:HA	1.98	0.45
7:W:426:ARG:O	7:W:429:MET:HG3	2.17	0.45
4:H:122:LYS:HB2	4:H:122:LYS:HE2	1.78	0.45
5:I:9:DT:H2''	5:I:10:DG:C8	2.52	0.45
5:I:-74:DC:H2''	5:I:-73:DA:C8	2.52	0.45
7:W:506:SER:O	7:W:558:SER:HA	2.16	0.45
3:G:32:ARG:HH22	4:H:32:GLU:CD	2.25	0.45
6:J:-37:DG:H2''	6:J:-36:DT:C7	2.47	0.45
7:W:179:LYS:O	7:W:181:ARG:NH2	2.50	0.45
6:J:-32:DC:H2''	6:J:-31:DA:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:SER:HB3	2:B:58:LEU:HD11	1.99	0.44
5:I:49:DC:H2''	5:I:50:DG:C8	2.53	0.44
3:C:79:ILE:HG12	3:C:82:HIS:CE1	2.53	0.44
5:I:73:DG:H1'	5:I:76:DC:C2	2.53	0.44
6:J:-50:DC:H5'	6:J:-50:DC:C6	2.52	0.44
6:J:-38:DC:H2''	6:J:-37:DG:C8	2.52	0.44
6:J:-56:DC:H2''	6:J:-55:DG:C8	2.53	0.44
7:W:307:ILE:HD11	7:W:324:VAL:HG21	1.99	0.44
7:W:450:LEU:O	7:W:454:ARG:CG	2.65	0.44
6:J:7:DC:H2''	6:J:8:DC:C6	2.54	0.43
1:E:50:GLU:OE1	2:F:39:ARG:NH1	2.51	0.43
1:A:107:THR:HG23	1:A:123:ASP:HB2	1.99	0.43
6:J:36:DC:H2''	6:J:37:DC:C5	2.53	0.43
5:I:-61:DT:H2''	5:I:-60:DA:H8	1.84	0.43
6:J:-6:DT:H2''	6:J:-5:DA:N7	2.33	0.43
5:I:-13:DA:H2''	5:I:-12:DA:C8	2.53	0.43
4:H:36:ILE:O	4:H:40:LYS:HG3	2.19	0.43
7:W:271:VAL:HG23	7:W:275:LEU:HD23	2.01	0.43
7:W:495:LEU:HD13	7:W:495:LEU:HA	1.80	0.43
5:I:37:DC:H2''	5:I:38:DG:C8	2.54	0.43
2:F:35:ARG:NH2	2:F:39:ARG:HH22	2.17	0.43
5:I:56:DG:H2''	5:I:57:DG:N7	2.34	0.43
7:W:619:GLU:O	7:W:623:MET:CG	2.49	0.43
5:I:-52:DC:H2''	5:I:-51:DG:H8	1.82	0.42
6:J:-23:DC:O4'	7:W:448:ASN:ND2	2.52	0.42
6:J:-37:DG:H2''	6:J:-36:DT:H71	2.01	0.42
7:W:482:SER:HB3	7:W:485:MET:HB2	2.01	0.42
2:B:84:MET:HA	2:B:87:VAL:HG22	2.00	0.42
7:W:405:PRO:HB2	7:W:408:LYS:NZ	2.34	0.42
7:W:280:TRP:HZ2	7:W:300:PHE:CD2	2.37	0.42
5:I:-61:DT:H2''	5:I:-60:DA:C8	2.53	0.42
5:I:-4:DG:H2''	5:I:-3:DA:C8	2.55	0.42
6:J:-32:DC:H2''	6:J:-31:DA:C8	2.55	0.42
3:G:79:ILE:HG12	3:G:82:HIS:CE1	2.55	0.42
5:I:35:DT:H2''	5:I:36:DA:C8	2.54	0.42
5:I:73:DG:H1'	5:I:76:DC:O2	2.20	0.42
7:W:527:CYS:SG	7:W:552:LYS:HD3	2.60	0.42
5:I:24:DC:OP1	7:W:624:LYS:NZ	2.51	0.41
5:I:-23:DT:H2''	5:I:-22:DG:H8	1.86	0.41
7:W:267:ARG:HD3	7:W:289:MET:HE3	2.01	0.41
7:W:412:ILE:HD12	7:W:607:PHE:HE1	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:473:THR:OG1	7:W:477:HIS:NE2	2.49	0.41
2:B:89:ALA:O	2:B:93:GLN:HG2	2.20	0.41
5:I:50:DG:H2''	5:I:51:DG:H8	1.84	0.41
7:W:192:ILE:HD12	7:W:192:ILE:HA	1.67	0.41
7:W:553:PHE:CD2	7:W:554:VAL:HG23	2.55	0.41
3:C:26:PRO:HB2	3:C:29:ARG:HB3	2.01	0.41
7:W:450:LEU:HD21	7:W:581:TRP:CH2	2.55	0.41
3:C:63:LEU:HD13	4:D:42:LEU:HB2	2.03	0.41
7:W:494:LYS:O	7:W:498:GLN:HB2	2.21	0.41
7:W:203:LEU:HD23	7:W:203:LEU:HA	1.91	0.41
4:D:58:ILE:HG23	2:F:98:TYR:HB3	2.03	0.41
4:H:121:ALA:O	4:H:122:LYS:HD3	2.21	0.41
6:J:-55:DG:H2''	6:J:-54:DA:C8	2.55	0.41
7:W:168:PHE:CE2	7:W:172:PRO:HG3	2.56	0.41
7:W:495:LEU:O	7:W:500:SER:N	2.54	0.41
5:I:-5:DG:H2''	5:I:-4:DG:C8	2.56	0.41
5:I:67:DT:H2''	5:I:68:DC:C6	2.55	0.41
7:W:290:LEU:HD11	7:W:327:PHE:HE2	1.86	0.41
7:W:494:LYS:HA	7:W:494:LYS:HD2	1.83	0.41
7:W:587:LEU:HA	7:W:590:MET:HG2	2.02	0.41
7:W:264:LYS:HE3	7:W:264:LYS:HB3	1.90	0.40
1:A:65:LEU:HB3	1:A:66:PRO:HD3	2.03	0.40
1:A:126:LEU:HD22	1:E:113:HIS:CG	2.56	0.40
3:G:15:LYS:O	3:G:20:ARG:NH1	2.55	0.40
4:H:48:ASP:OD1	4:H:48:ASP:N	2.49	0.40
5:I:58:DC:H2''	5:I:59:DA:C8	2.56	0.40
5:I:72:DA:H2''	5:I:73:DG:C8	2.56	0.40
5:I:73:DG:N3	5:I:76:DC:H5''	2.36	0.40
6:J:-45:DA:H2''	6:J:-44:DA:H8	1.86	0.40
6:J:-25:DA:H2''	6:J:-24:DG:C8	2.54	0.40
1:A:113:HIS:CG	1:E:126:LEU:HD22	2.56	0.40
6:J:-31:DA:H2'	6:J:-30:DG:C8	2.57	0.40
6:J:8:DC:H2''	6:J:9:DG:H8	1.85	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%)	92 (98%)	2 (2%)	0	100	100
2	B	83/103 (81%)	82 (99%)	1 (1%)	0	100	100
2	F	78/103 (76%)	76 (97%)	2 (3%)	0	100	100
3	C	107/130 (82%)	106 (99%)	1 (1%)	0	100	100
3	G	107/130 (82%)	105 (98%)	2 (2%)	0	100	100
4	D	94/126 (75%)	93 (99%)	1 (1%)	0	100	100
4	H	94/126 (75%)	92 (98%)	2 (2%)	0	100	100
7	W	436/1052 (41%)	408 (94%)	27 (6%)	1 (0%)	44	74
All	All	1188/2042 (58%)	1146 (96%)	41 (4%)	1 (0%)	50	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	W	566	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%)	85 (100%)	0	100	100
1	E	84/111 (76%)	83 (99%)	1 (1%)	67	83
2	B	69/79 (87%)	69 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	F	66/79 (84%)	63 (96%)	3 (4%)	23	53
3	C	85/102 (83%)	85 (100%)	0	100	100
3	G	85/102 (83%)	84 (99%)	1 (1%)	67	83
4	D	80/106 (76%)	78 (98%)	2 (2%)	42	69
4	H	82/106 (77%)	82 (100%)	0	100	100
7	W	407/939 (43%)	396 (97%)	11 (3%)	40	67
All	All	1043/1735 (60%)	1025 (98%)	18 (2%)	56	78

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	90	GLU
4	D	113	LYS
1	E	59	GLU
2	F	25	ASN
2	F	43	VAL
2	F	50	ILE
3	G	73	ASN
7	W	168	PHE
7	W	192	ILE
7	W	261	ILE
7	W	416	LEU
7	W	428	LEU
7	W	447	LEU
7	W	494	LYS
7	W	495	LEU
7	W	517	ASP
7	W	557	LEU
7	W	601	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	108	ASN
2	B	25	ASN
4	D	46	HIS
4	D	81	ASN
1	E	68	GLN
2	F	75	HIS

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Mol	Chain	Res	Type
3	G	24	GLN
3	G	73	ASN
3	G	89	ASN
4	H	81	ASN
7	W	567	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	1101	-	24,29,29	0.87	0	29,45,45	1.23	2 (6%)

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	1101	-	-	0/12/32/32	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	W	1101	ADP	N3-C2-N1	-3.72	123.62	128.67
8	W	1101	ADP	C4-C5-N7	-2.65	106.53	109.34

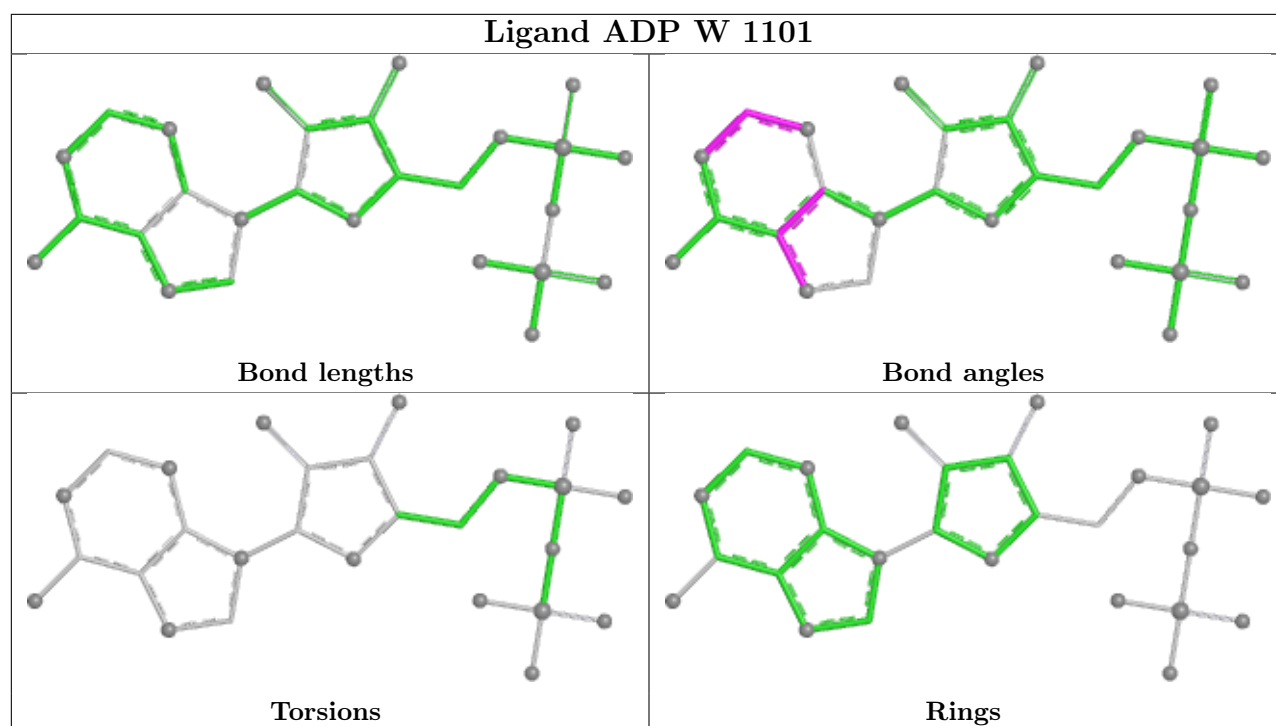
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

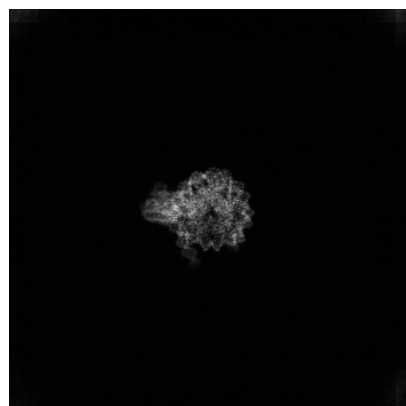
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47422. 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

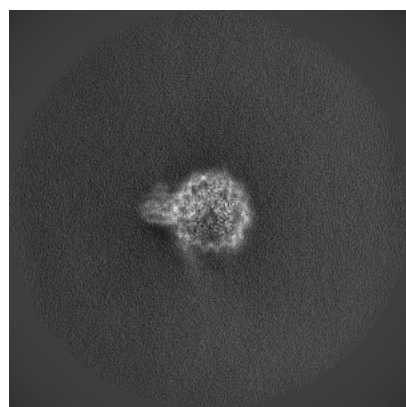


Y

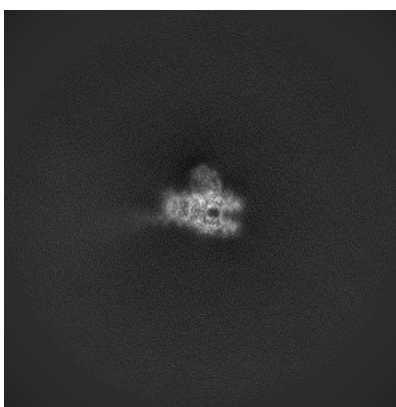


Z

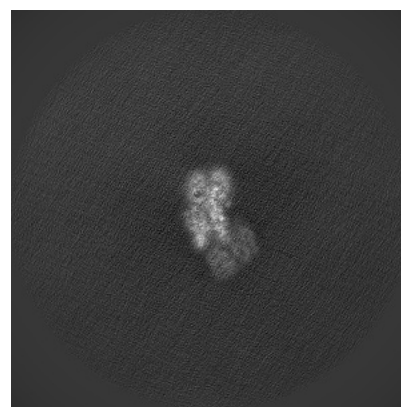
#### 6.1.2 Raw map



X



Y



Z

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

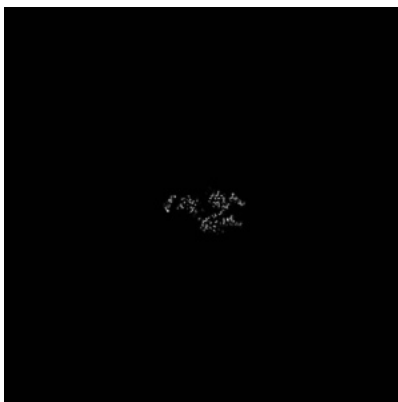


## 6.2 Central slices [i](#)

### 6.2.1 Primary map



X Index: 248

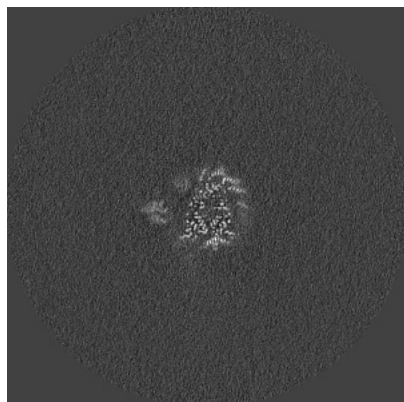


Y Index: 248

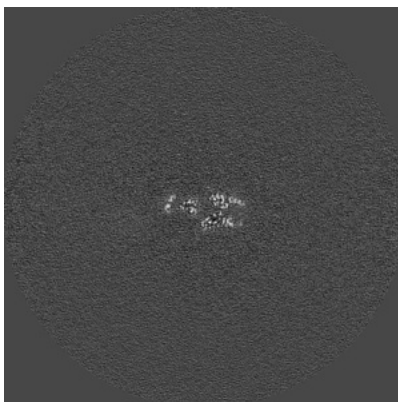


Z Index: 248

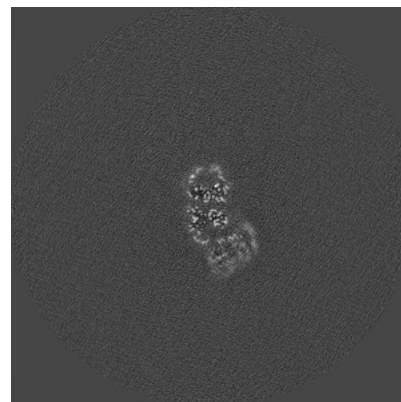
### 6.2.2 Raw map



X Index: 192



Y Index: 192

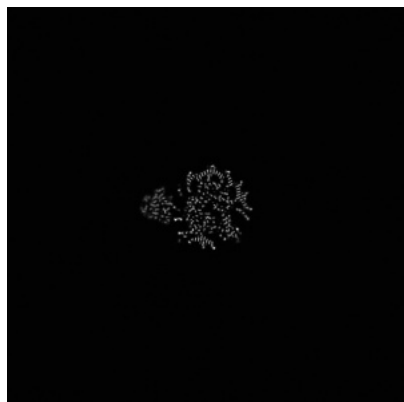


Z Index: 192

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

## 6.3 Largest variance slices [i](#)

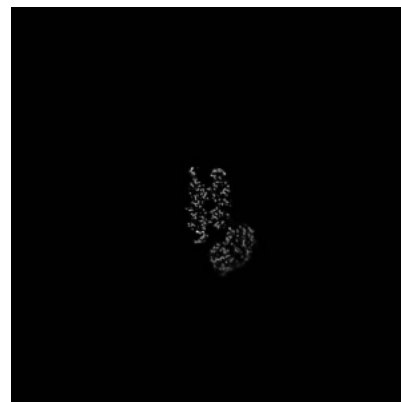
### 6.3.1 Primary map



X Index: 255

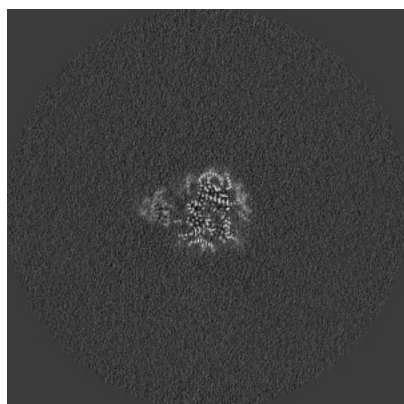


Y Index: 225

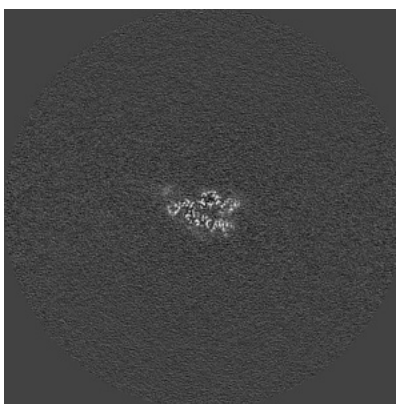


Z Index: 254

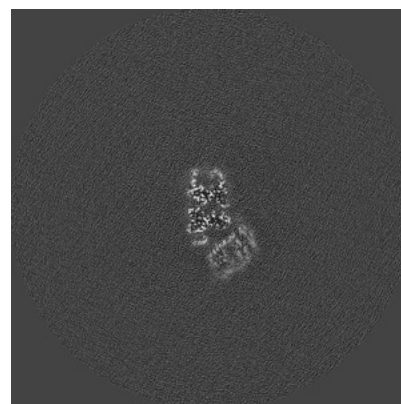
### 6.3.2 Raw map



X Index: 196



Y Index: 211



Z Index: 194

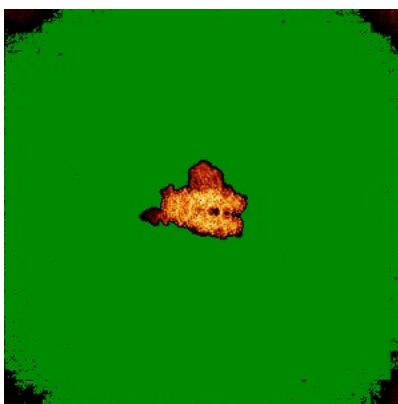
The images above show the largest variance slices of the map in three orthogonal directions.

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

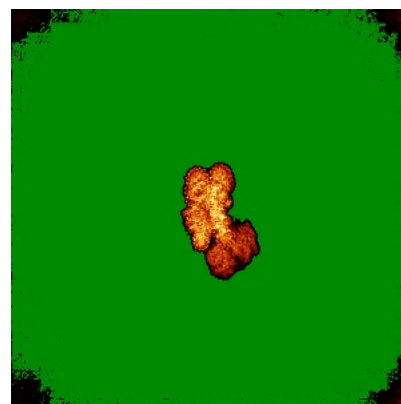
### 6.4.1 Primary map



X

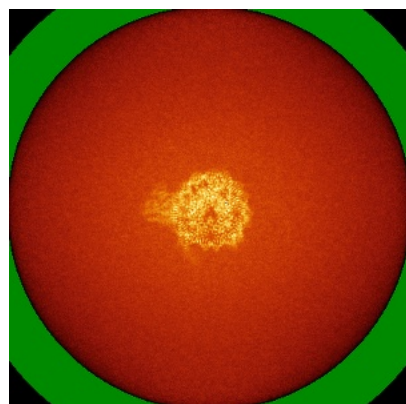


Y

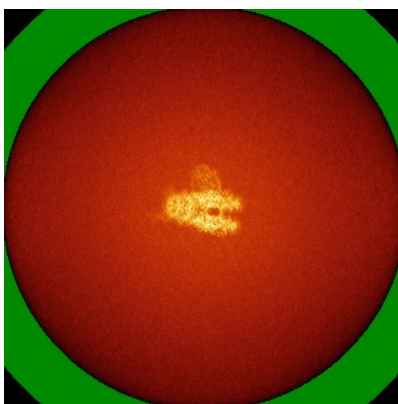


Z

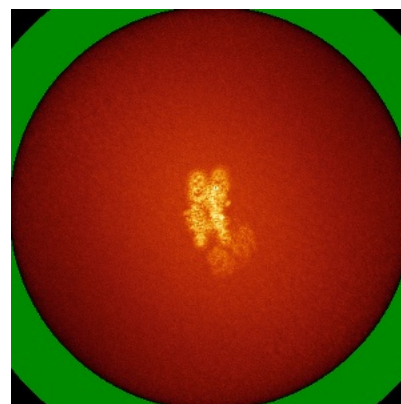
### 6.4.2 Raw map



X



Y

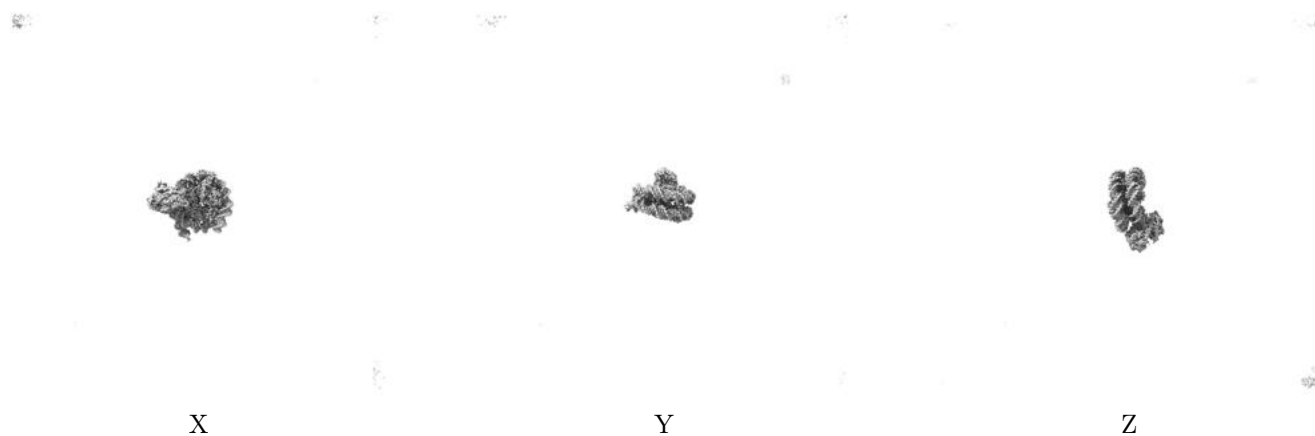


Z

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.

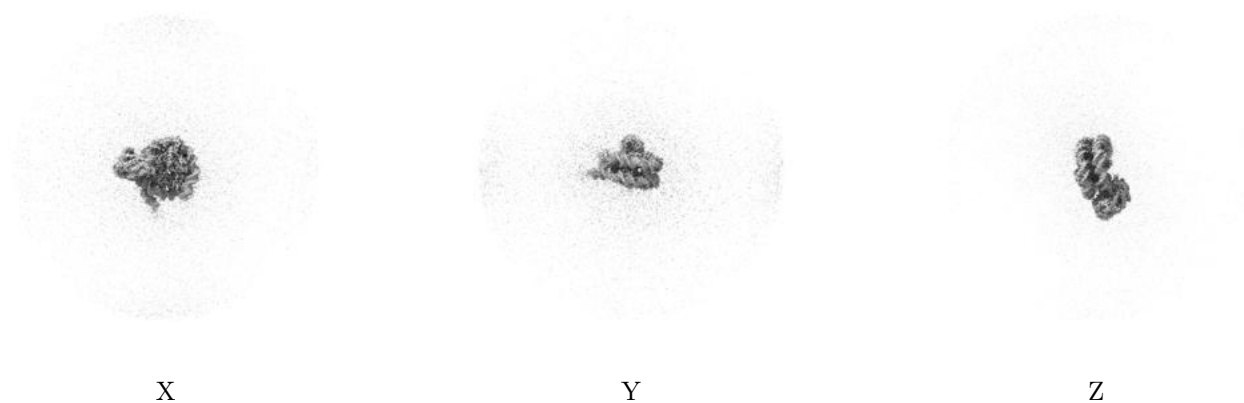
## 6.5 Orthogonal surface views [i](#)

### 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.

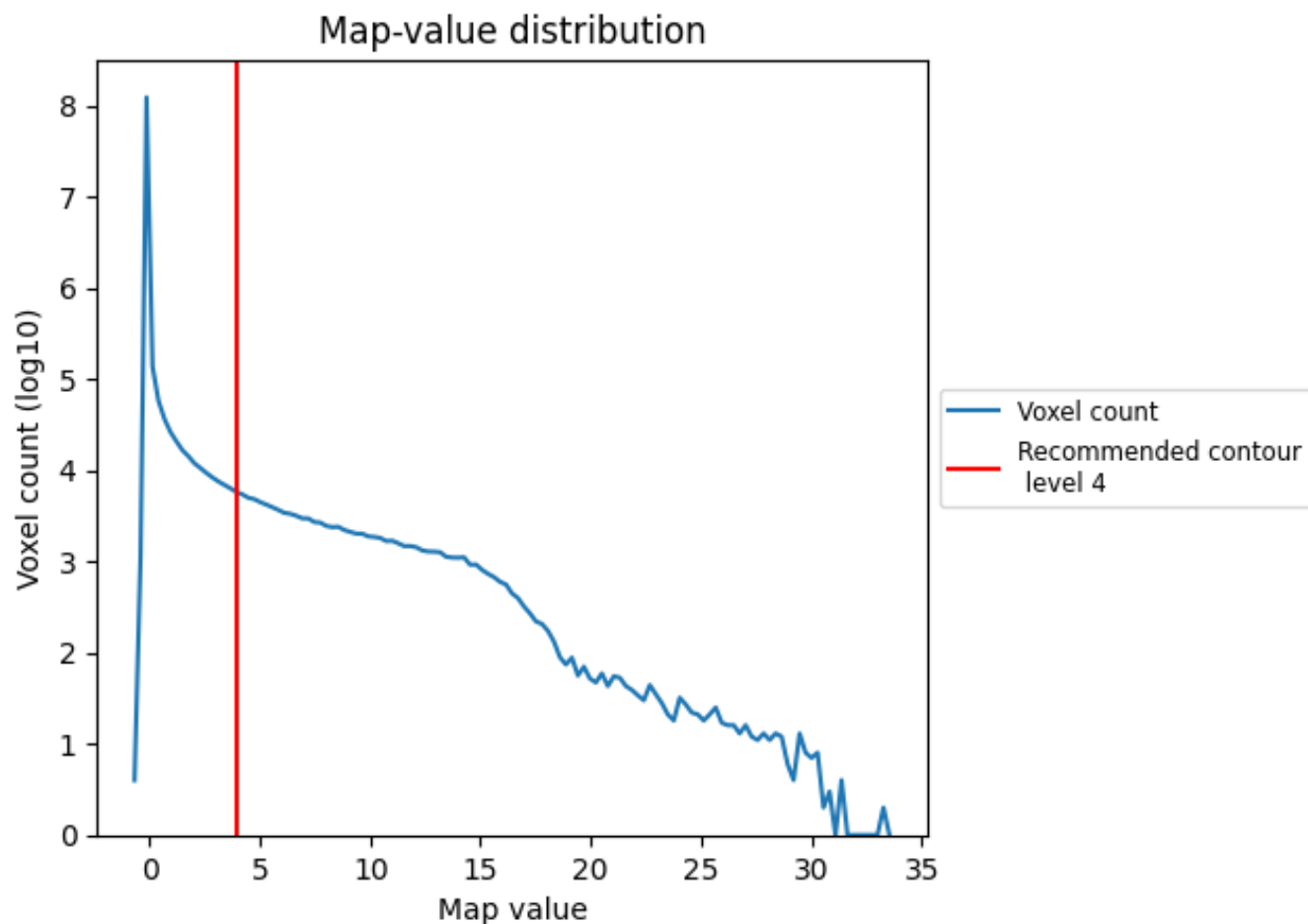
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

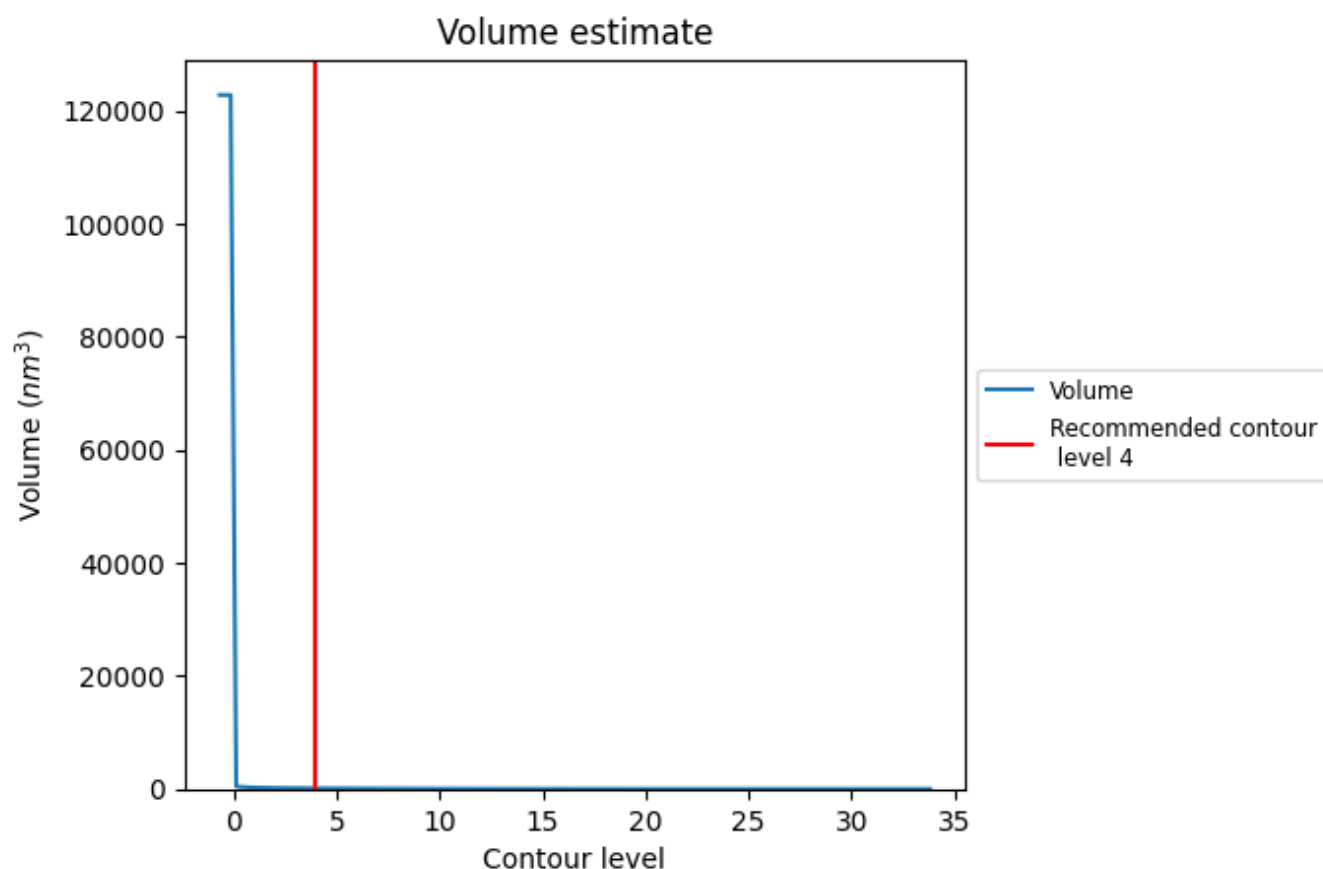
This section contains the results of statistical analysis of the map.

### 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.

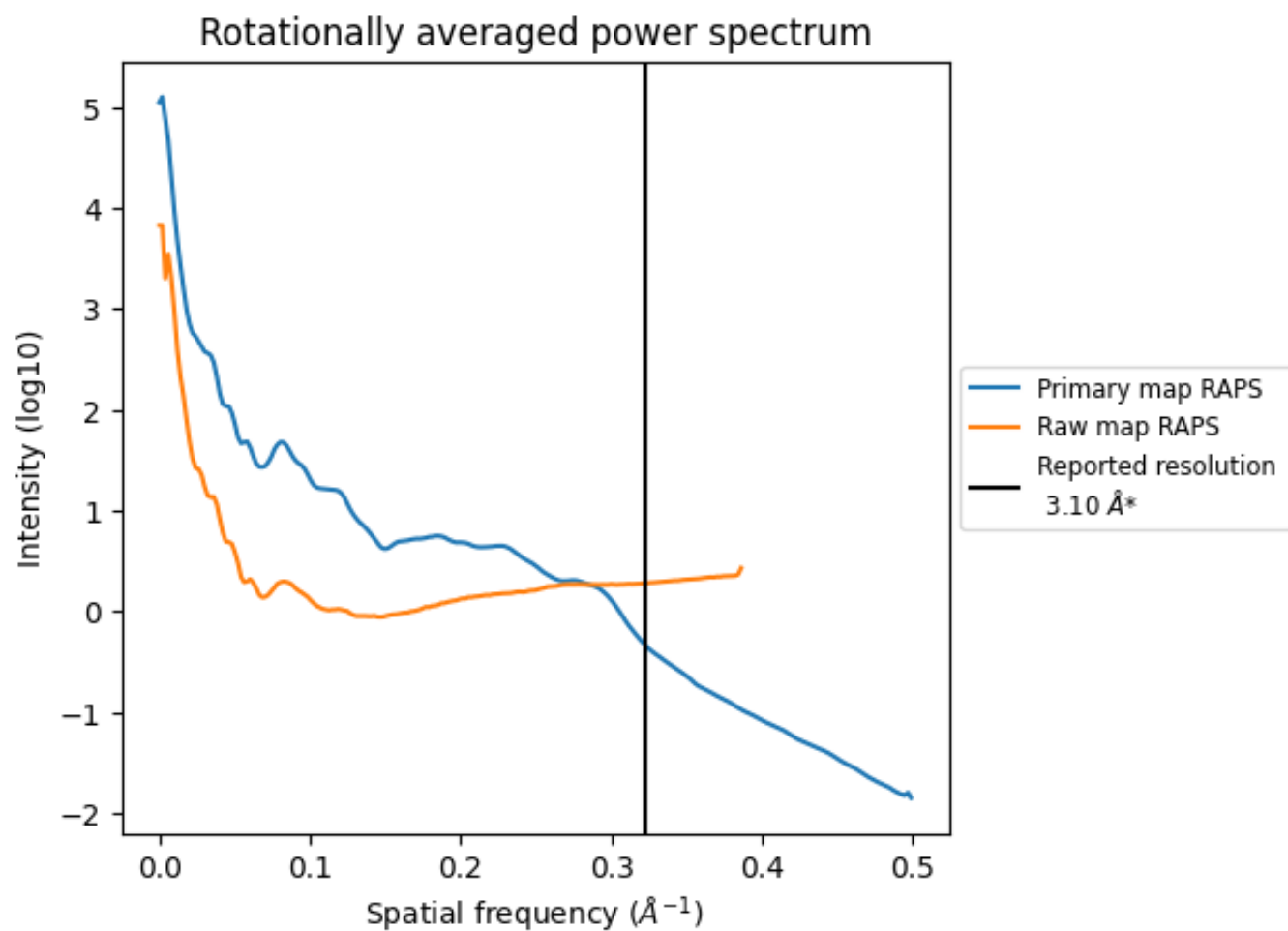
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 106  $\text{nm}^3$ ; this corresponds to an approximate mass of 96 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 ⓘ

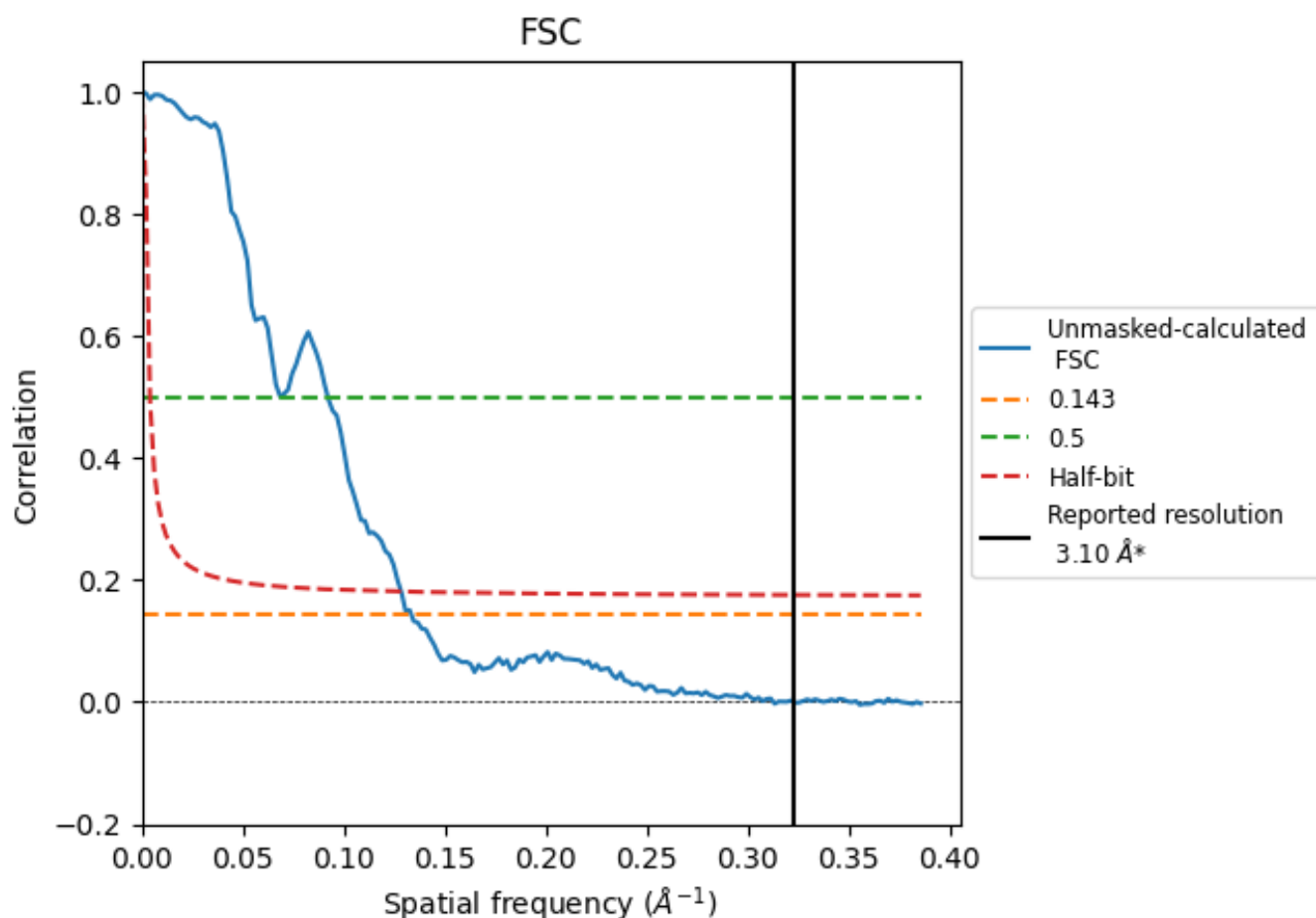


\*Reported resolution corresponds to spatial frequency of 0.323  $\text{\AA}^{-1}$

## 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  $0.323 \text{ \AA}^{-1}$



## 8.2 Resolution estimates [i](#)

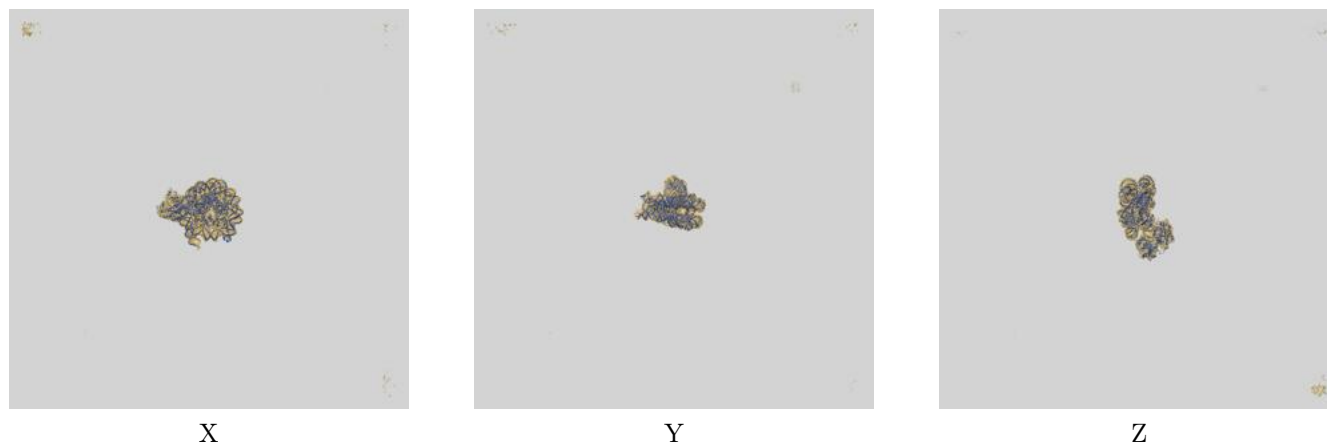
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.50	10.88	7.79

\*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 7.50 differs from the reported value 3.1 by more than 10 %

## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-47422 and PDB model 9E1V. Per-residue inclusion information can be found in section [3](#) on page [7](#).

### 9.1 Map-model overlay [i](#)



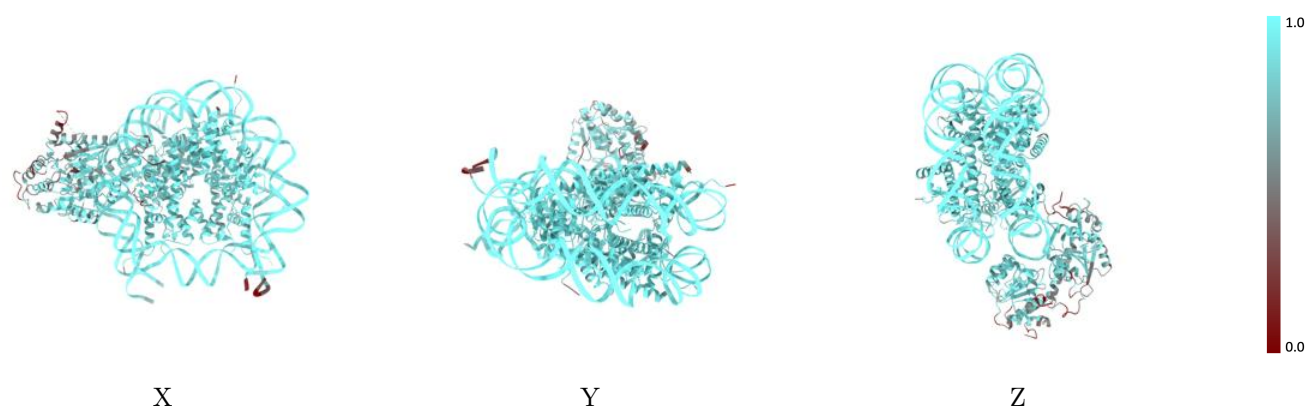
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



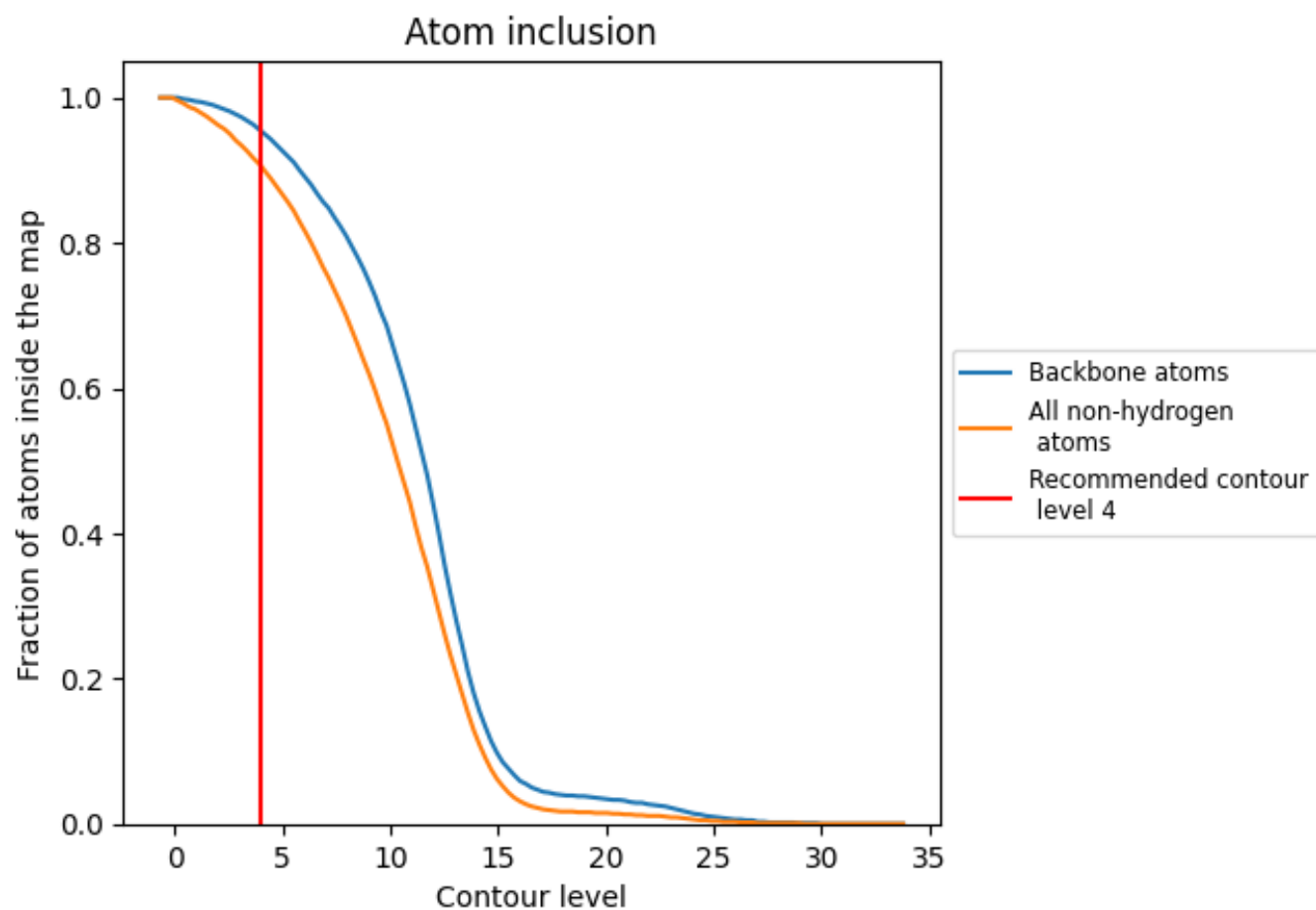
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 95% of all backbone atoms, 91% 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	<div><div></div></div> 0.9060	<div><div></div></div> 0.5860
A	<div><div></div></div> 0.9560	<div><div></div></div> 0.6640
B	<div><div></div></div> 0.9250	<div><div></div></div> 0.6490
C	<div><div></div></div> 0.9590	<div><div></div></div> 0.6660
D	<div><div></div></div> 0.9600	<div><div></div></div> 0.6680
E	<div><div></div></div> 0.9720	<div><div></div></div> 0.6740
F	<div><div></div></div> 0.9630	<div><div></div></div> 0.6620
G	<div><div></div></div> 0.9640	<div><div></div></div> 0.6610
H	<div><div></div></div> 0.9540	<div><div></div></div> 0.6630
I	<div><div></div></div> 0.9600	<div><div></div></div> 0.5870
J	<div><div></div></div> 0.9640	<div><div></div></div> 0.5930
W	<div><div></div></div> 0.7250	<div><div></div></div> 0.4500

1.0

0.0

<0.0