



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 07:21 AM UTC

PDB ID : 6JM9 / pdb_00006jm9
EMDB ID : EMD-9843
Title : cryo-EM structure of DOT1L bound to unmodified nucleosome
Authors : Jang, S.; Song, J.J.
Deposited on : 2019-03-07
Resolution : 7.30 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

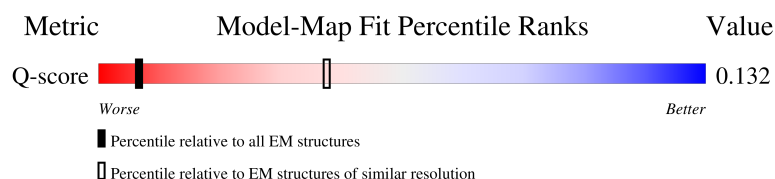
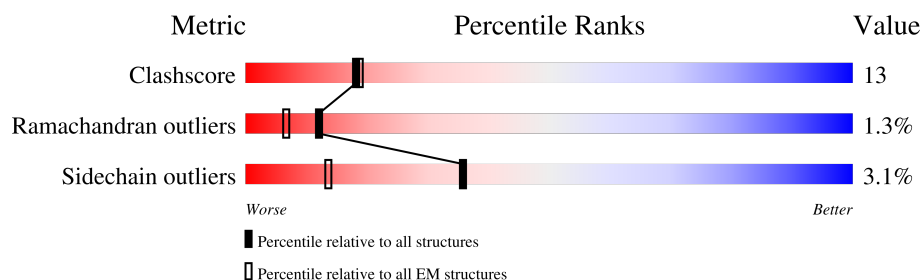
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.30 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	436 (6.80 - 7.80)

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	I	123	
2	J	123	
3	A	98	
3	E	98	

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Mol	Chain	Length	Quality of chain
4	B	87	
4	F	87	
5	C	107	
5	G	107	
6	D	94	
6	H	94	
7	X	328	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
8	SAM	X	500	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 13827 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 DNA chain called DNA strand I.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	I	123	Total	C	N	O	P	0	0
			2517	1203	453	738	123		

- Molecule 2 is a DNA chain called DNA strand J.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	J	123	Total	C	N	O	P	0	0
			2526	1206	459	738	123		

- Molecule 3 is a protein called Histone H3.2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	98	Total	C	N	O	S	0	0
			807	508	156	140	3		
3	E	98	Total	C	N	O	S	0	0
			807	508	156	140	3		

- Molecule 4 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	82	Total	C	N	O	S	0	0
			653	412	127	113	1		
4	F	87	Total	C	N	O	S	0	0
			703	442	142	118	1		

- Molecule 5 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	C	107	Total	C	N	O	0	0
			825	520	161	144		
5	G	106	Total	C	N	O	0	0
			818	516	160	142		

- Molecule 6 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	94	Total	C	N	O	S	0	0
			736	463	132	139	2		
6	H	94	Total	C	N	O	S	0	0
			736	463	132	139	2		

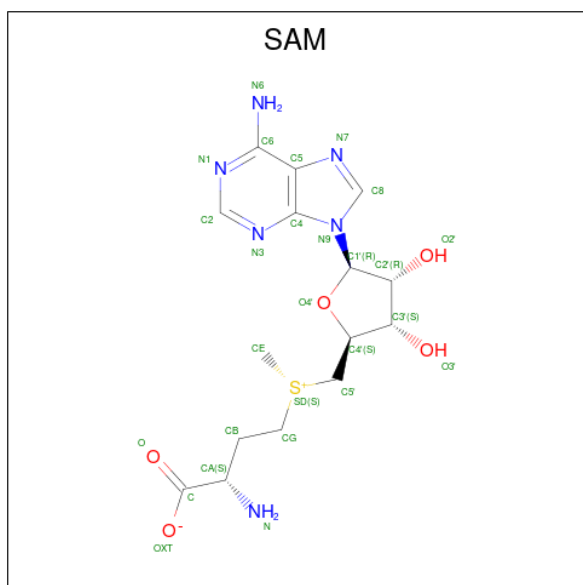
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	29	THR	-	expression tag	UNP P02281
H	29	THR	-	expression tag	UNP P02281

- Molecule 7 is a protein called Histone-lysine N-methyltransferase, H3 lysine-79 specific.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	X	328	Total	C	N	O	S	0	0
			2672	1706	455	499	12		

- Molecule 8 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: $C_{15}H_{22}N_6O_5S$).

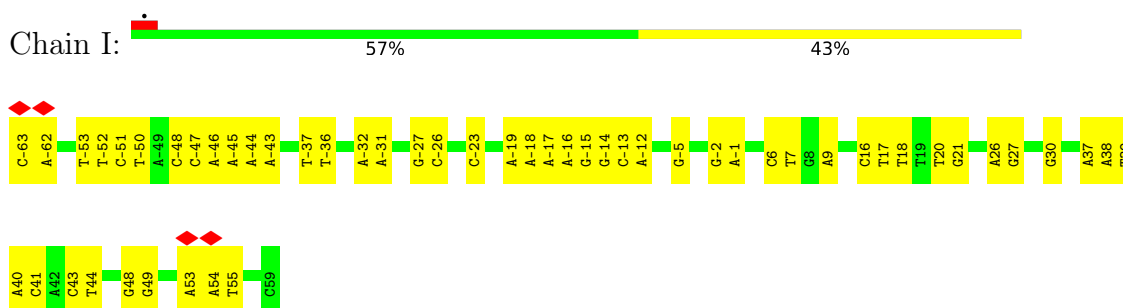


Mol	Chain	Residues	Atoms					AltConf
8	X	1	Total	C	N	O	S	0
			27	15	6	5	1	

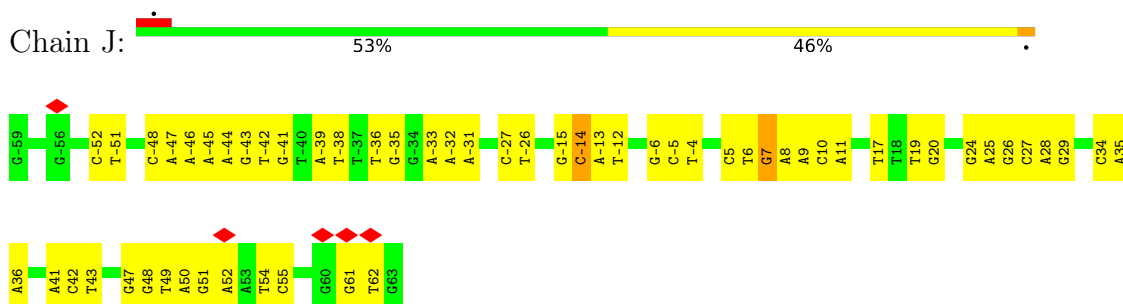
3 Residue-property plots [i](#)

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.

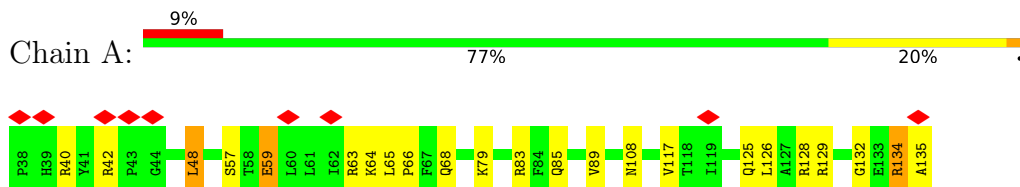
- Molecule 1: DNA strand I



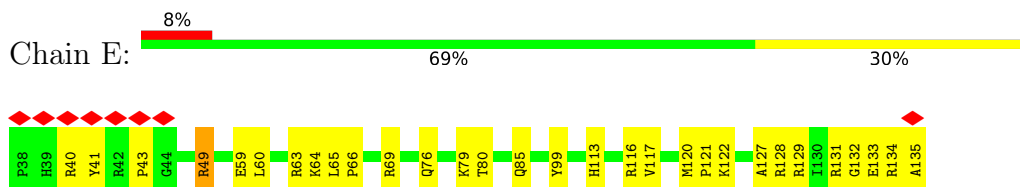
- Molecule 2: DNA strand J



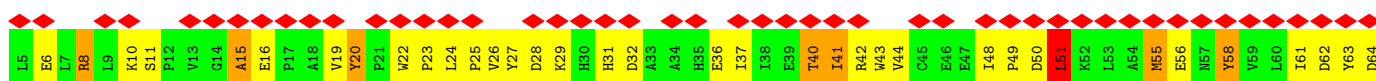
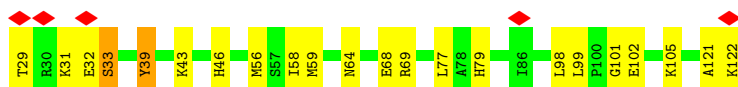
- Molecule 3: Histone H3.2

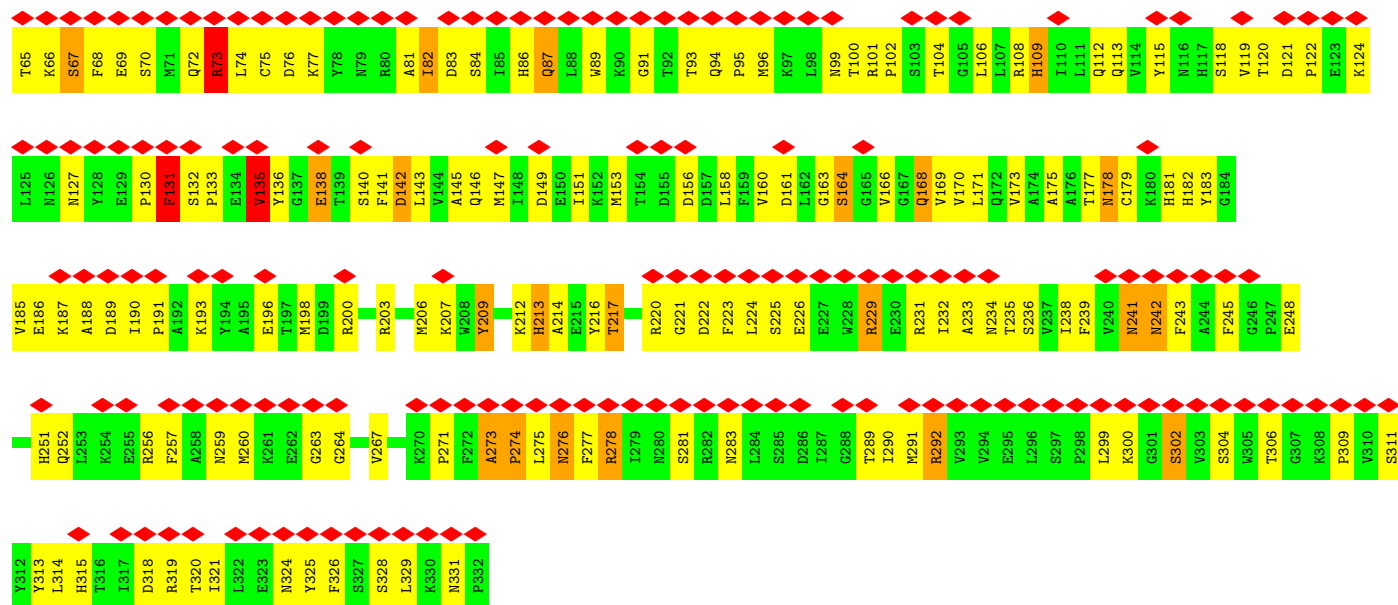


- Molecule 3: Histone H3.2



- Molecule 4: Histone H4





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	21229	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	37.28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.087	Depositor
Minimum map value	-0.023	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.021	Depositor
Map size ($\text{\AA}$)	211.99998, 211.99998, 211.99998	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

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

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	I	0.29	0/2822	0.66	0/4352
2	J	0.31	0/2834	0.68	2/4373 (0.0%)
3	A	0.67	0/819	1.04	4/1097 (0.4%)
3	E	0.86	0/819	1.07	4/1097 (0.4%)
4	B	0.72	0/660	1.03	4/883 (0.5%)
4	F	0.88	0/711	1.04	2/948 (0.2%)
5	C	0.82	0/835	1.00	1/1127 (0.1%)
5	G	0.65	0/828	0.91	1/1117 (0.1%)
6	D	0.84	1/747 (0.1%)	1.04	1/1004 (0.1%)
6	H	0.71	1/747 (0.1%)	0.93	1/1004 (0.1%)
7	X	2.29	96/2742 (3.5%)	2.47	213/3718 (5.7%)
All	All	1.13	98/14564 (0.7%)	1.30	233/20720 (1.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	J	0	2
6	D	0	1
7	X	0	9
All	All	0	12

All (98) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	X	264	GLY	CA-C	10.52	1.61	1.52
7	X	311	SER	CA-C	-9.63	1.41	1.52
7	X	179	CYS	CA-C	-9.29	1.41	1.52
7	X	200	ARG	CD-NE	8.93	1.58	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	X	26	VAL	CA-C	-8.36	1.42	1.52
7	X	109	HIS	ND1-CE1	8.26	1.40	1.32
7	X	275	LEU	CA-C	-8.08	1.42	1.52
7	X	132	SER	N-CA	-8.05	1.38	1.45
7	X	20	TYR	C-N	7.95	1.43	1.33
7	X	43	TRP	CA-C	-7.89	1.42	1.52
7	X	40	THR	N-CA	-7.77	1.37	1.46
7	X	8	ARG	NE-CZ	7.72	1.41	1.33
7	X	181	HIS	ND1-CE1	7.71	1.40	1.32
7	X	6	GLU	C-N	7.63	1.43	1.33
7	X	51	LEU	CA-C	-7.53	1.43	1.52
7	X	16	GLU	CA-C	7.41	1.60	1.52
7	X	182	HIS	ND1-CE1	7.33	1.39	1.32
7	X	171	LEU	N-CA	-7.27	1.37	1.46
7	X	58	TYR	CA-C	-7.24	1.43	1.53
7	X	221	GLY	CA-C	-7.23	1.41	1.51
7	X	276	ASN	CA-CB	7.19	1.62	1.52
7	X	86	HIS	N-CA	-7.18	1.37	1.46
7	X	229	ARG	NE-CZ	7.08	1.40	1.33
7	X	31	HIS	ND1-CE1	7.04	1.39	1.32
7	X	41	ILE	N-CA	-7.02	1.38	1.46
7	X	277	PHE	CA-CB	6.90	1.62	1.53
7	X	32	ASP	CA-C	-6.58	1.44	1.52
7	X	220	ARG	C-N	6.53	1.43	1.33
7	X	239	PHE	N-CA	-6.36	1.38	1.46
7	X	289	THR	C-N	6.33	1.41	1.33
7	X	27	TYR	C-N	6.30	1.41	1.33
7	X	189	ASP	C-N	6.30	1.40	1.33
7	X	212	LYS	CA-C	-6.25	1.44	1.52
7	X	178	ASN	N-CA	6.24	1.53	1.45
7	X	263	GLY	C-N	6.24	1.41	1.33
7	X	168	GLN	C-N	6.23	1.41	1.33
7	X	209	TYR	C-N	6.22	1.42	1.33
7	X	108	ARG	CD-NE	6.20	1.54	1.46
7	X	74	LEU	C-N	6.18	1.41	1.33
7	X	151	ILE	CA-C	-6.16	1.46	1.52
7	X	65	THR	CA-C	-6.16	1.44	1.52
7	X	138	GLU	CA-CB	6.07	1.63	1.53
7	X	213	HIS	ND1-CE1	5.98	1.38	1.32
7	X	299	LEU	CA-C	-5.97	1.45	1.52
7	X	291	MET	N-CA	5.96	1.53	1.46
7	X	251	HIS	CG-ND1	5.92	1.44	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	X	213	HIS	C-N	5.87	1.42	1.33
7	X	127	ASN	N-CA	-5.83	1.39	1.46
7	X	319	ARG	CZ-NH1	5.80	1.40	1.32
7	X	127	ASN	CA-CB	5.79	1.60	1.53
7	X	119	VAL	CA-C	-5.76	1.46	1.52
7	X	203	ARG	C-N	5.70	1.41	1.33
7	X	242	ASN	C-N	5.69	1.41	1.33
7	X	25	PRO	N-CD	-5.67	1.39	1.47
6	H	56	MET	SD-CE	5.66	1.93	1.79
7	X	149	ASP	CA-CB	5.65	1.62	1.53
7	X	76	ASP	CA-CB	5.63	1.62	1.53
7	X	173	VAL	CA-CB	5.62	1.61	1.54
7	X	315	HIS	C-N	5.62	1.41	1.33
7	X	118	SER	N-CA	-5.57	1.39	1.46
7	X	131	PHE	C-N	5.56	1.39	1.33
7	X	234	ASN	C-N	5.54	1.41	1.33
7	X	158	LEU	C-N	5.54	1.40	1.33
7	X	22	TRP	CA-C	5.54	1.58	1.52
7	X	66	LYS	C-N	5.53	1.41	1.33
7	X	73	ARG	CD-NE	5.53	1.53	1.46
7	X	231	ARG	CA-C	-5.50	1.45	1.52
7	X	115	TYR	CA-CB	5.49	1.61	1.53
7	X	99	ASN	CA-C	-5.48	1.45	1.52
7	X	142	ASP	CA-C	-5.46	1.45	1.52
7	X	309	PRO	CA-CB	-5.46	1.46	1.53
7	X	207	LYS	CA-C	-5.38	1.45	1.52
7	X	256	ARG	C-N	5.38	1.41	1.33
7	X	183	TYR	N-CA	5.32	1.52	1.45
7	X	15	ALA	C-O	-5.32	1.17	1.24
7	X	248	GLU	C-N	5.30	1.40	1.33
7	X	112	GLN	C-N	5.29	1.40	1.33
6	D	56	MET	SD-CE	5.27	1.92	1.79
7	X	232	ILE	CA-CB	-5.26	1.48	1.54
7	X	214	ALA	N-CA	-5.23	1.39	1.46
7	X	217	THR	C-N	5.23	1.40	1.33
7	X	135	VAL	CA-C	5.21	1.59	1.52
7	X	74	LEU	C-O	-5.20	1.18	1.24
7	X	260	MET	C-N	5.16	1.40	1.33
7	X	183	TYR	CZ-OH	5.15	1.48	1.38
7	X	42	ARG	CA-CB	5.15	1.61	1.53
7	X	236	SER	C-N	5.15	1.40	1.33
7	X	229	ARG	C-N	5.14	1.41	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	X	19	VAL	C-O	-5.11	1.18	1.24
7	X	156	ASP	CA-C	-5.11	1.46	1.52
7	X	149	ASP	N-CA	-5.10	1.40	1.46
7	X	102	PRO	CA-CB	5.08	1.60	1.53
7	X	42	ARG	CZ-NH2	5.06	1.40	1.33
7	X	164	SER	CA-CB	5.06	1.62	1.53
7	X	75	CYS	C-N	5.05	1.40	1.33
7	X	313	TYR	C-N	5.04	1.40	1.33
7	X	100	THR	N-CA	-5.03	1.40	1.46
7	X	206	MET	CA-CB	5.02	1.61	1.53

All (233) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	X	161	ASP	CA-CB-CG	12.18	124.78	112.60
3	A	64	LYS	N-CA-C	8.54	120.28	110.97
7	X	278	ARG	NE-CZ-NH2	-8.50	111.55	119.20
3	A	117	VAL	N-CA-C	-8.49	105.05	113.20
7	X	94	GLN	CA-C-O	-8.32	112.09	120.66
7	X	131	PHE	CA-CB-CG	-8.20	105.60	113.80
3	E	117	VAL	N-CA-C	-8.08	105.26	113.10
3	A	85	GLN	N-CA-C	-8.08	99.86	110.53
7	X	140	SER	CA-C-N	8.07	131.43	120.54
7	X	140	SER	C-N-CA	8.07	131.43	120.54
7	X	67	SER	CA-C-N	7.87	130.67	120.44
7	X	67	SER	C-N-CA	7.87	130.67	120.44
7	X	259	ASN	CA-CB-CG	-7.86	104.75	112.60
7	X	28	ASP	CA-CB-CG	7.73	120.33	112.60
7	X	49	PRO	CA-C-N	7.71	130.62	120.28
7	X	49	PRO	C-N-CA	7.71	130.62	120.28
7	X	169	VAL	CA-C-N	7.64	130.19	120.56
7	X	169	VAL	C-N-CA	7.64	130.19	120.56
7	X	145	ALA	CA-C-O	-7.64	112.32	120.42
7	X	331	ASN	CA-CB-CG	-7.59	105.01	112.60
7	X	248	GLU	CA-C-N	7.55	130.81	120.46
7	X	248	GLU	C-N-CA	7.55	130.81	120.46
7	X	10	LYS	CA-C-N	7.48	131.12	120.49
7	X	10	LYS	C-N-CA	7.48	131.12	120.49
7	X	300	LYS	N-CA-C	-7.48	97.03	109.07
7	X	84	SER	N-CA-CB	7.41	120.75	110.01
7	X	147	MET	CA-C-N	7.40	130.60	120.46
7	X	147	MET	C-N-CA	7.40	130.60	120.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	X	169	VAL	O-C-N	7.39	129.58	121.90
7	X	239	PHE	N-CA-CB	7.23	121.92	110.57
7	X	321	ILE	CA-C-N	7.18	129.90	120.28
7	X	321	ILE	C-N-CA	7.18	129.90	120.28
7	X	101	ARG	NE-CZ-NH1	7.17	128.67	121.50
3	E	64	LYS	N-CA-C	7.16	118.87	111.14
7	X	149	ASP	N-CA-C	7.08	119.08	111.36
7	X	48	ILE	CA-C-N	7.08	126.61	119.24
7	X	48	ILE	C-N-CA	7.08	126.61	119.24
7	X	257	PHE	CA-CB-CG	-7.08	106.72	113.80
7	X	113	GLN	O-C-N	7.00	129.28	122.07
7	X	44	VAL	O-C-N	6.96	128.90	121.87
7	X	37	ILE	CA-C-N	6.94	129.97	120.46
7	X	37	ILE	C-N-CA	6.94	129.97	120.46
7	X	326	PHE	N-CA-CB	6.94	120.33	110.12
4	B	29	ILE	N-CA-C	-6.89	96.60	107.15
7	X	141	PHE	CA-C-N	6.74	129.31	120.28
7	X	141	PHE	C-N-CA	6.74	129.31	120.28
7	X	22	TRP	CA-C-O	-6.70	113.12	119.55
7	X	260	MET	N-CA-C	6.68	119.92	110.23
6	H	85	THR	N-CA-C	6.62	119.73	109.07
6	D	99	LEU	N-CA-C	6.62	118.40	110.07
7	X	213	HIS	CG-CD2-NE2	6.59	113.79	107.20
7	X	283	ASN	CA-CB-CG	6.57	119.17	112.60
7	X	256	ARG	N-CA-C	-6.55	104.32	112.90
7	X	96	MET	CA-C-N	6.54	130.43	120.82
7	X	96	MET	C-N-CA	6.54	130.43	120.82
7	X	94	GLN	CA-C-N	6.52	126.54	119.89
7	X	94	GLN	C-N-CA	6.52	126.54	119.89
7	X	328	SER	CA-CB-OG	6.52	124.14	111.10
2	J	-14	DC	C5'-C4'-C3'	-6.52	105.12	114.90
7	X	83	ASP	CA-CB-CG	-6.49	106.11	112.60
7	X	193	LYS	O-C-N	6.49	128.75	122.07
7	X	87	GLN	CA-C-N	6.48	129.61	120.28
7	X	87	GLN	C-N-CA	6.48	129.61	120.28
7	X	121	ASP	CA-CB-CG	-6.47	106.13	112.60
7	X	252	GLN	CA-C-N	6.46	129.47	120.29
7	X	252	GLN	C-N-CA	6.46	129.47	120.29
7	X	143	LEU	CA-C-O	6.46	127.35	120.70
7	X	16	GLU	CA-C-N	6.45	127.90	119.84
7	X	16	GLU	C-N-CA	6.45	127.90	119.84
7	X	213	HIS	CE1-NE2-CD2	-6.45	102.56	109.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	X	42	ARG	N-CA-CB	6.42	119.55	110.12
7	X	278	ARG	NE-CZ-NH1	6.42	127.92	121.50
7	X	306	THR	N-CA-C	-6.39	105.41	113.72
7	X	56	GLU	CA-CB-CG	-6.37	101.36	114.10
7	X	36	GLU	N-CA-CB	6.34	119.44	110.12
7	X	8	ARG	O-C-N	-6.34	115.89	123.31
7	X	147	MET	CA-C-O	-6.34	114.17	120.82
7	X	89	TRP	CA-C-N	6.33	131.28	120.72
7	X	89	TRP	C-N-CA	6.33	131.28	120.72
7	X	82	ILE	O-C-N	6.32	128.00	121.87
7	X	106	LEU	O-C-N	-6.28	115.31	122.09
7	X	95	PRO	N-CA-CB	6.25	108.57	103.32
7	X	309	PRO	CA-C-O	-6.25	114.21	121.34
7	X	229	ARG	NE-CZ-NH1	-6.23	115.27	121.50
7	X	120	THR	N-CA-C	-6.21	105.29	112.92
7	X	324	ASN	OD1-CG-ND2	-6.21	116.39	122.60
5	C	118	LYS	CB-CA-C	-6.11	108.52	115.79
7	X	135	VAL	CA-C-N	6.10	129.77	121.05
7	X	135	VAL	C-N-CA	6.10	129.77	121.05
7	X	302	SER	O-C-N	-6.06	114.53	122.59
7	X	216	TYR	CB-CG-CD1	-6.04	111.74	120.80
7	X	191	PRO	CA-C-N	6.03	128.86	120.29
7	X	191	PRO	C-N-CA	6.03	128.86	120.29
7	X	143	LEU	CA-C-N	6.03	128.98	120.42
7	X	143	LEU	C-N-CA	6.03	128.98	120.42
7	X	55	MET	N-CA-C	-6.02	105.43	112.89
7	X	91	GLY	CA-C-N	6.00	128.32	120.28
7	X	91	GLY	C-N-CA	6.00	128.32	120.28
7	X	278	ARG	CA-C-N	5.98	128.66	120.35
7	X	278	ARG	C-N-CA	5.98	128.66	120.35
7	X	207	LYS	CA-C-N	5.93	128.50	120.38
7	X	207	LYS	C-N-CA	5.93	128.50	120.38
7	X	58	TYR	CB-CA-C	-5.89	108.78	115.79
7	X	190	ILE	CA-C-N	5.88	125.43	119.19
7	X	190	ILE	C-N-CA	5.88	125.43	119.19
7	X	170	VAL	CA-C-N	5.88	128.08	120.44
7	X	170	VAL	C-N-CA	5.88	128.08	120.44
4	F	92	ARG	CB-CA-C	-5.86	101.07	110.79
7	X	73	ARG	CA-C-N	5.85	128.40	120.44
7	X	73	ARG	C-N-CA	5.85	128.40	120.44
7	X	11	SER	CA-C-N	5.85	125.39	119.19
7	X	11	SER	C-N-CA	5.85	125.39	119.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	X	241	ASN	CA-CB-CG	5.82	118.42	112.60
3	E	85	GLN	N-CA-C	-5.82	101.67	110.28
7	X	86	HIS	CB-CA-C	-5.82	99.86	110.63
7	X	304	SER	O-C-N	5.82	130.33	122.59
7	X	267	VAL	CA-C-O	5.80	126.74	120.53
7	X	318	ASP	CA-CB-CG	-5.80	106.80	112.60
7	X	50	ASP	CA-C-N	5.80	128.33	120.44
7	X	50	ASP	C-N-CA	5.80	128.33	120.44
4	B	30	THR	N-CA-C	5.79	118.37	110.55
7	X	50	ASP	O-C-N	-5.79	115.98	122.12
7	X	70	SER	N-CA-CB	5.78	118.71	110.16
7	X	290	ILE	O-C-N	-5.77	115.80	122.09
7	X	160	VAL	O-C-N	5.77	129.30	123.07
7	X	36	GLU	CA-C-O	-5.76	114.44	120.55
7	X	238	ILE	CA-CB-CG1	5.74	120.17	110.40
7	X	86	HIS	CE1-NE2-CD2	-5.74	103.26	109.00
7	X	99	ASN	N-CA-C	-5.72	105.03	113.61
7	X	72	GLN	CA-C-O	-5.72	113.64	120.10
7	X	206	MET	N-CA-C	5.72	117.51	111.28
7	X	292	ARG	N-CA-C	-5.70	100.38	109.96
7	X	84	SER	O-C-N	5.70	127.94	122.07
7	X	320	THR	CA-C-N	5.69	127.73	120.56
7	X	320	THR	C-N-CA	5.69	127.73	120.56
7	X	271	PRO	N-CA-C	-5.69	100.75	112.47
4	B	46	ILE	N-CA-C	5.68	116.30	108.12
7	X	198	MET	CA-C-N	5.67	127.82	120.44
7	X	198	MET	C-N-CA	5.67	127.82	120.44
7	X	314	LEU	N-CA-C	-5.67	99.27	108.52
3	A	134	ARG	N-CA-C	-5.67	106.91	113.88
7	X	260	MET	N-CA-CB	5.67	118.38	109.83
7	X	86	HIS	ND1-CE1-NE2	5.66	114.06	108.40
4	F	30	THR	N-CA-C	5.65	118.17	110.55
7	X	124	LYS	CB-CG-CD	5.64	124.28	111.30
7	X	233	ALA	N-CA-C	5.64	117.43	111.28
7	X	239	PHE	N-CA-C	-5.64	99.99	109.07
7	X	127	ASN	N-CA-C	-5.63	99.34	108.41
7	X	170	VAL	O-C-N	5.62	127.42	121.91
7	X	42	ARG	NE-CZ-NH2	-5.62	114.14	119.20
7	X	64	ASP	CA-C-N	5.60	127.78	120.28
7	X	64	ASP	C-N-CA	5.60	127.78	120.28
7	X	32	ASP	N-CA-CB	5.59	121.42	111.69
7	X	188	ALA	O-C-N	-5.59	116.50	123.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	X	130	PRO	CA-C-O	-5.58	115.19	121.43
7	X	277	PHE	CA-C-O	5.55	126.93	120.49
7	X	69	GLU	CA-C-N	5.55	128.16	120.29
7	X	69	GLU	C-N-CA	5.55	128.16	120.29
7	X	122	PRO	CA-C-O	-5.55	111.48	118.86
7	X	238	ILE	O-C-N	-5.54	117.28	123.26
7	X	274	PRO	CA-C-N	5.53	128.48	120.79
7	X	274	PRO	C-N-CA	5.53	128.48	120.79
7	X	231	ARG	CA-C-N	5.53	127.64	120.56
7	X	231	ARG	C-N-CA	5.53	127.64	120.56
7	X	196	GLU	CA-C-N	5.51	128.11	120.29
7	X	196	GLU	C-N-CA	5.51	128.11	120.29
7	X	216	TYR	CB-CG-CD2	5.51	129.06	120.80
7	X	302	SER	CA-C-N	5.50	131.88	121.97
7	X	302	SER	C-N-CA	5.50	131.88	121.97
7	X	328	SER	N-CA-CB	5.50	118.68	110.22
7	X	109	HIS	CB-CG-CD2	-5.49	124.06	131.20
7	X	158	LEU	CA-C-N	-5.49	115.43	123.00
7	X	158	LEU	C-N-CA	-5.49	115.43	123.00
7	X	42	ARG	NE-CZ-NH1	5.48	126.98	121.50
7	X	108	ARG	CA-C-N	5.46	127.60	120.28
7	X	108	ARG	C-N-CA	5.46	127.60	120.28
7	X	318	ASP	N-CA-CB	5.46	119.06	110.71
7	X	229	ARG	CD-NE-CZ	-5.45	116.78	124.40
7	X	273	ALA	CA-C-N	5.44	125.44	119.89
7	X	273	ALA	C-N-CA	5.44	125.44	119.89
7	X	104	THR	N-CA-C	5.41	117.18	111.28
7	X	101	ARG	NE-CZ-NH2	-5.38	114.35	119.20
7	X	6	GLU	N-CA-C	-5.38	101.32	108.74
7	X	166	VAL	CA-C-O	5.37	126.25	119.48
7	X	329	LEU	CA-C-N	5.35	131.77	121.18
7	X	329	LEU	C-N-CA	5.35	131.77	121.18
7	X	75	CYS	N-CA-CB	5.31	117.71	110.01
7	X	27	TYR	N-CA-C	-5.29	106.50	113.12
7	X	130	PRO	O-C-N	5.28	129.69	122.99
7	X	181	HIS	CE1-NE2-CD2	-5.28	103.72	109.00
7	X	145	ALA	O-C-N	5.27	128.16	122.15
5	G	70	ALA	N-CA-C	-5.26	105.55	111.28
4	B	43	VAL	N-CA-C	5.25	115.83	108.89
7	X	68	PHE	CB-CG-CD2	5.24	129.61	120.70
7	X	86	HIS	O-C-N	-5.24	116.09	122.22
7	X	106	LEU	CA-C-N	5.23	127.29	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	X	106	LEU	C-N-CA	5.23	127.29	120.28
7	X	28	ASP	N-CA-C	-5.22	100.52	107.88
7	X	24	LEU	CA-C-O	-5.21	114.33	119.49
7	X	281	SER	CA-C-N	5.21	131.50	121.54
7	X	281	SER	C-N-CA	5.21	131.50	121.54
7	X	93	THR	N-CA-C	-5.21	102.77	110.48
3	E	41	TYR	N-CA-C	-5.19	102.79	110.48
7	X	189	ASP	N-CA-C	5.19	116.62	111.07
7	X	231	ARG	NE-CZ-NH1	5.19	126.69	121.50
7	X	328	SER	CA-C-O	-5.19	114.24	120.10
7	X	325	TYR	O-C-N	5.18	127.40	122.07
7	X	76	ASP	CA-C-N	5.17	127.21	120.28
7	X	76	ASP	C-N-CA	5.17	127.21	120.28
7	X	189	ASP	CA-CB-CG	5.17	117.77	112.60
7	X	91	GLY	CA-C-O	-5.16	116.06	121.53
7	X	226	GLU	CA-C-O	-5.16	115.08	120.55
7	X	251	HIS	ND1-CE1-NE2	5.14	113.54	108.40
7	X	82	ILE	CA-C-O	-5.14	115.60	120.95
7	X	156	ASP	CA-CB-CG	5.14	117.74	112.60
7	X	81	ALA	CA-C-N	5.13	127.49	120.46
7	X	81	ALA	C-N-CA	5.13	127.49	120.46
7	X	225	SER	O-C-N	-5.13	117.93	123.42
7	X	16	GLU	CA-C-O	-5.12	114.63	119.55
7	X	309	PRO	N-CA-CB	5.12	107.86	103.31
7	X	44	VAL	CA-CB-CG1	5.11	119.08	110.40
7	X	83	ASP	N-CA-CB	5.10	117.62	110.12
7	X	319	ARG	NH1-CZ-NH2	-5.10	112.67	119.30
7	X	326	PHE	CA-C-N	5.10	127.11	120.28
7	X	326	PHE	C-N-CA	5.10	127.11	120.28
7	X	169	VAL	CA-C-O	-5.05	115.44	121.05
7	X	292	ARG	NE-CZ-NH2	-5.05	114.65	119.20
7	X	183	TYR	N-CA-C	5.04	117.34	109.52
2	J	7	DG	C5'-C4'-C3'	-5.04	107.35	114.90
7	X	23	PRO	CA-C-N	5.01	129.28	121.17
7	X	23	PRO	C-N-CA	5.01	129.28	121.17
7	X	68	PHE	N-CA-CB	5.00	117.26	110.01
7	X	153	MET	N-CA-CB	5.00	118.42	110.57

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	D	39	TYR	Sidechain
2	J	-12	DT	Sidechain
2	J	-6	DG	Sidechain
7	X	136	TYR	Sidechain
7	X	20	TYR	Sidechain
7	X	209	TYR	Sidechain
7	X	229	ARG	Sidechain
7	X	292	ARG	Sidechain
7	X	58	TYR	Sidechain
7	X	63	TYR	Sidechain
7	X	73	ARG	Sidechain
7	X	8	ARG	Sidechain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I	2517	0	1390	55	0
2	J	2526	0	1390	63	0
3	A	807	0	844	37	0
3	E	807	0	844	38	0
4	B	653	0	696	19	0
4	F	703	0	755	20	0
5	C	825	0	884	26	0
5	G	818	0	877	23	0
6	D	736	0	760	25	0
6	H	736	0	760	13	0
7	X	2672	0	2615	94	0
8	X	27	0	16	64	0
All	All	13827	0	11831	339	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 13.

All (339) 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:X:245:PHE:CZ	8:X:500:SAM:H5'1	1.16	1.66
7:X:245:PHE:HZ	8:X:500:SAM:C5'	1.03	1.63
7:X:223:PHE:CD1	8:X:500:SAM:N3	1.74	1.53
7:X:223:PHE:CD2	8:X:500:SAM:C5	1.97	1.45
7:X:241:ASN:ND2	8:X:500:SAM:CE	1.93	1.30
7:X:223:PHE:CG	8:X:500:SAM:C2	2.17	1.26
7:X:223:PHE:CG	8:X:500:SAM:N3	2.03	1.25
7:X:223:PHE:CD2	8:X:500:SAM:C4	2.20	1.24
7:X:223:PHE:CE2	8:X:500:SAM:C5	2.04	1.24
7:X:138:GLU:H	8:X:500:SAM:CA	1.45	1.20
7:X:223:PHE:CG	8:X:500:SAM:C4	2.25	1.19
7:X:224:LEU:HG	8:X:500:SAM:C5	1.65	1.17
7:X:163:GLY:O	8:X:500:SAM:N	1.78	1.16
7:X:224:LEU:HG	8:X:500:SAM:N7	1.61	1.15
7:X:241:ASN:HD21	8:X:500:SAM:HE2	1.08	1.14
7:X:224:LEU:CD1	8:X:500:SAM:N7	2.11	1.13
7:X:241:ASN:ND2	8:X:500:SAM:HE2	1.54	1.13
7:X:138:GLU:H	8:X:500:SAM:HA	1.12	1.13
7:X:245:PHE:CE1	8:X:500:SAM:H5'1	1.83	1.12
6:D:46:HIS:CE1	7:X:278:ARG:HG3	1.84	1.12
2:J:-46:DA:H2''	2:J:-45:DA:H5''	1.27	1.11
6:D:46:HIS:HE1	7:X:278:ARG:HG3	1.01	1.08
7:X:133:PRO:O	8:X:500:SAM:H2'	1.54	1.07
7:X:163:GLY:O	8:X:500:SAM:HG2	1.53	1.07
7:X:223:PHE:CD2	8:X:500:SAM:C6	2.36	1.07
7:X:223:PHE:CE2	8:X:500:SAM:N7	1.97	1.07
7:X:224:LEU:CG	8:X:500:SAM:N7	2.17	1.07
7:X:223:PHE:CD1	8:X:500:SAM:C4	2.19	1.06
7:X:245:PHE:CZ	8:X:500:SAM:C5'	1.93	1.06
4:B:22:LEU:HD22	7:X:29:LYS:HE3	1.06	1.04
3:A:128:ARG:HD3	3:A:134:ARG:HH12	1.22	1.03
7:X:241:ASN:ND2	8:X:500:SAM:HE3	1.70	1.02
7:X:245:PHE:HZ	8:X:500:SAM:H5'2	1.19	1.02
7:X:138:GLU:N	8:X:500:SAM:CA	2.14	1.01
1:I:26:DA:H2''	1:I:27:DG:H5'	1.41	0.99
7:X:223:PHE:CE1	8:X:500:SAM:N3	2.20	0.98
4:F:87:VAL:HG11	4:F:102:GLY:HA3	1.45	0.98
5:C:33:LEU:HD23	5:C:36:LYS:HD3	1.42	0.98
5:G:17:ARG:HH12	5:G:31:HIS:HD2	0.98	0.97
7:X:163:GLY:O	8:X:500:SAM:CG	2.12	0.97
3:E:49:ARG:HG3	3:E:49:ARG:HH11	1.27	0.96
3:A:128:ARG:HH11	3:A:134:ARG:HH12	1.11	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:22:LEU:CD2	7:X:29:LYS:HE3	1.95	0.95
5:C:17:ARG:HH12	5:C:31:HIS:CD2	1.83	0.94
3:A:128:ARG:HH11	3:A:134:ARG:NH1	1.64	0.93
2:J:41:DA:H2''	2:J:42:DC:H5''	1.49	0.93
5:C:17:ARG:HH12	5:C:31:HIS:HD2	0.94	0.93
2:J:26:DG:H2''	2:J:27:DC:C5	2.03	0.93
4:B:22:LEU:HD22	7:X:29:LYS:CE	1.97	0.92
3:E:116:ARG:CZ	3:E:120:MET:HE2	2.01	0.91
5:C:55:LEU:O	5:C:59:THR:HG23	1.72	0.89
5:G:17:ARG:HH12	5:G:31:HIS:CD2	1.89	0.88
3:A:128:ARG:HD3	3:A:134:ARG:NH1	1.89	0.88
2:J:-46:DA:C2'	2:J:-45:DA:H5''	2.03	0.87
6:D:46:HIS:HE1	7:X:278:ARG:CG	1.89	0.85
3:A:128:ARG:NH1	3:A:134:ARG:NH1	2.28	0.82
3:E:120:MET:CE	3:E:122:LYS:HD3	2.08	0.82
7:X:241:ASN:CG	8:X:500:SAM:HE3	2.06	0.81
3:A:129:ARG:HD2	3:A:135:ALA:HB2	1.62	0.81
7:X:138:GLU:H	8:X:500:SAM:C	1.86	0.81
3:A:125:GLN:HG2	3:A:134:ARG:HH21	1.48	0.79
3:E:120:MET:HE3	3:E:122:LYS:HD3	1.62	0.79
7:X:224:LEU:HD11	8:X:500:SAM:N7	1.96	0.79
5:C:17:ARG:NH1	5:C:31:HIS:HD2	1.76	0.79
7:X:224:LEU:CG	8:X:500:SAM:C5	2.56	0.78
7:X:138:GLU:N	8:X:500:SAM:C	2.23	0.78
2:J:42:DC:H2'	2:J:43:DT:H71	1.64	0.78
5:C:71:ARG:HH21	7:X:276:ASN:HB3	1.49	0.78
2:J:49:DT:OP1	6:D:31:LYS:HG2	1.84	0.77
7:X:163:GLY:HA2	7:X:223:PHE:CE1	2.20	0.77
2:J:5:DC:H2''	2:J:6:DT:C7	2.14	0.77
7:X:163:GLY:C	8:X:500:SAM:HN2	1.92	0.77
2:J:41:DA:C2'	2:J:42:DC:H5''	2.15	0.76
7:X:245:PHE:CZ	8:X:500:SAM:H5'2	2.01	0.76
1:I:17:DT:OP2	3:E:69:ARG:NH2	2.20	0.75
1:I:26:DA:C2'	1:I:27:DG:H5'	2.17	0.74
7:X:241:ASN:HD22	8:X:500:SAM:CG	2.01	0.73
2:J:17:DT:OP1	3:A:66:PRO:HG3	1.89	0.73
2:J:-46:DA:H2''	2:J:-45:DA:C5'	2.13	0.73
2:J:-46:DA:H4'	6:H:30:ARG:HD3	1.72	0.72
5:G:17:ARG:NH1	5:G:31:HIS:HD2	1.82	0.72
2:J:28:DA:H2''	2:J:29:DG:C8	2.25	0.71
7:X:224:LEU:HD12	8:X:500:SAM:N7	2.04	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:105:LYS:NZ	7:X:131:PHE:CE1	2.58	0.70
1:I:-45:DA:H2''	1:I:-44:DA:H5''	1.73	0.70
1:I:-48:DC:H2''	1:I:-47:DC:H5'	1.74	0.70
1:I:17:DT:P	3:E:69:ARG:HH22	2.14	0.70
2:J:-39:DA:H2''	2:J:-38:DT:OP2	1.92	0.70
2:J:5:DC:H2''	2:J:6:DT:H71	1.74	0.69
2:J:-48:DC:H1'	2:J:-47:DA:C5	2.29	0.68
2:J:24:DG:H2''	2:J:25:DA:N7	2.09	0.68
5:G:84:GLN:OE1	5:G:88:ARG:HD2	1.94	0.67
7:X:223:PHE:CD2	7:X:224:LEU:HG	2.28	0.67
5:C:32:ARG:HH22	6:D:32:GLU:CD	2.03	0.66
4:F:87:VAL:CG1	4:F:102:GLY:HA3	2.24	0.66
1:I:-45:DA:C2'	1:I:-44:DA:H5''	2.25	0.65
5:G:15:LYS:HG3	5:G:19:SER:OG	1.97	0.65
1:I:20:DT:H2''	1:I:21:DG:H5'	1.78	0.64
5:C:118:LYS:C	5:C:119:LYS:HD3	2.21	0.64
6:D:46:HIS:CE1	7:X:278:ARG:CG	2.71	0.64
2:J:-14:DC:H2''	2:J:-13:DA:C8	2.32	0.64
7:X:241:ASN:HD22	8:X:500:SAM:CB	2.10	0.64
3:A:129:ARG:HA	3:A:134:ARG:HB2	1.79	0.64
2:J:54:DT:H2''	2:J:55:DC:OP2	1.98	0.63
3:E:76:GLN:NE2	4:F:19:ARG:NH1	2.47	0.63
2:J:-43:DG:O3'	5:G:14:ALA:HB1	1.98	0.63
1:I:-13:DC:H5''	3:A:63:ARG:CZ	2.29	0.62
7:X:223:PHE:CG	8:X:500:SAM:C5	2.68	0.62
2:J:10:DC:H2''	2:J:11:DA:C8	2.34	0.62
3:E:76:GLN:HE22	4:F:19:ARG:NH1	1.96	0.62
1:I:39:DT:OP2	5:G:35:ARG:NH2	2.31	0.62
7:X:223:PHE:CG	8:X:500:SAM:C6	2.83	0.62
2:J:34:DC:H2''	2:J:35:DA:N7	2.15	0.62
7:X:223:PHE:HE2	8:X:500:SAM:N7	1.87	0.62
7:X:241:ASN:HD21	8:X:500:SAM:CE	1.80	0.62
7:X:138:GLU:N	8:X:500:SAM:HA	1.95	0.62
1:I:-13:DC:H5''	3:A:63:ARG:NH1	2.14	0.61
2:J:-27:DC:H2''	2:J:-26:DT:H71	1.81	0.61
3:E:134:ARG:O	3:E:135:ALA:OXT	2.18	0.61
7:X:223:PHE:CG	8:X:500:SAM:N1	2.60	0.61
7:X:163:GLY:O	8:X:500:SAM:HG1	1.98	0.61
3:E:49:ARG:HH11	3:E:49:ARG:CG	2.03	0.61
2:J:41:DA:H2''	2:J:42:DC:C5'	2.25	0.61
7:X:187:LYS:HB2	8:X:500:SAM:C4	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:49:ARG:HG3	3:E:49:ARG:NH1	2.06	0.60
7:X:186:GLU:OE1	8:X:500:SAM:O3'	2.19	0.60
6:D:105:LYS:NZ	7:X:131:PHE:CZ	2.65	0.60
3:A:125:GLN:HG2	3:A:134:ARG:NH2	2.16	0.60
2:J:-32:DA:H1'	2:J:-31:DA:O5'	2.03	0.59
3:A:128:ARG:NH1	3:A:134:ARG:HH12	1.88	0.59
7:X:163:GLY:CA	7:X:223:PHE:CE1	2.86	0.59
7:X:223:PHE:CE2	7:X:224:LEU:HG	2.38	0.59
1:I:-37:DT:H2''	1:I:-36:DT:OP2	2.03	0.58
3:A:134:ARG:HH11	3:A:134:ARG:HG3	1.68	0.58
3:E:120:MET:HE1	3:E:122:LYS:HD3	1.83	0.58
3:E:132:GLY:HA2	3:E:135:ALA:HB2	1.86	0.57
1:I:-14:DG:H2''	1:I:-13:DC:C6	2.38	0.57
5:C:29:ARG:NH2	6:D:33:SER:O	2.38	0.57
5:G:84:GLN:CD	5:G:88:ARG:HD2	2.29	0.57
7:X:222:ASP:OD1	8:X:500:SAM:C6	2.51	0.57
1:I:-23:DC:H1'	3:A:83:ARG:HH21	1.69	0.57
1:I:-16:DA:H2''	1:I:-15:DG:C8	2.39	0.57
6:D:121:ALA:O	6:D:122:LYS:HB2	2.05	0.57
6:H:122:LYS:HG3	6:H:122:LYS:OXT	2.04	0.57
7:X:241:ASN:HD22	8:X:500:SAM:CE	2.12	0.57
3:E:128:ARG:HE	3:E:134:ARG:HH21	1.52	0.57
2:J:-5:DC:H5'	3:E:43:PRO:HG2	1.85	0.57
3:E:129:ARG:HG3	3:E:135:ALA:HA	1.86	0.57
7:X:187:LYS:HB3	8:X:500:SAM:O2'	2.04	0.57
3:E:116:ARG:NH2	3:E:120:MET:HE2	2.20	0.56
2:J:19:DT:H2''	2:J:20:DG:C8	2.41	0.56
5:C:119:LYS:HD3	5:C:119:LYS:N	2.19	0.56
6:D:39:TYR:CZ	6:D:43:LYS:HE2	2.41	0.55
2:J:25:DA:H1'	3:A:83:ARG:NH1	2.21	0.55
3:A:126:LEU:HD22	3:E:113:HIS:CG	2.41	0.55
3:E:49:ARG:CG	3:E:49:ARG:NH1	2.66	0.55
1:I:18:DT:H5''	3:E:63:ARG:HH12	1.70	0.55
1:I:-63:DC:H1'	1:I:-62:DA:C8	2.41	0.55
1:I:-45:DA:H2''	1:I:-44:DA:C5'	2.37	0.55
7:X:241:ASN:HD22	8:X:500:SAM:HG1	1.71	0.54
5:C:62:ILE:CG2	6:D:59:MET:HE1	2.38	0.54
2:J:5:DC:H2''	2:J:6:DT:C5	2.42	0.54
2:J:-44:DA:OP2	5:G:32:ARG:HD3	2.08	0.54
1:I:-46:DA:H2	2:J:47:DG:N2	2.05	0.54
5:G:102:ILE:HG23	6:H:58:ILE:HD13	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:57:SER:HB2	3:A:59:GLU:OE2	2.07	0.53
4:B:31:LYS:HB3	4:B:32:PRO:HD3	1.90	0.53
2:J:-42:DT:H5'	5:G:14:ALA:HB2	1.90	0.53
3:A:68:GLN:HE21	3:A:89:VAL:HG21	1.74	0.53
7:X:41:ILE:HG21	7:X:55:MET:HE2	1.91	0.53
1:I:41:DC:H4'	1:I:41:DC:OP1	2.08	0.53
1:I:-53:DT:H2''	1:I:-52:DT:OP2	2.08	0.52
2:J:29:DG:OP1	6:H:29:THR:HG22	2.09	0.52
5:C:62:ILE:HG21	6:D:59:MET:HE1	1.90	0.52
4:F:87:VAL:HG11	4:F:102:GLY:CA	2.29	0.52
3:E:116:ARG:NH1	3:E:120:MET:HE2	2.25	0.52
4:B:75:HIS:CE1	6:D:77:LEU:HD21	2.44	0.52
7:X:223:PHE:CD1	8:X:500:SAM:C2	2.57	0.52
1:I:40:DA:H2''	1:I:41:DC:O5'	2.10	0.52
5:C:37:GLY:HA3	5:C:39:TYR:CE2	2.45	0.52
1:I:49:DG:H5'	6:H:30:ARG:NH2	2.26	0.51
1:I:54:DA:H2''	1:I:55:DT:OP2	2.09	0.51
2:J:6:DT:H2''	2:J:7:DG:C8	2.46	0.51
5:G:35:ARG:HG2	5:G:35:ARG:HH11	1.76	0.51
5:G:69:ALA:O	5:G:73:ASN:ND2	2.37	0.51
4:B:84:MET:HE1	4:B:102:GLY:CA	2.40	0.51
2:J:61:DG:H2''	2:J:62:DT:OP2	2.11	0.51
3:A:79:LYS:HD2	4:B:74:GLU:CG	2.41	0.51
7:X:62:ASP:C	7:X:73:ARG:HH22	2.19	0.51
5:C:25:PHE:CZ	5:C:59:THR:HG21	2.46	0.50
1:I:-52:DT:H2''	1:I:-51:DC:O5'	2.11	0.50
3:A:79:LYS:HD2	4:B:74:GLU:CD	2.36	0.50
1:I:-12:DA:OP1	4:B:23:ARG:NH2	2.45	0.49
3:E:76:GLN:HE22	4:F:19:ARG:HH11	1.58	0.49
4:F:59:LYS:O	4:F:63:GLU:HG3	2.12	0.49
2:J:48:DG:H2''	2:J:49:DT:H5'	1.94	0.49
3:A:79:LYS:HD2	4:B:74:GLU:HG2	1.95	0.49
4:F:17:ARG:HB3	4:F:18:HIS:CD2	2.47	0.49
1:I:-45:DA:H1'	1:I:-44:DA:H5''	1.94	0.49
2:J:51:DG:H2''	2:J:52:DA:OP2	2.12	0.48
7:X:223:PHE:HD2	8:X:500:SAM:C6	2.18	0.48
1:I:41:DC:H42	2:J:-41:DG:H1	1.61	0.48
4:B:30:THR:HB	4:B:32:PRO:HD2	1.95	0.48
3:E:128:ARG:HH21	3:E:134:ARG:NH2	2.11	0.48
2:J:7:DG:H2''	2:J:8:DA:C8	2.48	0.48
3:A:57:SER:CB	3:A:59:GLU:OE2	2.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:128:ARG:HD2	3:E:133:GLU:OE1	2.13	0.48
2:J:-36:DT:H2''	2:J:-35:DG:N7	2.28	0.48
3:A:63:ARG:O	3:A:66:PRO:HD2	2.13	0.48
3:A:65:LEU:HB3	3:A:66:PRO:HD3	1.95	0.48
4:B:22:LEU:O	4:B:23:ARG:HB2	2.13	0.48
5:C:32:ARG:NH1	6:D:32:GLU:OE2	2.44	0.48
6:D:64:ASN:O	6:D:68:GLU:HG3	2.13	0.48
1:I:-47:DC:H1'	1:I:-46:DA:C5	2.49	0.48
1:I:-13:DC:OP1	3:A:63:ARG:HD2	2.14	0.48
1:I:48:DG:H3'	6:H:36:ILE:HD11	1.95	0.47
1:I:-5:DG:OP1	3:A:42:ARG:CZ	2.61	0.47
3:A:132:GLY:HA2	3:A:135:ALA:HB3	1.95	0.47
2:J:9:DA:N3	3:A:40:ARG:NH2	2.56	0.47
5:C:71:ARG:HH22	7:X:276:ASN:HD22	1.61	0.47
3:E:65:LEU:HB3	3:E:66:PRO:HD3	1.95	0.47
6:D:39:TYR:CE2	6:D:43:LYS:HE2	2.50	0.47
1:I:53:DA:H1'	1:I:54:DA:H5'	1.96	0.47
2:J:-15:DG:H2''	2:J:-14:DC:O5'	2.15	0.47
5:C:80:PRO:HG3	6:D:58:ILE:HD12	1.96	0.47
5:G:84:GLN:O	5:G:88:ARG:HG2	2.14	0.47
3:A:48:LEU:CD2	5:G:117:PRO:HD3	2.45	0.47
1:I:-46:DA:C2	2:J:47:DG:N2	2.83	0.46
2:J:8:DA:OP2	4:B:35:ARG:NH2	2.44	0.46
3:A:129:ARG:CD	3:A:135:ALA:HB2	2.41	0.46
2:J:-27:DC:H2''	2:J:-26:DT:C7	2.45	0.46
7:X:164:SER:O	8:X:500:SAM:HA	2.16	0.46
2:J:-46:DA:H4'	6:H:30:ARG:CD	2.44	0.46
2:J:42:DC:H2''	2:J:43:DT:O5'	2.15	0.46
3:E:128:ARG:HB2	3:E:134:ARG:HE	1.81	0.46
1:I:-47:DC:H1'	1:I:-46:DA:C4	2.51	0.46
7:X:245:PHE:CZ	8:X:500:SAM:C4'	2.91	0.46
2:J:-33:DA:C6	2:J:-32:DA:N6	2.84	0.46
6:D:79:HIS:CE1	5:G:38:ASN:OD1	2.69	0.46
1:I:-44:DA:H5'	1:I:-44:DA:H8	1.80	0.46
4:F:30:THR:CB	4:F:32:PRO:HD2	2.45	0.46
6:H:29:THR:HG23	6:H:29:THR:O	2.16	0.46
3:E:120:MET:HE3	3:E:122:LYS:CD	2.41	0.45
1:I:18:DT:OP1	3:E:63:ARG:NH1	2.48	0.45
1:I:9:DA:N3	3:E:40:ARG:NH2	2.61	0.45
1:I:43:DC:C2'	1:I:44:DT:H72	2.46	0.45
4:F:30:THR:OG1	4:F:32:PRO:HD2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:X:273:ALA:HB1	7:X:274:PRO:HD2	1.98	0.45
2:J:35:DA:C6	2:J:36:DA:C6	3.03	0.45
6:H:43:LYS:HD3	6:H:43:LYS:HA	1.61	0.45
7:X:135:VAL:O	8:X:500:SAM:SD	2.75	0.45
1:I:-19:DA:H2''	1:I:-18:DA:C8	2.51	0.45
5:G:37:GLY:HA3	5:G:39:TYR:CE2	2.51	0.45
2:J:-43:DG:H5''	5:G:16:THR:HA	1.98	0.45
4:B:24:ASP:O	4:B:27:GLN:HB2	2.17	0.45
5:C:119:LYS:O	5:C:120:THR:HB	2.17	0.45
6:D:69:ARG:HD2	6:D:98:LEU:HD11	1.99	0.45
5:G:35:ARG:HG2	5:G:35:ARG:NH1	2.32	0.44
7:X:164:SER:HA	8:X:500:SAM:N	2.32	0.44
5:C:71:ARG:HE	7:X:278:ARG:HD3	1.81	0.44
4:F:59:LYS:NZ	4:F:63:GLU:OE2	2.34	0.44
7:X:163:GLY:HA2	7:X:223:PHE:CD1	2.52	0.44
1:I:30:DG:OP1	6:D:29:THR:HG22	2.17	0.44
1:I:39:DT:H2''	1:I:40:DA:O5'	2.17	0.44
1:I:37:DA:H2''	1:I:38:DA:OP2	2.18	0.44
4:F:19:ARG:NH2	4:F:22:LEU:HD11	2.33	0.44
4:F:19:ARG:HH22	4:F:22:LEU:HD11	1.83	0.44
4:B:52:GLU:OE2	4:B:55:ARG:NH1	2.49	0.44
4:B:59:LYS:O	4:B:63:GLU:HG3	2.18	0.44
5:C:33:LEU:HA	5:C:36:LYS:HG2	2.00	0.44
1:I:-18:DA:H2''	1:I:-17:DA:C8	2.53	0.43
1:I:16:DC:H2''	1:I:17:DT:H71	2.00	0.43
6:D:102:GLU:OE2	6:D:105:LYS:HD2	2.18	0.43
2:J:28:DA:H2''	2:J:29:DG:H8	1.77	0.43
5:C:47:ALA:N	5:C:48:PRO:HD2	2.33	0.43
3:E:116:ARG:CZ	3:E:120:MET:CE	2.87	0.43
6:H:102:GLU:OE1	6:H:106:HIS:CE1	2.71	0.43
4:F:18:HIS:O	4:F:19:ARG:HB2	2.19	0.43
5:C:71:ARG:NH2	7:X:276:ASN:HB3	2.26	0.43
1:I:-2:DG:H1'	1:I:-1:DA:C8	2.54	0.43
2:J:-32:DA:H4'	2:J:-31:DA:OP1	2.18	0.43
3:E:79:LYS:HG3	4:F:74:GLU:OE2	2.18	0.43
7:X:87:GLN:NE2	7:X:87:GLN:HA	2.33	0.43
2:J:-5:DC:C5'	3:E:43:PRO:HG2	2.48	0.43
2:J:-45:DA:H2''	2:J:-44:DA:C8	2.53	0.43
5:C:25:PHE:HZ	5:C:59:THR:HG21	1.83	0.43
6:D:29:THR:O	6:D:29:THR:HG23	2.19	0.43
1:I:-43:DA:OP2	5:C:32:ARG:HD3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:7:DG:H5'	4:B:46:ILE:O	2.19	0.43
2:J:26:DG:H5'	4:B:79:LYS:HD2	2.01	0.43
5:C:79:ILE:HG12	5:C:82:HIS:CE1	2.54	0.43
3:A:128:ARG:HB2	3:A:134:ARG:NH1	2.34	0.43
6:D:105:LYS:HB2	6:D:105:LYS:HE3	1.81	0.43
7:X:40:THR:HA	7:X:109:HIS:CE1	2.53	0.43
1:I:-18:DA:H2''	1:I:-17:DA:N7	2.34	0.42
6:H:102:GLU:HG3	6:H:106:HIS:CE1	2.54	0.42
7:X:163:GLY:N	7:X:223:PHE:CD1	2.87	0.42
2:J:-32:DA:C1'	2:J:-31:DA:O5'	2.66	0.42
4:F:31:LYS:HE3	4:F:35:ARG:HH22	1.84	0.42
7:X:163:GLY:HA2	7:X:223:PHE:HE1	1.77	0.42
7:X:187:LYS:HB2	8:X:500:SAM:N3	2.34	0.42
3:E:76:GLN:NE2	4:F:19:ARG:HH12	2.17	0.42
5:C:71:ARG:HD3	7:X:278:ARG:CZ	2.49	0.42
2:J:24:DG:H2''	2:J:25:DA:C8	2.53	0.42
3:E:79:LYS:HD3	3:E:80:THR:N	2.35	0.42
7:X:163:GLY:CA	7:X:223:PHE:CD1	3.03	0.42
3:E:127:ALA:O	3:E:131:ARG:HG3	2.19	0.42
2:J:-52:DC:H2''	2:J:-51:DT:OP2	2.19	0.42
3:A:48:LEU:HD21	5:G:117:PRO:HD3	2.01	0.42
4:B:84:MET:HE1	4:B:102:GLY:HA3	2.01	0.42
5:G:64:GLU:OE1	6:H:45:VAL:HG13	2.19	0.41
1:I:-45:DA:C1'	1:I:-44:DA:H5''	2.49	0.41
2:J:-47:DA:H2''	2:J:-46:DA:OP2	2.19	0.41
7:X:186:GLU:OE2	8:X:500:SAM:O3'	2.38	0.41
1:I:-27:DG:H2''	1:I:-26:DC:C6	2.55	0.41
4:F:65:VAL:HG22	4:F:93:GLN:OE1	2.19	0.41
7:X:51:LEU:HD11	7:X:82:ILE:HD13	2.01	0.41
7:X:175:ALA:HA	7:X:213:HIS:HA	2.02	0.41
1:I:18:DT:H5''	3:E:63:ARG:NH1	2.36	0.41
2:J:-5:DC:H2''	2:J:-4:DT:H71	2.02	0.41
3:A:128:ARG:CD	3:A:134:ARG:NH1	2.71	0.41
3:A:108:ASN:HD21	5:G:115:LEU:HD11	1.85	0.41
2:J:-42:DT:C5'	5:G:14:ALA:HB2	2.51	0.41
2:J:49:DT:H1'	2:J:50:DA:C8	2.56	0.41
1:I:-50:DT:H6	1:I:-50:DT:H2'	1.74	0.41
2:J:-32:DA:H1'	2:J:-31:DA:C5'	2.50	0.41
3:E:99:TYR:OH	3:E:133:GLU:OE1	2.33	0.41
4:F:30:THR:HB	4:F:32:PRO:HD2	2.02	0.41
7:X:223:PHE:CD2	7:X:223:PHE:C	2.99	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:30:DG:OP1	6:D:29:THR:CG2	2.69	0.41
6:H:29:THR:O	6:H:30:ARG:C	2.64	0.41
4:F:31:LYS:HE3	4:F:35:ARG:NH2	2.36	0.40
7:X:164:SER:CA	8:X:500:SAM:HN2	2.34	0.40
7:X:186:GLU:CD	8:X:500:SAM:O3'	2.64	0.40
1:I:6:DC:H2''	1:I:7:DT:C6	2.56	0.40
3:A:134:ARG:HH11	3:A:134:ARG:CG	2.34	0.40
3:E:60:LEU:HD23	3:E:60:LEU:HA	1.87	0.40
1:I:-32:DA:H2''	1:I:-31:DA:O5'	2.21	0.40
3:A:125:GLN:CG	3:A:134:ARG:HH21	2.27	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	A	96/98 (98%)	96 (100%)	0	0	100	100
3	E	96/98 (98%)	95 (99%)	1 (1%)	0	100	100
4	B	80/87 (92%)	78 (98%)	0	2 (2%)	4	26
4	F	85/87 (98%)	81 (95%)	1 (1%)	3 (4%)	3	20
5	C	105/107 (98%)	101 (96%)	4 (4%)	0	100	100
5	G	104/107 (97%)	102 (98%)	2 (2%)	0	100	100
6	D	92/94 (98%)	90 (98%)	1 (1%)	1 (1%)	11	46
6	H	92/94 (98%)	88 (96%)	2 (2%)	2 (2%)	5	29
7	X	326/328 (99%)	303 (93%)	17 (5%)	6 (2%)	6	34
All	All	1076/1100 (98%)	1034 (96%)	28 (3%)	14 (1%)	12	42

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	F	19	ARG
7	X	67	SER
4	B	22	LEU
6	D	101	GLY
6	H	101	GLY
7	X	131	PHE
7	X	243	PHE
4	F	20	LYS
4	B	23	ARG
4	F	18	HIS
7	X	15	ALA
7	X	302	SER
6	H	30	ARG
7	X	135	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	85/85 (100%)	83 (98%)	2 (2%)	43	64
3	E	85/85 (100%)	82 (96%)	3 (4%)	32	53
4	B	67/72 (93%)	66 (98%)	1 (2%)	57	72
4	F	72/72 (100%)	72 (100%)	0	100	100
5	C	85/85 (100%)	79 (93%)	6 (7%)	13	35
5	G	84/85 (99%)	83 (99%)	1 (1%)	63	75
6	D	80/80 (100%)	79 (99%)	1 (1%)	61	74
6	H	80/80 (100%)	77 (96%)	3 (4%)	29	50
7	X	294/294 (100%)	282 (96%)	12 (4%)	27	48
All	All	932/938 (99%)	903 (97%)	29 (3%)	36	56

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	48	LEU

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Mol	Chain	Res	Type
3	A	59	GLU
4	B	22	LEU
5	C	29	ARG
5	C	59	THR
5	C	76	THR
5	C	81	ARG
5	C	109	PRO
5	C	119	LYS
6	D	33	SER
3	E	49	ARG
3	E	59	GLU
3	E	121	PRO
5	G	88	ARG
6	H	31	LYS
6	H	33	SER
6	H	103	LEU
7	X	51	LEU
7	X	61	ILE
7	X	77	LYS
7	X	142	ASP
7	X	146	GLN
7	X	168	GLN
7	X	177	THR
7	X	178	ASN
7	X	185	VAL
7	X	217	THR
7	X	235	THR
7	X	242	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	68	GLN
3	A	76	GLN
3	A	108	ASN
4	B	27	GLN
5	C	24	GLN
5	C	31	HIS
6	D	46	HIS
6	D	79	HIS
3	E	68	GLN
3	E	76	GLN

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Mol	Chain	Res	Type
4	F	18	HIS
5	G	31	HIS
6	H	44	GLN
6	H	79	HIS
6	H	106	HIS
7	X	30	HIS
7	X	79	ASN
7	X	87	GLN
7	X	109	HIS
7	X	146	GLN
7	X	168	GLN
7	X	178	ASN
7	X	234	ASN
7	X	241	ASN
7	X	242	ASN
7	X	259	ASN
7	X	276	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	SAM	X	500	-	27,29,29	0.74	0	34,42,42	1.07	2 (5%)

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	SAM	X	500	-	-	2/17/33/33	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	X	500	SAM	O2'-C2'-C3'	3.13	121.84	111.82
8	X	500	SAM	O3'-C3'-C4'	-2.01	105.31	111.08

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	X	500	SAM	N-CA-CB-CG
8	X	500	SAM	C-CA-CB-CG

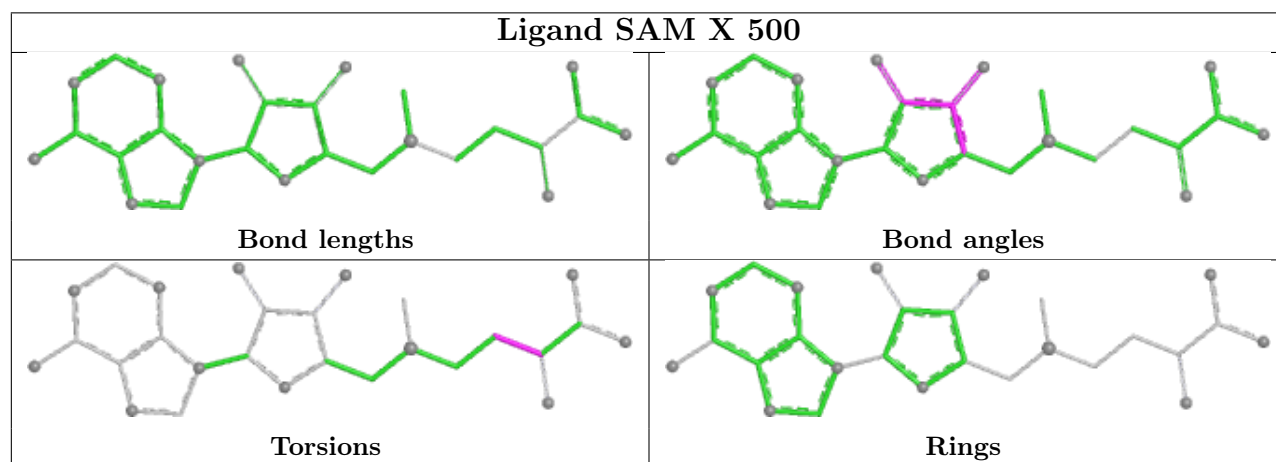
There are no ring outliers.

1 monomer is involved in 64 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	X	500	SAM	64	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.

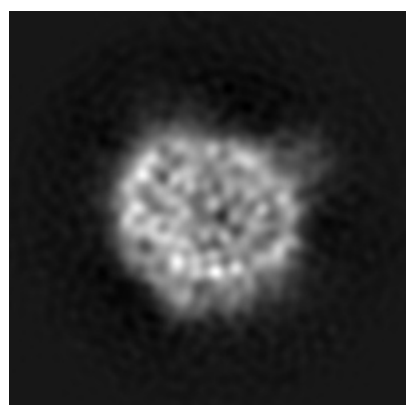
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9843. These allow visual inspection of the internal detail of the map and identification of artifacts.

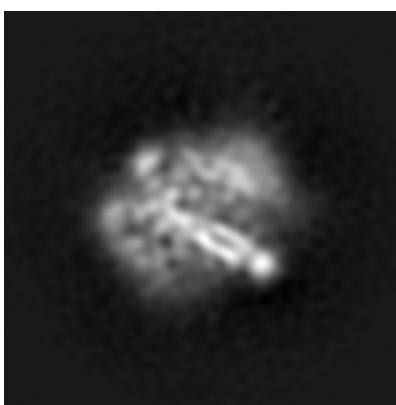
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

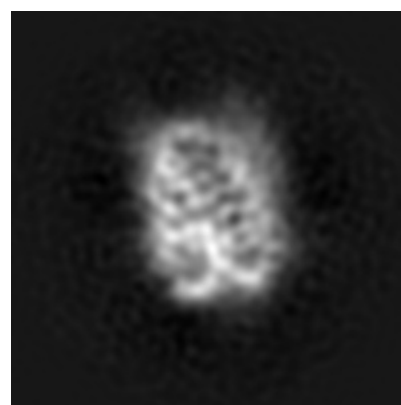
6.1.1 Primary map



X



Y

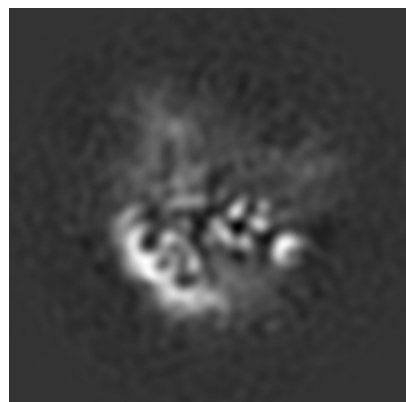


Z

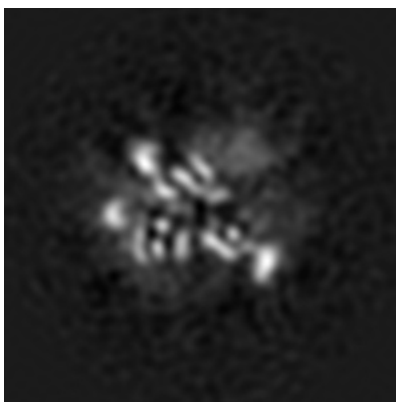
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

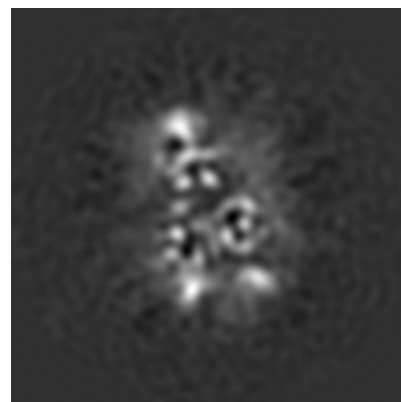
6.2.1 Primary map



X Index: 100



Y Index: 100

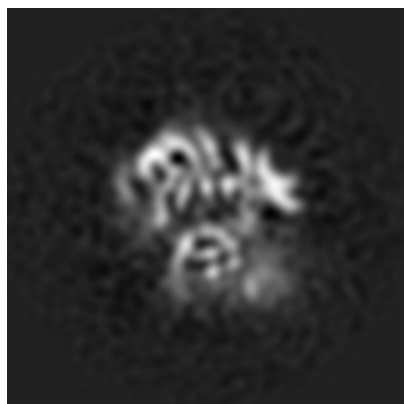


Z Index: 100

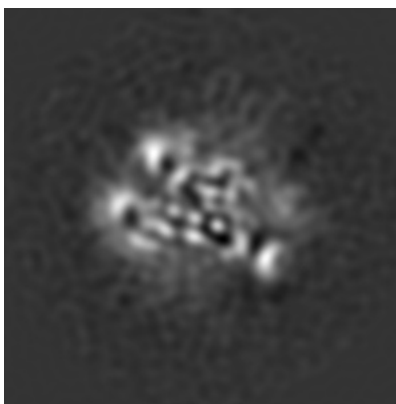
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

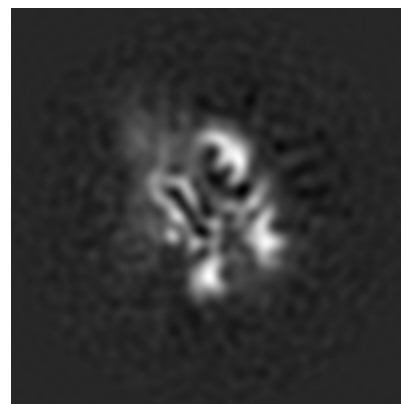
6.3.1 Primary map



X Index: 78



Y Index: 83

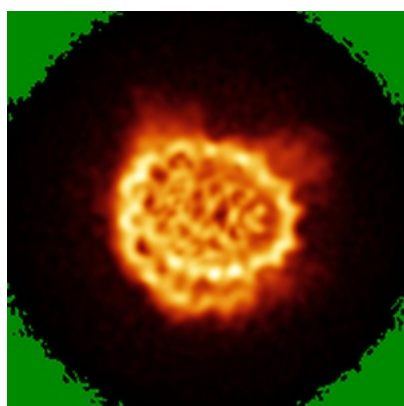


Z Index: 75

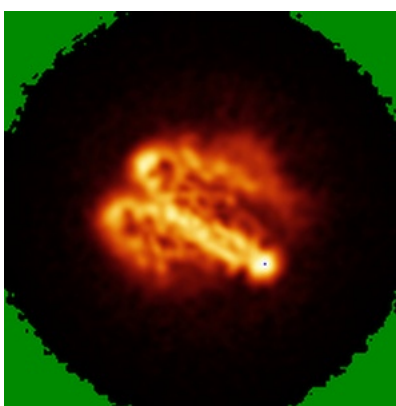
The images above show the largest variance slices of the map in three orthogonal directions.

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

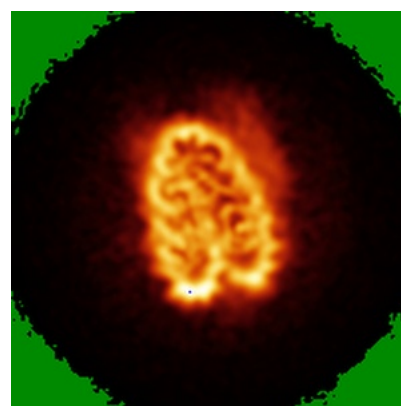
6.4.1 Primary map



X



Y

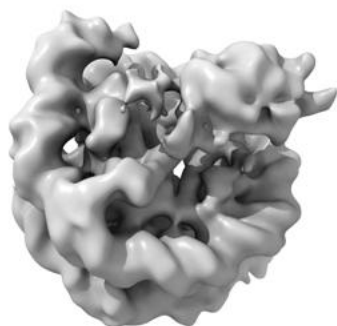


Z

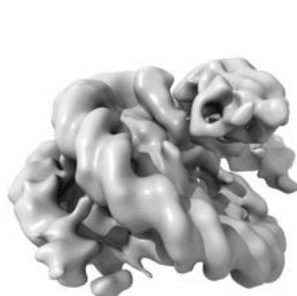
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

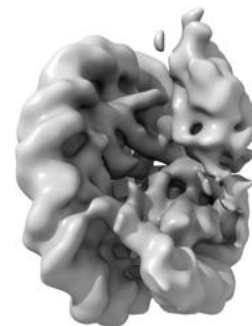
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.021. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

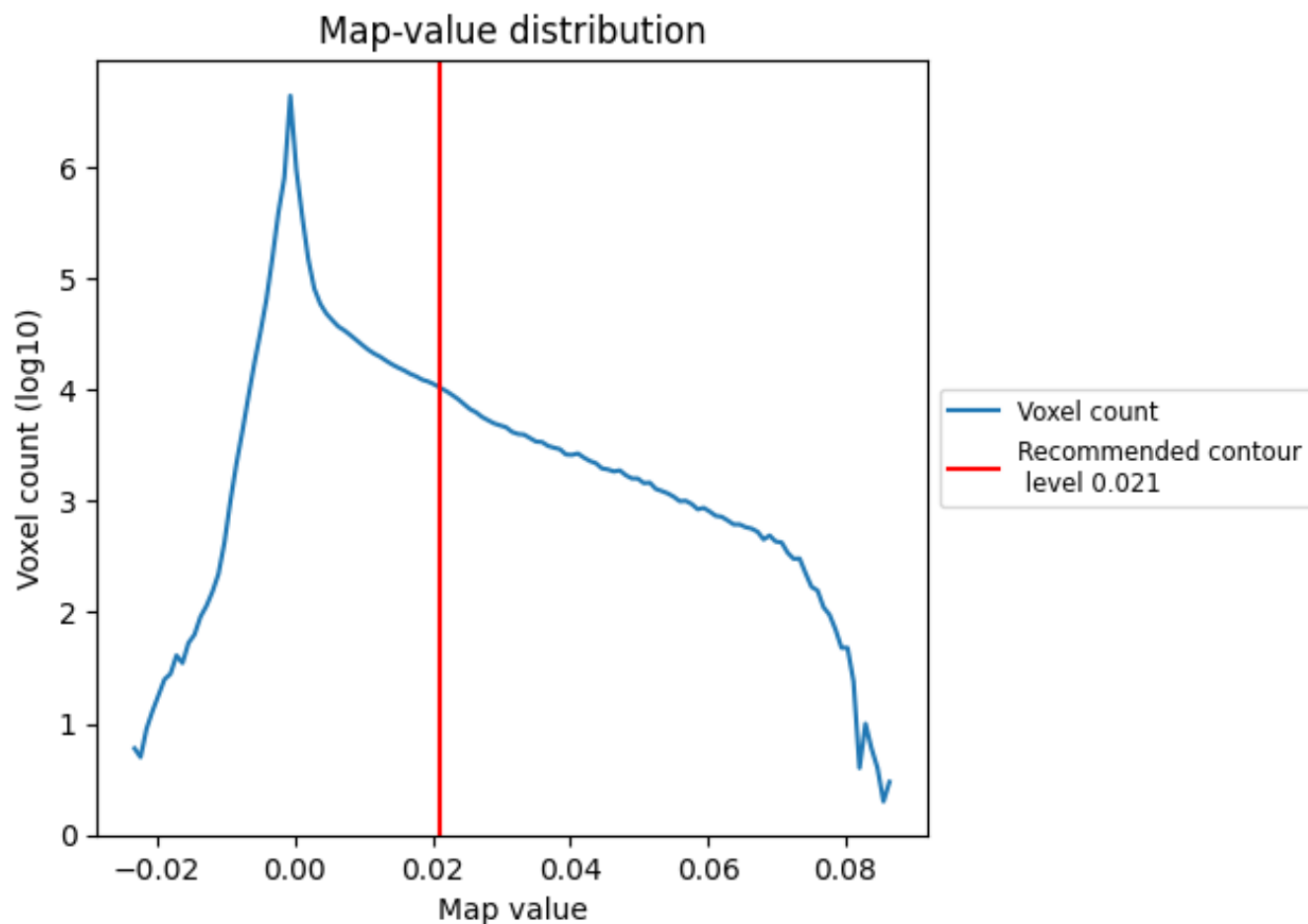
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

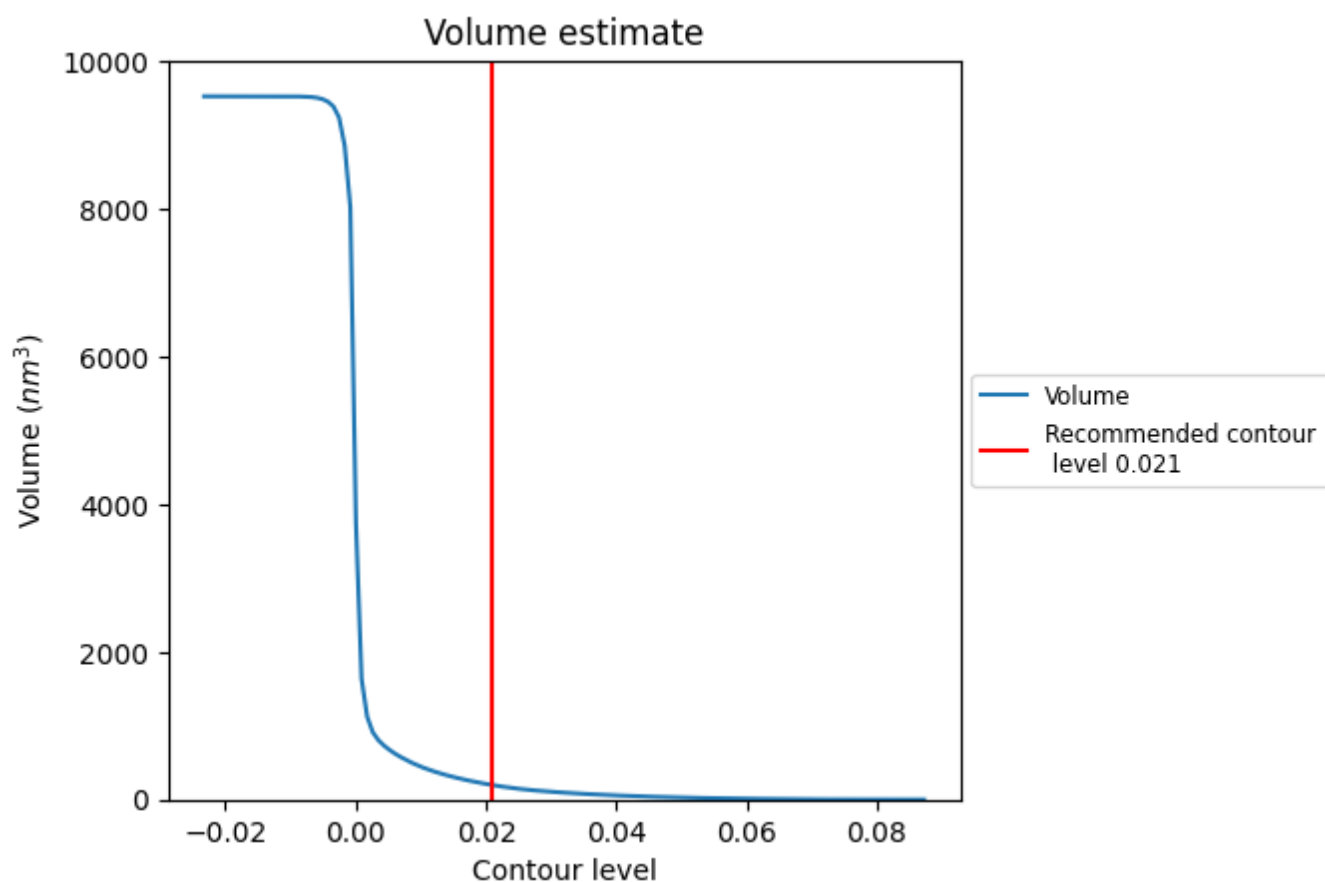
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

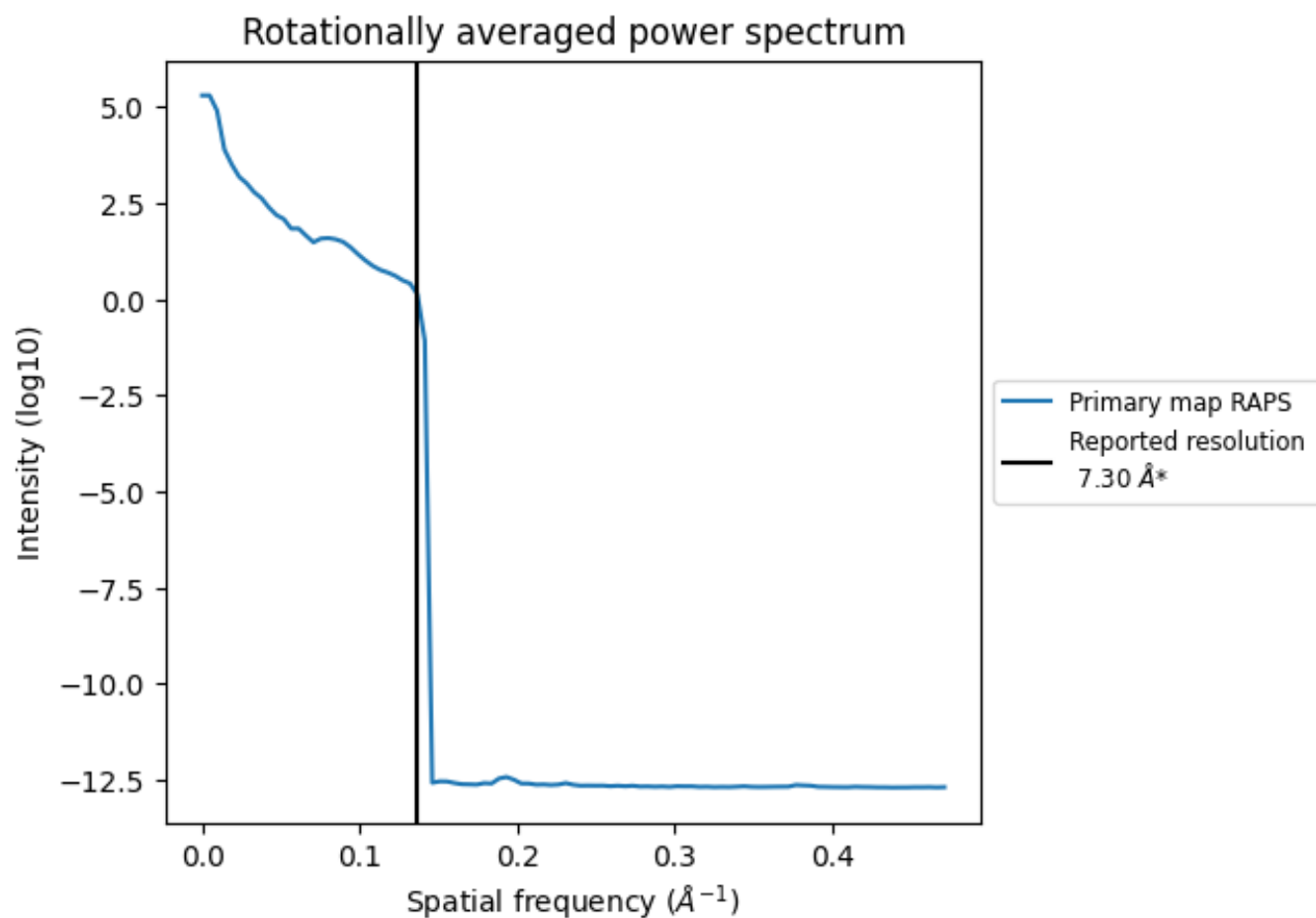
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 197 nm³; this corresponds to an approximate mass of 178 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 ⓘ

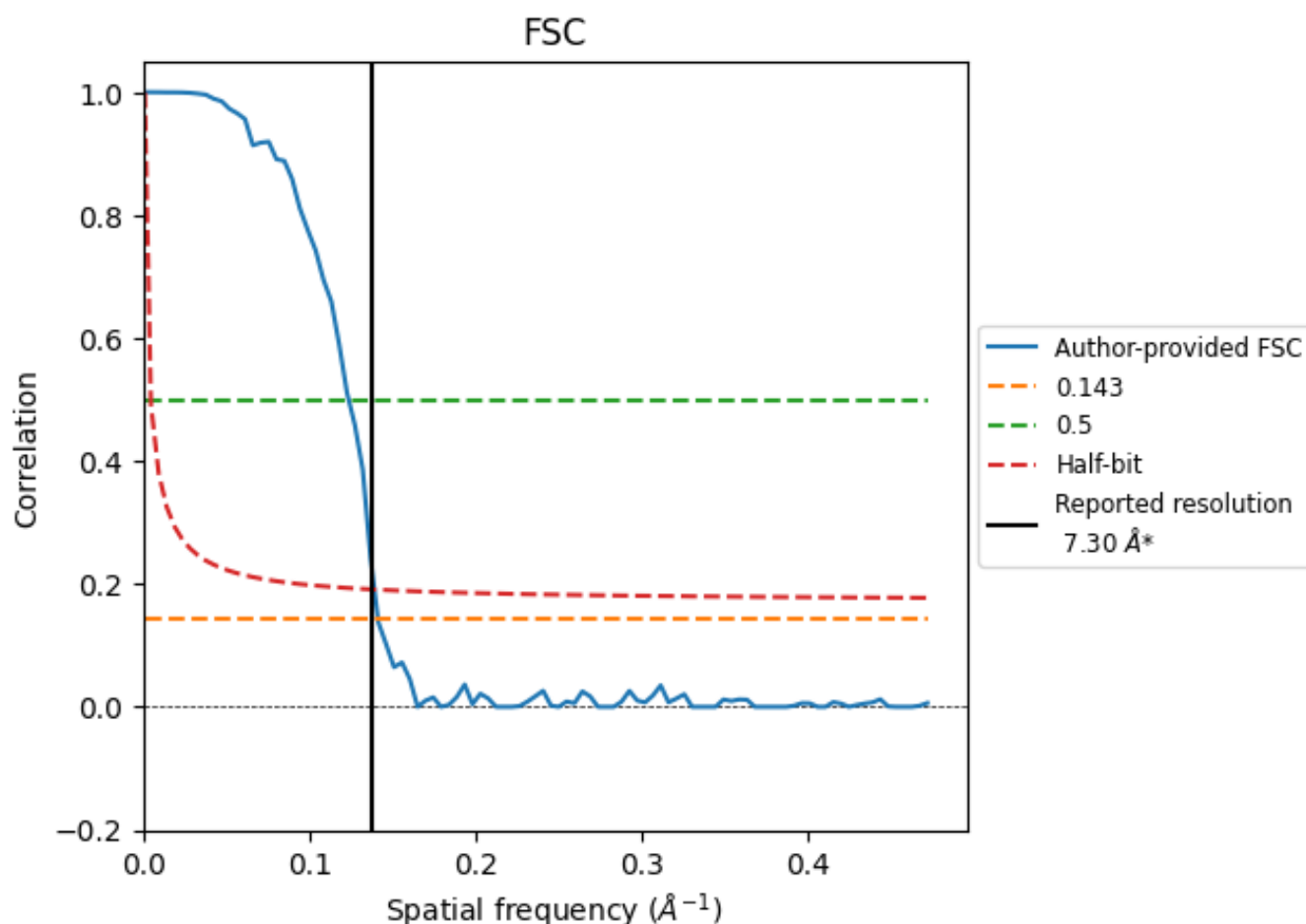


*Reported resolution corresponds to spatial frequency of 0.137 $\text{\AA}^{-1}$

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 0.137 Å⁻¹

8.2 Resolution estimates [i](#)

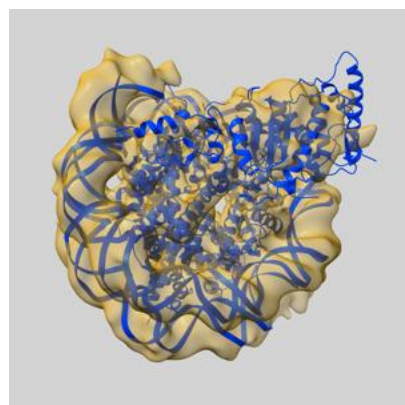
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.30	-	-
Author-provided FSC curve	7.08	8.09	7.19
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

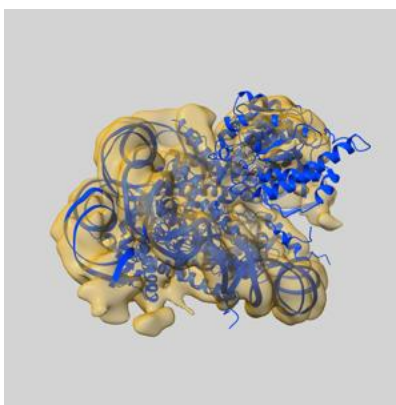
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9843 and PDB model 6JM9. Per-residue inclusion information can be found in section [3](#) on page [6](#).

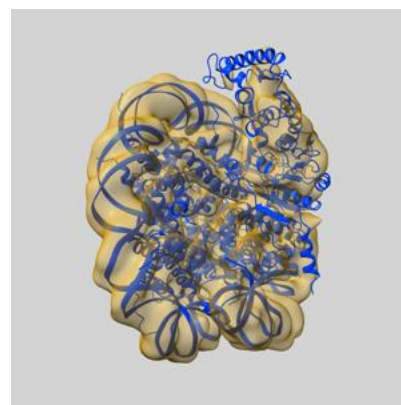
9.1 Map-model overlay [i](#)



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.021 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](#)



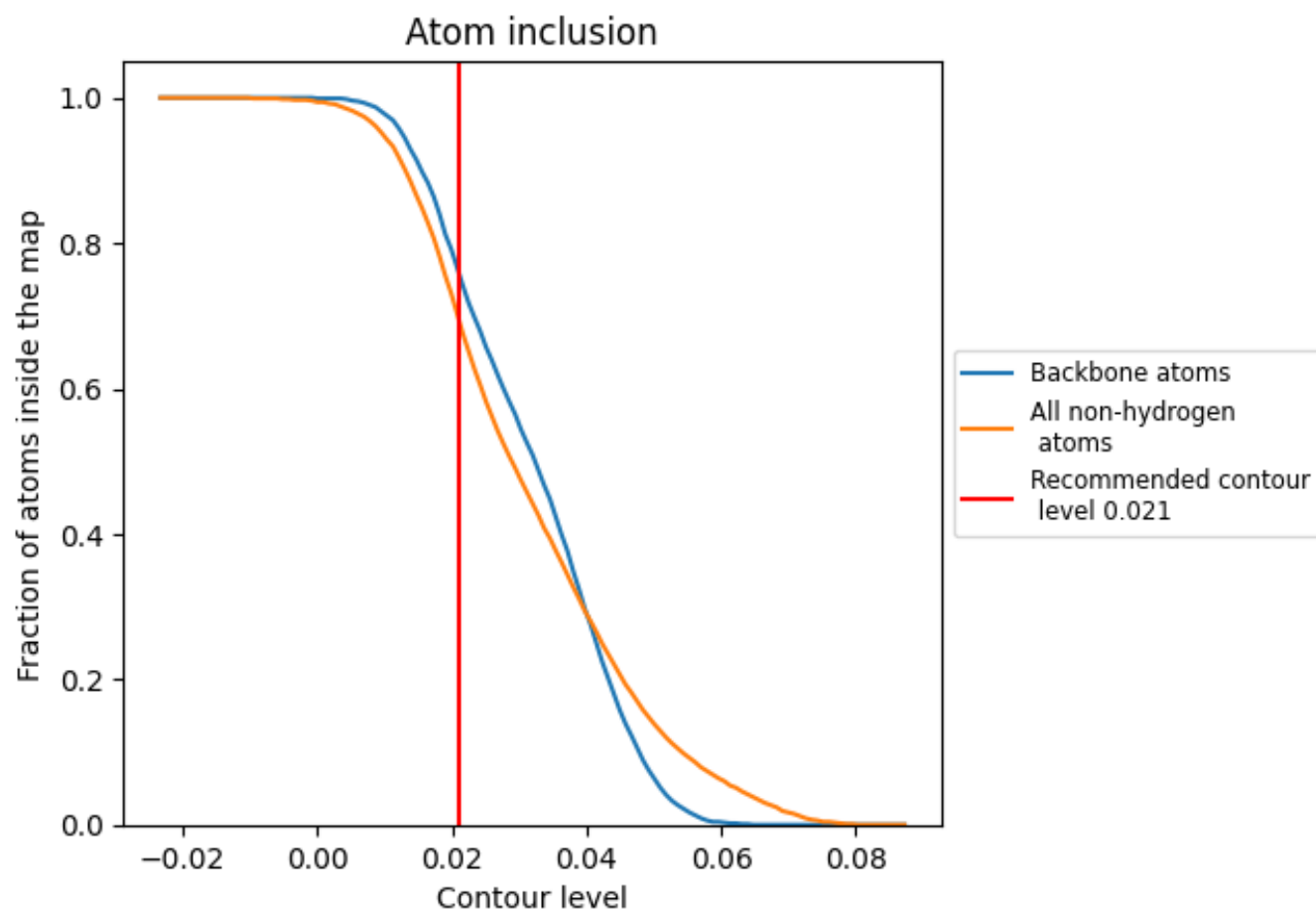
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.021).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 70% 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 (0.021) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6960	0.1320
A	0.6960	0.1250
B	0.6950	0.1270
C	0.6640	0.1490
D	0.7410	0.1430
E	0.6780	0.1190
F	0.6730	0.1240
G	0.7140	0.1440
H	0.7650	0.1540
I	0.8900	0.1710
J	0.8810	0.1710
X	0.3170	0.0530

1.0
0.0
<0.0