



Full wwPDB EM Validation Report ⓘ

Jun 23, 2026 – 02:18 PM JST

PDB ID : 8YUP / pdb_00008yup
EMDB ID : EMD-39578
Title : E. coli 70S ribosome complexed with P. putida tRNA^{Ile2} and A4 mRNA
Authors : Akiyama, N.; Ishiguro, K.; Shirouzu, M.; Suzuki, T.
Deposited on : 2024-03-28
Resolution : 2.39 Å (reported)
Based on initial model : 7K00

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 : 1.8.5 (274361), CSD as541be (2020)
MolProbity : **FAILED**
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

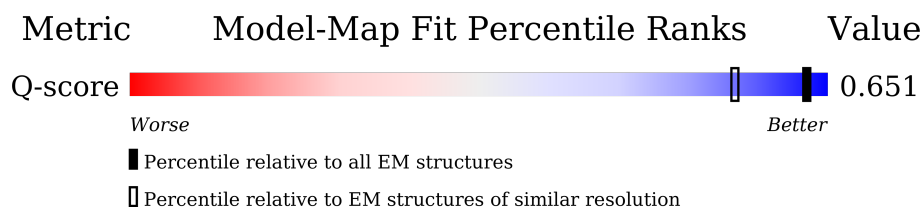
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.39 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	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	4884 (1.90 - 2.89)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 141910 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 RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1519	Total	C	N	O	P	0	0
			32612	14552	5986	10555	1519		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 6 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	103	Total	C	N	O	S	0	0
			839	530	151	151	7		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	117	Total	C	N	O	S	0	0
			877	540	173	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	conflict	UNP P0A7R9

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 22 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	a	2753	Total	C	N	O	P	0	0
			59130	26384	10897	19096	2753		

- Molecule 23 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	c	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	d	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 26 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	e	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 27 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	f	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 28 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	g	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	h	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 30 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	i	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 31 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	j	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 32 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	k	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 33 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	l	136	Total	C	N	O	S	0	0
			1075	686	205	177	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	82	MS6	MET	conflict	UNP P0ADY7

- Molecule 34 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	m	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 35 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	n	116	Total	C	N	O		0	0
			892	552	178	162			

- Molecule 36 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	o	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 37 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	p	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 38 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	q	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 39 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	r	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 40 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	s	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 41 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	t	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 42 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	u	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 43 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	v	78	Total	C	N	O	S	0	0
			586	362	116	107	1		

- Molecule 44 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	w	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 45 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	x	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 46 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	y	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 47 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	z	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 48 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	0	51	Total	C	N	O		0	0
			417	269	76	72			

- Molecule 49 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 50 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 51 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 52 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 53 is a RNA chain called P-site tRNA^{Glu}.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	V	76	Total	C	N	O	P	S	0	0
			1619	724	288	530	76	1		

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	W	12	Total	C	N	O	P	0	0
			260	117	52	79	12		

- Molecule 55 is a RNA chain called A-site tRNAIle2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	X	77	Total	C	N	O	P	0	0
			1663	747	292	547	77		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	A	90	Total	Mg	0
			90	90	
56	N	2	Total	Mg	0
			2	2	
56	Q	1	Total	Mg	0
			1	1	
56	a	207	Total	Mg	0
			207	207	
56	b	5	Total	Mg	0
			5	5	
56	c	1	Total	Mg	0
			1	1	
56	d	1	Total	Mg	0
			1	1	
56	p	1	Total	Mg	0
			1	1	
56	z	1	Total	Mg	0
			1	1	

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	156265	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.287	Depositor
Minimum map value	-0.116	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.0268	Depositor
Map size (Å)	439.10498, 439.10498, 439.10498	wwPDB
Map dimensions	530, 530, 530	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8285, 0.8285, 0.8285	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

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4.3.2 Protein sidechains [i](#)

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4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

56 non-standard protein/DNA/RNA residues are 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	$\# Z > 2$
25	MEQ	d	150	25	8,9,10	1.24	1 (12%)	5,10,12	1.40	2 (40%)
53	U8U	V	35	53,54	19,24,25	2.58	6 (31%)	23,34,37	1.14	3 (13%)
33	MS6	l	82	33	5,7,8	1.65	1 (20%)	2,7,9	2.20	1 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	PSU	a	2604	22	18,21,22	3.78	6 (33%)	22,30,33	1.88	4 (18%)
22	PSU	a	955	22	18,21,22	3.82	6 (33%)	22,30,33	1.86	5 (22%)
1	G7M	A	527	1	23,26,27	2.77	9 (39%)	35,39,42	1.62	7 (20%)
12	D2T	L	89	12	7,9,10	1.69	2 (28%)	6,11,13	1.27	1 (16%)
53	5MU	V	54	53	19,22,23	4.71	5 (26%)	28,32,35	3.43	10 (35%)
55	PSU	X	55	55	18,21,22	3.87	7 (38%)	22,30,33	1.87	5 (22%)
33	4D4	l	81	33	9,11,12	1.52	2 (22%)	8,13,15	2.01	3 (37%)
22	6MZ	a	1618	22	22,25,26	2.71	4 (18%)	30,36,39	2.28	9 (30%)
22	PSU	a	2457	22	18,21,22	3.72	6 (33%)	22,30,33	2.09	5 (22%)
1	PSU	A	516	1,56	18,21,22	3.80	6 (33%)	22,30,33	1.79	6 (27%)
53	PSU	V	55	53	18,21,22	3.96	6 (33%)	22,30,33	1.96	6 (27%)
55	A1LZ3	X	34	55,54	23,28,29	2.19	5 (21%)	24,38,41	1.04	3 (12%)
1	4OC	A	1402	1	20,23,24	3.05	8 (40%)	26,32,35	1.04	2 (7%)
55	H2U	X	16	55	18,21,22	0.56	0	21,30,33	1.37	4 (19%)
22	PSU	a	2580	22	18,21,22	3.83	7 (38%)	22,30,33	1.79	4 (18%)
22	5MU	a	747	22	19,22,23	4.68	6 (31%)	28,32,35	3.56	9 (32%)
1	UR3	A	1498	1	19,22,23	2.71	8 (42%)	26,32,35	1.31	1 (3%)
55	H2U	X	17	55	18,21,22	0.52	0	21,30,33	1.09	2 (9%)
1	2MG	A	1516	1	23,26,27	2.58	8 (34%)	32,38,41	2.17	11 (34%)
22	PSU	a	746	56,22	18,21,22	3.84	7 (38%)	22,30,33	1.77	5 (22%)
55	PSU	X	39	55	18,21,22	3.90	6 (33%)	22,30,33	1.78	5 (22%)
22	G7M	a	2069	22	23,26,27	2.76	9 (39%)	35,39,42	1.81	11 (31%)
55	H2U	X	20(A)	55	18,21,22	0.52	0	21,30,33	1.10	1 (4%)
1	5MC	A	967	1	18,22,23	3.74	8 (44%)	26,32,35	1.05	2 (7%)
22	2MG	a	2445	22	23,26,27	2.63	8 (34%)	32,38,41	2.14	9 (28%)
55	T6A	X	37	55	31,34,35	2.01	6 (19%)	44,49,52	2.23	11 (25%)
53	2MA	V	38	53	22,25,26	3.82	8 (36%)	33,37,40	2.83	10 (30%)
22	1MG	a	745	22	22,26,27	2.56	7 (31%)	33,39,42	1.69	9 (27%)
55	H2U	X	20	55	18,21,22	0.55	0	21,30,33	0.93	1 (4%)
22	2MA	a	2503	56,22	22,25,26	3.89	8 (36%)	33,37,40	2.77	9 (27%)
22	5MU	a	1939	22	19,22,23	4.63	7 (36%)	28,32,35	3.68	9 (32%)
22	2MG	a	1835	22	23,26,27	2.59	8 (34%)	32,38,41	2.09	10 (31%)
55	3AU	X	47	55	24,28,29	2.69	9 (37%)	33,40,43	1.27	4 (12%)
55	5MU	X	54	55	19,22,23	4.68	7 (36%)	28,32,35	3.60	9 (32%)
55	G7M	X	46	55	23,26,27	2.79	8 (34%)	35,39,42	1.76	8 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	PSU	a	1917	22	18,21,22	3.85	6 (33%)	22,30,33	1.80	5 (22%)
22	PSU	a	1911	22	18,21,22	3.85	6 (33%)	22,30,33	1.92	6 (27%)
22	5MC	a	1962	22	18,22,23	3.67	8 (44%)	26,32,35	0.99	2 (7%)
22	H2U	a	2449	22	18,21,22	0.53	0	21,30,33	0.83	1 (4%)
22	OMU	a	2552	22	19,22,23	2.84	7 (36%)	26,31,34	1.73	5 (19%)
22	3TD	a	1915	22	18,22,23	4.26	7 (38%)	22,32,35	1.69	2 (9%)
1	MA6	A	1518	1	23,26,27	1.26	4 (17%)	34,38,41	2.28	11 (32%)
1	MA6	A	1519	1	23,26,27	1.30	4 (17%)	34,38,41	2.33	11 (32%)
53	PSU	V	13	53	18,21,22	3.90	6 (33%)	22,30,33	1.91	5 (22%)
11	IAS	K	119	11	6,7,8	1.07	0	6,8,10	1.23	0
22	PSU	a	2504	22	18,21,22	3.82	6 (33%)	22,30,33	1.84	5 (22%)
1	2MG	A	1207	1	23,26,27	2.63	7 (30%)	32,38,41	2.10	9 (28%)
22	PSU	a	2605	22	18,21,22	3.82	6 (33%)	22,30,33	1.87	4 (18%)
1	5MC	A	1407	1	18,22,23	3.66	8 (44%)	26,32,35	1.05	2 (7%)
22	6MZ	a	2030	22	22,25,26	2.63	3 (13%)	30,36,39	2.40	11 (36%)
22	OMG	a	2251	56,53,22	23,26,27	2.56	8 (34%)	33,38,41	1.94	9 (27%)
1	2MG	A	966	1	23,26,27	2.63	7 (30%)	32,38,41	2.25	9 (28%)
22	OMC	a	2498	56,22	19,22,23	2.94	8 (42%)	26,31,34	0.87	1 (3%)

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
25	MEQ	d	150	25	-	4/8/9/11	-
53	U8U	V	35	53,54	-	0/9/28/29	0/2/2/2
33	MS6	l	82	33	-	1/4/6/8	-
22	PSU	a	2604	22	-	0/7/25/26	0/2/2/2
22	PSU	a	955	22	-	0/7/25/26	0/2/2/2
1	G7M	A	527	1	-	2/7/25/26	0/3/3/3
12	D2T	L	89	12	-	4/7/12/14	-
53	5MU	V	54	53	-	2/7/25/26	0/2/2/2
55	PSU	X	55	55	-	0/7/25/26	0/2/2/2
33	4D4	l	81	33	-	1/11/12/14	-
22	6MZ	a	1618	22	-	0/9/27/28	0/3/3/3
22	PSU	a	2457	22	-	0/7/25/26	0/2/2/2
1	PSU	A	516	1,56	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
53	PSU	V	55	53	-	2/7/25/26	0/2/2/2
55	A1LZ3	X	34	55,54	-	0/13/33/34	0/2/2/2
1	4OC	A	1402	1	-	0/9/29/30	0/2/2/2
55	H2U	X	16	55	-	3/7/38/39	0/2/2/2
22	PSU	a	2580	22	-	0/7/25/26	0/2/2/2
22	5MU	a	747	22	-	1/7/25/26	0/2/2/2
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
55	H2U	X	17	55	-	3/7/38/39	0/2/2/2
1	2MG	A	1516	1	-	0/9/27/28	0/3/3/3
22	PSU	a	746	56,22	-	1/7/25/26	0/2/2/2
55	PSU	X	39	55	-	0/7/25/26	0/2/2/2
22	G7M	a	2069	22	-	2/7/25/26	0/3/3/3
55	H2U	X	20(A)	55	-	5/7/38/39	0/2/2/2
1	5MC	A	967	1	-	0/7/25/26	0/2/2/2
22	2MG	a	2445	22	-	0/9/27/28	0/3/3/3
55	T6A	X	37	55	-	5/23/41/42	0/3/3/3
53	2MA	V	38	53	-	0/7/25/26	0/3/3/3
22	1MG	a	745	22	-	0/7/25/26	0/3/3/3
55	H2U	X	20	55	-	2/7/38/39	0/2/2/2
22	2MA	a	2503	56,22	-	2/7/25/26	0/3/3/3
22	5MU	a	1939	22	-	0/7/25/26	0/2/2/2
22	2MG	a	1835	22	-	0/9/27/28	0/3/3/3
55	3AU	X	47	55	-	7/16/34/35	0/2/2/2
55	5MU	X	54	55	-	2/7/25/26	0/2/2/2
55	G7M	X	46	55	-	0/7/25/26	0/3/3/3
22	PSU	a	1917	22	-	0/7/25/26	0/2/2/2
22	PSU	a	1911	22	-	0/7/25/26	0/2/2/2
22	5MC	a	1962	22	-	0/7/25/26	0/2/2/2
22	H2U	a	2449	22	-	0/7/38/39	0/2/2/2
22	OMU	a	2552	22	-	0/9/27/28	0/2/2/2
22	3TD	a	1915	22	-	2/7/25/26	0/2/2/2
1	MA6	A	1518	1	-	0/11/29/30	0/3/3/3
1	MA6	A	1519	1	-	3/11/29/30	0/3/3/3
53	PSU	V	13	53	-	2/7/25/26	0/2/2/2
11	IAS	K	119	11	-	0/7/7/8	-
22	PSU	a	2504	22	-	2/7/25/26	0/2/2/2
1	2MG	A	1207	1	-	0/9/27/28	0/3/3/3
22	PSU	a	2605	22	-	0/7/25/26	0/2/2/2
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	6MZ	a	2030	22	-	1/9/27/28	0/3/3/3
22	OMG	a	2251	56,53,22	-	1/9/27/28	0/3/3/3
1	2MG	A	966	1	-	1/9/27/28	0/3/3/3
22	OMC	a	2498	56,22	-	0/9/27/28	0/2/2/2

All (316) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	a	1915	3TD	C6-C5	12.75	1.50	1.35
22	a	2503	2MA	C4-N3	12.21	1.49	1.34
53	V	38	2MA	C4-N3	11.70	1.49	1.34
22	a	1618	6MZ	C6-N6	11.56	1.46	1.34
22	a	2030	6MZ	C6-N6	11.08	1.46	1.34
53	V	54	5MU	C6-N1	10.88	1.56	1.38
53	V	54	5MU	C2-N1	10.79	1.55	1.38
55	X	54	5MU	C2-N1	10.61	1.55	1.38
22	a	747	5MU	C6-N1	10.55	1.56	1.38
55	X	54	5MU	C6-N1	10.55	1.56	1.38
22	a	1939	5MU	C6-N1	10.54	1.56	1.38
22	a	747	5MU	C2-N1	10.40	1.55	1.38
22	a	1939	5MU	C2-N1	10.09	1.54	1.38
53	V	55	PSU	C6-C5	9.84	1.46	1.35
53	V	13	PSU	C6-C5	9.67	1.46	1.35
55	X	55	PSU	C6-C5	9.65	1.46	1.35
55	X	39	PSU	C6-C5	9.64	1.46	1.35
22	a	1911	PSU	C6-C5	9.60	1.46	1.35
22	a	2504	PSU	C6-C5	9.58	1.46	1.35
22	a	955	PSU	C6-C5	9.56	1.46	1.35
22	a	746	PSU	C6-C5	9.51	1.46	1.35
22	a	1917	PSU	C6-C5	9.50	1.46	1.35
22	a	2605	PSU	C6-C5	9.48	1.46	1.35
1	A	1407	5MC	C6-C5	9.44	1.50	1.34
22	a	2580	PSU	C6-C5	9.40	1.46	1.35
1	A	967	5MC	C6-C5	9.36	1.50	1.34
22	a	1962	5MC	C6-C5	9.31	1.49	1.34
55	X	39	PSU	C2-N1	9.30	1.49	1.36
53	V	13	PSU	C2-N1	9.28	1.49	1.36
22	a	2605	PSU	C2-N1	9.28	1.49	1.36
53	V	55	PSU	C2-N1	9.26	1.49	1.36
22	a	2604	PSU	C6-C5	9.24	1.46	1.35
55	X	55	PSU	C2-N1	9.16	1.49	1.36
55	X	54	5MU	C4-C5	9.15	1.60	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	a	1915	3TD	C2-N1	9.15	1.49	1.37
22	a	2580	PSU	C2-N1	9.14	1.49	1.36
22	a	747	5MU	C4-C5	9.14	1.60	1.44
53	V	54	5MU	C4-C5	9.13	1.59	1.44
22	a	1911	PSU	C2-N1	9.10	1.49	1.36
1	A	516	PSU	C2-N1	9.08	1.49	1.36
22	a	1939	5MU	C4-C5	9.07	1.59	1.44
22	a	2604	PSU	C2-N1	9.06	1.49	1.36
22	a	2457	PSU	C6-C5	9.05	1.45	1.35
1	A	516	PSU	C6-C5	9.04	1.45	1.35
22	a	1917	PSU	C2-N1	9.01	1.48	1.36
22	a	746	PSU	C2-N1	9.00	1.48	1.36
22	a	955	PSU	C2-N1	8.92	1.48	1.36
22	a	2504	PSU	C2-N1	8.84	1.48	1.36
22	a	2457	PSU	C2-N1	8.78	1.48	1.36
55	X	34	A1LZ3	C2-N2	8.16	1.45	1.33
1	A	966	2MG	C2-N3	7.63	1.46	1.31
22	a	747	5MU	C4-N3	-7.59	1.24	1.38
1	A	1207	2MG	C2-N3	7.58	1.46	1.31
22	a	1939	5MU	C4-N3	-7.54	1.24	1.38
22	a	2445	2MG	C2-N3	7.51	1.46	1.31
22	a	1835	2MG	C2-N3	7.35	1.46	1.31
55	X	54	5MU	C4-N3	-7.33	1.25	1.38
22	a	2503	2MA	C2-N3	7.32	1.47	1.34
1	A	1516	2MG	C2-N3	7.30	1.45	1.31
53	V	38	2MA	C2-N3	7.29	1.47	1.34
53	V	54	5MU	C4-N3	-7.21	1.25	1.38
1	A	967	5MC	C4-N3	7.12	1.46	1.34
22	a	1962	5MC	C4-N3	7.11	1.46	1.34
22	a	2251	OMG	C4-N3	7.09	1.51	1.34
53	V	55	PSU	C2-N3	6.95	1.49	1.37
22	a	1911	PSU	C2-N3	6.83	1.49	1.37
55	X	39	PSU	C2-N3	6.78	1.49	1.37
1	A	1407	5MC	C4-N3	6.76	1.45	1.34
22	a	2504	PSU	C2-N3	6.76	1.49	1.37
1	A	1207	2MG	C4-N3	6.74	1.50	1.34
55	X	55	PSU	C2-N3	6.73	1.49	1.37
1	A	1498	UR3	C2-N1	6.73	1.48	1.38
22	a	1917	PSU	C2-N3	6.71	1.49	1.37
1	A	516	PSU	C2-N3	6.70	1.49	1.37
53	V	13	PSU	C2-N3	6.67	1.48	1.37
22	a	955	PSU	C2-N3	6.66	1.48	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	a	1939	5MU	C6-C5	6.61	1.45	1.34
22	a	2457	PSU	C2-N3	6.61	1.48	1.37
22	a	2552	OMU	C2-N1	6.60	1.49	1.38
1	A	1402	4OC	C4-N3	6.59	1.44	1.32
22	a	747	5MU	C6-C5	6.58	1.45	1.34
22	a	746	PSU	C2-N3	6.58	1.48	1.37
55	X	54	5MU	C6-C5	6.52	1.45	1.34
53	V	54	5MU	C6-C5	6.52	1.45	1.34
55	X	46	G7M	C4-N3	6.51	1.49	1.34
55	X	46	G7M	C2-N2	6.49	1.49	1.34
22	a	2604	PSU	C2-N3	6.43	1.48	1.37
1	A	527	G7M	C2-N2	6.40	1.49	1.34
1	A	966	2MG	C4-N3	6.40	1.49	1.34
22	a	2445	2MG	C4-N3	6.39	1.49	1.34
22	a	2580	PSU	C2-N3	6.39	1.48	1.37
53	V	38	2MA	C2-N1	6.37	1.45	1.34
22	a	2605	PSU	C2-N3	6.37	1.48	1.37
22	a	1835	2MG	C4-N3	6.36	1.49	1.34
22	a	2503	2MA	C2-N1	6.33	1.45	1.34
1	A	967	5MC	C2-N3	6.33	1.49	1.36
1	A	527	G7M	C4-N3	6.32	1.49	1.34
22	a	2069	G7M	C4-N3	6.30	1.49	1.34
22	a	2069	G7M	C2-N2	6.29	1.49	1.34
22	a	2552	OMU	C2-N3	6.29	1.49	1.38
1	A	1402	4OC	C6-C5	6.23	1.49	1.35
22	a	1962	5MC	C2-N3	6.19	1.48	1.36
1	A	1498	UR3	C6-C5	6.13	1.49	1.35
22	a	1915	3TD	C6-N1	6.12	1.46	1.36
1	A	1407	5MC	C2-N3	6.11	1.48	1.36
1	A	1516	2MG	C4-N3	6.10	1.48	1.34
55	X	47	3AU	C2-N3	6.07	1.49	1.38
22	a	2498	OMC	C2-N3	6.04	1.48	1.36
22	a	745	1MG	C4-N3	6.00	1.48	1.34
22	a	2498	OMC	C6-C5	5.97	1.48	1.35
22	a	745	1MG	C2-N3	5.90	1.45	1.34
22	a	745	1MG	C2-N2	5.90	1.44	1.34
55	X	47	3AU	C6-C5	5.83	1.48	1.35
55	X	46	G7M	C2-N3	5.72	1.47	1.33
55	X	47	3AU	C2-N1	5.70	1.46	1.38
55	X	37	T6A	C10-N6	5.70	1.49	1.37
53	V	35	U8U	C2-N3	5.68	1.50	1.37
22	a	2552	OMU	C6-C5	5.67	1.48	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1402	4OC	C2-N3	5.66	1.47	1.36
1	A	527	G7M	C2-N3	5.64	1.46	1.33
55	X	37	T6A	C6-N6	5.51	1.50	1.39
53	V	35	U8U	C6-C5	5.47	1.50	1.34
22	a	2503	2MA	C5-C6	5.38	1.56	1.41
22	a	2251	OMG	C2-N3	5.35	1.46	1.33
22	a	2069	G7M	C2-N3	5.33	1.46	1.33
53	V	38	2MA	C5-C6	5.29	1.55	1.41
53	V	55	PSU	C6-N1	5.23	1.44	1.36
1	A	516	PSU	C6-N1	5.13	1.44	1.36
22	a	2604	PSU	C6-N1	5.13	1.44	1.36
1	A	967	5MC	C6-N1	5.13	1.46	1.38
1	A	1498	UR3	C2-N3	5.08	1.48	1.39
55	X	37	T6A	C10-N11	5.04	1.46	1.35
53	V	13	PSU	C6-N1	5.03	1.44	1.36
22	a	1835	2MG	C2-N1	5.02	1.44	1.36
22	a	1917	PSU	C6-N1	5.02	1.44	1.36
55	X	39	PSU	C6-N1	5.01	1.44	1.36
1	A	1516	2MG	C2-N1	4.98	1.44	1.36
22	a	2445	2MG	C2-N1	4.95	1.44	1.36
22	a	1962	5MC	C6-N1	4.94	1.46	1.38
22	a	2503	2MA	C6-N6	-4.90	1.21	1.34
53	V	38	2MA	C6-N6	-4.89	1.21	1.34
1	A	1407	5MC	C6-N1	4.87	1.46	1.38
55	X	55	PSU	C6-N1	4.85	1.44	1.36
22	a	746	PSU	C6-N1	4.85	1.44	1.36
22	a	2605	PSU	C6-N1	4.83	1.44	1.36
1	A	1207	2MG	C2-N1	4.83	1.44	1.36
1	A	966	2MG	C2-N1	4.82	1.44	1.36
22	a	2580	PSU	C6-N1	4.81	1.44	1.36
22	a	2504	PSU	C6-N1	4.78	1.44	1.36
22	a	2251	OMG	C2-N2	4.76	1.45	1.34
22	a	2498	OMC	C4-N4	4.74	1.45	1.33
22	a	955	PSU	C6-N1	4.70	1.44	1.36
22	a	2498	OMC	C4-N3	4.69	1.44	1.34
53	V	35	U8U	C6-N1	4.67	1.46	1.38
22	a	1911	PSU	C6-N1	4.66	1.44	1.36
22	a	2498	OMC	C2-N1	4.56	1.49	1.40
22	a	2457	PSU	C6-N1	4.54	1.43	1.36
22	a	1915	3TD	C2-N3	4.46	1.48	1.38
1	A	1402	4OC	C4-N4	4.43	1.45	1.35
1	A	527	G7M	C5-N7	-4.42	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	X	46	G7M	C5-N7	-4.27	1.34	1.39
1	A	967	5MC	C2-N1	4.20	1.49	1.40
1	A	1407	5MC	C2-N1	4.16	1.49	1.40
1	A	967	5MC	C4-N4	4.11	1.44	1.34
22	a	2069	G7M	C5-N7	-4.10	1.34	1.39
53	V	35	U8U	C4-N3	4.00	1.46	1.38
1	A	1402	4OC	C2-N1	3.96	1.48	1.40
1	A	1402	4OC	C5-C4	3.94	1.49	1.40
22	a	2069	G7M	C5-C6	3.93	1.54	1.43
1	A	1407	5MC	C4-N4	3.93	1.44	1.34
55	X	34	A1LZ3	CZ-N	3.92	1.45	1.32
22	a	1962	5MC	C4-N4	3.90	1.44	1.34
55	X	47	3AU	C4-N3	3.85	1.46	1.40
22	a	1962	5MC	C2-N1	3.83	1.48	1.40
1	A	527	G7M	C5-C6	3.77	1.53	1.43
55	X	46	G7M	C5-C6	3.70	1.53	1.43
53	V	35	U8U	C2-S2	-3.69	1.62	1.67
55	X	47	3AU	O2-C2	-3.65	1.15	1.22
22	a	2503	2MA	C6-N1	3.51	1.40	1.35
33	l	81	4D4	CZ-NE	3.50	1.40	1.33
55	X	47	3AU	C6-N1	3.47	1.46	1.38
55	X	34	A1LZ3	C4-N4	3.40	1.45	1.35
33	l	82	MS6	CB-CA	3.40	1.58	1.53
53	V	38	2MA	C6-N1	3.38	1.39	1.35
1	A	516	PSU	C4-N3	3.33	1.45	1.38
53	V	55	PSU	C4-N3	3.29	1.45	1.38
55	X	47	3AU	C11-C10	3.29	1.59	1.52
22	a	2504	PSU	C4-N3	3.25	1.44	1.38
55	X	55	PSU	C4-N3	3.23	1.44	1.38
22	a	2457	PSU	C4-N3	3.22	1.44	1.38
22	a	745	1MG	C5-C6	3.21	1.53	1.45
22	a	1911	PSU	C4-N3	3.21	1.44	1.38
22	a	2552	OMU	C4-N3	3.20	1.44	1.38
22	a	1917	PSU	C4-N3	3.20	1.44	1.38
55	X	39	PSU	C4-N3	3.19	1.44	1.38
22	a	955	PSU	C4-N3	3.17	1.44	1.38
22	a	2498	OMC	C6-N1	3.16	1.45	1.38
1	A	1519	MA6	C6-N6	3.15	1.46	1.36
22	a	746	PSU	C4-N3	3.14	1.44	1.38
22	a	2503	2MA	C5-N7	-3.12	1.33	1.39
1	A	1518	MA6	C6-N6	3.11	1.46	1.36
1	A	1402	4OC	O2-C2	-3.11	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	a	2445	2MG	C5-N7	-3.10	1.33	1.39
22	a	2580	PSU	C4-N3	3.10	1.44	1.38
12	L	89	D2T	CB-SB	3.09	1.85	1.82
22	a	745	1MG	C5-N7	-3.09	1.33	1.39
22	a	2552	OMU	O4-C4	-3.09	1.18	1.24
53	V	13	PSU	C4-N3	3.08	1.44	1.38
53	V	38	2MA	C5-N7	-3.07	1.33	1.39
1	A	1402	4OC	C6-N1	3.06	1.45	1.38
22	a	2604	PSU	C4-N3	3.03	1.44	1.38
22	a	2251	OMG	C5-N7	-3.00	1.33	1.39
22	a	2498	OMC	O2-C2	-2.97	1.18	1.23
22	a	2251	OMG	O6-C6	-2.96	1.17	1.23
1	A	966	2MG	C5-N7	-2.96	1.33	1.39
22	a	1835	2MG	C5-N7	-2.96	1.33	1.39
1	A	1516	2MG	C5-N7	-2.95	1.33	1.39
22	a	2605	PSU	C4-N3	2.95	1.44	1.38
1	A	1498	UR3	C6-N1	2.93	1.45	1.38
22	a	2069	G7M	C6-N1	2.92	1.44	1.38
1	A	1519	MA6	C5-C4	-2.91	1.33	1.39
55	X	46	G7M	C2-N1	2.91	1.44	1.37
22	a	2552	OMU	O2-C2	-2.91	1.17	1.23
22	a	2251	OMG	C5-C6	2.86	1.55	1.44
55	X	46	G7M	C6-N1	2.86	1.44	1.38
1	A	527	G7M	C2-N1	2.80	1.44	1.37
22	a	2069	G7M	O6-C6	-2.78	1.18	1.23
22	a	2069	G7M	C2-N1	2.75	1.44	1.37
53	V	35	U8U	C4-C5	2.74	1.51	1.45
22	a	1915	3TD	C4-N3	2.72	1.46	1.40
22	a	1618	6MZ	C5-C4	-2.72	1.33	1.39
1	A	1518	MA6	C5-C4	-2.71	1.33	1.39
22	a	2580	PSU	O4-C4	-2.69	1.18	1.23
22	a	2030	6MZ	C5-C4	-2.69	1.34	1.39
1	A	527	G7M	C6-N1	2.67	1.43	1.38
1	A	1516	2MG	C5-C6	2.65	1.54	1.44
1	A	1519	MA6	C5-N7	-2.63	1.34	1.39
1	A	1207	2MG	O6-C6	-2.60	1.18	1.23
1	A	1407	5MC	O2-C2	-2.60	1.18	1.23
1	A	966	2MG	C5-C6	2.59	1.54	1.44
22	a	2445	2MG	O6-C6	-2.58	1.18	1.23
1	A	527	G7M	O6-C6	-2.56	1.18	1.23
22	a	1835	2MG	C5-C6	2.56	1.53	1.44
22	a	2251	OMG	C2-N1	2.56	1.44	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	a	2445	2MG	C5-C6	2.55	1.53	1.44
1	A	1518	MA6	C5-N7	-2.55	1.34	1.39
1	A	1207	2MG	C5-C6	2.55	1.53	1.44
1	A	1207	2MG	C5-N7	-2.54	1.34	1.39
1	A	966	2MG	O6-C6	-2.53	1.18	1.23
22	a	2498	OMC	C5-C4	2.53	1.48	1.42
22	a	747	5MU	O2-C2	-2.51	1.18	1.23
22	a	2457	PSU	O4-C4	-2.50	1.18	1.23
22	a	1962	5MC	O2-C2	-2.50	1.19	1.23
1	A	1498	UR3	O4-C4	-2.48	1.18	1.23
1	A	967	5MC	O2-C2	-2.47	1.19	1.23
1	A	966	2MG	C6-N1	2.45	1.43	1.38
22	a	746	PSU	O4-C4	-2.44	1.18	1.23
22	a	1835	2MG	C6-N1	2.44	1.43	1.38
55	X	46	G7M	O6-C6	-2.43	1.19	1.23
55	X	47	3AU	O4-C4	-2.43	1.18	1.23
22	a	745	1MG	C4-N9	-2.40	1.31	1.38
1	A	1516	2MG	C6-N1	2.40	1.43	1.38
1	A	1516	2MG	O6-C6	-2.38	1.19	1.23
22	a	955	PSU	O4-C4	-2.37	1.19	1.23
1	A	1519	MA6	C8-N9	-2.37	1.33	1.37
22	a	2251	OMG	C6-N1	2.37	1.43	1.38
33	l	81	4D4	OB-CB	-2.36	1.38	1.43
22	a	745	1MG	O6-C6	-2.36	1.18	1.23
55	X	34	A1LZ3	C6-N1	-2.35	1.32	1.35
22	a	2030	6MZ	C5-N7	-2.34	1.34	1.39
22	a	2504	PSU	O4-C4	-2.33	1.19	1.23
22	a	1939	5MU	O2-C2	-2.33	1.18	1.23
22	a	2445	2MG	C6-N1	2.32	1.43	1.38
1	A	1207	2MG	C6-N1	2.31	1.43	1.38
1	A	1498	UR3	O2-C2	-2.28	1.18	1.22
22	a	2605	PSU	O4-C4	-2.27	1.19	1.23
25	d	150	MEQ	CB-CA	2.27	1.56	1.53
55	X	34	A1LZ3	C4-N3	-2.26	1.31	1.35
53	V	38	2MA	CM2-C2	2.26	1.56	1.49
22	a	2580	PSU	O4'-C1'	-2.25	1.40	1.43
22	a	2503	2MA	CM2-C2	2.25	1.56	1.49
55	X	47	3AU	O30-C13	2.25	1.29	1.22
1	A	516	PSU	O4-C4	-2.25	1.19	1.23
53	V	13	PSU	O4-C4	-2.23	1.19	1.23
55	X	54	5MU	O2-C2	-2.22	1.19	1.23
22	a	1917	PSU	O4-C4	-2.21	1.19	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1498	UR3	C5-C4	2.20	1.49	1.43
22	a	1835	2MG	O6-C6	-2.20	1.19	1.23
22	a	1962	5MC	CM5-C5	2.18	1.56	1.50
55	X	37	T6A	O10-C10	-2.16	1.18	1.23
22	a	2604	PSU	O4-C4	-2.16	1.19	1.23
55	X	37	T6A	C5-C4	-2.15	1.35	1.39
22	a	1618	6MZ	C5-N7	-2.15	1.35	1.39
22	a	1939	5MU	O4-C4	-2.14	1.19	1.23
12	L	89	D2T	CB-CG	2.14	1.55	1.52
1	A	1518	MA6	C8-N9	-2.14	1.33	1.37
22	a	1915	3TD	O4-C4	-2.12	1.18	1.23
1	A	967	5MC	CM5-C5	2.12	1.55	1.50
22	a	1911	PSU	O4-C4	-2.12	1.19	1.23
55	X	55	PSU	O4-C4	-2.11	1.19	1.23
1	A	1516	2MG	C4-N9	-2.10	1.32	1.38
22	a	1835	2MG	C4-N9	-2.09	1.32	1.38
1	A	1498	UR3	C4-N3	2.09	1.45	1.40
22	a	1618	6MZ	C8-N9	-2.09	1.33	1.37
55	X	39	PSU	O4-C4	-2.09	1.19	1.23
1	A	1407	5MC	CM5-C5	2.06	1.55	1.50
22	a	2445	2MG	C4-N9	-2.06	1.32	1.38
22	a	746	PSU	O4'-C1'	-2.06	1.41	1.43
1	A	527	G7M	C8-N7	2.05	1.36	1.33
22	a	2552	OMU	C6-N1	2.05	1.42	1.38
53	V	55	PSU	O4-C4	-2.04	1.19	1.23
22	a	1915	3TD	O4'-C1'	-2.04	1.41	1.43
55	X	37	T6A	C6-N1	-2.03	1.31	1.35
55	X	55	PSU	C4-C5	2.03	1.49	1.44
22	a	2069	G7M	C8-N7	2.02	1.36	1.33
55	X	54	5MU	O4-C4	-2.02	1.19	1.23

All (314) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	a	1939	5MU	C5-C4-N3	12.48	125.96	115.31
55	X	54	5MU	C5-C4-N3	12.03	125.58	115.31
22	a	747	5MU	C5-C4-N3	11.57	125.19	115.31
53	V	54	5MU	C5-C4-N3	11.55	125.17	115.31
22	a	1939	5MU	C5-C6-N1	-10.50	112.53	123.34
22	a	747	5MU	C5-C6-N1	-10.00	113.05	123.34
55	X	54	5MU	C5-C6-N1	-9.72	113.34	123.34
53	V	54	5MU	C5-C6-N1	-9.09	113.98	123.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	a	2503	2MA	C5-C4-N3	-8.58	117.53	127.19
53	V	38	2MA	C4-N9-C1'	-7.77	108.08	126.59
53	V	38	2MA	C1'-N9-C8	7.53	144.13	127.14
53	V	38	2MA	C5-C4-N3	-7.46	118.80	127.19
1	A	966	2MG	C2-N3-C4	7.13	120.88	112.04
22	a	1835	2MG	C2-N3-C4	6.60	120.22	112.04
1	A	1516	2MG	C2-N3-C4	6.57	120.19	112.04
22	a	2445	2MG	C2-N3-C4	6.48	120.08	112.04
1	A	1207	2MG	C2-N3-C4	6.29	119.84	112.04
22	a	2503	2MA	C4-N9-C1'	-6.14	111.96	126.59
22	a	2503	2MA	N3-C4-N9	6.08	135.43	126.99
22	a	2503	2MA	C1'-N9-C8	6.01	140.70	127.14
22	a	2030	6MZ	N1-C2-N3	-5.85	119.45	128.60
1	A	1519	MA6	N1-C2-N3	-5.80	119.52	128.60
1	A	1518	MA6	N1-C2-N3	-5.73	119.64	128.60
55	X	37	T6A	C5-C4-N3	-5.70	119.32	126.75
55	X	37	T6A	N6-C10-N11	5.58	121.55	113.76
55	X	37	T6A	N3-C2-N1	-5.55	119.92	128.60
22	a	2552	OMU	C4-N3-C2	-5.41	119.45	126.58
22	a	1915	3TD	N1-C2-N3	5.39	120.39	116.14
1	A	966	2MG	C5-C4-N3	-5.35	119.78	128.46
22	a	2251	OMG	C5-C4-N3	-5.32	119.83	128.46
22	a	1618	6MZ	N1-C2-N3	-5.31	120.29	128.60
22	a	1618	6MZ	C5-C4-N3	-5.23	119.93	126.75
22	a	2445	2MG	C5-C4-N3	-5.16	120.09	128.46
22	a	2457	PSU	C4-N3-C2	-5.16	118.91	126.34
1	A	1498	UR3	C4-N3-C2	-5.10	119.77	124.56
22	a	2030	6MZ	C9-N6-C6	-4.97	118.59	122.87
55	X	54	5MU	C4-N3-C2	-4.96	120.93	127.35
22	a	1939	5MU	O4-C4-C5	-4.92	119.20	124.90
22	a	1939	5MU	C4-N3-C2	-4.90	121.01	127.35
22	a	2457	PSU	N1-C2-N3	4.89	120.67	115.13
22	a	1835	2MG	C5-C4-N3	-4.88	120.54	128.46
53	V	54	5MU	O4-C4-C5	-4.84	119.29	124.90
55	X	54	5MU	O4-C4-C5	-4.84	119.30	124.90
22	a	2030	6MZ	N9-C8-N7	-4.81	107.34	113.91
1	A	1519	MA6	C5-C4-N3	-4.80	120.49	126.75
22	a	955	PSU	C4-N3-C2	-4.78	119.45	126.34
1	A	1207	2MG	C5-C4-N3	-4.75	120.76	128.46
1	A	1519	MA6	N9-C8-N7	-4.74	107.43	113.91
55	X	54	5MU	N3-C2-N1	4.73	121.17	114.89
22	a	2030	6MZ	C5-C4-N3	-4.72	120.59	126.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	a	747	5MU	N3-C2-N1	4.71	121.14	114.89
22	a	746	PSU	C4-N3-C2	-4.71	119.56	126.34
53	V	38	2MA	N3-C4-N9	4.69	133.49	126.99
22	a	2604	PSU	C4-N3-C2	-4.68	119.60	126.34
1	A	1518	MA6	C5-C4-N3	-4.67	120.66	126.75
22	a	2069	G7M	C2-N3-C4	4.67	120.62	112.30
22	a	747	5MU	C4-N3-C2	-4.65	121.33	127.35
1	A	1516	2MG	C5-C4-N3	-4.64	120.94	128.46
22	a	2504	PSU	C4-N3-C2	-4.63	119.66	126.34
22	a	1917	PSU	C4-N3-C2	-4.63	119.67	126.34
22	a	2580	PSU	C4-N3-C2	-4.60	119.70	126.34
1	A	1518	MA6	C2-N1-C6	4.58	122.56	111.75
53	V	54	5MU	N3-C2-N1	4.58	120.96	114.89
53	V	13	PSU	C4-N3-C2	-4.57	119.76	126.34
53	V	55	PSU	C4-N3-C2	-4.56	119.77	126.34
55	X	55	PSU	C4-N3-C2	-4.53	119.81	126.34
22	a	1618	6MZ	N9-C8-N7	-4.52	107.74	113.91
22	a	745	1MG	C5-C4-N3	-4.51	121.14	128.46
22	a	747	5MU	O4-C4-C5	-4.51	119.67	124.90
22	a	1911	PSU	C4-N3-C2	-4.50	119.85	126.34
55	X	39	PSU	C4-N3-C2	-4.46	119.92	126.34
1	A	1519	MA6	C2-N1-C6	4.46	122.28	111.75
1	A	966	2MG	C2-N1-C6	-4.44	119.37	124.48
55	X	55	PSU	N1-C2-N3	4.43	120.15	115.13
53	V	54	5MU	C4-N3-C2	-4.40	121.65	127.35
22	a	2604	PSU	N1-C2-N3	4.40	120.12	115.13
1	A	1518	MA6	N9-C8-N7	-4.37	107.94	113.91
1	A	516	PSU	C4-N3-C2	-4.35	120.08	126.34
22	a	1939	5MU	N3-C2-N1	4.34	120.64	114.89
55	X	37	T6A	N9-C8-N7	-4.33	107.99	113.91
53	V	13	PSU	N1-C2-N3	4.32	120.03	115.13
22	a	2504	PSU	N1-C2-N3	4.32	120.03	115.13
53	V	55	PSU	N1-C2-N3	4.32	120.02	115.13
22	a	955	PSU	N1-C2-N3	4.31	120.02	115.13
1	A	1519	MA6	C4-C5-C6	4.30	120.69	115.88
55	X	37	T6A	C4-C5-C6	4.30	120.14	116.81
22	a	2605	PSU	N1-C2-N3	4.29	120.00	115.13
22	a	2251	OMG	C2-N3-C4	4.28	119.92	112.30
55	X	46	G7M	C2-N3-C4	4.25	119.88	112.30
22	a	1911	PSU	N1-C2-N3	4.23	119.92	115.13
22	a	2605	PSU	C4-N3-C2	-4.23	120.24	126.34
22	a	746	PSU	N1-C2-N3	4.22	119.91	115.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	a	2445	2MG	C2-N1-C6	-4.20	119.64	124.48
22	a	1618	6MZ	C4-C5-C6	4.16	120.03	116.81
1	A	1518	MA6	C4-C5-C6	4.15	120.52	115.88
55	X	39	PSU	N1-C2-N3	4.14	119.82	115.13
22	a	1917	PSU	N1-C2-N3	4.12	119.80	115.13
22	a	1915	3TD	C4-N3-C2	-4.12	120.14	124.61
1	A	527	G7M	C2-N3-C4	4.07	119.55	112.30
55	X	46	G7M	C5-C6-N1	4.06	120.26	111.79
22	a	2069	G7M	C5-C6-N1	4.04	120.23	111.79
53	V	38	2MA	N9-C8-N7	-4.02	108.42	113.91
22	a	2580	PSU	N1-C2-N3	4.01	119.68	115.13
22	a	747	5MU	C5M-C5-C6	-3.97	117.55	122.85
1	A	1516	2MG	C2-N1-C6	-3.96	119.92	124.48
1	A	1519	MA6	C5-N7-C8	3.96	109.14	103.51
1	A	516	PSU	N1-C2-N3	3.88	119.53	115.13
55	X	46	G7M	C5-C4-N3	-3.83	120.81	128.15
22	a	2552	OMU	N3-C2-N1	3.82	119.96	114.89
33	l	81	4D4	NE-CZ-NH2	3.81	127.40	120.70
1	A	1207	2MG	C2-N1-C6	-3.74	120.17	124.48
55	X	54	5MU	C5M-C5-C6	-3.72	117.88	122.85
55	X	37	T6A	C2-N3-C4	3.72	120.53	111.75
1	A	527	G7M	C5-C6-N1	3.69	119.49	111.79
1	A	527	G7M	C5-C4-N3	-3.67	121.11	128.15
22	a	745	1MG	C2-N3-C4	3.66	120.20	111.98
22	a	2069	G7M	C5-C4-N3	-3.65	121.14	128.15
53	V	54	5MU	C5M-C5-C6	-3.65	117.97	122.85
53	V	54	5MU	C5M-C5-C4	3.65	122.78	118.77
22	a	747	5MU	C5M-C5-C4	3.63	122.76	118.77
55	X	46	G7M	O6-C6-C5	-3.62	119.90	128.06
22	a	1911	PSU	C6-C5-C4	3.60	120.72	118.20
1	A	1518	MA6	C5-N7-C8	3.58	108.60	103.51
53	V	55	PSU	C6-C5-C4	3.58	120.70	118.20
22	a	2030	6MZ	C2-N3-C4	3.57	120.18	111.75
55	X	54	5MU	C5M-C5-C4	3.56	122.68	118.77
22	a	1835	2MG	C2-N1-C6	-3.53	120.42	124.48
22	a	2251	OMG	N9-C4-N3	3.52	133.01	125.94
22	a	2552	OMU	C5-C4-N3	3.52	120.10	114.84
1	A	966	2MG	N9-C4-N3	3.50	132.97	125.94
22	a	1939	5MU	C5M-C5-C6	-3.50	118.17	122.85
55	X	47	3AU	C4-N3-C2	-3.48	120.26	124.63
22	a	2605	PSU	C6-C5-C4	3.48	120.63	118.20
1	A	1207	2MG	N9-C8-N7	-3.46	106.88	113.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	a	1939	5MU	C5M-C5-C4	3.45	122.57	118.77
22	a	1618	6MZ	C2-N3-C4	3.44	119.88	111.75
55	X	20(A)	H2U	C5-C4-N3	-3.42	112.81	116.65
55	X	37	T6A	C5-N7-C8	3.42	108.36	103.51
53	V	13	PSU	C6-C5-C4	3.41	120.58	118.20
22	a	2445	2MG	N9-C4-N3	3.41	132.78	125.94
22	a	1618	6MZ	N3-C4-N9	3.39	132.68	127.08
22	a	2251	OMG	N9-C8-N7	-3.38	107.02	113.39
1	A	1519	MA6	C2-N3-C4	3.38	119.74	111.75
22	a	2457	PSU	O2-C2-N1	-3.37	119.08	122.79
22	a	2503	2MA	N9-C8-N7	-3.36	109.31	113.91
22	a	2030	6MZ	C5-N7-C8	3.36	108.28	103.51
1	A	1516	2MG	N9-C8-N7	-3.33	107.11	113.39
22	a	2069	G7M	O6-C6-C5	-3.33	120.55	128.06
22	a	1962	5MC	C5-C6-N1	-3.32	119.92	123.34
55	X	16	H2U	C5-C4-N3	-3.31	112.93	116.65
1	A	1407	5MC	C5-C6-N1	-3.30	119.94	123.34
55	X	37	T6A	N3-C4-N9	3.30	132.52	127.08
22	a	2605	PSU	C6-N1-C2	-3.30	119.31	122.68
22	a	2251	OMG	C2-N1-C6	-3.29	119.11	125.10
1	A	1518	MA6	C2-N3-C4	3.27	119.48	111.75
22	a	2457	PSU	C6-C5-C4	3.27	120.48	118.20
22	a	745	1MG	N9-C8-N7	-3.24	107.28	113.39
55	X	37	T6A	O10-C10-N6	-3.21	118.20	123.62
22	a	2445	2MG	N9-C8-N7	-3.20	107.37	113.39
1	A	1519	MA6	C4-C5-N7	-3.19	106.74	110.62
55	X	34	A1LZ3	C2-N3-C4	3.19	120.78	117.84
53	V	38	2MA	C5-N7-C8	3.18	108.03	103.51
55	X	46	G7M	N9-C4-N3	3.18	132.32	125.94
53	V	13	PSU	C6-N1-C2	-3.17	119.44	122.68
22	a	1618	6MZ	C5-N7-C8	3.17	108.01	103.51
1	A	1207	2MG	N9-C4-N3	3.15	132.27	125.94
22	a	2503	2MA	N3-C2-N1	-3.15	119.92	125.72
55	X	55	PSU	C6-N1-C2	-3.15	119.47	122.68
1	A	527	G7M	O6-C6-C5	-3.13	121.00	128.06
1	A	966	2MG	N9-C8-N7	-3.11	107.53	113.39
55	X	39	PSU	C6-N1-C2	-3.11	119.50	122.68
22	a	2604	PSU	C6-C5-C4	3.10	120.37	118.20
55	X	17	H2U	C5-C4-N3	-3.10	113.17	116.65
22	a	1835	2MG	N9-C4-N3	3.09	132.15	125.94
53	V	55	PSU	C6-N1-C2	-3.09	119.52	122.68
1	A	516	PSU	C6-N1-C2	-3.09	119.53	122.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	a	2503	2MA	C6-C5-C4	3.08	121.33	117.18
55	X	47	3AU	C5-C4-N3	3.08	119.56	115.50
33	l	82	MS6	CE-SD-CG	3.08	110.98	100.40
55	X	16	H2U	O2-C2-N1	3.08	126.97	123.11
1	A	967	5MC	C5-C6-N1	-3.04	120.21	123.34
22	a	2457	PSU	C6-N1-C2	-3.03	119.59	122.68
22	a	2552	OMU	O4-C4-C5	-3.03	119.84	125.16
22	a	1835	2MG	N9-C8-N7	-3.02	107.70	113.39
55	X	46	G7M	C2-N1-C6	-3.01	119.61	125.10
1	A	1518	MA6	C4-C5-N7	-2.97	107.01	110.62
53	V	38	2MA	C6-C5-C4	2.96	121.16	117.18
22	a	2504	PSU	C6-N1-C2	-2.95	119.67	122.68
53	V	35	U8U	C5-C4-N3	2.95	119.11	114.97
22	a	1911	PSU	C6-N1-C2	-2.93	119.69	122.68
22	a	1939	5MU	O2-C2-N1	-2.92	118.91	122.79
22	a	2604	PSU	C6-N1-C2	-2.91	119.71	122.68
1	A	966	2MG	C5-C6-N1	2.89	120.52	113.19
22	a	2030	6MZ	C4-C5-C6	2.87	119.03	116.81
22	a	2069	G7M	C2-N1-C6	-2.86	119.88	125.10
22	a	746	PSU	C6-N1-C2	-2.85	119.76	122.68
22	a	2069	G7M	CN7-N7-C5	2.84	130.30	126.77
53	V	38	2MA	N3-C2-N1	-2.84	120.50	125.72
22	a	1835	2MG	N1-C2-N3	-2.84	119.57	123.95
22	a	2503	2MA	C5-N7-C8	2.83	107.53	103.51
22	a	1911	PSU	O2-C2-N1	-2.83	119.68	122.79
55	X	20	H2U	C5-C4-N3	-2.82	113.48	116.65
55	X	46	G7M	CN7-N7-C5	2.81	130.26	126.77
22	a	2504	PSU	O2-C2-N1	-2.80	119.71	122.79
55	X	55	PSU	C6-C5-C4	2.79	120.15	118.20
53	V	35	U8U	O4-C4-C5	-2.78	120.82	124.96
1	A	966	2MG	N1-C2-N3	-2.78	119.65	123.95
1	A	527	G7M	CN7-N7-C5	2.78	130.22	126.77
1	A	1207	2MG	N1-C2-N3	-2.77	119.67	123.95
22	a	2580	PSU	C6-N1-C2	-2.77	119.86	122.68
22	a	1939	5MU	O4-C4-N3	-2.75	114.84	120.12
1	A	1207	2MG	C5-C6-N1	2.73	120.11	113.19
1	A	1516	2MG	N1-C2-N3	-2.72	119.74	123.95
22	a	2251	OMG	C5-C6-N1	2.71	120.08	113.19
1	A	527	G7M	N9-C4-N3	2.71	131.38	125.94
22	a	955	PSU	C6-C5-C4	2.71	120.09	118.20
55	X	54	5MU	O2-C2-N1	-2.70	119.20	122.79
22	a	1618	6MZ	C9-N6-C6	-2.68	120.56	122.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1518	MA6	N1-C6-N6	-2.67	114.16	117.08
22	a	1962	5MC	CM5-C5-C6	-2.67	119.28	122.85
22	a	2445	2MG	O6-C6-C5	-2.65	119.56	126.60
22	a	955	PSU	C6-N1-C2	-2.64	119.98	122.68
22	a	1917	PSU	C6-N1-C2	-2.64	119.99	122.68
1	A	1516	2MG	C5-C6-N1	2.63	119.87	113.19
1	A	966	2MG	O6-C6-C5	-2.63	119.63	126.60
22	a	1917	PSU	C6-C5-C4	2.62	120.03	118.20
22	a	2445	2MG	C5-C6-N1	2.62	119.85	113.19
53	V	55	PSU	O2-C2-N1	-2.62	119.91	122.79
22	a	1618	6MZ	C4-N9-C8	2.61	108.56	105.73
55	X	54	5MU	O4-C4-N3	-2.60	115.12	120.12
22	a	955	PSU	O2-C2-N1	-2.60	119.93	122.79
22	a	747	5MU	O4-C4-N3	-2.60	115.13	120.12
1	A	1516	2MG	N9-C4-N3	2.59	131.14	125.94
1	A	527	G7M	C2-N1-C6	-2.59	120.38	125.10
22	a	747	5MU	O2-C2-N1	-2.58	119.36	122.79
55	X	55	PSU	O2-C2-N1	-2.58	119.95	122.79
22	a	745	1MG	C5-C6-N1	2.57	119.88	114.91
22	a	2030	6MZ	N3-C4-N9	2.55	131.29	127.08
33	l	81	4D4	CB-CA-C	-2.55	107.70	111.77
22	a	2030	6MZ	C4-N9-C8	2.54	108.48	105.73
22	a	2580	PSU	O4'-C1'-C2'	2.52	108.69	105.14
22	a	1835	2MG	C5-C6-N1	2.50	119.55	113.19
22	a	2069	G7M	N9-C4-N3	2.50	130.95	125.94
55	X	39	PSU	C6-C5-C4	2.47	119.92	118.20
22	a	2445	2MG	N1-C2-N3	-2.46	120.14	123.95
1	A	516	PSU	C6-C5-C4	2.46	119.92	118.20
1	A	1518	MA6	C5-C4-N9	2.46	108.65	105.78
22	a	2251	OMG	O6-C6-C5	-2.46	120.07	126.60
22	a	746	PSU	C6-C5-C4	2.46	119.92	118.20
1	A	516	PSU	O2-C2-N1	-2.42	120.13	122.79
1	A	1207	2MG	O6-C6-C5	-2.42	120.19	126.60
1	A	1516	2MG	C8-N7-C5	2.41	108.61	104.24
1	A	1402	4OC	C6-C5-C4	2.41	119.91	116.96
1	A	1516	2MG	O6-C6-C5	-2.41	120.22	126.60
1	A	1519	MA6	C5-C4-N9	2.40	108.58	105.78
22	a	2251	OMG	C1'-N9-C4	-2.40	119.37	126.50
22	a	2251	OMG	C8-N7-C5	2.40	108.58	104.24
53	V	54	5MU	O4-C4-N3	-2.39	115.54	120.12
22	a	2504	PSU	C6-C5-C4	2.36	119.85	118.20
1	A	967	5MC	CM5-C5-C6	-2.36	119.70	122.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1402	4OC	CM4-N4-C4	-2.36	117.85	122.45
55	X	17	H2U	C4-N3-C2	2.36	127.75	125.79
22	a	2503	2MA	CM2-C2-N3	2.35	120.83	117.15
1	A	516	PSU	O4'-C1'-C2'	2.34	108.45	105.14
22	a	2030	6MZ	C4-C5-N7	-2.34	107.77	110.62
22	a	2069	G7M	CN7-N7-C8	-2.33	121.24	124.84
22	a	2069	G7M	N2-C2-N1	2.33	121.68	116.71
1	A	1519	MA6	N3-C4-N9	2.33	130.92	127.08
22	a	2449	H2U	C5-C4-N3	-2.32	114.05	116.65
22	a	745	1MG	C8-N7-C5	2.31	108.42	104.24
33	l	81	4D4	O-C-CA	-2.30	118.75	124.78
22	a	1917	PSU	O2-C2-N1	-2.30	120.26	122.79
53	V	54	5MU	C6-N1-C2	-2.29	118.98	121.30
1	A	1407	5MC	CM5-C5-C6	-2.29	119.80	122.85
22	a	1835	2MG	O6-C6-C5	-2.28	120.55	126.60
55	X	37	T6A	C4-C5-N7	-2.28	107.84	110.62
12	L	89	D2T	O-C-CA	-2.27	118.83	124.78
22	a	2069	G7M	N9-C8-N7	-2.26	106.63	112.21
55	X	16	H2U	O2-C2-N3	-2.25	117.31	121.50
53	V	35	U8U	C1'-N1-C6	-2.25	117.38	121.12
1	A	1516	2MG	C1'-N9-C4	-2.25	119.82	126.50
55	X	34	A1LZ3	C5-C4-N3	-2.25	119.13	121.72
53	V	13	PSU	O2-C2-N1	-2.25	120.32	122.79
22	a	746	PSU	O2-C2-N1	-2.24	120.32	122.79
25	d	150	MEQ	OE1-CD-CG	2.24	126.11	122.02
22	a	2552	OMU	O2-C2-N1	-2.24	119.81	122.79
22	a	745	1MG	N9-C4-N3	2.23	130.43	125.94
53	V	54	5MU	O2-C2-N1	-2.23	119.82	122.79
1	A	1519	MA6	C4-N9-C8	2.20	108.11	105.73
55	X	39	PSU	O2-C2-N1	-2.19	120.38	122.79
1	A	1518	MA6	N3-C4-N9	2.19	130.70	127.08
22	a	2445	2MG	C8-N7-C5	2.19	108.20	104.24
53	V	55	PSU	O4'-C1'-C2'	2.18	108.22	105.14
22	a	2069	G7M	N1-C2-N3	-2.17	119.28	123.32
1	A	1207	2MG	C8-N7-C5	2.17	108.17	104.24
1	A	966	2MG	C8-N7-C5	2.16	108.15	104.24
22	a	2498	OMC	O2-C2-N3	-2.16	118.81	122.33
22	a	1835	2MG	CM2-N2-C2	-2.16	119.09	123.86
53	V	38	2MA	CM2-C2-N3	2.16	120.52	117.15
22	a	745	1MG	C1'-N9-C8	-2.13	120.64	126.70
55	X	46	G7M	CN7-N7-C8	-2.12	121.56	124.84
25	d	150	MEQ	CG-CD-NE2	-2.11	113.35	116.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	a	1911	PSU	O4'-C1'-C2'	2.11	108.12	105.14
22	a	1835	2MG	C8-N7-C5	2.10	108.04	104.24
53	V	38	2MA	C4-C5-N7	-2.09	108.07	110.62
1	A	1516	2MG	C4-C5-N7	-2.09	107.41	110.72
22	a	745	1MG	C4-C5-N7	-2.09	107.42	110.72
55	X	16	H2U	C4-N3-C2	2.07	127.51	125.79
22	a	745	1MG	CM1-N1-C6	2.07	120.86	117.69
55	X	47	3AU	O31-C13-C12	2.05	120.37	113.38
55	X	37	T6A	C5-C4-N9	2.05	108.16	105.78
55	X	47	3AU	C6-N1-C2	-2.04	119.97	121.79
55	X	34	A1LZ3	N4-C4-N3	2.03	119.71	116.49
22	a	2030	6MZ	C5-C4-N9	2.01	108.12	105.78

There are no chirality outliers.

All (61) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	L	89	D2T	CA-CB-CG-OD1
12	L	89	D2T	CA-CB-CG-OD2
25	d	150	MEQ	C-CA-CB-CG
53	V	13	PSU	C3'-C4'-C5'-O5'
22	a	2251	OMG	C1'-C2'-O2'-CM2
55	X	20	H2U	O4'-C4'-C5'-O5'
55	X	20	H2U	C3'-C4'-C5'-O5'
55	X	20(A)	H2U	O4'-C4'-C5'-O5'
55	X	20(A)	H2U	C3'-C4'-C5'-O5'
55	X	37	T6A	N11-C12-C13-ODA
55	X	37	T6A	N11-C12-C13-ODB
55	X	37	T6A	C14-C12-C13-ODA
55	X	37	T6A	C14-C12-C13-ODB
55	X	47	3AU	N3-C10-C11-C12
55	X	47	3AU	C10-C11-C12-N40
55	X	47	3AU	N40-C12-C13-O31
53	V	54	5MU	O4'-C4'-C5'-O5'
55	X	16	H2U	C2'-C1'-N1-C2
53	V	13	PSU	O4'-C4'-C5'-O5'
55	X	54	5MU	O4'-C4'-C5'-O5'
55	X	16	H2U	C2'-C1'-N1-C6
25	d	150	MEQ	NE2-CD-CG-CB
25	d	150	MEQ	OE1-CD-CG-CB
1	A	527	G7M	C3'-C4'-C5'-O5'
22	a	1915	3TD	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
53	V	55	PSU	C4'-C5'-O5'-P
53	V	54	5MU	C3'-C4'-C5'-O5'
22	a	1915	3TD	O4'-C4'-C5'-O5'
22	a	2504	PSU	O4'-C4'-C5'-O5'
55	X	54	5MU	C3'-C4'-C5'-O5'
1	A	1519	MA6	O4'-C4'-C5'-O5'
55	X	17	H2U	C3'-C4'-C5'-O5'
55	X	47	3AU	N40-C12-C13-O30
12	L	89	D2T	CG-CB-SB-CB1
55	X	20(A)	H2U	C4'-C5'-O5'-P
55	X	47	3AU	C10-C11-C12-C13
25	d	150	MEQ	N-CA-CB-CG
1	A	527	G7M	O4'-C4'-C5'-O5'
33	l	82	MS6	CB-CG-SD-CE
1	A	966	2MG	C3'-C4'-C5'-O5'
22	a	747	5MU	C3'-C4'-C5'-O5'
1	A	1519	MA6	C3'-C4'-C5'-O5'
22	a	2504	PSU	C3'-C4'-C5'-O5'
53	V	55	PSU	O4'-C1'-C5-C4
55	X	37	T6A	C13-C12-N11-C10
55	X	47	3AU	C11-C12-C13-O31
55	X	16	H2U	O4'-C4'-C5'-O5'
55	X	17	H2U	O4'-C4'-C5'-O5'
12	L	89	D2T	SB-CB-CG-OD2
55	X	47	3AU	C11-C12-C13-O30
22	a	2030	6MZ	O4'-C4'-C5'-O5'
55	X	17	H2U	C4'-C5'-O5'-P
22	a	746	PSU	O4'-C1'-C5-C6
55	X	20(A)	H2U	O4'-C1'-N1-C6
22	a	2069	G7M	C4'-C5'-O5'-P
22	a	2503	2MA	C4'-C5'-O5'-P
22	a	2069	G7M	O4'-C4'-C5'-O5'
22	a	2503	2MA	O4'-C4'-C5'-O5'
33	l	81	4D4	O-C-CA-CB
1	A	1519	MA6	C4'-C5'-O5'-P
55	X	20(A)	H2U	C2'-C1'-N1-C2

There are no ring outliers.

No monomer is involved in short contacts.

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 309 ligands modelled in this entry, 309 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

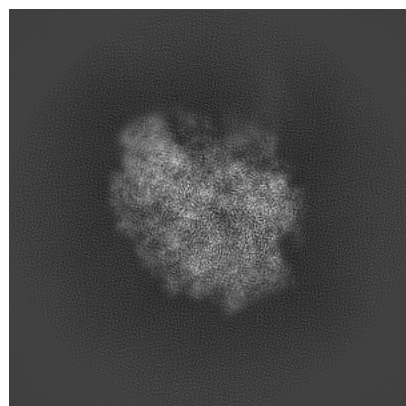
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39578. These allow visual inspection of the internal detail of the map and identification of artifacts.

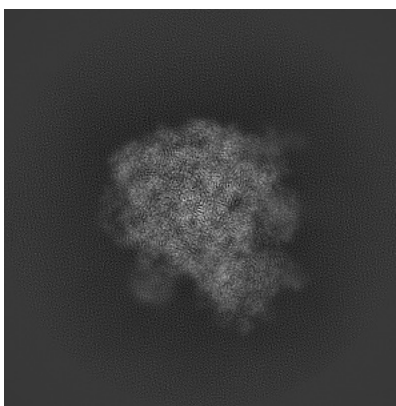
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

5.1 Orthogonal projections [i](#)

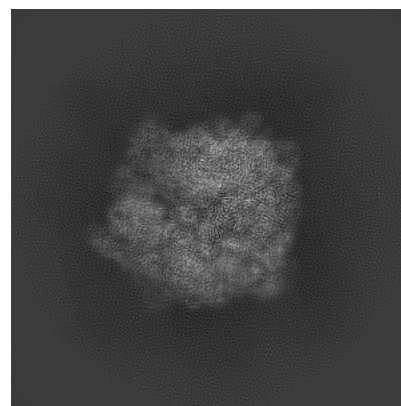
5.1.1 Primary map



X

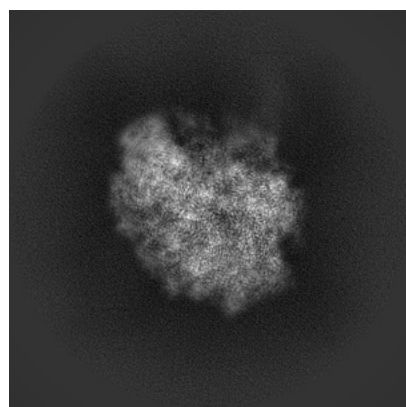


Y

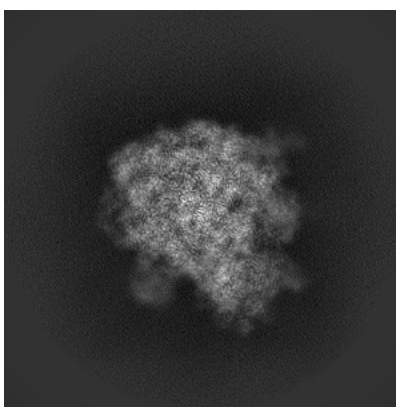


Z

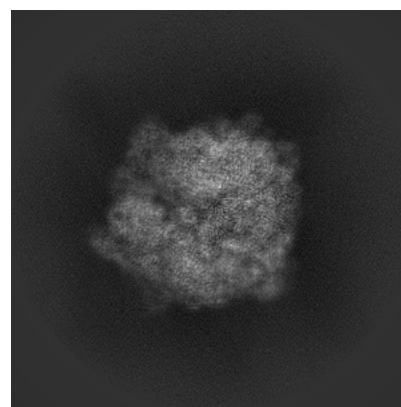
5.1.2 Raw map



X



Y

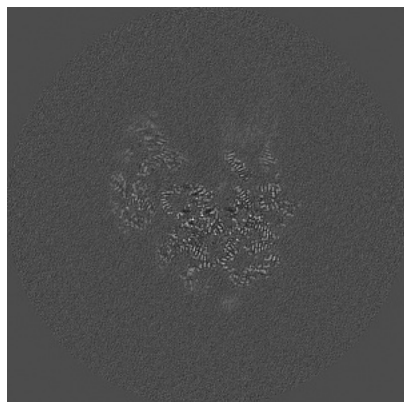


Z

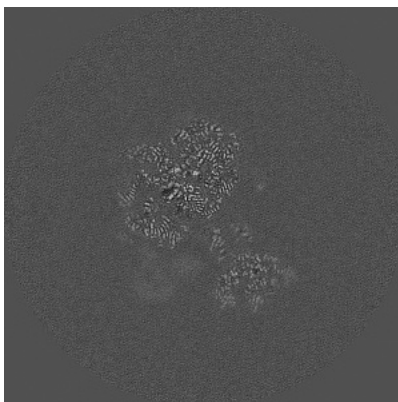
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

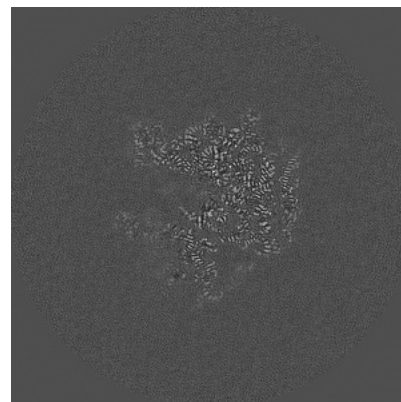
5.2.1 Primary map



X Index: 265

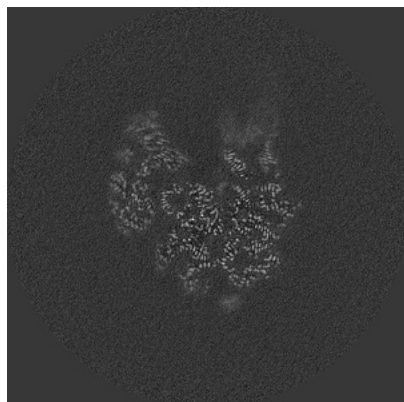


Y Index: 265

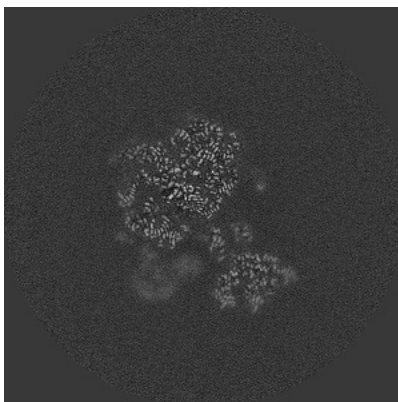


Z Index: 265

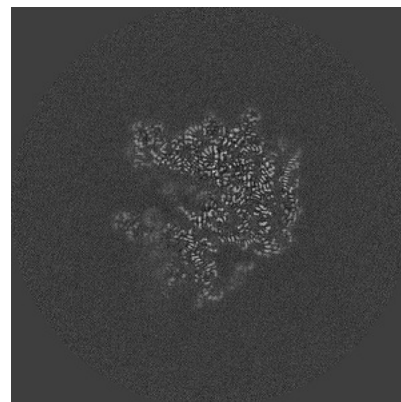
5.2.2 Raw map



X Index: 265



Y Index: 265

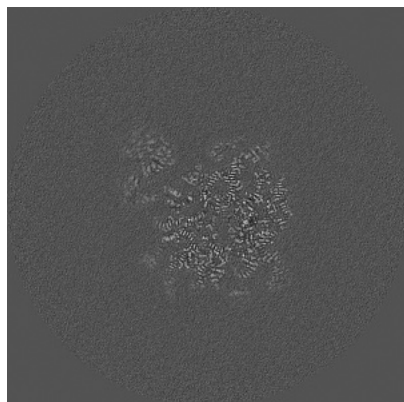


Z Index: 265

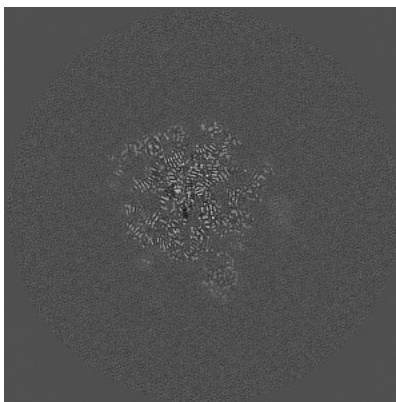
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

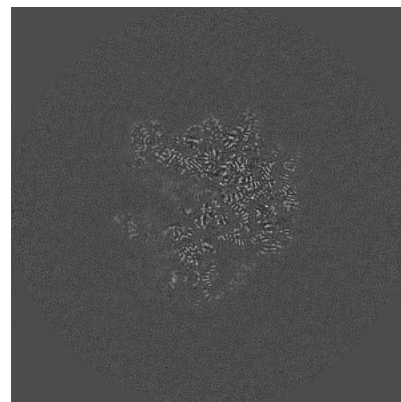
5.3.1 Primary map



X Index: 297

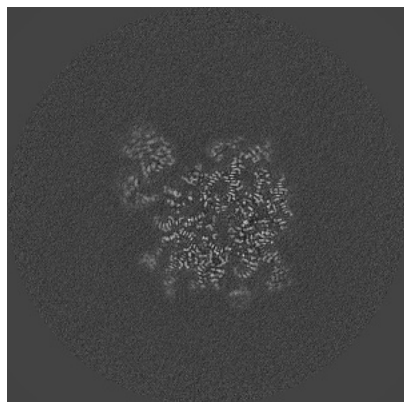


Y Index: 319

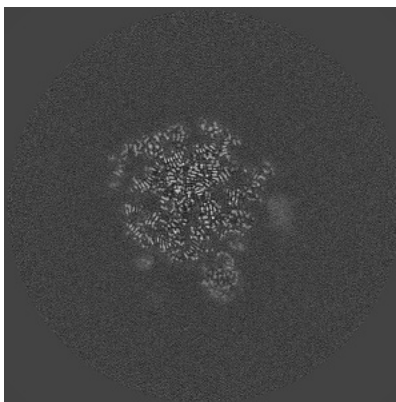


Z Index: 268

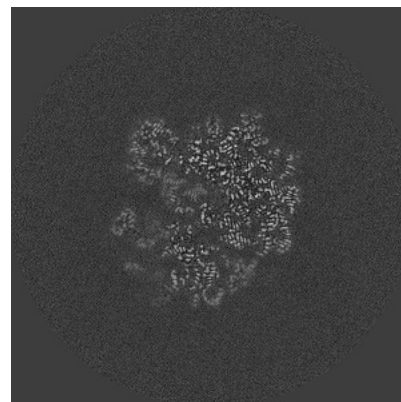
5.3.2 Raw map



X Index: 297



Y Index: 319

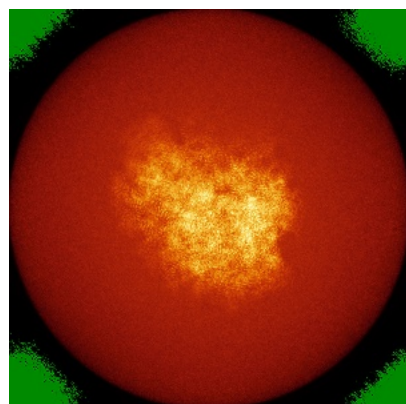


Z Index: 272

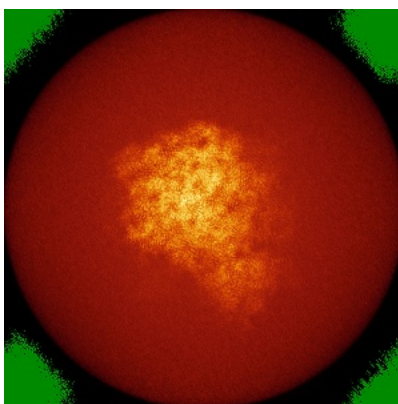
The images above show the largest variance slices of the map in three orthogonal directions.

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

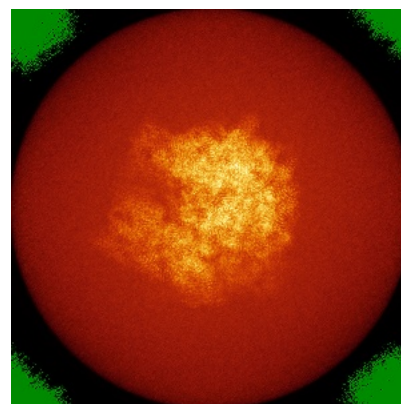
5.4.1 Primary map



X

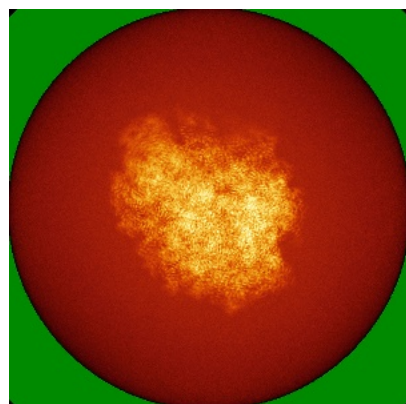


Y

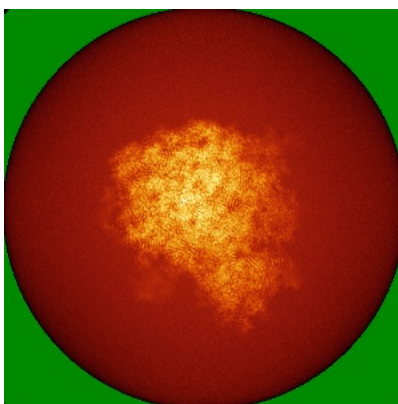


Z

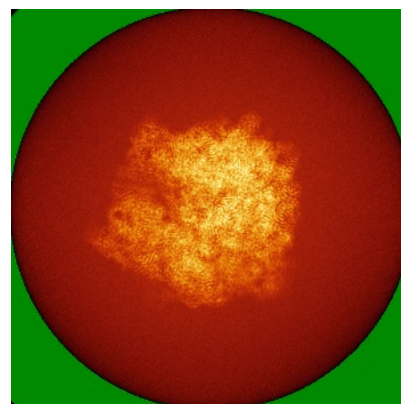
5.4.2 Raw map



X



Y

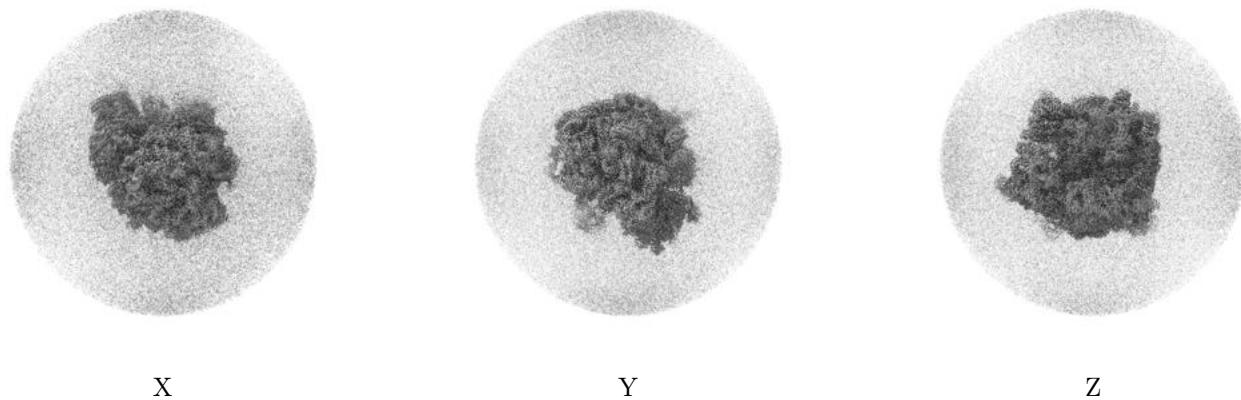


Z

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.

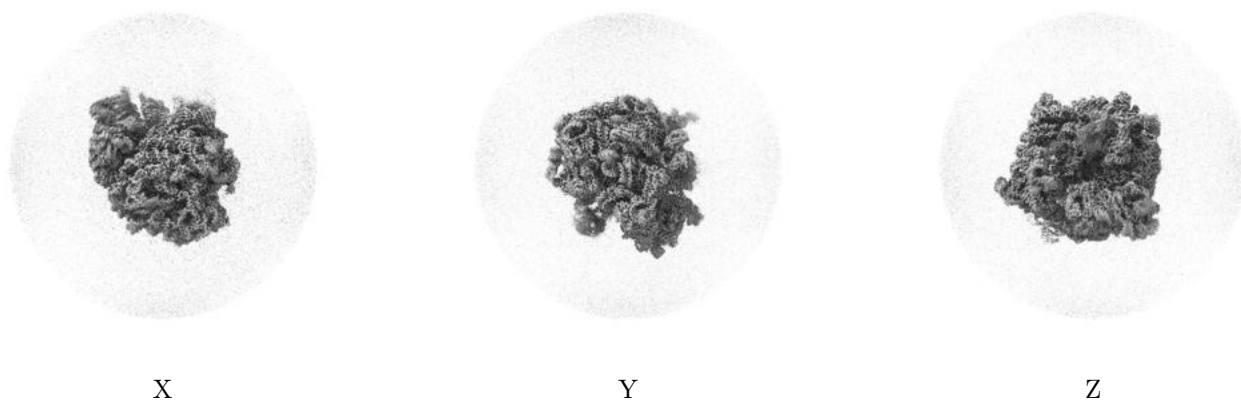
5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0268. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

5.5.2 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.

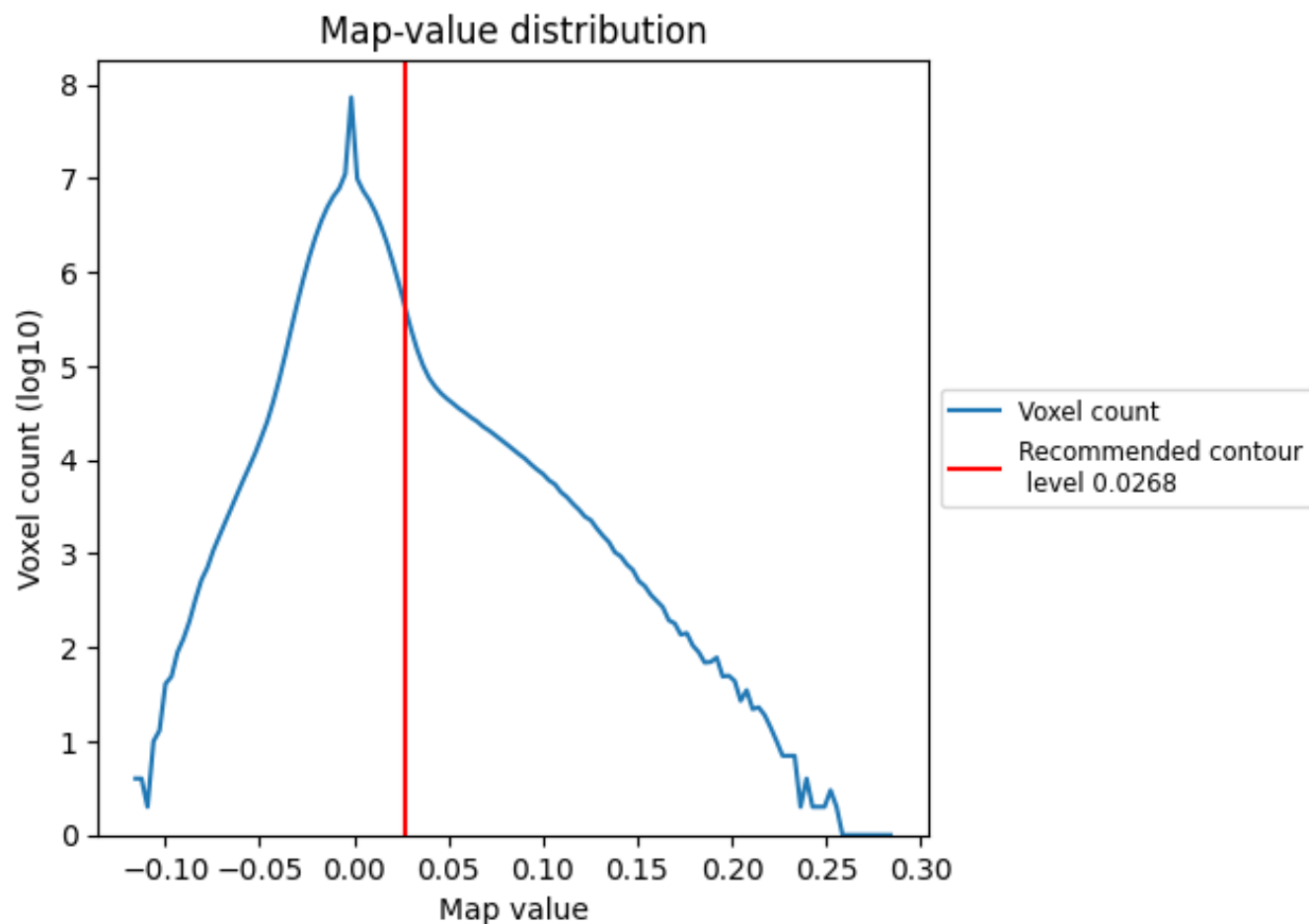
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

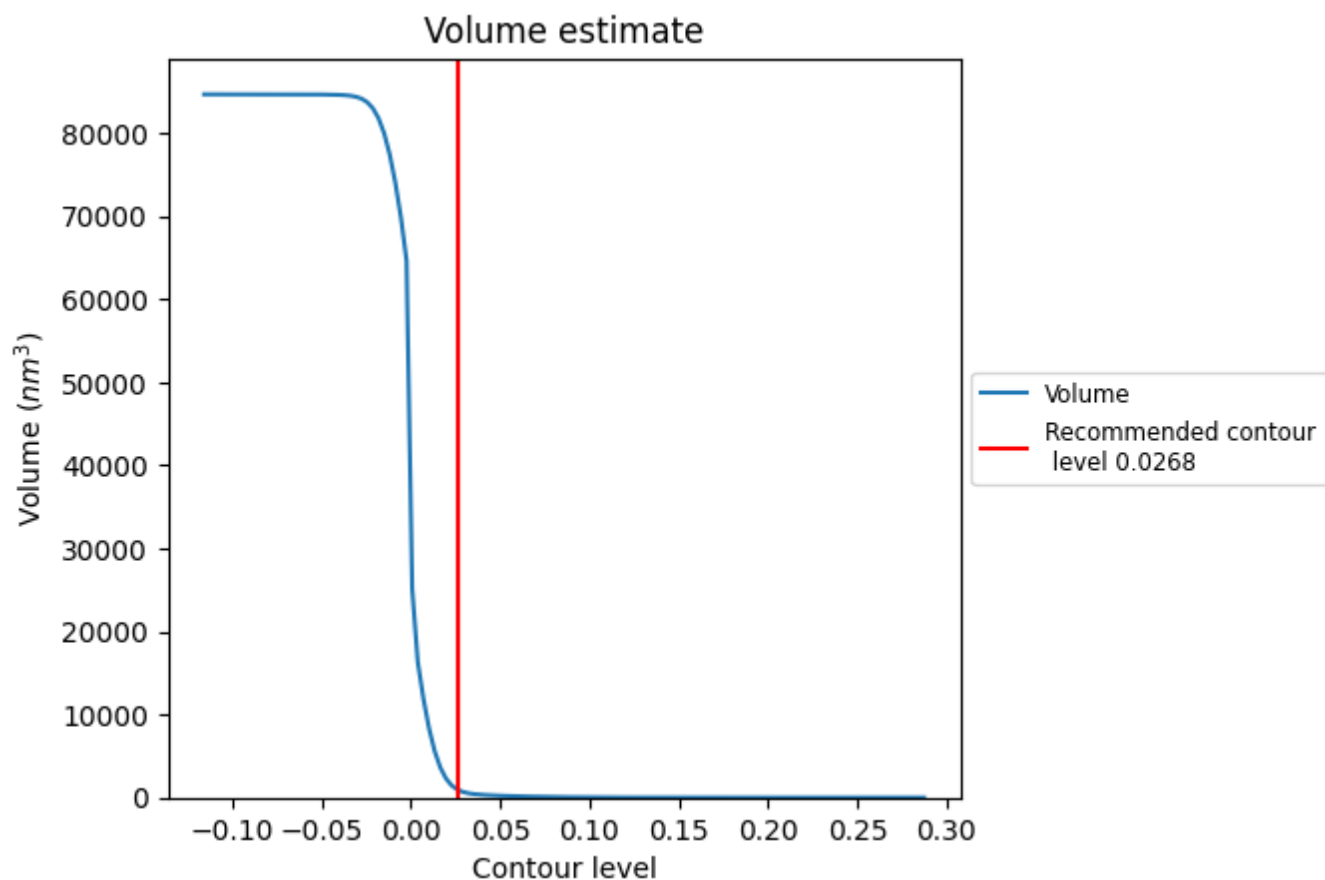
This section contains the results of statistical analysis of the map.

6.1 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.

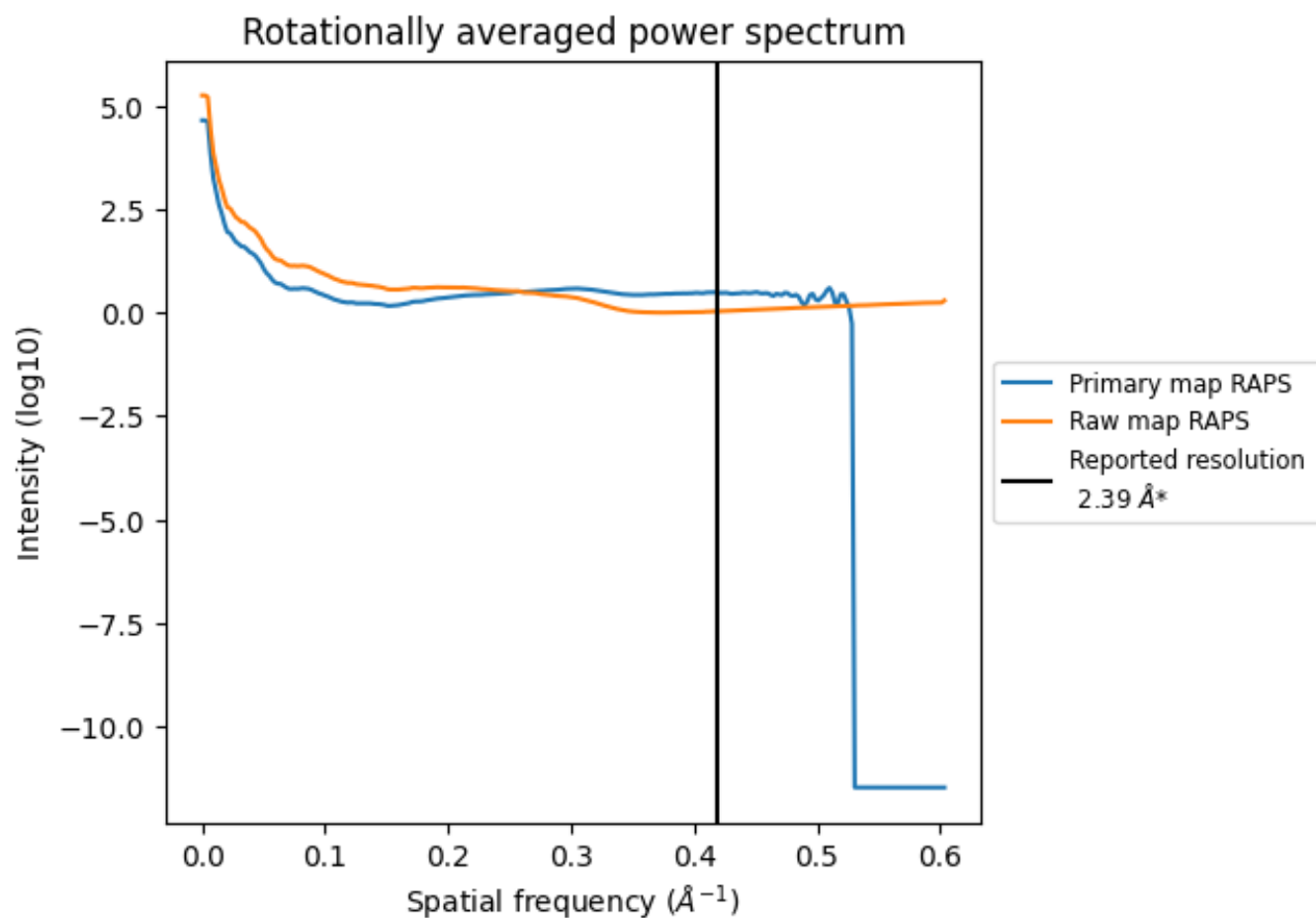
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 900 nm^3 ; this corresponds to an approximate mass of 813 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.

6.3 Rotationally averaged power spectrum ⓘ

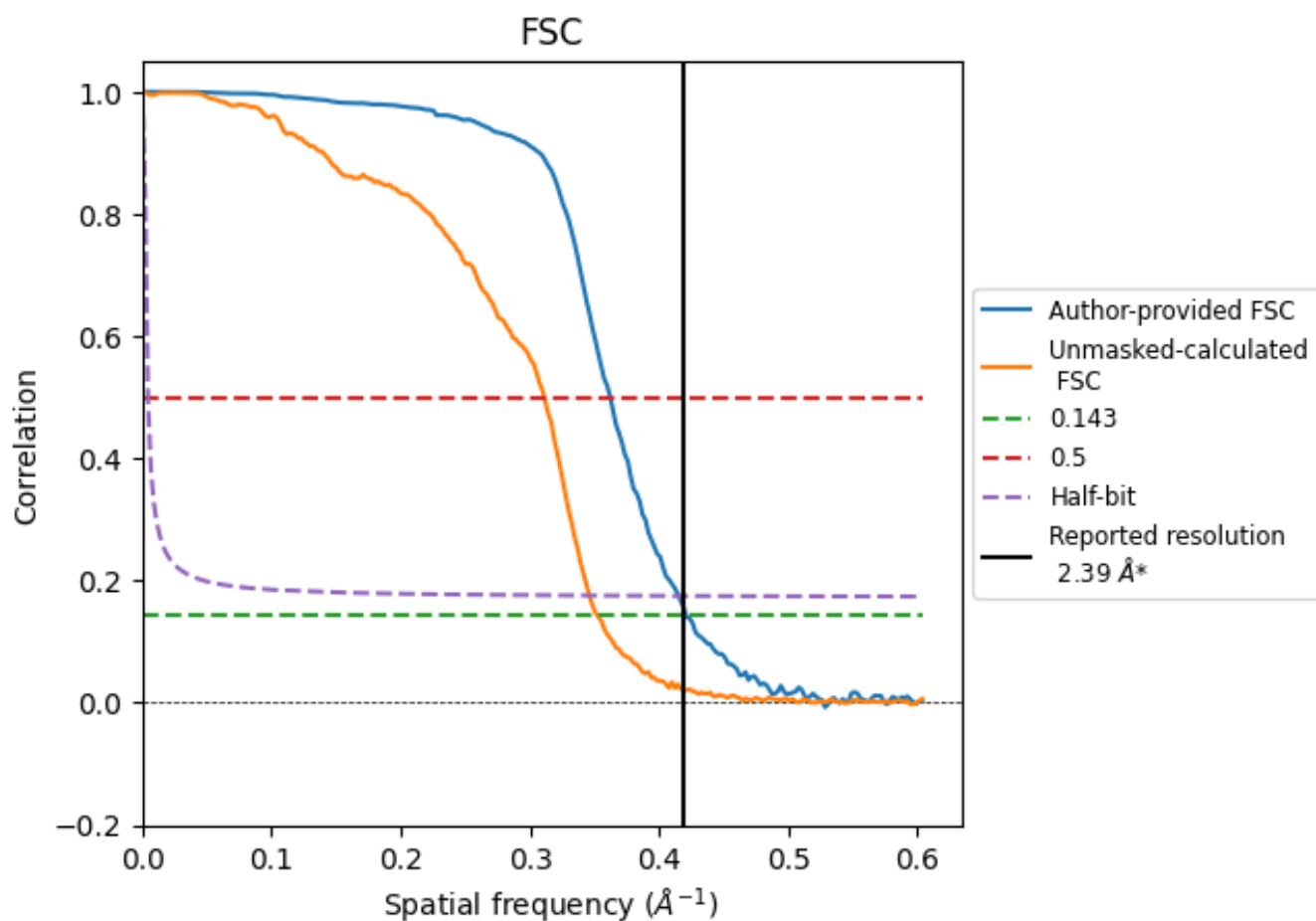


*Reported resolution corresponds to spatial frequency of 0.418 Å⁻¹

7 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.

7.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.418 $\text{\AA}^{-1}$

7.2 Resolution estimates [i](#)

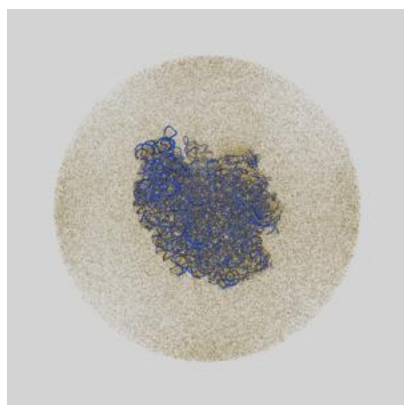
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.39	-	-
Author-provided FSC curve	2.38	2.76	2.41
Unmasked-calculated*	2.84	3.21	2.89

*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 2.84 differs from the reported value 2.39 by more than 10 %

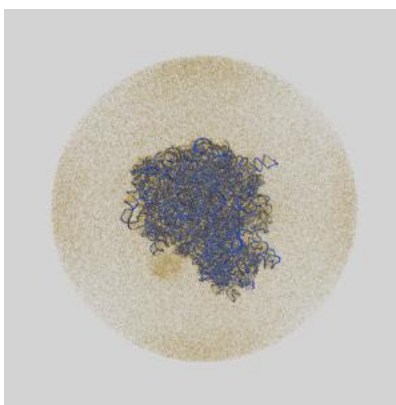
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-39578 and PDB model 8YUP. Per-residue inclusion information can be found in section ?? on page ??.

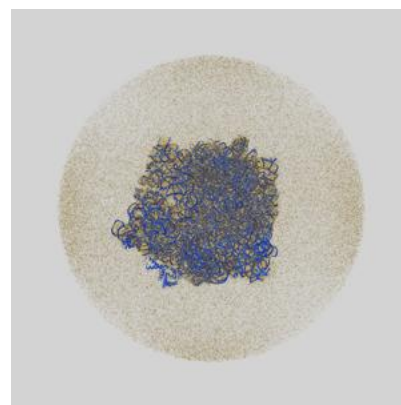
8.1 Map-model overlay [i](#)



X



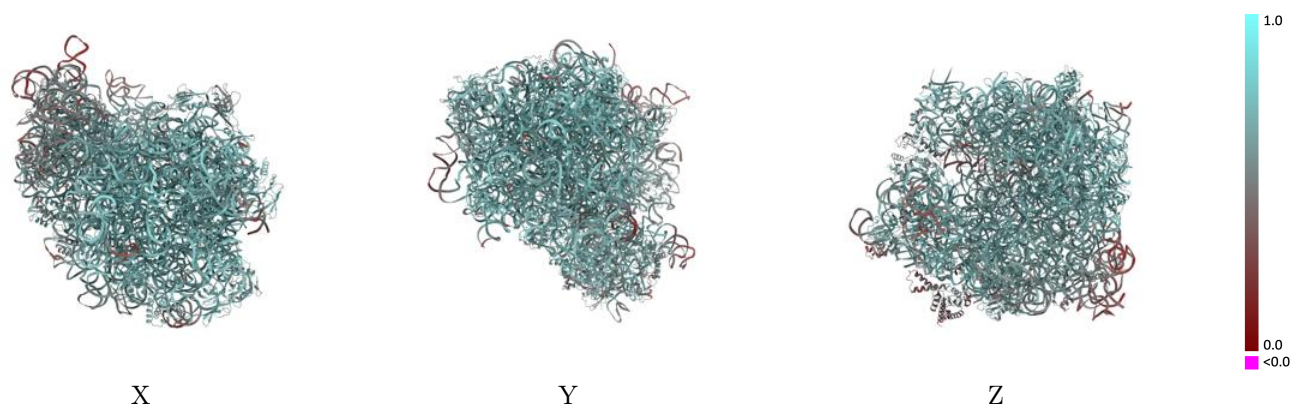
Y



Z

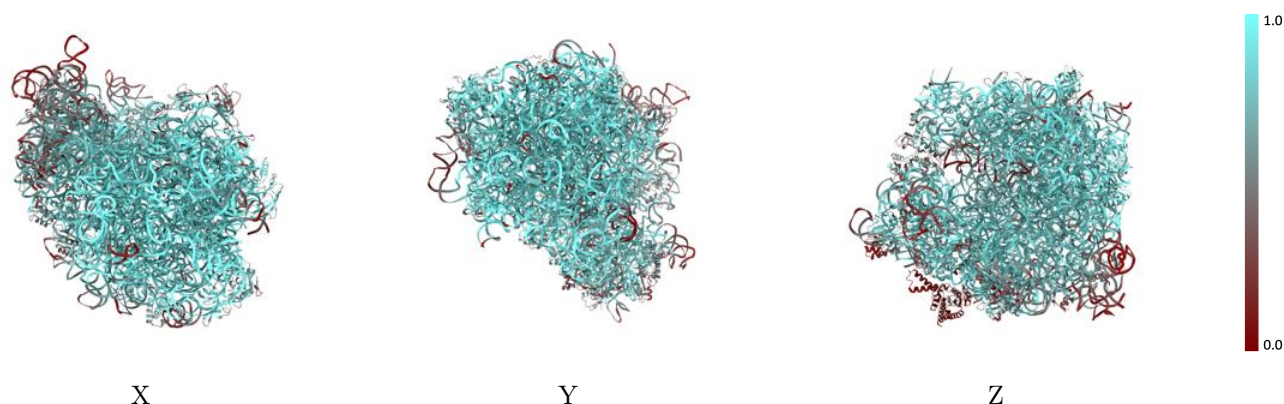
The images above show the 3D surface view of the map at the recommended contour level 0.0268 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



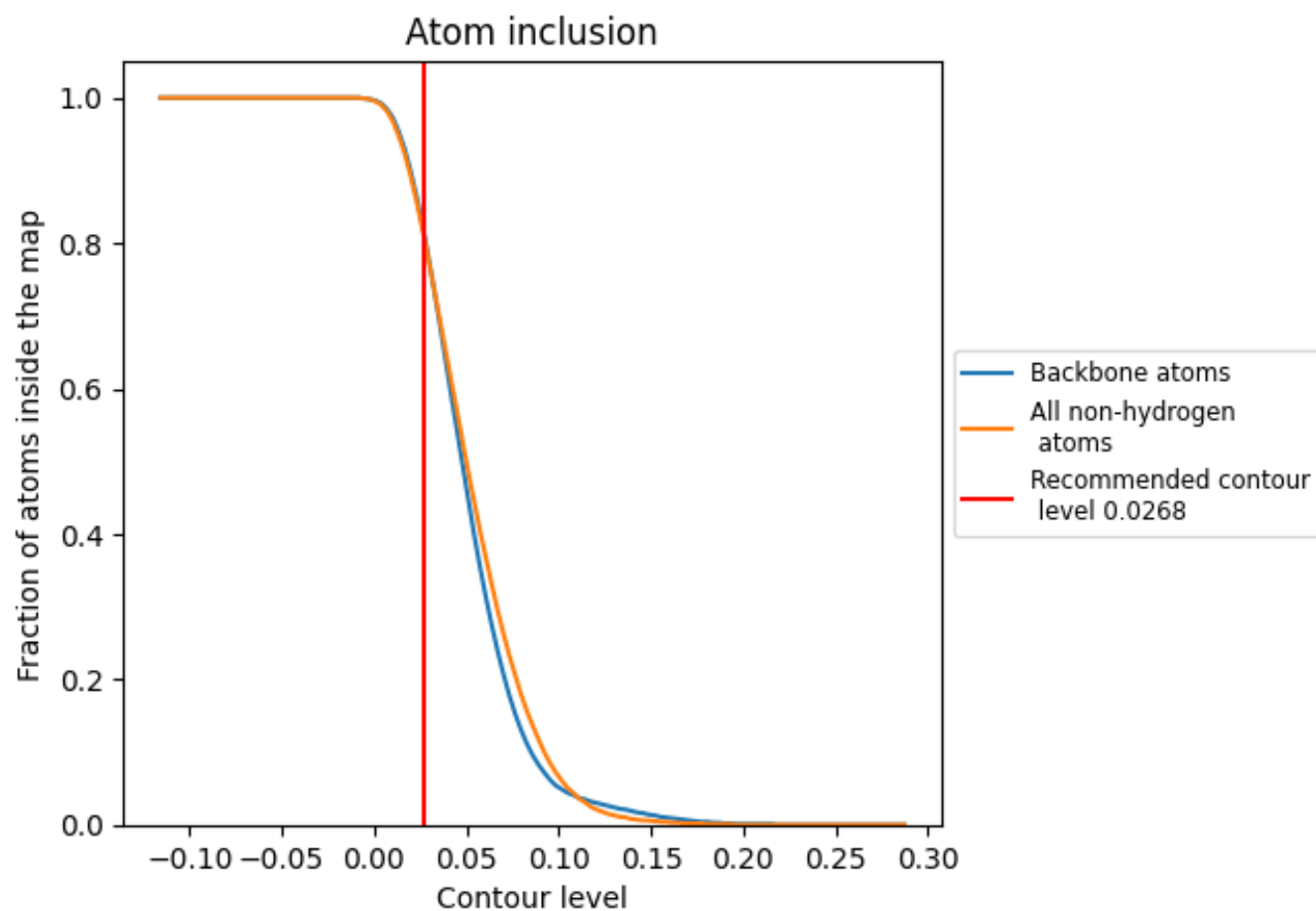
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

8.3 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 (0.0268).

8.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0268) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8120	 0.6510
0	 0.8310	 0.6800
1	 0.9410	 0.7260
2	 0.9570	 0.7370
3	 0.8900	 0.6910
4	 0.4060	 0.5080
A	 0.7840	 0.6180
B	 0.1100	 0.4330
C	 0.7140	 0.6340
D	 0.4010	 0.5310
E	 0.8030	 0.6660
F	 0.5420	 0.5650
G	 0.5570	 0.5780
H	 0.7780	 0.6520
I	 0.6580	 0.6030
J	 0.5060	 0.5480
K	 0.6930	 0.6200
L	 0.7360	 0.6480
M	 0.6720	 0.6080
N	 0.7540	 0.6440
O	 0.7260	 0.6290
P	 0.5040	 0.5480
Q	 0.5570	 0.5610
R	 0.6670	 0.5980
S	 0.6550	 0.6080
T	 0.4530	 0.5040
U	 0.3290	 0.4930
V	 0.6390	 0.5620
W	 0.7190	 0.5970
X	 0.6350	 0.5610
a	 0.9090	 0.6870
b	 0.8590	 0.6520
c	 0.9330	 0.7320
d	 0.8970	 0.7110
e	 0.7550	 0.6570



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Chain	Atom inclusion	Q-score
f	 0.6110	 0.5880
g	 0.5680	 0.5780
h	 0.4600	 0.5650
i	 0.9150	 0.7130
j	 0.8710	 0.7110
k	 0.8620	 0.6930
l	 0.8980	 0.7110
m	 0.9580	 0.7290
n	 0.7930	 0.6480
o	 0.8580	 0.6990
p	 0.9380	 0.7260
q	 0.8260	 0.6790
r	 0.8790	 0.6950
s	 0.7510	 0.6410
t	 0.6990	 0.6200
u	 0.7750	 0.6600
v	 0.9090	 0.7170
w	 0.8600	 0.6950
x	 0.6460	 0.6000
y	 0.8650	 0.6890
z	 0.8810	 0.7040