



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 24, 2024 – 05:13 PM EDT

PDB ID : 6CAP  
Title : Crystal Structure of 30S ribosomal subunit from *Thermus thermophilus* in complex with Sisomicin  
Authors : DeMirici, H.  
Deposited on : 2018-01-31  
Resolution : 3.40 Å (reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.37.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.37.1

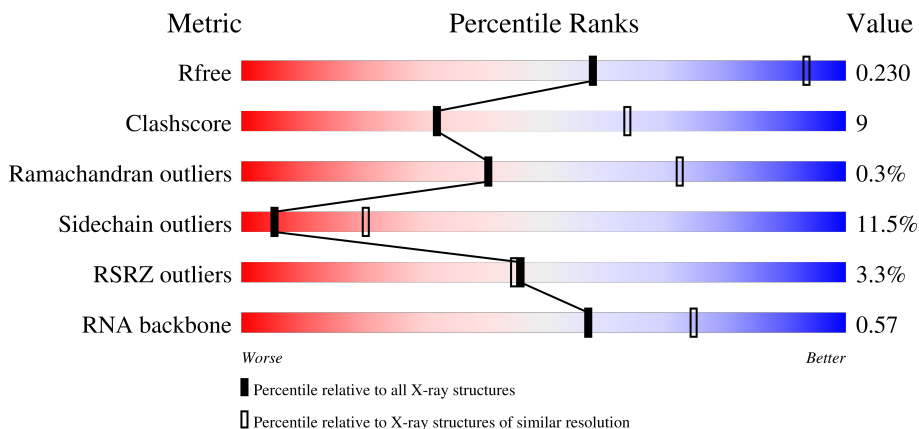
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



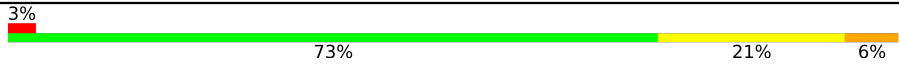

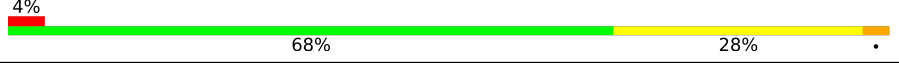
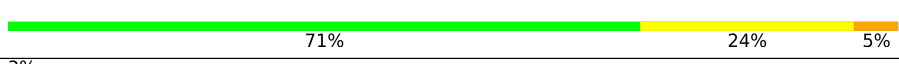

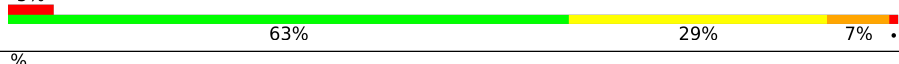


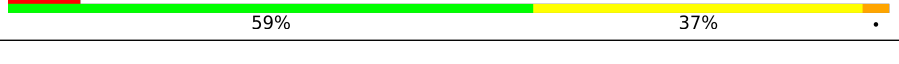


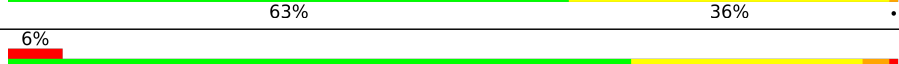

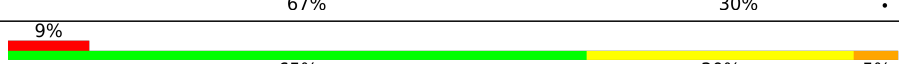
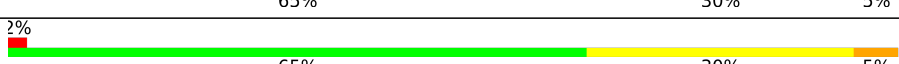
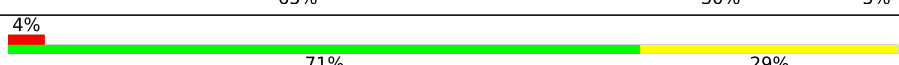

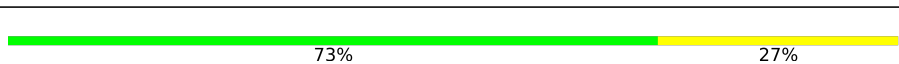

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)
RNA backbone	3102	1006 (3.84-2.96)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1522	 2% 59% 32% 8% ..
2	B	234	 2% 66% 30% .
3	C	206	 8% 65% 31% .
4	D	208	 5% 64% 32% .

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Mol	Chain	Length	Quality of chain
5	E	150	
6	F	101	
7	G	155	
8	H	138	
9	I	127	
10	J	98	
11	K	116	
12	L	124	
13	M	118	
14	N	60	
15	O	87	
16	P	83	
17	Q	99	
18	R	70	
19	S	80	
20	T	99	
21	U	24	
22	Y	6	
23	W	15	

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
24	MG	A	1631	-	-	-	X
24	MG	A	1639	-	-	-	X
24	MG	A	1663	-	-	-	X
24	MG	A	1665	-	-	-	X
24	MG	A	1674	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	MG	A	1682	-	-	-	X
24	MG	A	1706	-	-	-	X
24	MG	A	1709	-	-	-	X
24	MG	A	1721	-	-	-	X
24	MG	A	1723	-	-	-	X
24	MG	A	1729	-	-	-	X
24	MG	A	1733	-	-	-	X
24	MG	A	1752	-	-	-	X
24	MG	A	1753	-	-	-	X
24	MG	A	1754	-	-	-	X
24	MG	A	1759	-	-	-	X
24	MG	A	1761	-	-	-	X
24	MG	A	1762	-	-	-	X
24	MG	A	1769	-	-	-	X
24	MG	A	1772	-	-	-	X
24	MG	A	1780	-	-	-	X
24	MG	A	1791	-	-	-	X
24	MG	A	1793	-	-	-	X
24	MG	A	1794	-	-	-	X
24	MG	A	1797	-	-	-	X
24	MG	A	1802	-	-	-	X
24	MG	A	1804	-	-	-	X
24	MG	A	1805	-	-	-	X
24	MG	A	1808	-	-	-	X
24	MG	A	1811	-	-	-	X
24	MG	A	1815	-	-	-	X
24	MG	A	1817	-	-	-	X
24	MG	K	201	-	-	-	X
24	MG	L	201	-	-	-	X
24	MG	L	202	-	-	-	X
24	MG	L	203	-	-	-	X

## 2 Entry composition

There are 27 unique types of molecules in this entry. The entry contains 52675 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Ribosomal RNA rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	A	1512	32644	14540	6040	10546	1518	0	6	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	13	C	U	conflict	GB 55771382

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	234	1900	1213	341	341	5	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	206	1612	1016	314	281	1	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	208	1703	1066	339	291	7	0	0	0

- Molecule 5 is a protein called RIBOSOMAL PROTEIN S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	150	1146	724	217	201	4	0	0	0

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	F	101	843	531	155	154	3	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
7	G	155	1257	781	252	218	6	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
8	H	138	1116	705	215	193	3	0	0	0

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
9	I	127	1010	639	197	174	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
10	J	98	792	498	156	137	1	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
11	K	116	864	537	164	160	3	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
12	L	124	972	612	195	163	2	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
13	M	118	937	579	193	163	2	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
14	N	60	492	312	104	72	4	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
15	O	87	729	457	146	124	2	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
16	P	83	700	443	139	117	1	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
17	Q	99	823	528	152	141	2	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	96	GLN	GLU	conflict	UNP P0DOY7

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
18	R	70	574	367	112	95	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	80	Total	C	N	O	S	0	0	0
			647	414	119	112	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	T	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	U	24	Total	C	N	O	0	0	0
			208	128	50	30			

- Molecule 22 is a RNA chain called RNA (5'-R(\*UP\*UP\*UP\*UP\*UP\*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	Y	6	Total	C	N	O	P	0	0	0
			117	54	12	46	5			

- Molecule 23 is a RNA chain called RNA (5'-R(\*GP\*GP\*GP\*AP\*UP\*UP\*GP\*AP\*AP\*AP\*AP\*UP\*CP\*CP\*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	W	15	Total	C	N	O	P	0	0	0
			319	144	60	101	14			

- Molecule 24 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	A	216	Total	Mg	0	0
			216	216		
24	B	3	Total	Mg	0	0
			3	3		
24	C	5	Total	Mg	0	0
			5	5		
24	D	3	Total	Mg	0	0
			3	3		
24	E	1	Total	Mg	0	0
			1	1		
24	F	1	Total	Mg	0	0
			1	1		

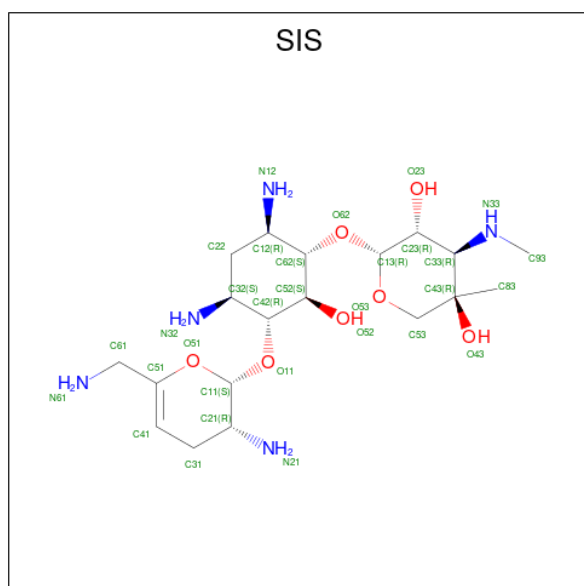
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	H	2	Total	Mg	0	0
			2	2		
24	K	4	Total	Mg	0	0
			4	4		
24	L	3	Total	Mg	0	0
			3	3		
24	M	5	Total	Mg	0	0
			5	5		
24	P	3	Total	Mg	0	0
			3	3		
24	Q	3	Total	Mg	0	0
			3	3		
24	S	1	Total	Mg	0	0
			1	1		
24	T	1	Total	Mg	0	0
			1	1		
24	W	1	Total	Mg	0	0
			1	1		

- Molecule 25 is (1S,2S,3R,4S,6R)-4,6-diamino-3-[[[(2S,3R)-3-amino-6-(aminomethyl)-3,4-dihydro-2H-pyran-2-yl]oxy]-2-hydroxycyclohexyl 3-deoxy-4-C-methyl-3-(methylamino)-beta-L-a rabinopyranoside (three-letter code: SIS) (formula: C<sub>19</sub>H<sub>37</sub>N<sub>5</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
25	A	1	Total	C	N	O	0	0
			31	19	5	7		

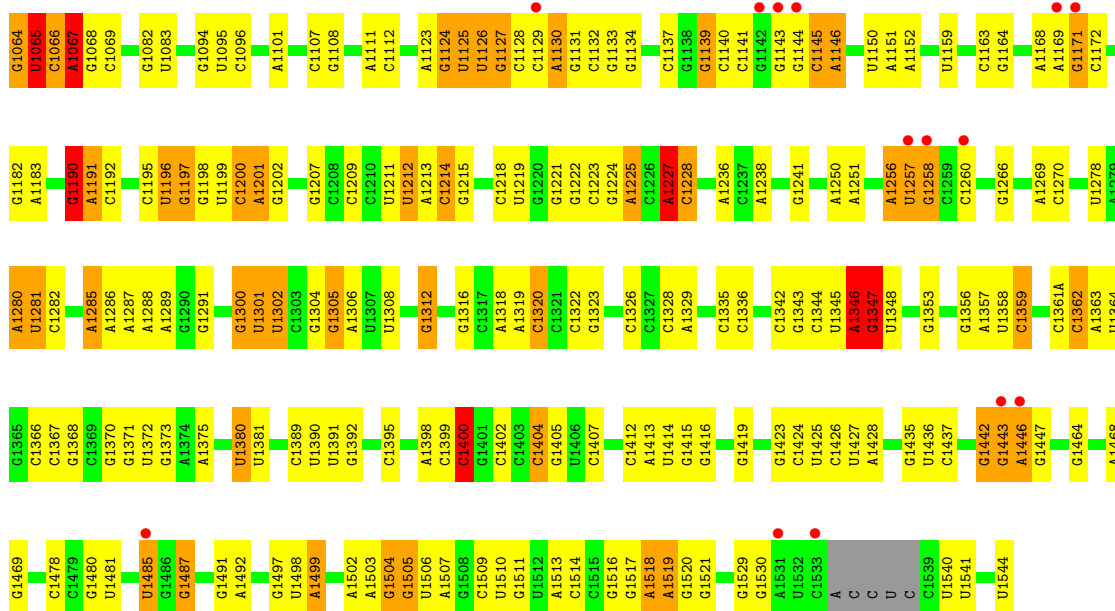
- Molecule 26 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
26	D	1	Total	Zn	0	0
			1	1		
26	N	1	Total	Zn	0	0
			1	1		

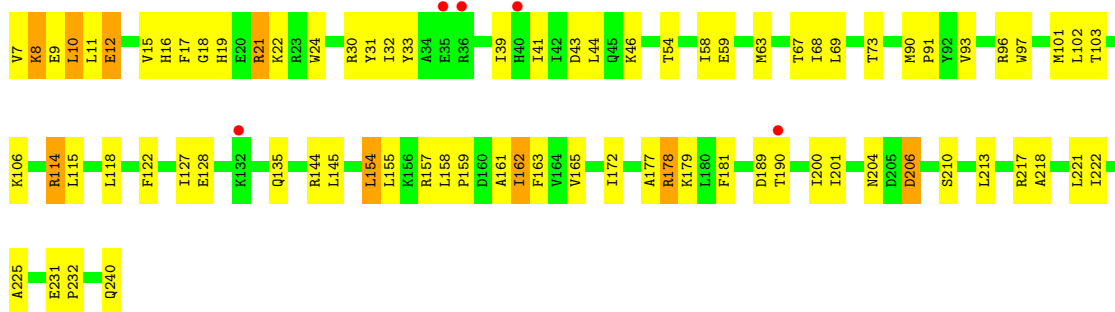
- Molecule 27 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
27	A	192	Total	O	0	0
			192	192		
27	C	1	Total	O	0	0
			1	1		
27	D	1	Total	O	0	0
			1	1		
27	E	6	Total	O	0	0
			6	6		
27	K	11	Total	O	0	0
			11	11		
27	L	3	Total	O	0	0
			3	3		
27	N	1	Total	O	0	0
			1	1		
27	O	1	Total	O	0	0
			1	1		
27	Q	2	Total	O	0	0
			2	2		
27	T	4	Total	O	0	0
			4	4		

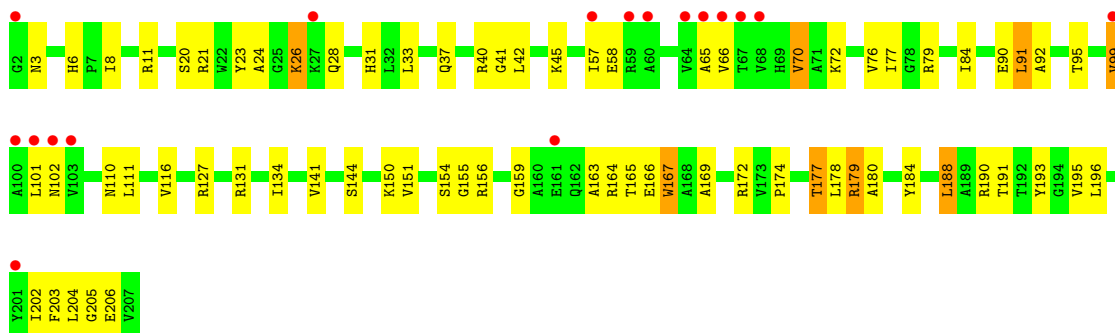




• Molecule 2: 30S ribosomal protein S2

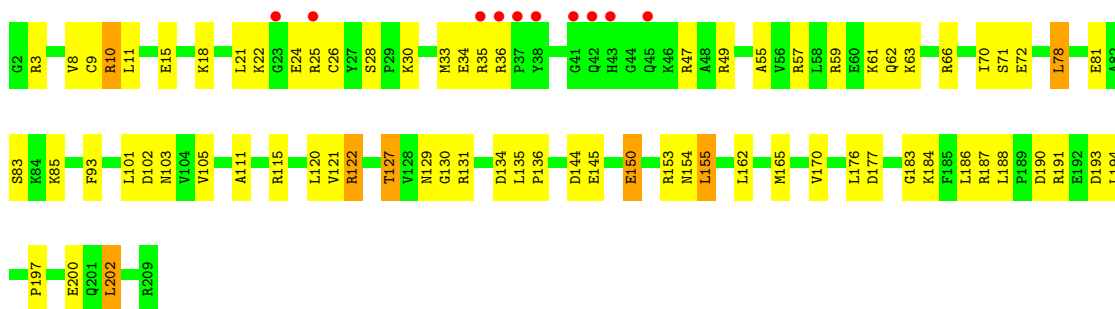


• Molecule 3: 30S ribosomal protein S3

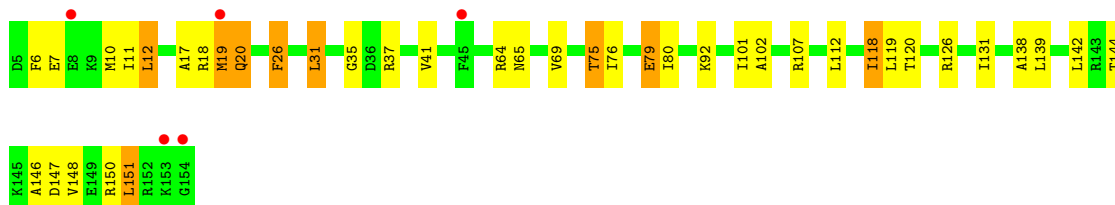
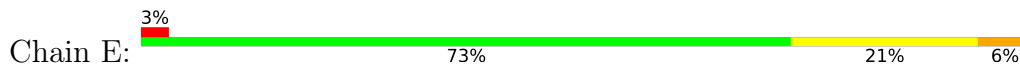


• Molecule 4: 30S ribosomal protein S4

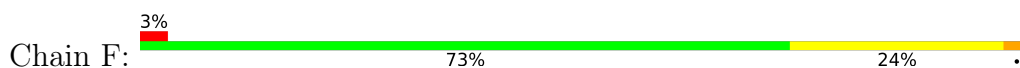




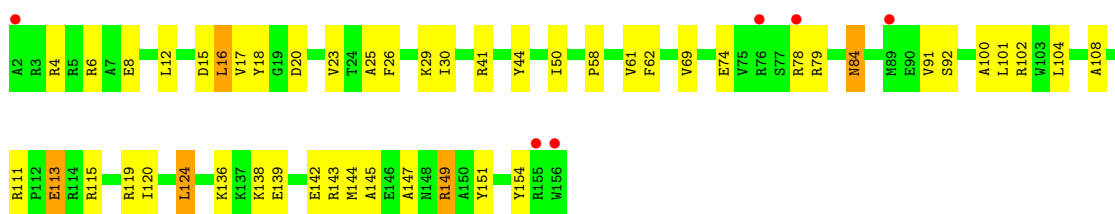
- Molecule 5: RIBOSOMAL PROTEIN S5



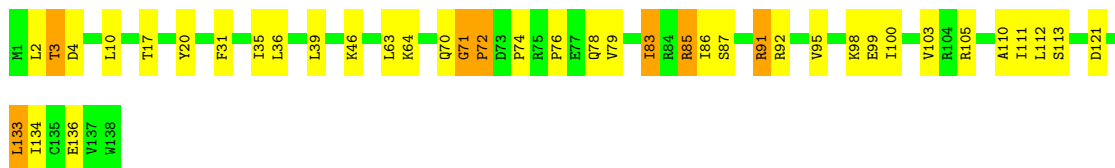
- Molecule 6: 30S ribosomal protein S6



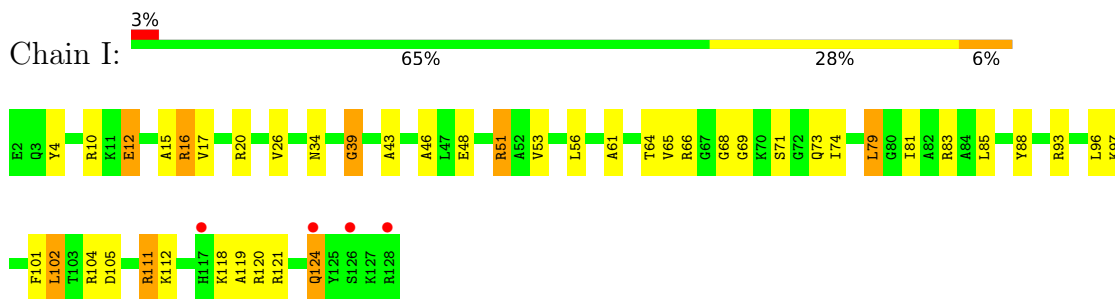
- Molecule 7: 30S ribosomal protein S7



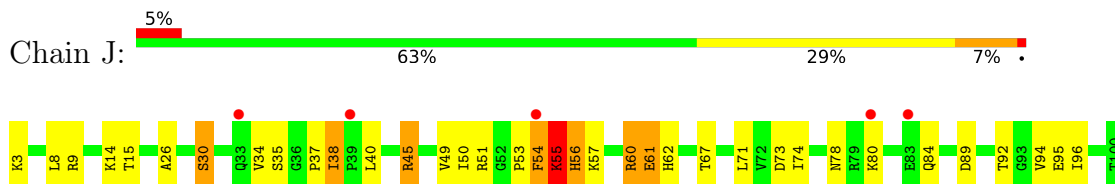
- Molecule 8: 30S ribosomal protein S8



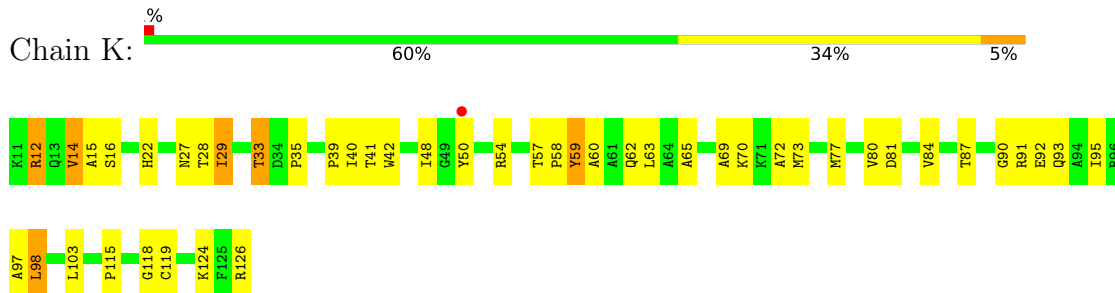
- Molecule 9: 30S ribosomal protein S9



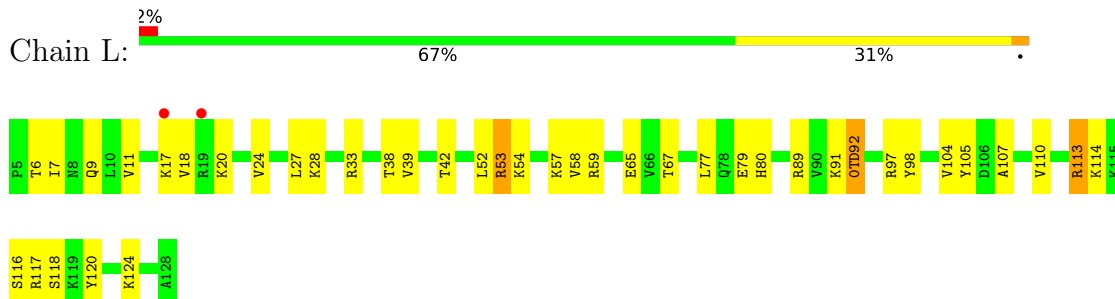
- Molecule 10: 30S ribosomal protein S10



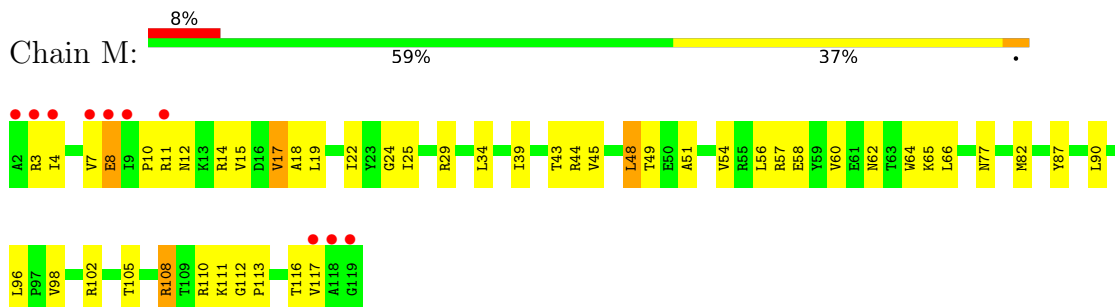
- Molecule 11: 30S ribosomal protein S11



- Molecule 12: 30S ribosomal protein S12



- Molecule 13: 30S ribosomal protein S13



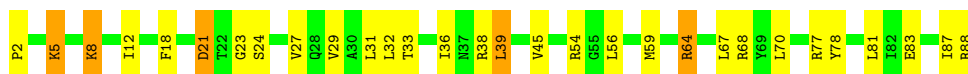
- Molecule 14: 30S ribosomal protein S14 type Z

Chain N:  67% 32%



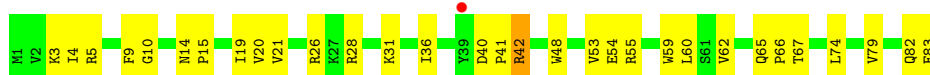
- Molecule 15: 30S ribosomal protein S15

Chain O:  66% 29% 6%



- Molecule 16: 30S ribosomal protein S16

Chain P:  63% 36%



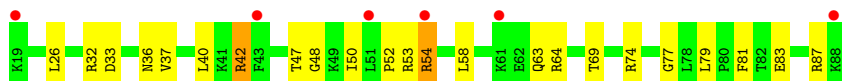
- Molecule 17: 30S ribosomal protein S17

Chain Q:  70% 26% 6%



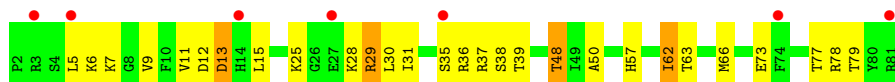
- Molecule 18: 30S ribosomal protein S18

Chain R:  67% 30% 9%



- Molecule 19: 30S ribosomal protein S19

Chain S:  65% 30% 9%



- Molecule 20: 30S ribosomal protein S20

Chain T:  65% 30% 5%





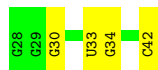
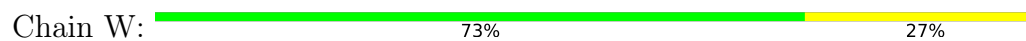
- Molecule 21: 30S ribosomal protein Thx



- Molecule 22: RNA (5'-R(\*UP\*UP\*UP\*UP\*UP\*U)-3')



- Molecule 23: RNA (5'-R(\*GP\*GP\*GP\*AP\*UP\*UP\*GP\*AP\*AP\*AP\*AP\*UP\*CP\*CP\*C)-3')





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	400.97Å 400.97Å 175.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.91 – 3.40 39.91 – 3.12	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.91-3.40) 82.1 (39.91-3.12)	Depositor EDS
$R_{merge}$	1.01	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	-0.05 (at 3.12Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.183 , 0.230 0.183 , 0.230	Depositor DCC
$R_{free}$ test set	2000 reflections (0.82%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	86.1	Xtrriage
Anisotropy	0.204	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.23 , 72.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	52675	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	142.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.50% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PSU, UR3, MA6, 2MG, 4OC, G7M, MG, ZN, SIS, M2G, 0TD, 5MC

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.37	0/36139	0.93	40/56396 (0.1%)
2	B	0.30	0/1935	0.48	0/2609
3	C	0.29	0/1636	0.49	0/2205
4	D	0.31	0/1733	0.46	0/2318
5	E	0.33	0/1162	0.52	0/1564
6	F	0.27	0/856	0.47	0/1154
7	G	0.29	0/1276	0.43	0/1709
8	H	0.33	0/1136	0.52	0/1527
9	I	0.29	0/1029	0.52	1/1379 (0.1%)
10	J	0.28	0/805	0.56	0/1082
11	K	0.32	0/879	0.49	0/1187
12	L	0.32	0/977	0.54	0/1306
13	M	0.29	0/947	0.49	0/1270
14	N	0.31	0/501	0.50	0/664
15	O	0.28	0/740	0.46	0/987
16	P	0.31	0/716	0.51	0/963
17	Q	0.31	0/836	0.52	1/1117 (0.1%)
18	R	0.29	0/579	0.48	0/768
19	S	0.28	0/661	0.51	0/890
20	T	0.29	0/765	0.47	0/1007
21	U	0.29	0/212	0.44	0/277
22	Y	0.33	0/128	0.99	0/196
23	W	0.33	0/357	0.86	0/555
All	All	0.35	0/56005	0.82	42/83130 (0.1%)

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
3	C	0	2
8	H	0	1
10	J	0	2
13	M	0	2
20	T	0	1
All	All	0	8

There are no bond length outliers.

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	328	C	C2-N1-C1'	8.92	128.61	118.80
1	A	839	U	C2-N1-C1'	7.61	126.83	117.70
1	A	254	G	O5'-P-OP1	-7.59	98.86	105.70
1	A	839	U	N1-C2-O2	7.57	128.10	122.80
1	A	299	G	C5-C6-N1	-7.18	107.91	111.50

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	166	GLU	Peptide
3	C	179	ARG	Peptide
8	H	71	GLY	Peptide
10	J	54	PHE	Peptide
10	J	55	LYS	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32644	0	16507	372	0
2	B	1900	0	1951	46	0
3	C	1612	0	1676	40	0
4	D	1703	0	1763	43	0
5	E	1146	0	1207	25	0
6	F	843	0	857	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	G	1257	0	1296	33	0
8	H	1116	0	1177	29	0
9	I	1010	0	1037	29	0
10	J	792	0	835	25	0
11	K	864	0	881	29	0
12	L	972	0	1058	24	0
13	M	937	0	995	30	0
14	N	492	0	529	19	0
15	O	729	0	768	16	0
16	P	700	0	720	16	0
17	Q	823	0	893	20	0
18	R	574	0	644	17	0
19	S	647	0	673	20	0
20	T	763	0	861	22	0
21	U	208	0	221	5	0
22	Y	117	0	62	1	0
23	W	319	0	164	0	0
24	A	216	0	0	0	0
24	B	3	0	0	0	0
24	C	5	0	0	0	0
24	D	3	0	0	0	0
24	E	1	0	0	0	0
24	F	1	0	0	0	0
24	H	2	0	0	0	0
24	K	4	0	0	0	0
24	L	3	0	0	0	0
24	M	5	0	0	0	0
24	P	3	0	0	0	0
24	Q	3	0	0	0	0
24	S	1	0	0	0	0
24	T	1	0	0	0	0
24	W	1	0	0	0	0
25	A	31	0	37	2	0
26	D	1	0	0	0	0
26	N	1	0	0	0	0
27	A	192	0	0	2	0
27	C	1	0	0	0	0
27	D	1	0	0	0	0
27	E	6	0	0	0	0
27	K	11	0	0	1	0
27	L	3	0	0	0	0
27	N	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	O	1	0	0	0	0
27	Q	2	0	0	0	0
27	T	4	0	0	0	0
All	All	52675	0	36812	774	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 774 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)
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.50	0.91
20:T:100:ILE:HG22	20:T:102:GLY:H	1.41	0.86
14:N:8:GLU:HB2	14:N:11:LYS:HE3	1.58	0.84
1:A:456:C:H42	1:A:476:G:H1	1.30	0.80
3:C:33:LEU:HD21	14:N:53:LEU:HD22	1.65	0.78

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	
2	B	232/234 (99%)	216 (93%)	16 (7%)	0	100	100
3	C	204/206 (99%)	182 (89%)	22 (11%)	0	100	100
4	D	206/208 (99%)	197 (96%)	9 (4%)	0	100	100
5	E	148/150 (99%)	140 (95%)	8 (5%)	0	100	100
6	F	99/101 (98%)	95 (96%)	4 (4%)	0	100	100
7	G	153/155 (99%)	144 (94%)	9 (6%)	0	100	100
8	H	136/138 (99%)	129 (95%)	5 (4%)	2 (2%)	10	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	125/127 (98%)	113 (90%)	12 (10%)	0	100	100
10	J	96/98 (98%)	80 (83%)	13 (14%)	3 (3%)	4	23
11	K	114/116 (98%)	109 (96%)	5 (4%)	0	100	100
12	L	121/124 (98%)	114 (94%)	7 (6%)	0	100	100
13	M	116/118 (98%)	99 (85%)	16 (14%)	1 (1%)	17	49
14	N	58/60 (97%)	49 (84%)	9 (16%)	0	100	100
15	O	85/87 (98%)	84 (99%)	1 (1%)	0	100	100
16	P	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
17	Q	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
18	R	68/70 (97%)	64 (94%)	4 (6%)	0	100	100
19	S	78/80 (98%)	71 (91%)	7 (9%)	0	100	100
20	T	97/99 (98%)	88 (91%)	8 (8%)	1 (1%)	15	46
21	U	22/24 (92%)	20 (91%)	2 (9%)	0	100	100
All	All	2336/2377 (98%)	2162 (93%)	167 (7%)	7 (0%)	41	72

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	J	55	LYS
10	J	56	HIS
10	J	54	PHE
8	H	72	PRO
8	H	71	GLY

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	
2	B	202/202 (100%)	174 (86%)	28 (14%)	3	13
3	C	160/160 (100%)	135 (84%)	25 (16%)	2	11
4	D	180/180 (100%)	159 (88%)	21 (12%)	5	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	115/115 (100%)	100 (87%)	15 (13%)	4	16
6	F	90/90 (100%)	85 (94%)	5 (6%)	21	51
7	G	126/126 (100%)	114 (90%)	12 (10%)	8	29
8	H	119/119 (100%)	110 (92%)	9 (8%)	13	41
9	I	98/98 (100%)	85 (87%)	13 (13%)	4	15
10	J	87/88 (99%)	74 (85%)	13 (15%)	3	12
11	K	88/88 (100%)	78 (89%)	10 (11%)	5	21
12	L	103/103 (100%)	93 (90%)	10 (10%)	8	28
13	M	94/94 (100%)	82 (87%)	12 (13%)	4	16
14	N	49/49 (100%)	46 (94%)	3 (6%)	18	48
15	O	79/79 (100%)	68 (86%)	11 (14%)	3	13
16	P	72/72 (100%)	63 (88%)	9 (12%)	4	17
17	Q	94/94 (100%)	86 (92%)	8 (8%)	10	35
18	R	61/61 (100%)	58 (95%)	3 (5%)	25	55
19	S	71/71 (100%)	61 (86%)	10 (14%)	3	13
20	T	76/76 (100%)	66 (87%)	10 (13%)	4	15
21	U	19/19 (100%)	18 (95%)	1 (5%)	22	52
All	All	1983/1984 (100%)	1755 (88%)	228 (12%)	5	20

5 of 228 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	I	12	GLU
20	T	57	ARG
11	K	29	ILE
20	T	53	LEU
17	Q	53	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	204	ASN
3	C	37	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1504/1522 (98%)	246 (16%)	46 (3%)
22	Y	5/6 (83%)	2 (40%)	0
23	W	14/15 (93%)	4 (28%)	0
All	All	1523/1543 (98%)	252 (16%)	46 (3%)

5 of 252 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	7	G
1	A	9	G
1	A	32	A
1	A	39	G

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	992	U
1	A	1201	A
1	A	1049	U
1	A	1145	C
1	A	1257	U

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

17 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
1	MA6	A	1518[A]	1	18,26,27	0.80	1 (5%)	19,38,41	0.67	0
1	4OC	A	1402	1	20,23,24	1.17	3 (15%)	26,32,35	0.78	1 (3%)
1	MA6	A	1519[B]	1	18,26,27	1.29	3 (16%)	19,38,41	0.60	0



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	M2G	A	966	1	20,27,28	1.44	3 (15%)	22,40,43	1.46	3 (13%)
1	5MC	A	1407	1	18,22,23	1.13	2 (11%)	26,32,35	0.98	2 (7%)
1	UR3	A	1498	1	19,22,23	1.25	2 (10%)	26,32,35	1.12	1 (3%)
1	MA6	A	1519[A]	1	18,26,27	0.79	0	19,38,41	0.69	0
1	PSU	A	516	24,1	18,21,22	1.18	1 (5%)	22,30,33	1.59	4 (18%)
12	0TD	L	92	12	7,9,10	0.94	0	6,11,13	1.77	2 (33%)
1	5MC	A	967	1	18,22,23	1.08	2 (11%)	26,32,35	0.93	1 (3%)
1	PSU	A	1541	1	18,21,22	1.09	1 (5%)	22,30,33	1.63	3 (13%)
1	5MC	A	1404	1	18,22,23	1.11	2 (11%)	26,32,35	1.05	2 (7%)
1	G7M	A	527	1	20,26,27	1.23	2 (10%)	17,39,42	0.86	1 (5%)
1	2MG	A	1207	1	18,26,27	1.50	4 (22%)	16,38,41	1.32	2 (12%)
1	PSU	A	1540	1	18,21,22	1.13	1 (5%)	22,30,33	1.55	4 (18%)
1	MA6	A	1518[B]	1	18,26,27	1.27	2 (11%)	19,38,41	0.74	0
1	5MC	A	1400	1	18,22,23	1.14	2 (11%)	26,32,35	1.03	2 (7%)

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
1	MA6	A	1518[A]	1	-	2/7/29/30	0/3/3/3
1	4OC	A	1402	1	-	2/9/29/30	0/2/2/2
1	MA6	A	1519[B]	1	-	4/7/29/30	0/3/3/3
1	M2G	A	966	1	-	3/7/29/30	0/3/3/3
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
1	UR3	A	1498	1	-	2/7/25/26	0/2/2/2
1	MA6	A	1519[A]	1	-	4/7/29/30	0/3/3/3
1	PSU	A	516	24,1	-	0/7/25/26	0/2/2/2
12	0TD	L	92	12	-	2/7/12/14	-
1	5MC	A	967	1	-	2/7/25/26	0/2/2/2
1	PSU	A	1541	1	-	1/7/25/26	0/2/2/2
1	5MC	A	1404	1	-	0/7/25/26	0/2/2/2
1	G7M	A	527	1	-	2/3/25/26	0/3/3/3
1	2MG	A	1207	1	-	0/5/27/28	0/3/3/3
1	PSU	A	1540	1	-	0/7/25/26	0/2/2/2
1	MA6	A	1518[B]	1	-	1/7/29/30	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MC	A	1400	1	-	2/7/25/26	0/2/2/2

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	G7M	C2-N2	4.07	1.43	1.34
1	A	1540	PSU	C6-C5	3.94	1.39	1.35
1	A	516	PSU	C6-C5	3.93	1.39	1.35
1	A	1498	UR3	C2-N1	3.92	1.44	1.38
1	A	966	M2G	C2-N3	3.86	1.35	1.30

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1541	PSU	C4-N3-C2	-4.35	120.06	126.34
1	A	516	PSU	C4-N3-C2	-4.21	120.27	126.34
1	A	1540	PSU	C4-N3-C2	-4.06	120.49	126.34
1	A	1541	PSU	N1-C2-N3	3.96	119.62	115.13
1	A	516	PSU	N1-C2-N3	3.90	119.55	115.13

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	967	5MC	O4'-C4'-C5'-O5'
1	A	1519[A]	MA6	C3'-C4'-C5'-O5'
1	A	1519[A]	MA6	C5-C6-N6-C9
1	A	1519[B]	MA6	C5-C6-N6-C9
1	A	1519[B]	MA6	N1-C6-N6-C9

There are no ring outliers.

10 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1518[A]	MA6	1	0
1	A	1519[B]	MA6	3	0
1	A	966	M2G	1	0
1	A	1519[A]	MA6	1	0
12	L	92	OTD	1	0
1	A	967	5MC	1	0
1	A	1404	5MC	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	527	G7M	1	0
1	A	1518[B]	MA6	3	0
1	A	1400	5MC	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 255 ligands modelled in this entry, 254 are monoatomic - leaving 1 for Mogul analysis.

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	SIS	A	1792	-	28,33,33	1.24	2 (7%)	28,49,49	1.03	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	SIS	A	1792	-	-	2/9/65/65	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	1792	SIS	C31-C41	-4.71	1.40	1.50
25	A	1792	SIS	C61-C51	-3.77	1.39	1.48

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	1792	SIS	C93-N33-C33	-3.12	109.84	114.38

There are no chirality outliers.

All (2) torsion outliers are listed below:

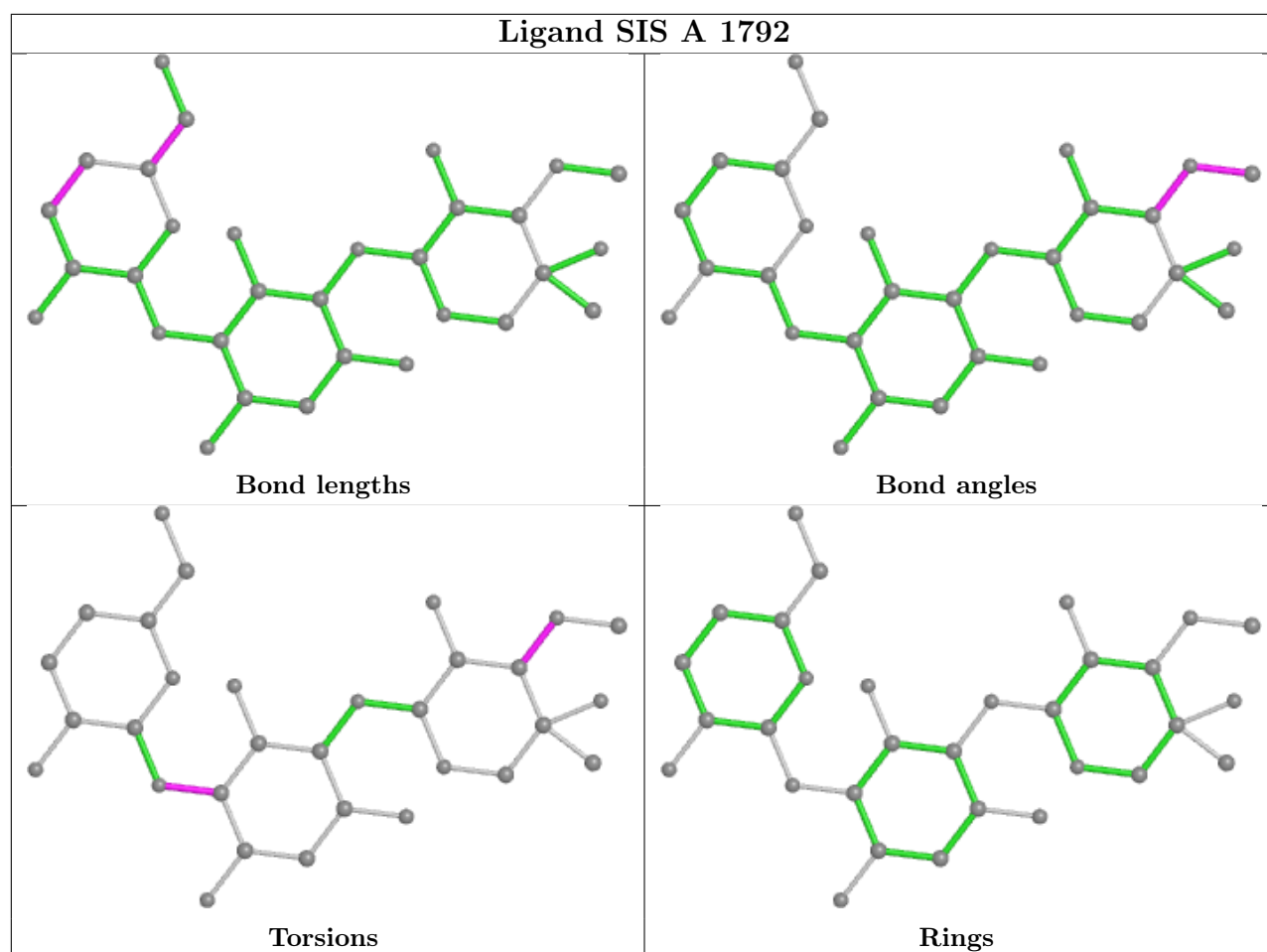
Mol	Chain	Res	Type	Atoms
25	A	1792	SIS	C23-C33-N33-C93
25	A	1792	SIS	C52-C42-O11-C11

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	A	1792	SIS	2	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 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	1498/1522 (98%)	-0.09	36 (2%) 59 57	90, 129, 208, 321	0
2	B	234/234 (100%)	-0.14	5 (2%) 63 62	110, 156, 242, 273	0
3	C	206/206 (100%)	0.15	17 (8%) 11 13	127, 161, 211, 242	0
4	D	208/208 (100%)	0.06	10 (4%) 30 31	98, 140, 186, 241	0
5	E	150/150 (100%)	0.01	5 (3%) 46 45	92, 118, 155, 215	0
6	F	101/101 (100%)	-0.11	3 (2%) 50 49	113, 155, 188, 220	0
7	G	155/155 (100%)	0.09	6 (3%) 39 38	111, 143, 198, 255	0
8	H	138/138 (100%)	-0.34	0 100 100	87, 114, 150, 162	0
9	I	127/127 (100%)	0.08	4 (3%) 49 48	123, 154, 204, 230	0
10	J	98/98 (100%)	0.17	5 (5%) 28 28	125, 185, 259, 314	0
11	K	116/116 (100%)	-0.07	1 (0%) 84 83	90, 126, 172, 188	0
12	L	123/124 (99%)	-0.04	2 (1%) 72 70	83, 129, 183, 252	0
13	M	118/118 (100%)	0.20	10 (8%) 10 12	116, 150, 198, 288	0
14	N	60/60 (100%)	0.04	0 100 100	117, 150, 207, 269	0
15	O	87/87 (100%)	-0.21	0 100 100	100, 132, 175, 210	0
16	P	83/83 (100%)	0.05	1 (1%) 79 77	97, 129, 169, 222	0
17	Q	99/99 (100%)	0.05	6 (6%) 21 22	88, 116, 156, 172	0
18	R	70/70 (100%)	0.34	6 (8%) 10 12	97, 138, 204, 227	0
19	S	80/80 (100%)	0.41	7 (8%) 10 11	136, 171, 226, 273	0
20	T	99/99 (100%)	0.08	2 (2%) 65 64	101, 128, 175, 216	0
21	U	24/24 (100%)	0.16	1 (4%) 36 35	113, 146, 189, 199	0
22	Y	6/6 (100%)	0.64	1 (16%) 1 2	161, 167, 236, 265	0
23	W	15/15 (100%)	-0.11	0 100 100	146, 159, 244, 247	0
All	All	3895/3920 (99%)	-0.02	128 (3%) 46 45	83, 138, 208, 321	0

The worst 5 of 128 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1129	C	8.3
7	G	156	TRP	7.4
1	A	1003(A)	G	6.9
20	T	106	ALA	6.1
4	D	42	GLN	5.9

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
1	PSU	A	1540	20/21	0.86	0.39	208,219,231,237	0
1	PSU	A	1541	20/21	0.88	0.33	210,228,262,308	0
1	PSU	A	516	20/21	0.92	0.15	146,154,162,165	0
1	MA6	A	1518[B]	24/25	0.93	0.26	100,108,119,121	24
1	G7M	A	527	24/25	0.93	0.20	105,113,126,128	0
1	MA6	A	1518[A]	24/25	0.93	0.26	100,102,108,109	24
1	MA6	A	1519[A]	24/25	0.94	0.27	98,100,109,125	24
1	MA6	A	1519[B]	24/25	0.94	0.27	99,105,109,112	24
1	4OC	A	1402	22/23	0.95	0.22	103,107,119,123	0
12	0TD	L	92	10/11	0.95	0.19	132,154,192,194	0
1	5MC	A	1404	21/22	0.96	0.18	99,108,113,115	0
1	2MG	A	1207	24/25	0.96	0.13	127,142,156,160	0
1	5MC	A	1407	21/22	0.97	0.17	103,117,127,135	0
1	5MC	A	1400	21/22	0.97	0.16	101,126,143,146	0
1	5MC	A	967	21/22	0.97	0.17	111,125,130,136	0
1	M2G	A	966	25/26	0.97	0.17	129,134,151,152	0
1	UR3	A	1498	21/22	0.98	0.18	101,107,122,134	0

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
24	MG	A	1639	1/1	0.10	0.48	193,193,193,193	0
24	MG	A	1811	1/1	0.16	0.60	137,137,137,137	0
24	MG	A	1717	1/1	0.30	0.24	127,127,127,127	0
24	MG	M	202	1/1	0.33	0.30	125,125,125,125	0
24	MG	D	304	1/1	0.41	0.19	130,130,130,130	0
24	MG	A	1803	1/1	0.41	0.21	160,160,160,160	0
24	MG	L	203	1/1	0.45	0.54	118,118,118,118	0
24	MG	A	1804	1/1	0.50	0.45	150,150,150,150	0
24	MG	A	1813	1/1	0.51	0.18	112,112,112,112	0
24	MG	A	1759	1/1	0.51	0.56	113,113,113,113	0
24	MG	A	1733	1/1	0.53	0.64	120,120,120,120	0
24	MG	A	1762	1/1	0.55	0.66	101,101,101,101	0
24	MG	M	201	1/1	0.56	0.26	123,123,123,123	0
24	MG	T	201	1/1	0.57	0.24	387,387,387,387	0
24	MG	Q	202	1/1	0.58	0.12	133,133,133,133	0
24	MG	A	1808	1/1	0.58	0.54	132,132,132,132	0
24	MG	A	1793	1/1	0.60	1.33	372,372,372,372	0
24	MG	A	1791	1/1	0.60	0.40	131,131,131,131	0
24	MG	M	203	1/1	0.62	0.10	129,129,129,129	0
24	MG	A	1684	1/1	0.62	0.38	109,109,109,109	0
24	MG	A	1682	1/1	0.62	0.42	131,131,131,131	0
24	MG	B	303	1/1	0.63	0.28	126,126,126,126	0
24	MG	A	1795	1/1	0.63	0.34	395,395,395,395	0
24	MG	A	1763	1/1	0.66	0.24	110,110,110,110	0
24	MG	A	1805	1/1	0.68	0.67	151,151,151,151	0
24	MG	A	1771	1/1	0.68	0.34	116,116,116,116	0
24	MG	A	1802	1/1	0.68	1.61	126,126,126,126	0
24	MG	A	1631	1/1	0.69	0.55	108,108,108,108	0
24	MG	A	1817	1/1	0.69	0.44	146,146,146,146	0
24	MG	A	1799	1/1	0.69	0.17	147,147,147,147	0
24	MG	A	1709	1/1	0.69	0.77	142,142,142,142	0
24	MG	A	1754	1/1	0.69	0.55	87,87,87,87	0
24	MG	A	1761	1/1	0.70	0.86	94,94,94,94	0
24	MG	A	1672	1/1	0.70	0.13	120,120,120,120	0
24	MG	A	1744	1/1	0.72	0.34	121,121,121,121	0
24	MG	A	1729	1/1	0.72	0.47	107,107,107,107	0
24	MG	A	1663	1/1	0.72	0.54	112,112,112,112	0
24	MG	C	305	1/1	0.73	0.13	124,124,124,124	0
24	MG	A	1615	1/1	0.73	0.12	134,134,134,134	0
24	MG	E	201	1/1	0.73	0.13	166,166,166,166	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
24	MG	K	201	1/1	0.73	1.16	343,343,343,343	0
24	MG	A	1741	1/1	0.73	0.39	101,101,101,101	0
24	MG	A	1794	1/1	0.74	0.50	215,215,215,215	0
24	MG	A	1797	1/1	0.74	0.43	111,111,111,111	0
24	MG	A	1667	1/1	0.75	0.37	87,87,87,87	0
24	MG	M	205	1/1	0.75	0.12	118,118,118,118	0
24	MG	C	302	1/1	0.75	0.15	120,120,120,120	0
24	MG	A	1707	1/1	0.75	0.16	121,121,121,121	0
24	MG	A	1624	1/1	0.76	0.33	106,106,106,106	0
24	MG	A	1740	1/1	0.76	0.32	86,86,86,86	0
24	MG	A	1772	1/1	0.76	0.46	97,97,97,97	0
24	MG	A	1780	1/1	0.76	0.49	84,84,84,84	0
24	MG	M	204	1/1	0.76	0.10	111,111,111,111	0
24	MG	A	1720	1/1	0.76	0.14	77,77,77,77	0
24	MG	A	1674	1/1	0.76	0.52	117,117,117,117	0
24	MG	L	201	1/1	0.76	0.47	113,113,113,113	0
24	MG	C	301	1/1	0.77	0.30	104,104,104,104	0
24	MG	A	1787	1/1	0.77	0.15	102,102,102,102	0
24	MG	A	1721	1/1	0.77	0.43	97,97,97,97	0
24	MG	A	1669	1/1	0.78	0.20	125,125,125,125	0
24	MG	A	1706	1/1	0.78	0.65	172,172,172,172	0
24	MG	A	1815	1/1	0.78	0.92	120,120,120,120	0
24	MG	L	202	1/1	0.78	0.45	118,118,118,118	0
24	MG	A	1781	1/1	0.79	0.35	117,117,117,117	0
24	MG	A	1697	1/1	0.79	0.14	154,154,154,154	0
24	MG	A	1790	1/1	0.79	0.31	98,98,98,98	0
24	MG	A	1769	1/1	0.79	0.70	122,122,122,122	0
24	MG	A	1665	1/1	0.79	0.59	75,75,75,75	0
24	MG	A	1752	1/1	0.79	0.58	98,98,98,98	0
24	MG	A	1753	1/1	0.79	0.60	110,110,110,110	0
24	MG	D	302	1/1	0.80	0.12	97,97,97,97	0
24	MG	A	1723	1/1	0.80	0.45	105,105,105,105	0
24	MG	A	1719	1/1	0.80	0.23	126,126,126,126	0
24	MG	A	1722	1/1	0.80	0.17	94,94,94,94	0
24	MG	A	1809	1/1	0.80	0.78	120,120,120,120	0
24	MG	A	1734	1/1	0.80	0.19	94,94,94,94	0
24	MG	A	1739	1/1	0.80	0.47	111,111,111,111	0
24	MG	A	1750	1/1	0.81	0.18	88,88,88,88	0
24	MG	A	1786	1/1	0.81	0.74	98,98,98,98	0
24	MG	A	1687	1/1	0.81	0.29	121,121,121,121	0
24	MG	K	203	1/1	0.81	0.56	103,103,103,103	0
24	MG	C	304	1/1	0.81	0.53	146,146,146,146	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
24	MG	P	101	1/1	0.81	0.24	112,112,112,112	0
24	MG	A	1601	1/1	0.81	0.48	98,98,98,98	0
24	MG	A	1626	1/1	0.81	0.51	128,128,128,128	0
24	MG	A	1760	1/1	0.82	0.28	80,80,80,80	0
24	MG	A	1608	1/1	0.82	0.16	120,120,120,120	0
24	MG	A	1801	1/1	0.82	0.37	124,124,124,124	0
24	MG	A	1683	1/1	0.82	0.10	129,129,129,129	0
24	MG	A	1810	1/1	0.82	0.61	153,153,153,153	0
24	MG	A	1725	1/1	0.82	0.37	95,95,95,95	0
24	MG	A	1796	1/1	0.83	0.29	115,115,115,115	0
24	MG	A	1698	1/1	0.83	0.22	138,138,138,138	0
24	MG	A	1690	1/1	0.83	0.32	150,150,150,150	0
24	MG	A	1730	1/1	0.83	0.60	101,101,101,101	0
24	MG	W	101	1/1	0.83	0.18	123,123,123,123	0
24	MG	A	1645	1/1	0.84	0.56	184,184,184,184	0
24	MG	A	1617	1/1	0.84	0.32	80,80,80,80	0
24	MG	A	1806	1/1	0.84	0.81	139,139,139,139	0
24	MG	A	1700	1/1	0.84	0.09	118,118,118,118	0
24	MG	A	1696	1/1	0.84	0.34	99,99,99,99	0
24	MG	K	204	1/1	0.84	0.37	110,110,110,110	0
24	MG	A	1633	1/1	0.85	0.47	105,105,105,105	0
24	MG	H	201	1/1	0.86	0.48	76,76,76,76	0
24	MG	A	1623	1/1	0.86	0.26	116,116,116,116	0
24	MG	A	1774	1/1	0.86	0.24	111,111,111,111	0
24	MG	A	1647	1/1	0.86	0.26	157,157,157,157	0
24	MG	A	1648	1/1	0.86	0.20	107,107,107,107	0
24	MG	A	1680	1/1	0.86	0.57	104,104,104,104	0
24	MG	A	1757	1/1	0.86	0.14	101,101,101,101	0
24	MG	A	1716	1/1	0.86	0.30	101,101,101,101	0
24	MG	A	1816	1/1	0.87	0.43	181,181,181,181	0
24	MG	A	1728	1/1	0.87	0.36	93,93,93,93	0
24	MG	A	1710	1/1	0.87	0.32	79,79,79,79	0
24	MG	A	1691	1/1	0.87	0.31	83,83,83,83	0
24	MG	A	1666	1/1	0.87	0.78	93,93,93,93	0
24	MG	A	1634	1/1	0.87	0.20	149,149,149,149	0
24	MG	A	1735	1/1	0.87	0.14	105,105,105,105	0
24	MG	A	1638	1/1	0.87	0.81	94,94,94,94	0
24	MG	A	1602	1/1	0.87	1.74	244,244,244,244	0
24	MG	A	1686	1/1	0.87	0.39	106,106,106,106	0
24	MG	A	1605	1/1	0.87	0.64	89,89,89,89	0
24	MG	A	1724	1/1	0.87	0.28	111,111,111,111	0
24	MG	A	1679	1/1	0.87	0.30	101,101,101,101	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
24	MG	A	1783	1/1	0.88	0.27	114,114,114,114	0
24	MG	A	1610	1/1	0.88	0.17	106,106,106,106	0
24	MG	A	1642	1/1	0.88	0.49	101,101,101,101	0
24	MG	A	1712	1/1	0.88	0.29	116,116,116,116	0
24	MG	A	1737	1/1	0.88	0.12	112,112,112,112	0
24	MG	A	1607	1/1	0.88	0.29	90,90,90,90	0
24	MG	A	1646	1/1	0.88	0.08	99,99,99,99	0
24	MG	A	1789	1/1	0.89	0.42	84,84,84,84	0
24	MG	A	1798	1/1	0.89	0.74	107,107,107,107	0
24	MG	H	202	1/1	0.89	0.20	106,106,106,106	0
24	MG	A	1777	1/1	0.89	0.14	144,144,144,144	0
24	MG	A	1685	1/1	0.89	0.10	106,106,106,106	0
24	MG	A	1630	1/1	0.89	1.02	93,93,93,93	0
24	MG	P	103	1/1	0.89	0.21	111,111,111,111	0
24	MG	A	1658	1/1	0.89	0.90	108,108,108,108	0
24	MG	A	1662	1/1	0.89	0.44	102,102,102,102	0
24	MG	A	1699	1/1	0.89	0.15	88,88,88,88	0
24	MG	A	1715	1/1	0.90	0.19	71,71,71,71	0
24	MG	A	1812	1/1	0.90	0.24	124,124,124,124	0
24	MG	A	1622	1/1	0.90	0.25	129,129,129,129	0
24	MG	A	1668	1/1	0.90	0.37	142,142,142,142	0
24	MG	A	1807	1/1	0.90	0.25	110,110,110,110	0
24	MG	Q	201	1/1	0.90	0.26	119,119,119,119	0
24	MG	A	1652	1/1	0.90	0.50	96,96,96,96	0
24	MG	A	1627	1/1	0.90	0.48	88,88,88,88	0
24	MG	A	1661	1/1	0.90	0.24	109,109,109,109	0
24	MG	A	1727	1/1	0.91	0.19	109,109,109,109	0
24	MG	A	1676	1/1	0.91	0.10	113,113,113,113	0
24	MG	A	1619	1/1	0.91	0.25	89,89,89,89	0
24	MG	A	1660	1/1	0.91	0.17	149,149,149,149	0
24	MG	A	1800	1/1	0.91	0.45	109,109,109,109	0
24	MG	A	1732	1/1	0.91	0.33	104,104,104,104	0
24	MG	A	1681	1/1	0.91	0.24	80,80,80,80	0
24	MG	A	1603	1/1	0.91	0.21	116,116,116,116	0
24	MG	A	1702	1/1	0.91	0.17	110,110,110,110	0
24	MG	A	1675	1/1	0.91	0.22	142,142,142,142	0
24	MG	A	1758	1/1	0.91	0.14	129,129,129,129	0
24	MG	A	1779	1/1	0.91	0.30	114,114,114,114	0
24	MG	A	1677	1/1	0.92	0.19	104,104,104,104	0
24	MG	A	1678	1/1	0.92	0.07	107,107,107,107	0
24	MG	A	1764	1/1	0.92	0.61	93,93,93,93	0
24	MG	D	303	1/1	0.92	0.11	157,157,157,157	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
24	MG	A	1671	1/1	0.92	0.26	87,87,87,87	0
24	MG	A	1655	1/1	0.92	0.42	177,177,177,177	0
24	MG	A	1756	1/1	0.92	0.21	120,120,120,120	0
24	MG	A	1726	1/1	0.92	0.35	114,114,114,114	0
24	MG	A	1688	1/1	0.92	0.15	138,138,138,138	0
24	MG	K	202	1/1	0.92	0.83	353,353,353,353	0
24	MG	A	1657	1/1	0.92	0.20	85,85,85,85	0
24	MG	A	1651	1/1	0.92	0.23	81,81,81,81	0
24	MG	A	1640	1/1	0.92	0.19	138,138,138,138	0
24	MG	A	1775	1/1	0.93	0.10	94,94,94,94	0
24	MG	A	1649	1/1	0.93	0.27	103,103,103,103	0
24	MG	A	1616	1/1	0.93	0.57	85,85,85,85	0
24	MG	A	1613	1/1	0.93	0.10	147,147,147,147	0
24	MG	A	1713	1/1	0.93	0.44	120,120,120,120	0
24	MG	A	1782	1/1	0.93	0.11	118,118,118,118	0
24	MG	A	1628	1/1	0.93	0.17	92,92,92,92	0
24	MG	A	1767	1/1	0.93	0.19	93,93,93,93	0
24	MG	A	1656	1/1	0.93	0.18	140,140,140,140	0
24	MG	A	1705	1/1	0.93	0.28	108,108,108,108	0
24	MG	A	1693	1/1	0.93	0.63	116,116,116,116	0
24	MG	S	101	1/1	0.93	0.12	99,99,99,99	0
24	MG	A	1773	1/1	0.93	0.42	78,78,78,78	0
24	MG	A	1629	1/1	0.93	0.13	139,139,139,139	0
24	MG	A	1644	1/1	0.94	0.30	82,82,82,82	0
24	MG	A	1612	1/1	0.94	0.09	124,124,124,124	0
24	MG	A	1632	1/1	0.94	0.07	112,112,112,112	0
24	MG	A	1635	1/1	0.94	0.20	122,122,122,122	0
24	MG	B	302	1/1	0.94	0.64	139,139,139,139	0
24	MG	A	1701	1/1	0.94	0.45	196,196,196,196	0
24	MG	A	1749	1/1	0.94	0.23	88,88,88,88	0
24	MG	A	1641	1/1	0.94	0.31	104,104,104,104	0
24	MG	C	303	1/1	0.94	0.09	118,118,118,118	0
24	MG	A	1695	1/1	0.94	0.15	124,124,124,124	0
24	MG	A	1776	1/1	0.94	0.09	144,144,144,144	0
24	MG	A	1637	1/1	0.94	0.35	115,115,115,115	0
24	MG	A	1742	1/1	0.95	0.26	100,100,100,100	0
24	MG	A	1770	1/1	0.95	0.20	78,78,78,78	0
24	MG	A	1659	1/1	0.95	0.21	104,104,104,104	0
24	MG	A	1784	1/1	0.95	0.18	109,109,109,109	0
24	MG	A	1746	1/1	0.95	0.14	95,95,95,95	0
24	MG	A	1748	1/1	0.95	0.17	98,98,98,98	0
24	MG	A	1692	1/1	0.95	0.21	108,108,108,108	0

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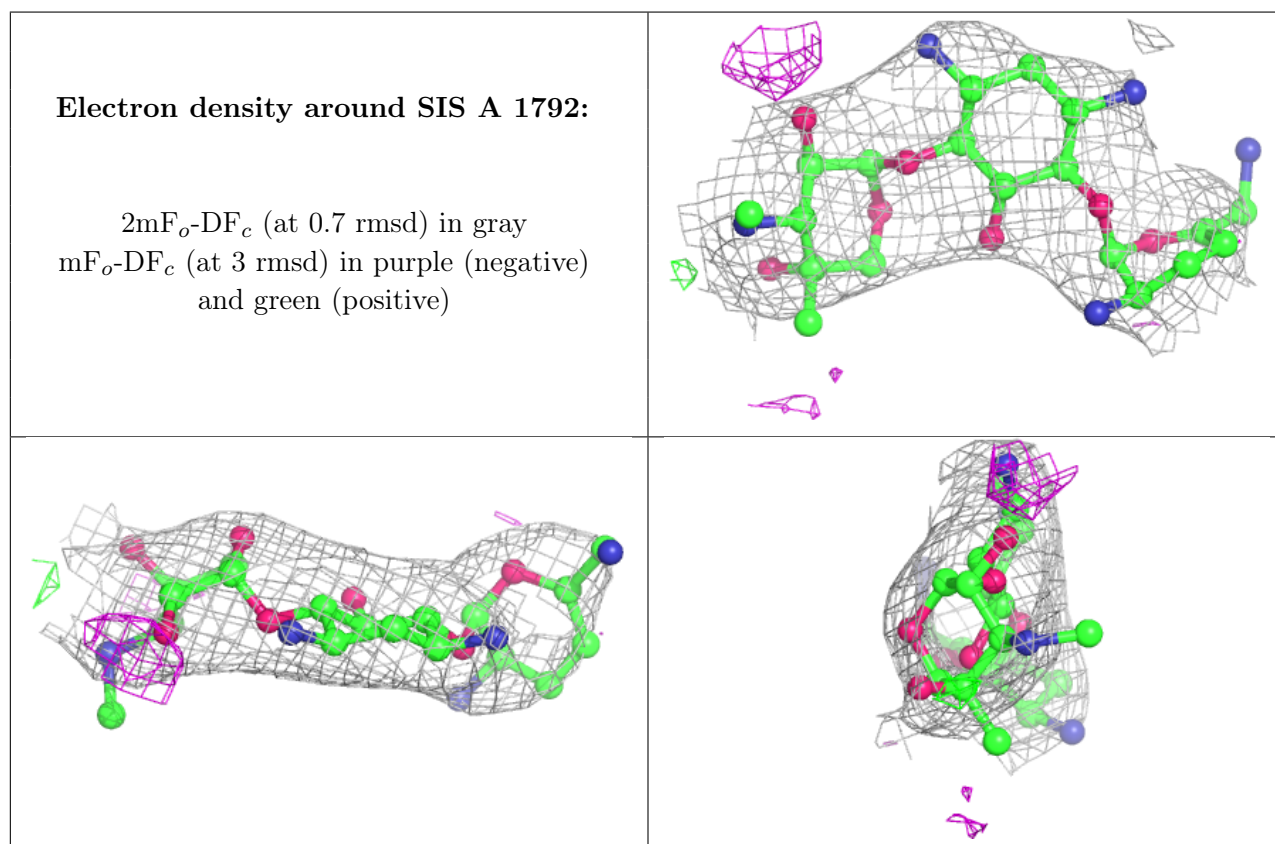
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
24	MG	A	1708	1/1	0.95	0.27	150,150,150,150	0
24	MG	A	1751	1/1	0.95	0.19	91,91,91,91	0
24	MG	A	1703	1/1	0.95	0.25	163,163,163,163	0
24	MG	Q	203	1/1	0.95	0.18	110,110,110,110	0
24	MG	A	1778	1/1	0.95	0.38	104,104,104,104	0
24	MG	A	1704	1/1	0.95	0.23	118,118,118,118	0
24	MG	A	1673	1/1	0.95	0.15	106,106,106,106	0
24	MG	A	1670	1/1	0.96	0.09	112,112,112,112	0
24	MG	P	102	1/1	0.96	0.44	75,75,75,75	0
24	MG	A	1745	1/1	0.96	0.24	83,83,83,83	0
24	MG	A	1621	1/1	0.96	0.28	109,109,109,109	0
24	MG	A	1814	1/1	0.96	0.17	116,116,116,116	0
24	MG	A	1765	1/1	0.96	0.10	79,79,79,79	0
24	MG	A	1785	1/1	0.96	0.34	131,131,131,131	0
24	MG	A	1718	1/1	0.96	0.61	105,105,105,105	0
24	MG	A	1768	1/1	0.96	0.43	107,107,107,107	0
25	SIS	A	1792	31/31	0.96	0.24	85,103,118,122	0
24	MG	A	1731	1/1	0.97	0.09	62,62,62,62	0
24	MG	A	1747	1/1	0.97	0.26	92,92,92,92	0
24	MG	B	301	1/1	0.97	0.11	82,82,82,82	0
24	MG	A	1643	1/1	0.97	0.10	87,87,87,87	0
24	MG	A	1650	1/1	0.97	0.36	107,107,107,107	0
24	MG	A	1766	1/1	0.97	0.09	79,79,79,79	0
24	MG	A	1620	1/1	0.97	0.20	102,102,102,102	0
24	MG	A	1606	1/1	0.97	0.15	122,122,122,122	0
24	MG	A	1689	1/1	0.97	0.14	130,130,130,130	0
24	MG	A	1738	1/1	0.97	0.09	120,120,120,120	0
24	MG	A	1788	1/1	0.97	0.23	114,114,114,114	0
24	MG	A	1653	1/1	0.97	0.40	130,130,130,130	0
24	MG	A	1755	1/1	0.97	0.20	99,99,99,99	0
24	MG	A	1604	1/1	0.97	0.10	116,116,116,116	0
24	MG	A	1664	1/1	0.97	0.09	95,95,95,95	0
24	MG	A	1636	1/1	0.97	0.14	95,95,95,95	0
24	MG	A	1743	1/1	0.97	0.22	99,99,99,99	0
24	MG	A	1694	1/1	0.97	0.26	112,112,112,112	0
24	MG	A	1611	1/1	0.97	0.20	92,92,92,92	0
26	ZN	N	101	1/1	0.97	0.21	130,130,130,130	0
24	MG	A	1711	1/1	0.98	0.12	90,90,90,90	0
24	MG	F	201	1/1	0.98	0.06	108,108,108,108	0
24	MG	A	1609	1/1	0.98	0.06	84,84,84,84	0
24	MG	A	1618	1/1	0.98	0.26	135,135,135,135	0
24	MG	A	1714	1/1	0.98	0.21	86,86,86,86	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
24	MG	A	1736	1/1	0.98	0.09	112,112,112,112	0
24	MG	A	1625	1/1	0.98	0.10	57,57,57,57	0
24	MG	A	1654	1/1	0.98	0.20	88,88,88,88	0
26	ZN	D	301	1/1	0.98	0.34	113,113,113,113	0
24	MG	A	1614	1/1	0.98	0.07	110,110,110,110	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.