Full wwPDB X-ray Structure Validation Report ⓘ

Oct 12, 2020 – 10:56 AM EDT

PDB ID	:	5WNV
Title	:	Crystal Structure of 30S ribosomal subunit from Thermus thermophilus
Authors	:	DeMirci, H.
Deposited on	:	2017-08-01
Resolution	:	3.30 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

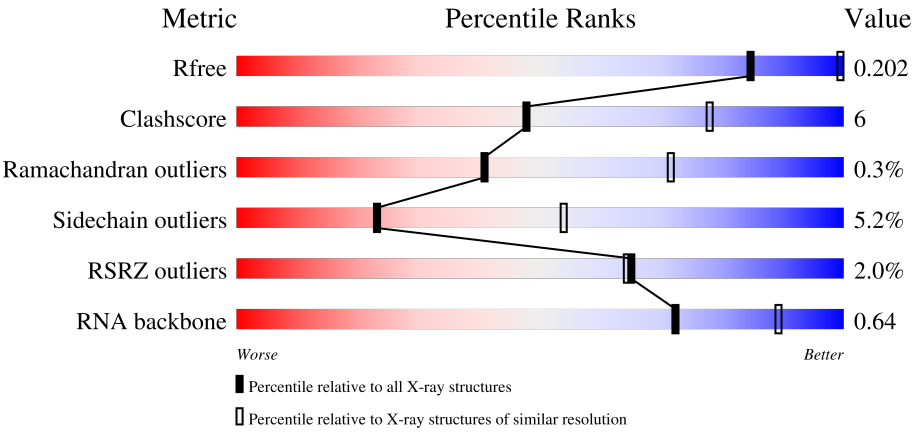
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.14.6
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.14.6

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)
RNA backbone	3102	1117 (3.70-2.90)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	65% 27% 7%
2	B	236	6% 78% 20%
3	C	207	% 79% 19%
4	D	208	2% 82% 18%

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Mol	Chain	Length	Quality of chain
5	E	151	76% 21%
6	F	101	% 83% 15%
7	G	155	3% 75% 25%
8	H	138	75% 24%
9	I	127	4% 72% 26%
10	J	99	14% 74% 22%
11	K	119	3% 78% 20%
12	L	125	6% 73% 23%
13	M	118	3% 68% 31%
14	N	60	3% 77% 22%
15	O	88	% 89% 10%
16	P	84	85% 15%
17	Q	99	84% 16%
18	R	73	4% 82% 15%
19	S	81	4% 79% 19%
20	T	99	83% 14%
21	U	25	16% 84% 16%
22	a	6	17% 67% 33%
23	b	15	7% 60% 40%

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
23	12A	b	37	X	-	-	-
24	MG	A	1620	-	-	-	X
24	MG	A	1629	-	-	-	X
24	MG	A	1666	-	-	-	X
24	MG	A	1671	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	MG	A	1677	-	-	-	X
24	MG	A	1681	-	-	-	X
24	MG	A	1687	-	-	-	X
24	MG	A	1690	-	-	-	X
24	MG	A	1692	-	-	-	X
24	MG	A	1704	-	-	-	X
24	MG	A	1710	-	-	-	X
24	MG	A	1714	-	-	-	X
24	MG	A	1715	-	-	-	X
24	MG	A	1716	-	-	-	X
24	MG	A	1720	-	-	-	X
24	MG	A	1729	-	-	-	X
24	MG	A	1743	-	-	-	X
24	MG	A	1744	-	-	-	X
24	MG	A	1748	-	-	-	X
24	MG	A	1749	-	-	-	X
24	MG	A	1757	-	-	-	X
24	MG	A	1762	-	-	-	X
24	MG	A	1782	-	-	-	X
24	MG	A	1785	-	-	-	X
24	MG	A	1792	-	-	-	X
24	MG	A	1794	-	-	-	X
24	MG	A	1795	-	-	-	X
24	MG	A	1802	-	-	-	X
24	MG	A	1804	-	-	-	X
24	MG	A	1807	-	-	-	X
24	MG	A	1812	-	-	-	X
24	MG	A	1817	-	-	-	X
24	MG	A	1823	-	-	-	X
24	MG	A	1824	-	-	-	X
24	MG	A	1827	-	-	-	X
24	MG	A	1829	-	-	-	X
25	K	A	1834	-	-	-	X
25	K	A	1838	-	-	-	X
25	K	A	1841	-	-	-	X
25	K	A	1843	-	-	-	X
25	K	A	1847	-	-	-	X
25	K	A	1849	-	-	-	X
25	K	A	1852	-	-	-	X
25	K	E	202	-	-	-	X

2 Entry composition (i)

There are 28 unique types of molecules in this entry. The entry contains 52620 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	32504	14477	6011	10505	1511	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1534	C	A	conflict	GB 55771382
A	1535	A	C	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	236	1874	1195	336	338	5	0	0	1

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	207	1613	1016	315	281	1	0	0	1

- 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 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	151	1147	724	218	201	4	0	0	1

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	99	Total	C	N	O	S	0	0	1
			793	498	157	137	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	125	Total	C	N	O	S	0	0	1
			973	612	196	163	2			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	O	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	P	84	Total	C	N	O	S	0	0	1
			701	443	140	117	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	R	73	Total	C	N	O	0	0	0
			598	381	118	99			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	81	Total	C	N	O	S	0	0	1
			648	414	120	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	25	Total	C	N	O	0	0	1
			209	128	51	30			

- Molecule 22 is a RNA chain called RNA (5'-R(P*UP*AP*GP*AP*CP*UP*(70U)P*UP*U P*(12A)P*AP*(PSU)P*CP*UP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	a	6	Total	C	N	O	P	0	0	0
			124	58	21	40	5			

- Molecule 23 is a RNA chain called RNA (5'-R(P*UP*AP*GP*AP*CP*UP*(70U)P*UP*U P*(12A)P*AP*(PSU)P*CP*UP*A)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
23	b	15	Total	C	N	O	P	S	0	0	0
			329	150	51	111	15	2			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	P	3	Total	Mg	0	0
			3	3		
24	G	1	Total	Mg	0	0
			1	1		
24	Q	2	Total	Mg	0	0
			2	2		
24	D	1	Total	Mg	0	0
			1	1		
24	E	1	Total	Mg	0	0
			1	1		
24	H	1	Total	Mg	0	0
			1	1		
24	A	235	Total	Mg	0	0
			235	235		
24	T	1	Total	Mg	0	0
			1	1		

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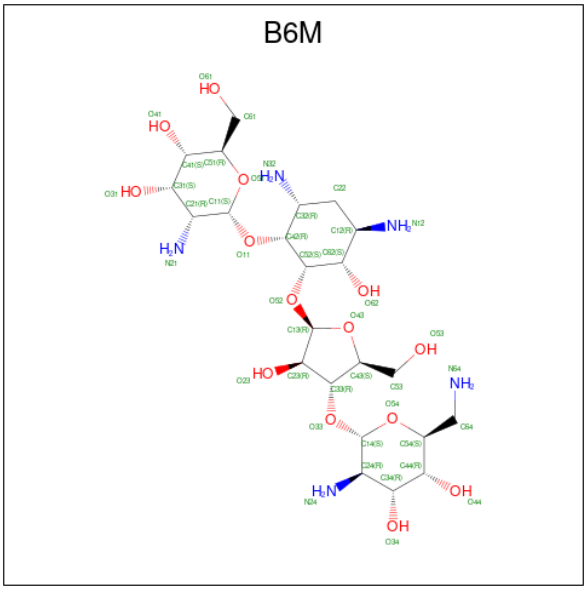
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
24	N	1	Total Mg 1 1	0	0
24	L	1	Total Mg 1 1	0	0
24	S	3	Total Mg 3 3	0	0
24	F	1	Total Mg 1 1	0	0

- Molecule 25 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
25	A	21	Total K 21 21	0	0
25	E	1	Total K 1 1	0	0

- Molecule 26 is (1R,2S,3S,4R,6R)-4,6-diamino-2-{[3-O-(2,6-diamino-2,6-dideoxy-alpha-L-altropyranosyl)-beta-L-arabinofuranosyl]oxy}-3-hydroxycyclohexyl 2-amino-2-deoxy-alpha-D-allopyranoside (three-letter code: B6M) (formula: $C_{23}H_{45}N_5O_{14}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
26	A	1	Total C N O 42 23 5 14	0	0

- Molecule 27 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 28 is water.

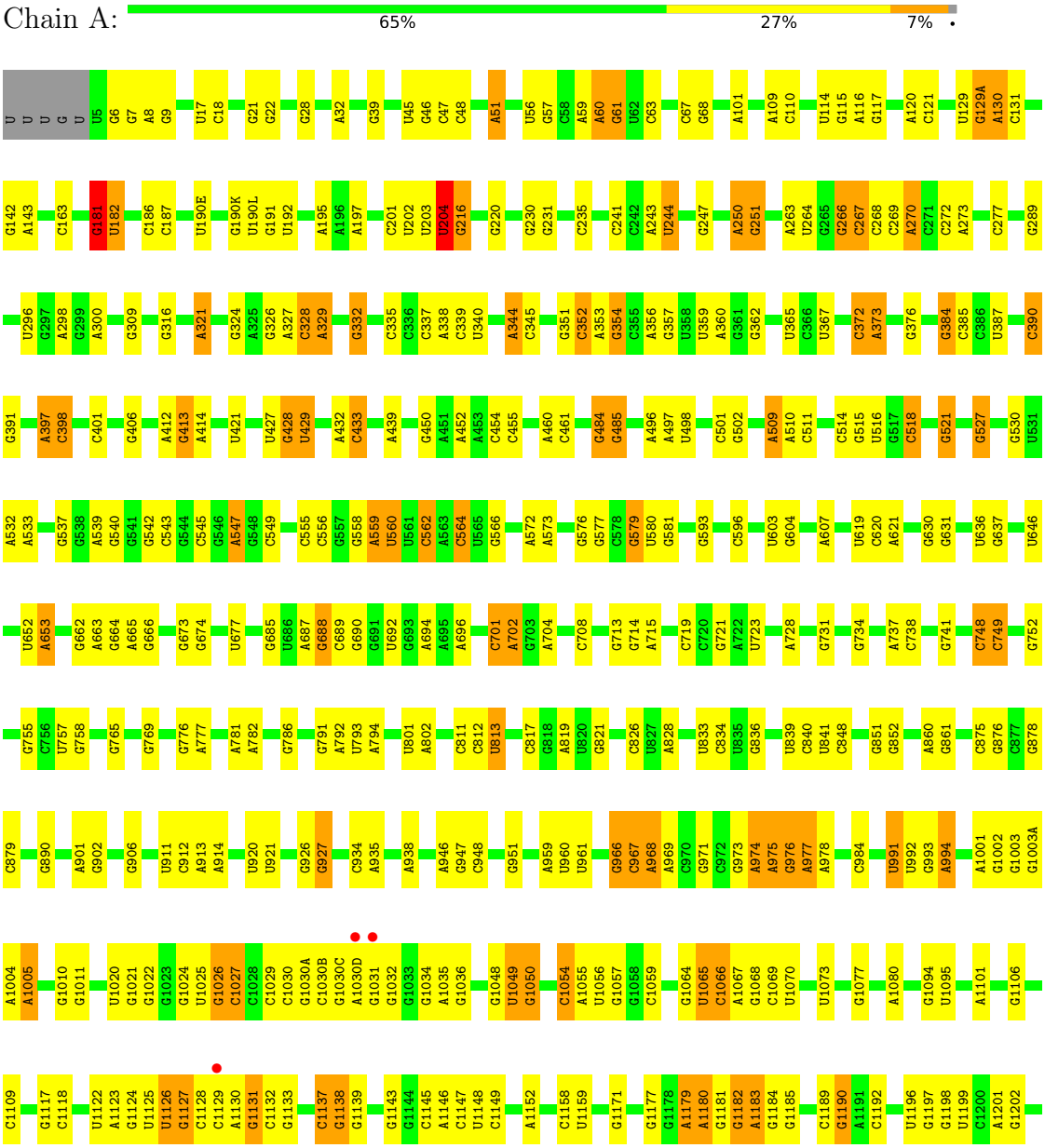
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
28	A	214	Total O 214 214	0	0
28	D	3	Total O 3 3	0	0
28	E	4	Total O 4 4	0	0
28	K	1	Total O 1 1	0	0
28	L	3	Total O 3 3	0	0
28	N	1	Total O 1 1	0	0
28	T	1	Total O 1 1	0	0

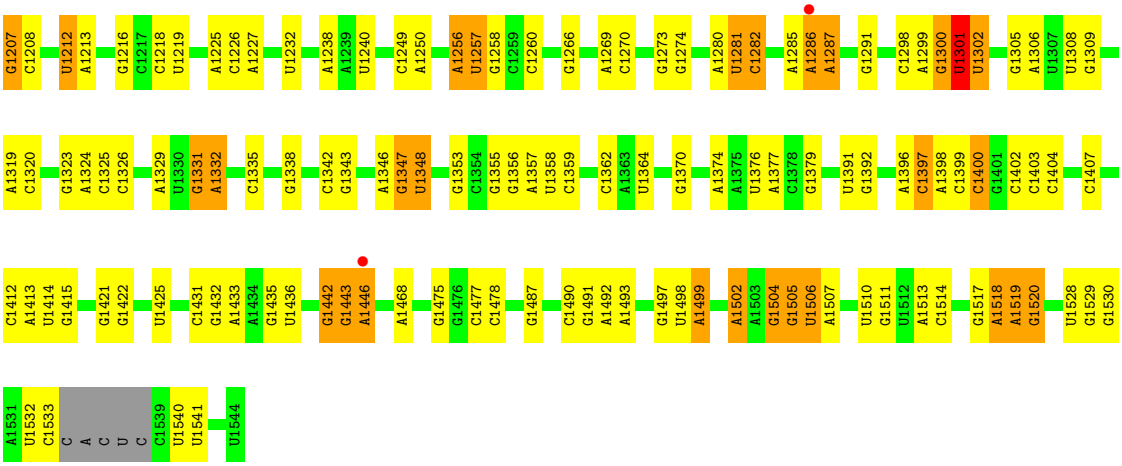
3 Residue-property plots (i)

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

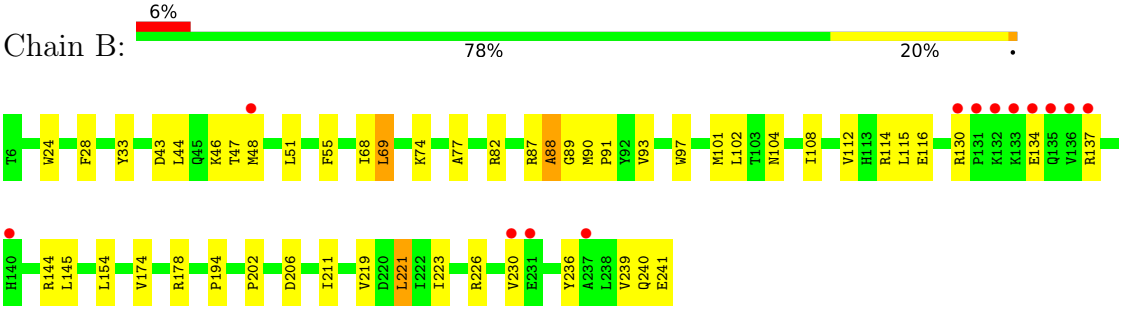
- Molecule 1: 16S Ribosomal RNA rRNA

Chain A:

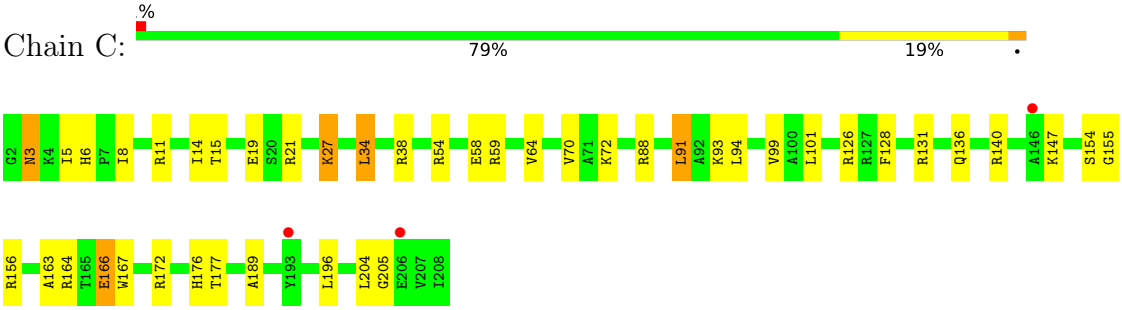




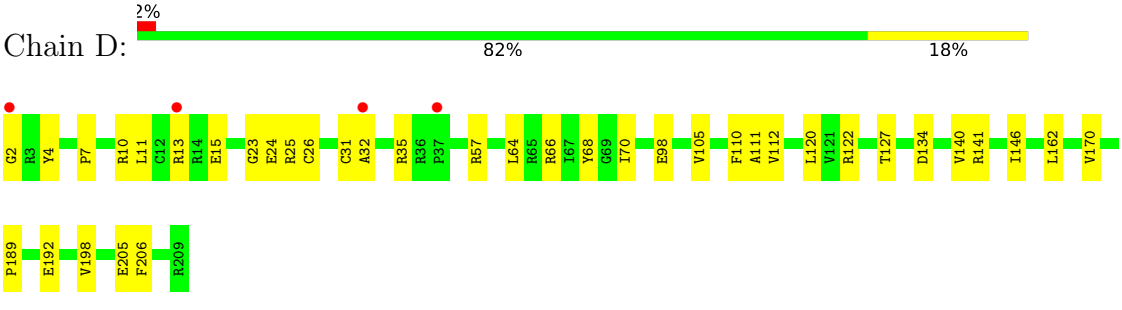
• Molecule 2: 30S ribosomal protein S2



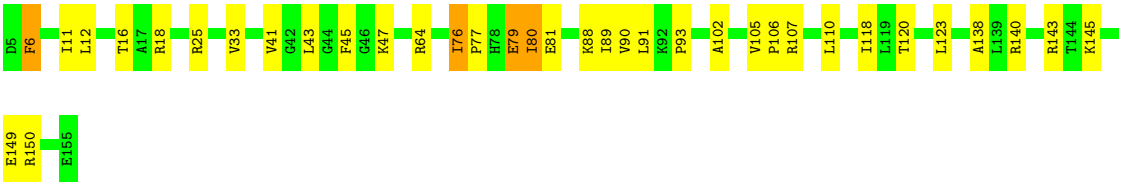
• Molecule 3: 30S ribosomal protein S3



• Molecule 4: 30S ribosomal protein S4

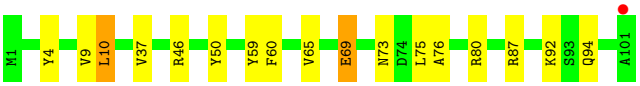


• Molecule 5: 30S ribosomal protein S5



• Molecule 6: 30S ribosomal protein S6

Chain F:

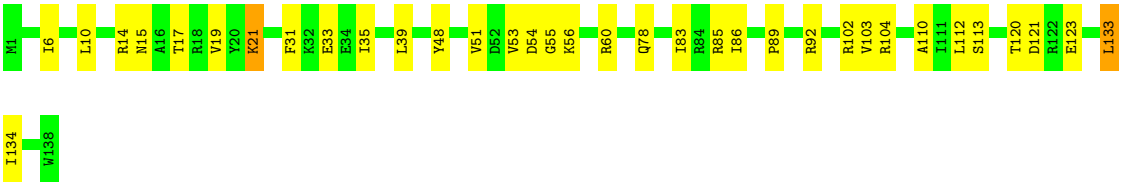


• Molecule 7: 30S ribosomal protein S7

Chain G:

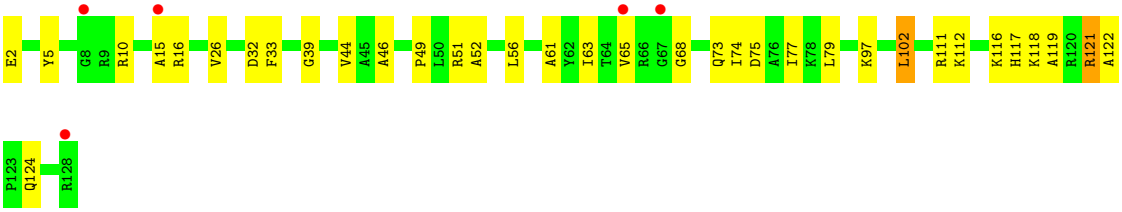
• Molecule 8: 30S ribosomal protein S8

Chain H:



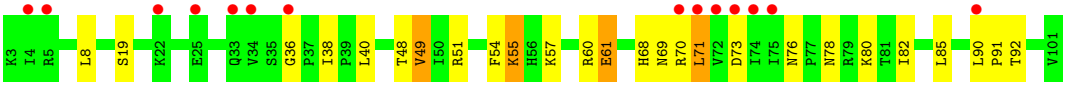
• Molecule 9: 30S ribosomal protein S9

Chain I:

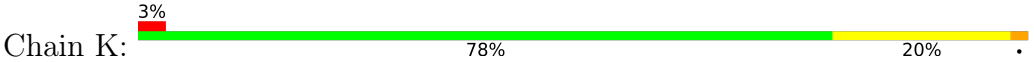


• Molecule 10: 30S ribosomal protein S10

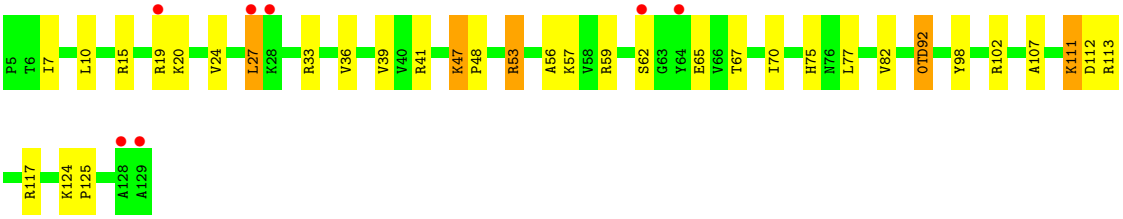
Chain J:



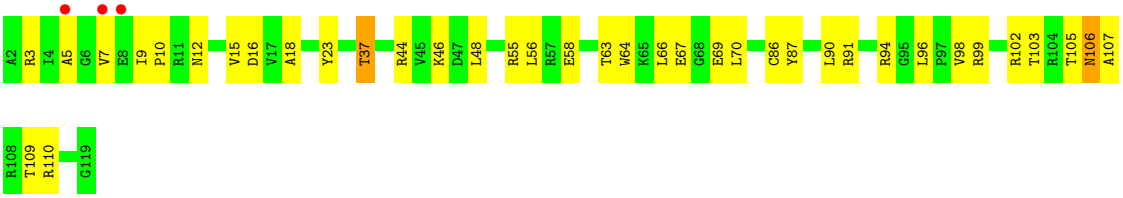
• Molecule 11: 30S ribosomal protein S11



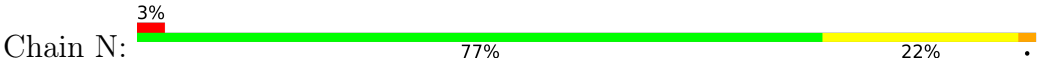
• Molecule 12: 30S ribosomal protein S12

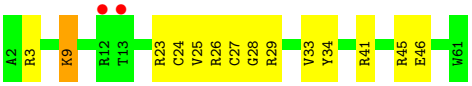


• Molecule 13: 30S ribosomal protein S13

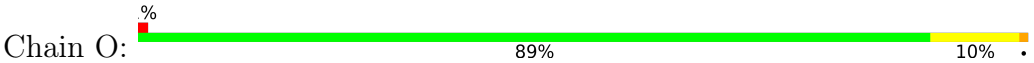


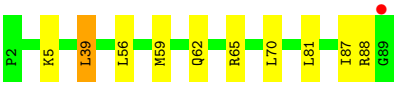
• Molecule 14: 30S ribosomal protein S14 type Z





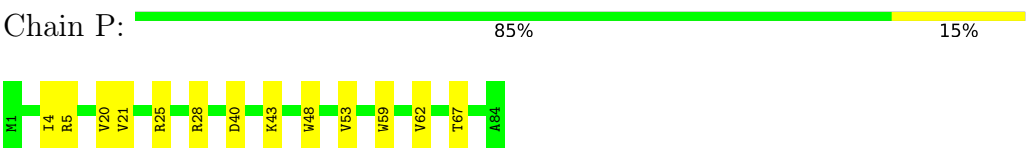
• Molecule 15: 30S ribosomal protein S15





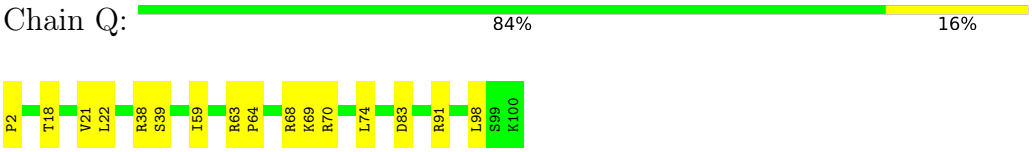
• Molecule 16: 30S ribosomal protein S16

Chain P:



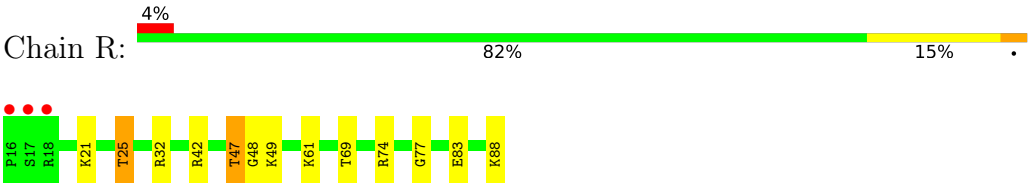
• Molecule 17: 30S ribosomal protein S17

Chain Q:



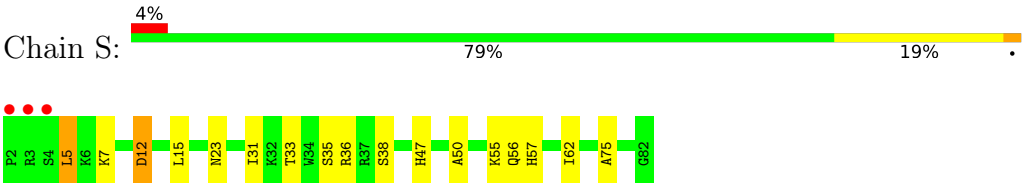
• Molecule 18: 30S ribosomal protein S18

Chain R:



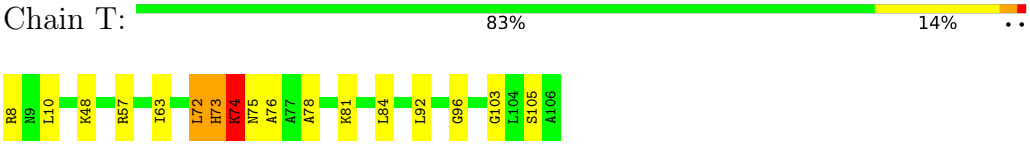
• Molecule 19: 30S ribosomal protein S19

Chain S:



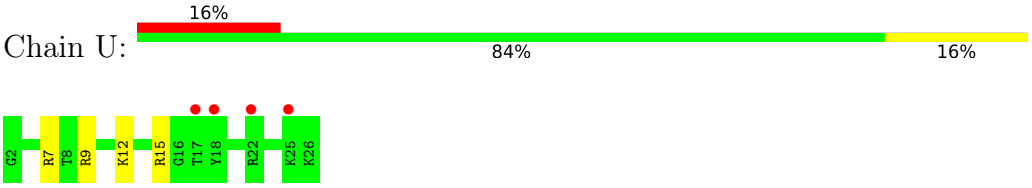
• Molecule 20: 30S ribosomal protein S20

Chain T:



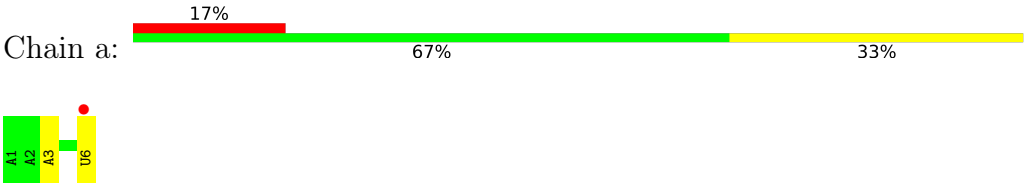
• Molecule 21: 30S ribosomal protein Thx

Chain U:



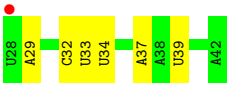
• Molecule 22: RNA (5'-R(P*UP*AP*GP*AP*CP*UP*(70U)P*UP*UP*(12A)P*AP*(PSU)P*CP*UP*A)-3')

Chain a:



• Molecule 23: RNA (5'-R(P*UP*AP*GP*AP*CP*UP*(70U)P*UP*UP*(12A)P*AP*(PSU)P*CP*UP*A)-3')

Chain b:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	400.00Å 400.00Å 173.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.80 – 3.30 39.80 – 2.92	Depositor EDS
% Data completeness (in resolution range)	99.9 (39.80-3.30) 81.8 (39.80-2.92)	Depositor EDS
R_{merge}	0.57	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	-0.28 (at 2.90Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.179 , 0.203 0.179 , 0.202	Depositor DCC
R_{free} test set	2000 reflections (0.68%)	wwPDB-VP
Wilson B-factor (Å^2)	91.1	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 88.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	52620	wwPDB-VP
Average B, all atoms (Å^2)	136.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.42% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 12A, ZN, MA6, 70U, K, 0TD, MG, 2MG, 5MC, UR3, 4OC, M2G, 7MG, A2M, B6M, PSU

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	0.17	0/36037	0.76	5/56239 (0.0%)
2	B	0.24	0/1909	0.40	0/2579
3	C	0.24	0/1637	0.44	0/2207
4	D	0.24	0/1733	0.40	0/2318
5	E	0.25	0/1163	0.44	0/1566
6	F	0.23	0/856	0.40	0/1154
7	G	0.24	0/1276	0.38	0/1709
8	H	0.24	0/1136	0.43	0/1527
9	I	0.25	0/1029	0.44	0/1379
10	J	0.24	0/806	0.49	0/1084
11	K	0.24	0/900	0.44	0/1213
12	L	0.24	0/978	0.48	0/1308
13	M	0.23	0/947	0.42	0/1270
14	N	0.24	0/501	0.41	0/664
15	O	0.23	0/745	0.38	0/992
16	P	0.23	0/717	0.43	0/965
17	Q	0.24	0/836	0.43	0/1117
18	R	0.23	0/604	0.39	0/801
19	S	0.24	0/662	0.46	0/892
20	T	0.24	0/765	0.38	0/1007
21	U	0.21	0/213	0.39	0/279
22	a	0.14	0/112	0.64	0/172
23	b	0.15	0/277	0.78	1/423 (0.2%)
All	All	0.20	0/55839	0.67	6/82865 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1
13	M	0	1
20	T	0	1
23	b	1	0
All	All	1	3

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	b	29	A	OP1-P-O3'	6.45	119.38	105.20
1	A	1301	U	P-O3'-C3'	5.53	126.33	119.70
1	A	1158	C	N1-C2-O2	5.42	122.15	118.90
1	A	1158	C	C2-N1-C1'	5.39	124.73	118.80
1	A	204	U	C2-N1-C1'	5.18	123.92	117.70
1	A	181	G	OP2-P-O3'	5.10	116.41	105.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
23	b	37	12A	C1'

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	88	ALA	Peptide
13	M	106	ASN	Peptide
20	T	74	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	32504	0	16434	281	1
2	B	1874	0	1887	25	0
3	C	1613	0	1677	30	0
4	D	1703	0	1763	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	1147	0	1207	21	0
6	F	843	0	857	11	0
7	G	1257	0	1296	21	0
8	H	1116	0	1177	21	0
9	I	1010	0	1037	24	0
10	J	793	0	835	19	0
11	K	885	0	904	14	0
12	L	973	0	1058	22	0
13	M	937	0	995	19	0
14	N	492	0	529	11	0
15	O	734	0	771	4	0
16	P	701	0	720	7	0
17	Q	823	0	891	11	0
18	R	598	0	670	11	0
19	S	648	0	673	7	0
20	T	763	0	861	8	0
21	U	209	0	221	3	0
22	a	124	0	67	0	0
23	b	329	0	171	0	0
24	A	235	0	0	0	0
24	D	1	0	0	0	0
24	E	1	0	0	0	0
24	F	1	0	0	0	0
24	G	1	0	0	0	0
24	H	1	0	0	0	0
24	L	1	0	0	0	0
24	N	1	0	0	0	0
24	P	3	0	0	0	0
24	Q	2	0	0	0	0
24	S	3	0	0	0	0
24	T	1	0	0	0	0
25	A	21	0	0	0	0
25	E	1	0	0	0	0
26	A	42	0	0	1	0
27	D	1	0	0	0	0
27	N	1	0	0	0	0
28	A	214	0	0	3	0
28	D	3	0	0	1	0
28	E	4	0	0	0	0
28	K	1	0	0	1	0
28	L	3	0	0	0	0
28	N	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	T	1	0	0	0	0
All	All	52620	0	36701	523	1

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 6.

All (523) 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)
8:H:10:LEU:HD22	8:H:83:ILE:HD11	1.70	0.73
2:B:223:ILE:HD13	2:B:230:VAL:H	1.54	0.73
1:A:664:G:H22	1:A:741:G:H1	1.35	0.73
7:G:143:ARG:O	7:G:147:ALA:HB2	1.89	0.73
11:K:123:LYS:HA	11:K:126:ARG:HG3	1.69	0.72
1:A:1266:G:N2	1:A:1269:A:OP2	2.23	0.71
5:E:80:ILE:HD12	5:E:138:ALA:HB1	1.72	0.71
12:L:41:ARG:HE	12:L:57:LYS:HE2	1.55	0.70
1:A:235:C:N4	28:A:1903:HOH:O	2.26	0.69
1:A:677:U:H3	1:A:713:G:H22	1.40	0.69
1:A:1422:G:H1	1:A:1478:C:H42	1.40	0.69
1:A:975:A:H4'	1:A:976:G:H5"	1.75	0.69
1:A:501:C:OP1	12:L:117:ARG:NH2	2.25	0.68
11:K:15:ALA:HA	11:K:77:MET:HA	1.75	0.68
2:B:134:GLU:HG2	2:B:137:ARG:HH21	1.59	0.67
1:A:1073:U:O2	2:B:104:ASN:ND2	2.28	0.67
1:A:266:G:H5'	1:A:268:C:H41	1.60	0.67
2:B:77:ALA:HB2	2:B:211:ILE:HD13	1.75	0.67
12:L:57:LYS:HG2	12:L:67:THR:HG22	1.77	0.67
1:A:537:G:OP1	12:L:113:ARG:NH2	2.27	0.67
20:T:74:LYS:O	20:T:76:ALA:N	2.28	0.66
9:I:51:ARG:HG3	9:I:56:LEU:HD21	1.76	0.66
5:E:102:ALA:O	5:E:107:ARG:NH1	2.29	0.65
1:A:1505:G:O2'	1:A:1506:U:OP2	2.14	0.65
12:L:53:ARG:NH1	12:L:92:0TD:OD2	2.30	0.65
16:P:4:ILE:HG12	16:P:21:VAL:HG22	1.77	0.65
3:C:189:ALA:HB3	3:C:196:LEU:HB2	1.79	0.64
1:A:1493:A:OP1	26:A:1856:B6M:O41	2.14	0.64
6:F:9:VAL:HB	6:F:87:ARG:HB2	1.79	0.64
1:A:976:G:OP2	1:A:1358:U:O2'	2.16	0.64
6:F:10:LEU:HD12	6:F:59:TYR:HB3	1.79	0.64
1:A:509:A:N3	1:A:543:C:O2'	2.30	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:80:ILE:HG13	5:E:91:LEU:HB2	1.79	0.63
9:I:112:LYS:HA	9:I:119:ALA:HB2	1.79	0.63
19:S:50:ALA:HB1	19:S:57:HIS:HB3	1.80	0.63
3:C:14:ILE:HG22	3:C:15:THR:HG23	1.81	0.63
3:C:156:ARG:H	3:C:163:ALA:HA	1.64	0.63
13:M:23:TYR:HB3	13:M:67:GLU:HG2	1.80	0.63
1:A:427:U:OP1	4:D:13:ARG:NH2	2.32	0.63
11:K:18:ARG:NH1	11:K:35:PRO:O	2.32	0.62
11:K:22:HIS:HB3	11:K:29:ILE:HG23	1.82	0.62
1:A:1518:MA6:H93	1:A:1519:MA6:H92	1.81	0.62
5:E:140:ARG:O	5:E:143:ARG:NH2	2.32	0.62
3:C:131:ARG:HH11	3:C:166:GLU:HG3	1.65	0.62
8:H:113:SER:HB2	8:H:134:ILE:HD11	1.81	0.62
10:J:19:SER:HB3	10:J:91:PRO:HG3	1.82	0.62
1:A:1347:G:O6	9:I:10:ARG:NH2	2.31	0.62
12:L:47:LYS:HG3	12:L:48:PRO:HD3	1.81	0.62
3:C:11:ARG:NH1	3:C:177:THR:O	2.33	0.62
3:C:27:LYS:HD3	3:C:27:LYS:H	1.65	0.61
3:C:70:VAL:HG12	3:C:72:LYS:H	1.65	0.61
9:I:46:ALA:HB2	9:I:74:ILE:HG23	1.82	0.61
1:A:1326:C:OP1	21:U:12:LYS:NZ	2.34	0.61
14:N:9:LYS:HE2	14:N:23:ARG:HB2	1.82	0.61
15:O:62:GLN:OE1	15:O:65:ARG:NH2	2.33	0.61
7:G:143:ARG:O	7:G:147:ALA:CB	2.47	0.61
9:I:10:ARG:HG2	9:I:75:ASP:HB2	1.83	0.60
1:A:401:C:O2'	1:A:621:A:N3	2.33	0.60
2:B:174:VAL:O	2:B:178:ARG:HG2	2.00	0.60
4:D:7:PRO:HB2	4:D:10:ARG:HD2	1.81	0.60
1:A:6:G:H4'	1:A:298:A:H4'	1.84	0.60
1:A:372:C:H4'	1:A:373:A:O5'	2.02	0.60
1:A:765:G:N2	1:A:813:U:OP2	2.35	0.59
1:A:542:G:OP1	4:D:10:ARG:NH2	2.34	0.59
1:A:1240:U:OP1	7:G:119:ARG:NH1	2.34	0.59
7:G:111:ARG:NH2	7:G:126:ASP:OD2	2.34	0.59
11:K:122:LYS:NZ	28:K:201:HOH:O	2.36	0.59
1:A:298:A:N6	28:A:1904:HOH:O	2.30	0.59
1:A:521:G:N7	12:L:53:ARG:NH2	2.50	0.59
1:A:951:G:OP2	13:M:102:ARG:NH2	2.36	0.59
7:G:54:THR:HG22	7:G:56:GLN:H	1.68	0.59
8:H:53:VAL:HG12	8:H:54:ASP:H	1.67	0.59
1:A:1301:U:O2'	1:A:1302:U:O5'	2.21	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:39:LEU:HD13	15:O:56:LEU:HB2	1.85	0.58
1:A:1005:A:N6	1:A:1024:G:O2'	2.35	0.58
7:G:28:ASN:OD1	7:G:36:LYS:NZ	2.37	0.58
10:J:38:ILE:HD12	10:J:71:LEU:HD12	1.85	0.58
3:C:6:HIS:HD2	3:C:8:ILE:H	1.51	0.58
1:A:1319:A:H5'	19:S:5:LEU:HD22	1.84	0.58
1:A:636:U:H5'	17:Q:2:PRO:HG3	1.84	0.58
9:I:15:ALA:HB2	9:I:65:VAL:HG13	1.86	0.58
1:A:974:A:OP2	14:N:29:ARG:NH2	2.37	0.57
5:E:88:LYS:HB3	5:E:123:LEU:HB2	1.86	0.57
5:E:81:GLU:HG3	5:E:90:VAL:HG22	1.86	0.57
18:R:25:THR:HB	18:R:42:ARG:HH22	1.70	0.57
1:A:811:C:O2'	1:A:901:A:N1	2.37	0.57
3:C:59:ARG:HG2	3:C:64:VAL:HG22	1.86	0.57
14:N:26:ARG:NH2	14:N:46:GLU:OE1	2.37	0.57
11:K:58:PRO:HB2	11:K:93:GLN:HG3	1.85	0.57
1:A:413:G:N2	1:A:429:U:OP2	2.38	0.56
1:A:1249:C:O2'	9:I:73:GLN:NE2	2.39	0.56
1:A:362:G:N2	1:A:365:U:OP2	2.38	0.56
8:H:103:VAL:HG12	8:H:104:ARG:HG2	1.86	0.56
10:J:38:ILE:HB	10:J:71:LEU:HB3	1.87	0.56
1:A:1301:U:HO2'	1:A:1302:U:P	2.27	0.56
1:A:1425:U:H3	1:A:1475:G:H1	1.52	0.56
1:A:1442:G:O6	1:A:1446:A:N6	2.39	0.56
1:A:316:G:OP2	1:A:351:G:O2'	2.24	0.56
1:A:1124:G:N7	1:A:1145:C:O2'	2.35	0.56
1:A:1402:4OC:HM22	1:A:1403:C:H5'	1.88	0.56
1:A:1065:U:H4'	1:A:1066:C:O5'	2.05	0.56
10:J:8:LEU:HB2	10:J:70:ARG:HB2	1.86	0.56
1:A:1309:G:N7	13:M:99:ARG:NH2	2.53	0.56
1:A:1510:U:H2'	1:A:1511:G:C8	2.41	0.56
19:S:33:THR:HG22	19:S:35:SER:H	1.70	0.56
5:E:102:ALA:HB1	5:E:106:PRO:HG2	1.89	0.55
1:A:1122:U:O4	1:A:1123:A:N6	2.40	0.55
5:E:33:VAL:HG22	5:E:43:LEU:HD23	1.88	0.55
7:G:146:GLU:HG2	7:G:149:ARG:HD3	1.88	0.55
1:A:1049:U:H4'	1:A:1050:G:O5'	2.06	0.55
10:J:49:VAL:HG23	14:N:41:ARG:HB2	1.88	0.55
18:R:32:ARG:HA	18:R:69:THR:HG21	1.88	0.55
1:A:1391:U:H2'	1:A:1392:G:C8	2.41	0.55
1:A:558:G:OP2	1:A:559:A:O2'	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:A:O2'	1:A:564:C:N3	2.36	0.55
4:D:23:GLY:HA3	4:D:112:VAL:HG22	1.89	0.55
1:A:685:G:N2	1:A:704:A:OP2	2.38	0.55
1:A:1137:C:H4'	1:A:1138:G:C2	2.43	0.54
1:A:1498:UR3:H1'	1:A:1499:A:OP2	2.07	0.54
2:B:87:ARG:HH21	2:B:219:VAL:HB	1.72	0.54
1:A:946:A:H2'	1:A:947:G:C8	2.42	0.54
1:A:1399:C:H4'	1:A:1400:5MC:H5"	1.89	0.54
1:A:562:C:H1'	12:L:15:ARG:HG3	1.88	0.54
2:B:48:MET:HA	2:B:51:LEU:HB2	1.90	0.54
1:A:45:U:H2'	1:A:46:G:C8	2.43	0.54
1:A:1412:C:H2'	1:A:1413:A:C8	2.42	0.54
1:A:1392:G:N2	1:A:1502:A:H8	2.06	0.54
1:A:708:C:OP1	11:K:85:ARG:NH2	2.34	0.54
12:L:56:ALA:HB2	12:L:70:ILE:HD11	1.90	0.54
1:A:250:A:H4'	1:A:251:G:O5'	2.07	0.53
10:J:8:LEU:O	10:J:69:ASN:HA	2.07	0.53
13:M:86:CYS:SG	13:M:87:TYR:N	2.81	0.53
1:A:1183:A:O2'	1:A:1185:G:OP2	2.27	0.53
9:I:32:ASP:OD1	9:I:33:PHE:N	2.42	0.53
1:A:1207:2MG:HM23	1:A:1208:C:H1'	1.89	0.53
1:A:1056:U:H5'	3:C:163:ALA:HB2	1.90	0.53
1:A:390:C:O3'	16:P:28:ARG:NH2	2.41	0.53
1:A:1182:G:H4'	1:A:1183:A:O5'	2.09	0.53
11:K:110:ASP:OD2	18:R:88:LYS:NZ	2.39	0.53
4:D:141:ARG:NH2	28:D:401:HOH:O	2.41	0.53
7:G:113:GLU:HB2	7:G:119:ARG:HG3	1.91	0.53
1:A:1035:A:H2'	1:A:1036:G:H8	1.73	0.53
4:D:26:CYS:HA	4:D:31:CYS:HB2	1.91	0.53
8:H:51:VAL:HG21	8:H:60:ARG:HG3	1.91	0.53
1:A:8:A:N6	4:D:205:GLU:O	2.42	0.53
1:A:967:5MC:H5"	1:A:968:A:OP2	2.08	0.53
1:A:1057:G:H5"	3:C:154:SER:HB2	1.91	0.53
1:A:1059:C:O3'	14:N:45:ARG:NH2	2.41	0.53
3:C:58:GLU:HB3	10:J:92:THR:HG21	1.91	0.53
12:L:111:LYS:HE3	12:L:112:ASP:H	1.74	0.52
11:K:57:THR:HG22	11:K:59:TYR:H	1.73	0.52
1:A:1030(A):G:N2	1:A:1030(D):A:OP2	2.39	0.52
7:G:152:ALA:O	7:G:155:ARG:NH1	2.43	0.52
8:H:112:LEU:HD23	8:H:133:LEU:HA	1.91	0.52
9:I:116:LYS:HD2	9:I:122:ALA:HA	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:48:GLY:O	18:R:74:ARG:NH2	2.42	0.52
1:A:890:G:O2'	1:A:906:G:O6	2.20	0.52
1:A:826:C:O2	8:H:15:ASN:ND2	2.42	0.52
10:J:57:LYS:HE2	10:J:60:ARG:NH2	2.24	0.52
2:B:55:PHE:HD2	2:B:221:LEU:HG	1.74	0.52
12:L:59:ARG:NH1	12:L:65:GLU:OE2	2.42	0.52
2:B:74:LYS:NZ	2:B:206:ASP:OD1	2.34	0.52
9:I:26:VAL:HG13	9:I:61:ALA:HB3	1.92	0.52
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.92	0.52
1:A:662:G:H2'	1:A:663:A:C8	2.45	0.51
3:C:91:LEU:HD21	3:C:99:VAL:HG22	1.90	0.51
1:A:619:U:N3	4:D:134:ASP:OD1	2.35	0.51
4:D:140:VAL:HG11	4:D:146:ILE:HD11	1.90	0.51
1:A:1035:A:H2'	1:A:1036:G:C8	2.44	0.51
12:L:36:VAL:HG22	12:L:82:VAL:HG22	1.91	0.51
1:A:1031:G:H2'	1:A:1032:G:C8	2.45	0.51
1:A:1192:C:O2	5:E:25:ARG:NH2	2.27	0.51
4:D:68:TYR:HB3	4:D:70:ILE:HD13	1.92	0.51
5:E:110:LEU:HD13	5:E:118:ILE:HG21	1.91	0.51
1:A:21:G:H2'	1:A:22:G:C8	2.46	0.51
1:A:352:C:O2'	1:A:354:G:OP1	2.23	0.51
16:P:40:ASP:HB3	16:P:48:TRP:HB2	1.93	0.51
1:A:966:M2G:HM13	1:A:967:5MC:H1'	1.92	0.51
3:C:21:ARG:HG3	3:C:58:GLU:HG2	1.93	0.51
1:A:1498:UR3:O5'	1:A:1498:UR3:H6	2.11	0.51
1:A:673:G:H2'	1:A:674:G:C8	2.46	0.51
3:C:38:ARG:HB3	3:C:94:LEU:HD21	1.92	0.51
15:O:56:LEU:HA	15:O:59:MET:HE2	1.93	0.51
1:A:1499:A:H1'	1:A:1520:G:H5'	1.93	0.51
1:A:501:C:H2'	1:A:502:G:H8	1.74	0.51
17:Q:68:ARG:H	17:Q:70:ARG:NH1	2.08	0.51
1:A:1070:U:OP1	5:E:18:ARG:NH1	2.44	0.51
1:A:1435:G:H2'	1:A:1436:U:C6	2.46	0.51
1:A:337:C:H2'	1:A:338:A:C8	2.45	0.51
7:G:62:PHE:HA	7:G:124:LEU:HD12	1.92	0.51
9:I:44:VAL:O	9:I:51:ARG:NH2	2.44	0.51
1:A:1413:A:H2	1:A:1487:G:H22	1.59	0.50
1:A:56:U:H2'	1:A:57:G:C8	2.46	0.50
1:A:501:C:H2'	1:A:502:G:C8	2.46	0.50
1:A:1080:A:H5"	5:E:16:THR:HG21	1.93	0.50
2:B:33:TYR:HB2	2:B:43:ASP:HA	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:121:ASP:N	8:H:121:ASP:OD1	2.44	0.50
8:H:86:ILE:HD12	8:H:133:LEU:HD22	1.94	0.50
1:A:269:C:H2'	1:A:270:A:C8	2.47	0.50
12:L:75:HIS:HA	12:L:102:ARG:HH22	1.77	0.50
1:A:1124:G:O2'	1:A:1126:U:O4	2.29	0.50
1:A:1226:C:OP2	13:M:103:THR:OG1	2.22	0.50
1:A:539:A:H2'	1:A:540:G:C8	2.47	0.50
1:A:947:G:H4'	1:A:1332:A:H2	1.76	0.50
9:I:49:PRO:O	9:I:52:ALA:HB3	2.12	0.50
9:I:65:VAL:HG21	9:I:77:ILE:HD11	1.94	0.50
1:A:1256:A:HO2'	1:A:1257:U:P	2.35	0.49
1:A:1504:G:OP1	1:A:1507:A:H4'	2.12	0.49
1:A:59:A:H5"	1:A:387:U:H5"	1.94	0.49
1:A:1179:A:O2'	1:A:1180:A:OP1	2.28	0.49
1:A:1250:A:H4'	9:I:68:GLY:N	2.26	0.49
1:A:181:G:H4'	1:A:182:U:H5'	1.94	0.49
3:C:155:GLY:HA2	3:C:164:ARG:H	1.76	0.49
4:D:11:LEU:HD13	4:D:66:ARG:HD3	1.94	0.49
7:G:46:ALA:O	7:G:50:ILE:HG12	2.13	0.49
2:B:112:VAL:O	2:B:116:GLU:HG2	2.12	0.49
2:B:91:PRO:HG3	2:B:154:LEU:HB2	1.94	0.49
9:I:117:HIS:HB2	9:I:121:ARG:HB3	1.95	0.49
17:Q:68:ARG:H	17:Q:70:ARG:HH11	1.60	0.49
1:A:1031:G:H2'	1:A:1032:G:H8	1.78	0.49
9:I:97:LYS:HA	9:I:102:LEU:HD11	1.93	0.49
1:A:1034:G:H2'	1:A:1035:A:C8	2.48	0.49
1:A:1532:U:H2'	1:A:1533:C:H3'	1.95	0.49
1:A:514:C:H2'	1:A:515:G:H8	1.78	0.49
13:M:3:ARG:HE	13:M:7:VAL:HA	1.77	0.49
1:A:1308:U:H2'	1:A:1309:G:H8	1.77	0.49
1:A:337:C:H2'	1:A:338:A:H8	1.76	0.49
7:G:111:ARG:HB2	7:G:119:ARG:HG2	1.95	0.49
1:A:1026:G:O6	1:A:1027:C:N4	2.46	0.48
1:A:1443:G:H4'	1:A:1446:A:O5'	2.12	0.48
1:A:580:U:H2'	1:A:581:G:O4'	2.12	0.48
4:D:98:GLU:HG2	4:D:189:PRO:HG3	1.95	0.48
17:Q:83:ASP:N	17:Q:83:ASP:OD1	2.46	0.48
2:B:97:TRP:HZ2	2:B:102:LEU:HD13	1.78	0.48
1:A:1026:G:H3'	1:A:1027:C:H5"	1.96	0.48
1:A:1064:G:H21	1:A:1190:G:H2'	1.78	0.48
1:A:1356:G:H2'	1:A:1357:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1152:A:OP1	10:J:68:HIS:ND1	2.45	0.48
3:C:19:GLU:HG2	3:C:54:ARG:HE	1.78	0.48
19:S:23:ASN:OD1	19:S:47:HIS:NE2	2.40	0.48
3:C:64:VAL:HB	3:C:99:VAL:HG21	1.95	0.48
7:G:75:VAL:HG21	7:G:86:GLN:HB3	1.96	0.48
1:A:277:C:H5"	17:Q:68:ARG:NH2	2.28	0.48
1:A:7:G:H5'	1:A:298:A:O4'	2.13	0.48
1:A:1106:G:H5"	3:C:172:ARG:HG2	1.95	0.48
5:E:79:GLU:HG3	5:E:93:PRO:HD2	1.95	0.48
11:K:72:ALA:HB1	11:K:77:MET:HE2	1.94	0.48
19:S:12:ASP:HB2	19:S:38:SER:HB3	1.95	0.48
1:A:652:U:O4	1:A:752:G:O2'	2.24	0.48
1:A:579:G:H5'	1:A:728:A:H1'	1.95	0.48
4:D:64:LEU:HD23	4:D:198:VAL:HG21	1.95	0.48
4:D:57:ARG:HB3	4:D:206:PHE:HB2	1.96	0.48
1:A:1379:G:OP1	7:G:6:ARG:NH1	2.46	0.48
1:A:1128:C:H42	1:A:1143:G:H22	1.61	0.48
1:A:1132:C:H2'	1:A:1133:G:H8	1.78	0.48
1:A:454:C:OP2	1:A:455:C:N4	2.38	0.48
1:A:60:A:H4'	1:A:61:G:O5'	2.13	0.48
1:A:593:G:H1	1:A:646:U:H3	1.61	0.48
1:A:1286:A:H2'	1:A:1287:A:H4'	1.95	0.47
1:A:560:U:H5'	1:A:566:G:N2	2.29	0.47
4:D:24:GLU:HG2	4:D:25:ARG:H	1.79	0.47
11:K:80:VAL:HG11	11:K:103:LEU:HD13	1.96	0.47
1:A:1414:U:H2'	1:A:1415:G:H8	1.79	0.47
20:T:92:LEU:O	20:T:96:GLY:N	2.33	0.47
2:B:44:LEU:H	2:B:44:LEU:HD12	1.79	0.47
15:O:87:ILE:HG22	15:O:88:ARG:H	1.79	0.47
1:A:376:G:H5"	16:P:5:ARG:HB2	1.94	0.47
1:A:1301:U:H1'	1:A:1302:U:OP1	2.14	0.47
1:A:692:U:O2'	1:A:694:A:N7	2.40	0.47
9:I:16:ARG:O	9:I:63:ILE:HA	2.14	0.47
12:L:124:LYS:HD3	12:L:125:PRO:HD2	1.97	0.47
13:M:12:ASN:OD1	13:M:46:LYS:NZ	2.40	0.47
13:M:96:LEU:O	13:M:110:ARG:NH1	2.48	0.47
2:B:101:MET:HA	2:B:108:ILE:HG13	1.96	0.47
2:B:88:ALA:HB1	2:B:226:ARG:HH21	1.79	0.47
10:J:48:THR:O	14:N:34:TYR:OH	2.33	0.47
1:A:1308:U:H2'	1:A:1309:G:C8	2.50	0.47
1:A:1306:A:N6	1:A:1331:G:H1'	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:243:A:H4'	1:A:244:U:H5'	1.97	0.47
1:A:413:G:H1'	1:A:428:G:N2	2.30	0.47
1:A:1325:C:P	21:U:15:ARG:HH21	2.38	0.47
1:A:1189:C:H5"	3:C:5:ILE:HG12	1.96	0.47
1:A:1329:A:N7	21:U:7:ARG:NH2	2.63	0.47
1:A:28:G:O2'	1:A:296:U:OP1	2.30	0.47
1:A:991:U:O4	1:A:1212:U:O2'	2.22	0.47
4:D:4:TYR:CG	4:D:4:TYR:O	2.68	0.47
1:A:1291:G:H4'	9:I:39:GLY:HA3	1.97	0.47
5:E:76:ILE:HG13	5:E:77:PRO:HD2	1.96	0.46
2:B:130:ARG:HD3	2:B:130:ARG:HA	1.73	0.46
1:A:737:A:H1'	6:F:73:ASN:HD21	1.81	0.46
1:A:1054:C:H2'	1:A:1055:A:H5"	1.98	0.46
1:A:875:C:O2'	8:H:14:ARG:NH1	2.48	0.46
1:A:973:G:H3'	1:A:974:A:H5"	1.96	0.46
8:H:120:THR:H	8:H:123:GLU:HB2	1.81	0.46
1:A:1020:U:H2'	1:A:1021:G:H8	1.80	0.46
1:A:1218:C:H2'	1:A:1219:U:C6	2.50	0.46
1:A:1342:C:H2'	1:A:1343:G:C8	2.51	0.46
3:C:64:VAL:H	3:C:99:VAL:HB	1.80	0.46
18:R:47:THR:HA	18:R:83:GLU:HB2	1.98	0.46
1:A:1323:G:H2'	1:A:1324:A:C8	2.51	0.46
1:A:266:G:H5"	1:A:267:C:C5	2.51	0.46
1:A:757:U:H2'	1:A:758:G:O4'	2.16	0.46
1:A:1432:G:O2'	1:A:1468:A:N6	2.48	0.46
1:A:190(L):U:O2	20:T:105:SER:OG	2.27	0.46
5:E:45:PHE:CE2	5:E:47:LYS:HD2	2.50	0.46
8:H:6:ILE:O	8:H:10:LEU:HG	2.16	0.46
1:A:335:C:O2'	1:A:1433:A:N3	2.40	0.46
1:A:501:C:H1'	1:A:549:C:H1'	1.96	0.46
1:A:791:G:O6	1:A:792:A:N6	2.48	0.46
1:A:344:A:H5'	1:A:345:C:C5	2.51	0.46
1:A:977:A:H2'	1:A:978:A:H5"	1.98	0.46
13:M:5:ALA:HB1	13:M:66:LEU:HD13	1.97	0.46
1:A:1402:4OC:H2'	1:A:1403:C:O4'	2.15	0.45
1:A:514:C:H2'	1:A:515:G:C8	2.51	0.45
1:A:769:G:H4'	1:A:1513:A:H4'	1.98	0.45
3:C:88:ARG:HE	3:C:101:LEU:HB3	1.81	0.45
5:E:6:PHE:HA	5:E:6:PHE:HD1	1.70	0.45
13:M:98:VAL:HG23	13:M:110:ARG:HH12	1.81	0.45
1:A:1027:C:N4	1:A:1036:G:O6	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1305:G:H22	1:A:1331:G:H2'	1.82	0.45
1:A:927:G:OP1	1:A:1505:G:N2	2.49	0.45
1:A:938:A:N6	28:A:1905:HOH:O	2.39	0.45
4:D:64:LEU:HB2	4:D:198:VAL:HG11	1.99	0.45
10:J:90:LEU:N	10:J:91:PRO:HD2	2.31	0.45
13:M:37:THR:HG22	13:M:55:ARG:HD2	1.98	0.45
1:A:264:U:H4'	17:Q:63:ARG:HD3	1.99	0.45
1:A:1305:G:N2	1:A:1331:G:H2'	2.32	0.45
2:B:88:ALA:O	2:B:90:MET:N	2.46	0.45
12:L:7:ILE:HD13	12:L:10:LEU:HD12	1.97	0.45
1:A:1502:A:H2	1:A:1505:G:H1	1.62	0.45
1:A:696:A:N3	1:A:786:G:O2'	2.39	0.45
2:B:239:VAL:O	2:B:241:GLU:N	2.50	0.45
1:A:372:C:H1'	1:A:373:A:OP2	2.16	0.45
2:B:47:THR:HA	2:B:202:PRO:HG2	1.98	0.45
8:H:19:VAL:HG23	8:H:21:LYS:HD3	1.99	0.45
10:J:71:LEU:HD13	10:J:73:ASP:HB2	1.99	0.45
6:F:46:ARG:HB2	6:F:60:PHE:CE2	2.51	0.45
13:M:90:LEU:O	13:M:94:ARG:HG2	2.17	0.45
9:I:44:VAL:HG12	9:I:51:ARG:HH22	1.81	0.45
1:A:1298:C:H4'	1:A:1299:A:C4	2.52	0.45
1:A:1513:A:H2'	1:A:1514:C:C6	2.51	0.45
10:J:40:LEU:HB3	10:J:69:ASN:HB2	1.99	0.45
1:A:186:C:H2'	1:A:187:C:C6	2.52	0.45
1:A:390:C:H2'	1:A:391:G:C8	2.52	0.45
1:A:701:C:H4'	1:A:702:A:O5'	2.16	0.45
6:F:4:TYR:CE2	6:F:92:LYS:HG2	2.52	0.45
7:G:65:ALA:O	7:G:69:VAL:HG23	2.17	0.45
20:T:63:ILE:HG21	20:T:81:LYS:HG3	1.98	0.45
1:A:309:G:O2'	1:A:607:A:N1	2.50	0.44
9:I:44:VAL:HG12	9:I:51:ARG:NH2	2.32	0.44
1:A:1431:C:H2'	1:A:1432:G:O4'	2.17	0.44
1:A:324:G:N1	1:A:327:A:OP2	2.50	0.44
7:G:74:GLU:HG2	7:G:91:VAL:HG22	1.99	0.44
4:D:105:VAL:HG13	4:D:110:PHE:HB2	1.99	0.44
5:E:145:LYS:O	5:E:149:GLU:HG2	2.17	0.44
1:A:673:G:O3'	6:F:87:ARG:NH2	2.50	0.44
13:M:63:THR:HG23	13:M:64:TRP:CD2	2.52	0.44
1:A:976:G:H5'	1:A:1358:U:O2'	2.16	0.44
2:B:88:ALA:HB1	2:B:226:ARG:NH2	2.33	0.44
1:A:1109:C:OP2	3:C:176:HIS:ND1	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:11:ILE:HD12	5:E:105:VAL:HA	1.99	0.44
8:H:17:THR:O	8:H:78:GLN:NE2	2.44	0.44
17:Q:21:VAL:HG21	17:Q:59:ILE:HD11	2.00	0.44
10:J:54:PHE:CD2	10:J:55:LYS:HG2	2.52	0.44
13:M:3:ARG:HA	13:M:9:ILE:HG13	2.00	0.44
1:A:204:U:H4'	1:A:216:G:C8	2.52	0.44
1:A:636:U:H2'	1:A:637:G:C8	2.53	0.44
1:A:653:A:C8	8:H:56:LYS:HG2	2.53	0.44
11:K:34:ASP:OD1	11:K:38:ASN:N	2.50	0.44
13:M:15:VAL:HG21	13:M:48:LEU:HD21	1.99	0.44
1:A:689:C:H2'	1:A:690:G:O4'	2.17	0.44
17:Q:18:THR:HG23	17:Q:69:LYS:HE3	2.00	0.44
18:R:21:LYS:O	18:R:25:THR:OG1	2.27	0.44
11:K:27:ASN:OD1	11:K:28:THR:N	2.50	0.44
1:A:1148:U:H2'	1:A:1149:C:O4'	2.17	0.43
1:A:235:C:H5'	17:Q:70:ARG:HG2	2.00	0.43
1:A:1048:G:H5"	14:N:3:ARG:HG3	2.00	0.43
1:A:994:A:N7	1:A:1216:G:H4'	2.34	0.43
6:F:94:GLN:HB3	18:R:32:ARG:HH11	1.82	0.43
1:A:1147:C:HO2'	9:I:5:TYR:HH	1.65	0.43
1:A:328:C:H4'	1:A:329:A:O5'	2.17	0.43
1:A:558:G:C8	1:A:559:A:H2'	2.54	0.43
1:A:559:A:H4'	1:A:560:U:O5'	2.17	0.43
1:A:911:U:H2'	1:A:912:C:C6	2.52	0.43
4:D:111:ALA:HB2	4:D:120:LEU:HD12	1.99	0.43
4:D:110:PHE:HD1	4:D:162:LEU:HD21	1.83	0.43
7:G:45:ASP:O	7:G:49:ILE:HG13	2.17	0.43
14:N:24:CYS:HB3	14:N:29:ARG:H	1.83	0.43
1:A:1131:G:H2'	1:A:1132:C:C6	2.53	0.43
8:H:51:VAL:HG11	8:H:60:ARG:HH11	1.84	0.43
1:A:518:C:H2'	1:A:530:G:N3	2.34	0.43
2:B:115:LEU:HD13	2:B:145:LEU:HB3	2.00	0.43
4:D:32:ALA:HA	4:D:35:ARG:HG2	2.01	0.43
1:A:1127:G:N2	1:A:1146:A:H62	2.17	0.43
1:A:321:A:H61	1:A:332:G:H1	1.66	0.43
1:A:688:G:O2'	1:A:704:A:N1	2.46	0.43
1:A:757:U:O2'	1:A:879:C:O2	2.36	0.43
1:A:1123:A:H4'	10:J:36:GLY:HA3	2.00	0.43
12:L:70:ILE:HD13	12:L:77:LEU:HD12	2.00	0.43
1:A:1010:G:H2'	1:A:1011:G:H8	1.82	0.43
1:A:1118:C:H1'	1:A:1179:A:C5	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1198:G:H2'	1:A:1199:U:C6	2.54	0.43
1:A:130:A:H1'	1:A:263:A:O2'	2.19	0.43
3:C:147:LYS:HE2	3:C:205:GLY:H	1.83	0.43
6:F:50:TYR:CE2	18:R:77:GLY:HA2	2.54	0.43
8:H:110:ALA:HB3	8:H:121:ASP:HB3	2.00	0.43
12:L:24:VAL:HG13	12:L:98:TYR:CE1	2.53	0.43
19:S:55:LYS:HG2	19:S:56:GLN:HG3	1.99	0.43
1:A:339:C:H2'	1:A:340:U:C6	2.54	0.43
1:A:738:C:H5"	6:F:69:GLU:HB3	2.00	0.43
1:A:1273:G:H2'	1:A:1274:G:O4'	2.19	0.43
1:A:129:U:O3'	1:A:129(A):G:H3'	2.19	0.43
1:A:663:A:H5"	18:R:61:LYS:HE3	2.01	0.42
3:C:64:VAL:HG23	3:C:99:VAL:HG11	2.01	0.42
8:H:53:VAL:O	8:H:55:GLY:N	2.52	0.42
1:A:186:C:H5'	20:T:78:ALA:HB1	2.01	0.42
1:A:129(A):G:H21	1:A:190(E):U:H3'	1.84	0.42
7:G:51:GLN:C	7:G:53:LYS:H	2.22	0.42
17:Q:22:LEU:HD11	17:Q:39:SER:HB2	2.01	0.42
1:A:1347:G:O2'	1:A:1348:U:P	2.77	0.42
1:A:1518:MA6:H93	1:A:1519:MA6:C9	2.47	0.42
1:A:555:C:H2'	1:A:556:C:C6	2.54	0.42
1:A:801:U:H2'	1:A:802:A:C8	2.54	0.42
2:B:68:ILE:O	2:B:90:MET:HB3	2.19	0.42
6:F:37:VAL:HA	6:F:65:VAL:HG12	2.01	0.42
1:A:1001:A:H2'	1:A:1002:G:C8	2.54	0.42
1:A:142:G:H2'	1:A:143:A:H8	1.84	0.42
1:A:547:A:OP2	4:D:2:GLY:N	2.51	0.42
4:D:110:PHE:CD1	4:D:162:LEU:HD21	2.54	0.42
11:K:69:ALA:O	11:K:73:MET:HG2	2.20	0.42
1:A:1077:G:N2	1:A:1080:A:OP2	2.49	0.42
1:A:1232:U:H5"	9:I:124:GLN:O	2.19	0.42
1:A:1355:G:H2'	1:A:1356:G:C8	2.54	0.42
1:A:384:G:H2'	1:A:385:C:C6	2.55	0.42
1:A:603:U:H2'	1:A:604:G:C8	2.55	0.42
1:A:878:G:H5"	8:H:89:PRO:O	2.18	0.42
13:M:16:ASP:N	13:M:16:ASP:OD1	2.53	0.42
1:A:1034:G:H2'	1:A:1035:A:H8	1.83	0.42
1:A:241:C:H4'	12:L:19:ARG:HH22	1.83	0.42
1:A:833:U:H2'	1:A:834:C:C6	2.55	0.42
1:A:836:G:C6	1:A:851:G:C6	3.08	0.42
1:A:851:G:H2'	1:A:852:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:948:C:OP1	13:M:107:ALA:HA	2.20	0.42
2:B:28:PHE:HD1	2:B:194:PRO:HG3	1.83	0.42
1:A:1306:A:H61	1:A:1331:G:H1'	1.84	0.42
5:E:90:VAL:O	5:E:120:THR:HA	2.19	0.42
12:L:27:LEU:O	12:L:33:ARG:NH1	2.53	0.42
1:A:272:C:H2'	1:A:273:A:H8	1.84	0.42
1:A:67:C:H2'	1:A:68:G:C8	2.54	0.42
1:A:748:C:H1'	1:A:749:C:OP2	2.20	0.42
6:F:76:ALA:O	6:F:80:ARG:HG3	2.20	0.42
10:J:82:ILE:HA	10:J:85:LEU:HB2	2.01	0.42
18:R:47:THR:HG22	18:R:48:GLY:H	1.85	0.42
1:A:1392:G:H21	1:A:1502:A:H8	1.65	0.42
3:C:136:GLN:O	3:C:140:ARG:HG3	2.19	0.42
3:C:93:LYS:HA	3:C:93:LYS:HD3	1.94	0.42
1:A:1069:C:O2'	1:A:1192:C:H1'	2.20	0.42
1:A:719:C:O2'	18:R:49:LYS:HB3	2.20	0.42
3:C:126:ARG:HH21	3:C:128:PHE:HD1	1.68	0.42
10:J:76:ASN:O	10:J:78:ASN:N	2.53	0.42
1:A:1003:G:H2'	1:A:1003(A):G:C8	2.55	0.41
1:A:1225:A:H5"	1:A:1226:C:OP2	2.19	0.41
1:A:1477:C:H2'	1:A:1478:C:C6	2.55	0.41
1:A:713:G:H2'	1:A:714:G:C8	2.54	0.41
14:N:27:CYS:SG	14:N:29:ARG:HB2	2.60	0.41
1:A:1396:A:H4'	1:A:1397:C:H5"	2.02	0.41
17:Q:63:ARG:HG2	17:Q:64:PRO:HD2	2.02	0.41
1:A:1376:U:H2'	1:A:1377:A:C8	2.56	0.41
1:A:230:G:H2'	1:A:231:G:O4'	2.20	0.41
1:A:397:A:H5'	1:A:398:C:OP1	2.20	0.41
3:C:3:ASN:N	3:C:3:ASN:OD1	2.53	0.41
10:J:51:ARG:CZ	10:J:61:GLU:HG3	2.50	0.41
1:A:191:G:N2	20:T:103:GLY:O	2.42	0.41
1:A:17:U:H2'	1:A:18:C:C6	2.55	0.41
1:A:51:A:N7	1:A:114:U:O2'	2.51	0.41
1:A:851:G:H2'	1:A:852:G:C8	2.54	0.41
12:L:27:LEU:HB2	12:L:62:SER:OG	2.19	0.41
1:A:359:U:H2'	1:A:360:A:C8	2.56	0.41
7:G:75:VAL:HG11	7:G:144:MET:HB3	2.02	0.41
12:L:77:LEU:HD21	12:L:107:ALA:HB2	2.03	0.41
1:A:1128:C:H42	1:A:1143:G:H1	1.69	0.41
1:A:1256:A:O2'	1:A:1257:U:O5'	2.35	0.41
1:A:450:G:OP1	16:P:43:LYS:NZ	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:111:ARG:HB3	7:G:113:GLU:HG2	2.02	0.41
1:A:1505:G:HO2'	1:A:1506:U:P	2.39	0.41
1:A:776:G:N2	1:A:802:A:OP2	2.52	0.41
5:E:81:GLU:HG2	5:E:88:LYS:HE2	2.02	0.41
1:A:192:U:H1'	20:T:103:GLY:HA2	2.01	0.41
1:A:1029:C:H2'	1:A:1030:C:C6	2.56	0.41
1:A:1177:G:O5'	9:I:97:LYS:NZ	2.54	0.41
1:A:1300:G:HO2'	1:A:1301:U:P	2.44	0.41
1:A:959:A:HO2'	1:A:984:C:HO2'	1.66	0.41
2:B:69:LEU:HD21	2:B:93:VAL:HG23	2.02	0.41
9:I:65:VAL:HG11	9:I:73:GLN:HB3	2.03	0.41
1:A:1281:U:O2'	1:A:1282:C:OP1	2.30	0.41
1:A:1490:C:H2'	1:A:1491:G:H8	1.86	0.41
1:A:620:C:H2'	1:A:621:A:O4'	2.21	0.41
7:G:15:ASP:OD1	7:G:44:TYR:OH	2.36	0.41
1:A:356:A:H2'	1:A:357:G:O4'	2.21	0.41
1:A:1020:U:H2'	1:A:1021:G:C8	2.56	0.40
1:A:484:G:H4'	1:A:485:G:O5'	2.21	0.40
5:E:76:ILE:O	5:E:93:PRO:HB3	2.20	0.40
20:T:72:LEU:HD22	20:T:72:LEU:HA	1.88	0.40
1:A:1021:G:H2'	1:A:1022:G:C8	2.56	0.40
8:H:33:GLU:HG3	8:H:48:TYR:CE2	2.56	0.40
12:L:53:ARG:HD2	12:L:53:ARG:N	2.36	0.40
13:M:87:TYR:O	13:M:91:ARG:HG2	2.21	0.40
1:A:1300:G:O2'	1:A:1301:U:P	2.79	0.40
1:A:1346:A:N1	1:A:1374:A:H5"	2.37	0.40
1:A:190(K):G:H2'	1:A:190(L):U:C6	2.56	0.40
1:A:714:G:H2'	1:A:715:A:C8	2.56	0.40
1:A:860:A:H2'	1:A:861:G:O4'	2.21	0.40
3:C:34:LEU:HD11	14:N:25:VAL:HG21	2.03	0.40
1:A:110:C:O2'	16:P:25:ARG:O	2.31	0.40
1:A:109:A:C6	1:A:326:G:C6	3.09	0.40
14:N:23:ARG:NH1	14:N:28:GLY:O	2.55	0.40
16:P:59:TRP:HA	16:P:62:VAL:HG22	2.04	0.40
19:S:36:ARG:NH2	19:S:75:ALA:O	2.49	0.40
1:A:1030(B):C:H2'	1:A:1030(C):G:O4'	2.21	0.40
1:A:432:A:H3'	1:A:433:C:H5"	2.02	0.40
1:A:920:U:H2'	1:A:921:U:C6	2.57	0.40
8:H:31:PHE:O	8:H:35:ILE:HG13	2.22	0.40
10:J:71:LEU:HA	10:J:71:LEU:HD22	1.94	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203:U:OP2	1:A:1335:C:O2'[3_545]	2.19	0.01

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	234/236 (99%)	214 (92%)	18 (8%)	2 (1%)	17 48
3	C	205/207 (99%)	187 (91%)	18 (9%)	0	100 100
4	D	206/208 (99%)	200 (97%)	6 (3%)	0	100 100
5	E	149/151 (99%)	146 (98%)	3 (2%)	0	100 100
6	F	99/101 (98%)	99 (100%)	0	0	100 100
7	G	153/155 (99%)	148 (97%)	5 (3%)	0	100 100
8	H	136/138 (99%)	130 (96%)	6 (4%)	0	100 100
9	I	125/127 (98%)	113 (90%)	12 (10%)	0	100 100
10	J	97/99 (98%)	80 (82%)	16 (16%)	1 (1%)	15 46
11	K	117/119 (98%)	108 (92%)	9 (8%)	0	100 100
12	L	122/125 (98%)	113 (93%)	9 (7%)	0	100 100
13	M	116/118 (98%)	108 (93%)	7 (6%)	1 (1%)	17 48
14	N	58/60 (97%)	55 (95%)	3 (5%)	0	100 100
15	O	86/88 (98%)	84 (98%)	2 (2%)	0	100 100
16	P	82/84 (98%)	80 (98%)	2 (2%)	0	100 100
17	Q	97/99 (98%)	93 (96%)	4 (4%)	0	100 100
18	R	71/73 (97%)	68 (96%)	3 (4%)	0	100 100
19	S	79/81 (98%)	74 (94%)	5 (6%)	0	100 100
20	T	97/99 (98%)	88 (91%)	6 (6%)	3 (3%)	4 23
21	U	23/25 (92%)	21 (91%)	2 (9%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	2352/2393 (98%)	2209 (94%)	136 (6%)	7 (0%)	41 71

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	T	75	ASN
20	T	74	LYS
2	B	240	GLN
20	T	73	HIS
10	J	55	LYS
13	M	106	ASN
2	B	89	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	194/204 (95%)	186 (96%)	8 (4%)	30 61
3	C	160/161 (99%)	153 (96%)	7 (4%)	28 59
4	D	180/180 (100%)	175 (97%)	5 (3%)	43 70
5	E	115/116 (99%)	106 (92%)	9 (8%)	12 38
6	F	90/90 (100%)	87 (97%)	3 (3%)	38 66
7	G	126/126 (100%)	120 (95%)	6 (5%)	25 56
8	H	119/119 (100%)	113 (95%)	6 (5%)	24 55
9	I	98/98 (100%)	92 (94%)	6 (6%)	18 48
10	J	87/89 (98%)	83 (95%)	4 (5%)	27 58
11	K	90/90 (100%)	86 (96%)	4 (4%)	28 59
12	L	103/103 (100%)	97 (94%)	6 (6%)	20 50
13	M	94/94 (100%)	86 (92%)	8 (8%)	10 35
14	N	49/49 (100%)	47 (96%)	2 (4%)	30 61
15	O	79/79 (100%)	75 (95%)	4 (5%)	24 54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
16	P	72/72 (100%)	69 (96%)	3 (4%)	30 60
17	Q	94/94 (100%)	90 (96%)	4 (4%)	29 59
18	R	64/64 (100%)	62 (97%)	2 (3%)	40 67
19	S	71/71 (100%)	65 (92%)	6 (8%)	10 35
20	T	76/76 (100%)	68 (90%)	8 (10%)	7 25
21	U	19/20 (95%)	18 (95%)	1 (5%)	22 53
All	All	1980/1995 (99%)	1878 (95%)	102 (5%)	23 54

All (102) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	24	TRP
2	B	46	LYS
2	B	69	LEU
2	B	82	ARG
2	B	114	ARG
2	B	144	ARG
2	B	221	LEU
2	B	236	TYR
3	C	3	ASN
3	C	27	LYS
3	C	34	LEU
3	C	91	LEU
3	C	166	GLU
3	C	167	TRP
3	C	204	LEU
4	D	15	GLU
4	D	122	ARG
4	D	127	THR
4	D	170	VAL
4	D	192	GLU
5	E	6	PHE
5	E	12	LEU
5	E	41	VAL
5	E	64	ARG
5	E	76	ILE
5	E	79	GLU
5	E	80	ILE
5	E	89	ILE
5	E	150	ARG

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Mol	Chain	Res	Type
6	F	10	LEU
6	F	69	GLU
6	F	75	LEU
7	G	8	GLU
7	G	11	GLN
7	G	48	LYS
7	G	52	GLU
7	G	114	ARG
7	G	156	TRP
8	H	21	LYS
8	H	39	LEU
8	H	85	ARG
8	H	92	ARG
8	H	102	ARG
8	H	133	LEU
9	I	2	GLU
9	I	79	LEU
9	I	102	LEU
9	I	111	ARG
9	I	118	LYS
9	I	121	ARG
10	J	49	VAL
10	J	61	GLU
10	J	71	LEU
10	J	80	LYS
11	K	11	LYS
11	K	29	ILE
11	K	92	GLU
11	K	126	ARG
12	L	20	LYS
12	L	27	LEU
12	L	39	VAL
12	L	47	LYS
12	L	53	ARG
12	L	111	LYS
13	M	37	THR
13	M	44	ARG
13	M	56	LEU
13	M	58	GLU
13	M	69	GLU
13	M	70	LEU
13	M	105	THR

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Mol	Chain	Res	Type
13	M	109	THR
14	N	9	LYS
14	N	33	VAL
15	O	5	LYS
15	O	39	LEU
15	O	70	LEU
15	O	81	LEU
16	P	20	VAL
16	P	53	VAL
16	P	67	THR
17	Q	38	ARG
17	Q	74	LEU
17	Q	91	ARG
17	Q	98	LEU
18	R	25	THR
18	R	47	THR
19	S	5	LEU
19	S	7	LYS
19	S	12	ASP
19	S	15	LEU
19	S	31	ILE
19	S	62	ILE
20	T	8	ARG
20	T	10	LEU
20	T	48	LYS
20	T	57	ARG
20	T	72	LEU
20	T	73	HIS
20	T	74	LYS
20	T	84	LEU
21	U	9	ARG

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

Mol	Chain	Res	Type
3	C	6	HIS
9	I	73	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1507/1522 (99%)	203 (13%)	36 (2%)
22	a	5/6 (83%)	1 (20%)	0
23	b	12/15 (80%)	2 (16%)	0
All	All	1524/1543 (98%)	206 (13%)	36 (2%)

All (206) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	51	A
1	A	61	G
1	A	63	C
1	A	101	A
1	A	116	A
1	A	117	G
1	A	120	A
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	163	C
1	A	182	U
1	A	195	A
1	A	197	A
1	A	201	C
1	A	202	U
1	A	204	U
1	A	216	G
1	A	220	G
1	A	244	U
1	A	247	G
1	A	251	G
1	A	267	C
1	A	270	A
1	A	289	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	332	G

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Mol	Chain	Res	Type
1	A	344	A
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	373	A
1	A	384	G
1	A	390	C
1	A	397	A
1	A	398	C
1	A	406	G
1	A	412	A
1	A	413	G
1	A	414	A
1	A	421	U
1	A	429	U
1	A	433	C
1	A	439	A
1	A	452	A
1	A	460	A
1	A	461	C
1	A	485	G
1	A	497	A
1	A	498	U
1	A	509	A
1	A	510	A
1	A	511	C
1	A	518	C
1	A	521	G
1	A	527	7MG
1	A	532	A
1	A	533	A
1	A	545	C
1	A	547	A
1	A	559	A
1	A	560	U
1	A	562	C
1	A	564	C
1	A	572	A
1	A	573	A
1	A	576	G
1	A	577	G

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Mol	Chain	Res	Type
1	A	579	G
1	A	596	C
1	A	630	G
1	A	631	G
1	A	653	A
1	A	665	A
1	A	666	G
1	A	687	A
1	A	688	G
1	A	702	A
1	A	721	G
1	A	723	U
1	A	731	G
1	A	734	G
1	A	749	C
1	A	755	G
1	A	777	A
1	A	781	A
1	A	782	A
1	A	793	U
1	A	794	A
1	A	813	U
1	A	817	C
1	A	819	A
1	A	821	G
1	A	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	876	G
1	A	902	G
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	960	U
1	A	961	U
1	A	968	A
1	A	969	A
1	A	971	G

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Mol	Chain	Res	Type
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1004	A
1	A	1005	A
1	A	1025	U
1	A	1026	G
1	A	1027	C
1	A	1050	G
1	A	1054	C
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1117	G
1	A	1125	U
1	A	1126	U
1	A	1127	G
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1159	U
1	A	1171	G
1	A	1180	A
1	A	1181	G
1	A	1182	G
1	A	1183	A
1	A	1184	G
1	A	1190	G
1	A	1196	U
1	A	1197	G
1	A	1201	A

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Mol	Chain	Res	Type
1	A	1202	G
1	A	1212	U
1	A	1213	A
1	A	1227	A
1	A	1238	A
1	A	1257	U
1	A	1258	G
1	A	1260	C
1	A	1270	C
1	A	1280	A
1	A	1282	C
1	A	1286	A
1	A	1287	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1320	C
1	A	1332	A
1	A	1338	G
1	A	1348	U
1	A	1353	G
1	A	1359	C
1	A	1362	C
1	A	1364	U
1	A	1370	G
1	A	1397	C
1	A	1398	A
1	A	1421	G
1	A	1442	G
1	A	1443	G
1	A	1446	A
1	A	1492	A
1	A	1497	G
1	A	1499	A
1	A	1502	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1517	G
1	A	1520	G
1	A	1529	G
1	A	1530	G

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Mol	Chain	Res	Type
22	a	6	U
23	b	32	C
23	b	33	U

All (36) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	60	A
1	A	115	G
1	A	129(A)	G
1	A	181	G
1	A	250	A
1	A	266	G
1	A	328	C
1	A	372	C
1	A	428	G
1	A	484	G
1	A	496	A
1	A	509	A
1	A	559	A
1	A	687	A
1	A	701	C
1	A	748	C
1	A	812	C
1	A	913	A
1	A	960	U
1	A	1049	U
1	A	1065	U
1	A	1067	A
1	A	1129	C
1	A	1179	A
1	A	1182	G
1	A	1201	A
1	A	1256	A
1	A	1281	U
1	A	1285	A
1	A	1300	G
1	A	1301	U
1	A	1331	G
1	A	1347	G
1	A	1443	G
1	A	1505	G

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Mol	Chain	Res	Type
1	A	1528	U

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

19 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	5MC	A	967	1	15,22,23	0.86	0	19,32,35	1.03	1 (5%)
1	4OC	A	1402	1	16,23,24	0.76	0	17,32,35	0.76	0
1	PSU	A	516	1,24	17,21,22	1.44	4 (23%)	20,30,33	3.65	5 (25%)
1	2MG	A	1207	1	19,26,27	2.00	2 (10%)	21,38,41	2.04	3 (14%)
1	MA6	A	1518	1	19,26,27	0.72	0	18,38,41	0.82	1 (5%)
1	5MC	A	1404	1	15,22,23	0.87	0	19,32,35	0.99	1 (5%)
23	PSU	b	39	23	17,21,22	1.42	3 (17%)	20,30,33	3.56	5 (25%)
23	70U	b	34	22,23	19,26,27	2.77	7 (36%)	21,37,40	2.05	3 (14%)
1	5MC	A	1407	1	15,22,23	0.87	0	19,32,35	0.98	1 (5%)
1	MA6	A	1519	1	19,26,27	0.70	0	18,38,41	0.87	1 (5%)
1	PSU	A	1541	1,24	17,21,22	1.44	4 (23%)	20,30,33	3.63	5 (25%)
22	A2M	a	3	22,23	18,25,26	0.92	1 (5%)	18,36,39	1.42	2 (11%)
12	0TD	L	92	12	4,9,10	1.00	0	3,11,13	1.84	1 (33%)
1	5MC	A	1400	1	15,22,23	0.88	0	19,32,35	1.02	1 (5%)
1	UR3	A	1498	1	14,22,23	0.72	0	15,32,35	0.97	0
23	12A	b	37	23	26,35,37	5.25	12 (46%)	28,50,55	2.78	10 (35%)
1	M2G	A	966	1	20,27,28	1.81	4 (20%)	22,40,43	2.49	5 (22%)
1	7MG	A	527	1	22,26,27	2.05	7 (31%)	28,39,42	1.63	8 (28%)
1	PSU	A	1540	1	17,21,22	1.42	3 (17%)	20,30,33	3.63	5 (25%)

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	5MC	A	967	1	-	0/5/25/26	0/2/2/2
1	4OC	A	1402	1	-	3/9/29/30	0/2/2/2
1	PSU	A	516	1,24	-	0/7/25/26	0/2/2/2
1	5MC	A	1404	1	-	0/5/25/26	0/2/2/2
1	MA6	A	1518	1	-	2/7/29/30	0/3/3/3
1	2MG	A	1207	1	-	0/5/27/28	0/3/3/3
23	PSU	b	39	23	-	0/7/25/26	0/2/2/2
23	70U	b	34	22,23	-	4/11/31/32	0/2/2/2
1	5MC	A	1407	1	-	0/5/25/26	0/2/2/2
1	MA6	A	1519	1	-	1/7/29/30	0/3/3/3
1	PSU	A	1541	1,24	-	1/7/25/26	0/2/2/2
22	A2M	a	3	22,23	-	1/5/27/28	0/3/3/3
12	0TD	L	92	12	-	2/3/12/14	-
1	5MC	A	1400	1	-	2/5/25/26	0/2/2/2
1	UR3	A	1498	1	-	0/5/25/26	0/2/2/2
23	12A	b	37	23	1/1/8/11	3/16/42/44	0/3/3/3
1	M2G	A	966	1	-	0/7/29/30	0/3/3/3
1	7MG	A	527	1	-	2/7/37/38	0/3/3/3
1	PSU	A	1540	1	-	0/7/25/26	0/2/2/2

All (47) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	b	37	12A	C2'-C1'	-14.97	1.31	1.53
23	b	37	12A	O4'-C1'	14.56	1.61	1.41
23	b	37	12A	C6-N6	9.20	1.52	1.36
23	b	37	12A	C2-S2	7.19	1.81	1.75
23	b	34	70U	C2-S2	7.14	1.81	1.66
1	A	1207	2MG	C2-N2	6.32	1.39	1.34
23	b	34	70U	O4-C4	6.15	1.40	1.24
1	A	966	M2G	C6-N1	5.68	1.42	1.33
23	b	37	12A	O4'-C4'	-5.65	1.32	1.45
1	A	527	7MG	C8-N9	-5.35	1.33	1.45
23	b	37	12A	CC-N	5.16	1.46	1.35
1	A	1207	2MG	C6-N1	5.15	1.42	1.33
1	A	527	7MG	C2-N2	4.58	1.43	1.33
23	b	37	12A	O2'-C2'	4.11	1.52	1.43
23	b	34	70U	C5M-C5	4.08	1.57	1.51
1	A	527	7MG	C4-N3	3.93	1.39	1.34
23	b	37	12A	CC-N6	3.65	1.45	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	b	34	70U	O9-C8	3.62	1.44	1.33
1	A	966	M2G	C2-N2	3.38	1.40	1.34
23	b	34	70U	O9-C9	-3.29	1.37	1.45
1	A	966	M2G	C2-N1	3.27	1.40	1.34
23	b	37	12A	O3'-C3'	-3.25	1.35	1.43
23	b	39	PSU	C2-N1	-3.22	1.31	1.38
23	b	37	12A	OO-CC	-3.20	1.16	1.23
1	A	516	PSU	C2-N1	-3.20	1.31	1.38
1	A	1541	PSU	C2-N1	-3.18	1.31	1.38
1	A	1540	PSU	C2-N1	-3.18	1.31	1.38
23	b	37	12A	CA-N	-3.11	1.40	1.46
23	b	39	PSU	C2-N3	-3.10	1.32	1.38
1	A	516	PSU	C2-N3	-3.09	1.32	1.38
1	A	1541	PSU	C2-N3	-3.08	1.32	1.38
1	A	1540	PSU	C2-N3	-3.03	1.32	1.38
23	b	37	12A	O5'-C5'	-2.92	1.37	1.44
1	A	966	M2G	C4-N3	2.77	1.40	1.35
22	a	3	A2M	C6-N6	2.68	1.43	1.34
23	b	34	70U	C6-C5	2.66	1.43	1.37
1	A	527	7MG	CM7-N7	-2.46	1.41	1.46
1	A	516	PSU	O4-C4	-2.45	1.18	1.24
1	A	1541	PSU	O4-C4	-2.42	1.18	1.24
1	A	1540	PSU	O4-C4	-2.41	1.18	1.24
1	A	527	7MG	C6-N1	2.41	1.37	1.33
23	b	39	PSU	O4-C4	-2.38	1.18	1.24
1	A	527	7MG	C2-N3	-2.10	1.31	1.35
23	b	34	70U	C4-N3	-2.10	1.29	1.33
1	A	527	7MG	C5-C4	-2.06	1.34	1.39
1	A	516	PSU	O4'-C1'	-2.00	1.41	1.44
1	A	1541	PSU	O4'-C1'	-2.00	1.41	1.44

All (58) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	516	PSU	N1-C2-N3	-11.34	119.41	128.43
1	A	1540	PSU	N1-C2-N3	-11.32	119.43	128.43
1	A	1541	PSU	N1-C2-N3	-11.29	119.45	128.43
23	b	39	PSU	N1-C2-N3	-10.98	119.70	128.43
23	b	37	12A	C2M-S2-C2	9.97	109.71	102.27
1	A	516	PSU	C4-N3-C2	8.85	122.61	115.14
1	A	1540	PSU	C4-N3-C2	8.79	122.57	115.14
1	A	1541	PSU	C4-N3-C2	8.76	122.54	115.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	b	39	PSU	C4-N3-C2	8.61	122.41	115.14
1	A	966	M2G	C5-C6-N1	-8.56	111.72	123.43
1	A	1207	2MG	C5-C6-N1	-7.63	113.00	123.43
1	A	966	M2G	C6-N1-C2	5.96	123.28	116.18
23	b	34	70U	O9-C8-C5M	5.83	119.54	111.45
23	b	34	70U	C2-N3-C4	5.33	121.38	115.93
23	b	37	12A	N6-CC-N	4.94	120.67	113.76
23	b	39	PSU	C5-C4-N3	-4.59	119.44	125.36
1	A	516	PSU	C5-C4-N3	-4.54	119.52	125.36
1	A	1540	PSU	C5-C4-N3	-4.51	119.55	125.36
1	A	1541	PSU	C5-C4-N3	-4.49	119.58	125.36
22	a	3	A2M	N3-C2-N1	-4.49	121.67	128.68
23	b	37	12A	C2-N3-C4	4.43	121.43	115.32
1	A	1541	PSU	C6-N1-C2	3.95	121.88	115.36
23	b	34	70U	C5-C4-N3	-3.93	119.49	125.25
1	A	516	PSU	C6-N1-C2	3.93	121.83	115.36
1	A	1540	PSU	C6-N1-C2	3.93	121.83	115.36
1	A	1207	2MG	C6-N1-C2	3.89	122.14	115.18
23	b	39	PSU	C6-N1-C2	3.87	121.74	115.36
23	b	39	PSU	C5-C6-N1	-3.62	119.99	124.44
1	A	1541	PSU	C5-C6-N1	-3.56	120.07	124.44
1	A	527	7MG	C5-C4-N3	-3.55	120.69	126.49
23	b	37	12A	O4'-C1'-C2'	-3.53	101.76	106.93
1	A	1540	PSU	C5-C6-N1	-3.52	120.12	124.44
1	A	527	7MG	N3-C4-N9	3.48	131.38	126.91
1	A	516	PSU	C5-C6-N1	-3.48	120.17	124.44
23	b	37	12A	OO-CC-N6	-3.37	117.92	123.62
1	A	527	7MG	N7-C8-N9	3.35	108.16	103.38
1	A	966	M2G	N3-C2-N2	2.95	120.17	117.18
23	b	37	12A	C3'-C2'-C1'	-2.84	96.70	100.98
22	a	3	A2M	C4-C5-N7	-2.67	106.61	109.40
12	L	92	0TD	CSB-SB-CB	-2.67	96.61	101.85
23	b	37	12A	N3-C2-N1	-2.65	122.11	126.98
1	A	966	M2G	N1-C2-N2	-2.63	114.53	117.19
1	A	527	7MG	C6-N1-C2	2.56	120.00	115.93
23	b	37	12A	CA-N-CC	2.48	125.39	122.75
1	A	1519	MA6	N1-C6-N6	-2.39	114.54	117.06
1	A	527	7MG	C2-N3-C4	2.39	120.50	113.89
1	A	1207	2MG	C4-C5-N7	2.34	111.83	109.40
23	b	37	12A	C4-C5-N7	-2.28	107.02	109.40
1	A	966	M2G	C2-N3-C4	-2.28	112.69	115.28
1	A	527	7MG	N1-C2-N3	-2.27	121.86	125.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1404	5MC	C2-N3-C4	2.23	118.71	116.02
1	A	527	7MG	C4-N9-C1'	-2.22	121.33	126.60
1	A	1518	MA6	N1-C6-N6	-2.17	114.77	117.06
23	b	37	12A	C5'-C4'-C3'	-2.08	107.39	115.18
1	A	1400	5MC	N4-C4-N3	-2.08	114.09	117.03
1	A	527	7MG	N2-C2-N1	2.04	120.42	117.25
1	A	967	5MC	N4-C4-N3	-2.02	114.18	117.03
1	A	1407	5MC	N4-C4-N3	-2.01	114.19	117.03

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
23	b	37	12A	C1'

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	b	34	70U	C5M-C8-O9-C9
12	L	92	0TD	CA-CB-SB-CSB
12	L	92	0TD	CG-CB-SB-CSB
1	A	527	7MG	O4'-C4'-C5'-O5'
1	A	527	7MG	C3'-C4'-C5'-O5'
23	b	34	70U	O8-C8-O9-C9
1	A	1402	4OC	O4'-C4'-C5'-O5'
1	A	1400	5MC	O4'-C4'-C5'-O5'
1	A	1400	5MC	C3'-C4'-C5'-O5'
1	A	1518	MA6	O4'-C4'-C5'-O5'
23	b	34	70U	O4'-C4'-C5'-O5'
1	A	1518	MA6	C3'-C4'-C5'-O5'
23	b	37	12A	O4'-C4'-C5'-O5'
1	A	1402	4OC	C3'-C4'-C5'-O5'
23	b	34	70U	C3'-C4'-C5'-O5'
23	b	37	12A	C3'-C4'-C5'-O5'
22	a	3	A2M	C3'-C2'-O2'-CM'
1	A	1541	PSU	O4'-C1'-C5-C4
1	A	1402	4OC	C5-C4-N4-CM4
1	A	1519	MA6	C4'-C5'-O5'-P
23	b	37	12A	CB-CA-N-CC

There are no ring outliers.

9 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	967	5MC	2	0
1	A	1402	4OC	2	0
1	A	1207	2MG	1	0
1	A	1518	MA6	2	0
1	A	1519	MA6	2	0
12	L	92	0TD	1	0
1	A	1400	5MC	1	0
1	A	1498	UR3	2	0
1	A	966	M2G	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 276 ligands modelled in this entry, 275 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	$\#\|Z\| > 2$
26	B6M	A	1856	-	45,45,45	3.38	14 (31%)	64,67,67	1.42	9 (14%)

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
26	B6M	A	1856	-	-	8/18/94/94	0/4/4/4

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	A	1856	B6M	C23-C33	-13.42	1.23	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	A	1856	B6M	O43-C43	-7.64	1.27	1.45
26	A	1856	B6M	C64-C54	-6.10	1.43	1.52
26	A	1856	B6M	C34-C24	-5.19	1.47	1.53
26	A	1856	B6M	C13-C23	5.14	1.59	1.52
26	A	1856	B6M	O43-C13	4.97	1.50	1.41
26	A	1856	B6M	O54-C54	4.87	1.56	1.44
26	A	1856	B6M	C33-C43	4.81	1.65	1.52
26	A	1856	B6M	O51-C11	4.21	1.52	1.41
26	A	1856	B6M	C31-C21	-4.10	1.48	1.53
26	A	1856	B6M	O23-C23	4.10	1.52	1.43
26	A	1856	B6M	O33-C33	3.90	1.54	1.43
26	A	1856	B6M	O52-C13	-3.67	1.31	1.41
26	A	1856	B6M	C24-N24	2.52	1.51	1.47

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	A	1856	B6M	C13-O52-C52	-3.91	108.30	117.96
26	A	1856	B6M	C14-O33-C33	-3.88	108.36	117.96
26	A	1856	B6M	C11-O11-C42	-2.56	111.64	117.96
26	A	1856	B6M	C22-C12-C62	2.53	113.86	110.04
26	A	1856	B6M	O51-C51-C41	2.46	114.15	109.69
26	A	1856	B6M	C13-C23-C33	2.23	104.78	102.10
26	A	1856	B6M	O51-C11-C21	2.18	114.95	110.06
26	A	1856	B6M	C52-C62-C12	2.14	114.85	109.63
26	A	1856	B6M	O52-C13-C23	2.14	112.39	107.96

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
26	A	1856	B6M	C23-C13-O52-C52
26	A	1856	B6M	O43-C13-O52-C52
26	A	1856	B6M	C24-C14-O33-C33
26	A	1856	B6M	C44-C54-C64-N64
26	A	1856	B6M	O51-C11-O11-C42
26	A	1856	B6M	O51-C51-C61-O61
26	A	1856	B6M	C41-C51-C61-O61
26	A	1856	B6M	O54-C14-O33-C33

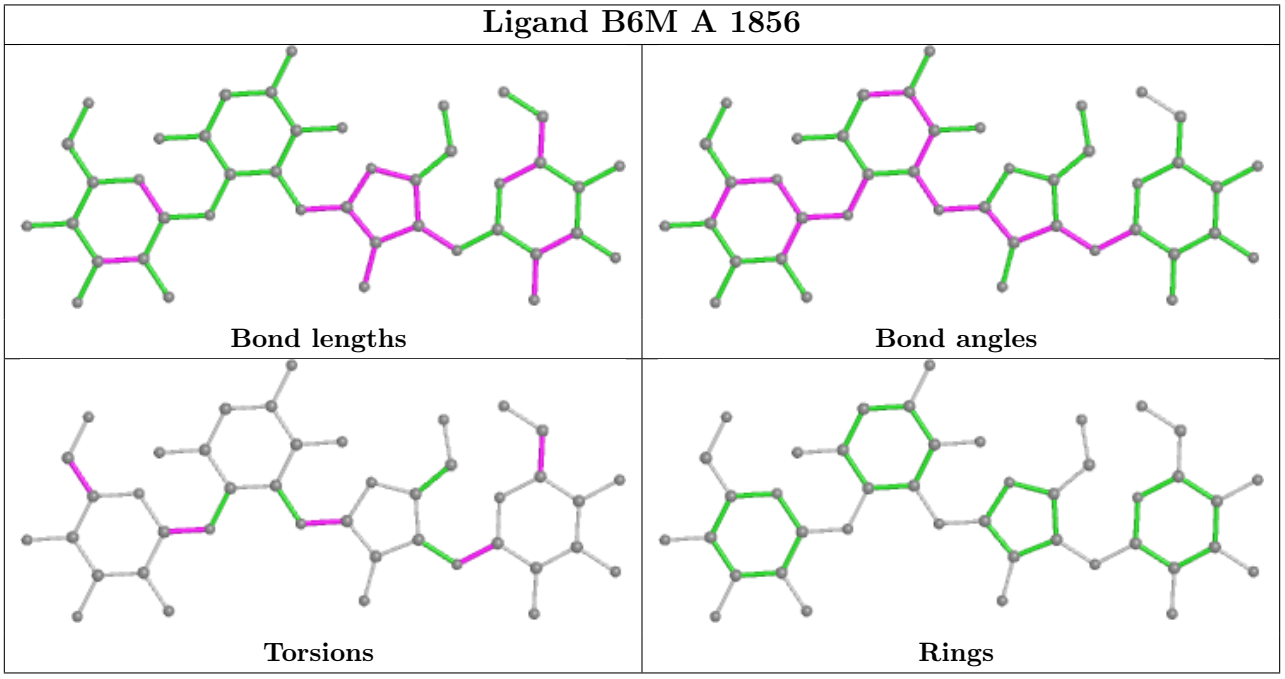
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
26	A	1856	B6M	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.

Ligand B6M A 1856



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

6.1 Protein, DNA and RNA chains

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^{th} 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^2)	Q<0.9
1	A	1498/1522 (98%)	-0.51	5 (0%) 94 94	81, 118, 205, 326	0
2	B	236/236 (100%)	-0.02	13 (5%) 25 23	110, 161, 240, 298	0
3	C	207/207 (100%)	-0.20	3 (1%) 75 75	101, 166, 215, 244	0
4	D	208/208 (100%)	-0.15	4 (1%) 66 65	96, 136, 189, 284	0
5	E	151/151 (100%)	-0.34	0 100 100	83, 117, 159, 241	0
6	F	101/101 (100%)	-0.28	1 (0%) 82 82	109, 154, 187, 217	0
7	G	155/155 (100%)	-0.36	4 (2%) 56 53	107, 144, 204, 252	0
8	H	138/138 (100%)	-0.37	0 100 100	80, 109, 147, 196	0
9	I	127/127 (100%)	0.18	5 (3%) 39 37	113, 169, 214, 294	0
10	J	99/99 (100%)	0.83	14 (14%) 2 2	114, 193, 282, 323	0
11	K	119/119 (100%)	-0.03	3 (2%) 57 54	90, 119, 167, 249	0
12	L	124/125 (99%)	0.10	7 (5%) 24 23	83, 131, 182, 244	0
13	M	118/118 (100%)	-0.07	3 (2%) 57 54	107, 142, 187, 288	0
14	N	60/60 (100%)	0.14	2 (3%) 46 44	122, 149, 186, 272	0
15	O	88/88 (100%)	-0.08	1 (1%) 80 81	93, 129, 177, 241	0
16	P	84/84 (100%)	-0.24	0 100 100	84, 121, 155, 230	0
17	Q	99/99 (100%)	-0.27	0 100 100	82, 110, 161, 177	0
18	R	73/73 (100%)	-0.10	3 (4%) 37 35	99, 130, 231, 287	0
19	S	81/81 (100%)	0.12	3 (3%) 41 38	108, 161, 221, 274	0
20	T	99/99 (100%)	-0.09	0 100 100	90, 120, 167, 209	0
21	U	25/25 (100%)	0.90	4 (16%) 1 2	111, 138, 198, 239	0
22	a	5/6 (83%)	1.04	1 (20%) 1 1	145, 179, 202, 251	0
23	b	12/15 (80%)	1.14	1 (8%) 11 11	155, 247, 304, 319	0
All	All	3907/3936 (99%)	-0.24	77 (1%) 65 64	80, 132, 213, 326	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
11	K	128	ALA	10.2
12	L	129	ALA	8.8
14	N	12	ARG	7.8
10	J	34	VAL	7.5
15	O	89	GLY	7.1
2	B	131	PRO	6.8
11	K	129	SER	6.5
2	B	132	LYS	5.4
10	J	72	VAL	5.4
2	B	134	GLU	5.3
10	J	33	GLN	5.2
14	N	13	THR	4.7
2	B	133	LYS	4.3
2	B	130	ARG	4.2
10	J	71	LEU	4.2
10	J	74	ILE	4.2
21	U	18	TYR	4.1
2	B	135	GLN	3.7
9	I	15	ALA	3.7
1	A	1129	C	3.5
19	S	4	SER	3.5
13	M	7	VAL	3.5
2	B	140	HIS	3.5
10	J	22	LYS	3.4
12	L	19	ARG	3.4
9	I	67	GLY	3.4
12	L	28	LYS	3.4
7	G	2	ALA	3.4
3	C	206	GLU	3.4
12	L	64	TYR	3.4
10	J	73	ASP	3.3
11	K	127	LYS	3.3
10	J	70	ARG	3.3
19	S	2	PRO	3.2
9	I	8	GLY	3.2
10	J	36	GLY	3.2
9	I	128	ARG	3.1
19	S	3	ARG	3.1
10	J	90	LEU	3.1
10	J	5	ARG	3.0
2	B	136	VAL	3.0
4	D	37	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
3	C	193	TYR	2.9
21	U	22	ARG	2.9
22	a	6	U	2.8
18	R	17	SER	2.8
12	L	128	ALA	2.8
1	A	1030(D)	A	2.8
18	R	16	PRO	2.8
6	F	101	ALA	2.8
10	J	75	ILE	2.7
12	L	27	LEU	2.6
2	B	237	ALA	2.6
2	B	231	GLU	2.6
12	L	62	SER	2.5
7	G	156	TRP	2.5
10	J	25	GLU	2.5
1	A	1286	A	2.4
4	D	32	ALA	2.4
10	J	4	ILE	2.4
3	C	146	ALA	2.4
18	R	18	ARG	2.3
13	M	5	ALA	2.2
4	D	2	GLY	2.2
7	G	80	VAL	2.2
7	G	82	GLY	2.2
13	M	8	GLU	2.2
4	D	13	ARG	2.1
1	A	1446	A	2.1
2	B	48	MET	2.1
21	U	17	THR	2.1
23	b	28	U	2.1
1	A	1031	G	2.1
9	I	65	VAL	2.1
2	B	230	VAL	2.1
21	U	25	LYS	2.0
2	B	137	ARG	2.0

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^{th} 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^2)	Q<0.9
23	PSU	b	39	20/21	0.80	0.28	185,236,260,272	0
1	PSU	A	1540	20/21	0.83	0.25	171,206,249,254	0
1	PSU	A	1541	20/21	0.89	0.17	149,178,203,217	0
23	12A	b	37	33/35	0.90	0.34	147,204,225,226	0
22	A2M	a	3	23/24	0.90	0.23	107,144,212,225	0
1	PSU	A	516	20/21	0.93	0.11	120,133,163,163	0
23	70U	b	34	25/26	0.95	0.19	128,171,208,215	0
1	7MG	A	527	24/25	0.95	0.18	83,111,133,156	0
12	0TD	L	92	10/11	0.95	0.48	113,162,268,274	0
1	2MG	A	1207	24/25	0.96	0.15	116,142,153,169	0
1	5MC	A	1400	21/22	0.96	0.16	83,111,130,137	0
1	UR3	A	1498	21/22	0.96	0.18	88,97,113,144	0
1	5MC	A	967	21/22	0.97	0.11	93,117,133,147	0
1	4OC	A	1402	22/23	0.97	0.19	92,97,115,147	0
1	5MC	A	1407	21/22	0.97	0.14	92,101,115,140	0
1	MA6	A	1519	24/25	0.97	0.22	83,91,103,126	0
1	M2G	A	966	25/26	0.97	0.14	87,123,143,173	0
1	MA6	A	1518	24/25	0.97	0.15	86,97,116,125	0
1	5MC	A	1404	21/22	0.97	0.17	85,89,102,108	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, 95th 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^2)	Q<0.9
24	MG	A	1782	1/1	-0.08	1.42	136,136,136,136	0
24	MG	A	1678	1/1	0.15	0.19	137,137,137,137	0
24	MG	A	1762	1/1	0.24	0.58	117,117,117,117	0
24	MG	A	1720	1/1	0.25	1.12	131,131,131,131	0
24	MG	A	1802	1/1	0.36	1.48	138,138,138,138	0
24	MG	A	1769	1/1	0.37	0.27	120,120,120,120	0
24	MG	A	1795	1/1	0.39	0.65	114,114,114,114	0
24	MG	L	201	1/1	0.40	0.16	121,121,121,121	0
24	MG	A	1666	1/1	0.41	0.60	115,115,115,115	0
24	MG	A	1748	1/1	0.42	0.68	128,128,128,128	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
24	MG	A	1794	1/1	0.51	1.79	124,124,124,124	0
24	MG	A	1744	1/1	0.51	0.63	98,98,98,98	0
24	MG	A	1819	1/1	0.52	0.30	137,137,137,137	0
24	MG	A	1601	1/1	0.52	0.37	163,163,163,163	0
24	MG	A	1807	1/1	0.52	0.54	144,144,144,144	0
24	MG	A	1729	1/1	0.53	1.04	138,138,138,138	0
24	MG	A	1677	1/1	0.53	0.44	109,109,109,109	0
24	MG	A	1704	1/1	0.53	0.68	102,102,102,102	0
25	K	A	1853	1/1	0.54	0.26	161,161,161,161	0
24	MG	A	1781	1/1	0.57	0.32	112,112,112,112	0
24	MG	A	1827	1/1	0.57	0.94	133,133,133,133	0
25	K	A	1840	1/1	0.57	0.33	181,181,181,181	0
24	MG	A	1799	1/1	0.58	0.14	100,100,100,100	0
25	K	A	1847	1/1	0.61	0.42	194,194,194,194	0
24	MG	A	1793	1/1	0.62	0.26	99,99,99,99	0
24	MG	A	1725	1/1	0.62	0.12	116,116,116,116	0
24	MG	A	1831	1/1	0.62	0.33	142,142,142,142	0
24	MG	P	103	1/1	0.65	0.17	107,107,107,107	0
24	MG	A	1714	1/1	0.66	0.66	135,135,135,135	0
24	MG	A	1620	1/1	0.66	0.97	110,110,110,110	0
24	MG	A	1786	1/1	0.67	0.31	94,94,94,94	0
24	MG	A	1716	1/1	0.67	0.49	104,104,104,104	0
24	MG	A	1815	1/1	0.69	0.39	106,106,106,106	0
24	MG	A	1817	1/1	0.70	0.45	122,122,122,122	0
24	MG	A	1783	1/1	0.70	0.28	122,122,122,122	0
25	K	A	1849	1/1	0.71	0.44	187,187,187,187	0
24	MG	A	1638	1/1	0.71	0.08	96,96,96,96	0
25	K	A	1843	1/1	0.72	0.41	158,158,158,158	0
24	MG	A	1804	1/1	0.72	0.63	126,126,126,126	0
25	K	A	1852	1/1	0.72	0.54	205,205,205,205	0
24	MG	A	1715	1/1	0.72	1.35	128,128,128,128	0
24	MG	A	1701	1/1	0.72	0.26	116,116,116,116	0
24	MG	A	1829	1/1	0.72	0.40	117,117,117,117	0
24	MG	A	1780	1/1	0.72	0.30	94,94,94,94	0
24	MG	A	1824	1/1	0.73	0.56	113,113,113,113	0
24	MG	A	1681	1/1	0.73	0.75	110,110,110,110	0
24	MG	A	1785	1/1	0.73	0.52	108,108,108,108	0
24	MG	A	1854	1/1	0.73	0.09	135,135,135,135	0
24	MG	A	1710	1/1	0.73	1.58	137,137,137,137	0
24	MG	A	1813	1/1	0.74	0.19	120,120,120,120	0
24	MG	A	1757	1/1	0.74	0.86	133,133,133,133	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
24	MG	A	1823	1/1	0.74	1.08	123,123,123,123	0
24	MG	A	1630	1/1	0.74	0.28	132,132,132,132	0
24	MG	A	1749	1/1	0.74	0.67	86,86,86,86	0
25	K	A	1834	1/1	0.75	0.73	166,166,166,166	0
24	MG	A	1607	1/1	0.75	0.10	128,128,128,128	0
25	K	A	1841	1/1	0.76	0.45	182,182,182,182	0
24	MG	A	1690	1/1	0.76	1.15	127,127,127,127	0
24	MG	A	1671	1/1	0.76	0.46	108,108,108,108	0
24	MG	A	1776	1/1	0.76	0.18	91,91,91,91	0
24	MG	A	1736	1/1	0.76	0.35	124,124,124,124	0
24	MG	A	1773	1/1	0.76	0.20	96,96,96,96	0
25	K	A	1838	1/1	0.77	1.19	188,188,188,188	0
24	MG	A	1657	1/1	0.77	0.33	102,102,102,102	0
24	MG	A	1719	1/1	0.77	0.31	107,107,107,107	0
24	MG	A	1812	1/1	0.77	0.47	116,116,116,116	0
24	MG	A	1779	1/1	0.77	0.16	170,170,170,170	0
24	MG	A	1629	1/1	0.78	0.94	111,111,111,111	0
24	MG	A	1743	1/1	0.78	1.41	121,121,121,121	0
24	MG	A	1692	1/1	0.78	0.53	94,94,94,94	0
24	MG	A	1814	1/1	0.78	0.14	139,139,139,139	0
25	K	E	202	1/1	0.78	0.87	156,156,156,156	0
24	MG	P	102	1/1	0.79	0.12	110,110,110,110	0
24	MG	A	1825	1/1	0.79	0.18	148,148,148,148	0
24	MG	A	1826	1/1	0.79	0.23	117,117,117,117	0
24	MG	A	1687	1/1	0.79	0.64	105,105,105,105	0
25	K	A	1851	1/1	0.79	0.22	189,189,189,189	0
24	MG	A	1792	1/1	0.79	0.43	118,118,118,118	0
24	MG	A	1806	1/1	0.80	0.34	95,95,95,95	0
24	MG	A	1683	1/1	0.81	0.59	94,94,94,94	0
24	MG	A	1634	1/1	0.81	0.10	98,98,98,98	0
24	MG	A	1700	1/1	0.81	0.73	143,143,143,143	0
24	MG	A	1818	1/1	0.81	0.37	125,125,125,125	0
24	MG	Q	201	1/1	0.82	0.11	112,112,112,112	0
24	MG	A	1664	1/1	0.82	0.13	119,119,119,119	0
24	MG	A	1706	1/1	0.82	0.66	106,106,106,106	0
24	MG	A	1708	1/1	0.83	0.25	118,118,118,118	0
24	MG	A	1770	1/1	0.83	0.58	98,98,98,98	0
24	MG	A	1803	1/1	0.83	0.12	83,83,83,83	0
24	MG	N	101	1/1	0.83	0.20	155,155,155,155	0
24	MG	A	1619	1/1	0.83	0.22	110,110,110,110	0
24	MG	A	1699	1/1	0.83	0.46	165,165,165,165	0
24	MG	A	1698	1/1	0.83	0.08	144,144,144,144	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
25	K	A	1844	1/1	0.83	0.27	185,185,185,185	0
24	MG	A	1707	1/1	0.84	0.58	114,114,114,114	0
25	K	A	1833	1/1	0.84	0.62	188,188,188,188	0
24	MG	A	1745	1/1	0.84	0.41	123,123,123,123	0
25	K	A	1845	1/1	0.84	0.43	182,182,182,182	0
24	MG	A	1627	1/1	0.84	1.03	170,170,170,170	0
24	MG	A	1822	1/1	0.84	0.11	127,127,127,127	0
24	MG	A	1766	1/1	0.84	0.12	149,149,149,149	0
24	MG	A	1765	1/1	0.84	0.09	146,146,146,146	0
24	MG	A	1832	1/1	0.85	0.37	140,140,140,140	0
24	MG	A	1855	1/1	0.85	0.13	141,141,141,141	0
24	MG	A	1675	1/1	0.85	0.18	146,146,146,146	0
24	MG	A	1761	1/1	0.85	0.91	97,97,97,97	0
24	MG	A	1778	1/1	0.85	0.13	172,172,172,172	0
24	MG	A	1750	1/1	0.85	0.26	109,109,109,109	0
24	MG	A	1796	1/1	0.85	0.73	112,112,112,112	0
24	MG	A	1732	1/1	0.85	0.39	114,114,114,114	0
24	MG	G	201	1/1	0.85	0.28	105,105,105,105	0
24	MG	A	1739	1/1	0.85	0.50	97,97,97,97	0
24	MG	A	1809	1/1	0.85	0.11	85,85,85,85	0
24	MG	A	1631	1/1	0.85	0.24	107,107,107,107	0
24	MG	A	1703	1/1	0.85	0.14	82,82,82,82	0
24	MG	A	1645	1/1	0.86	0.47	121,121,121,121	0
24	MG	A	1654	1/1	0.86	0.24	111,111,111,111	0
24	MG	A	1805	1/1	0.86	0.40	94,94,94,94	0
24	MG	Q	202	1/1	0.86	0.33	119,119,119,119	0
24	MG	A	1636	1/1	0.86	0.14	106,106,106,106	0
24	MG	A	1747	1/1	0.86	0.43	112,112,112,112	0
24	MG	A	1752	1/1	0.86	0.12	105,105,105,105	0
24	MG	A	1784	1/1	0.87	1.05	134,134,134,134	0
24	MG	A	1713	1/1	0.87	0.30	113,113,113,113	0
24	MG	A	1623	1/1	0.87	0.61	78,78,78,78	0
24	MG	A	1791	1/1	0.87	0.31	133,133,133,133	0
24	MG	A	1702	1/1	0.87	0.57	88,88,88,88	0
24	MG	A	1610	1/1	0.87	0.16	71,71,71,71	0
24	MG	H	201	1/1	0.88	0.33	124,124,124,124	0
24	MG	A	1625	1/1	0.88	0.11	129,129,129,129	0
24	MG	A	1737	1/1	0.88	0.82	97,97,97,97	0
24	MG	A	1790	1/1	0.88	0.97	143,143,143,143	0
24	MG	A	1717	1/1	0.88	0.29	89,89,89,89	0
24	MG	A	1828	1/1	0.88	0.62	102,102,102,102	0
24	MG	A	1616	1/1	0.88	0.39	102,102,102,102	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
24	MG	A	1730	1/1	0.88	0.60	98,98,98,98	0
24	MG	A	1635	1/1	0.88	0.23	156,156,156,156	0
24	MG	A	1768	1/1	0.88	0.12	138,138,138,138	0
24	MG	A	1641	1/1	0.88	0.10	85,85,85,85	0
27	ZN	D	301	1/1	0.88	0.42	209,209,209,209	0
25	K	A	1837	1/1	0.88	0.75	201,201,201,201	0
24	MG	A	1712	1/1	0.89	0.20	80,80,80,80	0
24	MG	A	1759	1/1	0.89	0.22	121,121,121,121	0
24	MG	A	1661	1/1	0.89	0.24	132,132,132,132	0
24	MG	A	1622	1/1	0.89	0.21	127,127,127,127	0
24	MG	S	101	1/1	0.89	0.11	91,91,91,91	0
24	MG	A	1659	1/1	0.89	0.38	83,83,83,83	0
24	MG	A	1640	1/1	0.89	0.49	101,101,101,101	0
24	MG	A	1857	1/1	0.89	0.15	99,99,99,99	0
25	K	A	1836	1/1	0.89	0.70	190,190,190,190	0
24	MG	S	103	1/1	0.89	0.09	112,112,112,112	0
24	MG	A	1767	1/1	0.89	0.55	180,180,180,180	0
24	MG	A	1801	1/1	0.89	0.45	86,86,86,86	0
24	MG	A	1663	1/1	0.89	0.29	98,98,98,98	0
24	MG	A	1798	1/1	0.89	0.50	105,105,105,105	0
24	MG	D	302	1/1	0.90	0.15	104,104,104,104	0
24	MG	P	101	1/1	0.90	0.34	91,91,91,91	0
24	MG	A	1672	1/1	0.90	0.67	90,90,90,90	0
24	MG	A	1693	1/1	0.90	0.24	110,110,110,110	0
24	MG	A	1633	1/1	0.90	0.27	131,131,131,131	0
24	MG	A	1709	1/1	0.90	0.20	121,121,121,121	0
24	MG	A	1624	1/1	0.90	0.43	112,112,112,112	0
24	MG	A	1789	1/1	0.90	0.78	149,149,149,149	0
24	MG	A	1637	1/1	0.90	0.32	109,109,109,109	0
24	MG	A	1718	1/1	0.90	0.35	119,119,119,119	0
24	MG	A	1808	1/1	0.90	0.66	126,126,126,126	0
25	K	A	1846	1/1	0.91	0.79	232,232,232,232	0
24	MG	A	1787	1/1	0.91	0.14	116,116,116,116	0
24	MG	A	1797	1/1	0.91	0.29	135,135,135,135	0
24	MG	A	1653	1/1	0.91	0.47	117,117,117,117	0
24	MG	A	1741	1/1	0.91	0.57	113,113,113,113	0
24	MG	S	102	1/1	0.91	0.19	92,92,92,92	0
24	MG	A	1647	1/1	0.91	0.28	88,88,88,88	0
24	MG	A	1742	1/1	0.91	0.13	117,117,117,117	0
24	MG	A	1756	1/1	0.91	0.25	96,96,96,96	0
24	MG	A	1609	1/1	0.91	0.87	111,111,111,111	0
24	MG	A	1810	1/1	0.91	0.23	120,120,120,120	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
24	MG	A	1679	1/1	0.91	0.36	131,131,131,131	0
24	MG	A	1760	1/1	0.91	0.25	106,106,106,106	0
24	MG	A	1724	1/1	0.91	0.36	120,120,120,120	0
24	MG	A	1695	1/1	0.91	0.19	100,100,100,100	0
24	MG	A	1755	1/1	0.92	0.10	95,95,95,95	0
24	MG	A	1753	1/1	0.92	0.24	124,124,124,124	0
24	MG	A	1668	1/1	0.92	0.20	104,104,104,104	0
24	MG	A	1731	1/1	0.92	0.20	86,86,86,86	0
24	MG	A	1686	1/1	0.92	0.41	95,95,95,95	0
24	MG	A	1763	1/1	0.92	0.19	98,98,98,98	0
24	MG	A	1820	1/1	0.92	0.17	97,97,97,97	0
24	MG	A	1642	1/1	0.92	0.36	110,110,110,110	0
24	MG	A	1830	1/1	0.92	0.21	107,107,107,107	0
24	MG	A	1626	1/1	0.93	0.53	90,90,90,90	0
24	MG	A	1650	1/1	0.93	0.40	110,110,110,110	0
24	MG	A	1684	1/1	0.93	0.36	123,123,123,123	0
24	MG	A	1682	1/1	0.93	0.41	217,217,217,217	0
24	MG	A	1800	1/1	0.93	0.35	89,89,89,89	0
24	MG	A	1746	1/1	0.93	0.15	109,109,109,109	0
24	MG	A	1614	1/1	0.93	0.35	90,90,90,90	0
24	MG	A	1656	1/1	0.93	0.10	144,144,144,144	0
24	MG	A	1705	1/1	0.94	0.28	121,121,121,121	0
24	MG	A	1617	1/1	0.94	0.25	92,92,92,92	0
24	MG	A	1613	1/1	0.94	0.22	96,96,96,96	0
24	MG	A	1691	1/1	0.94	0.15	111,111,111,111	0
24	MG	A	1665	1/1	0.94	0.39	110,110,110,110	0
26	B6M	A	1856	42/42	0.94	0.15	78,107,127,155	0
24	MG	A	1606	1/1	0.94	0.47	103,103,103,103	0
24	MG	A	1618	1/1	0.94	0.31	98,98,98,98	0
24	MG	A	1660	1/1	0.94	1.13	109,109,109,109	0
24	MG	T	201	1/1	0.94	0.26	90,90,90,90	0
24	MG	A	1646	1/1	0.94	0.30	118,118,118,118	0
24	MG	A	1694	1/1	0.94	0.46	164,164,164,164	0
24	MG	A	1643	1/1	0.94	0.26	142,142,142,142	0
24	MG	A	1735	1/1	0.94	0.14	70,70,70,70	0
24	MG	A	1674	1/1	0.94	0.09	137,137,137,137	0
24	MG	A	1621	1/1	0.94	0.69	89,89,89,89	0
25	K	A	1839	1/1	0.94	0.88	166,166,166,166	0
24	MG	A	1696	1/1	0.94	0.36	115,115,115,115	0
24	MG	A	1821	1/1	0.94	0.18	97,97,97,97	0
24	MG	A	1788	1/1	0.94	0.19	91,91,91,91	0
24	MG	E	201	1/1	0.94	0.16	133,133,133,133	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
24	MG	A	1603	1/1	0.94	0.28	131,131,131,131	0
24	MG	A	1697	1/1	0.94	0.41	100,100,100,100	0
24	MG	A	1676	1/1	0.95	0.18	115,115,115,115	0
24	MG	A	1777	1/1	0.95	0.31	91,91,91,91	0
24	MG	A	1655	1/1	0.95	0.20	131,131,131,131	0
24	MG	A	1722	1/1	0.95	0.15	87,87,87,87	0
25	K	A	1848	1/1	0.95	0.11	169,169,169,169	0
24	MG	A	1652	1/1	0.95	0.22	146,146,146,146	0
24	MG	A	1811	1/1	0.95	0.20	106,106,106,106	0
24	MG	A	1751	1/1	0.95	0.75	182,182,182,182	0
24	MG	A	1644	1/1	0.95	0.60	119,119,119,119	0
24	MG	A	1775	1/1	0.95	0.52	89,89,89,89	0
24	MG	A	1658	1/1	0.95	0.18	83,83,83,83	0
24	MG	A	1727	1/1	0.95	0.32	105,105,105,105	0
25	K	A	1850	1/1	0.95	0.38	177,177,177,177	0
24	MG	A	1685	1/1	0.95	0.37	93,93,93,93	0
24	MG	A	1726	1/1	0.95	0.50	118,118,118,118	0
24	MG	A	1628	1/1	0.95	0.08	110,110,110,110	0
24	MG	A	1670	1/1	0.95	0.31	139,139,139,139	0
25	K	A	1835	1/1	0.95	0.38	133,133,133,133	0
24	MG	A	1673	1/1	0.96	0.52	104,104,104,104	0
24	MG	A	1669	1/1	0.96	0.17	123,123,123,123	0
24	MG	A	1602	1/1	0.96	0.45	105,105,105,105	0
24	MG	A	1772	1/1	0.96	0.20	130,130,130,130	0
24	MG	A	1688	1/1	0.96	0.04	138,138,138,138	0
24	MG	A	1689	1/1	0.96	0.25	119,119,119,119	0
24	MG	A	1667	1/1	0.96	0.23	189,189,189,189	0
24	MG	A	1711	1/1	0.96	0.14	123,123,123,123	0
24	MG	A	1774	1/1	0.96	0.38	116,116,116,116	0
24	MG	A	1738	1/1	0.96	0.32	93,93,93,93	0
24	MG	A	1680	1/1	0.96	0.16	134,134,134,134	0
24	MG	A	1771	1/1	0.96	0.29	110,110,110,110	0
24	MG	A	1733	1/1	0.96	0.09	104,104,104,104	0
24	MG	A	1651	1/1	0.96	0.17	127,127,127,127	0
24	MG	A	1734	1/1	0.96	0.32	93,93,93,93	0
24	MG	A	1764	1/1	0.96	0.29	130,130,130,130	0
24	MG	A	1740	1/1	0.96	0.25	87,87,87,87	0
24	MG	A	1662	1/1	0.96	0.16	123,123,123,123	0
24	MG	A	1728	1/1	0.97	0.18	123,123,123,123	0
24	MG	A	1632	1/1	0.97	0.18	90,90,90,90	0
24	MG	A	1758	1/1	0.97	0.09	86,86,86,86	0
24	MG	A	1649	1/1	0.97	0.16	118,118,118,118	0

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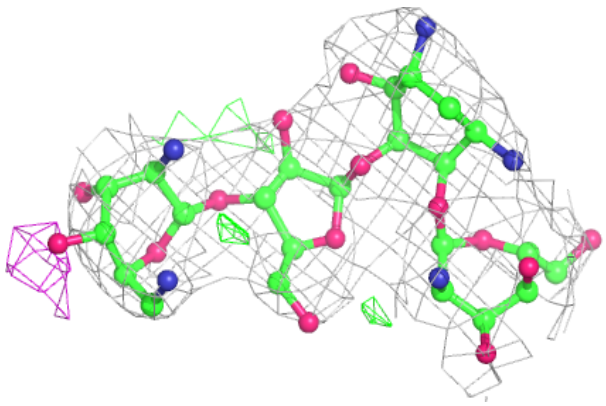
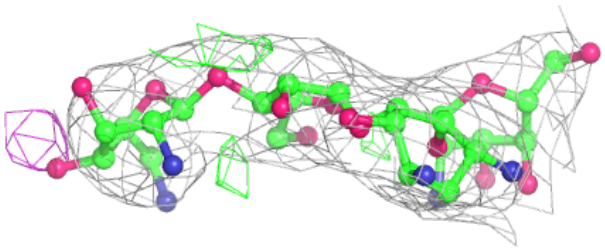
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
24	MG	A	1612	1/1	0.97	0.12	125,125,125,125	0
25	K	A	1842	1/1	0.97	0.30	160,160,160,160	0
24	MG	A	1611	1/1	0.97	0.04	115,115,115,115	0
24	MG	A	1723	1/1	0.97	0.11	101,101,101,101	0
24	MG	A	1639	1/1	0.97	0.15	80,80,80,80	0
24	MG	A	1605	1/1	0.97	0.14	110,110,110,110	0
24	MG	A	1604	1/1	0.97	0.18	135,135,135,135	0
24	MG	F	201	1/1	0.97	0.06	100,100,100,100	0
24	MG	A	1816	1/1	0.97	0.14	83,83,83,83	0
24	MG	A	1721	1/1	0.97	0.15	58,58,58,58	0
24	MG	A	1648	1/1	0.97	0.48	101,101,101,101	0
27	ZN	N	102	1/1	0.98	0.16	124,124,124,124	0
24	MG	A	1615	1/1	0.98	0.33	116,116,116,116	0
24	MG	A	1754	1/1	0.98	0.42	84,84,84,84	0
24	MG	A	1608	1/1	0.99	0.21	94,94,94,94	0

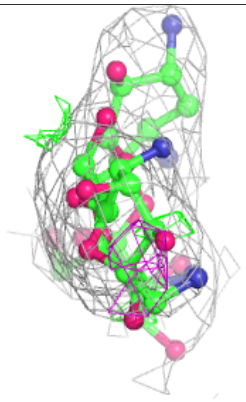
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around B6M A 1856:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)







6.5 Other polymers (i)

There are no such residues in this entry.