



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:30 PM GMT

PDB ID : 4X65
Title : Crystal Structure of 30S ribosomal subunit from *Thermus thermophilus*
Authors : Demirci, H.; Chen, J.; Choi, J.; Soltis, M.; Puglisi, J.D.
Deposited on : 2014-12-06
Resolution : 3.35 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
<http://wwpdb.org/validation/2016/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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

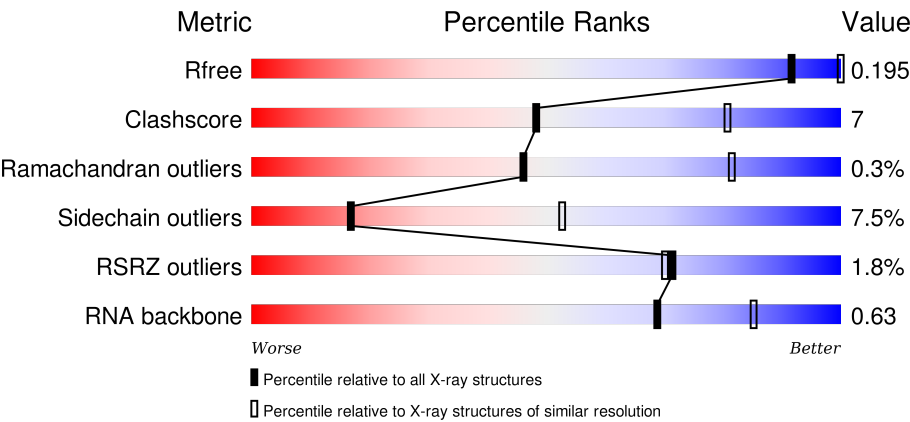
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.35 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.



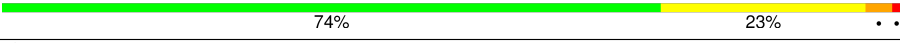










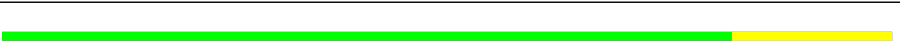




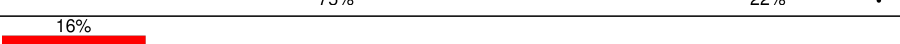
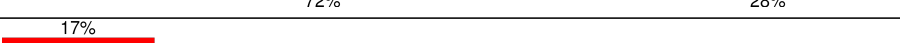

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1004 (3.40-3.28)
Clashscore	102246	1072 (3.40-3.28)
Ramachandran outliers	100387	1055 (3.40-3.28)
Sidechain outliers	100360	1054 (3.40-3.28)
RSRZ outliers	91569	1009 (3.40-3.28)
RNA backbone	2183	1007 (3.88-2.80)

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. 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	<div><div>%</div><div><div></div><div>61%</div><div>32%</div><div>6%</div><div>.</div></div></div>
2	B	236	<div><div>3%</div><div><div></div><div>80%</div><div>18%</div><div>.</div></div></div>
3	C	207	<div><div>%</div><div><div></div><div>75%</div><div>23%</div><div>.</div></div></div>
4	D	208	<div><div>2%</div><div><div></div><div>77%</div><div>20%</div><div>.</div></div></div>

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Mol	Chain	Length	Quality of chain
5	E	151	
6	F	101	
7	G	155	
8	H	138	
9	I	127	
10	J	99	
11	K	119	
12	L	125	
13	M	118	
14	N	60	
15	O	88	
16	P	84	
17	Q	99	
18	R	73	
19	S	81	
20	T	99	
21	U	25	
22	a	6	
23	b	11	

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	PAR	A	1602	-	-	-	X
24	PAR	A	1603	-	-	-	X
24	PAR	A	1605	-	-	-	X
24	PAR	A	1606	-	-	-	X
25	MG	A	1613	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	MG	A	1624	-	-	-	X
25	MG	A	1630	-	-	-	X
25	MG	A	1637	-	-	-	X
25	MG	A	1667	-	-	-	X
25	MG	A	1702	-	-	-	X
25	MG	A	1714	-	-	-	X
25	MG	A	1717	-	-	-	X
25	MG	A	1727	-	-	-	X
25	MG	A	1746	-	-	-	X
25	MG	A	1752	-	-	-	X
25	MG	A	1767	-	-	-	X
25	MG	A	1770	-	-	-	X
25	MG	A	1772	-	-	-	X
25	MG	A	1775	-	-	-	X
25	MG	A	1781	-	-	-	X
25	MG	A	1793	-	-	-	X
25	MG	A	1801	-	-	-	X
25	MG	A	1818	-	-	-	X
25	MG	A	1857	-	-	-	X
25	MG	A	1861	-	-	-	X
25	MG	A	1875	-	-	-	X
25	MG	A	1878	-	-	-	X
25	MG	A	1879	-	-	-	X
25	MG	C	301	-	-	-	X
26	K	A	1912	-	-	-	X

2 Entry composition

There are 28 unique types of molecules in this entry. The entry contains 52840 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 rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1512	Total	C	N	O	P	0	0	0
			32504	14477	6011	10505	1511			

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
2	B	236	Total	C	N	O	S	0	0	1
			1874	1195	336	338	5			

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

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

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

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

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

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

- 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				

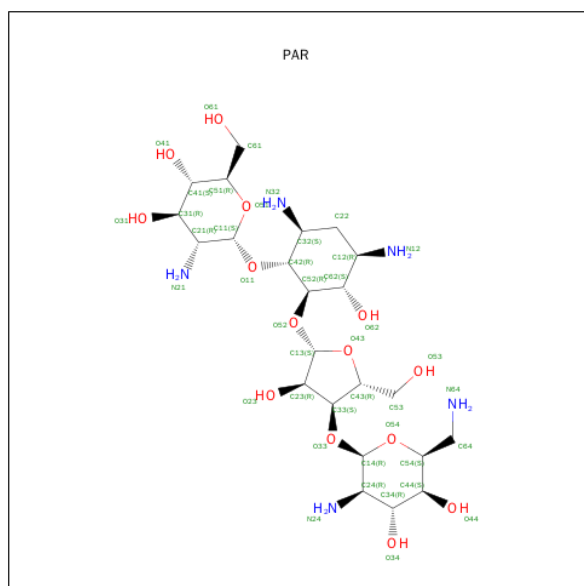
- Molecule 22 is a RNA chain called RNA (5'-D(*AP*(MA6)P*AP*UP*UP*U)-3').

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'-D(P*GP*AP*CP*UP*(70U)P*UP*UP*(12A)P*AP*(PSU)P*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	b	11	Total	C	N	O	P	S	0	0
			247	112	37	85	11	2		

- Molecule 24 is PAROMOMYCIN (three-letter code: PAR) (formula: C₂₃H₄₅N₅O₁₄).



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

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

- Molecule 25 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	P	4	Total	Mg	0	0
			4	4		
25	G	2	Total	Mg	0	0
			2	2		
25	Q	3	Total	Mg	0	0
			3	3		
25	D	1	Total	Mg	0	0
			1	1		
25	E	1	Total	Mg	0	0
			1	1		
25	H	2	Total	Mg	0	0
			2	2		
25	b	1	Total	Mg	0	0
			1	1		
25	C	1	Total	Mg	0	0
			1	1		
25	A	295	Total	Mg	0	0
			295	295		
25	T	1	Total	Mg	0	0
			1	1		
25	L	2	Total	Mg	0	0
			2	2		
25	S	3	Total	Mg	0	0
			3	3		
25	F	1	Total	Mg	0	0
			1	1		

- Molecule 26 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
26	G	1	Total K 1 1	0	0
26	A	44	Total K 44 44	0	0
26	E	1	Total K 1 1	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

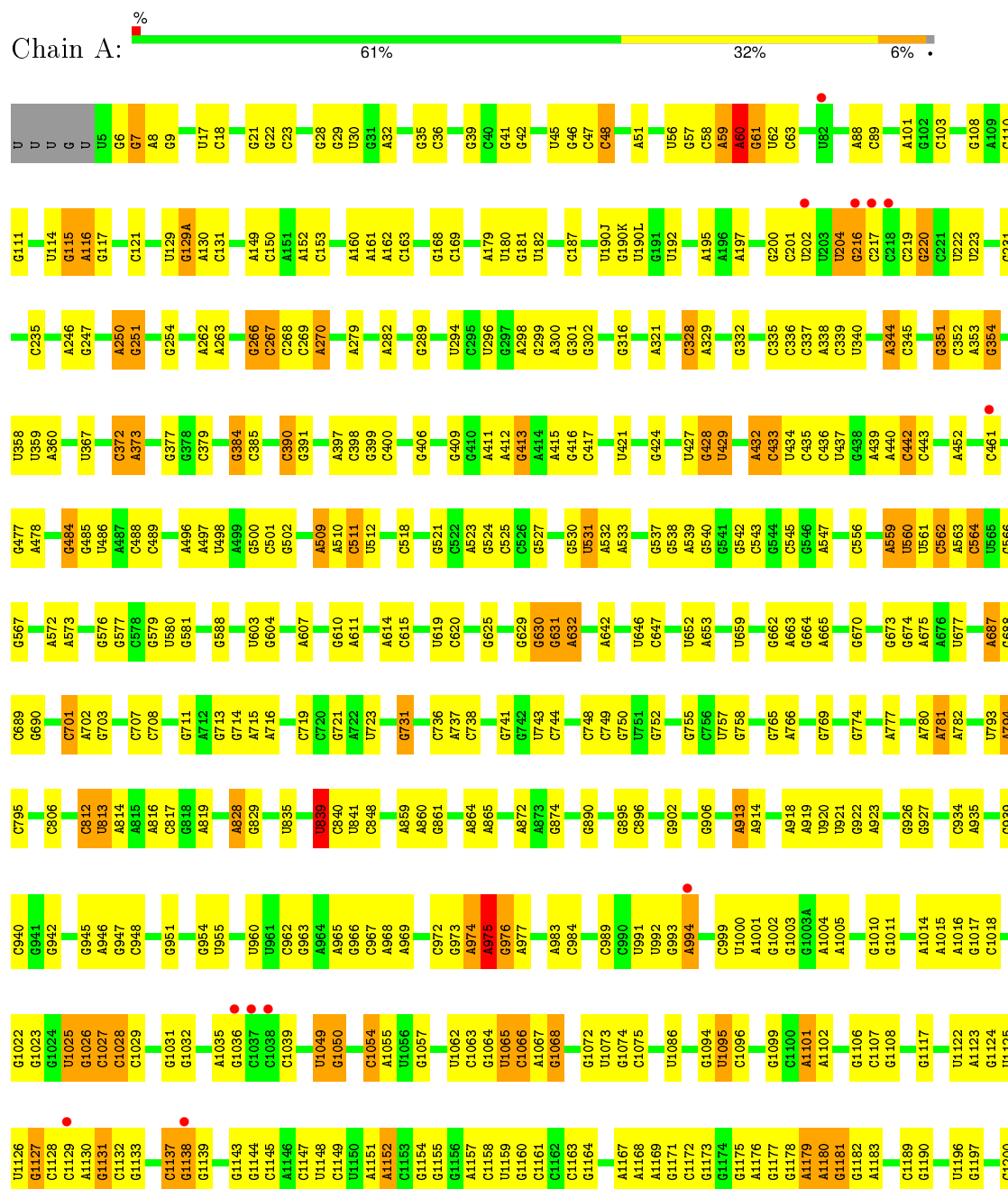
- Molecule 28 is water.

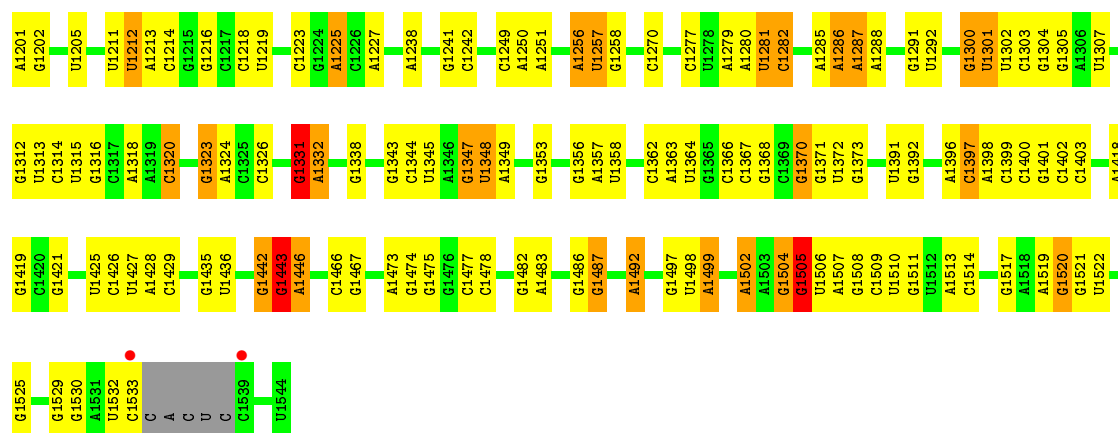
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
28	A	216	Total O 216 216	0	0
28	D	1	Total O 1 1	0	0
28	E	5	Total O 5 5	0	0
28	K	1	Total O 1 1	0	0
28	L	3	Total O 3 3	0	0
28	O	1	Total O 1 1	0	0
28	Q	1	Total O 1 1	0	0
28	T	1	Total O 1 1	0	0

3 Residue-property plots

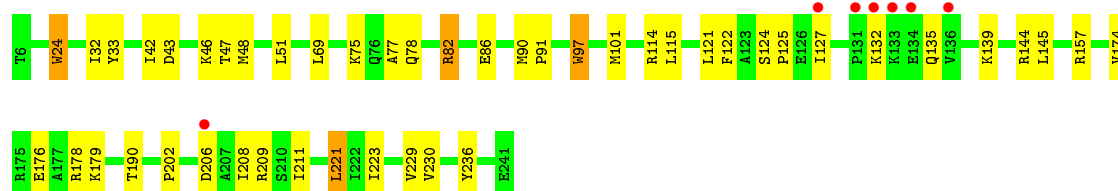
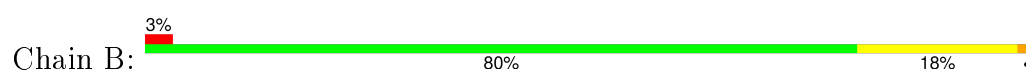
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 rRNA

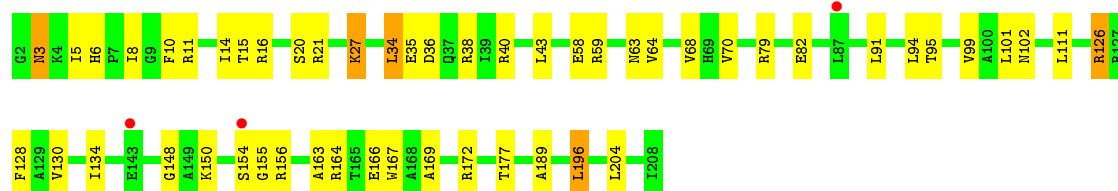
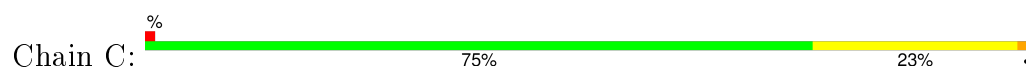




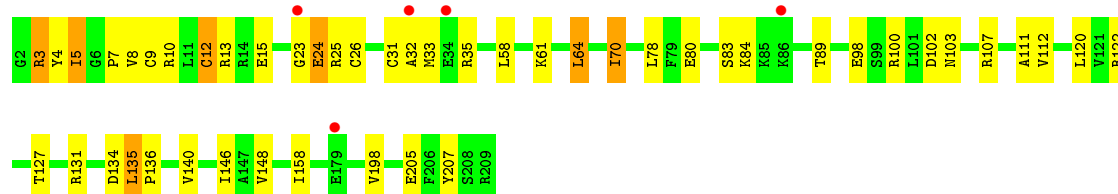
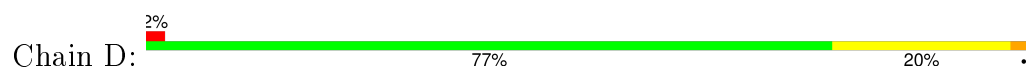
• Molecule 2: 30S ribosomal protein S2



• Molecule 3: 30S ribosomal protein S3

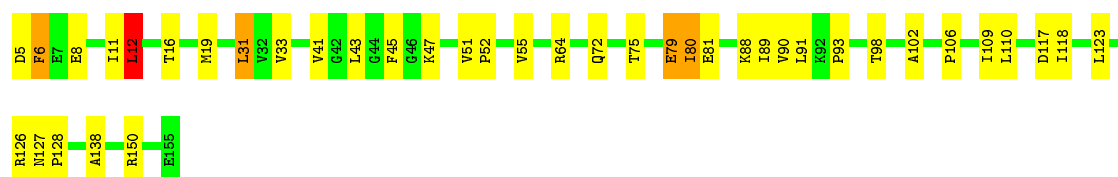


• Molecule 4: 30S ribosomal protein S4

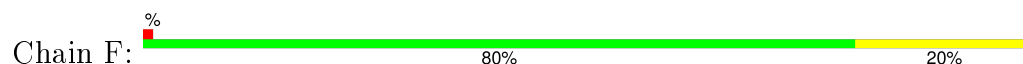


• Molecule 5: 30S ribosomal protein S5

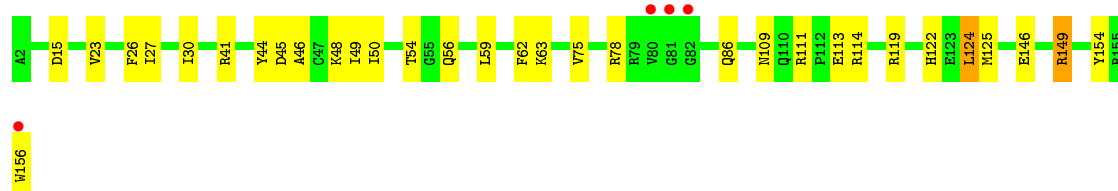
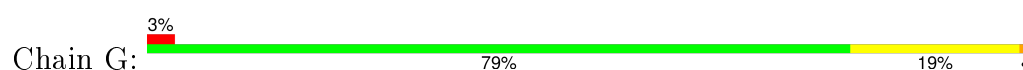




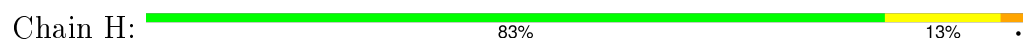
- Molecule 6: 30S ribosomal protein S6



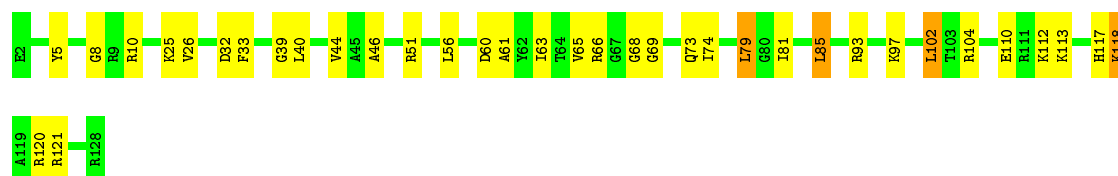
- Molecule 7: 30S ribosomal protein S7



- Molecule 8: 30S ribosomal protein S8



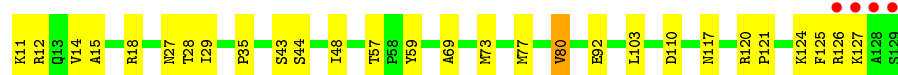
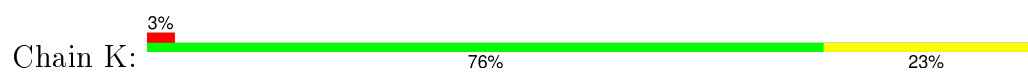
- Molecule 9: 30S ribosomal protein S9



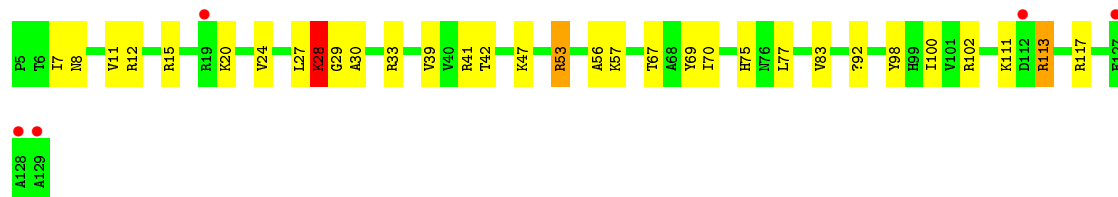
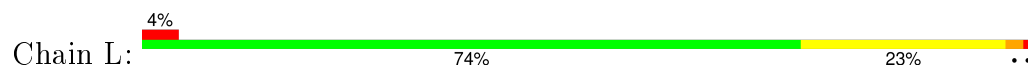
- Molecule 10: 30S ribosomal protein S10



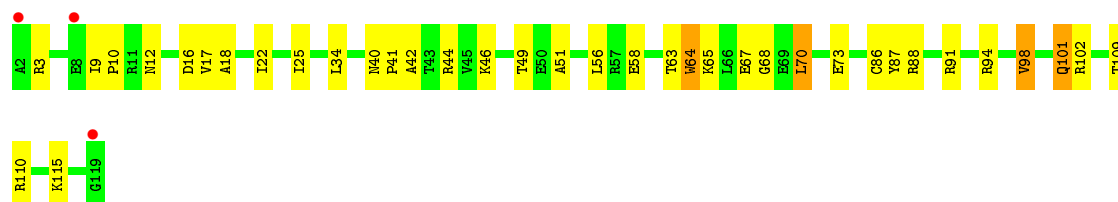
- Molecule 11: 30S ribosomal protein S11



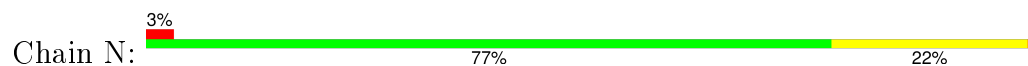
- Molecule 12: 30S ribosomal protein S12



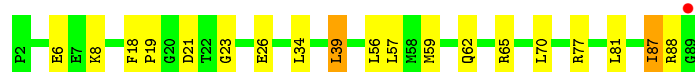
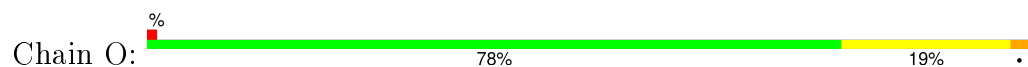
- Molecule 13: 30S ribosomal protein S13



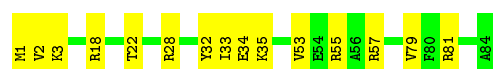
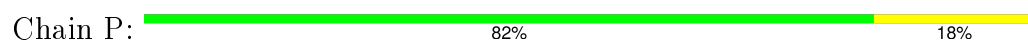
- Molecule 14: 30S ribosomal protein S14 type Z




- Molecule 15: 30S ribosomal protein S15



- Molecule 16: 30S ribosomal protein S16




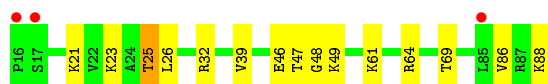
- Molecule 17: 30S ribosomal protein S17

Chain Q:  78% 22%



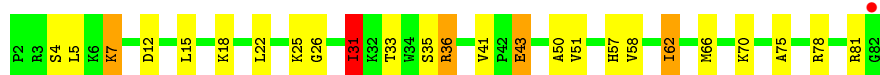
- Molecule 18: 30S ribosomal protein S18

Chain R:  4% 79% 19%




- Molecule 19: 30S ribosomal protein S19

Chain S:  69% 25% 5%



- Molecule 20: 30S ribosomal protein S20

Chain T:  2% 75% 22%




- Molecule 21: 30S ribosomal protein Thx

Chain U:  16% 72% 28%




- Molecule 22: RNA (5'-D(*AP*(MA6)P*AP*UP*UP*U)-3')

Chain a:  17% 83% 17%



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

Chain b:  18% 82% 18%



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	401.44Å 401.44Å 175.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.96 – 3.35 34.96 – 3.36	Depositor EDS
% Data completeness (in resolution range)	99.5 (34.96-3.35) 79.8 (34.96-3.36)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.96 (at 3.39Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1938)	Depositor
R, R_{free}	0.184 , 0.210 0.193 , 0.195	Depositor DCC
R_{free} test set	8617 reflections (5.60%)	DCC
Wilson B-factor (Å ²)	58.2	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 57.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 171129 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	52840	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.65% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: 12A, PAR, MA6, ZN, 70U, K, 0TD, MG, 6MZ, 2MG, 5MC, UR3, 4OC, M2G, 7MG, 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	0.49	0/36037	0.84	23/56239 (0.0%)
2	B	0.26	0/1909	0.42	0/2579
3	C	0.28	0/1637	0.44	0/2207
4	D	0.32	0/1733	0.46	1/2318 (0.0%)
5	E	0.36	0/1163	0.51	1/1566 (0.1%)
6	F	0.26	0/856	0.42	0/1154
7	G	0.27	0/1276	0.44	0/1709
8	H	0.35	0/1136	0.45	0/1527
9	I	0.28	0/1029	0.45	0/1379
10	J	0.27	0/806	0.49	0/1084
11	K	0.32	0/900	0.49	0/1213
12	L	0.35	0/978	0.52	0/1308
13	M	0.27	0/947	0.44	0/1270
14	N	0.32	0/501	0.43	0/664
15	O	0.27	0/745	0.42	0/992
16	P	0.34	0/717	0.47	0/965
17	Q	0.35	0/836	0.48	0/1117
18	R	0.28	0/604	0.41	0/801
19	S	0.24	0/662	0.49	0/892
20	T	0.30	0/765	0.52	0/1007
21	U	0.28	0/213	0.43	0/279
22	a	0.32	0/111	0.91	0/168
23	b	0.83	1/184 (0.5%)	0.74	0/277
All	All	0.44	1/55745 (0.0%)	0.74	25/82715 (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
10	J	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	b	30	G	OP3-P	-10.57	1.48	1.61

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	328	C	C2-N1-C1'	7.65	127.22	118.80
1	A	839	U	C2-N1-C1'	7.51	126.71	117.70
1	A	254	G	O5'-P-OP1	-7.09	99.32	105.70
1	A	839	U	N1-C2-O2	6.94	127.66	122.80
1	A	328	C	N1-C2-O2	6.31	122.69	118.90
1	A	839	U	N3-C2-O2	-5.93	118.05	122.20
1	A	60	A	P-O3'-C3'	5.82	126.69	119.70
4	D	12	CYS	CA-CB-SG	5.81	124.46	114.00
1	A	913	A	P-O3'-C3'	5.78	126.64	119.70
1	A	108	G	O4'-C1'-N9	5.61	112.69	108.20
1	A	1331	G	P-O3'-C3'	5.56	126.37	119.70
1	A	812	C	P-O3'-C3'	5.52	126.33	119.70
1	A	328	C	C6-N1-C2	-5.44	118.12	120.30
1	A	975	A	O4'-C1'-N9	-5.42	103.86	108.20
1	A	328	C	P-O3'-C3'	5.38	126.16	119.70
1	A	687	A	P-O3'-C3'	5.37	126.15	119.70
1	A	1054	C	C2-N1-C1'	5.28	124.61	118.80
1	A	328	C	C5-C6-N1	5.24	123.62	121.00
1	A	328	C	N3-C2-O2	-5.20	118.26	121.90
1	A	328	C	C6-N1-C1'	-5.13	114.64	120.80
1	A	839	U	C6-N1-C1'	-5.12	114.04	121.20
1	A	701	C	P-O3'-C3'	5.04	125.75	119.70
5	E	12	LEU	CA-CB-CG	5.02	126.85	115.30
1	A	1505	G	C8-N9-C4	-5.02	104.39	106.40
1	A	1443	G	P-O3'-C3'	5.01	125.71	119.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	J	87	THR	Peptide

5.2 Too-close contacts ⓘ

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	354	0
2	B	1874	0	1887	23	0
3	C	1613	0	1677	32	0
4	D	1703	0	1763	28	0
5	E	1147	0	1207	26	0
6	F	843	0	857	11	0
7	G	1257	0	1296	18	0
8	H	1116	0	1177	15	0
9	I	1010	0	1037	29	0
10	J	793	0	835	24	0
11	K	885	0	904	16	0
12	L	973	0	1058	20	0
13	M	937	0	995	19	0
14	N	492	0	529	9	0
15	O	734	0	771	8	0
16	P	701	0	720	7	0
17	Q	823	0	891	15	0
18	R	598	0	670	10	0
19	S	648	0	673	16	0
20	T	763	0	861	17	0
21	U	209	0	221	4	0
22	a	124	0	67	0	0
23	b	247	0	129	0	0
24	A	252	0	270	13	0
25	A	295	0	0	0	0
25	C	1	0	0	0	0
25	D	1	0	0	0	0
25	E	1	0	0	0	0
25	F	1	0	0	0	0
25	G	2	0	0	0	0
25	H	2	0	0	0	0
25	L	2	0	0	0	0
25	P	4	0	0	0	0
25	Q	3	0	0	0	0
25	S	3	0	0	0	0
25	T	1	0	0	0	0
25	b	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	A	44	0	0	0	0
26	E	1	0	0	0	0
26	G	1	0	0	0	0
27	D	1	0	0	0	0
27	N	1	0	0	0	0
28	A	216	0	0	2	0
28	D	1	0	0	0	0
28	E	5	0	0	0	0
28	K	1	0	0	0	0
28	L	3	0	0	0	0
28	O	1	0	0	0	0
28	Q	1	0	0	0	0
28	T	1	0	0	0	0
All	All	52840	0	36929	635	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 7.

All (635) 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)
1:A:235:C:H5'	17:Q:70:ARG:HG2	1.52	0.91
1:A:48:C:OP1	24:A:1603:PAR:N12	2.10	0.82
1:A:662:G:N7	24:A:1604:PAR:N12	2.28	0.82
1:A:537:G:OP1	12:L:113:ARG:NH2	2.13	0.81
11:K:15:ALA:HA	11:K:77:MET:HA	1.63	0.79
1:A:1502:A:H2	1:A:1505:G:H1	1.31	0.78
1:A:951:G:OP2	13:M:102:ARG:NH2	2.18	0.77
1:A:501:C:OP1	12:L:117:ARG:NH2	2.18	0.77
1:A:1086:U:H3	1:A:1099:G:H22	1.33	0.76
1:A:664:G:H22	1:A:741:G:H1	1.35	0.75
8:H:10:LEU:HD22	8:H:83:ILE:HD11	1.68	0.75
11:K:57:THR:HG22	11:K:59:TYR:H	1.52	0.74
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.70	0.73
12:L:53:ARG:NH1	12:L:92:0TD:OD2	2.21	0.72
3:C:64:VAL:HG23	3:C:99:VAL:HG11	1.70	0.72
1:A:975:A:H4'	1:A:976:G:H5"	1.71	0.72
4:D:32:ALA:HA	4:D:35:ARG:HG2	1.70	0.72
3:C:156:ARG:H	3:C:163:ALA:HA	1.56	0.71
1:A:1427:U:H2'	1:A:1428:A:H8	1.56	0.70
1:A:1435:G:H2'	1:A:1436:U:C6	2.27	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:82:ILE:HA	10:J:85:LEU:HB2	1.73	0.70
1:A:266:G:H5'	1:A:268:C:H41	1.55	0.69
3:C:14:ILE:HG22	3:C:15:THR:HG23	1.73	0.69
1:A:713:G:H2'	1:A:714:G:C8	2.28	0.69
5:E:80:ILE:HD13	5:E:138:ALA:HB1	1.75	0.69
17:Q:66:SER:O	17:Q:70:ARG:NH1	2.28	0.67
1:A:542:G:OP1	4:D:10:ARG:NH2	2.27	0.67
1:A:673:G:H2'	1:A:674:G:C8	2.30	0.67
19:S:50:ALA:HB1	19:S:57:HIS:HB3	1.74	0.67
7:G:146:GLU:HA	7:G:149:ARG:HG2	1.76	0.67
1:A:1307:U:OP1	13:M:101:GLN:NE2	2.28	0.66
2:B:223:ILE:HD13	2:B:230:VAL:H	1.60	0.66
18:R:32:ARG:HA	18:R:69:THR:HG21	1.77	0.66
1:A:1200:C:O2'	1:A:1205:U:O4	2.14	0.66
1:A:765:G:N2	1:A:813:U:OP2	2.25	0.66
12:L:53:ARG:HG2	12:L:69:TYR:HE1	1.60	0.66
12:L:28:LYS:HB3	12:L:30:ALA:HB2	1.76	0.66
1:A:1122:U:O4	1:A:1123:A:N6	2.29	0.65
1:A:1326:C:OP1	21:U:12:LYS:NZ	2.29	0.65
1:A:432:A:O2'	1:A:433:C:OP1	2.13	0.65
1:A:153:C:H42	1:A:168:G:H1	1.43	0.64
1:A:60:A:H4'	1:A:61:G:O5'	1.97	0.64
1:A:1391:U:H2'	1:A:1392:G:C8	2.32	0.64
1:A:835:U:OP1	18:R:64:ARG:NH2	2.28	0.64
1:A:974:A:OP2	14:N:41:ARG:NH1	2.31	0.63
1:A:298:A:N6	28:A:2149:HOH:O	2.31	0.63
13:M:91:ARG:HB2	13:M:98:VAL:HG13	1.80	0.63
10:J:89:ASP:HB2	10:J:91:PRO:HD2	1.79	0.63
1:A:1027:C:HO2'	1:A:1028:C:H6	1.45	0.63
2:B:77:ALA:HB2	2:B:211:ILE:HD13	1.80	0.63
1:A:427:U:OP1	4:D:13:ARG:NH2	2.30	0.63
1:A:1425:U:H3	1:A:1475:G:H1	1.47	0.63
1:A:1010:G:H2'	1:A:1011:G:H8	1.64	0.62
1:A:103:C:OP1	20:T:17:ARG:NH1	2.33	0.62
17:Q:67:LYS:HA	17:Q:70:ARG:HH12	1.64	0.62
1:A:946:A:H2'	1:A:947:G:C8	2.35	0.62
19:S:5:LEU:HD21	19:S:70:LYS:HZ1	1.65	0.61
1:A:1147:C:HO2'	9:I:5:TYR:HH	1.48	0.61
12:L:24:VAL:HG13	12:L:98:TYR:HE2	1.65	0.61
1:A:1347:G:O6	9:I:10:ARG:NH2	2.30	0.61
7:G:109:ASN:OD1	7:G:119:ARG:NH2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1504:G:OP1	1:A:1507:A:H4'	2.00	0.61
5:E:110:LEU:HD13	5:E:118:ILE:HG21	1.83	0.60
10:J:48:THR:HA	10:J:62:HIS:HB3	1.83	0.60
19:S:33:THR:HG22	19:S:35:SER:H	1.66	0.60
1:A:677:U:H3	1:A:713:G:H22	1.49	0.60
1:A:1075:C:OP1	2:B:179:LYS:NZ	2.34	0.60
20:T:10:LEU:HG	20:T:12:ALA:H	1.65	0.60
19:S:36:ARG:NH2	19:S:75:ALA:O	2.31	0.60
7:G:78:ARG:NH1	7:G:154:TYR:O	2.35	0.59
1:A:920:U:H2'	1:A:921:U:C6	2.37	0.59
2:B:33:TYR:HB2	2:B:43:ASP:HA	1.84	0.59
8:H:41:ARG:NH1	8:H:123:GLU:OE2	2.35	0.59
1:A:1435:G:H2'	1:A:1436:U:H6	1.67	0.59
1:A:736:C:H2'	1:A:737:A:C8	2.38	0.59
1:A:413:G:N2	1:A:429:U:OP2	2.35	0.59
2:B:75:LYS:HA	2:B:78:GLN:HB2	1.85	0.59
1:A:562:C:H1'	12:L:15:ARG:HG3	1.85	0.58
9:I:8:GLY:HA2	9:I:79:LEU:HD13	1.85	0.58
5:E:79:GLU:HG3	5:E:93:PRO:HD2	1.85	0.58
1:A:250:A:H4'	1:A:251:G:O5'	2.03	0.58
1:A:1356:G:H2'	1:A:1357:A:C8	2.39	0.58
9:I:25:LYS:N	9:I:60:ASP:OD1	2.37	0.58
7:G:15:ASP:OD1	7:G:44:TYR:OH	2.22	0.58
17:Q:83:ASP:N	17:Q:83:ASP:OD1	2.35	0.58
5:E:33:VAL:HG22	5:E:43:LEU:HD23	1.85	0.58
9:I:46:ALA:HB2	9:I:74:ILE:HG23	1.85	0.58
13:M:49:THR:HG22	13:M:51:ALA:H	1.68	0.58
1:A:1057:G:H5''	3:C:154:SER:HB2	1.86	0.58
12:L:41:ARG:HH21	12:L:57:LYS:NZ	2.02	0.58
24:A:1604:PAR:N21	24:A:1604:PAR:O53	2.35	0.57
3:C:58:GLU:HB3	10:J:92:THR:HG21	1.86	0.57
1:A:1427:U:H2'	1:A:1428:A:C8	2.39	0.57
1:A:1345:U:OP1	9:I:120:ARG:NH1	2.36	0.57
3:C:3:ASN:N	3:C:3:ASN:OD1	2.36	0.57
1:A:1249:C:O2'	9:I:73:GLN:NE2	2.37	0.57
13:M:88:ARG:HG2	13:M:98:VAL:HG12	1.85	0.57
8:H:113:SER:HB2	8:H:134:ILE:HD11	1.86	0.57
10:J:57:LYS:HE2	10:J:60:ARG:NH2	2.19	0.57
1:A:372:C:H4'	1:A:373:A:O5'	2.05	0.57
1:A:750:G:N3	15:O:23:GLY:HA3	2.20	0.57
1:A:1137:C:H4'	1:A:1138:G:C2	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1026:G:H3'	1:A:1027:C:H5''	1.86	0.56
5:E:81:GLU:HG2	5:E:88:LYS:HE2	1.87	0.56
1:A:1124:G:N7	1:A:1145:C:O2'	2.29	0.56
1:A:890:G:O2'	1:A:906:G:O6	2.20	0.56
7:G:54:THR:HG22	7:G:56:GLN:H	1.70	0.56
2:B:174:VAL:O	2:B:178:ARG:HG2	2.05	0.56
3:C:64:VAL:HB	3:C:99:VAL:HG21	1.87	0.56
1:A:976:G:OP2	1:A:1358:U:O2'	2.23	0.56
1:A:1281:U:H5''	1:A:1282:C:H5	1.68	0.56
2:B:176:GLU:HA	2:B:179:LYS:HB2	1.87	0.56
1:A:948:C:OP1	13:M:109:THR:HG22	2.05	0.56
7:G:113:GLU:HB2	7:G:119:ARG:HG3	1.88	0.56
1:A:1132:C:H2'	1:A:1133:G:H8	1.69	0.56
24:A:1606:PAR:HN21	24:A:1606:PAR:H322	1.54	0.56
15:O:87:ILE:HG22	15:O:88:ARG:H	1.70	0.56
1:A:738:C:OP2	6:F:92:LYS:NZ	2.36	0.56
6:F:100:ASN:ND2	18:R:23:LYS:O	2.38	0.56
24:A:1605:PAR:HN61	24:A:1605:PAR:H532	1.71	0.56
1:A:190(J):U:H2'	1:A:190(K):G:C8	2.41	0.56
1:A:975:A:H5'	1:A:975:A:H8	1.71	0.56
10:J:49:VAL:HG23	14:N:41:ARG:HB2	1.88	0.55
1:A:190(J):U:H2'	1:A:190(K):G:H8	1.71	0.55
1:A:269:C:H2'	1:A:270:A:H8	1.71	0.55
1:A:714:G:H2'	1:A:715:A:C8	2.41	0.55
3:C:155:GLY:HA2	3:C:164:ARG:H	1.71	0.55
1:A:279:A:OP2	17:Q:95:TYR:OH	2.19	0.55
11:K:80:VAL:HG21	11:K:103:LEU:HD13	1.87	0.55
1:A:390:C:O3'	16:P:28:ARG:NH2	2.40	0.55
11:K:110:ASP:OD2	18:R:88:LYS:NZ	2.40	0.55
1:A:1525:G:OP1	11:K:120:ARG:NH2	2.39	0.55
8:H:24:THR:HG22	8:H:63:LEU:HD21	1.89	0.55
1:A:1502:A:H2	1:A:1505:G:N1	2.03	0.55
4:D:7:PRO:HB2	4:D:10:ARG:HD2	1.88	0.55
10:J:49:VAL:HG23	14:N:41:ARG:HD2	1.89	0.55
1:A:1189:C:H5''	3:C:5:ILE:HG12	1.88	0.55
5:E:102:ALA:HB1	5:E:106:PRO:HG2	1.88	0.55
1:A:1049:U:H4'	1:A:1050:G:O5'	2.06	0.55
5:E:88:LYS:HB3	5:E:123:LEU:HB2	1.87	0.54
15:O:26:GLU:OE1	15:O:77:ARG:NH1	2.38	0.54
1:A:1291:G:H4'	9:I:39:GLY:HA3	1.90	0.54
9:I:51:ARG:HG3	9:I:56:LEU:HD21	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:80:ILE:HD12	5:E:91:LEU:HB2	1.90	0.54
1:A:192:U:H1'	20:T:103:GLY:HA2	1.88	0.53
1:A:625:G:O6	24:A:1605:PAR:N24	2.41	0.53
15:O:56:LEU:HA	15:O:59:MET:HE2	1.89	0.53
1:A:114:U:H5''	24:A:1603:PAR:H52	1.91	0.53
1:A:619:U:N3	4:D:134:ASP:OD1	2.25	0.53
6:F:4:TYR:CZ	6:F:72:VAL:HG21	2.44	0.53
1:A:1143:G:H2'	1:A:1144:G:C8	2.44	0.53
1:A:204:U:H4'	1:A:216:G:C8	2.43	0.53
3:C:6:HIS:HD2	3:C:8:ILE:H	1.56	0.53
1:A:1250:A:H4'	9:I:68:GLY:N	2.23	0.53
1:A:360:A:H61	24:A:1603:PAR:H44	1.72	0.53
1:A:1391:U:H2'	1:A:1392:G:H8	1.74	0.53
1:A:1004:A:OP1	1:A:1025:U:N3	2.32	0.53
1:A:1323:G:H2'	1:A:1324:A:C8	2.42	0.53
20:T:10:LEU:HD12	20:T:11:SER:H	1.73	0.53
15:O:39:LEU:HD13	15:O:56:LEU:HB2	1.91	0.53
1:A:1313:U:O4	19:S:4:SER:OG	2.25	0.53
9:I:97:LYS:HA	9:I:102:LEU:HD11	1.91	0.53
1:A:190(K):G:H2'	1:A:190(L):U:H6	1.74	0.53
1:A:1532:U:H2'	1:A:1533:C:H3'	1.91	0.53
1:A:384:G:H2'	1:A:385:C:C6	2.44	0.53
13:M:12:ASN:OD1	13:M:46:LYS:NZ	2.42	0.53
1:A:1368:G:OP2	9:I:112:LYS:HD3	2.09	0.53
3:C:5:ILE:HD13	3:C:10:PHE:HB2	1.91	0.53
19:S:18:LYS:HG2	19:S:31:ILE:HD11	1.91	0.53
1:A:646:U:H2'	1:A:647:C:C6	2.43	0.53
16:P:22:THR:HA	16:P:33:ILE:HG13	1.91	0.52
10:J:32:ALA:HB2	10:J:76:ASN:HB2	1.91	0.52
7:G:75:VAL:HG21	7:G:86:GLN:HB3	1.91	0.52
1:A:1016:A:H2'	1:A:1017:G:O4'	2.09	0.52
3:C:36:ASP:OD1	3:C:59:ARG:NH2	2.41	0.52
14:N:16:PHE:HB2	14:N:19:ARG:HG3	1.91	0.52
1:A:674:G:H2'	1:A:675:A:H8	1.74	0.52
1:A:359:U:H2'	1:A:360:A:C8	2.44	0.52
20:T:57:ARG:HE	20:T:102:GLY:HA2	1.73	0.52
1:A:21:G:H2'	1:A:22:G:C8	2.44	0.52
4:D:111:ALA:HB2	4:D:120:LEU:HD12	1.92	0.52
1:A:360:A:N6	24:A:1603:PAR:H44	2.25	0.52
1:A:501:C:H2'	1:A:502:G:C8	2.45	0.52
10:J:57:LYS:HG3	10:J:60:ARG:HH21	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:646:U:H2'	1:A:647:C:H6	1.75	0.52
5:E:98:THR:N	5:E:117:ASP:OD2	2.43	0.52
1:A:28:G:O2'	1:A:296:U:OP1	2.25	0.52
2:B:32:ILE:HD11	2:B:190:THR:HG23	1.92	0.51
1:A:1095:U:H2'	1:A:1096:C:C6	2.45	0.51
6:F:9:VAL:HB	6:F:87:ARG:HB2	1.91	0.51
2:B:122:PHE:HA	2:B:127:ILE:HG12	1.91	0.51
1:A:1510:U:H2'	1:A:1511:G:C8	2.46	0.51
2:B:24:TRP:HB2	2:B:190:THR:HG22	1.91	0.51
1:A:1305:G:N2	1:A:1332:A:OP2	2.43	0.51
1:A:524:G:H2'	1:A:525:C:C6	2.46	0.51
7:G:45:ASP:O	7:G:48:LYS:HG2	2.10	0.51
20:T:67:ALA:O	20:T:73:HIS:ND1	2.42	0.51
1:A:7:G:H5'	1:A:298:A:O4'	2.10	0.51
1:A:983:A:O2'	1:A:1050:G:OP2	2.28	0.51
7:G:23:VAL:O	7:G:27:ILE:HG12	2.11	0.51
4:D:64:LEU:HG	4:D:198:VAL:HG11	1.92	0.51
17:Q:3:LYS:HB3	17:Q:61:GLU:HB3	1.91	0.51
1:A:1072:G:H2'	1:A:1073:U:C6	2.46	0.51
1:A:737:A:H2'	1:A:738:C:H6	1.76	0.51
1:A:390:C:H2'	1:A:391:G:H8	1.76	0.51
10:J:8:LEU:HB2	10:J:70:ARG:HB2	1.92	0.51
19:S:22:LEU:O	19:S:26:GLY:N	2.43	0.51
1:A:757:U:H2'	1:A:758:G:O4'	2.10	0.51
1:A:806:C:H4'	24:A:1606:PAR:H13	1.93	0.51
8:H:86:ILE:HD12	8:H:133:LEU:HD22	1.93	0.51
1:A:17:U:H2'	1:A:18:C:C6	2.46	0.51
8:H:85:ARG:NE	8:H:87:SER:O	2.44	0.51
1:A:153:C:N4	1:A:168:G:H1	2.09	0.51
1:A:1347:G:O2'	1:A:1348:U:P	2.69	0.51
3:C:155:GLY:HA3	3:C:163:ALA:HB1	1.94	0.50
1:A:1178:G:OP1	9:I:93:ARG:NH1	2.44	0.50
9:I:32:ASP:OD1	9:I:33:PHE:N	2.44	0.50
1:A:1399:C:H4'	1:A:1400:5MC:H5''	1.93	0.50
13:M:3:ARG:HD2	13:M:9:ILE:HD11	1.93	0.50
1:A:399:G:H2'	1:A:400:C:C6	2.46	0.50
1:A:743:U:H2'	1:A:744:C:C6	2.46	0.50
2:B:47:THR:HA	2:B:202:PRO:HG2	1.93	0.50
1:A:741:G:OP2	24:A:1604:PAR:O41	2.21	0.50
1:A:477:G:H2'	1:A:478:A:H8	1.75	0.50
1:A:1106:G:H5''	3:C:172:ARG:HG2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:538:G:H2'	1:A:539:A:H8	1.75	0.50
1:A:190(K):G:H2'	1:A:190(L):U:C6	2.47	0.50
5:E:12:LEU:HD13	5:E:31:LEU:HB2	1.92	0.50
1:A:1343:G:H2'	1:A:1344:C:C6	2.46	0.50
1:A:440:A:H3'	1:A:442:C:H6	1.77	0.50
1:A:1392:G:N2	1:A:1502:A:H8	2.10	0.50
1:A:59:A:H1'	1:A:354:G:N2	2.27	0.50
1:A:501:C:H2'	1:A:502:G:H8	1.76	0.50
1:A:1305:G:N2	1:A:1331:G:H1'	2.26	0.50
1:A:1256:A:HO2'	1:A:1257:U:P	2.34	0.50
13:M:63:THR:HG23	13:M:64:TRP:H	1.77	0.50
2:B:82:ARG:O	2:B:86:GLU:HB2	2.12	0.50
1:A:390:C:H2'	1:A:391:G:C8	2.47	0.49
11:K:27:ASN:OD1	11:K:28:THR:N	2.45	0.49
1:A:976:G:H5'	1:A:1358:U:O2'	2.13	0.49
1:A:737:A:H2'	1:A:738:C:C6	2.47	0.49
21:U:5:ASP:O	21:U:11:GLY:HA3	2.13	0.49
1:A:939:G:H2'	1:A:940:C:C6	2.47	0.49
4:D:70:ILE:HD11	4:D:100:ARG:CZ	2.43	0.49
6:F:23:LYS:O	6:F:27:GLN:HG2	2.12	0.49
1:A:6:G:H4'	1:A:298:A:H4'	1.95	0.49
1:A:1128:C:H42	1:A:1143:G:H1	1.60	0.49
18:R:26:LEU:HD21	18:R:39:VAL:HG23	1.94	0.49
1:A:731:G:OP1	1:A:766:A:H1'	2.12	0.49
1:A:1287:A:H2'	1:A:1288:A:C8	2.48	0.49
17:Q:24:GLU:HG2	17:Q:39:SER:HB3	1.94	0.49
1:A:359:U:H2'	1:A:360:A:H8	1.77	0.49
10:J:32:ALA:O	10:J:34:VAL:HG23	2.13	0.49
1:A:1286:A:H2'	1:A:1287:A:H4'	1.95	0.49
20:T:92:LEU:O	20:T:96:GLY:N	2.43	0.49
1:A:603:U:H2'	1:A:604:G:H8	1.78	0.49
3:C:20:SER:OG	3:C:40:ARG:NH2	2.38	0.49
17:Q:9:VAL:HG21	17:Q:84:LEU:HD13	1.94	0.49
1:A:1031:G:H2'	1:A:1032:G:C8	2.48	0.49
7:G:46:ALA:O	7:G:50:ILE:HG12	2.12	0.49
1:A:1513:A:H2'	1:A:1514:C:C6	2.48	0.49
8:H:25:ASP:OD1	8:H:25:ASP:N	2.45	0.49
1:A:1062:U:H2'	1:A:1063:C:C6	2.47	0.48
1:A:56:U:H2'	1:A:57:G:C8	2.48	0.48
1:A:1314:C:H2'	1:A:1315:U:H6	1.78	0.48
1:A:989:C:H42	1:A:1216:G:H1	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1035:A:H2'	1:A:1036:G:H8	1.77	0.48
1:A:384:G:H2'	1:A:385:C:H6	1.76	0.48
4:D:70:ILE:HD11	4:D:100:ARG:NH2	2.28	0.48
17:Q:59:ILE:HD13	17:Q:73:VAL:HA	1.94	0.48
2:B:97:TRP:CH2	2:B:101:MET:HB2	2.48	0.48
1:A:1250:A:H2'	1:A:1251:A:C8	2.48	0.48
11:K:69:ALA:O	11:K:73:MET:HG2	2.13	0.48
1:A:662:G:H2'	1:A:663:A:C8	2.48	0.48
1:A:1147:C:O2'	9:I:5:TYR:OH	2.21	0.48
1:A:1015:A:H2'	1:A:1016:A:C8	2.49	0.48
1:A:335:C:H2'	1:A:336:C:C6	2.48	0.48
13:M:22:ILE:HB	13:M:25:ILE:HB	1.96	0.48
1:A:1218:C:H2'	1:A:1219:U:C6	2.48	0.48
16:P:57:ARG:NH1	16:P:79:VAL:O	2.47	0.48
18:R:47:THR:HG22	18:R:48:GLY:H	1.79	0.48
1:A:1372:U:H2'	1:A:1373:G:O4'	2.13	0.48
1:A:269:C:H2'	1:A:270:A:C8	2.48	0.48
12:L:56:ALA:HB2	12:L:70:ILE:HD11	1.95	0.48
1:A:1028:C:H2'	1:A:1029:C:H6	1.79	0.48
9:I:8:GLY:HA3	9:I:79:LEU:HB3	1.95	0.48
2:B:124:SER:HB2	2:B:125:PRO:HD2	1.95	0.48
1:A:538:G:H2'	1:A:539:A:C8	2.49	0.47
1:A:1131:G:O2'	1:A:1132:C:O4'	2.20	0.47
1:A:1157:A:C2	1:A:1181:G:C4	3.01	0.47
1:A:659:U:OP2	15:O:8:LYS:NZ	2.47	0.47
1:A:200:G:H2'	1:A:201:C:O4'	2.14	0.47
1:A:580:U:H2'	1:A:581:G:O4'	2.13	0.47
17:Q:68:ARG:HG3	17:Q:68:ARG:O	2.14	0.47
13:M:16:ASP:OD1	13:M:17:VAL:N	2.43	0.47
1:A:839:U:H2'	1:A:839:U:O2	2.13	0.47
3:C:189:ALA:HB3	3:C:196:LEU:HB2	1.95	0.47
1:A:116:A:H5''	28:A:2017:HOH:O	2.12	0.47
1:A:1168:A:H2'	1:A:1169:A:C8	2.49	0.47
4:D:9:CYS:O	4:D:12:CYS:HB2	2.15	0.47
1:A:436:C:H2'	1:A:437:U:H6	1.78	0.47
1:A:652:U:O4	1:A:752:G:O2'	2.27	0.47
13:M:67:GLU:HB3	13:M:68:GLY:H	1.50	0.47
1:A:434:U:H2'	1:A:435:C:C6	2.50	0.47
1:A:975:A:H5'	1:A:975:A:C8	2.50	0.47
12:L:27:LEU:O	12:L:29:GLY:N	2.48	0.47
1:A:432:A:HO2'	1:A:433:C:P	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:6:HIS:CD2	3:C:8:ILE:HB	2.49	0.47
1:A:1073:U:C2	1:A:1074:G:C8	3.02	0.47
1:A:603:U:H2'	1:A:604:G:C8	2.50	0.47
16:P:18:ARG:HD3	16:P:35:LYS:HD2	1.96	0.47
1:A:994:A:OP1	1:A:994:A:C8	2.68	0.47
1:A:1466:C:H2'	1:A:1467:G:O4'	2.14	0.47
9:I:26:VAL:HG13	9:I:61:ALA:HB3	1.96	0.47
21:U:12:LYS:O	21:U:16:GLY:N	2.48	0.47
1:A:642:A:C8	8:H:115:SER:HA	2.50	0.47
1:A:1402:4OC:HM22	1:A:1403:C:H5'	1.95	0.47
1:A:1014:A:H2'	1:A:1015:A:C8	2.49	0.47
1:A:922:G:H2'	1:A:923:A:C8	2.50	0.47
1:A:1068:G:OP2	1:A:1068:G:H8	1.98	0.47
20:T:36:LEU:HD12	20:T:62:LEU:HD12	1.96	0.47
1:A:674:G:H2'	1:A:675:A:C8	2.50	0.46
1:A:1189:C:OP1	10:J:51:ARG:NH2	2.37	0.46
2:B:178:ARG:NH2	8:H:74:PRO:HB3	2.31	0.46
11:K:12:ARG:HD2	11:K:14:VAL:HG22	1.97	0.46
9:I:63:ILE:HG22	9:I:65:VAL:HG23	1.96	0.46
1:A:973:G:H3'	1:A:974:A:H5''	1.97	0.46
1:A:1003:G:N2	1:A:1039:C:C2	2.83	0.46
1:A:56:U:H2'	1:A:57:G:H8	1.79	0.46
1:A:299:G:H2'	1:A:300:A:C8	2.51	0.46
7:G:26:PHE:CE2	7:G:30:ILE:HD11	2.50	0.46
3:C:150:LYS:HG3	3:C:169:ALA:HB2	1.96	0.46
10:J:29:ARG:HB2	10:J:84:GLN:HE22	1.80	0.46
1:A:631:G:H5'	1:A:632:A:OP1	2.15	0.46
2:B:48:MET:HA	2:B:51:LEU:HB2	1.96	0.46
1:A:1124:G:H5'	10:J:35:SER:HB3	1.97	0.46
1:A:769:G:H4'	1:A:1513:A:H4'	1.97	0.46
1:A:630:G:H5'	1:A:631:G:OP2	2.15	0.46
1:A:179:A:H2'	1:A:180:U:C6	2.49	0.46
1:A:670:G:H21	6:F:73:ASN:HD21	1.63	0.46
9:I:44:VAL:O	9:I:51:ARG:NH2	2.49	0.46
1:A:921:U:O2	5:E:19:MET:HB2	2.15	0.46
16:P:34:GLU:OE2	16:P:55:ARG:HD3	2.16	0.46
4:D:102:ASP:OD1	4:D:103:ASN:N	2.48	0.46
1:A:860:A:H2'	1:A:861:G:O4'	2.15	0.46
1:A:416:G:H2'	1:A:417:C:H6	1.81	0.46
1:A:1392:G:H21	1:A:1502:A:H8	1.63	0.46
12:L:24:VAL:HG13	12:L:98:TYR:CE2	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:56:VAL:HG12	17:Q:77:VAL:HB	1.98	0.46
1:A:1148:U:H2'	1:A:1149:C:O4'	2.15	0.46
1:A:1031:G:H2'	1:A:1032:G:H8	1.81	0.46
1:A:110:C:H2'	1:A:111:G:O4'	2.16	0.46
4:D:31:CYS:C	4:D:33:MET:H	2.19	0.46
12:L:8:ASN:O	12:L:12:ARG:HG3	2.16	0.46
1:A:266:G:H5''	1:A:267:C:C5	2.51	0.46
1:A:1017:G:H2'	1:A:1018:C:C6	2.50	0.46
1:A:1316:G:N2	1:A:1318:A:H3'	2.31	0.46
15:O:62:GLN:OE1	15:O:65:ARG:NH2	2.48	0.46
11:K:57:THR:HG22	11:K:59:TYR:N	2.26	0.45
1:A:1001:A:H2'	1:A:1002:G:C8	2.51	0.45
1:A:563:A:H2'	1:A:567:G:C8	2.51	0.45
1:A:509:A:N3	1:A:543:C:O2'	2.37	0.45
1:A:399:G:H2'	1:A:400:C:H6	1.81	0.45
1:A:35:G:H2'	1:A:36:C:C6	2.51	0.45
1:A:523:A:H61	12:L:92:OTD:CG	2.29	0.45
1:A:610:G:C4	1:A:611:A:C8	3.04	0.45
1:A:631:G:O3'	1:A:632:A:H8	2.00	0.45
9:I:85:LEU:HA	9:I:85:LEU:HD12	1.86	0.45
18:R:46:GLU:CD	18:R:46:GLU:H	2.20	0.45
1:A:477:G:H2'	1:A:478:A:C8	2.50	0.45
1:A:337:C:H2'	1:A:338:A:H8	1.81	0.45
1:A:1521:G:H2'	1:A:1522:U:C6	2.52	0.45
20:T:89:ARG:NH2	20:T:105:SER:O	2.44	0.45
3:C:11:ARG:NH1	3:C:177:THR:O	2.49	0.45
3:C:38:ARG:HB3	3:C:94:LEU:HD21	1.98	0.45
10:J:14:LYS:HE2	10:J:14:LYS:HB3	1.67	0.45
1:A:1371:G:O3'	9:I:69:GLY:HA3	2.16	0.45
1:A:1521:G:H2'	1:A:1522:U:H6	1.82	0.45
13:M:40:ASN:HD21	13:M:42:ALA:HB3	1.81	0.45
24:A:1602:PAR:H23	24:A:1602:PAR:N21	2.30	0.45
1:A:1443:G:H4'	1:A:1446:A:O5'	2.16	0.45
1:A:560:U:H5'	1:A:566:G:C2	2.52	0.45
6:F:30:LEU:HD23	6:F:30:LEU:HA	1.83	0.45
19:S:50:ALA:HA	19:S:58:VAL:O	2.17	0.45
1:A:611:A:H2	1:A:629:G:H22	1.65	0.45
2:B:90:MET:HA	2:B:91:PRO:HD3	1.78	0.45
1:A:1175:G:H2'	1:A:1176:A:H8	1.81	0.45
1:A:222:U:H2'	1:A:223:U:C6	2.52	0.45
1:A:335:C:H2'	1:A:336:C:H6	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:814:A:H2'	1:A:816:A:H5''	1.98	0.45
14:N:27:CYS:SG	14:N:29:ARG:HB2	2.57	0.45
1:A:262:A:H2'	1:A:263:A:C8	2.52	0.45
1:A:1401:G:C2	1:A:1402:4OC:H1'	2.52	0.45
1:A:1176:A:H2'	1:A:1177:G:C8	2.52	0.45
1:A:1163:C:H2'	1:A:1164:G:H8	1.81	0.45
3:C:130:VAL:HG12	3:C:134:ILE:HD11	1.99	0.45
1:A:45:U:H2'	1:A:46:G:C8	2.52	0.45
7:G:59:LEU:HD11	7:G:63:LYS:HE3	1.99	0.45
20:T:67:ALA:HA	20:T:73:HIS:H	1.81	0.45
12:L:70:ILE:HD13	12:L:77:LEU:HD12	1.99	0.45
1:A:614:A:H2'	1:A:615:C:C6	2.52	0.45
1:A:620:C:C2	4:D:135:LEU:HD22	2.51	0.45
4:D:140:VAL:HG11	4:D:146:ILE:HD11	1.99	0.45
11:K:18:ARG:NH1	11:K:35:PRO:O	2.50	0.45
4:D:23:GLY:HA3	4:D:112:VAL:HG22	1.98	0.45
3:C:64:VAL:H	3:C:99:VAL:HB	1.81	0.44
9:I:112:LYS:HE3	9:I:117:HIS:O	2.16	0.44
14:N:46:GLU:O	14:N:50:LYS:HG3	2.17	0.44
8:H:39:LEU:HD12	8:H:39:LEU:HA	1.80	0.44
12:L:57:LYS:HD3	12:L:67:THR:HG22	2.00	0.44
5:E:98:THR:HB	5:E:117:ASP:HB3	2.00	0.44
3:C:27:LYS:HD3	3:C:27:LYS:H	1.81	0.44
10:J:51:ARG:HG3	10:J:60:ARG:O	2.17	0.44
13:M:3:ARG:HA	13:M:9:ILE:HG13	1.99	0.44
1:A:222:U:H2'	1:A:223:U:H6	1.83	0.44
1:A:895:G:H2'	1:A:896:C:C6	2.52	0.44
1:A:1499:A:H1'	1:A:1520:G:H5'	1.99	0.44
1:A:864:A:H2'	1:A:865:A:C8	2.52	0.44
6:F:79:LEU:HA	6:F:79:LEU:HD23	1.87	0.44
1:A:219:C:C4	1:A:220:G:C8	3.05	0.44
1:A:539:A:H2'	1:A:540:G:C8	2.53	0.44
1:A:1399:C:C2	1:A:1502:A:N6	2.85	0.44
1:A:344:A:H5'	1:A:345:C:C5	2.53	0.44
1:A:736:C:H2'	1:A:737:A:H8	1.79	0.44
7:G:122:HIS:HA	7:G:125:MET:HE2	2.00	0.44
12:L:7:ILE:O	12:L:11:VAL:HG23	2.18	0.44
4:D:148:VAL:HG11	4:D:158:ILE:HD13	1.98	0.44
1:A:1482:G:HO2'	1:A:1483:A:H8	1.61	0.44
1:A:484:G:H5'	1:A:486:U:O4'	2.17	0.44
1:A:192:U:C1'	20:T:103:GLY:HA2	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:35:GLU:HB3	3:C:59:ARG:HH22	1.83	0.44
1:A:1241:G:H2'	1:A:1242:C:H6	1.82	0.44
1:A:57:G:H2'	1:A:58:C:C6	2.53	0.44
1:A:560:U:H5'	1:A:566:G:N2	2.32	0.44
3:C:68:VAL:HG12	3:C:70:VAL:HG23	1.99	0.44
15:O:18:PHE:HB2	15:O:19:PRO:HD2	2.00	0.44
5:E:80:ILE:CD1	5:E:91:LEU:HB2	2.48	0.43
1:A:216:G:O2'	1:A:217:C:O4'	2.33	0.43
1:A:629:G:H2'	1:A:630:G:O4'	2.18	0.43
3:C:126:ARG:HE	3:C:128:PHE:HD2	1.66	0.43
1:A:918:A:H2'	1:A:919:A:C8	2.53	0.43
1:A:1473:A:H2'	1:A:1474:G:C8	2.54	0.43
10:J:60:ARG:HD3	10:J:60:ARG:HA	1.83	0.43
1:A:1128:C:OP1	9:I:66:ARG:NH1	2.51	0.43
5:E:11:ILE:HB	5:E:31:LEU:HB3	2.00	0.43
1:A:1163:C:C2	1:A:1164:G:C8	3.06	0.43
4:D:3:ARG:NH2	4:D:5:ILE:HD11	2.34	0.43
11:K:124:LYS:HD2	11:K:125:PHE:CZ	2.53	0.43
13:M:86:CYS:SG	13:M:87:TYR:N	2.91	0.43
9:I:110:GLU:OE2	9:I:113:LYS:NZ	2.52	0.43
5:E:33:VAL:HG11	5:E:109:ILE:HA	2.00	0.43
10:J:16:LEU:HD12	10:J:68:HIS:HB2	2.00	0.43
17:Q:9:VAL:HG22	17:Q:56:VAL:HG22	2.00	0.43
19:S:5:LEU:HD21	19:S:70:LYS:NZ	2.33	0.43
1:A:1525:G:P	11:K:120:ARG:HH22	2.42	0.43
5:E:31:LEU:HD23	5:E:31:LEU:HA	1.82	0.43
1:A:642:A:N7	8:H:115:SER:HA	2.34	0.43
20:T:62:LEU:HD23	20:T:62:LEU:HA	1.77	0.43
1:A:263:A:OP2	20:T:79:ARG:NH1	2.52	0.43
11:K:126:ARG:HB3	11:K:127:LYS:H	1.72	0.43
5:E:6:PHE:HA	5:E:6:PHE:HD1	1.73	0.43
16:P:18:ARG:NH1	16:P:32:TYR:OH	2.50	0.43
4:D:98:GLU:OE2	4:D:107:ARG:NE	2.36	0.43
1:A:962:C:H2'	1:A:963:G:O4'	2.19	0.43
9:I:69:GLY:O	9:I:73:GLN:HG3	2.19	0.43
10:J:34:VAL:HG22	10:J:74:ILE:HG23	1.99	0.43
1:A:1314:C:H2'	1:A:1315:U:C6	2.53	0.43
11:K:43:SER:OG	11:K:44:SER:N	2.52	0.43
1:A:954:G:H2'	1:A:955:U:C6	2.54	0.43
1:A:500:G:H2'	1:A:501:C:C6	2.53	0.43
2:B:211:ILE:H	2:B:211:ILE:HG13	1.70	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:530:G:HO2'	1:A:531:U:P	2.41	0.43
4:D:135:LEU:HA	4:D:136:PRO:HD3	1.88	0.43
1:A:1241:G:H2'	1:A:1242:C:C6	2.53	0.43
1:A:1151:A:C2	1:A:1152:A:C5	3.06	0.43
1:A:1366:C:H2'	1:A:1367:C:C6	2.54	0.43
1:A:168:G:C2	1:A:169:C:C5	3.07	0.43
13:M:65:LYS:NZ	13:M:73:GLU:OE2	2.50	0.43
1:A:1349:A:OP1	9:I:120:ARG:HB2	2.18	0.43
7:G:45:ASP:O	7:G:49:ILE:HG13	2.19	0.43
1:A:1035:A:H2'	1:A:1036:G:C8	2.54	0.43
1:A:1167:A:H2'	1:A:1168:A:C8	2.54	0.43
1:A:434:U:H2'	1:A:435:C:H6	1.83	0.43
18:R:21:LYS:O	18:R:25:THR:OG1	2.31	0.43
4:D:61:LYS:HE3	4:D:207:TYR:OH	2.19	0.43
1:A:1158:C:C4	1:A:1160:G:C8	3.06	0.43
6:F:46:ARG:HB2	6:F:60:PHE:CE2	2.53	0.43
2:B:115:LEU:HD13	2:B:145:LEU:HB3	2.01	0.43
7:G:111:ARG:HB2	7:G:119:ARG:HG2	2.01	0.42
1:A:57:G:H2'	1:A:58:C:H6	1.84	0.42
1:A:1498:UR3:O4'	1:A:1519:MA6:H2	2.19	0.42
1:A:1300:G:O2'	1:A:1301:U:P	2.77	0.42
12:L:41:ARG:HH21	12:L:57:LYS:HZ3	1.66	0.42
1:A:711:G:P	6:F:54:LYS:HZ1	2.42	0.42
4:D:78:LEU:HA	4:D:78:LEU:HD23	1.87	0.42
3:C:148:GLY:HA3	3:C:172:ARG:O	2.19	0.42
1:A:161:A:H2'	1:A:162:A:C8	2.55	0.42
1:A:564:C:O2'	8:H:91:ARG:NH2	2.53	0.42
1:A:1370:G:C2	1:A:1371:G:C8	3.06	0.42
10:J:8:LEU:HB3	10:J:16:LEU:HD22	2.01	0.42
5:E:45:PHE:CD2	5:E:47:LYS:HD2	2.55	0.42
1:A:1486:G:H2'	1:A:1487:G:O4'	2.20	0.42
1:A:409:G:OP1	4:D:25:ARG:HB3	2.20	0.42
1:A:537:G:H2'	1:A:538:G:C8	2.55	0.42
1:A:716:A:H1'	11:K:117:ASN:O	2.18	0.42
1:A:1277:C:O2'	1:A:1279:A:H1'	2.19	0.42
1:A:8:A:N6	4:D:205:GLU:O	2.52	0.42
1:A:432:A:H2'	1:A:433:C:O4'	2.19	0.42
1:A:974:A:H8	1:A:974:A:OP1	2.03	0.42
17:Q:24:GLU:OE1	17:Q:37:LYS:HD3	2.20	0.42
17:Q:40:LYS:HD2	17:Q:42:TYR:CZ	2.55	0.42
14:N:9:LYS:C	14:N:9:LYS:HD2	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:59:ILE:HA	17:Q:59:ILE:HD13	1.85	0.42
1:A:246:A:C2	1:A:282:A:C5	3.07	0.42
1:A:339:C:H2'	1:A:340:U:H6	1.85	0.42
1:A:1064:G:N2	1:A:1190:G:O2'	2.53	0.42
1:A:1320:C:O2	19:S:36:ARG:NH1	2.53	0.42
1:A:1072:G:H2'	1:A:1073:U:H6	1.83	0.42
9:I:81:ILE:O	9:I:85:LEU:HB2	2.20	0.42
2:B:132:LYS:HD2	2:B:135:GLN:HB2	2.02	0.42
1:A:828:A:H2'	1:A:829:G:O4'	2.19	0.42
14:N:24:CYS:HB2	14:N:40:CYS:HB3	2.02	0.42
1:A:1223:C:P	19:S:78:ARG:HH12	2.42	0.42
1:A:316:G:OP2	1:A:351:G:O2'	2.38	0.42
1:A:663:A:H5''	18:R:61:LYS:HE3	2.02	0.42
1:A:22:G:H2'	1:A:23:C:C6	2.55	0.42
1:A:1443:G:H4'	1:A:1446:A:C5'	2.50	0.42
13:M:34:LEU:HD13	13:M:41:PRO:HA	2.01	0.42
3:C:63:ASN:HA	3:C:99:VAL:HG12	2.01	0.42
2:B:223:ILE:HD13	2:B:230:VAL:N	2.32	0.42
1:A:972:C:O3'	10:J:57:LYS:HD3	2.20	0.42
1:A:1281:U:O2'	1:A:1282:C:OP1	2.36	0.42
1:A:1498:UR3:O2'	1:A:1499:A:OP2	2.27	0.42
10:J:5:ARG:HA	10:J:73:ASP:OD1	2.19	0.42
1:A:1107:C:C4	1:A:1108:G:C8	3.07	0.42
1:A:794:A:H2'	1:A:795:C:C6	2.55	0.42
1:A:1331:G:HO2'	1:A:1332:A:P	2.43	0.41
1:A:1473:A:H2'	1:A:1474:G:H8	1.85	0.41
1:A:302:G:N3	1:A:556:C:H4'	2.35	0.41
1:A:719:C:O2'	18:R:49:LYS:HB3	2.20	0.41
20:T:75:ASN:OD1	20:T:75:ASN:N	2.53	0.41
1:A:945:G:C2	1:A:946:A:C8	3.08	0.41
1:A:413:G:H1'	1:A:428:G:H21	1.85	0.41
2:B:42:ILE:HG21	2:B:202:PRO:O	2.21	0.41
2:B:221:LEU:HD22	2:B:221:LEU:HA	1.86	0.41
13:M:70:LEU:HA	13:M:70:LEU:HD23	1.91	0.41
1:A:152:A:C8	1:A:153:C:C5	3.09	0.41
1:A:160:A:H2'	1:A:161:A:O4'	2.21	0.41
1:A:511:C:C2	1:A:512:U:C5	3.08	0.41
1:A:29:G:O2'	1:A:30:U:H5'	2.20	0.41
1:A:41:G:H2'	1:A:42:G:C8	2.55	0.41
1:A:149:A:H2'	1:A:150:C:C6	2.55	0.41
1:A:294:U:OP1	1:A:610:G:O2'	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:560:U:H4'	1:A:561:U:H5''	2.01	0.41
1:A:1065:U:H1'	1:A:1066:C:OP2	2.21	0.41
1:A:1396:A:H4'	1:A:1397:C:H5''	2.00	0.41
3:C:111:LEU:HD23	3:C:111:LEU:HA	1.77	0.41
1:A:358:U:H2'	1:A:359:U:C6	2.55	0.41
1:A:1160:G:C6	1:A:1161:C:C5	3.09	0.41
5:E:51:VAL:HB	5:E:52:PRO:HD3	2.02	0.41
10:J:6:ILE:HD12	10:J:72:VAL:HG11	2.02	0.41
1:A:1172:C:H2'	1:A:1173:G:H8	1.84	0.41
1:A:1101:A:H4'	1:A:1102:A:O5'	2.20	0.41
1:A:689:C:H2'	1:A:690:G:O4'	2.21	0.41
4:D:24:GLU:C	4:D:26:CYS:H	2.23	0.41
12:L:75:HIS:HA	12:L:102:ARG:HH22	1.85	0.41
10:J:38:ILE:H	10:J:71:LEU:CB	2.32	0.41
1:A:1225:A:N3	1:A:1225:A:H2'	2.35	0.41
5:E:81:GLU:HG3	5:E:90:VAL:HG22	2.03	0.41
1:A:415:A:C4	1:A:416:G:C8	3.09	0.41
1:A:187:C:O2	20:T:105:SER:HB3	2.21	0.41
1:A:999:C:H2'	1:A:1000:U:H6	1.86	0.41
8:H:51:VAL:HG11	8:H:60:ARG:HG3	2.02	0.41
1:A:488:C:H2'	1:A:489:C:H6	1.84	0.41
1:A:1022:G:C2	1:A:1023:G:C8	3.09	0.41
1:A:1426:C:H2'	1:A:1427:U:C6	2.56	0.41
12:L:27:LEU:HB3	12:L:28:LYS:H	1.63	0.41
1:A:413:G:H1'	1:A:428:G:N2	2.35	0.41
5:E:45:PHE:CE2	5:E:47:LYS:HD2	2.56	0.41
1:A:1508:G:H2'	1:A:1509:C:H6	1.86	0.41
1:A:500:G:H2'	1:A:501:C:H6	1.86	0.41
1:A:1127:G:H21	1:A:1147:C:N4	2.19	0.41
1:A:1002:G:H2'	1:A:1003:G:C8	2.56	0.41
19:S:33:THR:HG22	19:S:35:SER:N	2.34	0.41
20:T:10:LEU:O	20:T:13:LEU:HG	2.20	0.41
1:A:1095:U:H2'	1:A:1096:C:H6	1.85	0.41
1:A:707:C:H2'	1:A:708:C:C6	2.55	0.41
3:C:34:LEU:HG	14:N:25:VAL:HG21	2.03	0.41
19:S:62:ILE:HA	19:S:66:MET:SD	2.61	0.41
24:A:1601:PAR:O44	24:A:1601:PAR:N64	2.54	0.41
1:A:780:A:O2'	1:A:781:A:H5''	2.21	0.41
4:D:80:GLU:O	4:D:84:LYS:HG3	2.21	0.41
1:A:62:U:O2'	1:A:379:C:O2	2.38	0.41
8:H:121:ASP:OD1	8:H:121:ASP:N	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:A:H2'	1:A:89:C:O4'	2.21	0.41
9:I:118:LYS:O	9:I:120:ARG:N	2.47	0.41
1:A:1442:G:C6	1:A:1446:A:N6	2.89	0.41
1:A:1303:C:H2'	1:A:1304:G:H5'	2.03	0.41
1:A:1211:U:H5'	1:A:1212:U:OP1	2.20	0.41
1:A:1477:C:H2'	1:A:1478:C:H6	1.86	0.41
19:S:7:LYS:H	19:S:7:LYS:HG3	1.65	0.41
1:A:1428:A:H2'	1:A:1429:C:C6	2.56	0.40
3:C:8:ILE:HG23	3:C:16:ARG:HG2	2.03	0.40
8:H:4:ASP:OD1	8:H:85:ARG:NH1	2.54	0.40
7:G:26:PHE:O	7:G:30:ILE:HG13	2.21	0.40
4:D:83:SER:HA	4:D:89:THR:HG23	2.03	0.40
1:A:1179:A:O2'	1:A:1180:A:OP1	2.34	0.40
1:A:872:A:C8	1:A:874:G:C8	3.09	0.40
1:A:377:G:OP1	16:P:3:LYS:HD3	2.21	0.40
1:A:114:U:O2'	1:A:115:G:H5'	2.21	0.40
21:U:12:LYS:HB3	21:U:22:ARG:HD2	2.03	0.40
7:G:62:PHE:HA	7:G:124:LEU:HD12	2.02	0.40
1:A:559:A:P	5:E:126:ARG:HH22	2.41	0.40
1:A:1418:A:H2'	1:A:1419:G:O4'	2.21	0.40
19:S:51:VAL:O	19:S:58:VAL:HG22	2.22	0.40
1:A:983:A:H5'	1:A:984:C:OP2	2.20	0.40
9:I:39:GLY:O	9:I:40:LEU:HD23	2.22	0.40
4:D:70:ILE:HD12	4:D:70:ILE:HA	1.81	0.40
5:E:127:ASN:HA	5:E:128:PRO:HD3	1.94	0.40
1:A:129:U:O3'	1:A:129(A):G:H3'	2.20	0.40
20:T:91:LEU:HA	20:T:91:LEU:HD23	1.93	0.40
3:C:101:LEU:HD23	3:C:102:ASN:N	2.36	0.40
1:A:1127:G:N2	1:A:1145:C:N3	2.70	0.40
4:D:3:ARG:CZ	4:D:5:ILE:HD11	2.52	0.40
5:E:51:VAL:O	5:E:55:VAL:HG23	2.21	0.40
5:E:72:GLN:O	5:E:75:THR:HG22	2.21	0.40
1:A:1492:A:OP1	12:L:47:LYS:N	2.55	0.40
11:K:120:ARG:HA	11:K:121:PRO:HD3	1.93	0.40
1:A:743:U:H2'	1:A:744:C:H6	1.85	0.40
1:A:41:G:H2'	1:A:42:G:H8	1.86	0.40
1:A:1154:G:H2'	1:A:1155:G:H8	1.86	0.40
19:S:41:VAL:HG23	19:S:43:GLU:HG2	2.02	0.40
1:A:1292:U:OP1	7:G:41:ARG:NH2	2.55	0.40
5:E:5:ASP:OD1	5:E:5:ASP:N	2.54	0.40
6:F:47:ARG:H	6:F:47:ARG:HG2	1.72	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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%)	206 (88%)	27 (12%)	1 (0%)	39	77
3	C	205/207 (99%)	190 (93%)	15 (7%)	0	100	100
4	D	206/208 (99%)	200 (97%)	5 (2%)	1 (0%)	34	73
5	E	149/151 (99%)	145 (97%)	4 (3%)	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%)	133 (98%)	3 (2%)	0	100	100
9	I	125/127 (98%)	114 (91%)	11 (9%)	0	100	100
10	J	97/99 (98%)	80 (82%)	15 (16%)	2 (2%)	9	43
11	K	117/119 (98%)	107 (92%)	10 (8%)	0	100	100
12	L	122/125 (98%)	114 (93%)	7 (6%)	1 (1%)	24	64
13	M	116/118 (98%)	110 (95%)	6 (5%)	0	100	100
14	N	58/60 (97%)	54 (93%)	4 (7%)	0	100	100
15	O	86/88 (98%)	84 (98%)	2 (2%)	0	100	100
16	P	82/84 (98%)	78 (95%)	4 (5%)	0	100	100
17	Q	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
18	R	71/73 (97%)	67 (94%)	4 (6%)	0	100	100
19	S	79/81 (98%)	71 (90%)	7 (9%)	1 (1%)	15	53
20	T	97/99 (98%)	85 (88%)	12 (12%)	0	100	100
21	U	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
All	All	2352/2393 (98%)	2193 (93%)	153 (6%)	6 (0%)	46	81

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	L	28	LYS
19	S	31	ILE
10	J	72	VAL
10	J	34	VAL
2	B	229	VAL
4	D	5	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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%)	179 (92%)	15 (8%)	16	51
3	C	160/161 (99%)	146 (91%)	14 (9%)	12	43
4	D	180/180 (100%)	168 (93%)	12 (7%)	20	58
5	E	115/116 (99%)	104 (90%)	11 (10%)	10	38
6	F	90/90 (100%)	85 (94%)	5 (6%)	26	65
7	G	126/126 (100%)	122 (97%)	4 (3%)	46	80
8	H	119/119 (100%)	110 (92%)	9 (8%)	16	52
9	I	98/98 (100%)	92 (94%)	6 (6%)	23	62
10	J	87/89 (98%)	80 (92%)	7 (8%)	15	49
11	K	90/90 (100%)	85 (94%)	5 (6%)	26	65
12	L	103/103 (100%)	93 (90%)	10 (10%)	10	37
13	M	94/94 (100%)	84 (89%)	10 (11%)	8	33
14	N	49/49 (100%)	45 (92%)	4 (8%)	14	48
15	O	79/79 (100%)	71 (90%)	8 (10%)	9	35
16	P	72/72 (100%)	68 (94%)	4 (6%)	26	65
17	Q	94/94 (100%)	91 (97%)	3 (3%)	46	80
18	R	64/64 (100%)	62 (97%)	2 (3%)	47	80
19	S	71/71 (100%)	62 (87%)	9 (13%)	5	24
20	T	76/76 (100%)	67 (88%)	9 (12%)	6	27
21	U	19/20 (95%)	17 (90%)	2 (10%)	8	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1980/1995 (99%)	1831 (92%)	149 (8%)	17	53

All (149) 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	97	TRP
2	B	114	ARG
2	B	121	LEU
2	B	139	LYS
2	B	144	ARG
2	B	157	ARG
2	B	206	ASP
2	B	208	ILE
2	B	209	ARG
2	B	221	LEU
2	B	236	TYR
3	C	3	ASN
3	C	21	ARG
3	C	27	LYS
3	C	34	LEU
3	C	43	LEU
3	C	79	ARG
3	C	82	GLU
3	C	91	LEU
3	C	95	THR
3	C	126	ARG
3	C	166	GLU
3	C	167	TRP
3	C	196	LEU
3	C	204	LEU
4	D	3	ARG
4	D	4	TYR
4	D	8	VAL
4	D	15	GLU
4	D	24	GLU
4	D	58	LEU
4	D	64	LEU
4	D	70	ILE

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Mol	Chain	Res	Type
4	D	122	ARG
4	D	127	THR
4	D	131	ARG
4	D	135	LEU
5	E	6	PHE
5	E	8	GLU
5	E	12	LEU
5	E	16	THR
5	E	31	LEU
5	E	41	VAL
5	E	64	ARG
5	E	79	GLU
5	E	80	ILE
5	E	89	ILE
5	E	150	ARG
6	F	10	LEU
6	F	43	LEU
6	F	69	GLU
6	F	70	ASP
6	F	86	ARG
7	G	114	ARG
7	G	124	LEU
7	G	149	ARG
7	G	156	TRP
8	H	21	LYS
8	H	24	THR
8	H	25	ASP
8	H	26	VAL
8	H	85	ARG
8	H	91	ARG
8	H	102	ARG
8	H	121	ASP
8	H	133	LEU
9	I	79	LEU
9	I	85	LEU
9	I	102	LEU
9	I	104	ARG
9	I	118	LYS
9	I	121	ARG
10	J	17	ASP
10	J	59	SER
10	J	62	HIS

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Mol	Chain	Res	Type
10	J	71	LEU
10	J	73	ASP
10	J	80	LYS
10	J	83	GLU
11	K	11	LYS
11	K	29	ILE
11	K	48	ILE
11	K	80	VAL
11	K	92	GLU
12	L	20	LYS
12	L	28	LYS
12	L	33	ARG
12	L	39	VAL
12	L	42	THR
12	L	53	ARG
12	L	83	VAL
12	L	100	ILE
12	L	111	LYS
12	L	113	ARG
13	M	44	ARG
13	M	56	LEU
13	M	58	GLU
13	M	64	TRP
13	M	70	LEU
13	M	94	ARG
13	M	98	VAL
13	M	101	GLN
13	M	110	ARG
13	M	115	LYS
14	N	9	LYS
14	N	11	LYS
14	N	22	THR
14	N	33	VAL
15	O	6	GLU
15	O	21	ASP
15	O	34	LEU
15	O	39	LEU
15	O	57	LEU
15	O	70	LEU
15	O	81	LEU
15	O	87	ILE
16	P	1	MET

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Mol	Chain	Res	Type
16	P	2	VAL
16	P	53	VAL
16	P	81	ARG
17	Q	52	LYS
17	Q	74	LEU
17	Q	98	LEU
18	R	25	THR
18	R	86	VAL
19	S	7	LYS
19	S	12	ASP
19	S	15	LEU
19	S	25	LYS
19	S	31	ILE
19	S	36	ARG
19	S	43	GLU
19	S	62	ILE
19	S	81	ARG
20	T	8	ARG
20	T	19	SER
20	T	42	GLN
20	T	48	LYS
20	T	57	ARG
20	T	73	HIS
20	T	74	LYS
20	T	75	ASN
20	T	84	LEU
21	U	6	ARG
21	U	9	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	6	HIS
9	I	73	GLN
13	M	106	ASN
15	O	46	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1507/1522 (99%)	216 (14%)	41 (2%)
22	a	4/6 (66%)	1 (25%)	0
23	b	8/11 (72%)	1 (12%)	0
All	All	1519/1539 (98%)	218 (14%)	41 (2%)

All (218) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
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	59	A
1	A	61	G
1	A	63	C
1	A	101	A
1	A	116	A
1	A	117	G
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	202	U
1	A	204	U
1	A	216	G
1	A	220	G
1	A	231	G
1	A	247	G
1	A	251	G
1	A	267	C
1	A	270	A
1	A	289	G
1	A	301	G
1	A	321	A
1	A	328	C
1	A	329	A

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Mol	Chain	Res	Type
1	A	332	G
1	A	344	A
1	A	351	G
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	411	A
1	A	412	A
1	A	413	G
1	A	421	U
1	A	424	G
1	A	429	U
1	A	433	C
1	A	439	A
1	A	442	C
1	A	443	C
1	A	452	A
1	A	461	C
1	A	484	G
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	531	U
1	A	532	A
1	A	533	A
1	A	545	C
1	A	547	A
1	A	559	A
1	A	560	U

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Mol	Chain	Res	Type
1	A	562	C
1	A	564	C
1	A	572	A
1	A	573	A
1	A	576	G
1	A	577	G
1	A	579	G
1	A	588	G
1	A	607	A
1	A	630	G
1	A	631	G
1	A	632	A
1	A	653	A
1	A	665	A
1	A	687	A
1	A	688	G
1	A	702	A
1	A	703	G
1	A	721	G
1	A	723	U
1	A	731	G
1	A	749	C
1	A	755	G
1	A	774	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	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	859	A
1	A	902	G
1	A	914	A
1	A	926	G
1	A	927	G

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Mol	Chain	Res	Type
1	A	934	C
1	A	935	A
1	A	942	G
1	A	960	U
1	A	966	M2G
1	A	967	5MC
1	A	968	A
1	A	969	A
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	1005	A
1	A	1025	U
1	A	1026	G
1	A	1027	C
1	A	1028	C
1	A	1050	G
1	A	1054	C
1	A	1055	A
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	1152	A
1	A	1159	U

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Mol	Chain	Res	Type
1	A	1171	G
1	A	1180	A
1	A	1181	G
1	A	1183	A
1	A	1196	U
1	A	1197	G
1	A	1201	A
1	A	1202	G
1	A	1212	U
1	A	1213	A
1	A	1214	C
1	A	1225	A
1	A	1227	A
1	A	1238	A
1	A	1257	U
1	A	1258	G
1	A	1270	C
1	A	1280	A
1	A	1281	U
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	1312	G
1	A	1320	C
1	A	1323	G
1	A	1331	G
1	A	1332	A
1	A	1338	G
1	A	1348	U
1	A	1353	G
1	A	1362	C
1	A	1363	A
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

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Mol	Chain	Res	Type
1	A	1446	A
1	A	1487	G
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
22	a	6	U
23	b	33	U

All (41) 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	329	A
1	A	352	C
1	A	372	C
1	A	428	G
1	A	432	A
1	A	484	G
1	A	496	A
1	A	509	A
1	A	532	A
1	A	559	A
1	A	687	A
1	A	701	C
1	A	748	C
1	A	793	U
1	A	812	C
1	A	913	A

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Mol	Chain	Res	Type
1	A	965	A
1	A	992	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	1212	U
1	A	1256	A
1	A	1281	U
1	A	1285	A
1	A	1300	G
1	A	1331	G
1	A	1347	G
1	A	1443	G
1	A	1505	G

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

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	2MG	A	1207	1	18,26,27	1.80	3 (16%)	21,38,41	2.10	2 (9%)
1	5MC	A	1400	1	14,22,23	0.76	0	17,32,35	1.00	1 (5%)
1	4OC	A	1402	1	15,23,24	0.66	0	21,32,35	1.00	2 (9%)
1	5MC	A	1404	1	14,22,23	0.74	0	17,32,35	0.89	0
1	5MC	A	1407	1	14,22,23	0.86	1 (7%)	17,32,35	1.09	2 (11%)
1	UR3	A	1498	1	13,22,23	0.70	0	18,32,35	1.21	1 (5%)
1	MA6	A	1518	1	18,26,27	0.78	1 (5%)	15,38,41	0.99	2 (13%)
1	MA6	A	1519	1	18,26,27	0.69	0	15,38,41	1.12	3 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	A	1540	1	15,21,22	1.33	3 (20%)	16,30,33	2.46	4 (25%)
1	PSU	A	1541	1,25	15,21,22	1.32	3 (20%)	16,30,33	2.40	3 (18%)
1	PSU	A	516	1,25	15,21,22	1.41	3 (20%)	16,30,33	2.56	3 (18%)
1	7MG	A	527	1	20,26,27	2.49	6 (30%)	23,39,42	2.03	5 (21%)
1	M2G	A	966	1	18,27,28	1.76	4 (22%)	22,40,43	2.18	4 (18%)
1	5MC	A	967	1	14,22,23	0.84	0	17,32,35	0.89	1 (5%)
12	0TD	L	92	12	4,9,10	1.02	0	4,11,13	2.45	3 (75%)
22	6MZ	a	2	22	17,25,26	1.21	2 (11%)	15,36,39	0.79	1 (6%)
23	70U	b	34	22,23	17,26,27	2.87	6 (35%)	21,37,40	2.28	3 (14%)
23	12A	b	37	25,23	25,36,37	2.83	4 (16%)	29,52,55	2.65	8 (27%)
23	PSU	b	39	23	15,21,22	1.32	3 (20%)	16,30,33	2.51	4 (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	2MG	A	1207	1	-	0/5/27/28	0/3/3/3
1	5MC	A	1400	1	-	0/3/25/26	0/2/2/2
1	4OC	A	1402	1	-	0/7/29/30	0/2/2/2
1	5MC	A	1404	1	-	0/3/25/26	0/2/2/2
1	5MC	A	1407	1	-	0/3/25/26	0/2/2/2
1	UR3	A	1498	1	-	0/3/25/26	0/2/2/2
1	MA6	A	1518	1	-	0/7/29/30	0/3/3/3
1	MA6	A	1519	1	-	0/7/29/30	0/3/3/3
1	PSU	A	1540	1	-	0/7/25/26	0/2/2/2
1	PSU	A	1541	1,25	-	0/7/25/26	0/2/2/2
1	PSU	A	516	1,25	-	0/7/25/26	0/2/2/2
1	7MG	A	527	1	-	0/7/37/38	0/3/3/3
1	M2G	A	966	1	-	0/7/29/30	0/3/3/3
1	5MC	A	967	1	-	0/3/25/26	0/2/2/2
12	0TD	L	92	12	-	0/2/12/14	0/0/0/0
22	6MZ	a	2	22	-	0/5/27/28	0/3/3/3
23	70U	b	34	22,23	-	0/9/31/32	0/2/2/2
23	12A	b	37	25,23	-	0/17/43/44	0/3/3/3
23	PSU	b	39	23	-	0/7/25/26	0/2/2/2

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	7MG	C8-N9	-7.81	1.34	1.45
23	b	34	70U	O9-C9	-3.18	1.37	1.45
1	A	516	PSU	C2-N1	-3.00	1.31	1.38
1	A	516	PSU	C2-N3	-2.96	1.32	1.38
23	b	39	PSU	C2-N1	-2.90	1.32	1.38
1	A	1540	PSU	C2-N3	-2.86	1.32	1.38
1	A	1540	PSU	C2-N1	-2.83	1.32	1.38
1	A	1541	PSU	C2-N3	-2.81	1.32	1.38
23	b	39	PSU	C2-N3	-2.77	1.32	1.38
1	A	1541	PSU	C2-N1	-2.72	1.32	1.38
1	A	527	7MG	CM7-N7	-2.62	1.41	1.46
1	A	516	PSU	O4-C4	-2.33	1.18	1.24
1	A	1540	PSU	O4-C4	-2.26	1.18	1.24
1	A	1541	PSU	O4-C4	-2.25	1.18	1.24
23	b	39	PSU	O4-C4	-2.23	1.18	1.24
1	A	1407	5MC	C4-N3	-2.20	1.31	1.35
1	A	527	7MG	C8-N7	-2.05	1.34	1.43
1	A	1518	MA6	C6-N1	2.03	1.36	1.34
22	a	2	6MZ	C6-N1	2.21	1.37	1.34
1	A	1207	2MG	C4-N3	2.22	1.39	1.35
1	A	527	7MG	C6-N1	2.44	1.37	1.33
23	b	34	70U	C6-C5	2.63	1.42	1.36
1	A	966	M2G	C4-N3	2.63	1.39	1.35
1	A	966	M2G	C2-N1	3.07	1.39	1.34
22	a	2	6MZ	C6-N6	3.15	1.40	1.35
1	A	966	M2G	C2-N2	3.33	1.40	1.34
23	b	34	70U	O9-C8	3.56	1.44	1.32
23	b	34	70U	C5M-C5	3.87	1.57	1.51
1	A	527	7MG	C2-N2	4.26	1.43	1.34
1	A	527	7MG	C4-N3	4.49	1.40	1.34
1	A	1207	2MG	C2-N2	4.75	1.39	1.34
23	b	37	12A	CC-N	4.91	1.49	1.35
23	b	37	12A	CC-N6	4.96	1.46	1.37
1	A	966	M2G	C6-N1	5.04	1.42	1.33
1	A	1207	2MG	C6-N1	5.15	1.42	1.33
23	b	37	12A	C6-N6	5.77	1.47	1.36
23	b	34	70U	O4-C4	6.21	1.40	1.24
23	b	34	70U	C2-S2	7.21	1.81	1.66
23	b	37	12A	C2-S2	10.31	1.84	1.75

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	966	M2G	C5-C6-N1	-8.68	112.18	123.52
1	A	1207	2MG	C5-C6-N1	-7.81	113.32	123.52
23	b	34	70U	C5-C4-N3	-6.64	119.23	125.19
1	A	527	7MG	C5-C4-N3	-6.13	120.49	126.74
23	b	37	12A	C6-N6-CC	-5.08	123.47	130.33
23	b	37	12A	OO-CC-N6	-3.77	117.83	123.59
1	A	1541	PSU	C5-C6-N1	-3.65	119.28	124.38
1	A	1540	PSU	C5-C6-N1	-3.61	119.34	124.38
23	b	39	PSU	C5-C6-N1	-3.49	119.51	124.38
1	A	516	PSU	C5-C6-N1	-3.07	120.10	124.38
23	b	37	12A	C-CA-N	-2.97	107.69	113.40
12	L	92	0TD	C-CA-N	-2.68	104.05	109.95
12	L	92	0TD	CB-CA-N	-2.66	104.51	109.83
1	A	527	7MG	C5-C6-N1	-2.65	119.45	123.39
23	b	39	PSU	C5-C1'-C2'	-2.63	110.97	115.44
12	L	92	0TD	CSB-SB-CB	-2.48	96.80	101.44
23	b	37	12A	N3-C2-N1	-2.48	122.27	126.84
1	A	966	M2G	N1-C2-N2	-2.35	114.57	117.14
1	A	1519	MA6	C1'-N9-C4	-2.32	124.21	126.81
1	A	527	7MG	N1-C2-N3	-2.13	122.03	125.51
1	A	1402	4OC	C6-C5-C4	-2.09	116.60	117.42
1	A	966	M2G	C2-N3-C4	-2.02	112.77	114.99
1	A	1540	PSU	C5-C1'-C2'	-2.02	112.00	115.44
1	A	1407	5MC	N4-C4-N3	-2.02	113.96	116.92
1	A	967	5MC	CM5-C5-C6	2.00	122.69	118.63
1	A	1518	MA6	N3-C2-N1	2.01	130.45	128.87
1	A	1519	MA6	N3-C2-N1	2.08	130.50	128.87
1	A	1519	MA6	C2-N1-C6	2.12	116.64	111.64
1	A	1518	MA6	C2-N1-C6	2.13	116.66	111.64
22	a	2	6MZ	N3-C2-N1	2.20	130.60	128.87
1	A	1400	5MC	CM5-C5-C6	2.27	123.22	118.63
1	A	1402	4OC	C2-N3-C4	2.28	118.33	115.43
1	A	1407	5MC	CM5-C5-C6	2.30	123.29	118.63
1	A	1498	UR3	C6-C5-C4	2.61	122.14	117.30
23	b	37	12A	C2-N1-C6	2.68	120.49	113.13
1	A	966	M2G	N3-C2-N2	2.76	120.19	117.14
23	b	39	PSU	O4'-C1'-C2'	2.86	107.78	104.69
1	A	516	PSU	O4'-C1'-C2'	2.89	107.81	104.69
1	A	1540	PSU	O4'-C1'-C2'	3.00	107.93	104.69
1	A	1541	PSU	O4'-C1'-C2'	3.02	107.96	104.69
23	b	37	12A	CA-N-CC	3.50	128.00	120.82
23	b	37	12A	N6-CC-N	3.77	119.90	113.75
1	A	527	7MG	C6-N1-C2	3.83	120.37	115.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	527	7MG	N3-C4-N9	4.09	132.27	126.98
1	A	1207	2MG	C6-N1-C2	4.61	121.84	115.24
23	b	34	70U	C2-N3-C4	4.66	121.08	115.89
23	b	34	70U	O9-C8-C5M	5.95	119.63	111.36
1	A	1541	PSU	C4-N3-C2	7.97	121.81	115.16
1	A	1540	PSU	C4-N3-C2	8.15	121.96	115.16
23	b	39	PSU	C4-N3-C2	8.32	122.10	115.16
1	A	516	PSU	C4-N3-C2	9.00	122.67	115.16
23	b	37	12A	C2M-S2-C2	10.15	109.47	102.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 7 short contacts:

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 371 ligands modelled in this entry, 365 are monoatomic - leaving 6 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
24	PAR	A	1601	-	45,45,45	1.21	4 (8%)	60,67,67	1.62	9 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	PAR	A	1602	-	45,45,45	1.34	6 (13%)	60,67,67	1.68	11 (18%)
24	PAR	A	1603	-	45,45,45	1.34	5 (11%)	60,67,67	1.65	11 (18%)
24	PAR	A	1604	-	45,45,45	1.29	7 (15%)	60,67,67	1.62	11 (18%)
24	PAR	A	1605	-	45,45,45	1.24	6 (13%)	60,67,67	1.62	10 (16%)
24	PAR	A	1606	-	45,45,45	1.45	6 (13%)	60,67,67	1.64	10 (16%)

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
24	PAR	A	1601	-	-	0/18/94/94	0/4/4/4
24	PAR	A	1602	-	-	0/18/94/94	0/4/4/4
24	PAR	A	1603	-	-	0/18/94/94	1/4/4/4
24	PAR	A	1604	-	-	0/18/94/94	1/4/4/4
24	PAR	A	1605	-	-	0/18/94/94	1/4/4/4
24	PAR	A	1606	-	-	0/18/94/94	0/4/4/4

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1601	PAR	C62-C52	2.03	1.58	1.52
24	A	1601	PAR	C33-C43	2.06	1.58	1.52
24	A	1604	PAR	C33-C43	2.15	1.58	1.52
24	A	1605	PAR	C33-C43	2.15	1.58	1.52
24	A	1603	PAR	C14-C24	2.25	1.56	1.52
24	A	1605	PAR	C14-C24	2.25	1.56	1.52
24	A	1604	PAR	C14-C24	2.26	1.56	1.52
24	A	1604	PAR	C31-C21	2.31	1.56	1.53
24	A	1603	PAR	C64-C54	2.34	1.55	1.52
24	A	1602	PAR	C64-C54	2.40	1.55	1.52
24	A	1605	PAR	C64-C54	2.43	1.55	1.52
24	A	1605	PAR	C13-C23	2.44	1.56	1.53
24	A	1604	PAR	C64-C54	2.50	1.55	1.52
24	A	1606	PAR	C64-C54	2.51	1.55	1.52
24	A	1602	PAR	C11-C21	2.56	1.57	1.52
24	A	1606	PAR	C62-C52	2.57	1.59	1.52
24	A	1602	PAR	C34-C24	2.58	1.56	1.53
24	A	1604	PAR	C13-C23	2.60	1.56	1.53
24	A	1602	PAR	C31-C21	2.60	1.56	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1604	PAR	C34-C24	2.61	1.56	1.53
24	A	1602	PAR	C14-C24	2.62	1.57	1.52
24	A	1606	PAR	C31-C21	2.67	1.57	1.53
24	A	1605	PAR	C34-C24	2.69	1.57	1.53
24	A	1606	PAR	C34-C24	2.69	1.57	1.53
24	A	1603	PAR	O43-C13	2.78	1.46	1.41
24	A	1601	PAR	C64-C54	2.87	1.56	1.52
24	A	1605	PAR	C52-C42	2.92	1.58	1.52
24	A	1604	PAR	C52-C42	3.10	1.58	1.52
24	A	1606	PAR	C13-C23	3.15	1.57	1.53
24	A	1601	PAR	C52-C42	3.36	1.59	1.52
24	A	1603	PAR	C52-C42	3.36	1.59	1.52
24	A	1602	PAR	C13-C23	3.73	1.57	1.53
24	A	1606	PAR	C52-C42	4.12	1.61	1.52
24	A	1603	PAR	C13-C23	4.39	1.58	1.53

All (62) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1601	PAR	C34-C24-N24	-3.43	104.55	110.72
24	A	1605	PAR	C34-C24-N24	-3.37	104.67	110.72
24	A	1603	PAR	C34-C24-N24	-3.34	104.71	110.72
24	A	1604	PAR	C34-C24-N24	-3.30	104.79	110.72
24	A	1606	PAR	C34-C24-N24	-3.29	104.80	110.72
24	A	1602	PAR	C34-C24-N24	-3.27	104.83	110.72
24	A	1601	PAR	O34-C34-C44	-3.11	103.34	110.36
24	A	1603	PAR	O34-C34-C44	-3.06	103.45	110.36
24	A	1606	PAR	O34-C34-C44	-3.03	103.53	110.36
24	A	1602	PAR	O34-C34-C44	-3.01	103.56	110.36
24	A	1604	PAR	O34-C34-C44	-3.01	103.57	110.36
24	A	1605	PAR	O34-C34-C44	-2.99	103.63	110.36
24	A	1603	PAR	C14-O33-C33	-2.66	110.93	118.00
24	A	1604	PAR	C13-O52-C52	-2.59	111.11	118.00
24	A	1606	PAR	C14-O33-C33	-2.57	111.16	118.00
24	A	1602	PAR	C14-O33-C33	-2.52	111.30	118.00
24	A	1601	PAR	C14-O33-C33	-2.50	111.35	118.00
24	A	1605	PAR	C14-O33-C33	-2.47	111.42	118.00
24	A	1605	PAR	C13-O52-C52	-2.43	111.54	118.00
24	A	1604	PAR	C14-O33-C33	-2.43	111.54	118.00
24	A	1602	PAR	C13-O52-C52	-2.33	111.80	118.00
24	A	1603	PAR	C13-O52-C52	-2.32	111.84	118.00
24	A	1601	PAR	C13-O52-C52	-2.23	112.07	118.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1606	PAR	C13-O52-C52	-2.10	112.41	118.00
24	A	1605	PAR	O33-C14-O54	-2.02	105.42	110.69
24	A	1606	PAR	O54-C54-C44	2.00	113.49	109.67
24	A	1604	PAR	O52-C52-C42	2.01	112.71	107.48
24	A	1604	PAR	O54-C54-C44	2.04	113.56	109.67
24	A	1603	PAR	C11-O51-C51	2.04	117.75	113.74
24	A	1603	PAR	C22-C32-C42	2.04	114.41	109.31
24	A	1606	PAR	O51-C51-C61	2.19	112.05	106.38
24	A	1601	PAR	O51-C51-C61	2.19	112.06	106.38
24	A	1602	PAR	O51-C51-C61	2.21	112.10	106.38
24	A	1604	PAR	O51-C51-C61	2.22	112.13	106.38
24	A	1602	PAR	C11-O51-C51	2.28	118.22	113.74
24	A	1605	PAR	O51-C51-C61	2.31	112.38	106.38
24	A	1603	PAR	O51-C51-C61	2.33	112.42	106.38
24	A	1602	PAR	C22-C12-C62	2.55	114.10	110.14
24	A	1605	PAR	C13-C23-C33	2.62	105.31	102.05
24	A	1601	PAR	C13-C23-C33	2.63	105.32	102.05
24	A	1604	PAR	O11-C11-O51	2.78	117.94	110.69
24	A	1606	PAR	O11-C11-O51	2.84	118.11	110.69
24	A	1604	PAR	C13-C23-C33	2.89	105.65	102.05
24	A	1603	PAR	O11-C11-O51	2.93	118.33	110.69
24	A	1605	PAR	O11-C11-O51	2.94	118.36	110.69
24	A	1601	PAR	O11-C11-O51	2.95	118.37	110.69
24	A	1602	PAR	O11-C11-O51	3.16	118.94	110.69
24	A	1601	PAR	O52-C13-C23	3.30	114.72	107.91
24	A	1606	PAR	C13-C23-C33	3.33	106.20	102.05
24	A	1603	PAR	O52-C13-C23	3.42	114.97	107.91
24	A	1606	PAR	O52-C13-C23	3.49	115.11	107.91
24	A	1605	PAR	O52-C13-C23	3.53	115.19	107.91
24	A	1602	PAR	O52-C13-C23	3.59	115.31	107.91
24	A	1602	PAR	C13-C23-C33	3.60	106.53	102.05
24	A	1603	PAR	C13-C23-C33	3.60	106.54	102.05
24	A	1604	PAR	O52-C13-C23	3.62	115.37	107.91
24	A	1605	PAR	O33-C14-C24	5.65	118.40	108.16
24	A	1604	PAR	O33-C14-C24	5.76	118.61	108.16
24	A	1601	PAR	O33-C14-C24	5.84	118.75	108.16
24	A	1603	PAR	O33-C14-C24	5.85	118.77	108.16
24	A	1602	PAR	O33-C14-C24	5.88	118.81	108.16
24	A	1606	PAR	O33-C14-C24	5.89	118.84	108.16

There are no chirality outliers.

There are no torsion outliers.

All (3) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	A	1603	PAR	C12-C22-C32-C42-C52-C62
24	A	1605	PAR	C12-C22-C32-C42-C52-C62
24	A	1604	PAR	C12-C22-C32-C42-C52-C62

6 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	A	1601	PAR	1	0
24	A	1602	PAR	1	0
24	A	1603	PAR	4	0
24	A	1604	PAR	3	0
24	A	1605	PAR	2	0
24	A	1606	PAR	2	0

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, 95th 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%)	-0.16	14 (0%) 85 86	40, 64, 136, 255	0
2	B	236/236 (100%)	-0.05	7 (2%) 54 54	45, 103, 182, 210	0
3	C	207/207 (100%)	-0.01	3 (1%) 78 79	58, 100, 148, 178	0
4	D	208/208 (100%)	-0.17	5 (2%) 62 61	45, 69, 120, 148	0
5	E	151/151 (100%)	-0.35	0 100 100	41, 59, 89, 176	0
6	F	101/101 (100%)	-0.18	1 (0%) 84 85	63, 95, 125, 169	0
7	G	155/155 (100%)	-0.21	4 (2%) 59 59	55, 80, 144, 176	0
8	H	138/138 (100%)	-0.43	0 100 100	40, 57, 83, 124	0
9	I	127/127 (100%)	-0.03	0 100 100	66, 97, 143, 181	0
10	J	99/99 (100%)	0.52	10 (10%) 9 9	44, 124, 198, 239	0
11	K	119/119 (100%)	0.07	4 (3%) 49 48	46, 65, 108, 199	0
12	L	124/125 (99%)	-0.13	5 (4%) 42 41	33, 63, 113, 247	0
13	M	118/118 (100%)	-0.08	3 (2%) 61 60	55, 85, 122, 219	0
14	N	60/60 (100%)	-0.03	2 (3%) 50 49	64, 82, 130, 187	0
15	O	88/88 (100%)	-0.06	1 (1%) 82 83	50, 73, 120, 190	0
16	P	84/84 (100%)	-0.35	0 100 100	42, 58, 82, 148	0
17	Q	99/99 (100%)	-0.27	0 100 100	41, 58, 96, 128	0
18	R	73/73 (100%)	-0.13	3 (4%) 41 39	48, 77, 150, 217	0
19	S	81/81 (100%)	0.14	1 (1%) 81 81	38, 105, 172, 212	0
20	T	99/99 (100%)	-0.16	2 (2%) 68 67	47, 62, 102, 173	0
21	U	25/25 (100%)	1.04	4 (16%) 3 2	53, 82, 113, 147	0
22	a	5/6 (83%)	0.68	1 (20%) 1 1	76, 81, 103, 113	0
23	b	8/11 (72%)	1.06	2 (25%) 1 1	82, 112, 151, 188	0
All	All	3903/3932 (99%)	-0.12	72 (1%) 71 70	33, 74, 143, 255	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
11	K	129	SER	11.3
11	K	128	ALA	10.1
12	L	129	ALA	6.7
21	U	26	LYS	6.5
15	O	89	GLY	4.6
1	A	1129	C	4.3
1	A	216	G	3.9
1	A	217	C	3.9
12	L	128	ALA	3.7
23	b	32	C	3.6
7	G	80	VAL	3.6
2	B	131	PRO	3.5
14	N	12	ARG	3.4
11	K	127	LYS	3.3
7	G	82	GLY	3.3
20	T	9	ASN	3.2
6	F	101	ALA	3.2
20	T	100	ILE	3.2
2	B	134	GLU	3.0
3	C	87	LEU	2.9
2	B	136	VAL	2.9
12	L	19	ARG	2.9
2	B	133	LYS	2.9
7	G	156	TRP	2.7
10	J	5	ARG	2.7
21	U	18	TYR	2.6
4	D	32	ALA	2.6
4	D	179	GLU	2.6
10	J	34	VAL	2.6
21	U	25	LYS	2.6
10	J	90	LEU	2.6
1	A	1533	C	2.6
4	D	23	GLY	2.6
1	A	1037	C	2.6
10	J	73	ASP	2.5
2	B	132	LYS	2.5
13	M	119	GLY	2.5
1	A	218	C	2.4
12	L	127	GLU	2.4
18	R	85	LEU	2.4
11	K	126	ARG	2.4
3	C	143	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
7	G	81	GLY	2.4
13	M	8	GLU	2.4
1	A	202	U	2.3
1	A	1539	C	2.3
18	R	17	SER	2.3
10	J	72	VAL	2.3
22	a	6	U	2.3
12	L	112	ASP	2.2
21	U	24	ARG	2.2
1	A	1038	C	2.2
19	S	82	GLY	2.2
10	J	74	ILE	2.2
3	C	154	SER	2.2
1	A	461	C	2.2
1	A	994	A	2.2
18	R	16	PRO	2.1
23	b	33	U	2.1
10	J	87	THR	2.1
1	A	1036	G	2.1
4	D	86	LYS	2.1
10	J	88	LEU	2.1
1	A	1138	G	2.1
10	J	89	ASP	2.1
10	J	100	THR	2.1
14	N	13	THR	2.1
2	B	127	ILE	2.0
13	M	2	ALA	2.0
1	A	82	U	2.0
4	D	34	GLU	2.0
2	B	206	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
1	M2G	A	966	25/26	0.95	0.21	-	56,59,63,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
1	PSU	A	1540	20/21	0.91	0.41	-	132,143,152,154	0
1	UR3	A	1498	21/22	0.96	0.19	-	45,46,48,52	0
1	4OC	A	1402	22/23	0.96	0.15	-	48,50,56,59	0
1	7MG	A	527	24/25	0.97	0.16	-	51,52,58,63	0
23	12A	b	37	34/35	0.93	0.26	-	72,81,96,101	0
1	5MC	A	1407	21/22	0.98	0.17	-	51,52,53,54	0
12	0TD	L	92	10/11	0.92	0.26	-	52,59,80,83	0
1	5MC	A	967	21/22	0.97	0.12	-	61,64,68,69	0
1	PSU	A	1541	20/21	0.91	0.26	-	125,131,139,142	0
22	6MZ	a	2	23/24	0.95	0.20	-	71,75,78,80	0
1	MA6	A	1518	24/25	0.97	0.19	-	46,47,48,48	0
1	5MC	A	1404	21/22	0.98	0.16	-	46,47,49,49	0
23	PSU	b	39	20/21	0.89	0.29	-	97,110,118,122	0
1	2MG	A	1207	24/25	0.95	0.17	-	82,87,93,95	0
1	MA6	A	1519	24/25	0.97	0.19	-	45,46,46,46	0
23	70U	b	34	25/26	0.91	0.22	-	80,98,116,126	0
1	5MC	A	1400	21/22	0.96	0.23	-	51,52,60,64	0
1	PSU	A	516	20/21	0.93	0.16	-	70,75,80,80	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
25	MG	A	1637	1/1	0.90	0.63	29.56	68,68,68,68	0
25	MG	A	1667	1/1	0.90	0.44	28.76	53,53,53,53	0
25	MG	A	1781	1/1	0.94	0.54	23.14	67,67,67,67	0
25	MG	A	1772	1/1	0.80	0.85	20.50	64,64,64,64	0
25	MG	A	1775	1/1	0.89	0.39	19.60	51,51,51,51	0
25	MG	A	1879	1/1	0.68	0.44	17.68	42,42,42,42	0
25	MG	A	1727	1/1	0.95	0.36	16.21	30,30,30,30	0
24	PAR	A	1602	42/42	0.78	0.42	15.18	134,165,193,223	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
25	MG	A	1793	1/1	0.82	0.42	14.06	65,65,65,65	0
25	MG	A	1875	1/1	0.96	0.33	13.99	59,59,59,59	0
25	MG	A	1770	1/1	0.90	0.34	13.59	52,52,52,52	0
25	MG	A	1630	1/1	0.98	0.29	11.83	19,19,19,19	0
25	MG	A	1767	1/1	0.92	0.35	11.73	41,41,41,41	0
25	MG	A	1613	1/1	0.86	0.30	7.20	55,55,55,55	0
24	PAR	A	1603	42/42	0.89	0.30	6.51	75,90,109,113	0
25	MG	A	1752	1/1	0.88	0.38	5.65	66,66,66,66	0
24	PAR	A	1606	42/42	0.88	0.34	4.94	102,106,112,114	0
25	MG	A	1717	1/1	0.83	0.30	4.82	75,75,75,75	0
25	MG	A	1746	1/1	0.82	0.24	4.63	21,21,21,21	0
25	MG	C	301	1/1	0.35	0.39	4.55	78,78,78,78	0
26	K	A	1912	1/1	0.84	0.24	4.29	109,109,109,109	0
25	MG	A	1818	1/1	0.97	0.30	3.88	45,45,45,45	0
25	MG	A	1624	1/1	0.98	0.25	3.20	58,58,58,58	0
25	MG	A	1861	1/1	0.91	0.20	3.19	34,34,34,34	0
25	MG	A	1878	1/1	0.92	0.25	3.12	46,46,46,46	0
25	MG	A	1702	1/1	0.98	0.30	2.96	39,39,39,39	0
25	MG	A	1801	1/1	0.89	0.23	2.50	57,57,57,57	0
25	MG	A	1714	1/1	0.98	0.25	2.41	69,69,69,69	0
25	MG	A	1857	1/1	0.86	0.34	2.23	41,41,41,41	0
24	PAR	A	1605	42/42	0.81	0.31	2.06	132,139,144,144	0
24	PAR	A	1601	42/42	0.94	0.21	1.75	36,49,76,84	0
24	PAR	A	1604	42/42	0.87	0.26	1.60	75,106,159,170	0
25	MG	A	1844	1/1	0.93	0.20	1.59	45,45,45,45	0
25	MG	P	104	1/1	0.88	0.25	1.47	63,63,63,63	0
25	MG	A	1762	1/1	0.88	0.21	1.43	49,49,49,49	0
25	MG	A	1645	1/1	0.89	0.18	1.32	133,133,133,133	0
25	MG	A	1627	1/1	0.99	0.26	0.98	67,67,67,67	0
25	MG	A	1780	1/1	0.95	0.17	0.97	46,46,46,46	0
25	MG	A	1945	1/1	0.90	0.28	0.96	68,68,68,68	0
25	MG	A	1854	1/1	0.85	0.22	0.67	62,62,62,62	0
25	MG	A	1723	1/1	0.94	0.19	0.58	33,33,33,33	0
25	MG	A	1711	1/1	0.88	0.17	0.56	33,33,33,33	0
27	ZN	D	301	1/1	0.98	0.33	0.50	47,47,47,47	0
25	MG	Q	201	1/1	0.91	0.19	0.21	63,63,63,63	0
25	MG	A	1617	1/1	0.96	0.17	0.02	24,24,24,24	0
25	MG	A	1706	1/1	0.92	0.18	-0.30	75,75,75,75	0
25	MG	A	1715	1/1	0.92	0.16	-0.31	44,44,44,44	0
25	MG	A	1623	1/1	0.84	0.15	-0.37	29,29,29,29	0
25	MG	Q	202	1/1	0.64	0.16	-0.44	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
25	MG	A	1719	1/1	0.97	0.14	-0.47	175,175,175,175	0
25	MG	A	1769	1/1	0.94	0.16	-0.47	42,42,42,42	0
25	MG	A	1622	1/1	0.94	0.15	-0.56	58,58,58,58	0
25	MG	A	1843	1/1	0.96	0.14	-0.58	50,50,50,50	0
25	MG	A	1740	1/1	0.90	0.17	-0.62	55,55,55,55	0
25	MG	A	1713	1/1	0.91	0.20	-0.70	62,62,62,62	0
25	MG	A	1763	1/1	0.86	0.16	-0.76	32,32,32,32	0
25	MG	A	1698	1/1	0.96	0.13	-0.78	193,193,193,193	0
25	MG	A	1811	1/1	0.94	0.12	-1.02	74,74,74,74	0
25	MG	T	201	1/1	0.90	0.14	-1.25	51,51,51,51	0
25	MG	A	1792	1/1	0.96	0.13	-1.29	45,45,45,45	0
25	MG	A	1657	1/1	0.87	0.15	-1.36	17,17,17,17	0
25	MG	D	302	1/1	0.95	0.07	-1.39	54,54,54,54	0
25	MG	A	1654	1/1	0.98	0.12	-1.52	70,70,70,70	0
25	MG	A	1658	1/1	0.89	0.13	-1.55	36,36,36,36	0
25	MG	A	1812	1/1	0.95	0.11	-1.90	56,56,56,56	0
25	MG	A	1651	1/1	0.92	0.13	-1.96	30,30,30,30	0
25	MG	A	1944	1/1	0.96	0.14	-2.01	47,47,47,47	0
27	ZN	N	101	1/1	0.96	0.12	-2.05	71,71,71,71	0
25	MG	A	1638	1/1	0.95	0.12	-2.51	45,45,45,45	0
25	MG	S	101	1/1	0.99	0.09	-2.51	37,37,37,37	0
25	MG	A	1669	1/1	0.94	0.09	-3.83	32,32,32,32	0
25	MG	A	1724	1/1	0.90	0.12	-4.87	37,37,37,37	0
25	MG	A	1664	1/1	0.94	0.11	-5.63	49,49,49,49	0
25	MG	A	1628	1/1	0.98	0.12	-6.18	45,45,45,45	0
26	K	A	1940	1/1	0.91	0.22	-	115,115,115,115	0
25	MG	A	1863	1/1	0.69	0.30	-	67,67,67,67	0
25	MG	S	102	1/1	0.94	0.16	-	51,51,51,51	0
25	MG	A	1725	1/1	0.84	0.35	-	49,49,49,49	0
25	MG	A	1827	1/1	0.83	0.41	-	65,65,65,65	0
25	MG	G	202	1/1	0.93	0.13	-	68,68,68,68	0
25	MG	A	1864	1/1	0.93	0.24	-	62,62,62,62	0
25	MG	A	1722	1/1	0.85	0.20	-	53,53,53,53	0
25	MG	A	1790	1/1	0.92	0.33	-	81,81,81,81	0
25	MG	A	1634	1/1	0.94	0.10	-	113,113,113,113	0
25	MG	A	1653	1/1	0.93	0.20	-	138,138,138,138	0
26	K	A	1938	1/1	0.80	0.24	-	119,119,119,119	0
25	MG	A	1670	1/1	0.91	0.25	-	53,53,53,53	0
26	K	A	1906	1/1	0.91	0.19	-	111,111,111,111	0
25	MG	A	1748	1/1	0.83	0.22	-	53,53,53,53	0
25	MG	A	1778	1/1	0.97	0.16	-	48,48,48,48	0
25	MG	A	1718	1/1	0.71	0.71	-	212,212,212,212	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
25	MG	A	1640	1/1	0.81	0.24	-	128,128,128,128	0
26	K	A	1907	1/1	0.54	0.20	-	118,118,118,118	0
25	MG	A	1621	1/1	0.96	0.12	-	51,51,51,51	0
25	MG	A	1659	1/1	0.96	0.13	-	95,95,95,95	0
25	MG	A	1616	1/1	0.82	0.31	-	56,56,56,56	0
25	MG	A	1819	1/1	0.89	0.22	-	69,69,69,69	0
26	K	A	1935	1/1	0.91	0.35	-	112,112,112,112	0
25	MG	A	1694	1/1	0.97	0.32	-	81,81,81,81	0
25	MG	A	1646	1/1	0.98	0.10	-	30,30,30,30	0
25	MG	A	1887	1/1	0.97	0.15	-	65,65,65,65	0
26	K	A	1909	1/1	0.79	0.32	-	97,97,97,97	0
25	MG	A	1682	1/1	0.92	0.12	-	80,80,80,80	0
25	MG	A	1787	1/1	0.83	0.30	-	66,66,66,66	0
25	MG	A	1821	1/1	0.82	0.14	-	208,208,208,208	0
26	K	A	1914	1/1	0.82	0.29	-	140,140,140,140	0
25	MG	A	1642	1/1	0.97	0.18	-	50,50,50,50	0
25	MG	P	101	1/1	0.98	0.16	-	36,36,36,36	0
25	MG	A	1675	1/1	0.96	0.13	-	78,78,78,78	0
25	MG	A	1703	1/1	0.94	0.26	-	48,48,48,48	0
25	MG	A	1815	1/1	0.77	0.32	-	57,57,57,57	0
25	MG	A	1839	1/1	0.87	0.30	-	58,58,58,58	0
25	MG	A	1828	1/1	0.74	0.41	-	60,60,60,60	0
26	K	A	1925	1/1	0.56	0.32	-	112,112,112,112	0
26	K	A	1929	1/1	0.73	0.26	-	122,122,122,122	0
26	K	A	1923	1/1	0.60	0.47	-	121,121,121,121	0
25	MG	A	1639	1/1	0.78	0.55	-	59,59,59,59	0
25	MG	A	1611	1/1	0.83	0.23	-	63,63,63,63	0
25	MG	A	1693	1/1	0.86	0.24	-	80,80,80,80	0
25	MG	A	1869	1/1	0.94	0.17	-	66,66,66,66	0
25	MG	A	1663	1/1	0.70	0.42	-	60,60,60,60	0
25	MG	A	1799	1/1	0.91	0.46	-	44,44,44,44	0
25	MG	A	1692	1/1	0.98	0.12	-	51,51,51,51	0
25	MG	A	1701	1/1	0.89	0.25	-	67,67,67,67	0
25	MG	A	1662	1/1	0.97	0.21	-	102,102,102,102	0
25	MG	A	1684	1/1	0.95	0.19	-	91,91,91,91	0
25	MG	A	1816	1/1	0.91	0.22	-	52,52,52,52	0
25	MG	A	1649	1/1	0.97	0.13	-	36,36,36,36	0
25	MG	A	1730	1/1	0.96	0.13	-	65,65,65,65	0
26	K	A	1920	1/1	0.72	0.32	-	124,124,124,124	0
26	K	A	1908	1/1	0.84	0.23	-	107,107,107,107	0
26	K	A	1924	1/1	0.95	0.15	-	84,84,84,84	0
25	MG	A	1683	1/1	0.94	0.15	-	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
25	MG	A	1771	1/1	0.87	0.23	-	56,56,56,56	0
25	MG	A	1756	1/1	0.80	0.21	-	70,70,70,70	0
26	K	A	1936	1/1	0.65	0.52	-	118,118,118,118	0
25	MG	A	1750	1/1	0.56	0.23	-	83,83,83,83	0
25	MG	A	1834	1/1	0.83	0.30	-	55,55,55,55	0
25	MG	A	1802	1/1	0.93	0.19	-	146,146,146,146	0
25	MG	A	1648	1/1	0.94	0.11	-	57,57,57,57	0
26	K	A	1941	1/1	0.88	0.40	-	110,110,110,110	0
25	MG	A	1733	1/1	0.96	0.12	-	36,36,36,36	0
25	MG	A	1761	1/1	0.84	0.24	-	66,66,66,66	0
25	MG	A	1696	1/1	0.95	0.14	-	101,101,101,101	0
25	MG	A	1842	1/1	0.94	0.22	-	63,63,63,63	0
25	MG	A	1647	1/1	0.94	0.14	-	73,73,73,73	0
25	MG	A	1708	1/1	0.92	0.13	-	87,87,87,87	0
25	MG	L	201	1/1	0.96	0.15	-	62,62,62,62	0
25	MG	A	1868	1/1	0.93	0.21	-	49,49,49,49	0
25	MG	A	1736	1/1	0.71	0.25	-	63,63,63,63	0
26	K	A	1910	1/1	0.71	0.23	-	119,119,119,119	0
25	MG	A	1876	1/1	0.73	0.41	-	63,63,63,63	0
25	MG	A	1806	1/1	0.86	0.28	-	118,118,118,118	0
25	MG	A	1880	1/1	0.90	0.23	-	64,64,64,64	0
26	K	A	1930	1/1	0.83	0.24	-	116,116,116,116	0
25	MG	A	1632	1/1	0.95	0.50	-	31,31,31,31	0
25	MG	A	1898	1/1	0.89	0.24	-	64,64,64,64	0
25	MG	A	1661	1/1	0.97	0.14	-	66,66,66,66	0
25	MG	A	1700	1/1	0.96	0.17	-	64,64,64,64	0
26	K	A	1904	1/1	0.96	0.30	-	102,102,102,102	0
25	MG	A	1810	1/1	0.69	0.44	-	53,53,53,53	0
25	MG	A	1619	1/1	0.94	0.11	-	69,69,69,69	0
25	MG	A	1739	1/1	0.93	0.50	-	62,62,62,62	0
25	MG	A	1720	1/1	0.61	0.30	-	65,65,65,65	0
25	MG	A	1855	1/1	0.92	0.16	-	61,61,61,61	0
25	MG	P	103	1/1	0.85	0.23	-	64,64,64,64	0
25	MG	A	1852	1/1	0.76	0.36	-	79,79,79,79	0
25	MG	A	1679	1/1	0.52	0.50	-	69,69,69,69	0
25	MG	A	1785	1/1	0.90	0.33	-	79,79,79,79	0
25	MG	H	201	1/1	0.62	0.23	-	57,57,57,57	0
25	MG	A	1897	1/1	0.92	0.46	-	66,66,66,66	0
25	MG	A	1704	1/1	0.87	0.78	-	67,67,67,67	0
25	MG	A	1867	1/1	0.94	0.35	-	61,61,61,61	0
25	MG	A	1620	1/1	0.98	0.10	-	69,69,69,69	0
25	MG	A	1768	1/1	0.78	0.25	-	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
25	MG	A	1860	1/1	0.86	0.31	-	53,53,53,53	0
25	MG	A	1734	1/1	0.83	0.33	-	49,49,49,49	0
25	MG	A	1786	1/1	0.92	0.33	-	60,60,60,60	0
25	MG	A	1837	1/1	0.91	0.34	-	46,46,46,46	0
25	MG	A	1886	1/1	0.92	0.25	-	67,67,67,67	0
26	K	A	1917	1/1	0.67	0.36	-	125,125,125,125	0
26	K	A	1919	1/1	0.98	0.14	-	103,103,103,103	0
25	MG	A	1676	1/1	0.91	0.33	-	51,51,51,51	0
25	MG	A	1871	1/1	0.94	0.18	-	47,47,47,47	0
25	MG	A	1807	1/1	0.81	0.32	-	85,85,85,85	0
25	MG	A	1831	1/1	0.90	0.33	-	73,73,73,73	0
25	MG	A	1877	1/1	0.90	0.32	-	76,76,76,76	0
26	K	A	1901	1/1	0.77	0.22	-	107,107,107,107	0
25	MG	A	1774	1/1	0.87	0.73	-	88,88,88,88	0
25	MG	A	1737	1/1	0.54	0.41	-	65,65,65,65	0
25	MG	A	1794	1/1	0.88	0.26	-	53,53,53,53	0
26	K	A	1900	1/1	0.86	0.19	-	108,108,108,108	0
25	MG	A	1838	1/1	0.63	0.46	-	82,82,82,82	0
25	MG	A	1760	1/1	0.96	0.26	-	48,48,48,48	0
25	MG	A	1615	1/1	0.96	0.23	-	48,48,48,48	0
26	K	A	1913	1/1	0.88	0.30	-	98,98,98,98	0
25	MG	A	1745	1/1	0.91	0.32	-	74,74,74,74	0
25	MG	A	1848	1/1	0.94	0.16	-	59,59,59,59	0
25	MG	S	103	1/1	0.90	0.10	-	81,81,81,81	0
25	MG	A	1656	1/1	0.93	0.10	-	77,77,77,77	0
25	MG	A	1726	1/1	0.93	0.38	-	246,246,246,246	0
25	MG	A	1784	1/1	0.96	0.18	-	31,31,31,31	0
25	MG	A	1826	1/1	0.94	0.15	-	36,36,36,36	0
25	MG	A	1798	1/1	0.82	0.30	-	58,58,58,58	0
26	K	A	1933	1/1	0.69	0.42	-	129,129,129,129	0
25	MG	A	1845	1/1	0.93	0.26	-	54,54,54,54	0
25	MG	A	1830	1/1	0.82	0.57	-	86,86,86,86	0
25	MG	A	1777	1/1	0.76	0.50	-	69,69,69,69	0
25	MG	Q	203	1/1	0.88	0.45	-	48,48,48,48	0
25	MG	A	1817	1/1	0.79	0.25	-	54,54,54,54	0
25	MG	A	1894	1/1	0.61	0.48	-	77,77,77,77	0
25	MG	A	1791	1/1	0.97	0.39	-	35,35,35,35	0
25	MG	A	1753	1/1	0.86	0.28	-	91,91,91,91	0
25	MG	A	1893	1/1	0.66	0.48	-	66,66,66,66	0
25	MG	A	1856	1/1	0.95	0.23	-	34,34,34,34	0
25	MG	A	1783	1/1	0.89	0.24	-	73,73,73,73	0
25	MG	A	1849	1/1	0.86	0.30	-	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
25	MG	A	1779	1/1	0.95	0.16	-	61,61,61,61	0
25	MG	A	1789	1/1	0.73	0.27	-	67,67,67,67	0
25	MG	A	1742	1/1	0.95	0.12	-	49,49,49,49	0
25	MG	A	1707	1/1	0.95	0.40	-	65,65,65,65	0
25	MG	A	1804	1/1	0.92	0.16	-	169,169,169,169	0
26	K	A	1927	1/1	0.50	0.37	-	144,144,144,144	0
25	MG	A	1800	1/1	0.85	0.45	-	62,62,62,62	0
25	MG	A	1825	1/1	0.92	0.32	-	62,62,62,62	0
25	MG	A	1665	1/1	0.97	0.15	-	69,69,69,69	0
25	MG	A	1629	1/1	0.87	0.32	-	53,53,53,53	0
25	MG	A	1883	1/1	0.91	0.14	-	64,64,64,64	0
25	MG	A	1823	1/1	0.89	0.24	-	59,59,59,59	0
25	MG	A	1677	1/1	0.97	0.08	-	78,78,78,78	0
25	MG	A	1862	1/1	0.90	0.21	-	60,60,60,60	0
25	MG	A	1766	1/1	0.95	0.16	-	56,56,56,56	0
25	MG	A	1870	1/1	0.92	0.23	-	62,62,62,62	0
25	MG	A	1728	1/1	0.85	0.27	-	26,26,26,26	0
25	MG	H	202	1/1	0.74	0.19	-	74,74,74,74	0
25	MG	A	1751	1/1	0.63	0.44	-	74,74,74,74	0
25	MG	A	1716	1/1	0.86	0.85	-	116,116,116,116	0
25	MG	A	1652	1/1	0.93	0.17	-	52,52,52,52	0
25	MG	A	1668	1/1	0.95	0.51	-	37,37,37,37	0
25	MG	A	1797	1/1	0.86	0.19	-	77,77,77,77	0
25	MG	A	1895	1/1	0.93	0.17	-	60,60,60,60	0
25	MG	A	1687	1/1	0.97	0.23	-	35,35,35,35	0
25	MG	A	1671	1/1	0.91	0.54	-	37,37,37,37	0
25	MG	P	102	1/1	0.59	0.22	-	64,64,64,64	0
25	MG	A	1612	1/1	0.92	0.10	-	40,40,40,40	0
25	MG	A	1858	1/1	0.70	0.36	-	59,59,59,59	0
25	MG	A	1641	1/1	0.88	0.32	-	108,108,108,108	0
26	K	A	1921	1/1	0.91	0.20	-	90,90,90,90	0
26	K	A	1918	1/1	0.96	0.32	-	91,91,91,91	0
25	MG	F	201	1/1	0.89	0.14	-	62,62,62,62	0
26	K	A	1905	1/1	0.80	0.67	-	117,117,117,117	0
25	MG	A	1608	1/1	0.97	0.24	-	69,69,69,69	0
25	MG	A	1851	1/1	0.84	0.74	-	70,70,70,70	0
25	MG	A	1841	1/1	0.83	0.45	-	75,75,75,75	0
25	MG	A	1809	1/1	0.75	0.46	-	77,77,77,77	0
25	MG	A	1754	1/1	0.94	0.14	-	49,49,49,49	0
25	MG	A	1759	1/1	0.93	0.23	-	57,57,57,57	0
25	MG	A	1749	1/1	0.89	0.20	-	39,39,39,39	0
25	MG	b	101	1/1	0.94	0.14	-	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
25	MG	A	1729	1/1	0.80	0.34	-	71,71,71,71	0
26	K	A	1934	1/1	0.85	0.16	-	112,112,112,112	0
25	MG	A	1618	1/1	0.92	0.11	-	106,106,106,106	0
25	MG	A	1695	1/1	0.92	0.13	-	77,77,77,77	0
25	MG	A	1896	1/1	0.88	0.17	-	63,63,63,63	0
25	MG	A	1686	1/1	0.95	0.20	-	60,60,60,60	0
25	MG	A	1731	1/1	0.80	0.28	-	43,43,43,43	0
25	MG	A	1712	1/1	0.91	0.19	-	94,94,94,94	0
26	K	E	202	1/1	0.76	0.79	-	124,124,124,124	0
25	MG	A	1824	1/1	0.83	0.23	-	49,49,49,49	0
25	MG	A	1672	1/1	0.87	0.19	-	51,51,51,51	0
25	MG	A	1832	1/1	0.92	0.46	-	46,46,46,46	0
26	K	A	1903	1/1	0.94	0.15	-	98,98,98,98	0
25	MG	A	1796	1/1	0.94	0.15	-	33,33,33,33	0
25	MG	A	1782	1/1	0.89	0.34	-	61,61,61,61	0
25	MG	A	1765	1/1	0.92	0.34	-	49,49,49,49	0
25	MG	A	1820	1/1	0.98	0.07	-	178,178,178,178	0
25	MG	A	1650	1/1	0.87	0.28	-	48,48,48,48	0
25	MG	A	1892	1/1	0.96	0.18	-	51,51,51,51	0
25	MG	A	1840	1/1	0.85	0.31	-	67,67,67,67	0
25	MG	A	1847	1/1	0.90	0.24	-	55,55,55,55	0
25	MG	A	1764	1/1	0.89	0.25	-	61,61,61,61	0
25	MG	A	1609	1/1	0.92	0.13	-	92,92,92,92	0
25	MG	A	1699	1/1	0.97	0.29	-	44,44,44,44	0
25	MG	A	1813	1/1	0.93	0.20	-	81,81,81,81	0
25	MG	A	1655	1/1	0.94	0.23	-	53,53,53,53	0
26	K	A	1902	1/1	0.83	0.27	-	115,115,115,115	0
25	MG	A	1636	1/1	0.89	0.31	-	33,33,33,33	0
25	MG	A	1853	1/1	0.94	0.37	-	61,61,61,61	0
25	MG	A	1890	1/1	0.80	0.25	-	68,68,68,68	0
25	MG	A	1758	1/1	0.96	0.16	-	49,49,49,49	0
26	K	A	1922	1/1	0.86	0.23	-	123,123,123,123	0
25	MG	A	1888	1/1	0.76	0.16	-	80,80,80,80	0
25	MG	A	1814	1/1	0.86	0.20	-	34,34,34,34	0
25	MG	A	1803	1/1	0.94	0.11	-	136,136,136,136	0
25	MG	A	1899	1/1	0.67	0.42	-	56,56,56,56	0
25	MG	A	1743	1/1	0.79	0.22	-	58,58,58,58	0
25	MG	A	1678	1/1	0.94	0.24	-	58,58,58,58	0
25	MG	A	1643	1/1	0.96	0.34	-	70,70,70,70	0
25	MG	A	1885	1/1	0.90	0.24	-	51,51,51,51	0
25	MG	A	1644	1/1	0.93	0.27	-	76,76,76,76	0
25	MG	A	1685	1/1	0.96	0.15	-	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
25	MG	A	1850	1/1	0.88	0.34	-	72,72,72,72	0
25	MG	A	1690	1/1	0.90	0.32	-	175,175,175,175	0
25	MG	A	1757	1/1	0.90	0.27	-	48,48,48,48	0
26	K	A	1928	1/1	0.82	0.34	-	130,130,130,130	0
25	MG	A	1755	1/1	0.92	0.17	-	56,56,56,56	0
25	MG	A	1859	1/1	0.91	0.21	-	55,55,55,55	0
25	MG	A	1721	1/1	0.91	0.24	-	77,77,77,77	0
25	MG	A	1795	1/1	0.93	0.23	-	64,64,64,64	0
25	MG	A	1681	1/1	0.93	0.17	-	191,191,191,191	0
25	MG	A	1673	1/1	0.81	0.39	-	60,60,60,60	0
25	MG	A	1732	1/1	0.92	0.28	-	167,167,167,167	0
25	MG	A	1626	1/1	0.96	0.20	-	53,53,53,53	0
25	MG	A	1705	1/1	0.93	0.13	-	125,125,125,125	0
25	MG	A	1744	1/1	0.80	0.42	-	58,58,58,58	0
25	MG	A	1614	1/1	0.96	0.09	-	67,67,67,67	0
25	MG	A	1866	1/1	0.79	0.31	-	75,75,75,75	0
26	K	A	1939	1/1	0.87	0.35	-	91,91,91,91	0
25	MG	A	1884	1/1	0.92	0.19	-	57,57,57,57	0
25	MG	A	1873	1/1	0.78	0.33	-	76,76,76,76	0
26	K	A	1916	1/1	0.76	0.21	-	103,103,103,103	0
25	MG	A	1635	1/1	0.84	0.43	-	56,56,56,56	0
25	MG	A	1660	1/1	0.96	0.15	-	0,0,0,0	0
25	MG	A	1822	1/1	0.88	0.18	-	41,41,41,41	0
25	MG	A	1836	1/1	0.88	0.41	-	78,78,78,78	0
26	K	A	1932	1/1	0.81	0.50	-	133,133,133,133	0
25	MG	A	1633	1/1	0.95	0.20	-	54,54,54,54	0
25	MG	A	1835	1/1	0.84	0.21	-	58,58,58,58	0
25	MG	A	1688	1/1	0.78	0.23	-	57,57,57,57	0
25	MG	A	1773	1/1	0.62	0.18	-	72,72,72,72	0
25	MG	A	1631	1/1	0.98	0.10	-	77,77,77,77	0
25	MG	A	1689	1/1	0.92	0.09	-	89,89,89,89	0
26	K	G	203	1/1	0.58	0.21	-	142,142,142,142	0
25	MG	A	1680	1/1	0.78	0.33	-	61,61,61,61	0
25	MG	A	1747	1/1	0.97	0.14	-	50,50,50,50	0
25	MG	A	1666	1/1	0.91	0.12	-	79,79,79,79	0
25	MG	A	1889	1/1	0.92	0.12	-	69,69,69,69	0
25	MG	A	1891	1/1	0.92	0.27	-	54,54,54,54	0
25	MG	A	1788	1/1	0.57	0.65	-	57,57,57,57	0
25	MG	A	1846	1/1	0.92	0.31	-	66,66,66,66	0
25	MG	A	1805	1/1	0.96	0.17	-	161,161,161,161	0
25	MG	A	1874	1/1	0.82	0.32	-	64,64,64,64	0
25	MG	A	1697	1/1	0.74	0.64	-	79,79,79,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
25	MG	A	1607	1/1	0.75	0.29	-	84,84,84,84	0
25	MG	A	1808	1/1	0.92	0.26	-	57,57,57,57	0
25	MG	A	1710	1/1	0.84	0.11	-	115,115,115,115	0
25	MG	A	1881	1/1	0.87	0.23	-	63,63,63,63	0
25	MG	E	201	1/1	0.93	0.07	-	90,90,90,90	0
25	MG	A	1865	1/1	0.91	0.25	-	49,49,49,49	0
25	MG	A	1610	1/1	0.92	0.14	-	66,66,66,66	0
25	MG	A	1735	1/1	0.85	0.26	-	54,54,54,54	0
26	K	A	1943	1/1	0.93	0.38	-	111,111,111,111	0
25	MG	A	1829	1/1	0.74	0.36	-	71,71,71,71	0
25	MG	A	1709	1/1	0.89	0.20	-	39,39,39,39	0
26	K	A	1911	1/1	0.89	0.38	-	113,113,113,113	0
25	MG	A	1625	1/1	0.93	0.21	-	59,59,59,59	0
25	MG	A	1738	1/1	0.96	0.16	-	58,58,58,58	0
25	MG	A	1691	1/1	0.97	0.11	-	85,85,85,85	0
26	K	A	1937	1/1	0.72	0.30	-	117,117,117,117	0
25	MG	A	1674	1/1	0.95	0.14	-	63,63,63,63	0
25	MG	A	1741	1/1	0.92	0.24	-	56,56,56,56	0
25	MG	A	1872	1/1	0.85	0.23	-	88,88,88,88	0
26	K	A	1931	1/1	0.90	0.28	-	120,120,120,120	0
26	K	A	1926	1/1	0.94	0.45	-	114,114,114,114	0
26	K	A	1915	1/1	0.56	0.32	-	109,109,109,109	0
25	MG	A	1776	1/1	0.88	0.27	-	53,53,53,53	0
25	MG	A	1882	1/1	0.79	0.39	-	70,70,70,70	0
25	MG	L	202	1/1	0.89	0.10	-	52,52,52,52	0
25	MG	A	1833	1/1	0.86	0.31	-	59,59,59,59	0
26	K	A	1942	1/1	0.56	0.66	-	146,146,146,146	0
25	MG	G	201	1/1	0.96	0.18	-	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.