



Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 11:08 am BST

PDB ID : 4LF6
Title : Crystal Structure of 30S ribosomal subunit from *Thermus thermophilus*
Authors : Demirci, H.; Belardinelli, R.; Carr, J.; Murphy IV, F.; Jogl, G.; Dahlberg, A.E.; Gregory, S.T.
Deposited on : 2013-06-26
Resolution : 3.31 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

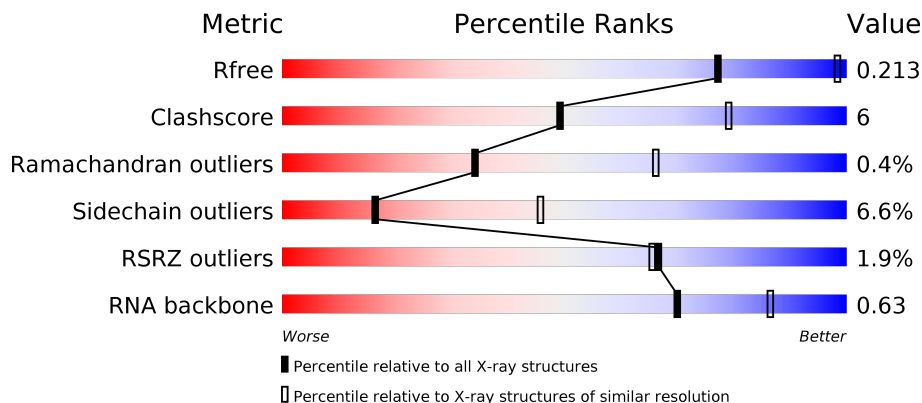
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



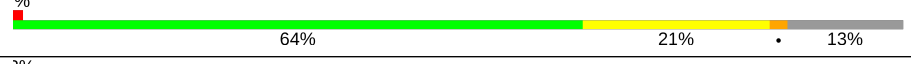

The reported resolution of this entry is 3.31 Å.

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









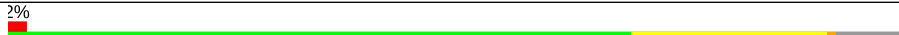
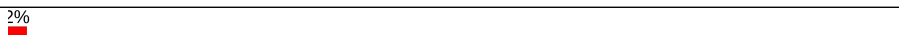
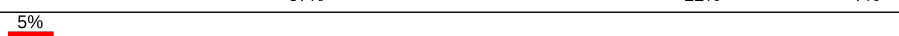








Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)
RNA backbone	3102	1117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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	 70% 25% 2% 2% 1%
2	B	256	 72% 20% 8% 2%
3	C	239	 64% 21% 13% 2%
4	D	209	 78% 18% 2%

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Mol	Chain	Length	Quality of chain
5	E	162	
6	F	101	
7	G	156	
8	H	138	
9	I	128	
10	J	105	
11	K	129	
12	L	135	
13	M	126	
14	N	61	
15	O	89	
16	P	88	
17	Q	105	
18	R	88	
19	S	93	
20	T	106	
21	U	27	

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
22	MG	A	1614	-	-	-	X
22	MG	A	1616	-	-	-	X
22	MG	A	1630	-	-	-	X
22	MG	A	1642	-	-	-	X
22	MG	A	1647	-	-	-	X
22	MG	A	1664	-	-	-	X
22	MG	A	1667	-	-	-	X
22	MG	A	1675	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	MG	A	1682	-	-	-	X
22	MG	A	1694	-	-	-	X
22	MG	A	1761	-	-	-	X
22	MG	A	1768	-	-	-	X
22	MG	A	1770	-	-	-	X
22	MG	A	1773	-	-	-	X
22	MG	A	1775	-	-	-	X
22	MG	A	1786	-	-	-	X
22	MG	A	1788	-	-	-	X
22	MG	A	1801	-	-	-	X
22	MG	A	1806	-	-	-	X
22	MG	A	1808	-	-	-	X
22	MG	A	1814	-	-	-	X
22	MG	C	302	-	-	-	X
22	MG	F	201	-	-	-	X
22	MG	N	102	-	-	-	X
23	K	A	1735	-	-	-	X
23	K	A	1742	-	-	-	X
23	K	A	1748	-	-	-	X
23	K	A	1750	-	-	-	X
23	K	A	1755	-	-	-	X
23	K	A	1760	-	-	-	X

2 Entry composition i

There are 26 unique types of molecules in this entry. The entry contains 52131 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
			Total	C	N	O	P			
1	A	1510	32462	14456	6009	10488	1509	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1533	C	A	CONFLICT	GB M26923.1
A	1534	A	C	CONFLICT	GB M26923.1

- Molecule 2 is a protein called ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	236	1874	1195	336	338	5	0	0	1

- Molecule 3 is a protein called ribosomal protein S3.

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

- Molecule 4 is a protein called ribosomal protein S4.

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

- Molecule 5 is a protein called ribosomal protein S5.

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

- Molecule 6 is a protein called ribosomal protein S6.

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

- Molecule 7 is a protein called ribosomal protein S7.

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

- Molecule 8 is a protein called ribosomal protein S8.

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

- Molecule 9 is a protein called ribosomal protein S9.

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

- Molecule 10 is a protein called ribosomal protein S10.

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

- Molecule 11 is a protein called ribosomal protein S11.

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

- Molecule 12 is a protein called ribosomal protein S12.

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

- Molecule 13 is a protein called ribosomal protein S13.

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

- Molecule 14 is a protein called ribosomal protein S14.

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

- Molecule 15 is a protein called ribosomal protein S15.

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

- Molecule 16 is a protein called ribosomal protein S16.

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

- Molecule 17 is a protein called ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
17	Q	104	857	547	160	148	2	0	0	0

- Molecule 18 is a protein called ribosomal protein S18.

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

- Molecule 19 is a protein called ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
19	S	81	648	414	120	112	2	0	0	1

- Molecule 20 is a protein called ribosomal protein S20.

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

- Molecule 21 is a protein called ribosomal protein THX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
21	U	25	209	128	51	30	0	0	1

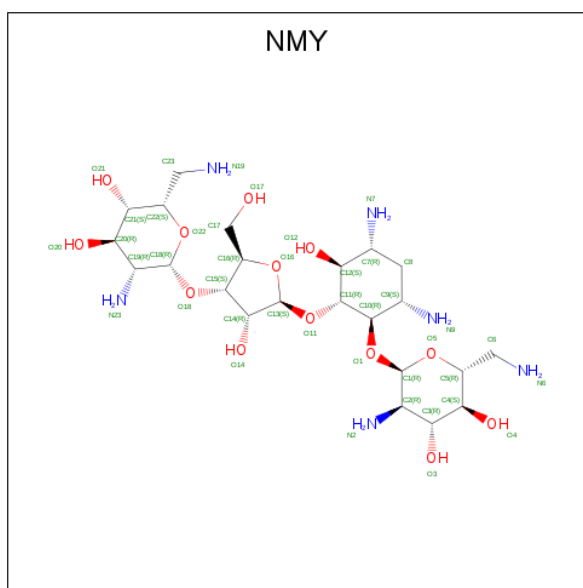
- Molecule 22 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	P	2	Total 2	Mg 2	0	0
22	Q	1	Total 1	Mg 1	0	0
22	D	2	Total 2	Mg 2	0	0
22	E	1	Total 1	Mg 1	0	0
22	H	2	Total 2	Mg 2	0	0
22	B	3	Total 3	Mg 3	0	0
22	C	2	Total 2	Mg 2	0	0
22	A	201	Total 201	Mg 201	0	0
22	N	2	Total 2	Mg 2	0	0
22	L	1	Total 1	Mg 1	0	0
22	F	1	Total 1	Mg 1	0	0
22	M	2	Total 2	Mg 2	0	0

- Molecule 23 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	A	30	Total 30	K 30	0	0

- Molecule 24 is NEOMYCIN (three-letter code: NMY) (formula: $C_{23}H_{46}N_6O_{13}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
24	A	1	Total	C	N	O	0	0
			42	23	6	13		
24	A	1	Total	C	N	O	0	0
			42	23	6	13		
24	A	1	Total	C	N	O	0	0
			42	23	6	13		
24	A	1	Total	C	N	O	0	0
			42	23	6	13		
24	A	1	Total	C	N	O	0	0
			42	23	6	13		

- Molecule 25 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

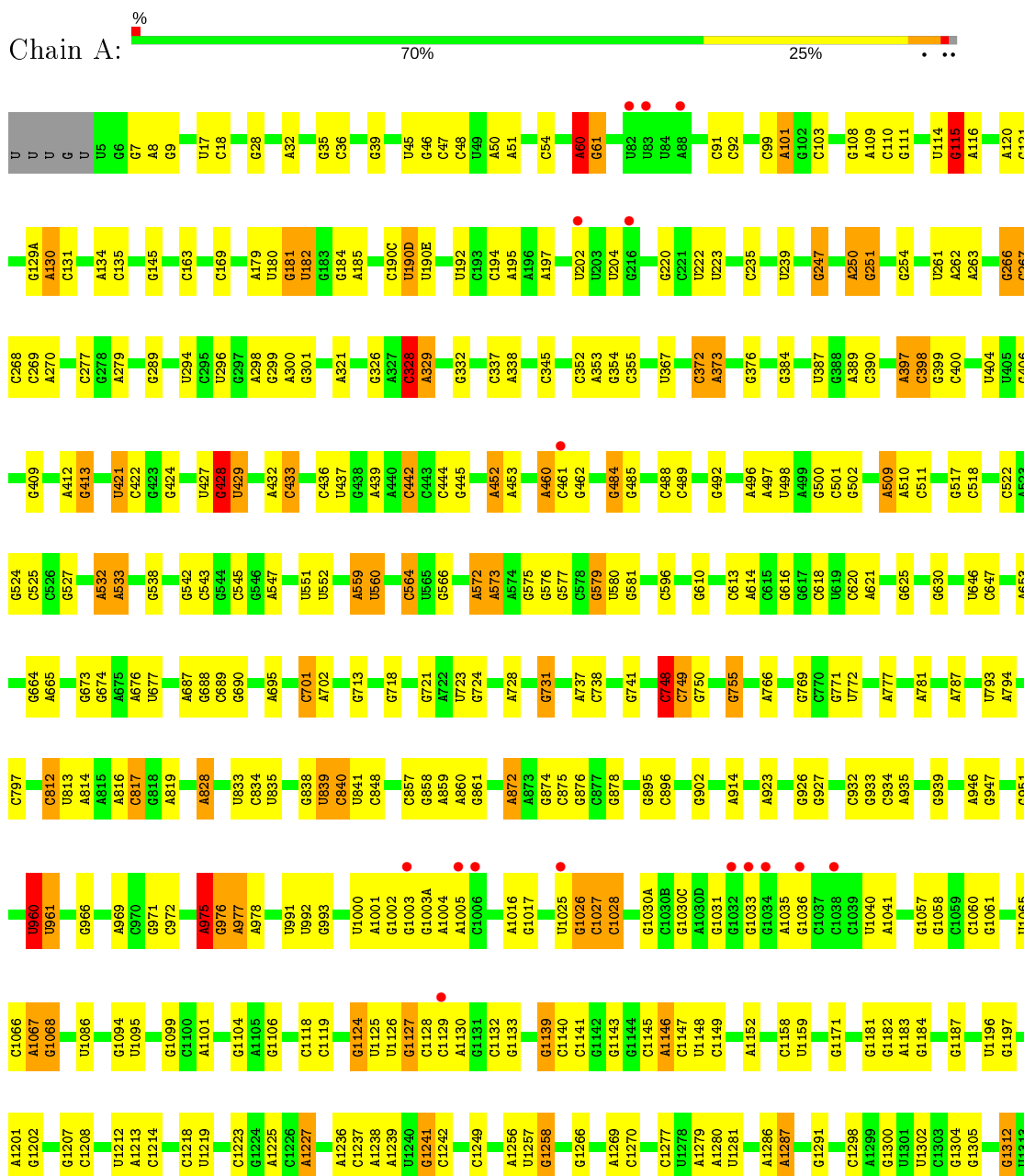
- Molecule 26 is water.

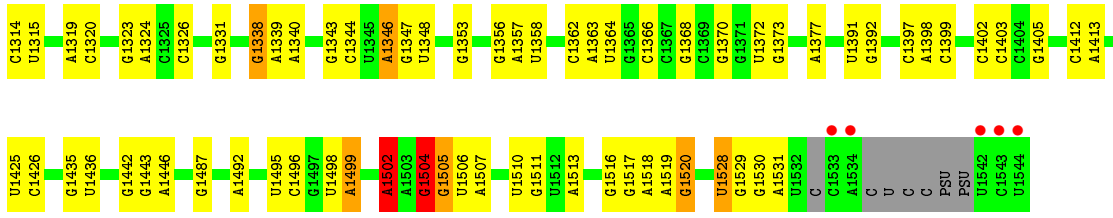
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
26	A	12	Total	O	0	0
			12	12		

3 Residue-property plots

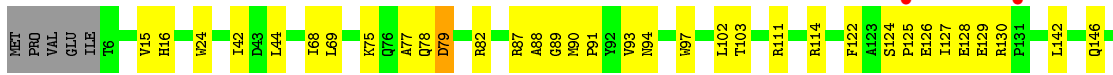
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

- Molecule 1: 16S rRNA





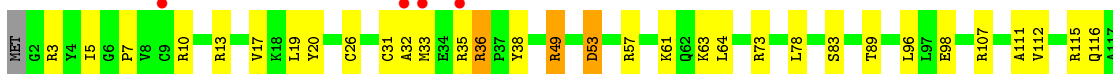
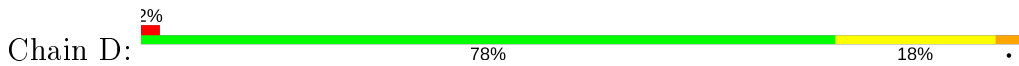
• Molecule 2: ribosomal protein S2



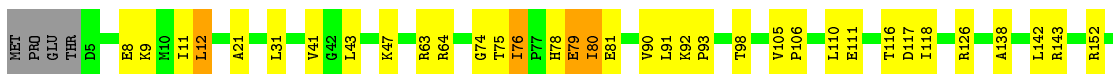
• Molecule 3: ribosomal protein S3

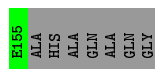


• Molecule 4: ribosomal protein S4

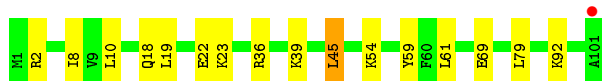
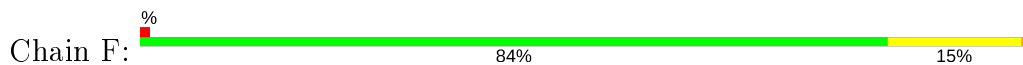


• Molecule 5: ribosomal protein S5

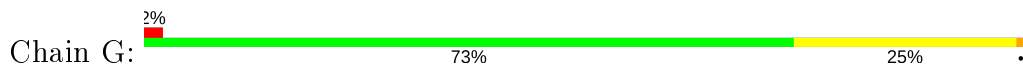




- Molecule 6: ribosomal protein S6



- Molecule 7: ribosomal protein S7



- Molecule 8: ribosomal protein S8



- Molecule 9: ribosomal protein S9



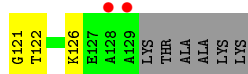
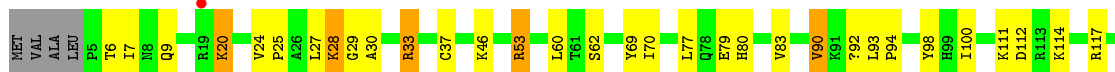
- Molecule 10: ribosomal protein S10



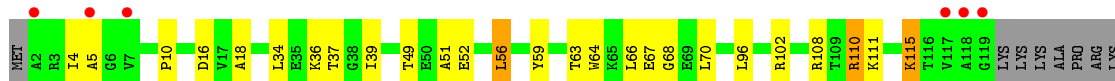
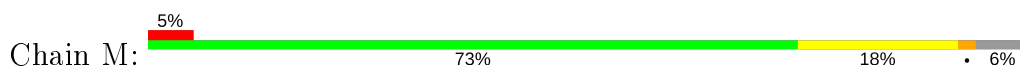
- Molecule 11: ribosomal protein S11



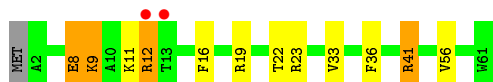
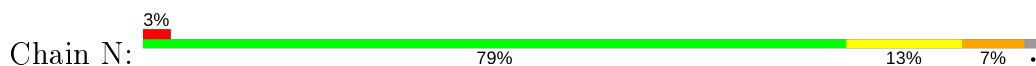
- Molecule 12: ribosomal protein S12



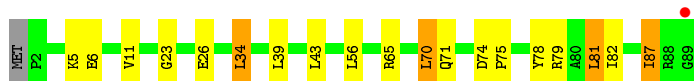
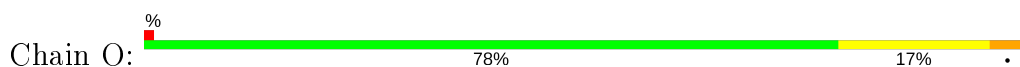
- Molecule 13: ribosomal protein S13



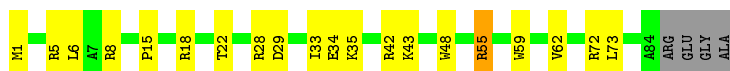
- Molecule 14: ribosomal protein S14



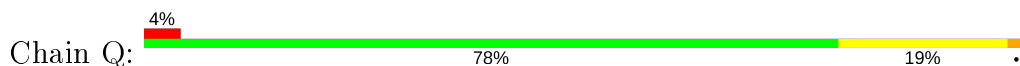
- Molecule 15: ribosomal protein S15



- Molecule 16: ribosomal protein S16

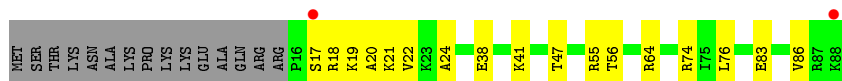


- Molecule 17: ribosomal protein S17

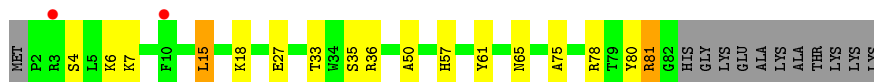




- Molecule 18: ribosomal protein S18



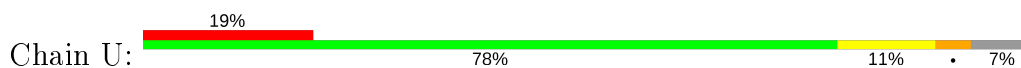
- Molecule 19: ribosomal protein S19



- Molecule 20: ribosomal protein S20



- Molecule 21: ribosomal protein THX



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	403.18Å 403.18Å 176.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.90 – 3.31 34.90 – 3.31	Depositor EDS
% Data completeness (in resolution range)	98.7 (34.90-3.31) 98.5 (34.90-3.31)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.92 (at 3.32Å)	Xtrriage
Refinement program	PHENIX dev_1119	Depositor
R, R_{free}	0.175 , 0.210 0.178 , 0.213	Depositor DCC
R_{free} test set	10690 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	96.4	Xtrriage
Anisotropy	0.272	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 67.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	52131	wwPDB-VP
Average B, all atoms (Å ²)	99.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.53% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, K, 0TD, ZN, NMY, 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	0.35	0/36091	0.80	30/56326 (0.1%)
2	B	0.28	0/1909	0.49	0/2579
3	C	0.27	0/1637	0.47	0/2207
4	D	0.31	0/1733	0.48	0/2318
5	E	0.34	0/1163	0.56	0/1566
6	F	0.25	0/856	0.45	0/1154
7	G	0.26	0/1276	0.43	0/1709
8	H	0.34	0/1136	0.52	0/1527
9	I	0.26	0/1029	0.50	0/1379
10	J	0.28	0/806	0.54	0/1084
11	K	0.28	0/900	0.51	0/1213
12	L	0.31	0/978	0.59	0/1308
13	M	0.26	0/947	0.45	0/1270
14	N	0.29	0/501	0.48	0/664
15	O	0.28	0/745	0.46	0/992
16	P	0.29	0/717	0.52	0/965
17	Q	0.34	0/870	0.57	0/1159
18	R	0.27	0/604	0.49	0/801
19	S	0.24	0/662	0.46	0/892
20	T	0.32	0/765	0.53	0/1007
21	U	0.26	0/213	0.44	0/279
All	All	0.33	0/55538	0.72	30/82399 (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
18	R	0	1
20	T	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	3

There are no bond length outliers.

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	328	C	C2-N1-C1'	8.28	127.91	118.80
1	A	328	C	N1-C2-O2	8.10	123.76	118.90
1	A	328	C	N3-C2-O2	-7.05	116.96	121.90
1	A	254	G	O5'-P-OP1	-6.99	99.41	105.70
1	A	1528	U	C2-N1-C1'	6.52	125.52	117.70
1	A	1528	U	P-O3'-C3'	6.15	127.08	119.70
1	A	1502	A	C5-N7-C8	-5.99	100.90	103.90
1	A	1502	A	N7-C8-N9	5.89	116.75	113.80
1	A	817	C	C6-N1-C2	5.74	122.60	120.30
1	A	1502	A	C6-C5-N7	-5.73	128.29	132.30
1	A	1158	C	C2-N1-C1'	5.65	125.02	118.80
1	A	328	C	C6-N1-C1'	-5.65	114.03	120.80
1	A	328	C	C6-N1-C2	-5.63	118.05	120.30
1	A	328	C	P-O3'-C3'	5.62	126.45	119.70
1	A	960	U	N1-C2-O2	5.60	126.72	122.80
1	A	60	A	P-O3'-C3'	5.40	126.18	119.70
1	A	1502	A	N1-C6-N6	5.39	121.83	118.60
1	A	428	G	P-O3'-C3'	5.33	126.10	119.70
1	A	1502	A	C4-C5-N7	5.32	113.36	110.70
1	A	1067	A	P-O3'-C3'	5.32	126.08	119.70
1	A	108	G	O4'-C1'-N9	5.28	112.42	108.20
1	A	1158	C	N1-C2-O2	5.28	122.07	118.90
1	A	812	C	P-O3'-C3'	5.20	125.94	119.70
1	A	748	C	P-O3'-C3'	5.15	125.88	119.70
1	A	484	G	P-O3'-C3'	5.07	125.79	119.70
1	A	975	A	O4'-C1'-N9	-5.06	104.15	108.20
1	A	115	G	P-O3'-C3'	5.05	125.76	119.70
1	A	1504	G	P-O3'-C3'	5.03	125.74	119.70
1	A	701	C	P-O3'-C3'	5.03	125.73	119.70
1	A	960	U	N3-C2-O2	-5.03	118.68	122.20

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
18	R	20	ALA	Peptide
20	T	73	HIS	Peptide
20	T	93	GLU	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32462	0	16406	218	0
2	B	1874	0	1887	25	0
3	C	1613	0	1677	28	0
4	D	1703	0	1763	26	0
5	E	1147	0	1207	24	0
6	F	843	0	857	10	0
7	G	1257	0	1296	25	0
8	H	1116	0	1177	27	0
9	I	1010	0	1037	24	0
10	J	793	0	835	23	0
11	K	885	0	904	19	0
12	L	973	0	1058	27	0
13	M	937	0	995	15	0
14	N	492	0	529	9	0
15	O	734	0	771	11	0
16	P	701	0	720	14	0
17	Q	857	0	928	13	0
18	R	598	0	670	11	0
19	S	648	0	673	11	0
20	T	763	0	861	19	0
21	U	209	0	221	3	0
22	A	201	0	0	0	0
22	B	3	0	0	0	0
22	C	2	0	0	0	0
22	D	2	0	0	0	0
22	E	1	0	0	0	0
22	F	1	0	0	0	0
22	H	2	0	0	0	0
22	L	1	0	0	0	0
22	M	2	0	0	0	0
22	N	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	P	2	0	0	0	0
22	Q	1	0	0	0	0
23	A	30	0	0	0	0
24	A	252	0	276	13	0
25	D	1	0	0	0	0
25	N	1	0	0	0	0
26	A	12	0	0	0	0
All	All	52131	0	36748	518	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 6.

All (518) 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:1086:U:H3	1:A:1099:G:H22	1.23	0.86
2:B:75:LYS:HA	2:B:78:GLN:HB2	1.60	0.83
1:A:664:G:H22	1:A:741:G:H1	1.27	0.81
1:A:279:A:OP2	17:Q:95:TYR:OH	1.98	0.81
19:S:33:THR:HG22	19:S:35:SER:H	1.47	0.79
18:R:38:GLU:HA	18:R:41:LYS:HD3	1.66	0.76
1:A:625:G:N7	24:A:1834:NMY:N19	2.34	0.75
12:L:53:ARG:NH1	12:L:92:OTD:OD2	2.20	0.75
2:B:103:THR:HG23	2:B:176:GLU:HG3	1.68	0.75
1:A:1057:G:H5''	3:C:154:SER:HB2	1.68	0.75
1:A:427:U:OP1	4:D:13:ARG:NH2	2.21	0.74
1:A:975:A:H4'	1:A:976:G:H5''	1.69	0.74
1:A:1405:G:O2'	1:A:1518:A:O2'	2.06	0.73
1:A:1502:A:H2	1:A:1505:G:H1	1.36	0.73
1:A:1028:C:N3	1:A:1033:G:N2	2.36	0.73
24:A:1834:NMY:O21	24:A:1834:NMY:N19	2.17	0.73
1:A:235:C:H5'	17:Q:70:ARG:HG2	1.69	0.72
3:C:156:ARG:H	3:C:163:ALA:HA	1.53	0.72
24:A:1834:NMY:N2	24:A:1834:NMY:O16	2.22	0.72
5:E:76:ILE:HG22	5:E:93:PRO:HG3	1.72	0.70
15:O:39:LEU:HD12	15:O:56:LEU:HB2	1.74	0.70
12:L:111:LYS:HZ2	12:L:112:ASP:H	1.39	0.70
1:A:387:U:OP1	24:A:1837:NMY:N9	2.24	0.69
5:E:80:ILE:HD12	5:E:138:ALA:HB1	1.73	0.69
10:J:34:VAL:HG13	10:J:74:ILE:HA	1.74	0.69
8:H:113:SER:HB2	8:H:134:ILE:HD11	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:542:G:OP1	4:D:10:ARG:NH2	2.27	0.68
7:G:146:GLU:HA	7:G:149:ARG:HB2	1.75	0.68
4:D:20:TYR:HD2	4:D:26:CYS:HB3	1.59	0.67
19:S:36:ARG:NH2	19:S:75:ALA:O	2.27	0.67
1:A:266:G:H5'	1:A:268:C:H41	1.58	0.67
10:J:49:VAL:HG13	14:N:41:ARG:HB2	1.76	0.66
1:A:266:G:H5''	1:A:267:C:C5	2.31	0.66
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.78	0.66
1:A:579:G:H5'	1:A:728:A:H1'	1.76	0.66
12:L:46:LYS:HB2	12:L:92:0TD:H8	1.77	0.65
1:A:517:G:N1	1:A:533:A:OP2	2.28	0.65
1:A:1518:A:H2'	1:A:1519:A:C8	2.31	0.65
1:A:1348:U:H4'	9:I:120:ARG:HG3	1.77	0.65
1:A:951:G:OP2	13:M:102:ARG:NH2	2.30	0.65
1:A:1392:G:H21	1:A:1502:A:H8	1.42	0.64
1:A:266:G:H5''	1:A:267:C:H5	1.61	0.64
10:J:34:VAL:HG12	10:J:35:SER:H	1.63	0.64
11:K:84:VAL:HG11	11:K:91:ARG:HE	1.63	0.64
12:L:33:ARG:HG2	12:L:62:SER:HB2	1.80	0.64
12:L:37:CYS:HB2	12:L:79:GLU:O	1.97	0.63
11:K:15:ALA:HA	11:K:77:MET:HA	1.80	0.63
1:A:1145:C:H4'	1:A:1146:A:H5'	1.81	0.63
1:A:413:G:N2	1:A:429:U:OP2	2.18	0.63
1:A:390:C:O3'	16:P:28:ARG:NH2	2.31	0.63
1:A:1392:G:N2	1:A:1502:A:H8	1.97	0.63
3:C:155:GLY:HA3	3:C:163:ALA:HB1	1.80	0.63
8:H:83:ILE:HG13	8:H:137:VAL:HG22	1.80	0.63
9:I:10:ARG:NH1	9:I:75:ASP:OD2	2.31	0.63
11:K:57:THR:HG22	11:K:59:TYR:H	1.64	0.63
16:P:28:ARG:NH1	16:P:29:ASP:OD1	2.32	0.62
1:A:1435:G:H2'	1:A:1436:U:C6	2.33	0.62
3:C:36:ASP:OD2	3:C:59:ARG:NH2	2.32	0.62
1:A:1366:C:O2'	10:J:60:ARG:NH2	2.32	0.62
13:M:4:ILE:HG22	13:M:5:ALA:H	1.65	0.62
1:A:560:U:H5'	1:A:566:G:N2	2.14	0.61
5:E:12:LEU:HD13	5:E:31:LEU:HB2	1.83	0.61
1:A:1026:G:H3'	1:A:1027:C:H5''	1.82	0.61
24:A:1835:NMY:O21	24:A:1835:NMY:N19	2.32	0.61
9:I:46:ALA:HB2	9:I:74:ILE:HG23	1.83	0.61
11:K:40:ILE:HG22	11:K:41:THR:HG23	1.83	0.61
20:T:45:GLN:HB2	20:T:91:LEU:HD13	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:91:ARG:NH2	11:K:110:ASP:OD1	2.33	0.61
1:A:460:A:O2'	1:A:462:G:N7	2.33	0.60
5:E:78:HIS:HD2	8:H:107:LEU:HD12	1.64	0.60
19:S:50:ALA:HB1	19:S:57:HIS:HB3	1.82	0.60
1:A:1377:A:HO2'	7:G:2:ALA:N	1.99	0.60
7:G:15:ASP:OD2	7:G:44:TYR:OH	2.20	0.60
1:A:738:C:OP2	6:F:92:LYS:NZ	2.33	0.60
20:T:67:ALA:HA	20:T:73:HIS:H	1.66	0.60
11:K:33:THR:HG22	11:K:39:PRO:HA	1.84	0.59
1:A:1028:C:H42	1:A:1033:G:H1	1.49	0.59
1:A:372:C:H4'	1:A:373:A:O5'	2.02	0.59
2:B:87:ARG:CZ	2:B:233:SER:HB3	2.32	0.59
1:A:975:A:H5'	1:A:975:A:H8	1.66	0.59
24:A:1836:NMY:O21	16:P:29:ASP:OD1	2.20	0.59
2:B:15:VAL:HG13	2:B:203:GLY:HA2	1.85	0.58
1:A:192:U:H1'	20:T:103:GLY:HA2	1.85	0.58
17:Q:48:GLU:HG3	17:Q:50:LYS:HB2	1.85	0.58
8:H:41:ARG:NH1	8:H:123:GLU:OE2	2.37	0.58
15:O:26:GLU:HG3	15:O:81:LEU:HG	1.86	0.58
2:B:77:ALA:HB2	2:B:211:ILE:HD13	1.85	0.58
9:I:111:ARG:NH1	9:I:113:LYS:HG2	2.19	0.57
3:C:11:ARG:NH1	3:C:177:THR:O	2.36	0.57
13:M:37:THR:HG23	13:M:39:ILE:HG13	1.87	0.57
15:O:70:LEU:HD13	15:O:78:TYR:HA	1.86	0.57
17:Q:45:HIS:CD2	17:Q:47:PRO:HG3	2.40	0.57
8:H:108:GLY:HA3	8:H:138:TRP:HB3	1.85	0.57
24:A:1837:NMY:N6	24:A:1837:NMY:O11	2.36	0.57
2:B:24:TRP:HB2	2:B:190:THR:HG22	1.85	0.57
1:A:184:G:H2'	1:A:185:A:H8	1.68	0.57
1:A:250:A:H4'	1:A:251:G:O5'	2.05	0.57
16:P:43:LYS:HG2	16:P:48:TRP:CD2	2.39	0.57
3:C:155:GLY:HA2	3:C:164:ARG:H	1.70	0.56
12:L:70:ILE:HG12	12:L:100:ILE:HD12	1.88	0.56
5:E:79:GLU:HB3	5:E:92:LYS:HG2	1.88	0.56
3:C:131:ARG:NH1	3:C:166:GLU:OE2	2.38	0.56
3:C:16:ARG:NH2	3:C:183:ASP:OD2	2.39	0.56
1:A:299:G:H2'	1:A:300:A:C8	2.40	0.56
10:J:99:LYS:HG2	10:J:100:THR:H	1.70	0.56
2:B:122:PHE:HA	2:B:127:ILE:HG12	1.87	0.56
11:K:12:ARG:HB2	11:K:75:TYR:HD2	1.71	0.56
12:L:27:LEU:O	12:L:29:GLY:N	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:102:LEU:HB2	2:B:176:GLU:HG2	1.87	0.56
5:E:11:ILE:HD13	5:E:105:VAL:HG13	1.88	0.56
1:A:328:C:H4'	1:A:329:A:H5'	1.87	0.55
1:A:1502:A:H2	1:A:1505:G:N1	2.02	0.55
1:A:239:U:O4	24:A:1835:NMY:N19	2.40	0.55
2:B:212:GLN:HE21	2:B:235:SER:HB2	1.71	0.55
7:G:38:LEU:O	7:G:42:ILE:HG13	2.06	0.55
1:A:1147:C:O2	9:I:16:ARG:NH1	2.40	0.55
24:A:1836:NMY:N19	24:A:1836:NMY:O21	2.39	0.55
1:A:45:U:H2'	1:A:46:G:C8	2.42	0.55
17:Q:68:ARG:H	17:Q:70:ARG:NH1	2.04	0.55
2:B:91:PRO:HB3	2:B:154:LEU:HB2	1.89	0.54
8:H:86:ILE:HD12	8:H:133:LEU:HD22	1.88	0.54
1:A:91:C:H2'	1:A:92:C:H6	1.72	0.54
16:P:22:THR:HA	16:P:33:ILE:HG13	1.89	0.54
1:A:580:U:H2'	1:A:581:G:O4'	2.06	0.54
13:M:49:THR:HB	13:M:52:GLU:HG2	1.90	0.54
16:P:15:PRO:HD2	16:P:42:ARG:HD2	1.89	0.54
10:J:8:LEU:HB3	10:J:16:LEU:HD21	1.89	0.54
11:K:84:VAL:HG21	11:K:95:ILE:HD11	1.90	0.54
20:T:60:GLU:HG3	20:T:81:LYS:HE3	1.89	0.54
1:A:835:U:OP1	18:R:64:ARG:NH2	2.39	0.54
1:A:1249:C:O2'	9:I:73:GLN:NE2	2.40	0.54
8:H:116:LYS:HE3	8:H:127:LEU:HD13	1.89	0.54
5:E:105:VAL:HB	5:E:106:PRO:HD3	1.89	0.54
1:A:750:G:N3	15:O:23:GLY:HA3	2.23	0.53
4:D:7:PRO:HB2	4:D:10:ARG:HD2	1.90	0.53
6:F:8:ILE:HB	6:F:61:LEU:HB2	1.90	0.53
1:A:279:A:C5	17:Q:98:LEU:HD12	2.44	0.53
2:B:16:HIS:HB3	2:B:44:LEU:HD21	1.91	0.53
10:J:16:LEU:HD13	10:J:70:ARG:HG2	1.91	0.53
20:T:50:GLU:HG3	20:T:100:ILE:HB	1.91	0.53
1:A:1035:A:H2'	1:A:1036:G:H8	1.74	0.53
1:A:946:A:H2'	1:A:947:G:C8	2.44	0.53
7:G:62:PHE:HD1	7:G:124:LEU:HD21	1.73	0.53
10:J:65:LEU:HB2	14:N:56:VAL:HG22	1.90	0.53
16:P:18:ARG:HD3	16:P:35:LYS:HD2	1.89	0.53
1:A:277:C:H5'	17:Q:68:ARG:HH12	1.73	0.53
1:A:676:A:H1'	11:K:115:PRO:HB3	1.91	0.53
4:D:32:ALA:HA	4:D:35:ARG:HB2	1.90	0.53
1:A:718:G:C8	11:K:116:HIS:HB3	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:A:H2'	1:A:180:U:C6	2.43	0.52
7:G:45:ASP:O	7:G:49:ILE:HG13	2.09	0.52
1:A:673:G:H2'	1:A:674:G:C8	2.44	0.52
4:D:57:ARG:HB3	4:D:206:PHE:HB2	1.91	0.52
9:I:5:TYR:HE1	9:I:16:ARG:HB3	1.75	0.52
20:T:69:GLY:O	20:T:73:HIS:ND1	2.43	0.52
3:C:137:ALA:HA	3:C:140:ARG:HE	1.75	0.52
9:I:65:VAL:HG11	9:I:73:GLN:HB3	1.92	0.52
1:A:1104:G:O5'	2:B:111:ARG:HD2	2.10	0.52
1:A:1338:G:H2'	1:A:1339:A:C8	2.45	0.51
1:A:1510:U:H2'	1:A:1511:G:C8	2.44	0.51
1:A:509:A:N3	1:A:543:C:O2'	2.33	0.51
7:G:69:VAL:HG21	7:G:104:LEU:HD21	1.92	0.51
3:C:134:ILE:HG22	3:C:168:ALA:HB3	1.91	0.51
1:A:559:A:OP1	5:E:126:ARG:NH2	2.32	0.51
2:B:78:GLN:O	2:B:94:ASN:ND2	2.34	0.51
1:A:17:U:H2'	1:A:18:C:C6	2.45	0.51
1:A:409:G:H1	1:A:433:C:H42	1.57	0.51
1:A:1339:A:H2'	1:A:1340:A:O4'	2.10	0.51
9:I:125:TYR:CD1	9:I:127:LYS:HB2	2.45	0.51
12:L:20:LYS:NZ	12:L:20:LYS:H	2.09	0.51
1:A:1218:C:H2'	1:A:1219:U:C6	2.45	0.51
9:I:9:ARG:HG2	9:I:14:VAL:HG22	1.92	0.51
12:L:24:VAL:HG13	12:L:98:TYR:HE2	1.75	0.51
7:G:51:GLN:C	7:G:53:LYS:H	2.14	0.51
1:A:564:C:O2'	8:H:91:ARG:NH2	2.43	0.50
3:C:147:LYS:HD3	3:C:205:GLY:H	1.77	0.50
12:L:24:VAL:HG13	12:L:98:TYR:CE2	2.45	0.50
1:A:328:C:H4'	1:A:329:A:C5'	2.41	0.50
1:A:718:G:O6	18:R:74:ARG:NH1	2.45	0.50
4:D:53:ASP:OD1	4:D:53:ASP:N	2.44	0.50
13:M:36:LYS:HD2	13:M:59:TYR:OH	2.12	0.50
1:A:572:A:H5'	1:A:573:A:OP2	2.11	0.50
3:C:148:GLY:HA3	3:C:172:ARG:O	2.11	0.50
1:A:923:A:OP1	5:E:21:ALA:HB2	2.11	0.50
2:B:88:ALA:O	2:B:90:MET:N	2.44	0.50
1:A:103:C:OP1	20:T:17:ARG:NH1	2.45	0.50
1:A:1391:U:H2'	1:A:1392:G:C8	2.46	0.50
1:A:404:U:H5'	4:D:122:ARG:HD2	1.94	0.50
1:A:269:C:H2'	1:A:270:A:C8	2.47	0.50
1:A:7:G:H5'	1:A:298:A:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:98:THR:N	5:E:117:ASP:OD1	2.45	0.50
9:I:8:GLY:HA3	9:I:79:LEU:HB3	1.93	0.50
5:E:9:LYS:NZ	5:E:111:GLU:OE1	2.43	0.50
3:C:6:HIS:CD2	3:C:8:ILE:HB	2.46	0.49
10:J:8:LEU:HB2	10:J:70:ARG:HB2	1.94	0.49
17:Q:67:LYS:O	17:Q:68:ARG:HB2	2.12	0.49
3:C:111:LEU:HD22	3:C:146:ALA:HB2	1.92	0.49
17:Q:101:ARG:HG2	17:Q:102:GLY:H	1.78	0.49
9:I:110:GLU:OE2	9:I:113:LYS:NZ	2.41	0.49
18:R:22:VAL:HB	18:R:56:THR:HA	1.94	0.49
1:A:222:U:H2'	1:A:223:U:C6	2.48	0.49
6:F:45:LEU:HD23	6:F:45:LEU:H	1.77	0.49
1:A:814:A:H2'	1:A:816:A:H5''	1.93	0.49
10:J:12:ASP:HB3	10:J:15:THR:HG22	1.93	0.49
10:J:82:ILE:HA	10:J:85:LEU:HB2	1.95	0.49
1:A:1040:U:H2'	1:A:1041:A:C8	2.48	0.49
1:A:261:U:OP2	20:T:79:ARG:NH2	2.45	0.49
1:A:1495:U:H2'	1:A:1496:C:C6	2.47	0.49
12:L:117:ARG:HB3	12:L:122:THR:HB	1.94	0.49
1:A:976:G:H5'	1:A:1358:U:O2'	2.12	0.49
3:C:152:ILE:HB	3:C:199:LYS:HB2	1.95	0.49
7:G:138:LYS:HE2	7:G:142:GLU:OE1	2.12	0.49
1:A:109:A:H2'	1:A:326:G:N2	2.27	0.48
1:A:1225:A:N3	1:A:1225:A:H2'	2.28	0.48
2:B:146:GLN:O	2:B:150:SER:HB3	2.14	0.48
10:J:6:ILE:HB	10:J:72:VAL:HB	1.94	0.48
10:J:3:LYS:N	10:J:77:PRO:HG3	2.29	0.48
1:A:1187:G:H5'	9:I:113:LYS:HE2	1.94	0.48
1:A:99:C:H2'	1:A:101:A:C8	2.49	0.48
7:G:50:ILE:HG21	7:G:58:PRO:HA	1.96	0.48
8:H:51:VAL:HG11	8:H:60:ARG:NH1	2.29	0.48
1:A:247:G:OP2	17:Q:100:LYS:HG3	2.13	0.48
4:D:98:GLU:OE2	4:D:107:ARG:NE	2.35	0.48
5:E:76:ILE:HG23	5:E:78:HIS:H	1.78	0.48
1:A:1356:G:H2'	1:A:1357:A:C8	2.49	0.48
6:F:10:LEU:HB2	6:F:59:TYR:HB3	1.95	0.48
19:S:15:LEU:HA	19:S:18:LYS:HB3	1.95	0.48
1:A:833:U:H2'	1:A:834:C:C6	2.50	0.47
3:C:6:HIS:HD2	3:C:9:GLY:H	1.62	0.47
4:D:78:LEU:HD23	4:D:78:LEU:HA	1.71	0.47
13:M:49:THR:HG22	13:M:51:ALA:H	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:524:G:H2'	1:A:525:C:C6	2.50	0.47
8:H:13:ILE:O	8:H:17:THR:HG23	2.15	0.47
1:A:1326:C:H5''	21:U:12:LYS:HE3	1.96	0.47
1:A:1499:A:H1'	1:A:1520:G:H5'	1.96	0.47
8:H:17:THR:HG22	8:H:63:LEU:HG	1.96	0.47
12:L:6:THR:OG1	12:L:9:GLN:HG3	2.14	0.47
20:T:74:LYS:H	20:T:74:LYS:HG3	1.41	0.47
6:F:8:ILE:HD11	6:F:79:LEU:HD13	1.95	0.47
12:L:90:VAL:HG21	12:L:93:LEU:HD12	1.97	0.47
1:A:337:C:H2'	1:A:338:A:C8	2.50	0.47
1:A:192:U:H4'	20:T:57:ARG:HD3	1.97	0.47
1:A:522:C:OP2	12:L:69:TYR:OH	2.24	0.47
2:B:178:ARG:O	8:H:71:GLY:HA2	2.15	0.47
19:S:80:TYR:CE1	19:S:81:ARG:HD3	2.50	0.47
1:A:421:U:H5'	1:A:422:C:C5	2.50	0.47
3:C:189:ALA:HB3	3:C:196:LEU:HB2	1.97	0.47
18:R:21:LYS:HD2	18:R:21:LYS:HA	1.67	0.47
18:R:47:THR:HA	18:R:83:GLU:HB2	1.95	0.47
1:A:192:U:C1'	20:T:103:GLY:HA2	2.45	0.47
1:A:1305:G:N2	1:A:1331:G:H1'	2.30	0.47
1:A:1504:G:OP1	1:A:1507:A:H4'	2.15	0.47
4:D:112:VAL:HG12	4:D:116:GLN:OE1	2.15	0.47
4:D:190:ASP:N	4:D:190:ASP:OD2	2.47	0.47
1:A:452:A:O3'	16:P:72:ARG:HD2	2.15	0.47
1:A:1127:G:H21	1:A:1147:C:N4	2.13	0.46
3:C:126:ARG:HH21	3:C:128:PHE:HD1	1.62	0.46
12:L:33:ARG:HA	12:L:33:ARG:HD2	1.69	0.46
7:G:46:ALA:O	7:G:50:ILE:HG12	2.15	0.46
1:A:1241:G:H2'	1:A:1242:C:C6	2.50	0.46
1:A:646:U:H2'	1:A:647:C:C6	2.50	0.46
2:B:68:ILE:O	2:B:90:MET:HB3	2.15	0.46
9:I:44:VAL:HG12	9:I:51:ARG:HH22	1.81	0.46
12:L:111:LYS:NZ	12:L:112:ASP:H	2.11	0.46
1:A:1277:C:O2'	1:A:1279:A:H1'	2.14	0.46
8:H:6:ILE:HD11	8:H:31:PHE:HD2	1.81	0.46
12:L:111:LYS:HA	12:L:111:LYS:HZ3	1.80	0.46
1:A:1236:A:H2'	1:A:1237:C:C6	2.50	0.46
11:K:98:LEU:HA	11:K:98:LEU:HD23	1.74	0.46
13:M:64:TRP:HB3	13:M:66:LEU:HD21	1.98	0.46
1:A:1518:A:H2'	1:A:1519:A:H8	1.80	0.46
1:A:839:U:H5'	1:A:840:C:H5	1.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:21:LYS:HB3	18:R:24:ALA:HB3	1.97	0.46
1:A:120:A:OP2	24:A:1835:NMY:O17	2.34	0.45
1:A:677:U:H3	1:A:713:G:H22	1.63	0.45
1:A:838:G:H2'	1:A:839:U:H5''	1.97	0.45
3:C:88:ARG:HA	3:C:91:LEU:HD22	1.97	0.45
1:A:1223:C:P	19:S:78:ARG:HH21	2.39	0.45
1:A:28:G:O2'	1:A:296:U:OP1	2.25	0.45
4:D:49:ARG:H	4:D:49:ARG:HD2	1.81	0.45
1:A:960:U:H1'	1:A:1223:C:H5'	1.97	0.45
1:A:975:A:H5'	1:A:975:A:C8	2.47	0.45
5:E:78:HIS:CD2	8:H:107:LEU:HD12	2.48	0.45
1:A:755:G:OP2	15:O:65:ARG:HD2	2.17	0.45
17:Q:97:SER:HA	17:Q:103:GLY:HA3	1.97	0.45
1:A:413:G:N2	1:A:428:G:H1'	2.31	0.45
15:O:82:ILE:HG12	15:O:87:ILE:HD12	1.98	0.45
20:T:92:LEU:HA	20:T:92:LEU:HD23	1.81	0.45
1:A:35:G:H2'	1:A:36:C:C6	2.52	0.45
4:D:57:ARG:NH2	4:D:205:GLU:OE2	2.49	0.45
11:K:79:SER:HB2	11:K:106:LYS:HE3	1.98	0.45
17:Q:26:GLN:HG2	17:Q:37:LYS:HG3	1.99	0.45
1:A:1016:A:H2'	1:A:1017:G:O4'	2.17	0.45
1:A:192:U:O2'	20:T:57:ARG:HG2	2.16	0.45
5:E:74:GLY:HA3	5:E:116:THR:HG22	1.99	0.45
1:A:427:U:OP2	4:D:36:ARG:NH2	2.50	0.45
10:J:75:ILE:HG22	10:J:76:ASN:H	1.82	0.45
14:N:16:PHE:HB2	14:N:19:ARG:HG3	1.99	0.45
1:A:1106:G:H5''	3:C:172:ARG:HG2	1.98	0.44
1:A:1057:G:H5''	3:C:154:SER:CB	2.42	0.44
1:A:748:C:H4'	1:A:749:C:O5'	2.17	0.44
8:H:10:LEU:HD22	8:H:83:ILE:HD11	1.99	0.44
4:D:32:ALA:HA	4:D:35:ARG:HG3	2.00	0.44
5:E:75:THR:OG1	5:E:76:ILE:N	2.51	0.44
5:E:78:HIS:CE1	5:E:142:LEU:HD23	2.52	0.44
12:L:27:LEU:HG	12:L:28:LYS:H	1.83	0.44
1:A:1286:A:H2'	1:A:1287:A:H4'	1.98	0.44
1:A:620:C:H2'	1:A:621:A:O4'	2.17	0.44
5:E:31:LEU:HA	5:E:31:LEU:HD23	1.81	0.44
7:G:145:ALA:O	7:G:146:GLU:HB2	2.17	0.44
1:A:194:C:OP1	20:T:61:SER:OG	2.34	0.44
1:A:399:G:H2'	1:A:400:C:C6	2.52	0.44
1:A:452:A:HO2'	1:A:453:A:H8	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:124:SER:HB2	2:B:125:PRO:HD2	1.98	0.44
3:C:120:VAL:O	3:C:124:ILE:HG13	2.18	0.44
1:A:620:C:N1	4:D:135:LEU:HD13	2.32	0.44
6:F:18:GLN:O	6:F:22:GLU:HG2	2.18	0.44
7:G:78:ARG:NH1	7:G:154:TYR:O	2.41	0.44
8:H:4:ASP:CG	8:H:85:ARG:HH11	2.20	0.44
11:K:57:THR:HG22	11:K:59:TYR:N	2.32	0.44
13:M:34:LEU:HA	13:M:37:THR:HG22	1.98	0.44
17:Q:22:LEU:HD11	17:Q:39:SER:HB2	1.99	0.44
1:A:1000:U:H2'	1:A:1001:A:C8	2.52	0.44
1:A:1227:A:OP2	13:M:111:LYS:HE3	2.18	0.44
1:A:731:G:OP1	1:A:766:A:H1'	2.18	0.44
2:B:195:ASP:O	8:H:68:ARG:NH2	2.51	0.44
1:A:860:A:H2'	1:A:861:G:O4'	2.17	0.44
3:C:91:LEU:HD21	3:C:99:VAL:HG22	1.99	0.44
10:J:34:VAL:CG1	10:J:74:ILE:HA	2.45	0.44
1:A:436:C:H2'	1:A:437:U:C6	2.53	0.44
20:T:59:ALA:O	20:T:63:ILE:HG13	2.17	0.44
1:A:1068:G:OP2	1:A:1068:G:H8	2.01	0.44
1:A:190(C):C:H2'	1:A:190(D):U:O4'	2.17	0.44
1:A:262:A:C6	1:A:263:A:C6	3.06	0.44
1:A:695:A:H61	1:A:797:C:H1'	1.83	0.44
9:I:43:ALA:HA	9:I:74:ILE:HD13	2.00	0.44
5:E:81:GLU:HG2	5:E:90:VAL:HG22	2.00	0.43
9:I:112:LYS:HD3	9:I:118:LYS:HA	2.00	0.43
9:I:125:TYR:HD1	9:I:127:LYS:HB2	1.83	0.43
10:J:87:THR:HG23	10:J:89:ASP:OD1	2.17	0.43
24:A:1832:NMY:O11	24:A:1832:NMY:H1	2.18	0.43
7:G:15:ASP:HB3	7:G:20:ASP:H	1.83	0.43
11:K:16:SER:O	11:K:35:PRO:HD3	2.17	0.43
1:A:1128:C:H42	1:A:1143:G:H1	1.65	0.43
1:A:114:U:O2'	1:A:115:G:H5'	2.18	0.43
1:A:1266:G:N2	1:A:1269:A:OP2	2.45	0.43
1:A:1402:4OC:H2'	1:A:1403:C:O4'	2.18	0.43
1:A:355:C:H5'	1:A:389:A:OP2	2.18	0.43
7:G:108:ALA:O	7:G:111:ARG:HB2	2.18	0.43
7:G:5:ARG:HG3	7:G:7:ALA:H	1.83	0.43
10:J:48:THR:HA	10:J:62:HIS:HB3	2.00	0.43
13:M:115:LYS:HB2	13:M:115:LYS:NZ	2.33	0.43
14:N:12:ARG:H	14:N:12:ARG:HD2	1.83	0.43
3:C:30:ARG:HB3	14:N:36:PHE:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1060:C:H2'	1:A:1061:G:H8	1.84	0.43
1:A:294:U:OP1	1:A:610:G:O2'	2.29	0.43
1:A:960:U:H4'	1:A:961:U:C5'	2.49	0.43
12:L:70:ILE:HD13	12:L:77:LEU:HD12	1.99	0.43
15:O:11:VAL:HG11	15:O:34:LEU:HD12	1.99	0.43
1:A:1139:G:H4'	1:A:1140:C:H5'	2.00	0.43
1:A:689:C:H2'	1:A:690:G:O4'	2.19	0.43
15:O:82:ILE:HA	15:O:87:ILE:HG13	2.01	0.43
1:A:135:C:O2	16:P:1:MET:HB2	2.18	0.43
20:T:50:GLU:HG3	20:T:100:ILE:HD12	2.01	0.43
1:A:1368:G:OP1	10:J:62:HIS:HE1	2.02	0.43
2:B:130:ARG:HD3	2:B:130:ARG:HA	1.71	0.43
4:D:83:SER:HA	4:D:89:THR:HG23	2.00	0.43
9:I:63:ILE:HG21	9:I:77:ILE:HG12	1.99	0.43
11:K:34:ASP:HB2	11:K:35:PRO:HD2	2.00	0.43
1:A:1312:G:N7	19:S:4:SER:HB3	2.34	0.43
1:A:1236:A:H4'	1:A:1304:G:H4'	2.00	0.43
1:A:1399:C:C2	1:A:1502:A:N6	2.87	0.43
1:A:872:A:C8	1:A:874:G:C8	3.07	0.43
21:U:5:ASP:O	21:U:11:GLY:HA3	2.19	0.43
1:A:181:G:H4'	1:A:182:U:H5'	2.01	0.43
1:A:444:C:H2'	1:A:445:G:H8	1.83	0.43
5:E:92:LYS:HA	5:E:93:PRO:HD3	1.89	0.43
1:A:1412:C:H2'	1:A:1413:A:C8	2.54	0.43
4:D:170:VAL:HG22	4:D:171:GLY:H	1.84	0.43
1:A:878:G:H5'	8:H:89:PRO:HG2	2.01	0.43
11:K:124:LYS:HE3	11:K:125:PHE:CE2	2.54	0.43
1:A:538:G:H5''	12:L:114:LYS:HB2	2.01	0.43
1:A:60:A:H4'	1:A:61:G:O5'	2.19	0.43
4:D:111:ALA:HB2	4:D:120:LEU:HD12	2.01	0.43
8:H:86:ILE:HG21	8:H:133:LEU:HD13	2.00	0.43
12:L:25:PRO:C	12:L:27:LEU:H	2.22	0.43
1:A:442:C:H42	1:A:492:G:H1	1.65	0.42
8:H:75:ARG:HA	8:H:76:PRO:HD3	1.76	0.42
12:L:46:LYS:HG3	12:L:94:PRO:HD3	2.01	0.42
1:A:376:G:H5''	16:P:5:ARG:HD2	2.01	0.42
1:A:1035:A:H2'	1:A:1036:G:C8	2.54	0.42
1:A:130:A:H1'	1:A:263:A:O2'	2.19	0.42
1:A:134:A:H2'	1:A:135:C:O4'	2.19	0.42
20:T:57:ARG:NH2	20:T:100:ILE:HD13	2.34	0.42
5:E:110:LEU:HD13	5:E:118:ILE:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:69:GLU:CD	6:F:69:GLU:H	2.22	0.42
1:A:1002:G:H2'	1:A:1003:G:C8	2.53	0.42
1:A:110:C:H2'	1:A:111:G:O4'	2.19	0.42
1:A:130:A:OP2	1:A:190(E):U:O2'	2.25	0.42
1:A:184:G:H2'	1:A:185:A:C8	2.53	0.42
2:B:79:ASP:HA	2:B:82:ARG:HG2	2.00	0.42
4:D:3:ARG:HD2	4:D:118:ARG:NE	2.34	0.42
11:K:109:VAL:HG22	18:R:86:VAL:HG12	2.01	0.42
20:T:73:HIS:HB3	20:T:74:LYS:H	1.61	0.42
1:A:731:G:H5'	1:A:766:A:H4'	2.01	0.42
1:A:933:G:OP2	7:G:3:ARG:HB3	2.19	0.42
14:N:9:LYS:HE2	14:N:23:ARG:HB2	2.01	0.42
14:N:9:LYS:HE3	14:N:9:LYS:HB3	1.78	0.42
1:A:532:A:H2'	1:A:532:A:N3	2.34	0.42
1:A:875:C:O2'	8:H:14:ARG:NH1	2.52	0.42
1:A:977:A:H2'	1:A:978:A:H5''	2.01	0.42
3:C:123:GLN:O	3:C:126:ARG:HG2	2.19	0.42
3:C:126:ARG:NE	3:C:128:PHE:HB2	2.34	0.42
1:A:1124:G:H4'	10:J:38:ILE:HD11	2.01	0.42
9:I:15:ALA:HB2	9:I:65:VAL:HG13	2.00	0.42
1:A:1147:C:HO2'	9:I:5:TYR:HH	1.67	0.42
9:I:69:GLY:O	9:I:73:GLN:HG3	2.19	0.42
16:P:8:ARG:N	16:P:29:ASP:OD2	2.52	0.42
1:A:1314:C:C5	19:S:6:LYS:HE2	2.55	0.42
21:U:6:ARG:HG2	21:U:6:ARG:H	1.71	0.42
1:A:432:A:H3'	1:A:433:C:H5''	2.02	0.42
6:F:39:LYS:HB2	6:F:39:LYS:HE3	1.90	0.42
8:H:121:ASP:OD1	8:H:121:ASP:N	2.53	0.42
1:A:1207:2MG:HM23	1:A:1208:C:H1'	2.02	0.42
1:A:1343:G:H2'	1:A:1344:C:C6	2.55	0.42
1:A:1372:U:H2'	1:A:1373:G:O4'	2.20	0.42
12:L:83:VAL:HG13	12:L:100:ILE:HG23	2.01	0.42
16:P:59:TRP:HA	16:P:62:VAL:HG22	2.02	0.42
18:R:17:SER:OG	18:R:55:ARG:HG2	2.20	0.42
19:S:80:TYR:CE1	19:S:81:ARG:HB2	2.54	0.42
8:H:56:LYS:HA	8:H:57:PRO:HD3	1.75	0.42
9:I:85:LEU:HA	9:I:85:LEU:HD13	1.94	0.42
12:L:53:ARG:HD2	12:L:53:ARG:N	2.35	0.42
1:A:1239:A:C4	1:A:1298:C:N4	2.88	0.41
1:A:1323:G:H2'	1:A:1324:A:C8	2.55	0.41
5:E:152:ARG:NH2	8:H:107:LEU:O	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:113:GLU:H	7:G:113:GLU:HG2	1.61	0.41
5:E:143:ARG:NH1	8:H:77:GLU:OE2	2.49	0.41
10:J:34:VAL:HG12	10:J:35:SER:N	2.33	0.41
13:M:96:LEU:O	13:M:110:ARG:NH1	2.53	0.41
1:A:1133:G:N2	1:A:1141:C:O2	2.51	0.41
1:A:551:U:H2'	1:A:552:U:C6	2.54	0.41
2:B:201:ILE:O	2:B:203:GLY:N	2.52	0.41
7:G:28:ASN:OD1	7:G:36:LYS:NZ	2.44	0.41
1:A:1040:U:H2'	1:A:1041:A:H8	1.84	0.41
1:A:1132:C:H2'	1:A:1133:G:H8	1.84	0.41
11:K:38:ASN:HA	11:K:39:PRO:HD3	1.88	0.41
18:R:76:LEU:HD23	18:R:76:LEU:HA	1.89	0.41
1:A:109:A:C6	1:A:326:G:C6	3.09	0.41
1:A:488:C:H2'	1:A:489:C:C6	2.55	0.41
1:A:857:C:H2'	1:A:858:G:O4'	2.20	0.41
1:A:8:A:N6	4:D:209:ARG:HB2	2.36	0.41
5:E:8:GLU:OE2	5:E:63:ARG:NH2	2.48	0.41
5:E:90:VAL:O	5:E:91:LEU:HD23	2.20	0.41
10:J:57:LYS:HE2	10:J:60:ARG:NH2	2.36	0.41
12:L:60:LEU:HB3	12:L:62:SER:HB3	2.01	0.41
1:A:737:A:H2'	1:A:738:C:C6	2.55	0.41
12:L:7:ILE:HA	12:L:7:ILE:HD13	1.87	0.41
3:C:12:LEU:HD23	3:C:12:LEU:HA	1.88	0.41
8:H:19:VAL:HG23	8:H:21:LYS:HD3	2.03	0.41
1:A:1425:U:H2'	1:A:1426:C:C6	2.55	0.41
24:A:1833:NMY:H18	24:A:1833:NMY:H16	1.27	0.41
1:A:620:C:C2	4:D:135:LEU:HD13	2.56	0.41
1:A:932:C:C5	7:G:3:ARG:HD3	2.55	0.41
2:B:42:ILE:HG21	2:B:202:PRO:O	2.20	0.41
4:D:63:LYS:NZ	4:D:197:PRO:O	2.43	0.41
1:A:1346:A:H2'	7:G:10:ARG:HH22	1.85	0.41
13:M:108:ARG:HH22	13:M:111:LYS:HE2	1.85	0.41
15:O:39:LEU:CD1	15:O:56:LEU:HB2	2.48	0.41
15:O:74:ASP:HA	15:O:75:PRO:HD2	1.90	0.41
24:A:1835:NMY:HN61	24:A:1835:NMY:H4	1.61	0.41
10:J:52:GLY:O	14:N:41:ARG:NH2	2.54	0.41
16:P:6:LEU:HD11	16:P:73:LEU:HD12	2.03	0.41
1:A:613:C:H2'	1:A:614:A:C8	2.55	0.41
1:A:1148:U:H2'	1:A:1149:C:O4'	2.21	0.41
4:D:36:ARG:HB3	4:D:38:TYR:CZ	2.56	0.41
6:F:2:ARG:NH2	6:F:69:GLU:HG2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:38:ILE:HB	10:J:71:LEU:HB2	2.03	0.41
12:L:117:ARG:O	12:L:121:GLY:N	2.54	0.41
1:A:1127:G:N2	1:A:1145:C:C2	2.89	0.41
1:A:1256:A:H5'	1:A:1258:G:C4	2.56	0.41
1:A:1516:G:H2'	1:A:1518:A:OP2	2.21	0.41
7:G:88:PRO:HG3	7:G:149:ARG:HA	2.02	0.41
13:M:52:GLU:O	13:M:56:LEU:HB2	2.20	0.41
13:M:67:GLU:HB3	13:M:68:GLY:H	1.64	0.41
15:O:43:LEU:HA	15:O:43:LEU:HD23	1.87	0.41
1:A:1030(A):G:N2	1:A:1030(C):G:H3'	2.37	0.40
1:A:1315:U:OP2	19:S:6:LYS:NZ	2.52	0.40
1:A:409:G:H1	1:A:433:C:N4	2.19	0.40
1:A:771:G:H2'	1:A:772:U:C6	2.55	0.40
1:A:828:A:OP1	1:A:828:A:H4'	2.21	0.40
14:N:8:GLU:O	14:N:11:LYS:HD3	2.22	0.40
20:T:36:LEU:HA	20:T:36:LEU:HD23	1.85	0.40
1:A:1291:G:OP1	7:G:37:ASN:ND2	2.53	0.40
1:A:397:A:H5'	1:A:398:C:OP1	2.20	0.40
4:D:31:CYS:C	4:D:33:MET:H	2.25	0.40
7:G:65:ALA:O	7:G:69:VAL:HG23	2.20	0.40
1:A:1118:C:H2'	1:A:1119:C:C6	2.56	0.40
1:A:1498:UR3:H6	1:A:1498:UR3:O5'	2.22	0.40
1:A:436:C:H2'	1:A:437:U:H6	1.86	0.40
1:A:500:G:H2'	1:A:501:C:C6	2.56	0.40
1:A:769:G:H4'	1:A:1513:A:H4'	2.04	0.40
2:B:126:GLU:O	2:B:129:GLU:HG2	2.20	0.40
3:C:52:LEU:HA	3:C:70:VAL:HA	2.03	0.40
16:P:34:GLU:OE2	16:P:55:ARG:HD3	2.21	0.40
1:A:501:C:H2'	1:A:502:G:C8	2.57	0.40
2:B:93:VAL:HG11	2:B:97:TRP:CD1	2.57	0.40
6:F:19:LEU:O	6:F:23:LYS:HG2	2.22	0.40
7:G:111:ARG:NH1	7:G:113:GLU:OE2	2.54	0.40
9:I:126:SER:OG	9:I:128:ARG:OXT	2.40	0.40
9:I:56:LEU:O	9:I:58:HIS:N	2.54	0.40
18:R:38:GLU:CD	18:R:38:GLU:H	2.25	0.40
19:S:80:TYR:CZ	19:S:81:ARG:HB2	2.56	0.40
1:A:1057:G:H2'	1:A:1058:G:O4'	2.22	0.40
1:A:328:C:O2	1:A:328:C:H2'	2.22	0.40
1:A:895:G:H2'	1:A:896:C:C6	2.57	0.40
8:H:102:ARG:H	8:H:102:ARG:HD2	1.87	0.40
11:K:48:ILE:HG22	11:K:49:GLY:H	1.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	234/256 (91%)	208 (89%)	24 (10%)	2 (1%)	17	48
3	C	205/239 (86%)	190 (93%)	15 (7%)	0	100	100
4	D	206/209 (99%)	200 (97%)	5 (2%)	1 (0%)	29	61
5	E	149/162 (92%)	145 (97%)	4 (3%)	0	100	100
6	F	99/101 (98%)	96 (97%)	3 (3%)	0	100	100
7	G	153/156 (98%)	145 (95%)	8 (5%)	0	100	100
8	H	136/138 (99%)	133 (98%)	3 (2%)	0	100	100
9	I	125/128 (98%)	109 (87%)	15 (12%)	1 (1%)	19	51
10	J	97/105 (92%)	78 (80%)	17 (18%)	2 (2%)	7	31
11	K	117/129 (91%)	107 (92%)	10 (8%)	0	100	100
12	L	122/135 (90%)	110 (90%)	10 (8%)	2 (2%)	9	36
13	M	116/126 (92%)	109 (94%)	7 (6%)	0	100	100
14	N	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
15	O	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
16	P	82/88 (93%)	80 (98%)	2 (2%)	0	100	100
17	Q	102/105 (97%)	95 (93%)	7 (7%)	0	100	100
18	R	71/88 (81%)	66 (93%)	4 (6%)	1 (1%)	11	38
19	S	79/93 (85%)	72 (91%)	7 (9%)	0	100	100
20	T	97/106 (92%)	88 (91%)	8 (8%)	1 (1%)	15	46
21	U	23/27 (85%)	22 (96%)	1 (4%)	0	100	100
All	All	2357/2541 (93%)	2189 (93%)	158 (7%)	10 (0%)	34	66

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	L	28	LYS
10	J	34	VAL
18	R	19	LYS
10	J	72	VAL
20	T	74	LYS
2	B	128	GLU
9	I	56	LEU
2	B	89	GLY
12	L	30	ALA
4	D	5	ILE

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	B	194/220 (88%)	185 (95%)	9 (5%)	27 58
3	C	160/188 (85%)	145 (91%)	15 (9%)	8 30
4	D	180/181 (99%)	166 (92%)	14 (8%)	12 38
5	E	115/123 (94%)	107 (93%)	8 (7%)	15 43
6	F	90/90 (100%)	87 (97%)	3 (3%)	38 66
7	G	126/127 (99%)	119 (94%)	7 (6%)	21 52
8	H	119/119 (100%)	109 (92%)	10 (8%)	11 35
9	I	98/99 (99%)	90 (92%)	8 (8%)	11 36
10	J	87/92 (95%)	81 (93%)	6 (7%)	15 44
11	K	90/99 (91%)	88 (98%)	2 (2%)	52 74
12	L	103/110 (94%)	97 (94%)	6 (6%)	20 50
13	M	94/101 (93%)	88 (94%)	6 (6%)	17 46
14	N	49/50 (98%)	43 (88%)	6 (12%)	5 20
15	O	79/80 (99%)	71 (90%)	8 (10%)	7 27
16	P	72/74 (97%)	71 (99%)	1 (1%)	67 82
17	Q	96/97 (99%)	90 (94%)	6 (6%)	18 47
18	R	64/77 (83%)	63 (98%)	1 (2%)	62 79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	S	71/80 (89%)	65 (92%)	6 (8%)	10	35
20	T	76/82 (93%)	69 (91%)	7 (9%)	9	31
21	U	19/22 (86%)	18 (95%)	1 (5%)	22	53
All	All	1982/2111 (94%)	1852 (93%)	130 (7%)	16	46

All (130) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	69	LEU
2	B	79	ASP
2	B	114	ARG
2	B	142	LEU
2	B	157	ARG
2	B	170	GLU
2	B	223	ILE
2	B	231	GLU
2	B	236	TYR
3	C	3	ASN
3	C	16	ARG
3	C	37	GLN
3	C	45	LYS
3	C	64	VAL
3	C	83	ARG
3	C	91	LEU
3	C	99	VAL
3	C	101	LEU
3	C	107	GLN
3	C	127	ARG
3	C	166	GLU
3	C	167	TRP
3	C	178	LEU
3	C	204	LEU
4	D	17	VAL
4	D	19	LEU
4	D	36	ARG
4	D	49	ARG
4	D	53	ASP
4	D	61	LYS
4	D	64	LEU
4	D	73	ARG
4	D	96	LEU

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Mol	Chain	Res	Type
4	D	115	ARG
4	D	119	GLN
4	D	122	ARG
4	D	135	LEU
4	D	190	ASP
5	E	12	LEU
5	E	41	VAL
5	E	43	LEU
5	E	47	LYS
5	E	64	ARG
5	E	76	ILE
5	E	79	GLU
5	E	80	ILE
6	F	36	ARG
6	F	45	LEU
6	F	54	LYS
7	G	8	GLU
7	G	11	GLN
7	G	54	THR
7	G	113	GLU
7	G	114	ARG
7	G	124	LEU
7	G	156	TRP
8	H	19	VAL
8	H	26	VAL
8	H	39	LEU
8	H	63	LEU
8	H	68	ARG
8	H	85	ARG
8	H	91	ARG
8	H	92	ARG
8	H	102	ARG
8	H	133	LEU
9	I	27	THR
9	I	38	GLN
9	I	79	LEU
9	I	85	LEU
9	I	102	LEU
9	I	108	VAL
9	I	118	LYS
9	I	121	ARG
10	J	16	LEU

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Mol	Chain	Res	Type
10	J	29	ARG
10	J	60	ARG
10	J	62	HIS
10	J	71	LEU
10	J	74	ILE
11	K	48	ILE
11	K	127	LYS
12	L	20	LYS
12	L	33	ARG
12	L	53	ARG
12	L	80	HIS
12	L	90	VAL
12	L	126	LYS
13	M	16	ASP
13	M	56	LEU
13	M	63	THR
13	M	70	LEU
13	M	110	ARG
13	M	115	LYS
14	N	8	GLU
14	N	9	LYS
14	N	12	ARG
14	N	22	THR
14	N	33	VAL
14	N	41	ARG
15	O	5	LYS
15	O	6	GLU
15	O	34	LEU
15	O	70	LEU
15	O	71	GLN
15	O	79	ARG
15	O	81	LEU
15	O	87	ILE
16	P	55	ARG
17	Q	38	ARG
17	Q	59	ILE
17	Q	74	LEU
17	Q	91	ARG
17	Q	98	LEU
17	Q	101	ARG
18	R	18	ARG
19	S	7	LYS

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Mol	Chain	Res	Type
19	S	15	LEU
19	S	27	GLU
19	S	61	TYR
19	S	65	ASN
19	S	81	ARG
20	T	8	ARG
20	T	19	SER
20	T	42	GLN
20	T	45	GLN
20	T	73	HIS
20	T	74	LYS
20	T	84	LEU
21	U	6	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	212	GLN
3	C	6	HIS
7	G	51	GLN
9	I	73	GLN
13	M	106	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1507/1522 (99%)	201 (13%)	28 (1%)

All (201) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	50	A
1	A	51	A
1	A	54	C
1	A	60	A

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Mol	Chain	Res	Type
1	A	61	G
1	A	101	A
1	A	116	A
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	145	G
1	A	163	C
1	A	169	C
1	A	182	U
1	A	190(D)	U
1	A	195	A
1	A	197	A
1	A	202	U
1	A	204	U
1	A	220	G
1	A	247	G
1	A	251	G
1	A	266	G
1	A	267	C
1	A	289	G
1	A	301	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	332	G
1	A	345	C
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	397	A
1	A	398	C
1	A	406	G
1	A	412	A
1	A	413	G
1	A	421	U
1	A	424	G
1	A	429	U

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Mol	Chain	Res	Type
1	A	433	C
1	A	439	A
1	A	442	C
1	A	452	A
1	A	460	A
1	A	461	C
1	A	485	G
1	A	497	A
1	A	498	U
1	A	509	A
1	A	510	A
1	A	511	C
1	A	518	C
1	A	527	7MG
1	A	532	A
1	A	533	A
1	A	545	C
1	A	547	A
1	A	559	A
1	A	560	U
1	A	564	C
1	A	572	A
1	A	573	A
1	A	576	G
1	A	577	G
1	A	579	G
1	A	596	C
1	A	616	G
1	A	618	C
1	A	630	G
1	A	653	A
1	A	665	A
1	A	687	A
1	A	688	G
1	A	702	A
1	A	721	G
1	A	723	U
1	A	724	G
1	A	731	G
1	A	749	C
1	A	755	G
1	A	777	A

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Mol	Chain	Res	Type
1	A	781	A
1	A	787	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	872	A
1	A	876	G
1	A	902	G
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	939	G
1	A	960	U
1	A	961	U
1	A	966	M2G
1	A	969	A
1	A	971	G
1	A	972	C
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	1003(A)	G
1	A	1004	A
1	A	1005	A
1	A	1025	U
1	A	1026	G
1	A	1027	C
1	A	1028	C
1	A	1031	G

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Mol	Chain	Res	Type
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	1124	G
1	A	1125	U
1	A	1126	U
1	A	1127	G
1	A	1129	C
1	A	1130	A
1	A	1139	G
1	A	1146	A
1	A	1152	A
1	A	1159	U
1	A	1171	G
1	A	1181	G
1	A	1182	G
1	A	1183	A
1	A	1184	G
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	1227	A
1	A	1238	A
1	A	1241	G
1	A	1257	U
1	A	1258	G
1	A	1270	C
1	A	1280	A
1	A	1281	U
1	A	1287	A
1	A	1300	G
1	A	1302	U
1	A	1312	G
1	A	1319	A
1	A	1320	C

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Mol	Chain	Res	Type
1	A	1338	G
1	A	1346	A
1	A	1347	G
1	A	1353	G
1	A	1362	C
1	A	1363	A
1	A	1364	U
1	A	1370	G
1	A	1398	A
1	A	1442	G
1	A	1443	G
1	A	1446	A
1	A	1487	G
1	A	1492	A
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
1	A	1531	A

All (28) 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	352	C
1	A	372	C
1	A	428	G
1	A	484	G
1	A	496	A
1	A	509	A
1	A	559	A

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Mol	Chain	Res	Type
1	A	575	G
1	A	687	A
1	A	701	C
1	A	723	U
1	A	748	C
1	A	812	C
1	A	960	U
1	A	1065	U
1	A	1067	A
1	A	1182	G
1	A	1201	A
1	A	1397	C
1	A	1504	G
1	A	1528	U

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

11 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MC	A	967	1	15,22,23	0.94	0	19,32,35	0.93	0
1	5MC	A	1404	1	15,22,23	0.81	0	19,32,35	1.11	2 (10%)
1	4OC	A	1402	1	16,23,24	0.80	0	17,32,35	0.85	0
1	PSU	A	516	1,22	17,21,22	1.06	1 (5%)	20,30,33	3.21	5 (25%)
1	2MG	A	1207	1	19,26,27	2.14	4 (21%)	21,38,41	2.02	3 (14%)
1	5MC	A	1400	1	15,22,23	0.89	0	19,32,35	1.05	2 (10%)
1	5MC	A	1407	1	15,22,23	0.97	1 (6%)	19,32,35	1.12	1 (5%)
1	7MG	A	527	1	22,26,27	2.19	5 (22%)	28,39,42	1.80	7 (25%)
12	0TD	L	92	12	4,9,10	0.88	0	3,11,13	2.00	2 (66%)
1	UR3	A	1498	1	14,22,23	0.80	0	15,32,35	1.18	1 (6%)
1	M2G	A	966	1	20,27,28	1.92	4 (20%)	22,40,43	2.33	5 (22%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MC	A	967	1	-	0/5/25/26	0/2/2/2
1	5MC	A	1404	1	-	0/5/25/26	0/2/2/2
1	4OC	A	1402	1	-	2/9/29/30	0/2/2/2
1	PSU	A	516	1,22	-	0/7/25/26	0/2/2/2
1	2MG	A	1207	1	-	0/5/27/28	0/3/3/3
1	5MC	A	1400	1	-	2/5/25/26	0/2/2/2
1	5MC	A	1407	1	-	0/5/25/26	0/2/2/2
1	7MG	A	527	1	-	2/7/37/38	0/3/3/3
12	0TD	L	92	12	-	1/3/12/14	-
1	UR3	A	1498	1	-	0/5/25/26	0/2/2/2
1	M2G	A	966	1	-	0/7/29/30	0/3/3/3

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1207	2MG	C2-N2	6.46	1.39	1.34
1	A	527	7MG	C4-N3	6.11	1.42	1.34
1	A	966	M2G	C6-N1	5.76	1.43	1.33
1	A	1207	2MG	C6-N1	5.64	1.42	1.33
1	A	527	7MG	C2-N2	5.02	1.43	1.33
1	A	527	7MG	C8-N9	-4.42	1.35	1.45
1	A	966	M2G	C2-N1	3.70	1.41	1.34
1	A	966	M2G	C2-N2	3.49	1.40	1.34
1	A	516	PSU	C4-N3	3.19	1.38	1.33
1	A	527	7MG	C6-N1	3.07	1.38	1.33
1	A	966	M2G	C4-N3	2.96	1.40	1.35
1	A	1207	2MG	C4-N3	2.50	1.39	1.35
1	A	1407	5MC	C5-C4	2.40	1.45	1.41
1	A	527	7MG	CM7-N7	-2.12	1.42	1.46
1	A	1207	2MG	C2-N1	2.06	1.41	1.34

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	516	PSU	N1-C2-N3	-10.90	119.76	128.43
1	A	966	M2G	C5-C6-N1	-8.17	112.25	123.43
1	A	1207	2MG	C5-C6-N1	-7.46	113.23	123.43
1	A	516	PSU	C4-N3-C2	6.26	120.43	115.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	966	M2G	C6-N1-C2	5.71	122.98	116.18
1	A	527	7MG	N3-C4-N9	4.74	133.00	126.91
1	A	516	PSU	C5-C4-N3	-4.71	119.29	125.36
1	A	527	7MG	C5-C4-N3	-4.26	119.53	126.49
1	A	527	7MG	N7-C8-N9	3.88	108.93	103.38
1	A	1207	2MG	C6-N1-C2	3.84	122.05	115.18
1	A	516	PSU	C6-N1-C2	3.03	120.35	115.36
1	A	516	PSU	C5-C6-N1	-2.81	120.98	124.44
1	A	527	7MG	C6-N1-C2	2.68	120.19	115.93
12	L	92	0TD	CSB-SB-CB	-2.50	96.94	101.85
1	A	527	7MG	C2-N3-C4	2.47	120.71	113.89
1	A	527	7MG	C6-C5-C4	2.40	117.78	115.20
1	A	1498	UR3	C3'-C2'-C1'	2.36	104.53	100.98
1	A	1207	2MG	C4-C5-N7	2.35	111.85	109.40
1	A	1407	5MC	N4-C4-N3	-2.29	113.80	117.03
1	A	527	7MG	N1-C2-N3	-2.28	121.85	125.42
1	A	966	M2G	N3-C2-N2	2.23	119.45	117.18
1	A	1400	5MC	C2-N3-C4	2.23	118.71	116.02
1	A	1404	5MC	C2-N3-C4	2.15	118.61	116.02
12	L	92	0TD	O-C-CA	-2.15	119.15	124.78
1	A	966	M2G	C2-N3-C4	-2.12	112.87	115.28
1	A	966	M2G	N1-C2-N2	-2.07	115.09	117.19
1	A	1400	5MC	CM5-C5-C6	2.02	122.94	118.68
1	A	1404	5MC	CM5-C5-C6	2.02	122.94	118.68

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	527	7MG	O4'-C4'-C5'-O5'
1	A	527	7MG	C3'-C4'-C5'-O5'
12	L	92	0TD	CG-CB-SB-CSB
1	A	1402	4OC	O4'-C4'-C5'-O5'
1	A	1402	4OC	C3'-C4'-C5'-O5'
1	A	1400	5MC	O4'-C4'-C5'-O5'
1	A	1400	5MC	C3'-C4'-C5'-O5'

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1402	4OC	1	0
1	A	1207	2MG	1	0
12	L	92	0TD	2	0
1	A	1498	UR3	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 258 ligands modelled in this entry, 252 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	NMY	A	1834	-	45,45,45	1.59	8 (17%)	63,67,67	1.84	16 (25%)
24	NMY	A	1837	-	45,45,45	1.59	9 (20%)	63,67,67	1.91	17 (26%)
24	NMY	A	1833	-	45,45,45	1.46	6 (13%)	63,67,67	1.77	13 (20%)
24	NMY	A	1836	-	45,45,45	1.54	8 (17%)	63,67,67	2.22	16 (25%)
24	NMY	A	1832	-	45,45,45	1.46	8 (17%)	63,67,67	1.43	9 (14%)
24	NMY	A	1835	-	45,45,45	1.45	7 (15%)	63,67,67	1.46	13 (20%)

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	NMY	A	1834	-	-	8/18/94/94	0/4/4/4
24	NMY	A	1837	-	-	8/18/94/94	0/4/4/4
24	NMY	A	1833	-	-	6/18/94/94	0/4/4/4
24	NMY	A	1836	-	-	11/18/94/94	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	NMY	A	1832	-	-	6/18/94/94	0/4/4/4
24	NMY	A	1835	-	-	3/18/94/94	0/4/4/4

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1834	NMY	C13-C14	4.69	1.58	1.52
24	A	1837	NMY	C1-C2	3.89	1.60	1.52
24	A	1837	NMY	C6-C5	3.81	1.57	1.52
24	A	1836	NMY	C6-C5	3.66	1.57	1.52
24	A	1834	NMY	C6-C5	3.49	1.56	1.52
24	A	1833	NMY	C3-C2	3.47	1.57	1.53
24	A	1835	NMY	C6-C5	3.45	1.56	1.52
24	A	1833	NMY	C6-C5	3.41	1.56	1.52
24	A	1832	NMY	C6-C5	3.38	1.56	1.52
24	A	1837	NMY	C3-C2	3.35	1.57	1.53
24	A	1836	NMY	C1-C2	3.33	1.58	1.52
24	A	1834	NMY	C3-C2	3.31	1.57	1.53
24	A	1837	NMY	C13-C14	3.10	1.56	1.52
24	A	1835	NMY	C3-C2	3.09	1.57	1.53
24	A	1836	NMY	C3-C2	3.09	1.57	1.53
24	A	1836	NMY	C23-C22	3.09	1.56	1.52
24	A	1836	NMY	C18-C19	3.07	1.58	1.52
24	A	1832	NMY	C3-C2	2.98	1.57	1.53
24	A	1832	NMY	C13-C14	2.94	1.56	1.52
24	A	1836	NMY	C13-C14	2.93	1.56	1.52
24	A	1833	NMY	C1-C2	2.92	1.58	1.52
24	A	1834	NMY	C1-C2	2.89	1.58	1.52
24	A	1835	NMY	C1-C2	2.87	1.58	1.52
24	A	1833	NMY	C13-C14	2.86	1.56	1.52
24	A	1837	NMY	C18-C19	2.78	1.57	1.52
24	A	1833	NMY	C23-C22	2.77	1.55	1.52
24	A	1835	NMY	C13-C14	2.76	1.56	1.52
24	A	1832	NMY	C1-C2	2.73	1.57	1.52
24	A	1832	NMY	C23-C22	2.69	1.55	1.52
24	A	1837	NMY	C23-C22	2.67	1.55	1.52
24	A	1834	NMY	C18-C19	2.58	1.57	1.52
24	A	1834	NMY	C21-C22	2.54	1.58	1.53
24	A	1835	NMY	C23-C22	2.51	1.55	1.52
24	A	1835	NMY	C18-C19	2.49	1.57	1.52
24	A	1832	NMY	C18-C19	2.48	1.57	1.52
24	A	1834	NMY	C14-C15	2.35	1.58	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1832	NMY	C10-C11	2.30	1.57	1.52
24	A	1834	NMY	C23-C22	2.27	1.55	1.52
24	A	1837	NMY	C10-C11	2.17	1.56	1.52
24	A	1832	NMY	C10-C9	2.15	1.57	1.53
24	A	1836	NMY	C21-C22	2.11	1.57	1.53
24	A	1835	NMY	C10-C9	2.11	1.57	1.53
24	A	1837	NMY	C12-C7	2.06	1.58	1.53
24	A	1833	NMY	C18-C19	2.05	1.56	1.52
24	A	1836	NMY	C20-C19	2.05	1.56	1.53
24	A	1837	NMY	C20-C19	2.00	1.56	1.53

All (84) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1836	NMY	C13-C14-C15	-10.11	89.95	102.10
24	A	1836	NMY	C14-C15-C16	-6.52	91.66	103.22
24	A	1837	NMY	O1-C10-C11	5.68	121.92	107.48
24	A	1833	NMY	O11-C13-O16	-5.42	105.56	111.43
24	A	1837	NMY	C11-C10-C9	-5.25	101.35	111.16
24	A	1836	NMY	O11-C13-C14	5.13	118.59	107.96
24	A	1834	NMY	O18-C18-C19	5.12	117.03	108.22
24	A	1833	NMY	C11-C10-C9	-4.91	102.00	111.16
24	A	1832	NMY	O11-C13-O16	-4.34	106.73	111.43
24	A	1833	NMY	O21-C21-C20	-4.28	100.45	110.35
24	A	1833	NMY	O11-C11-C12	4.28	118.66	107.28
24	A	1833	NMY	O20-C20-C19	-4.15	102.76	110.22
24	A	1837	NMY	O11-C13-C14	4.04	116.33	107.96
24	A	1834	NMY	C11-C10-C9	-3.88	103.92	111.16
24	A	1832	NMY	O1-C10-C11	3.86	117.29	107.48
24	A	1836	NMY	O16-C13-C14	-3.79	100.10	104.98
24	A	1834	NMY	O20-C20-C19	-3.61	103.74	110.22
24	A	1836	NMY	O18-C18-C19	3.53	114.31	108.22
24	A	1834	NMY	O1-C10-C11	3.50	116.39	107.48
24	A	1834	NMY	O11-C13-C14	3.46	115.14	107.96
24	A	1837	NMY	O16-C13-C14	-3.44	100.55	104.98
24	A	1834	NMY	O21-C21-C20	-3.29	102.74	110.35
24	A	1836	NMY	O20-C20-C19	-3.29	104.31	110.22
24	A	1836	NMY	O1-C10-C11	3.25	115.75	107.48
24	A	1835	NMY	C11-C10-C9	-3.24	105.11	111.16
24	A	1835	NMY	O11-C13-O16	-3.20	107.96	111.43
24	A	1835	NMY	O21-C21-C20	-3.18	103.01	110.35
24	A	1837	NMY	C13-C14-C15	-3.15	98.32	102.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1837	NMY	O5-C5-C6	3.11	111.80	106.01
24	A	1837	NMY	O11-C11-C12	3.09	115.49	107.28
24	A	1833	NMY	O1-C10-C11	3.08	115.31	107.48
24	A	1837	NMY	O11-C13-O16	-3.07	108.11	111.43
24	A	1834	NMY	O22-C22-C21	3.04	115.21	109.69
24	A	1836	NMY	O1-C1-C2	3.01	113.41	108.22
24	A	1835	NMY	O20-C20-C19	-2.98	104.86	110.22
24	A	1832	NMY	O21-C21-C20	-2.97	103.49	110.35
24	A	1834	NMY	O11-C13-O16	-2.94	108.24	111.43
24	A	1833	NMY	O12-C12-C7	-2.93	104.44	109.81
24	A	1834	NMY	C18-C19-N23	2.92	115.46	110.20
24	A	1835	NMY	O11-C13-C14	2.91	113.99	107.96
24	A	1836	NMY	O21-C21-C20	-2.90	103.64	110.35
24	A	1837	NMY	O1-C1-C2	2.86	113.14	108.22
24	A	1832	NMY	O20-C20-C19	-2.86	105.08	110.22
24	A	1833	NMY	O1-C1-C2	2.75	112.95	108.22
24	A	1835	NMY	C13-C14-C15	-2.72	98.83	102.10
24	A	1837	NMY	C1-C2-N2	2.71	115.09	110.20
24	A	1837	NMY	O20-C20-C19	-2.69	105.38	110.22
24	A	1837	NMY	O11-C11-C10	2.61	114.12	107.48
24	A	1834	NMY	C18-O18-C15	-2.61	111.50	117.96
24	A	1833	NMY	C18-O18-C15	-2.57	111.61	117.96
24	A	1836	NMY	C11-C10-C9	-2.56	106.39	111.16
24	A	1837	NMY	O18-C18-C19	2.55	112.60	108.22
24	A	1837	NMY	O21-C21-C20	-2.52	104.52	110.35
24	A	1834	NMY	C20-C21-C22	2.52	114.73	110.24
24	A	1835	NMY	O16-C13-C14	-2.51	101.74	104.98
24	A	1832	NMY	O18-C18-O22	-2.45	103.83	110.67
24	A	1836	NMY	O12-C12-C7	-2.42	105.38	109.81
24	A	1832	NMY	O1-C1-C2	2.41	112.37	108.22
24	A	1836	NMY	O11-C11-C12	2.41	113.68	107.28
24	A	1834	NMY	O1-C1-O5	-2.40	103.96	110.67
24	A	1836	NMY	C1-C2-N2	2.36	114.46	110.20
24	A	1833	NMY	O20-C20-C21	-2.34	104.93	110.35
24	A	1835	NMY	C13-O11-C11	-2.34	112.16	117.96
24	A	1836	NMY	C18-O22-C22	-2.29	109.19	113.69
24	A	1834	NMY	O11-C11-C12	2.28	113.36	107.28
24	A	1832	NMY	C8-C7-C12	-2.28	106.60	110.04
24	A	1834	NMY	O22-C18-C19	-2.27	104.95	110.06
24	A	1835	NMY	O18-C18-C19	2.26	112.11	108.22
24	A	1837	NMY	O1-C1-O5	-2.23	104.44	110.67
24	A	1835	NMY	O18-C18-O22	-2.22	104.47	110.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1833	NMY	O18-C18-C19	2.18	111.98	108.22
24	A	1835	NMY	O1-C1-O5	-2.16	104.64	110.67
24	A	1836	NMY	C18-C19-N23	2.15	114.07	110.20
24	A	1834	NMY	C18-O22-C22	-2.14	109.50	113.69
24	A	1832	NMY	C11-C10-C9	-2.13	107.19	111.16
24	A	1837	NMY	C12-C11-C10	-2.13	106.80	111.66
24	A	1834	NMY	C14-C15-C16	-2.10	99.50	103.22
24	A	1835	NMY	O1-C10-C11	2.07	112.74	107.48
24	A	1835	NMY	C18-O18-C15	-2.07	112.85	117.96
24	A	1837	NMY	O5-C5-C4	2.06	113.44	109.69
24	A	1836	NMY	C4-C3-C2	-2.06	107.53	111.07
24	A	1832	NMY	O11-C13-C14	2.03	112.17	107.96
24	A	1833	NMY	O5-C5-C6	2.02	109.77	106.01
24	A	1833	NMY	C18-O22-C22	-2.02	109.72	113.69

There are no chirality outliers.

All (42) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	A	1837	NMY	C4-C5-C6-N6
24	A	1837	NMY	O5-C5-C6-N6
24	A	1837	NMY	C21-C22-C23-N19
24	A	1837	NMY	O22-C22-C23-N19
24	A	1834	NMY	C4-C5-C6-N6
24	A	1834	NMY	O5-C5-C6-N6
24	A	1834	NMY	C21-C22-C23-N19
24	A	1836	NMY	C14-C13-O11-C11
24	A	1836	NMY	O16-C13-O11-C11
24	A	1836	NMY	C19-C18-O18-C15
24	A	1833	NMY	C16-C15-O18-C18
24	A	1833	NMY	C19-C18-O18-C15
24	A	1833	NMY	C21-C22-C23-N19
24	A	1833	NMY	O22-C22-C23-N19
24	A	1835	NMY	C4-C5-C6-N6
24	A	1835	NMY	O5-C5-C6-N6
24	A	1837	NMY	C12-C11-O11-C13
24	A	1833	NMY	C12-C11-O11-C13
24	A	1836	NMY	O22-C18-O18-C15
24	A	1837	NMY	C11-C10-O1-C1
24	A	1835	NMY	O5-C1-O1-C10
24	A	1834	NMY	O22-C18-O18-C15
24	A	1832	NMY	O16-C13-O11-C11

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Mol	Chain	Res	Type	Atoms
24	A	1832	NMY	C11-C10-O1-C1
24	A	1834	NMY	C2-C1-O1-C10
24	A	1836	NMY	C12-C11-O11-C13
24	A	1836	NMY	C10-C11-O11-C13
24	A	1832	NMY	C14-C13-O11-C11
24	A	1832	NMY	C9-C10-O1-C1
24	A	1834	NMY	O22-C22-C23-N19
24	A	1836	NMY	O16-C16-C17-O17
24	A	1836	NMY	C4-C5-C6-N6
24	A	1836	NMY	C21-C22-C23-N19
24	A	1834	NMY	C14-C13-O11-C11
24	A	1837	NMY	C16-C15-O18-C18
24	A	1834	NMY	C14-C15-O18-C18
24	A	1836	NMY	C16-C15-O18-C18
24	A	1832	NMY	C14-C15-O18-C18
24	A	1832	NMY	C21-C22-C23-N19
24	A	1833	NMY	C14-C15-O18-C18
24	A	1837	NMY	C2-C1-O1-C10
24	A	1836	NMY	C11-C10-O1-C1

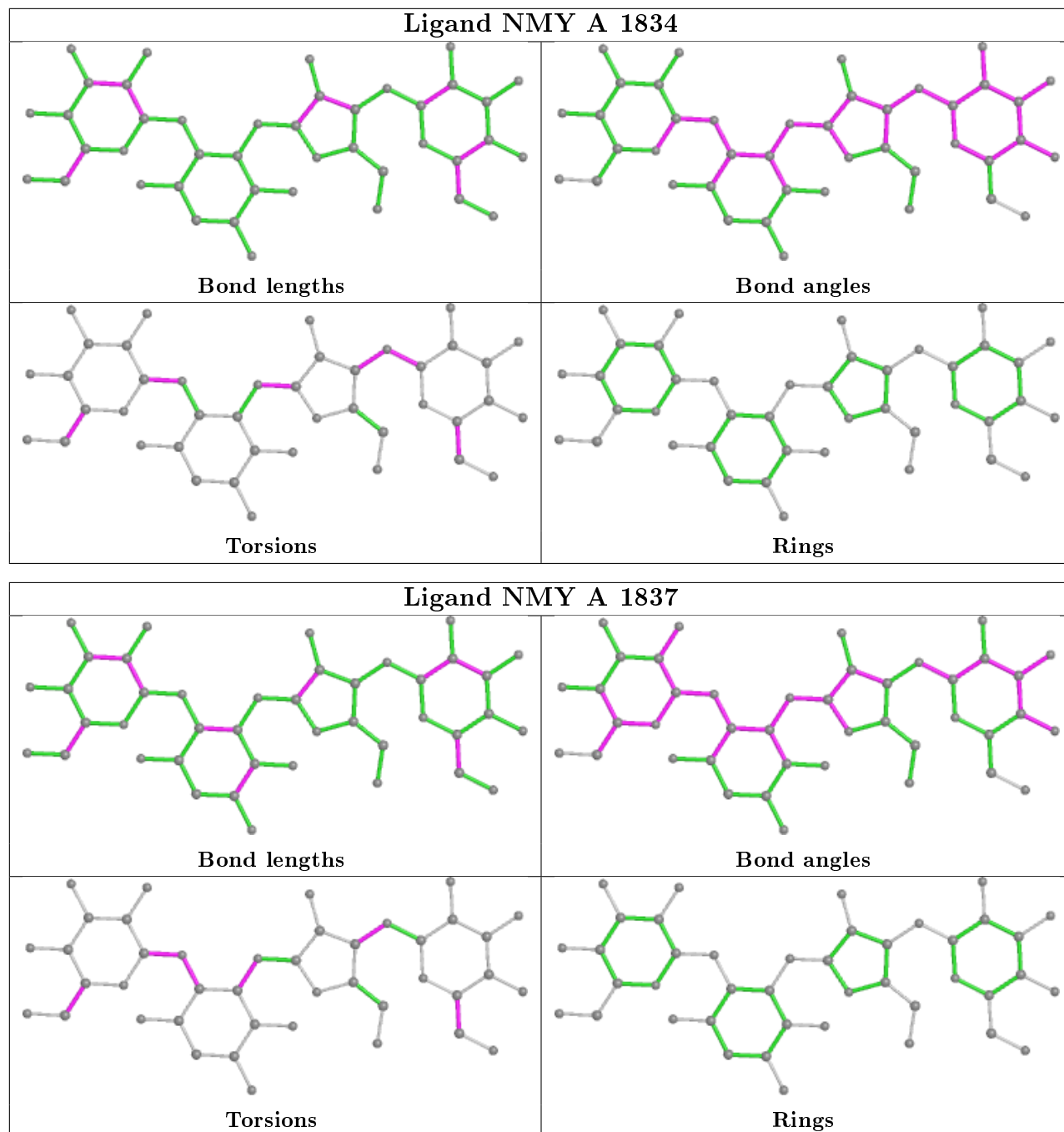
There are no ring outliers.

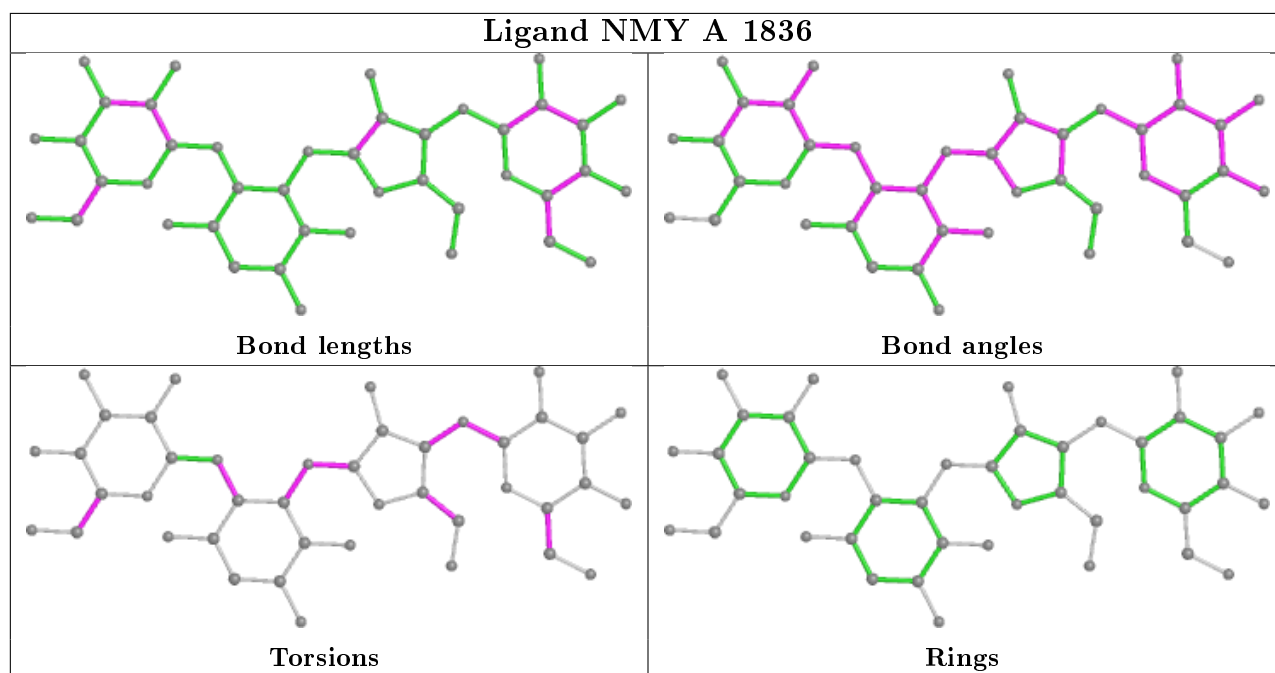
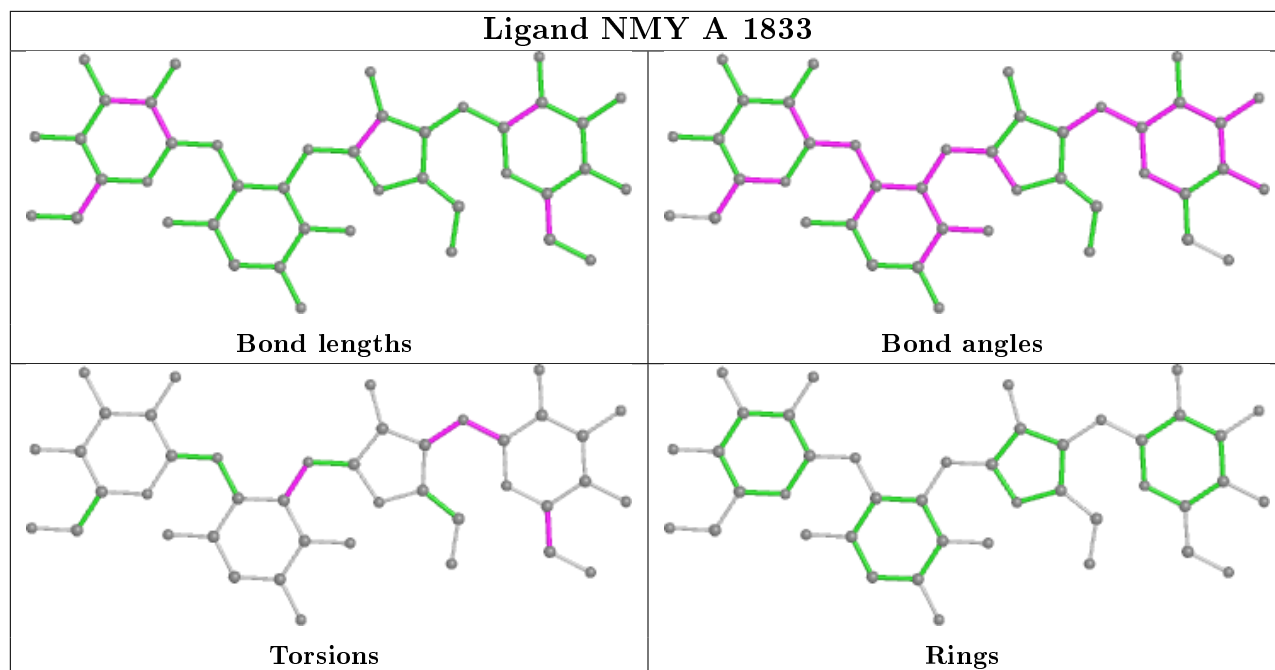
6 monomers are involved in 13 short contacts:

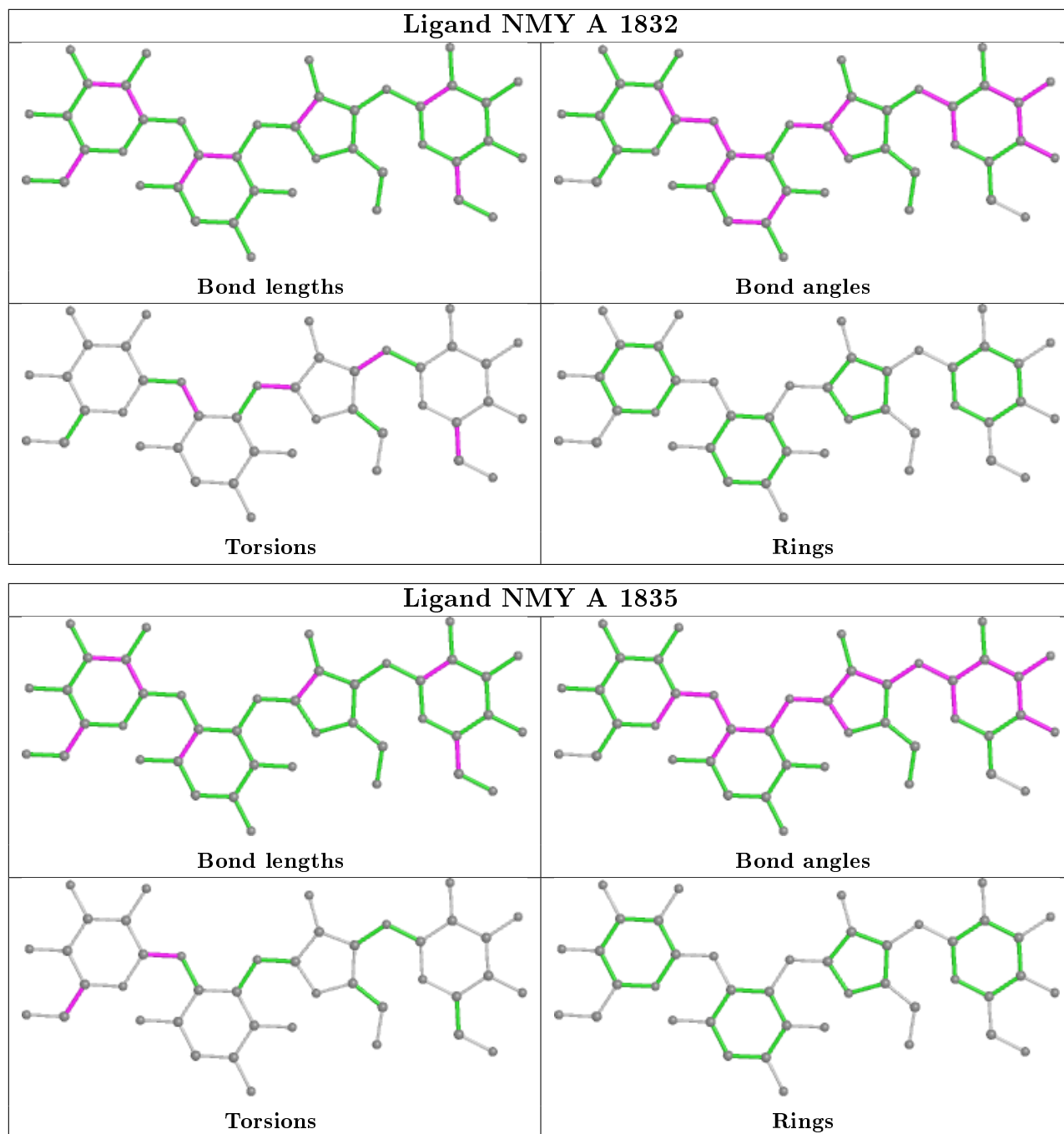
Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	A	1834	NMY	3	0
24	A	1837	NMY	2	0
24	A	1833	NMY	1	0
24	A	1836	NMY	2	0
24	A	1832	NMY	1	0
24	A	1835	NMY	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient

equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data i

6.1 Protein, DNA and RNA chains i

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	1500/1522 (98%)	-0.25	21 (1%) 75 75	51, 84, 177, 283	0
2	B	236/256 (92%)	-0.27	4 (1%) 70 68	60, 109, 189, 249	0
3	C	207/239 (86%)	-0.13	3 (1%) 75 75	50, 115, 159, 195	0
4	D	208/209 (99%)	-0.27	4 (1%) 66 65	63, 94, 134, 166	0
5	E	151/162 (93%)	-0.28	0 100 100	56, 75, 113, 167	0
6	F	101/101 (100%)	-0.48	1 (0%) 82 82	78, 118, 149, 179	0
7	G	155/156 (99%)	-0.31	3 (1%) 66 65	82, 115, 183, 212	0
8	H	138/138 (100%)	-0.47	0 100 100	46, 72, 102, 140	0
9	I	127/128 (99%)	-0.04	2 (1%) 72 70	79, 121, 162, 198	0
10	J	99/105 (94%)	0.41	5 (5%) 28 26	73, 140, 218, 252	0
11	K	119/129 (92%)	-0.02	3 (2%) 57 54	68, 93, 129, 150	0
12	L	124/135 (91%)	-0.10	3 (2%) 59 56	58, 87, 126, 215	0
13	M	118/126 (93%)	-0.19	6 (5%) 28 26	84, 114, 146, 183	0
14	N	60/61 (98%)	0.18	2 (3%) 46 44	81, 108, 151, 202	0
15	O	88/89 (98%)	-0.17	1 (1%) 80 81	57, 89, 135, 169	0
16	P	84/88 (95%)	-0.31	0 100 100	62, 80, 107, 189	0
17	Q	104/105 (99%)	0.25	4 (3%) 40 37	59, 78, 125, 196	0
18	R	73/88 (82%)	-0.02	2 (2%) 54 52	65, 97, 177, 232	0
19	S	81/93 (87%)	0.06	2 (2%) 57 54	47, 137, 180, 209	0
20	T	99/106 (93%)	-0.18	2 (2%) 65 64	64, 86, 136, 182	0
21	U	25/27 (92%)	1.23	5 (20%) 1 1	73, 106, 130, 206	0
All	All	3897/4063 (95%)	-0.18	73 (1%) 66 65	46, 94, 169, 283	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
17	Q	103	GLY	21.2
11	K	129	SER	17.9
17	Q	104	LYS	14.3
11	K	128	ALA	11.7
1	A	1129	C	9.3
17	Q	105	ALA	9.2
18	R	17	SER	6.0
17	Q	102	GLY	5.3
9	I	128	ARG	4.6
12	L	129	ALA	4.4
1	A	461	C	4.2
1	A	202	U	4.2
2	B	125	PRO	4.2
1	A	1006	C	4.1
1	A	1534	A	4.0
21	U	18	TYR	4.0
18	R	88	LYS	3.9
7	G	5	ARG	3.9
10	J	90	LEU	3.8
3	C	76	VAL	3.8
20	T	9	ASN	3.7
15	O	89	GLY	3.6
13	M	117	VAL	3.5
9	I	8	GLY	3.5
12	L	128	ALA	3.4
1	A	1034	G	3.3
2	B	131	PRO	3.3
21	U	26	LYS	3.2
21	U	17	THR	3.2
1	A	82	U	3.2
12	L	19	ARG	3.0
7	G	2	ALA	3.0
10	J	33	GLN	3.0
1	A	1542	U	2.9
19	S	3	ARG	2.9
13	M	118	ALA	2.9
14	N	12	ARG	2.9
2	B	231	GLU	2.8
6	F	101	ALA	2.8
21	U	25	LYS	2.8
14	N	13	THR	2.7
1	A	1005	A	2.7
21	U	24	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
19	S	10	PHE	2.6
1	A	1533	C	2.6
3	C	146	ALA	2.5
3	C	103	VAL	2.5
13	M	5	ALA	2.5
13	M	119	GLY	2.5
1	A	1003	G	2.5
1	A	1033	G	2.4
4	D	32	ALA	2.4
20	T	100	ILE	2.4
7	G	156	TRP	2.4
4	D	35	ARG	2.4
13	M	2	ALA	2.4
11	K	127	LYS	2.3
1	A	1038	C	2.3
1	A	1025	U	2.2
1	A	1036	G	2.2
10	J	71	LEU	2.2
4	D	33	MET	2.2
1	A	1544	U	2.2
4	D	9	CYS	2.1
1	A	1543	C	2.1
13	M	7	VAL	2.1
1	A	216	G	2.1
2	B	238	LEU	2.1
1	A	83	U	2.1
1	A	88	A	2.1
1	A	1032	G	2.0
10	J	73	ASP	2.0
10	J	6	ILE	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	PSU	A	516	20/21	0.94	0.16	87,90,100,100	0
1	5MC	A	1407	21/22	0.94	0.22	83,120,143,145	0
1	5MC	A	1400	21/22	0.95	0.20	67,83,106,112	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	2MG	A	1207	24/25	0.95	0.13	101,107,113,115	0
12	0TD	L	92	10/11	0.96	0.37	96,102,168,273	0
1	UR3	A	1498	21/22	0.96	0.22	71,77,98,103	0
1	5MC	A	967	21/22	0.97	0.14	59,76,83,84	0
1	5MC	A	1404	21/22	0.97	0.15	72,81,90,95	0
1	4OC	A	1402	22/23	0.98	0.16	70,75,83,91	0
1	7MG	A	527	24/25	0.98	0.19	66,72,94,98	0
1	M2G	A	966	25/26	0.98	0.13	70,81,95,98	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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
22	MG	A	1642	1/1	0.29	0.69	68,68,68,68	0
22	MG	A	1788	1/1	0.31	0.41	88,88,88,88	0
22	MG	A	1801	1/1	0.44	1.34	80,80,80,80	0
22	MG	A	1667	1/1	0.49	0.66	98,98,98,98	0
22	MG	A	1694	1/1	0.57	0.74	83,83,83,83	0
22	MG	C	302	1/1	0.60	0.71	106,106,106,106	0
22	MG	A	1633	1/1	0.61	0.35	93,93,93,93	0
22	MG	A	1814	1/1	0.61	1.16	87,87,87,87	0
22	MG	A	1647	1/1	0.63	0.46	83,83,83,83	0
22	MG	A	1761	1/1	0.64	0.53	51,51,51,51	0
22	MG	A	1770	1/1	0.65	0.53	102,102,102,102	0
22	MG	F	201	1/1	0.66	0.41	95,95,95,95	0
22	MG	A	1775	1/1	0.66	0.65	84,84,84,84	0
22	MG	A	1818	1/1	0.68	0.33	90,90,90,90	0
22	MG	A	1664	1/1	0.68	0.52	94,94,94,94	0
22	MG	A	1829	1/1	0.68	0.22	104,104,104,104	0
22	MG	A	1616	1/1	0.70	0.82	84,84,84,84	0
22	MG	A	1778	1/1	0.70	0.23	88,88,88,88	0
22	MG	A	1831	1/1	0.70	0.08	285,285,285,285	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
22	MG	A	1614	1/1	0.70	0.54	72,72,72,72	0
22	MG	A	1763	1/1	0.71	0.22	68,68,68,68	0
22	MG	A	1808	1/1	0.72	0.86	79,79,79,79	0
22	MG	A	1675	1/1	0.72	1.03	75,75,75,75	0
22	MG	N	102	1/1	0.72	1.08	92,92,92,92	0
23	K	A	1735	1/1	0.72	0.83	152,152,152,152	0
22	MG	A	1809	1/1	0.72	0.19	74,74,74,74	0
22	MG	A	1602	1/1	0.72	0.31	114,114,114,114	0
23	K	A	1742	1/1	0.74	1.22	138,138,138,138	0
22	MG	Q	201	1/1	0.74	0.14	71,71,71,71	0
22	MG	A	1773	1/1	0.74	0.56	69,69,69,69	0
23	K	A	1760	1/1	0.75	0.54	145,145,145,145	0
22	MG	A	1800	1/1	0.75	0.33	98,98,98,98	0
22	MG	A	1683	1/1	0.75	0.19	77,77,77,77	0
23	K	A	1750	1/1	0.76	1.09	143,143,143,143	0
22	MG	A	1826	1/1	0.77	0.18	81,81,81,81	0
22	MG	A	1786	1/1	0.78	0.80	71,71,71,71	0
22	MG	A	1682	1/1	0.78	1.20	84,84,84,84	0
22	MG	N	103	1/1	0.78	0.31	57,57,57,57	0
22	MG	A	1794	1/1	0.79	0.30	73,73,73,73	0
22	MG	A	1806	1/1	0.79	0.76	76,76,76,76	0
23	K	A	1748	1/1	0.79	0.53	136,136,136,136	0
23	K	A	1753	1/1	0.79	0.36	127,127,127,127	0
22	MG	A	1655	1/1	0.79	0.35	93,93,93,93	0
22	MG	A	1766	1/1	0.79	0.39	61,61,61,61	0
22	MG	A	1720	1/1	0.79	0.37	75,75,75,75	0
22	MG	A	1822	1/1	0.79	0.28	101,101,101,101	0
23	K	A	1755	1/1	0.79	0.53	147,147,147,147	0
22	MG	A	1657	1/1	0.80	0.28	70,70,70,70	0
23	K	A	1737	1/1	0.80	0.13	134,134,134,134	0
23	K	A	1751	1/1	0.80	0.34	160,160,160,160	0
22	MG	D	302	1/1	0.80	0.17	63,63,63,63	0
22	MG	A	1768	1/1	0.80	0.67	50,50,50,50	0
22	MG	A	1630	1/1	0.80	0.51	60,60,60,60	0
22	MG	M	202	1/1	0.80	0.29	85,85,85,85	0
22	MG	A	1781	1/1	0.80	0.55	87,87,87,87	0
22	MG	A	1799	1/1	0.81	0.34	98,98,98,98	0
22	MG	A	1730	1/1	0.81	1.47	74,74,74,74	0
22	MG	A	1795	1/1	0.81	0.45	96,96,96,96	0
22	MG	A	1615	1/1	0.81	0.59	95,95,95,95	0
22	MG	A	1776	1/1	0.81	0.57	85,85,85,85	0
22	MG	A	1659	1/1	0.81	0.31	94,94,94,94	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
22	MG	A	1772	1/1	0.82	0.69	66,66,66,66	0
22	MG	A	1810	1/1	0.82	0.55	65,65,65,65	0
22	MG	A	1762	1/1	0.82	0.39	89,89,89,89	0
22	MG	B	302	1/1	0.82	0.36	84,84,84,84	0
22	MG	P	101	1/1	0.82	0.46	68,68,68,68	0
23	K	A	1756	1/1	0.82	0.61	151,151,151,151	0
22	MG	A	1661	1/1	0.82	0.55	69,69,69,69	0
22	MG	A	1802	1/1	0.82	0.21	108,108,108,108	0
22	MG	B	303	1/1	0.82	0.09	83,83,83,83	0
22	MG	A	1721	1/1	0.82	0.28	77,77,77,77	0
22	MG	A	1815	1/1	0.83	0.55	81,81,81,81	0
23	K	A	1754	1/1	0.83	0.18	135,135,135,135	0
22	MG	A	1782	1/1	0.83	0.57	82,82,82,82	0
22	MG	A	1686	1/1	0.83	0.17	54,54,54,54	0
22	MG	A	1612	1/1	0.83	1.30	93,93,93,93	0
23	K	A	1759	1/1	0.83	0.13	145,145,145,145	0
22	MG	A	1767	1/1	0.83	0.65	62,62,62,62	0
22	MG	A	1821	1/1	0.83	0.45	73,73,73,73	0
22	MG	A	1765	1/1	0.83	0.63	55,55,55,55	0
23	K	A	1738	1/1	0.83	0.29	133,133,133,133	0
22	MG	A	1783	1/1	0.84	0.39	73,73,73,73	0
22	MG	H	202	1/1	0.84	0.46	49,49,49,49	0
22	MG	A	1803	1/1	0.84	0.21	66,66,66,66	0
22	MG	A	1805	1/1	0.84	1.02	79,79,79,79	0
22	MG	A	1665	1/1	0.84	0.42	84,84,84,84	0
22	MG	A	1610	1/1	0.84	0.24	89,89,89,89	0
22	MG	A	1724	1/1	0.84	0.29	51,51,51,51	0
22	MG	A	1726	1/1	0.84	0.43	70,70,70,70	0
22	MG	A	1797	1/1	0.84	0.17	68,68,68,68	0
23	K	A	1731	1/1	0.84	0.23	121,121,121,121	0
22	MG	A	1787	1/1	0.84	0.92	117,117,117,117	0
22	MG	A	1796	1/1	0.85	0.41	89,89,89,89	0
22	MG	A	1712	1/1	0.85	0.23	75,75,75,75	0
22	MG	A	1819	1/1	0.85	0.24	85,85,85,85	0
23	K	A	1739	1/1	0.85	0.28	140,140,140,140	0
22	MG	A	1658	1/1	0.85	1.07	76,76,76,76	0
22	MG	A	1792	1/1	0.85	0.83	68,68,68,68	0
22	MG	A	1780	1/1	0.85	0.34	75,75,75,75	0
22	MG	L	201	1/1	0.85	0.30	99,99,99,99	0
22	MG	A	1718	1/1	0.85	0.60	84,84,84,84	0
22	MG	A	1725	1/1	0.85	0.62	76,76,76,76	0
24	NMY	A	1834	42/42	0.86	0.28	62,120,200,201	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
24	NMY	A	1836	42/42	0.86	0.27	75,119,177,188	0
22	MG	A	1823	1/1	0.86	0.10	107,107,107,107	0
22	MG	H	201	1/1	0.86	0.21	74,74,74,74	0
24	NMY	A	1837	42/42	0.86	0.29	57,138,186,186	0
22	MG	A	1619	1/1	0.86	0.36	77,77,77,77	0
23	K	A	1749	1/1	0.86	0.67	115,115,115,115	0
22	MG	A	1777	1/1	0.86	0.58	96,96,96,96	0
22	MG	A	1711	1/1	0.86	0.58	90,90,90,90	0
22	MG	A	1652	1/1	0.87	0.49	64,64,64,64	0
23	K	A	1733	1/1	0.87	0.66	112,112,112,112	0
22	MG	A	1830	1/1	0.87	0.07	293,293,293,293	0
22	MG	A	1617	1/1	0.87	0.36	112,112,112,112	0
22	MG	A	1666	1/1	0.87	0.71	72,72,72,72	0
22	MG	A	1774	1/1	0.87	0.56	98,98,98,98	0
22	MG	A	1660	1/1	0.87	0.43	75,75,75,75	0
22	MG	A	1817	1/1	0.87	0.34	103,103,103,103	0
22	MG	A	1820	1/1	0.87	0.14	65,65,65,65	0
22	MG	A	1674	1/1	0.87	0.20	38,38,38,38	0
22	MG	A	1626	1/1	0.87	0.38	79,79,79,79	0
22	MG	A	1611	1/1	0.88	0.44	49,49,49,49	0
22	MG	C	301	1/1	0.88	0.21	66,66,66,66	0
22	MG	A	1679	1/1	0.88	0.57	62,62,62,62	0
22	MG	A	1653	1/1	0.88	0.70	63,63,63,63	0
22	MG	A	1816	1/1	0.88	0.55	67,67,67,67	0
22	MG	A	1727	1/1	0.88	0.25	54,54,54,54	0
22	MG	A	1684	1/1	0.88	0.52	68,68,68,68	0
24	NMY	A	1835	42/42	0.88	0.23	105,127,145,147	0
22	MG	A	1644	1/1	0.88	0.45	62,62,62,62	0
22	MG	A	1719	1/1	0.88	0.15	62,62,62,62	0
22	MG	A	1608	1/1	0.88	0.14	73,73,73,73	0
22	MG	A	1668	1/1	0.89	0.30	66,66,66,66	0
22	MG	A	1645	1/1	0.89	0.84	79,79,79,79	0
22	MG	A	1688	1/1	0.89	0.53	41,41,41,41	0
22	MG	A	1828	1/1	0.89	0.21	95,95,95,95	0
22	MG	A	1785	1/1	0.89	0.21	67,67,67,67	0
22	MG	A	1825	1/1	0.89	0.21	63,63,63,63	0
22	MG	A	1789	1/1	0.89	0.38	97,97,97,97	0
22	MG	A	1691	1/1	0.89	0.44	82,82,82,82	0
22	MG	A	1651	1/1	0.90	0.45	77,77,77,77	0
22	MG	A	1790	1/1	0.90	0.33	72,72,72,72	0
23	K	A	1747	1/1	0.90	0.45	112,112,112,112	0
22	MG	A	1728	1/1	0.90	0.32	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
22	MG	A	1811	1/1	0.90	0.27	79,79,79,79	0
22	MG	A	1812	1/1	0.90	0.21	103,103,103,103	0
22	MG	A	1715	1/1	0.90	0.34	68,68,68,68	0
23	K	A	1740	1/1	0.90	0.56	135,135,135,135	0
23	K	A	1741	1/1	0.90	0.95	154,154,154,154	0
22	MG	A	1723	1/1	0.91	0.26	55,55,55,55	0
22	MG	A	1618	1/1	0.91	0.87	58,58,58,58	0
22	MG	A	1603	1/1	0.91	0.78	69,69,69,69	0
22	MG	A	1623	1/1	0.91	1.33	86,86,86,86	0
22	MG	A	1813	1/1	0.91	0.64	88,88,88,88	0
22	MG	A	1827	1/1	0.91	0.15	102,102,102,102	0
23	K	A	1734	1/1	0.91	0.25	119,119,119,119	0
22	MG	A	1824	1/1	0.91	0.19	103,103,103,103	0
22	MG	A	1632	1/1	0.91	0.55	64,64,64,64	0
22	MG	B	301	1/1	0.91	0.29	96,96,96,96	0
22	MG	A	1793	1/1	0.92	1.08	69,69,69,69	0
22	MG	A	1685	1/1	0.92	0.50	55,55,55,55	0
22	MG	A	1798	1/1	0.92	0.92	85,85,85,85	0
22	MG	A	1613	1/1	0.92	0.54	86,86,86,86	0
22	MG	A	1673	1/1	0.92	0.44	57,57,57,57	0
22	MG	D	303	1/1	0.92	0.77	89,89,89,89	0
22	MG	A	1791	1/1	0.92	0.44	78,78,78,78	0
22	MG	A	1807	1/1	0.92	0.50	78,78,78,78	0
22	MG	A	1804	1/1	0.92	0.23	56,56,56,56	0
22	MG	A	1656	1/1	0.92	0.21	57,57,57,57	0
23	K	A	1743	1/1	0.92	0.30	137,137,137,137	0
22	MG	A	1670	1/1	0.92	0.28	57,57,57,57	0
22	MG	A	1692	1/1	0.92	0.87	72,72,72,72	0
22	MG	A	1706	1/1	0.93	0.76	73,73,73,73	0
23	K	A	1757	1/1	0.93	0.30	143,143,143,143	0
22	MG	A	1663	1/1	0.93	0.71	67,67,67,67	0
22	MG	A	1638	1/1	0.93	0.09	64,64,64,64	0
22	MG	A	1672	1/1	0.93	0.40	83,83,83,83	0
22	MG	A	1671	1/1	0.93	0.40	50,50,50,50	0
23	K	A	1744	1/1	0.93	0.46	121,121,121,121	0
22	MG	A	1690	1/1	0.93	1.55	70,70,70,70	0
22	MG	A	1722	1/1	0.93	0.08	35,35,35,35	0
22	MG	A	1680	1/1	0.93	0.75	46,46,46,46	0
22	MG	A	1681	1/1	0.93	0.44	75,75,75,75	0
22	MG	A	1784	1/1	0.93	0.58	90,90,90,90	0
22	MG	A	1620	1/1	0.93	1.23	53,53,53,53	0
22	MG	A	1696	1/1	0.93	0.53	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
22	MG	A	1769	1/1	0.93	0.48	73,73,73,73	0
22	MG	A	1771	1/1	0.93	0.69	58,58,58,58	0
22	MG	A	1609	1/1	0.93	0.94	86,86,86,86	0
22	MG	A	1709	1/1	0.94	0.53	66,66,66,66	0
22	MG	A	1693	1/1	0.94	0.28	72,72,72,72	0
23	K	A	1758	1/1	0.94	0.62	130,130,130,130	0
22	MG	A	1643	1/1	0.94	0.27	54,54,54,54	0
22	MG	A	1607	1/1	0.94	0.76	59,59,59,59	0
22	MG	A	1710	1/1	0.94	0.37	90,90,90,90	0
23	K	A	1736	1/1	0.94	0.56	108,108,108,108	0
22	MG	A	1676	1/1	0.94	0.25	60,60,60,60	0
22	MG	A	1716	1/1	0.94	0.20	49,49,49,49	0
23	K	A	1746	1/1	0.94	0.45	149,149,149,149	0
22	MG	A	1605	1/1	0.94	0.65	44,44,44,44	0
22	MG	A	1764	1/1	0.94	0.21	65,65,65,65	0
22	MG	A	1627	1/1	0.95	0.12	90,90,90,90	0
22	MG	A	1669	1/1	0.95	0.21	51,51,51,51	0
22	MG	A	1729	1/1	0.95	0.23	64,64,64,64	0
22	MG	A	1713	1/1	0.95	0.50	61,61,61,61	0
22	MG	A	1714	1/1	0.95	1.08	94,94,94,94	0
22	MG	A	1601	1/1	0.95	0.19	76,76,76,76	0
22	MG	A	1687	1/1	0.95	1.09	60,60,60,60	0
22	MG	A	1622	1/1	0.95	0.36	65,65,65,65	0
22	MG	A	1677	1/1	0.95	0.92	63,63,63,63	0
22	MG	A	1641	1/1	0.95	0.80	37,37,37,37	0
22	MG	A	1631	1/1	0.95	0.36	63,63,63,63	0
22	MG	A	1695	1/1	0.95	0.16	53,53,53,53	0
22	MG	A	1717	1/1	0.95	0.10	66,66,66,66	0
22	MG	A	1699	1/1	0.95	0.08	64,64,64,64	0
22	MG	A	1779	1/1	0.95	0.14	82,82,82,82	0
23	K	A	1732	1/1	0.95	0.19	104,104,104,104	0
24	NMY	A	1833	42/42	0.95	0.18	55,78,103,105	0
22	MG	A	1646	1/1	0.95	0.56	58,58,58,58	0
24	NMY	A	1832	42/42	0.95	0.21	54,85,153,163	0
22	MG	A	1635	1/1	0.96	0.48	41,41,41,41	0
22	MG	A	1604	1/1	0.96	0.16	79,79,79,79	0
22	MG	E	201	1/1	0.96	0.45	64,64,64,64	0
22	MG	A	1654	1/1	0.96	0.26	50,50,50,50	0
22	MG	A	1648	1/1	0.96	0.82	56,56,56,56	0
22	MG	A	1625	1/1	0.96	0.58	57,57,57,57	0
22	MG	A	1621	1/1	0.96	0.48	82,82,82,82	0
22	MG	A	1636	1/1	0.96	0.46	64,64,64,64	0

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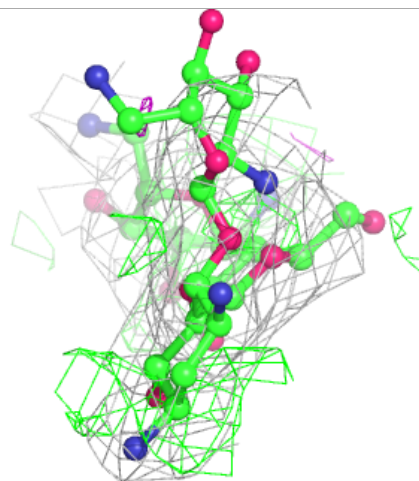
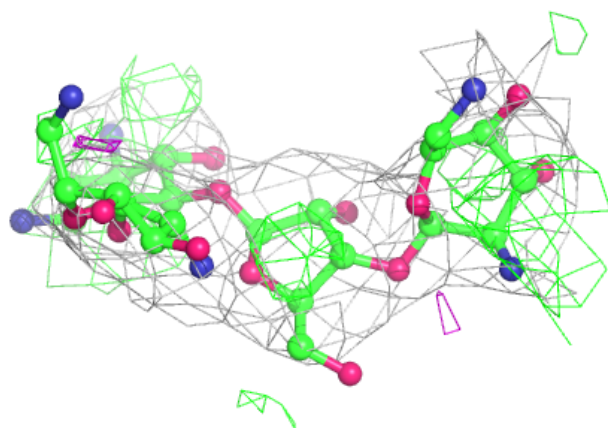
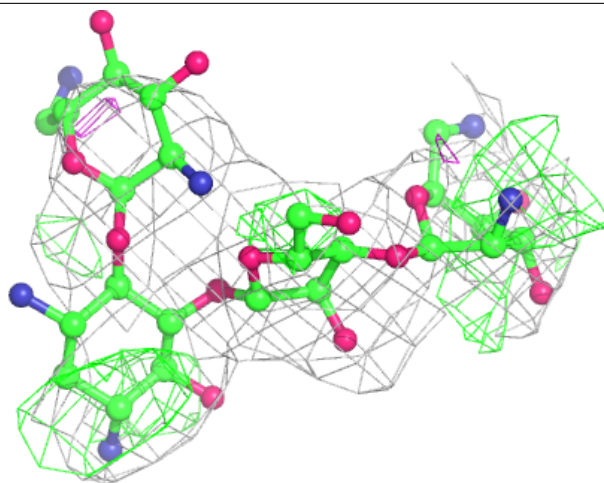
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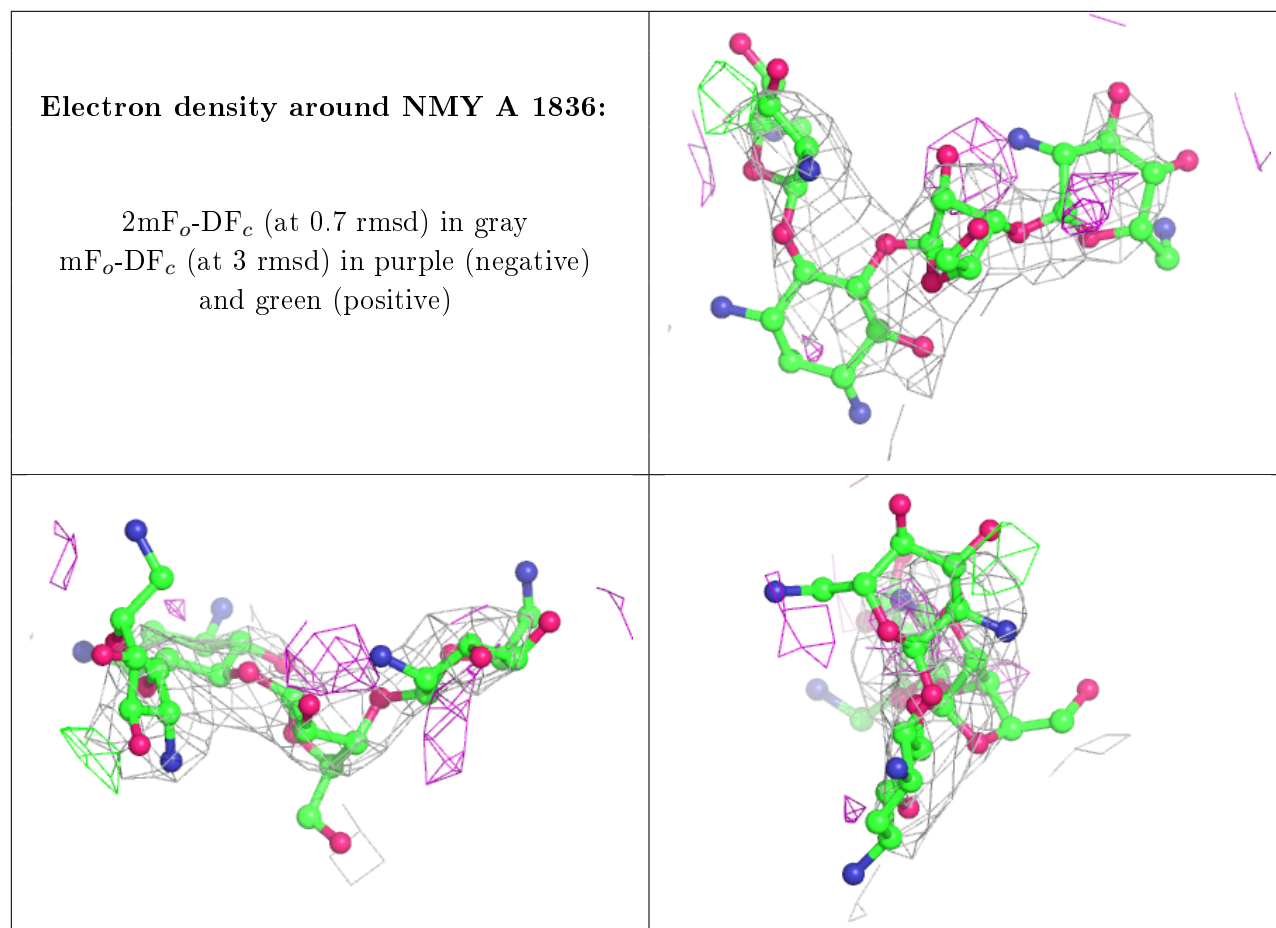
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
22	MG	A	1689	1/1	0.96	0.41	67,67,67,67	0
22	MG	M	201	1/1	0.96	0.27	72,72,72,72	0
22	MG	A	1678	1/1	0.97	0.29	35,35,35,35	0
22	MG	A	1606	1/1	0.97	1.43	72,72,72,72	0
22	MG	A	1628	1/1	0.97	0.62	57,57,57,57	0
22	MG	A	1637	1/1	0.97	0.38	67,67,67,67	0
22	MG	A	1650	1/1	0.97	0.19	41,41,41,41	0
22	MG	A	1700	1/1	0.97	0.20	38,38,38,38	0
22	MG	A	1649	1/1	0.97	0.48	40,40,40,40	0
22	MG	A	1697	1/1	0.97	0.23	36,36,36,36	0
22	MG	A	1708	1/1	0.97	0.40	63,63,63,63	0
22	MG	A	1639	1/1	0.97	0.27	28,28,28,28	0
22	MG	A	1624	1/1	0.97	0.53	39,39,39,39	0
22	MG	A	1629	1/1	0.97	0.49	43,43,43,43	0
22	MG	A	1662	1/1	0.97	0.18	51,51,51,51	0
23	K	A	1745	1/1	0.98	0.22	142,142,142,142	0
22	MG	A	1640	1/1	0.98	0.30	47,47,47,47	0
25	ZN	D	301	1/1	0.98	0.33	92,92,92,92	0
23	K	A	1752	1/1	0.98	0.62	115,115,115,115	0
22	MG	A	1698	1/1	0.98	0.64	47,47,47,47	0
22	MG	A	1702	1/1	0.98	0.29	40,40,40,40	0
22	MG	P	102	1/1	0.98	0.23	84,84,84,84	0
22	MG	A	1701	1/1	0.98	0.39	44,44,44,44	0
22	MG	A	1705	1/1	0.99	0.81	61,61,61,61	0
22	MG	A	1707	1/1	0.99	0.25	85,85,85,85	0
25	ZN	N	101	1/1	0.99	0.19	106,106,106,106	0
22	MG	A	1703	1/1	0.99	0.25	51,51,51,51	0
22	MG	A	1704	1/1	0.99	0.52	60,60,60,60	0
22	MG	A	1634	1/1	0.99	0.29	40,40,40,40	0

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

Electron density around NMY A 1834:

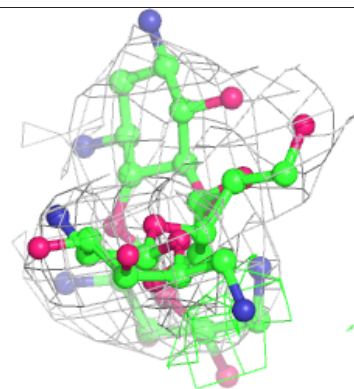
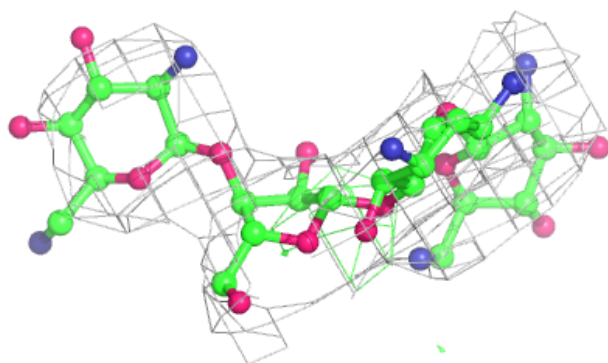
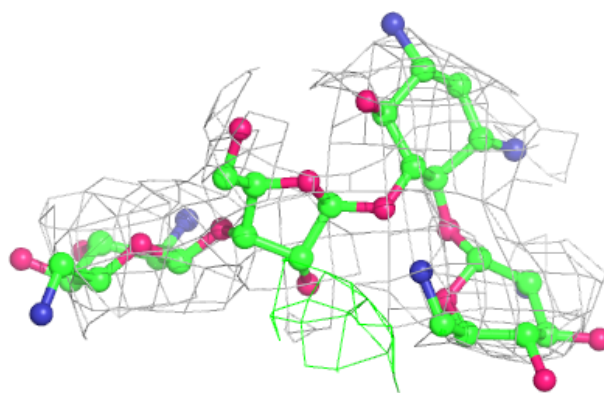
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





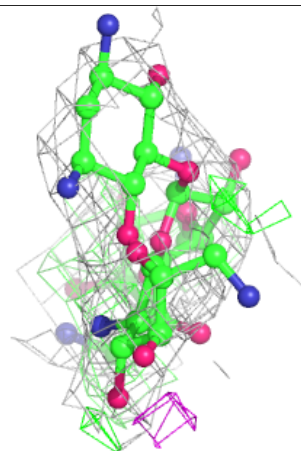
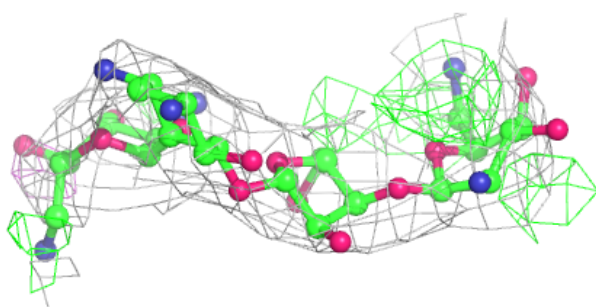
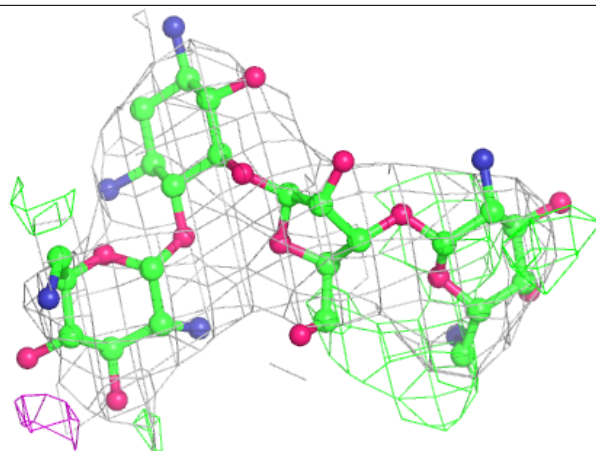
Electron density around NMY A 1837:

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

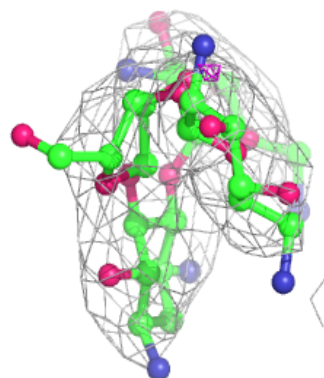
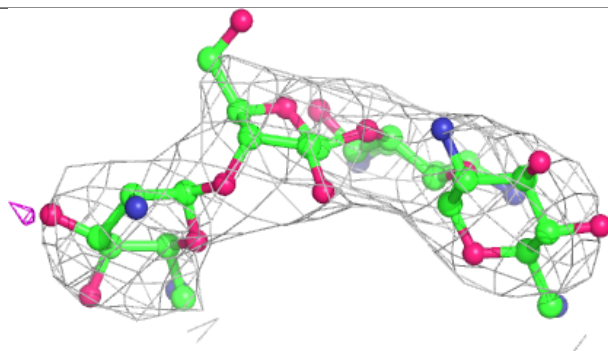
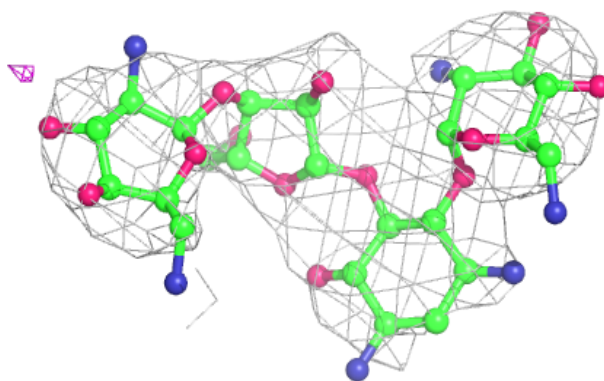


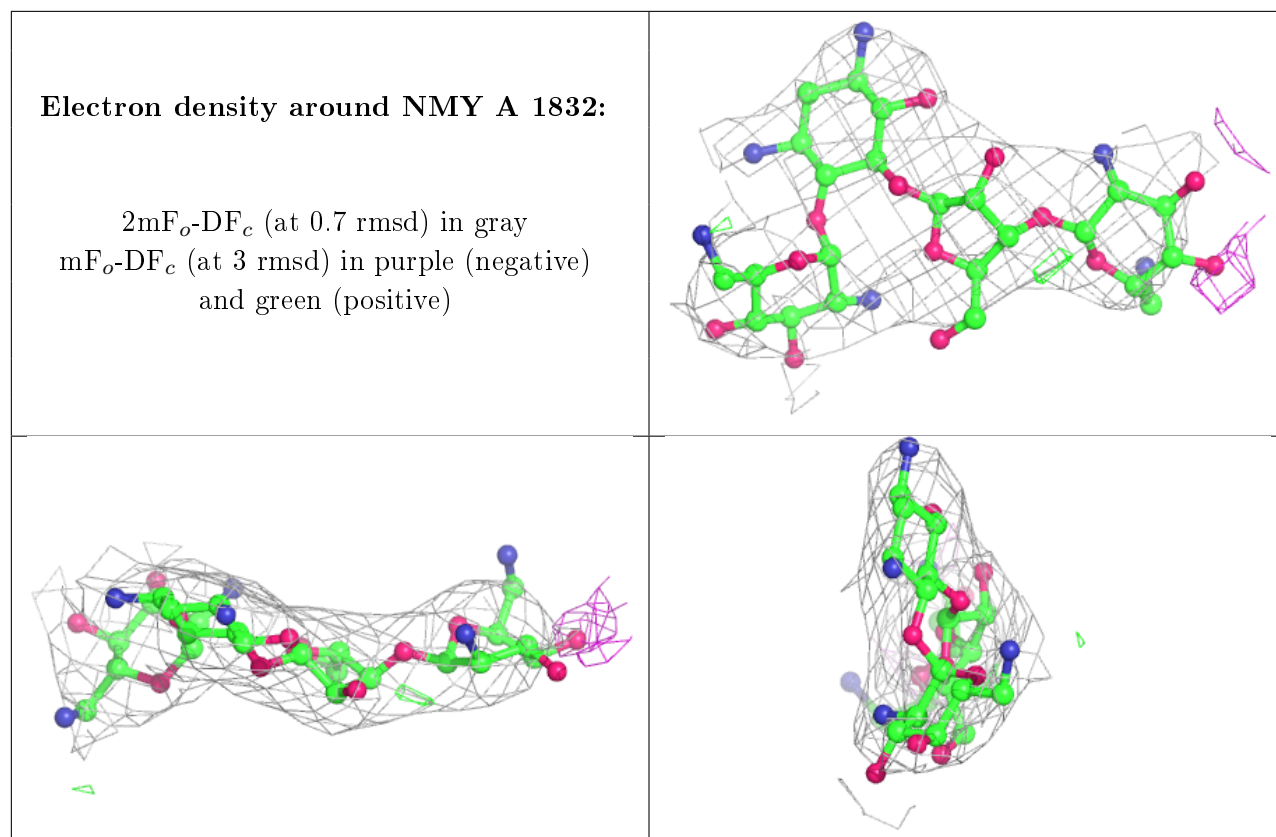
Electron density around NMY A 1835:

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

**Electron density around NMY A 1833:**

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





6.5 Other polymers [i](#)

There are no such residues in this entry.