



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 10:40 PM UTC

PDB ID : 4LF6 / pdb_00004lf6
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 types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

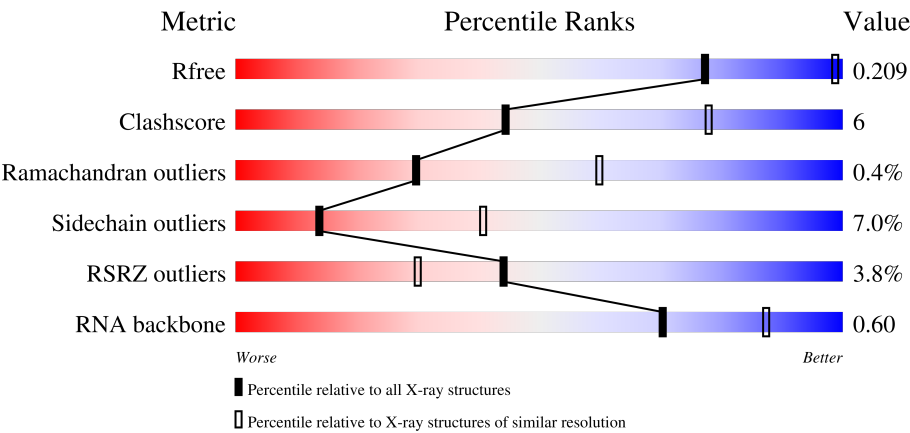
1 Overall quality at a glance i

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.



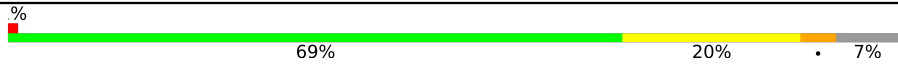
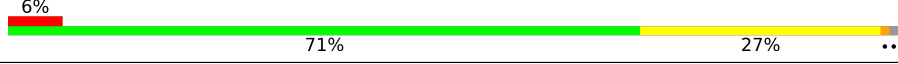
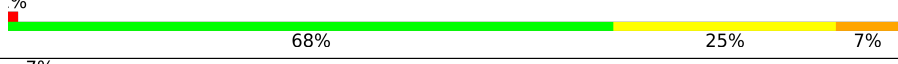
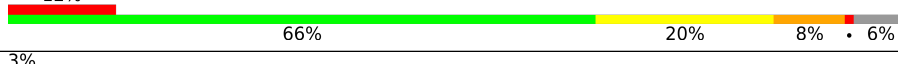
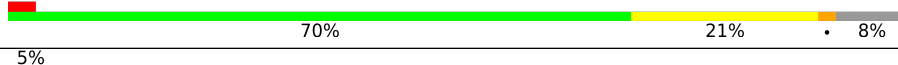
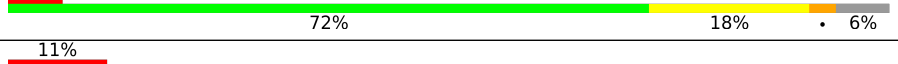
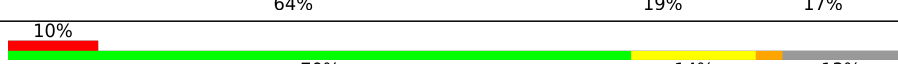
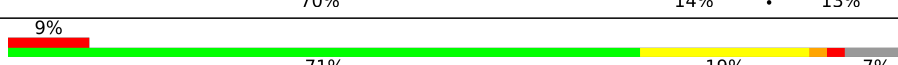
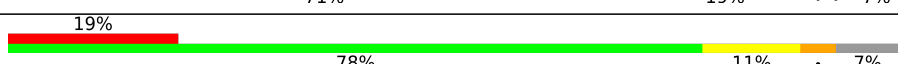
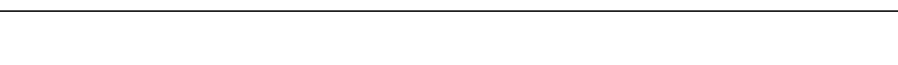
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)
RNA backbone	3983	1048 (3.60-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 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%5%
2	B	256	70%21%8%
3	C	239	64%21%13%
4	D	209	79%18%

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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	1602	-	-	-	X
22	MG	A	1615	-	-	-	X
22	MG	A	1655	-	-	-	X
22	MG	A	1658	-	-	-	X
22	MG	A	1667	-	-	-	X
22	MG	A	1772	-	-	-	X
22	MG	A	1777	-	-	-	X
22	MG	A	1781	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	MG	A	1787	-	-	-	X
22	MG	A	1788	-	-	-	X
22	MG	A	1795	-	-	-	X
22	MG	A	1800	-	-	-	X
22	MG	A	1802	-	-	-	X
22	MG	N	102	-	-	-	X
23	K	A	1735	-	-	-	X
23	K	A	1741	-	-	-	X
23	K	A	1750	-	-	-	X
23	K	A	1755	-	-	-	X

2 Entry composition

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
1	A	1510	Total	C	N	O	P	0	0	0
			32462	14456	6009	10488	1509			

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

- Molecule 3 is a protein called 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 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 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 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 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 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 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 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 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 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 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 ribosomal protein S14.

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 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 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 ribosomal protein S17.

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

- Molecule 18 is a protein called 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 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 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 ribosomal protein THX.

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

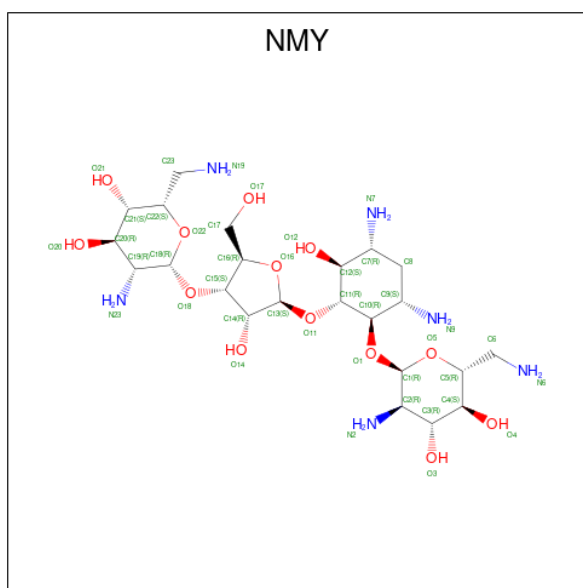
- Molecule 22 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 23 is POTASSIUM ION (CCD ID: K) (formula: K).

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

- Molecule 24 is NEOMYCIN (CCD ID: 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		
24	A	1	Total	C	N	O	0	0
			42	23	6	13		

- Molecule 25 is ZINC ION (CCD ID: 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		

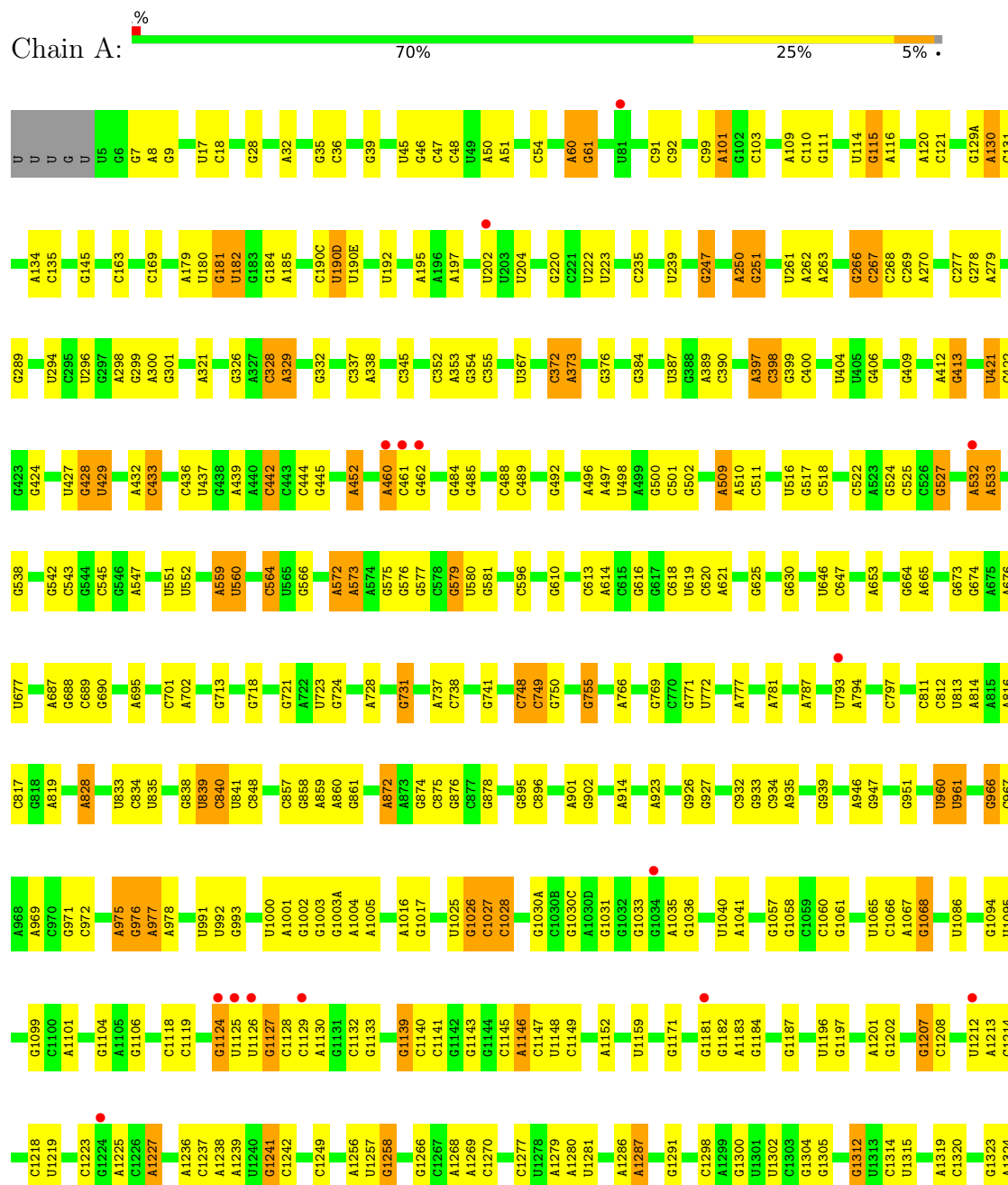
- Molecule 26 is water.

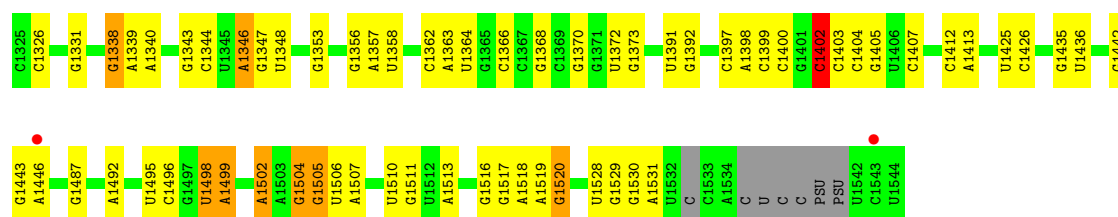
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
26	A	12	Total	O	0	0
			12	12		

3 Residue-property plots

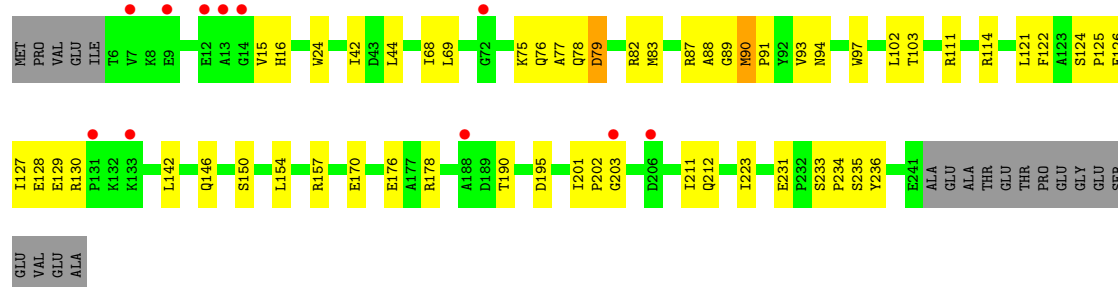
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: 16S rRNA

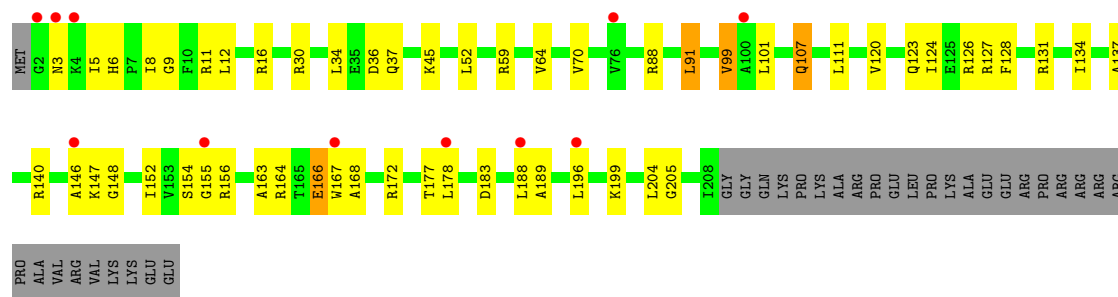




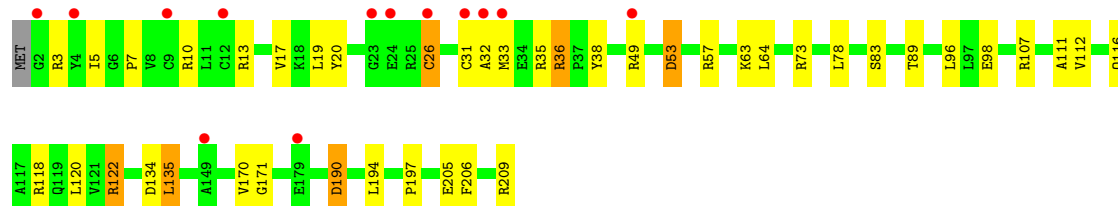
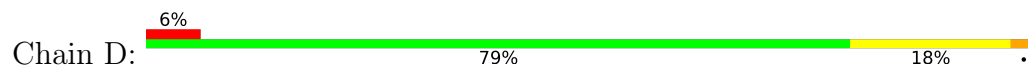
• Molecule 2: ribosomal protein S2



• Molecule 3: ribosomal protein S3

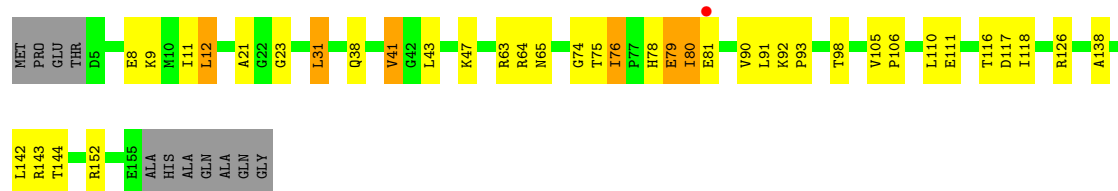


• Molecule 4: ribosomal protein S4

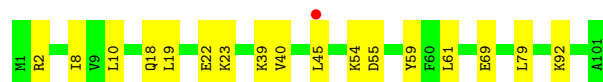
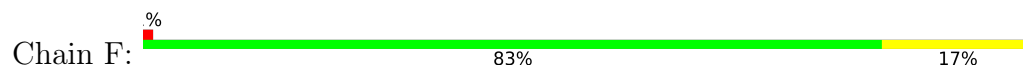


• Molecule 5: ribosomal protein S5

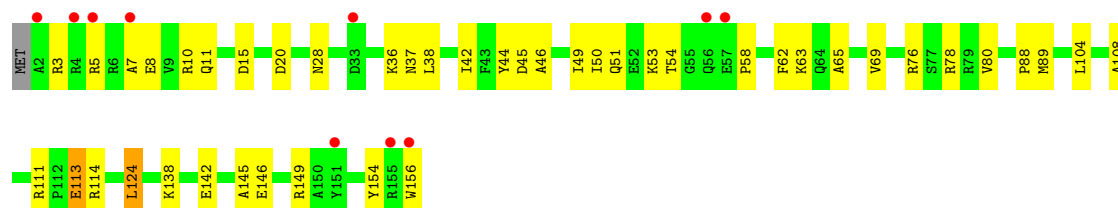
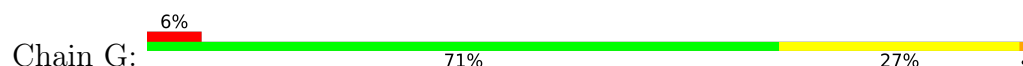




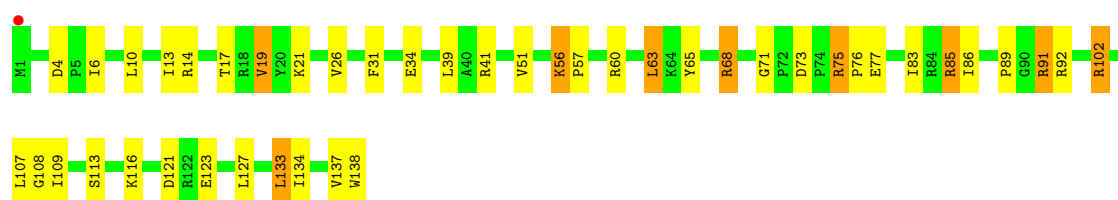
• Molecule 6: ribosomal protein S6



• Molecule 7: ribosomal protein S7



• Molecule 8: ribosomal protein S8

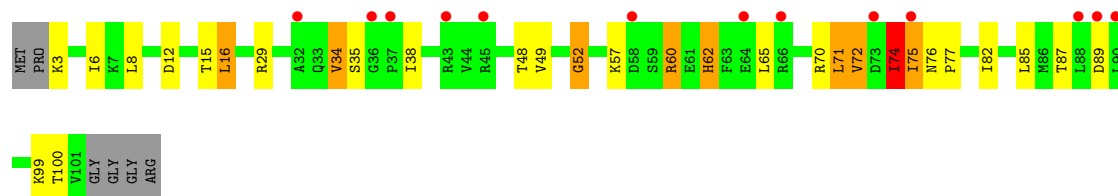


• Molecule 9: ribosomal protein S9

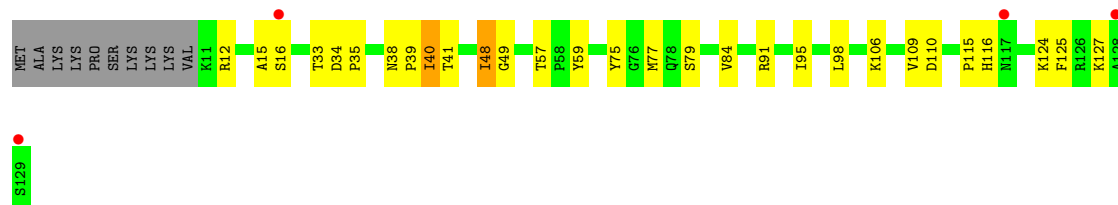


• Molecule 10: ribosomal protein S10

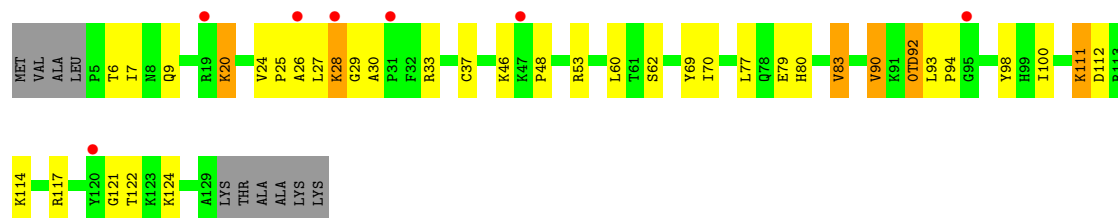




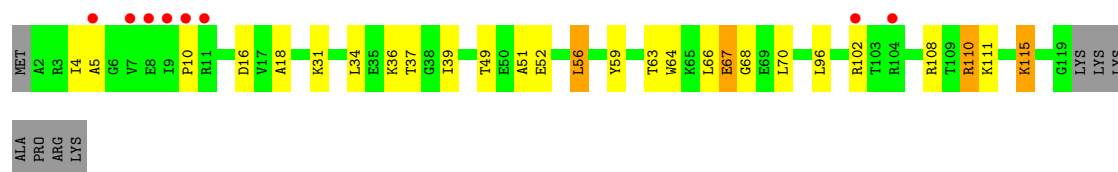
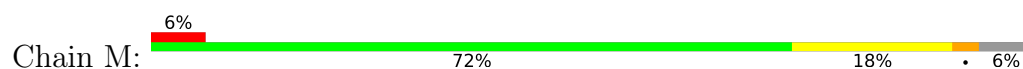
- Molecule 11: ribosomal protein S11



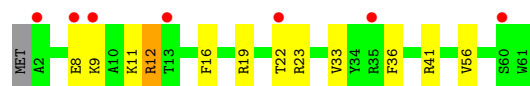
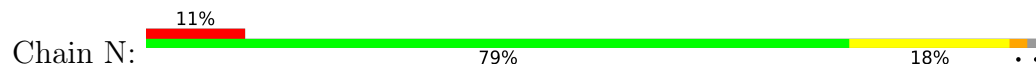
- Molecule 12: ribosomal protein S12



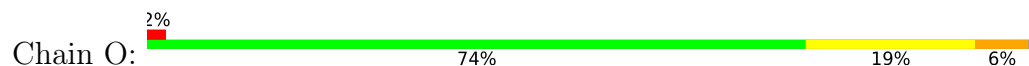
- Molecule 13: ribosomal protein S13

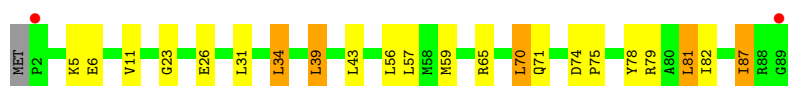


- Molecule 14: ribosomal protein S14

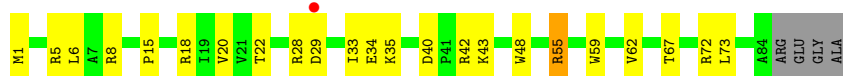


- Molecule 15: ribosomal protein S15

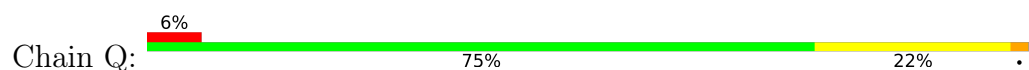




- Molecule 16: ribosomal protein S16



- Molecule 17: ribosomal protein S17



- Molecule 18: ribosomal protein S18



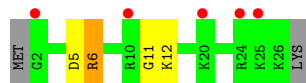
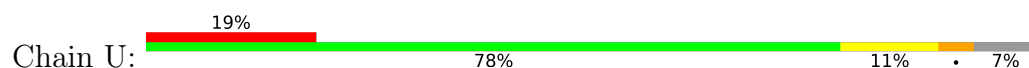
- Molecule 19: ribosomal protein S19



- 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) 98.4 (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)	Xtriage
Refinement program	PHENIX dev_1119	Depositor
R, R_{free}	0.175 , 0.210 0.176 , 0.209	Depositor DCC
R_{free} test set	10690 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	96.4	Xtriage
Anisotropy	0.272	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 76.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
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

Xtriage'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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: M2G, 7MG, K, MG, 4OC, PSU, 0TD, ZN, UR3, NMY, 5MC, 2MG

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	0.19	0/36091	0.36	0/56326
2	B	0.37	0/1909	0.84	3/2579 (0.1%)
3	C	0.36	0/1637	0.79	1/2207 (0.0%)
4	D	0.37	0/1733	0.82	1/2318 (0.0%)
5	E	0.47	0/1163	0.91	2/1566 (0.1%)
6	F	0.31	0/856	0.81	2/1154 (0.2%)
7	G	0.34	0/1276	0.78	0/1709
8	H	0.42	0/1136	0.92	6/1527 (0.4%)
9	I	0.35	0/1029	0.86	1/1379 (0.1%)
10	J	0.40	0/806	0.91	3/1084 (0.3%)
11	K	0.40	0/900	0.87	1/1213 (0.1%)
12	L	0.42	0/978	0.97	3/1308 (0.2%)
13	M	0.37	0/947	0.78	2/1270 (0.2%)
14	N	0.36	0/501	0.80	0/664
15	O	0.35	0/745	0.75	0/992
16	P	0.38	0/717	0.84	2/965 (0.2%)
17	Q	0.42	0/870	0.87	0/1159
18	R	0.36	0/604	0.79	0/801
19	S	0.31	0/662	0.77	0/892
20	T	0.41	0/765	0.81	1/1007 (0.1%)
21	U	0.31	0/213	0.73	0/279
All	All	0.27	0/55538	0.56	28/82399 (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 (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	26	CYS	N-CA-C	-8.10	103.40	113.28
12	L	26	ALA	N-CA-C	-7.56	103.95	113.02
2	B	76	GLN	N-CA-C	-6.63	103.87	112.23
5	E	23	GLY	N-CA-C	6.56	119.82	111.09
5	E	41	VAL	CB-CA-C	-6.00	102.93	111.34
16	P	40	ASP	CA-C-N	5.83	125.69	119.28
16	P	40	ASP	C-N-CA	5.83	125.69	119.28
6	F	55	ASP	CA-C-N	5.76	125.38	119.56
6	F	55	ASP	C-N-CA	5.76	125.38	119.56
20	T	96	GLY	N-CA-C	5.65	121.50	111.73
8	H	56	LYS	CA-C-N	5.52	125.70	119.90
8	H	56	LYS	C-N-CA	5.52	125.70	119.90
8	H	73	ASP	CA-C-N	5.47	125.56	119.87
8	H	73	ASP	C-N-CA	5.47	125.56	119.87
10	J	74	ILE	N-CA-C	5.46	116.62	109.58
13	M	67	GLU	N-CA-C	5.42	116.56	108.31
2	B	90	MET	CA-C-N	5.40	125.38	120.03
2	B	90	MET	C-N-CA	5.40	125.38	120.03
12	L	124	LYS	CA-C-N	5.38	125.37	119.89
12	L	124	LYS	C-N-CA	5.38	125.37	119.89
8	H	75	ARG	CA-C-N	5.34	125.31	120.03
8	H	75	ARG	C-N-CA	5.34	125.31	120.03
11	K	40	ILE	CB-CA-C	-5.22	107.27	111.71
3	C	5	ILE	CB-CA-C	-5.17	105.66	111.45
9	I	91	ASP	N-CA-C	-5.14	106.70	113.17
13	M	67	GLU	CB-CA-C	-5.05	110.73	116.54
10	J	52	GLY	CA-C-N	5.04	124.53	119.19
10	J	52	GLY	C-N-CA	5.04	124.53	119.19

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

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Mol	Chain	Res	Type	Group
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	219	0
2	B	1874	0	1887	26	0
3	C	1613	0	1677	29	0
4	D	1703	0	1763	27	0
5	E	1147	0	1207	24	0
6	F	843	0	857	10	0
7	G	1257	0	1296	26	0
8	H	1116	0	1177	28	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	25	0
13	M	937	0	995	15	0
14	N	492	0	529	9	0
15	O	734	0	771	12	0
16	P	701	0	720	14	0
17	Q	857	0	928	14	0
18	R	598	0	670	11	0
19	S	648	0	673	12	0
20	T	763	0	861	18	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
22	P	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	Q	1	0	0	0	0
23	A	30	0	0	0	0
24	A	252	0	276	14	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	525	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 (525) 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
12:L:111:LYS:HZ2	12:L:112:ASP:H	1.28	0.77
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:92:0TD:OD2	2.20	0.75
1:A:1057:G:H5''	3:C:154:SER:HB2	1.68	0.75
2:B:103:THR:HG23	2:B:176:GLU:HG3	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
12:L:48:PRO:HD2	12:L:92:0TD:H3	1.71	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:N19	24:A:1834:NMY:O21	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
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
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:413:G:N2	1:A:429:U:OP2	2.18	0.63
1:A:1145:C:H4'	1:A:1146:A:H5'	1.81	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
11:K:91:ARG:NH2	11:K:110:ASP:OD1	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:372:C:H4'	1:A:373:A:O5'	2.02	0.59
1:A:1028:C:H42	1:A:1033:G:H1	1.49	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:1834:NMY:H191	24:A:1834:NMY:HO21	1.49	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
2:B:83:MET:HE2	2:B:234:PRO:HG2	1.85	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:O11	24:A:1837:NMY:N6	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
7:G:76:ARG:HD2	7:G:89:MET:HE2	1.87	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
3:C:131:ARG:NH1	3:C:166:GLU:OE2	2.38	0.56
5:E:79:GLU:HB3	5:E:92:LYS:HG2	1.88	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:27:LEU:O	12:L:29:GLY:N	2.39	0.56
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:51:GLN:C	7:G:53:LYS:H	2.14	0.55
1:A:1147:C:O2	9:I:16:ARG:NH1	2.40	0.55
7:G:38:LEU:O	7:G:42:ILE:HG13	2.06	0.55
24:A:1836:NMY:O21	24:A:1836:NMY:N19	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:718:G:C8	11:K:116:HIS:HB3	2.43	0.53
4:D:32:ALA:HA	4:D:35:ARG:HB2	1.90	0.53
1:A:179:A:H2'	1:A:180:U:C6	2.43	0.52
1:A:278:G:OP2	17:Q:41:LYS:NZ	2.35	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:509:A:N3	1:A:543:C:O2'	2.33	0.51
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
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
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:103:C:OP1	20:T:17:ARG:NH1	2.45	0.50
1:A:130:A:OP2	1:A:190(E):U:O2'	2.25	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
5:E:9:LYS:NZ	5:E:111:GLU:OE1	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:404:U:H5'	4:D:122:ARG:HD2	1.94	0.50
1:A:1391:U:H2'	1:A:1392:G:C8	2.46	0.50
1:A:7:G:H5'	1:A:298:A:O4'	2.12	0.50
1:A:269:C:H2'	1:A:270:A:C8	2.47	0.50
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
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:261:U:OP2	20:T:79:ARG:NH2	2.45	0.49
1:A:1040:U:H2'	1:A:1041:A:C8	2.48	0.49
1:A:1495:U:H2'	1:A:1496:C:C6	2.47	0.49
8:H:4:ASP:CG	8:H:85:ARG:HH11	2.20	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:H2'	1:A:1225:A:N3	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:99:C:H2'	1:A:101:A:C8	2.49	0.48
1:A:247:G:OP2	17:Q:100:LYS:HG3	2.13	0.48
1:A:1187:G:H5'	9:I:113:LYS:HE2	1.94	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
12:L:25:PRO:C	12:L:27:LEU:H	2.22	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:192:U:H4'	20:T:57:ARG:HD3	1.97	0.47
1:A:337:C:H2'	1:A:338:A:C8	2.50	0.47
1:A:522:C:OP2	12:L:69:TYR:OH	2.24	0.47
6:F:69:GLU:CD	6:F:69:GLU:H	2.22	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:192:U:C1'	20:T:103:GLY:HA2	2.45	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:452:A:O3'	16:P:72:ARG:HD2	2.15	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:OD2	4:D:190:ASP:N	2.47	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:HD2	12:L:33:ARG:HA	1.69	0.46
7:G:46:ALA:O	7:G:50:ILE:HG12	2.15	0.46
1:A:646:U:H2'	1:A:647:C:C6	2.50	0.46
1:A:1241:G:H2'	1:A:1242: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
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
1:A:1236:A:H2'	1:A:1237:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:98:LEU:HD23	11:K:98:LEU:HA	1.74	0.46
13:M:64:TRP:HB3	13:M:66:LEU:HD21	1.98	0.46
1:A:839:U:H5'	1:A:840:C:H5	1.78	0.46
1:A:1518:A:H2'	1:A:1519:A:H8	1.80	0.46
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:28:G:O2'	1:A:296:U:OP1	2.25	0.45
1:A:1223:C:P	19:S:78:ARG:HH21	2.39	0.45
4:D:49:ARG:H	4:D:49:ARG:HD2	1.81	0.45
1:A:755:G:OP2	15:O:65:ARG:HD2	2.17	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
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
4:D:31:CYS:C	4:D:33:MET:H	2.25	0.45
15:O:82:ILE:HG12	15:O:87:ILE:HD12	1.98	0.45
20:T:92:LEU:HD23	20:T:92:LEU:HA	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:192:U:O2'	20:T:57:ARG:HG2	2.16	0.45
1:A:1016:A:H2'	1:A:1017:G:O4'	2.17	0.45
18:R:38:GLU:CD	18:R:38:GLU:H	2.25	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:748:C:H4'	1:A:749:C:O5'	2.17	0.44
1:A:1057:G:H5''	3:C:154:SER:CB	2.42	0.44
8:H:10:LEU:HD22	8:H:83:ILE:HD11	1.99	0.44
1:A:294:U:OP1	1:A:610:G:O2'	2.29	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:620:C:H2'	1:A:621:A:O4'	2.17	0.44
1:A:1268:A:N3	1:A:1326:C:O2'	2.44	0.44
1:A:1286:A:H2'	1:A:1287:A:H4'	1.98	0.44
5:E:31:LEU:HD23	5:E:31:LEU:HA	1.81	0.44
7:G:145:ALA:O	7:G:146:GLU:HB2	2.17	0.44
1:A:399:G:H2'	1:A:400:C:C6	2.52	0.44
1:A:620:C:N1	4:D:135:LEU:HD13	2.32	0.44
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
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
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:731:G:OP1	1:A:766:A:H1'	2.18	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
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
15:O:56:LEU:HA	15:O:59:MET:HE2	1.99	0.44
19:S:44:MET:C	19:S:62:ILE:HD11	2.43	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: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
1:A:1068:G:H8	1:A:1068:G:OP2	2.01	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:114:U:O2'	1:A:115:G:H5'	2.18	0.43
1:A:355:C:H5'	1:A:389:A:OP2	2.18	0.43
1:A:1128:C:H42	1:A:1143:G:H1	1.65	0.43
1:A:1266:G:N2	1:A:1269:A:OP2	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1402:4OC:H2'	1:A:1403:C:O4'	2.18	0.43
3:C:30:ARG:HB3	14:N:36:PHE:O	2.19	0.43
7:G:5:ARG:HG3	7:G:7:ALA:H	1.83	0.43
7:G:108:ALA:O	7:G:111:ARG:HB2	2.18	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
1:A:960:U:H4'	1:A:961:U:C5'	2.49	0.43
1:A:1060:C:H2'	1:A:1061:G:H8	1.84	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:135:C:O2	16:P:1:MET:HB2	2.18	0.43
1:A:689:C:H2'	1:A:690:G:O4'	2.19	0.43
1:A:1139:G:H4'	1:A:1140:C:H5'	2.00	0.43
15:O:82:ILE:HA	15:O:87:ILE:HG13	2.01	0.43
20:T:50:GLU:HG3	20:T:100:ILE:HD12	2.01	0.43
1:A:1312:G:N7	19:S:4:SER:HB3	2.34	0.43
1:A:1368:G:OP1	10:J:62:HIS:HE1	2.02	0.43
2:B:130:ARG:HA	2:B:130:ARG:HD3	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:872:A:C8	1:A:874:G:C8	3.07	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
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:878:G:H5'	8:H:89:PRO:HG2	2.01	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
11:K:124:LYS:HE3	11:K:125:PHE:CE2	2.54	0.43
1:A:60:A:H4'	1:A:61:G:O5'	2.19	0.43
1:A:538:G:H5''	12:L:114:LYS:HB2	2.01	0.43
1:A:619:U:H3	4:D:134:ASP:CG	2.27	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
1:A:376:G:H5''	16:P:5:ARG:HD2	2.01	0.42
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:46:LYS:HG3	12:L:94:PRO:HD3	2.01	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
1:A:1035:A:H2'	1:A:1036:G:C8	2.54	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
7:G:20:ASP:OD2	7:G:63:LYS:NZ	2.49	0.42
1:A:110:C:H2'	1:A:111:G:O4'	2.19	0.42
1:A:184:G:H2'	1:A:185:A:C8	2.53	0.42
1:A:1002:G:H2'	1:A:1003:G: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
4:D:63:LYS:NZ	4:D:197:PRO:O	2.43	0.42
14:N:9:LYS:HE3	14:N:9:LYS:HB3	1.78	0.42
14:N:9:LYS:HE2	14:N:23:ARG:HB2	2.01	0.42
1:A:532:A:N3	1:A:532:A:H2'	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
1:A:1124:G:H4'	10:J:38:ILE:HD11	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:1314:C:C5	19:S:6:LYS:HE2	2.55	0.42
9:I:15:ALA:HB2	9:I:65:VAL:HG13	2.00	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
21:U:6:ARG:H	21:U:6:ARG:HG2	1.71	0.42
1:A:432:A:H3'	1:A:433:C:H5''	2.02	0.42
3:C:107:GLN:CD	3:C:107:GLN:H	2.27	0.42
6:F:39:LYS:HE3	6:F:39:LYS:HB2	1.90	0.42
8:H:121:ASP:N	8:H:121:ASP:OD1	2.53	0.42
1:A:1207:2MG:HM23	1:A:1208:C:H1'	2.02	0.42
1:A:1315:U:OP2	19:S:6:LYS:NZ	2.52	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:HD13	9:I:85:LEU:HA	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:143:ARG:NH1	8:H:77:GLU:OE2	2.49	0.41
5:E:152:ARG:NH2	8:H:107:LEU:O	2.53	0.41
7:G:113:GLU:H	7:G:113:GLU:HG2	1.61	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:551:U:H2'	1:A:552:U:C6	2.54	0.41
1:A:1133:G:N2	1:A:1141:C:O2	2.51	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:8:A:N6	4:D:209:ARG:HB2	2.36	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:811:C:O2'	1:A:901:A:N1	2.51	0.41
1:A:857:C:H2'	1:A:858:G:O4'	2.20	0.41
1:A:1147:C:HO2'	9:I:5:TYR:HH	1.66	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:HD13	12:L:7:ILE:HA	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: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
1:A:1346:A:H2'	7:G:10:ARG:HH22	1.85	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
2:B:42:ILE:HG21	2:B:202:PRO:O	2.20	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:HD23	15:O:43:LEU:HA	1.87	0.41
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
1:A:1030(A):G:N2	1:A:1030(C):G:H3'	2.37	0.40
14:N:8:GLU:O	14:N:11:LYS:HD3	2.22	0.40
20:T:36:LEU:HD23	20:T:36:LEU:HA	1.85	0.40
1:A:397:A:H5'	1:A:398:C:OP1	2.20	0.40
1:A:1291:G:OP1	7:G:37:ASN:ND2	2.53	0.40
7:G:65:ALA:O	7:G:69:VAL:HG23	2.20	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
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
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:56:LEU:O	9:I:58:HIS:N	2.54	0.40
9:I:126:SER:OG	9:I:128:ARG:OXT	2.40	0.40
19:S:80:TYR:CZ	19:S:81:ARG:HB2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:C:H2'	1:A:328:C:O2	2.22	0.40
1:A:895:G:H2'	1:A:896:C:C6	2.57	0.40
1:A:1057:G:H2'	1:A:1058:G:O4'	2.22	0.40
8:H:21:LYS:O	8:H:65:TYR:OH	2.31	0.40
8:H:102:ARG:HD2	8:H:102:ARG:H	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%)	14	43
3	C	205/239 (86%)	190 (93%)	15 (7%)	0	100	100
4	D	206/209 (99%)	200 (97%)	5 (2%)	1 (0%)	24	55
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%)	16	45
10	J	97/105 (92%)	78 (80%)	17 (18%)	2 (2%)	5	26
11	K	117/129 (91%)	107 (92%)	10 (8%)	0	100	100
12	L	122/135 (90%)	110 (90%)	10 (8%)	2 (2%)	7	31
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	Q	102/105 (97%)	95 (93%)	7 (7%)	0	100	100
18	R	71/88 (81%)	66 (93%)	4 (6%)	1 (1%)	9	33
19	S	79/93 (85%)	72 (91%)	7 (9%)	0	100	100
20	T	97/106 (92%)	88 (91%)	8 (8%)	1 (1%)	12	40
21	U	23/27 (85%)	22 (96%)	1 (4%)	0	100	100
All	All	2357/2541 (93%)	2189 (93%)	158 (7%)	10 (0%)	30	60

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 ⓘ

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%)	184 (95%)	10 (5%)	21	49
3	C	160/188 (85%)	145 (91%)	15 (9%)	8	30
4	D	180/181 (99%)	169 (94%)	11 (6%)	17	45
5	E	115/123 (94%)	103 (90%)	12 (10%)	7	25
6	F	90/90 (100%)	88 (98%)	2 (2%)	45	66
7	G	126/127 (99%)	118 (94%)	8 (6%)	16	44
8	H	119/119 (100%)	107 (90%)	12 (10%)	7	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	I	98/99 (99%)	89 (91%)	9 (9%)	8	30
10	J	87/92 (95%)	80 (92%)	7 (8%)	11	36
11	K	90/99 (91%)	88 (98%)	2 (2%)	45	66
12	L	103/110 (94%)	98 (95%)	5 (5%)	22	51
13	M	94/101 (93%)	87 (93%)	7 (7%)	13	38
14	N	49/50 (98%)	46 (94%)	3 (6%)	17	45
15	O	79/80 (99%)	68 (86%)	11 (14%)	3	15
16	P	72/74 (97%)	69 (96%)	3 (4%)	26	55
17	Q	96/97 (99%)	88 (92%)	8 (8%)	10	34
18	R	64/77 (83%)	63 (98%)	1 (2%)	55	72
19	S	71/80 (89%)	67 (94%)	4 (6%)	19	47
20	T	76/82 (93%)	68 (90%)	8 (10%)	6	25
21	U	19/22 (86%)	18 (95%)	1 (5%)	20	49
All	All	1982/2111 (94%)	1843 (93%)	139 (7%)	14	41

All (139) 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	121	LEU
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	34	LEU
3	C	37	GLN
3	C	45	LYS
3	C	64	VAL
3	C	91	LEU
3	C	99	VAL
3	C	101	LEU
3	C	107	GLN

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Mol	Chain	Res	Type
3	C	127	ARG
3	C	166	GLU
3	C	167	TRP
3	C	178	LEU
3	C	188	LEU
3	C	204	LEU
4	D	17	VAL
4	D	19	LEU
4	D	36	ARG
4	D	53	ASP
4	D	64	LEU
4	D	73	ARG
4	D	96	LEU
4	D	122	ARG
4	D	135	LEU
4	D	190	ASP
4	D	194	LEU
5	E	12	LEU
5	E	31	LEU
5	E	38	GLN
5	E	41	VAL
5	E	43	LEU
5	E	47	LYS
5	E	64	ARG
5	E	65	ASN
5	E	76	ILE
5	E	79	GLU
5	E	80	ILE
5	E	144	THR
6	F	40	VAL
6	F	54	LYS
7	G	8	GLU
7	G	11	GLN
7	G	54	THR
7	G	80	VAL
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	34	GLU

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Mol	Chain	Res	Type
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	109	ILE
8	H	133	LEU
9	I	27	THR
9	I	38	GLN
9	I	79	LEU
9	I	85	LEU
9	I	96	LEU
9	I	102	LEU
9	I	108	VAL
9	I	118	LYS
9	I	121	ARG
10	J	16	LEU
10	J	29	ARG
10	J	60	ARG
10	J	62	HIS
10	J	71	LEU
10	J	74	ILE
10	J	75	ILE
11	K	48	ILE
11	K	127	LYS
12	L	20	LYS
12	L	80	HIS
12	L	83	VAL
12	L	90	VAL
12	L	111	LYS
13	M	16	ASP
13	M	31	LYS
13	M	56	LEU
13	M	63	THR
13	M	70	LEU
13	M	110	ARG
13	M	115	LYS
14	N	12	ARG
14	N	22	THR
14	N	33	VAL

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Mol	Chain	Res	Type
15	O	5	LYS
15	O	6	GLU
15	O	31	LEU
15	O	34	LEU
15	O	39	LEU
15	O	57	LEU
15	O	70	LEU
15	O	71	GLN
15	O	79	ARG
15	O	81	LEU
15	O	87	ILE
16	P	20	VAL
16	P	55	ARG
16	P	67	THR
17	Q	38	ARG
17	Q	53	LEU
17	Q	59	ILE
17	Q	74	LEU
17	Q	91	ARG
17	Q	98	LEU
17	Q	101	ARG
17	Q	104	LYS
18	R	18	ARG
19	S	15	LEU
19	S	62	ILE
19	S	65	ASN
19	S	81	ARG
20	T	8	ARG
20	T	17	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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	212	GLN
3	C	37	GLN

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Mol	Chain	Res	Type
4	D	43	HIS
4	D	119	GLN
7	G	51	GLN
8	H	82	HIS
9	I	3	GLN
9	I	73	GLN
10	J	69	ASN
10	J	78	ASN
19	S	14	HIS
20	T	16	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1508/1522 (99%)	203 (13%)	28 (1%)

All (203) 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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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	1402	4OC
1	A	1442	G
1	A	1443	G
1	A	1446	A

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Mol	Chain	Res	Type
1	A	1487	G
1	A	1492	A
1	A	1498	UR3
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
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

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Mol	Chain	Res	Type
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	PSU	A	516	1,22	18,21,22	1.14	1 (5%)	21,30,33	1.76	4 (19%)
1	5MC	A	967	1	19,22,23	0.96	1 (5%)	26,32,35	0.85	1 (3%)
1	4OC	A	1402	1	20,23,24	0.97	2 (10%)	25,32,35	0.79	0
1	M2G	A	966	1	24,27,28	1.22	4 (16%)	33,40,43	0.80	1 (3%)
1	2MG	A	1207	1	23,26,27	1.30	5 (21%)	33,38,41	1.13	4 (12%)
1	5MC	A	1407	1	19,22,23	1.15	2 (10%)	26,32,35	1.11	2 (7%)
1	7MG	A	527	1	23,26,27	3.69	4 (17%)	27,39,42	2.35	9 (33%)
1	5MC	A	1400	1	19,22,23	1.05	2 (10%)	26,32,35	0.95	1 (3%)
1	UR3	A	1498	1	19,22,23	0.51	0	26,32,35	0.96	0
12	0TD	L	92	12	8,9,10	1.92	1 (12%)	6,11,13	2.06	3 (50%)
1	5MC	A	1404	1	19,22,23	0.93	1 (5%)	26,32,35	0.91	2 (7%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	A	516	1,22	-	0/7/25/26	0/2/2/2
1	5MC	A	967	1	-	0/7/25/26	0/2/2/2
1	4OC	A	1402	1	-	2/9/29/30	0/2/2/2
1	M2G	A	966	1	-	0/11/29/30	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	2MG	A	1207	1	-	0/9/27/28	0/3/3/3
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
1	7MG	A	527	1	-	2/7/37/38	0/3/3/3
1	5MC	A	1400	1	-	2/7/25/26	0/2/2/2
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
12	0TD	L	92	12	-	3/7/12/14	-
1	5MC	A	1404	1	-	0/7/25/26	0/2/2/2

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	7MG	C8-N9	-16.27	1.35	1.45
12	L	92	0TD	CB-CA	-4.78	1.53	1.54
1	A	527	7MG	C2-N2	4.17	1.43	1.34
1	A	516	PSU	C6-C5	3.85	1.39	1.35
1	A	527	7MG	C4-N3	3.40	1.42	1.34
1	A	527	7MG	C5-N7	3.34	1.39	1.35
1	A	1407	5MC	C2-N1	3.21	1.46	1.40
1	A	966	M2G	C2-N2	2.97	1.40	1.35
1	A	1207	2MG	C2-N2	2.97	1.39	1.33
1	A	1207	2MG	C2-N1	2.72	1.41	1.36
1	A	966	M2G	C4-N3	2.64	1.40	1.34
1	A	1400	5MC	C2-N1	2.60	1.45	1.40
1	A	1404	5MC	C2-N3	2.56	1.41	1.36
1	A	967	5MC	C2-N3	2.43	1.41	1.36
1	A	1207	2MG	C8-N9	2.35	1.42	1.37
1	A	1207	2MG	C4-N3	2.33	1.39	1.34
1	A	1402	4OC	C2-N3	2.32	1.40	1.36
1	A	966	M2G	C6-N1	2.25	1.43	1.38
1	A	966	M2G	C8-N9	2.14	1.42	1.37
1	A	1207	2MG	C6-N1	2.14	1.42	1.38
1	A	1400	5MC	C2-N3	2.12	1.40	1.36
1	A	1407	5MC	C2-N3	2.12	1.40	1.36
1	A	1402	4OC	C2-N1	2.01	1.44	1.40

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	527	7MG	N9-C4-N3	5.14	133.00	125.46
1	A	527	7MG	C5-C6-N1	5.12	119.95	110.94
1	A	527	7MG	C2-N3-C4	4.88	120.71	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	527	7MG	C5-C4-N3	-4.58	119.53	128.13
1	A	516	PSU	N1-C2-N3	4.35	119.76	115.17
1	A	516	PSU	C4-N3-C2	-4.31	120.43	126.37
1	A	527	7MG	N9-C8-N7	3.92	108.93	103.37
1	A	527	7MG	O6-C6-C5	-3.02	120.21	127.62
12	L	92	0TD	CSB-SB-CB	-3.02	96.94	102.36
1	A	516	PSU	O2-C2-N1	-2.76	119.94	122.79
1	A	527	7MG	C2-N1-C6	-2.71	120.19	125.11
1	A	527	7MG	C6-C5-C4	-2.63	117.78	122.40
1	A	1407	5MC	N4-C4-N3	-2.60	113.80	118.51
1	A	1407	5MC	C5-C4-N3	2.59	124.41	121.75
12	L	92	0TD	OD1-CG-CB	-2.58	117.03	122.44
1	A	1207	2MG	C5-C4-N3	-2.58	124.29	128.39
1	A	516	PSU	C6-N1-C2	-2.52	120.35	122.69
1	A	1404	5MC	N4-C4-N3	-2.37	114.21	118.51
1	A	1207	2MG	N9-C4-N3	2.33	130.62	125.95
1	A	1207	2MG	O6-C6-N1	-2.29	115.81	120.11
1	A	1400	5MC	N4-C4-N3	-2.28	114.38	118.51
1	A	1404	5MC	C5-C4-N3	2.27	124.08	121.75
12	L	92	0TD	O-C-CA	-2.18	119.15	124.77
1	A	966	M2G	C5-C4-N3	-2.08	125.07	128.39
1	A	967	5MC	N4-C4-N3	-2.08	114.75	118.51
1	A	1207	2MG	C2-N1-C6	-2.07	122.05	124.55
1	A	527	7MG	C6-C5-N7	2.02	135.06	131.93

There are no chirality outliers.

All (9) 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'
1	A	1402	4OC	O4'-C4'-C5'-O5'
1	A	1400	5MC	O4'-C4'-C5'-O5'
1	A	1402	4OC	C3'-C4'-C5'-O5'
1	A	1400	5MC	C3'-C4'-C5'-O5'
12	L	92	0TD	CG-CB-SB-CSB
12	L	92	0TD	SB-CB-CG-OD1
12	L	92	0TD	SB-CB-CG-OD2

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
1	A	1498	UR3	1	0
12	L	92	0TD	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	1836	-	43,45,45	1.39	6 (13%)	62,67,67	2.16	15 (24%)
24	NMY	A	1837	-	43,45,45	1.47	8 (18%)	62,67,67	1.89	16 (25%)
24	NMY	A	1832	-	43,45,45	1.33	6 (13%)	62,67,67	1.44	8 (12%)
24	NMY	A	1835	-	43,45,45	1.33	5 (11%)	62,67,67	1.46	12 (19%)
24	NMY	A	1834	-	43,45,45	1.49	7 (16%)	62,67,67	1.85	15 (24%)
24	NMY	A	1833	-	43,45,45	1.33	4 (9%)	62,67,67	1.83	12 (19%)

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	1836	-	-	11/18/94/94	0/4/4/4
24	NMY	A	1837	-	-	8/18/94/94	0/4/4/4
24	NMY	A	1832	-	-	5/18/94/94	0/4/4/4
24	NMY	A	1835	-	-	3/18/94/94	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	NMY	A	1834	-	-	7/18/94/94	0/4/4/4
24	NMY	A	1833	-	-	6/18/94/94	0/4/4/4

All (36) 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	3.91	1.60	1.52
24	A	1833	NMY	C3-C2	3.47	1.57	1.53
24	A	1837	NMY	C3-C2	3.35	1.57	1.53
24	A	1836	NMY	C1-C2	3.34	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	C18-C19	3.08	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	1833	NMY	C1-C2	2.94	1.58	1.52
24	A	1836	NMY	C13-C14	2.93	1.56	1.52
24	A	1834	NMY	C1-C2	2.90	1.58	1.52
24	A	1835	NMY	C1-C2	2.88	1.58	1.52
24	A	1833	NMY	C13-C14	2.86	1.56	1.52
24	A	1837	NMY	C18-C19	2.79	1.57	1.52
24	A	1835	NMY	C13-C14	2.76	1.56	1.52
24	A	1832	NMY	C1-C2	2.74	1.57	1.52
24	A	1834	NMY	C18-C19	2.59	1.57	1.52
24	A	1834	NMY	C21-C22	2.52	1.58	1.53
24	A	1835	NMY	C18-C19	2.50	1.57	1.52
24	A	1832	NMY	C18-C19	2.49	1.57	1.52
24	A	1834	NMY	C14-C15	2.38	1.58	1.53
24	A	1832	NMY	C10-C11	2.31	1.57	1.52
24	A	1832	NMY	C10-C9	2.22	1.57	1.53
24	A	1837	NMY	C10-C11	2.19	1.56	1.52
24	A	1835	NMY	C10-C9	2.18	1.57	1.53
24	A	1837	NMY	C12-C7	2.14	1.58	1.53
24	A	1836	NMY	C21-C22	2.09	1.57	1.53
24	A	1837	NMY	C15-C16	2.06	1.58	1.52
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	1834	NMY	C10-C9	2.03	1.57	1.53
24	A	1837	NMY	C20-C19	2.00	1.56	1.53

All (78) 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	-6.61	91.66	103.24
24	A	1837	NMY	O1-C10-C11	5.71	121.92	107.42
24	A	1833	NMY	O11-C13-O16	-5.69	105.56	111.37
24	A	1834	NMY	O18-C18-C19	5.47	117.03	108.08
24	A	1837	NMY	C11-C10-C9	-5.37	101.35	111.31
24	A	1833	NMY	C11-C10-C9	-5.02	102.00	111.31
24	A	1832	NMY	O11-C13-O16	-4.54	106.73	111.37
24	A	1833	NMY	O11-C11-C12	4.50	118.66	107.23
24	A	1833	NMY	O21-C21-C20	-4.21	100.45	110.38
24	A	1833	NMY	O20-C20-C19	-4.15	102.76	110.22
24	A	1834	NMY	C11-C10-C9	-3.99	103.92	111.31
24	A	1832	NMY	O1-C10-C11	3.89	117.29	107.42
24	A	1836	NMY	O16-C13-C14	-3.84	100.10	104.98
24	A	1836	NMY	O18-C18-C19	3.81	114.31	108.08
24	A	1834	NMY	O20-C20-C19	-3.61	103.74	110.22
24	A	1834	NMY	O1-C10-C11	3.53	116.39	107.42
24	A	1837	NMY	O16-C13-C14	-3.49	100.55	104.98
24	A	1835	NMY	C11-C10-C9	-3.35	105.11	111.31
24	A	1835	NMY	O11-C13-O16	-3.33	107.96	111.37
24	A	1836	NMY	O20-C20-C19	-3.29	104.31	110.22
24	A	1836	NMY	O1-C10-C11	3.28	115.75	107.42
24	A	1836	NMY	O1-C1-C2	3.26	113.41	108.08
24	A	1837	NMY	O11-C11-C12	3.25	115.49	107.23
24	A	1834	NMY	O21-C21-C20	-3.24	102.74	110.38
24	A	1837	NMY	O11-C13-O16	-3.19	108.11	111.37
24	A	1837	NMY	C13-C14-C15	-3.15	98.32	102.10
24	A	1835	NMY	O21-C21-C20	-3.13	103.01	110.38
24	A	1833	NMY	O1-C10-C11	3.11	115.31	107.42
24	A	1837	NMY	O1-C1-C2	3.10	113.14	108.08
24	A	1834	NMY	O11-C13-O16	-3.06	108.24	111.37
24	A	1834	NMY	O22-C22-C21	3.06	115.21	109.70
24	A	1835	NMY	O20-C20-C19	-2.98	104.86	110.22
24	A	1837	NMY	O5-C5-C6	2.98	111.80	106.07
24	A	1833	NMY	O1-C1-C2	2.98	112.95	108.08
24	A	1833	NMY	O12-C12-C7	-2.92	104.44	109.90
24	A	1832	NMY	O21-C21-C20	-2.92	103.49	110.38
24	A	1834	NMY	C18-C19-N23	2.92	115.46	110.20
24	A	1832	NMY	O20-C20-C19	-2.86	105.08	110.22
24	A	1836	NMY	O21-C21-C20	-2.86	103.64	110.38
24	A	1837	NMY	O18-C18-C19	2.76	112.60	108.08
24	A	1834	NMY	C18-O18-C15	-2.73	111.50	117.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
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	1833	NMY	C18-O18-C15	-2.69	111.61	117.98
24	A	1836	NMY	C11-C10-C9	-2.65	106.39	111.31
24	A	1837	NMY	O11-C11-C10	2.64	114.12	107.42
24	A	1832	NMY	O1-C1-C2	2.62	112.37	108.08
24	A	1832	NMY	O18-C18-O22	-2.61	103.83	110.69
24	A	1834	NMY	O1-C1-O5	-2.56	103.96	110.69
24	A	1835	NMY	O16-C13-C14	-2.55	101.74	104.98
24	A	1836	NMY	O11-C11-C12	2.54	113.68	107.23
24	A	1837	NMY	O21-C21-C20	-2.49	104.52	110.38
24	A	1834	NMY	C20-C21-C22	2.48	114.73	110.23
24	A	1835	NMY	O18-C18-C19	2.47	112.11	108.08
24	A	1835	NMY	C13-O11-C11	-2.45	112.16	117.98
24	A	1836	NMY	O12-C12-C7	-2.42	105.38	109.90
24	A	1834	NMY	O11-C11-C12	2.41	113.36	107.23
24	A	1833	NMY	O18-C18-C19	2.38	111.98	108.08
24	A	1837	NMY	O1-C1-O5	-2.38	104.44	110.69
24	A	1835	NMY	O18-C18-O22	-2.37	104.47	110.69
24	A	1836	NMY	C1-C2-N2	2.36	114.46	110.20
24	A	1832	NMY	C8-C7-C12	-2.32	106.60	110.08
24	A	1834	NMY	O22-C18-C19	-2.32	104.95	110.08
24	A	1836	NMY	C18-O22-C22	-2.32	109.19	113.72
24	A	1833	NMY	O20-C20-C21	-2.31	104.93	110.38
24	A	1835	NMY	O1-C1-O5	-2.30	104.64	110.69
24	A	1832	NMY	C11-C10-C9	-2.22	107.19	111.31
24	A	1837	NMY	C12-C11-C10	-2.19	106.80	111.72
24	A	1834	NMY	C18-O22-C22	-2.16	109.50	113.72
24	A	1835	NMY	C18-O18-C15	-2.16	112.85	117.98
24	A	1836	NMY	C18-C19-N23	2.15	114.07	110.20
24	A	1834	NMY	C14-C15-C16	-2.14	99.50	103.24
24	A	1835	NMY	O1-C10-C11	2.10	112.74	107.42
24	A	1836	NMY	C4-C3-C2	-2.09	107.53	110.99
24	A	1837	NMY	O5-C5-C4	2.07	113.44	109.70
24	A	1833	NMY	C18-O22-C22	-2.05	109.72	113.72

There are no chirality outliers.

All (40) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	A	1833	NMY	C16-C15-O18-C18

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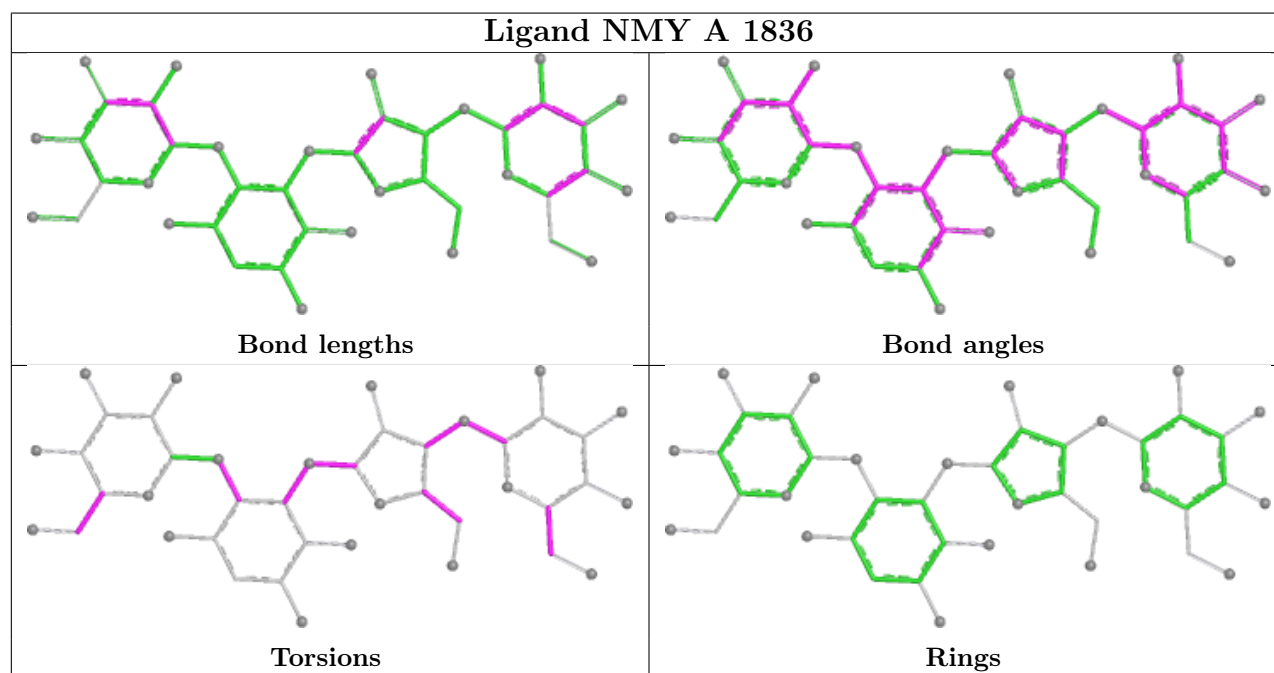
Mol	Chain	Res	Type	Atoms
24	A	1833	NMY	C19-C18-O18-C15
24	A	1833	NMY	O22-C22-C23-N19
24	A	1834	NMY	C4-C5-C6-N6
24	A	1834	NMY	O5-C5-C6-N6
24	A	1834	NMY	C21-C22-C23-N19
24	A	1835	NMY	C4-C5-C6-N6
24	A	1835	NMY	O5-C5-C6-N6
24	A	1836	NMY	C14-C13-O11-C11
24	A	1836	NMY	O16-C13-O11-C11
24	A	1836	NMY	C19-C18-O18-C15
24	A	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	1833	NMY	C12-C11-O11-C13
24	A	1837	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	C11-C10-O1-C1
24	A	1832	NMY	O16-C13-O11-C11
24	A	1833	NMY	C21-C22-C23-N19
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	1837	NMY	C2-C1-O1-C10
24	A	1836	NMY	C11-C10-O1-C1
24	A	1832	NMY	C14-C15-O18-C18
24	A	1833	NMY	C14-C15-O18-C18
24	A	1834	NMY	C14-C15-O18-C18
24	A	1836	NMY	C16-C15-O18-C18
24	A	1837	NMY	C16-C15-O18-C18

There are no ring outliers.

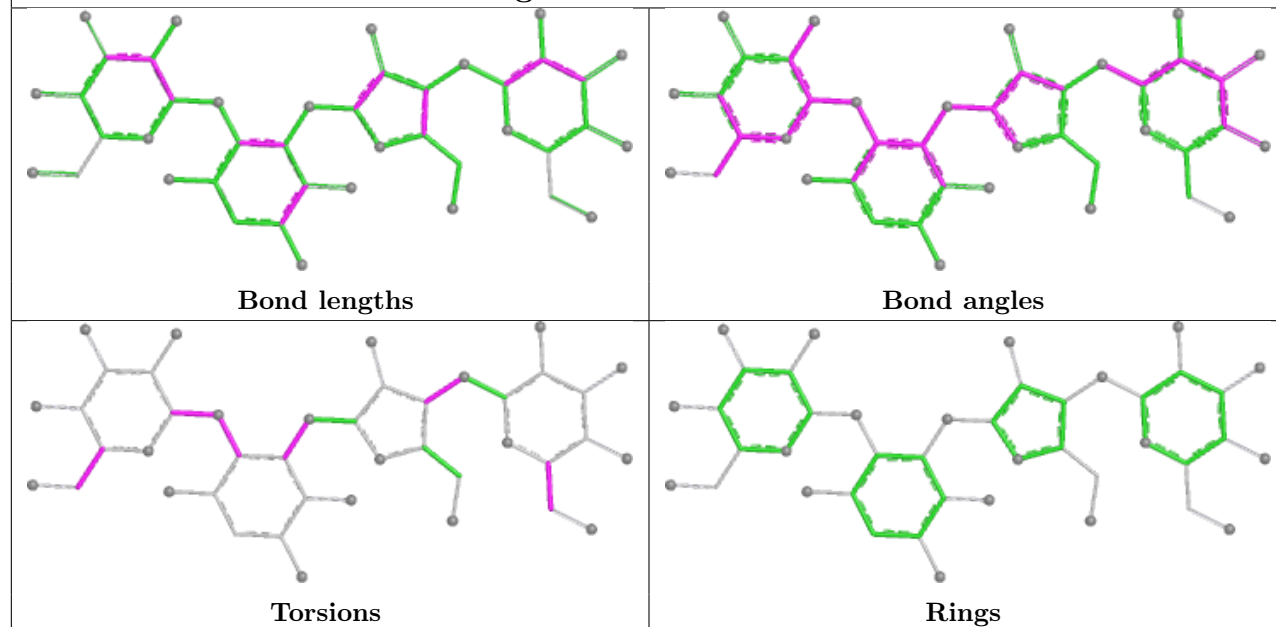
6 monomers are involved in 14 short contacts:

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

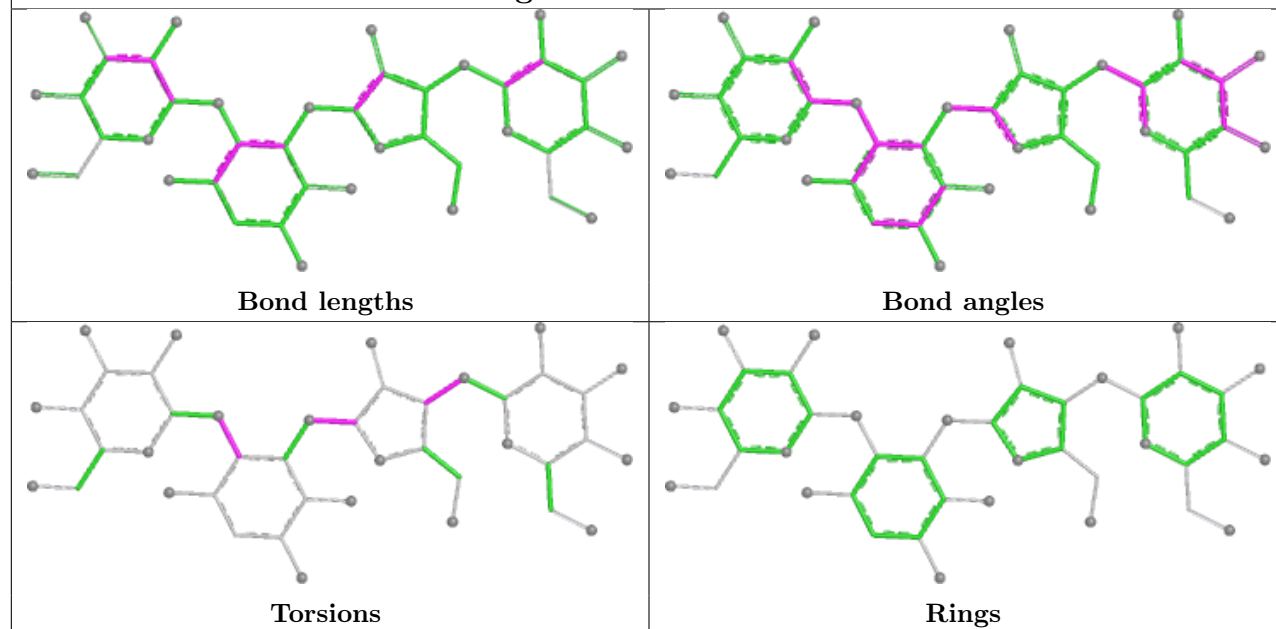
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



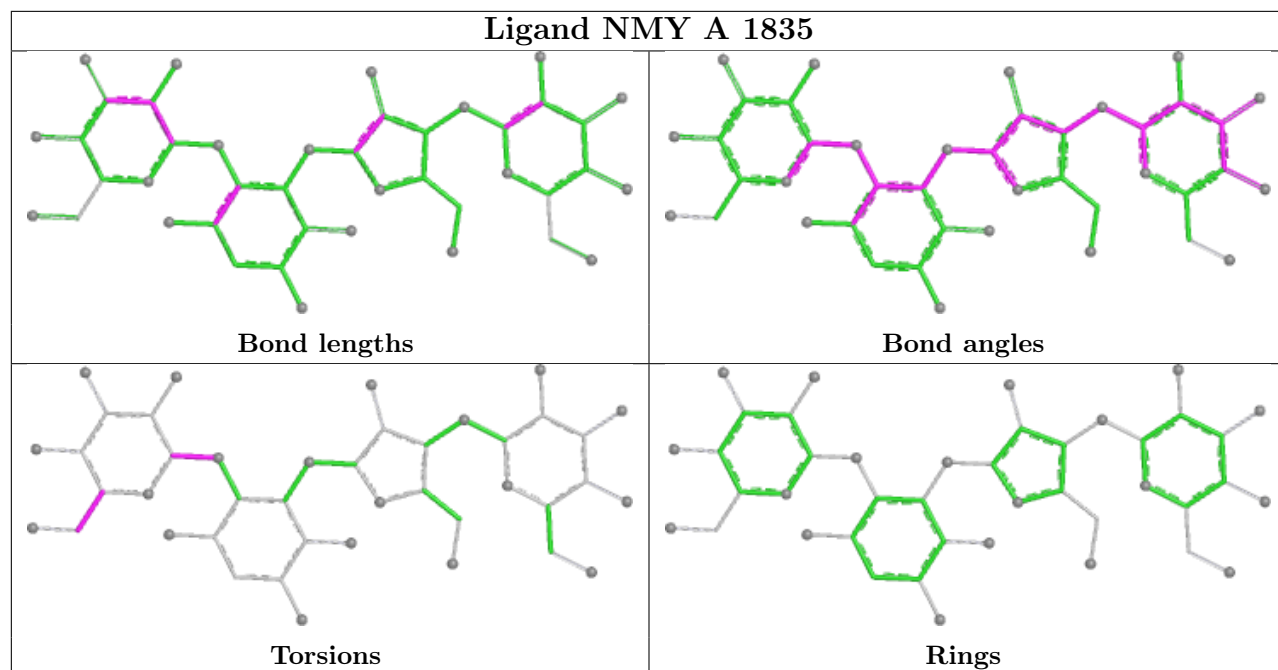
Ligand NMY A 1837



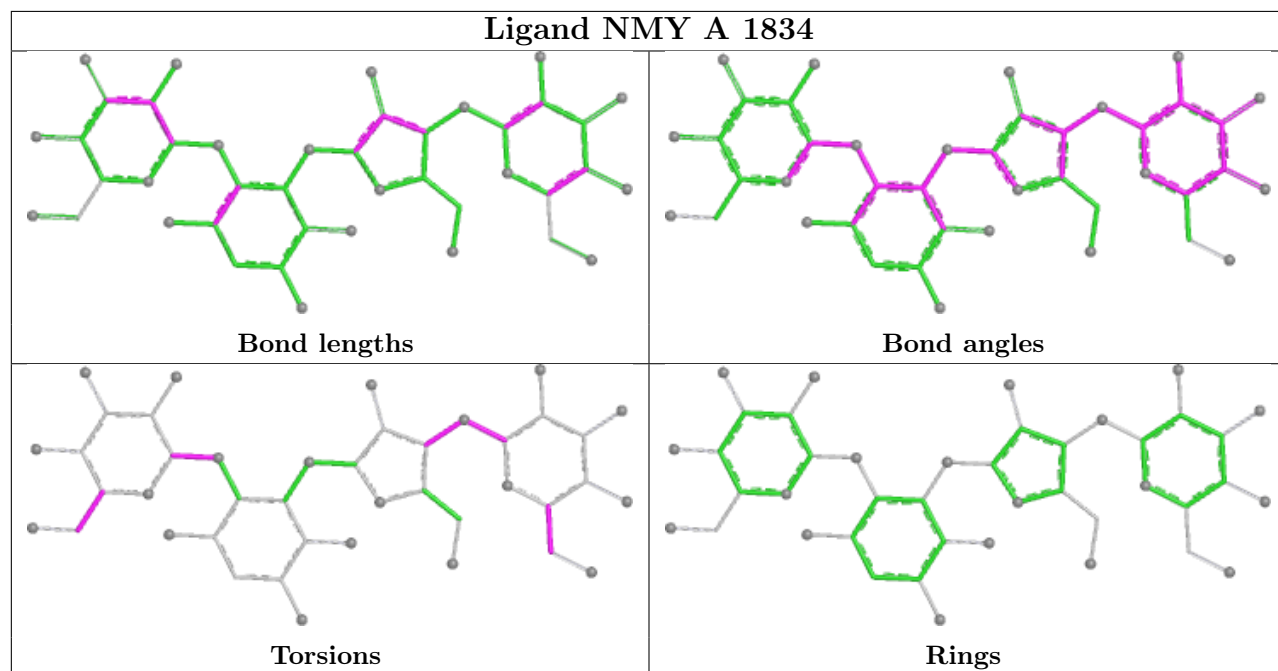
Ligand NMY A 1832

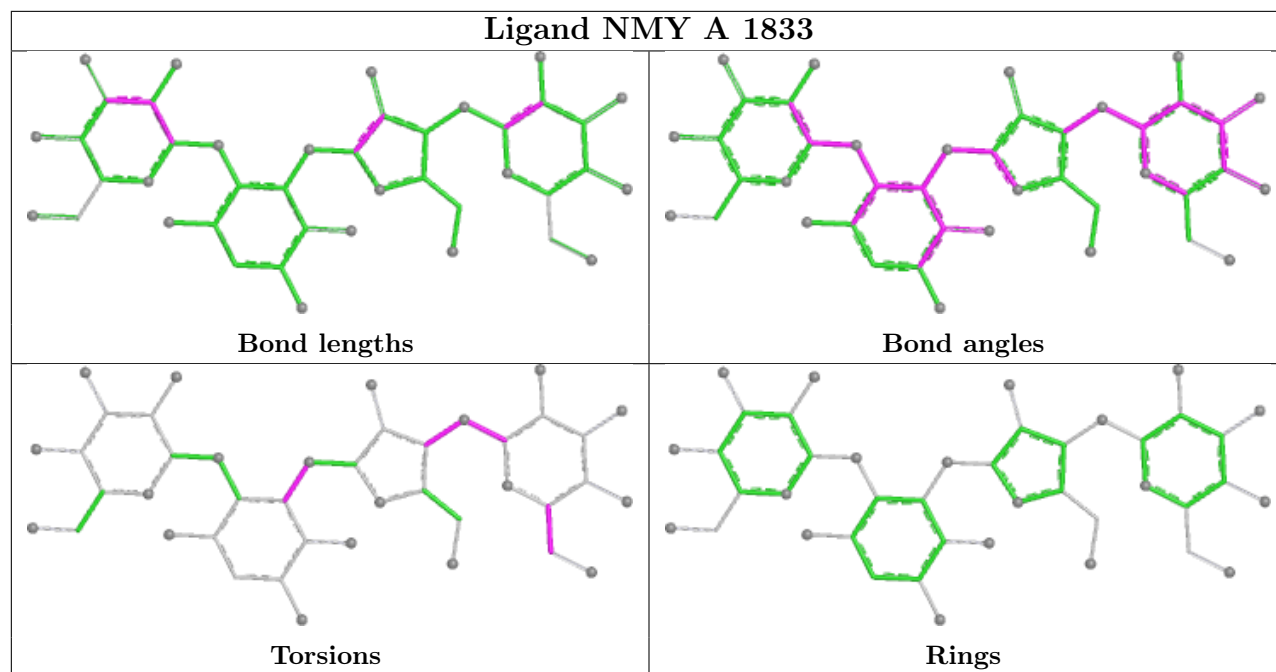


Ligand NMY A 1835



Ligand NMY A 1834





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%)	-0.49	17 (1%) 78 60	51, 84, 177, 283	0
2	B	236/256 (92%)	0.17	11 (4%) 36 24	60, 109, 189, 249	0
3	C	207/239 (86%)	0.18	11 (5%) 32 22	50, 115, 158, 195	0
4	D	208/209 (99%)	0.13	13 (6%) 26 17	63, 94, 134, 166	0
5	E	151/162 (93%)	-0.17	1 (0%) 84 70	56, 75, 113, 167	0
6	F	101/101 (100%)	-0.02	1 (0%) 79 63	78, 118, 149, 179	0
7	G	155/156 (99%)	0.32	10 (6%) 25 17	82, 115, 183, 212	0
8	H	138/138 (100%)	-0.42	1 (0%) 84 70	46, 72, 102, 140	0
9	I	127/128 (99%)	0.50	9 (7%) 22 15	79, 121, 162, 198	0
10	J	99/105 (94%)	0.99	13 (13%) 7 6	73, 140, 218, 252	0
11	K	119/129 (92%)	0.14	4 (3%) 48 32	68, 93, 129, 150	0
12	L	124/135 (91%)	0.26	7 (5%) 30 20	58, 87, 126, 215	0
13	M	118/126 (93%)	0.24	8 (6%) 23 16	84, 114, 146, 183	0
14	N	60/61 (98%)	0.66	7 (11%) 9 8	81, 108, 151, 202	0
15	O	88/89 (98%)	0.05	2 (2%) 61 42	57, 89, 135, 169	0
16	P	84/88 (95%)	-0.01	1 (1%) 76 58	62, 80, 107, 189	0
17	Q	104/105 (99%)	0.10	6 (5%) 29 19	59, 78, 125, 196	0
18	R	73/88 (82%)	0.14	4 (5%) 30 21	65, 97, 177, 232	0
19	S	81/93 (87%)	0.60	9 (11%) 10 9	47, 137, 180, 209	0
20	T	99/106 (93%)	0.40	10 (10%) 12 10	64, 86, 136, 182	0
21	U	25/27 (92%)	1.04	5 (20%) 3 2	73, 106, 130, 206	0
All	All	3897/4063 (95%)	-0.06	150 (3%) 44 30	46, 94, 169, 283	0

All (150) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
19	S	3	ARG	12.6
1	A	1129	C	10.9
11	K	129	SER	7.6
19	S	2	PRO	7.4
17	Q	105	ALA	7.1
17	Q	103	GLY	6.8
13	M	8	GLU	6.4
11	K	128	ALA	5.9
1	A	461	C	5.6
7	G	5	ARG	5.5
14	N	2	ALA	5.4
2	B	13	ALA	5.4
9	I	8	GLY	5.2
1	A	202	U	5.0
21	U	25	LYS	5.0
3	C	2	GLY	4.8
10	J	88	LEU	4.7
2	B	12	GLU	4.6
1	A	793	U	4.3
20	T	100	ILE	4.3
20	T	12	ALA	4.3
20	T	73	HIS	4.2
13	M	9	ILE	4.1
12	L	28	LYS	4.1
2	B	203	GLY	3.9
4	D	31	CYS	3.8
4	D	9	CYS	3.8
7	G	156	TRP	3.8
20	T	9	ASN	3.7
7	G	33	ASP	3.7
9	I	15	ALA	3.7
4	D	2	GLY	3.6
21	U	2	GLY	3.6
13	M	5	ALA	3.6
19	S	4	SER	3.6
17	Q	101	ARG	3.5
1	A	462	G	3.5
10	J	90	LEU	3.4
12	L	26	ALA	3.4
9	I	66	ARG	3.4
20	T	74	LYS	3.4
17	Q	100	LYS	3.3
19	S	6	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
10	J	32	ALA	3.2
17	Q	104	LYS	3.2
2	B	131	PRO	3.1
10	J	75	ILE	3.1
1	A	1034	G	3.1
2	B	72	GLY	3.1
3	C	188	LEU	3.1
3	C	3	ASN	3.1
9	I	128	ARG	3.0
3	C	100	ALA	3.0
3	C	167	TRP	3.0
10	J	37	PRO	2.9
18	R	17	SER	2.9
10	J	58	ASP	2.9
4	D	26	CYS	2.9
1	A	1125	U	2.9
10	J	43	ARG	2.9
1	A	81	U	2.8
20	T	11	SER	2.8
13	M	10	PRO	2.8
12	L	47	LYS	2.8
17	Q	102	GLY	2.8
13	M	104	ARG	2.8
12	L	19	ARG	2.8
7	G	57	GLU	2.8
1	A	1446	A	2.7
15	O	2	PRO	2.7
1	A	1224	G	2.7
11	K	117	ASN	2.7
19	S	7	LYS	2.7
4	D	32	ALA	2.7
18	R	16	PRO	2.7
3	C	146	ALA	2.7
7	G	2	ALA	2.7
7	G	56	GLN	2.6
20	T	68	LYS	2.6
14	N	8	GLU	2.6
13	M	11	ARG	2.6
7	G	7	ALA	2.6
21	U	24	ARG	2.6
18	R	20	ALA	2.6
2	B	206	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
19	S	10	PHE	2.6
10	J	73	ASP	2.6
21	U	10	ARG	2.5
1	A	1543	C	2.5
4	D	12	CYS	2.5
9	I	126	SER	2.5
4	D	24	GLU	2.5
6	F	45	LEU	2.5
2	B	9	GLU	2.4
10	J	89	ASP	2.4
20	T	10	LEU	2.4
1	A	1124	G	2.4
3	C	196	LEU	2.4
19	S	5	LEU	2.4
2	B	14	GLY	2.4
2	B	188	ALA	2.4
9	I	127	LYS	2.4
10	J	45	ARG	2.4
12	L	120	TYR	2.4
13	M	7	VAL	2.4
10	J	66	ARG	2.3
7	G	151	TYR	2.3
19	S	33	THR	2.3
19	S	30	LEU	2.3
2	B	133	LYS	2.3
21	U	20	LYS	2.3
7	G	4	ARG	2.3
16	P	29	ASP	2.3
3	C	4	LYS	2.2
3	C	76	VAL	2.2
15	O	89	GLY	2.2
1	A	460	A	2.2
9	I	102	LEU	2.2
14	N	22	THR	2.2
12	L	31	PRO	2.2
9	I	16	ARG	2.2
3	C	178	LEU	2.2
4	D	33	MET	2.2
1	A	532	A	2.2
4	D	149	ALA	2.1
7	G	155	ARG	2.1
10	J	64	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
3	C	155	GLY	2.1
11	K	16	SER	2.1
12	L	95	GLY	2.1
4	D	4	TYR	2.1
8	H	1	MET	2.1
9	I	2	GLU	2.1
10	J	36	GLY	2.1
18	R	83	GLU	2.1
2	B	7	VAL	2.1
14	N	9	LYS	2.1
4	D	49	ARG	2.1
1	A	1126	U	2.1
1	A	1212	U	2.1
4	D	23	GLY	2.1
14	N	60	SER	2.1
14	N	13	THR	2.1
13	M	102	ARG	2.0
20	T	103	GLY	2.0
4	D	179	GLU	2.0
1	A	1181	G	2.0
14	N	35	ARG	2.0
5	E	81	GLU	2.0
20	T	51	GLU	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(Å ²)	Q<0.9
1	5MC	A	1407	21/22	0.94	0.12	83,120,143,145	0
1	PSU	A	516	20/21	0.95	0.09	87,90,100,100	0
1	UR3	A	1498	21/22	0.95	0.10	71,77,98,103	0
12	0TD	L	92	10/11	0.95	0.16	96,102,168,273	0
1	5MC	A	1404	21/22	0.96	0.09	72,81,90,95	0
1	7MG	A	527	24/25	0.97	0.08	66,72,94,98	0
1	M2G	A	966	25/26	0.97	0.06	70,81,95,98	0
1	2MG	A	1207	24/25	0.97	0.07	101,107,113,115	0
1	5MC	A	1400	21/22	0.97	0.09	67,83,106,112	0
1	5MC	A	967	21/22	0.98	0.06	59,76,83,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	4OC	A	1402	22/23	0.98	0.08	70,75,83,91	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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($\text{\AA}^2$)	Q<0.9
22	MG	A	1802	1/1	0.30	0.41	108,108,108,108	0
22	MG	C	302	1/1	0.35	0.21	106,106,106,106	0
23	K	A	1742	1/1	0.47	0.34	138,138,138,138	0
22	MG	A	1829	1/1	0.52	0.26	104,104,104,104	0
22	MG	A	1655	1/1	0.53	0.41	93,93,93,93	0
22	MG	A	1830	1/1	0.53	0.19	293,293,293,293	0
22	MG	A	1660	1/1	0.54	0.35	75,75,75,75	0
22	MG	A	1776	1/1	0.55	0.32	85,85,85,85	0
22	MG	A	1602	1/1	0.56	0.47	114,114,114,114	0
22	MG	A	1814	1/1	0.57	0.36	87,87,87,87	0
22	MG	N	102	1/1	0.58	0.54	92,92,92,92	0
22	MG	A	1762	1/1	0.58	0.40	89,89,89,89	0
23	K	A	1753	1/1	0.58	0.37	127,127,127,127	0
22	MG	A	1667	1/1	0.61	0.63	98,98,98,98	0
22	MG	A	1823	1/1	0.61	0.25	107,107,107,107	0
22	MG	A	1615	1/1	0.62	0.47	95,95,95,95	0
22	MG	A	1772	1/1	0.63	0.45	66,66,66,66	0
23	K	A	1760	1/1	0.63	0.36	145,145,145,145	0
23	K	A	1751	1/1	0.65	0.20	160,160,160,160	0
22	MG	A	1788	1/1	0.65	0.41	88,88,88,88	0
23	K	A	1748	1/1	0.65	0.33	136,136,136,136	0
22	MG	A	1782	1/1	0.66	0.36	82,82,82,82	0
22	MG	A	1787	1/1	0.67	0.44	117,117,117,117	0
22	MG	A	1795	1/1	0.67	0.47	96,96,96,96	0
22	MG	A	1633	1/1	0.68	0.33	93,93,93,93	0
23	K	A	1755	1/1	0.69	0.40	147,147,147,147	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
22	MG	F	201	1/1	0.70	0.20	95,95,95,95	0
23	K	A	1747	1/1	0.71	0.25	112,112,112,112	0
22	MG	A	1789	1/1	0.71	0.33	97,97,97,97	0
22	MG	A	1822	1/1	0.72	0.15	101,101,101,101	0
22	MG	A	1778	1/1	0.74	0.29	88,88,88,88	0
23	K	A	1735	1/1	0.74	0.47	152,152,152,152	0
22	MG	L	201	1/1	0.74	0.33	99,99,99,99	0
22	MG	A	1824	1/1	0.75	0.21	103,103,103,103	0
22	MG	A	1809	1/1	0.75	0.23	74,74,74,74	0
22	MG	A	1774	1/1	0.75	0.33	98,98,98,98	0
22	MG	A	1658	1/1	0.75	0.45	76,76,76,76	0
22	MG	A	1725	1/1	0.75	0.26	76,76,76,76	0
23	K	A	1741	1/1	0.76	0.61	154,154,154,154	0
22	MG	A	1781	1/1	0.76	0.42	87,87,87,87	0
22	MG	A	1791	1/1	0.76	0.39	78,78,78,78	0
22	MG	A	1826	1/1	0.76	0.24	81,81,81,81	0
22	MG	A	1642	1/1	0.76	0.37	68,68,68,68	0
23	K	A	1731	1/1	0.76	0.20	121,121,121,121	0
22	MG	A	1800	1/1	0.76	0.41	98,98,98,98	0
23	K	A	1740	1/1	0.76	0.24	135,135,135,135	0
23	K	A	1733	1/1	0.77	0.19	112,112,112,112	0
22	MG	A	1796	1/1	0.77	0.12	89,89,89,89	0
23	K	A	1739	1/1	0.77	0.34	140,140,140,140	0
23	K	A	1750	1/1	0.78	0.42	143,143,143,143	0
22	MG	A	1773	1/1	0.79	0.20	69,69,69,69	0
22	MG	A	1710	1/1	0.79	0.35	90,90,90,90	0
22	MG	A	1720	1/1	0.80	0.50	75,75,75,75	0
22	MG	A	1763	1/1	0.80	0.28	68,68,68,68	0
22	MG	A	1688	1/1	0.80	0.37	41,41,41,41	0
22	MG	A	1827	1/1	0.80	0.23	102,102,102,102	0
22	MG	A	1784	1/1	0.80	0.32	90,90,90,90	0
22	MG	A	1818	1/1	0.80	0.34	90,90,90,90	0
22	MG	A	1819	1/1	0.80	0.24	85,85,85,85	0
23	K	A	1757	1/1	0.80	0.28	143,143,143,143	0
23	K	A	1759	1/1	0.80	0.18	145,145,145,145	0
22	MG	A	1777	1/1	0.80	0.47	96,96,96,96	0
22	MG	C	301	1/1	0.81	0.20	66,66,66,66	0
22	MG	A	1621	1/1	0.81	0.46	82,82,82,82	0
22	MG	A	1790	1/1	0.81	0.37	72,72,72,72	0
23	K	A	1744	1/1	0.82	0.34	121,121,121,121	0
22	MG	N	103	1/1	0.82	0.18	57,57,57,57	0
22	MG	A	1783	1/1	0.82	0.16	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
22	MG	A	1775	1/1	0.82	0.34	84,84,84,84	0
22	MG	A	1728	1/1	0.82	0.31	55,55,55,55	0
24	NMY	A	1837	42/42	0.82	0.16	57,138,186,186	0
22	MG	A	1828	1/1	0.83	0.13	95,95,95,95	0
22	MG	A	1798	1/1	0.83	0.58	85,85,85,85	0
22	MG	A	1686	1/1	0.83	0.27	54,54,54,54	0
22	MG	A	1622	1/1	0.83	0.27	65,65,65,65	0
23	K	A	1737	1/1	0.83	0.18	134,134,134,134	0
22	MG	A	1805	1/1	0.83	0.49	79,79,79,79	0
22	MG	A	1766	1/1	0.83	0.27	61,61,61,61	0
22	MG	A	1797	1/1	0.83	0.18	68,68,68,68	0
22	MG	M	202	1/1	0.83	0.18	85,85,85,85	0
22	MG	A	1815	1/1	0.83	0.49	81,81,81,81	0
22	MG	A	1804	1/1	0.84	0.16	56,56,56,56	0
24	NMY	A	1834	42/42	0.84	0.23	62,120,200,201	0
22	MG	B	301	1/1	0.84	0.17	96,96,96,96	0
22	MG	A	1659	1/1	0.85	0.18	94,94,94,94	0
22	MG	A	1801	1/1	0.85	0.36	80,80,80,80	0
22	MG	A	1726	1/1	0.85	0.25	70,70,70,70	0
22	MG	A	1785	1/1	0.85	0.27	67,67,67,67	0
23	K	A	1746	1/1	0.85	0.19	149,149,149,149	0
22	MG	H	201	1/1	0.85	0.21	74,74,74,74	0
22	MG	A	1771	1/1	0.85	0.48	58,58,58,58	0
22	MG	A	1799	1/1	0.85	0.37	98,98,98,98	0
23	K	A	1749	1/1	0.86	0.29	115,115,115,115	0
22	MG	A	1627	1/1	0.86	0.27	90,90,90,90	0
22	MG	A	1604	1/1	0.86	0.23	79,79,79,79	0
22	MG	A	1803	1/1	0.86	0.16	66,66,66,66	0
23	K	A	1754	1/1	0.86	0.27	135,135,135,135	0
22	MG	A	1706	1/1	0.86	0.38	73,73,73,73	0
23	K	A	1756	1/1	0.86	0.15	151,151,151,151	0
23	K	A	1743	1/1	0.86	0.11	137,137,137,137	0
22	MG	A	1640	1/1	0.86	0.20	47,47,47,47	0
22	MG	A	1682	1/1	0.86	0.44	84,84,84,84	0
22	MG	A	1813	1/1	0.86	0.18	88,88,88,88	0
22	MG	A	1724	1/1	0.86	0.12	51,51,51,51	0
22	MG	A	1792	1/1	0.87	0.32	68,68,68,68	0
22	MG	A	1661	1/1	0.87	0.26	69,69,69,69	0
22	MG	A	1647	1/1	0.87	0.40	83,83,83,83	0
22	MG	A	1651	1/1	0.87	0.32	77,77,77,77	0
22	MG	A	1631	1/1	0.87	0.27	63,63,63,63	0
22	MG	A	1611	1/1	0.87	0.27	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
22	MG	A	1689	1/1	0.87	0.29	67,67,67,67	0
22	MG	A	1644	1/1	0.87	0.32	62,62,62,62	0
22	MG	A	1646	1/1	0.87	0.40	58,58,58,58	0
24	NMY	A	1835	42/42	0.87	0.16	105,127,145,147	0
22	MG	A	1770	1/1	0.87	0.49	102,102,102,102	0
22	MG	A	1764	1/1	0.88	0.21	65,65,65,65	0
22	MG	A	1709	1/1	0.88	0.33	66,66,66,66	0
22	MG	A	1601	1/1	0.88	0.21	76,76,76,76	0
22	MG	A	1683	1/1	0.88	0.36	77,77,77,77	0
22	MG	A	1721	1/1	0.88	0.25	77,77,77,77	0
22	MG	A	1723	1/1	0.88	0.24	55,55,55,55	0
22	MG	A	1685	1/1	0.88	0.40	55,55,55,55	0
22	MG	A	1630	1/1	0.88	0.46	60,60,60,60	0
22	MG	A	1657	1/1	0.88	0.27	70,70,70,70	0
22	MG	A	1619	1/1	0.88	0.25	77,77,77,77	0
22	MG	A	1730	1/1	0.88	0.36	74,74,74,74	0
22	MG	D	302	1/1	0.88	0.15	63,63,63,63	0
22	MG	D	303	1/1	0.88	0.30	89,89,89,89	0
22	MG	A	1705	1/1	0.88	0.38	61,61,61,61	0
22	MG	A	1672	1/1	0.88	0.39	83,83,83,83	0
22	MG	A	1693	1/1	0.89	0.28	72,72,72,72	0
23	K	A	1752	1/1	0.89	0.35	115,115,115,115	0
22	MG	A	1699	1/1	0.89	0.10	64,64,64,64	0
22	MG	A	1761	1/1	0.89	0.35	51,51,51,51	0
23	K	A	1738	1/1	0.89	0.30	133,133,133,133	0
22	MG	A	1713	1/1	0.89	0.39	61,61,61,61	0
22	MG	A	1664	1/1	0.90	0.33	94,94,94,94	0
22	MG	A	1665	1/1	0.90	0.33	84,84,84,84	0
23	K	A	1732	1/1	0.90	0.18	104,104,104,104	0
22	MG	A	1645	1/1	0.90	0.54	79,79,79,79	0
22	MG	A	1632	1/1	0.90	0.30	64,64,64,64	0
22	MG	A	1652	1/1	0.90	0.32	64,64,64,64	0
22	MG	A	1673	1/1	0.91	0.15	57,57,57,57	0
22	MG	A	1643	1/1	0.91	0.25	54,54,54,54	0
22	MG	A	1624	1/1	0.91	0.30	39,39,39,39	0
22	MG	A	1711	1/1	0.91	0.38	90,90,90,90	0
22	MG	A	1712	1/1	0.91	0.24	75,75,75,75	0
22	MG	A	1684	1/1	0.91	0.40	68,68,68,68	0
23	K	A	1745	1/1	0.91	0.30	142,142,142,142	0
22	MG	A	1806	1/1	0.91	0.25	76,76,76,76	0
22	MG	A	1807	1/1	0.91	0.48	78,78,78,78	0
22	MG	A	1808	1/1	0.91	0.59	79,79,79,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
22	MG	A	1653	1/1	0.91	0.51	63,63,63,63	0
22	MG	A	1663	1/1	0.91	0.47	67,67,67,67	0
22	MG	A	1613	1/1	0.91	0.49	86,86,86,86	0
22	MG	A	1656	1/1	0.91	0.19	57,57,57,57	0
22	MG	A	1817	1/1	0.91	0.28	103,103,103,103	0
22	MG	A	1666	1/1	0.91	0.41	72,72,72,72	0
22	MG	Q	201	1/1	0.91	0.11	71,71,71,71	0
22	MG	A	1616	1/1	0.91	0.35	84,84,84,84	0
22	MG	A	1821	1/1	0.91	0.19	73,73,73,73	0
22	MG	A	1727	1/1	0.91	0.15	54,54,54,54	0
23	K	A	1734	1/1	0.91	0.25	119,119,119,119	0
22	MG	A	1617	1/1	0.91	0.63	112,112,112,112	0
22	MG	A	1729	1/1	0.91	0.18	64,64,64,64	0
24	NMY	A	1836	42/42	0.91	0.23	75,119,177,188	0
22	MG	A	1779	1/1	0.91	0.21	82,82,82,82	0
22	MG	A	1668	1/1	0.92	0.30	66,66,66,66	0
22	MG	A	1701	1/1	0.92	0.29	44,44,44,44	0
22	MG	A	1603	1/1	0.92	0.36	69,69,69,69	0
22	MG	H	202	1/1	0.92	0.07	49,49,49,49	0
22	MG	A	1614	1/1	0.92	0.24	72,72,72,72	0
22	MG	A	1675	1/1	0.92	0.56	75,75,75,75	0
22	MG	A	1662	1/1	0.92	0.20	51,51,51,51	0
22	MG	A	1623	1/1	0.92	0.65	86,86,86,86	0
23	K	A	1758	1/1	0.92	0.52	130,130,130,130	0
22	MG	P	102	1/1	0.92	0.27	84,84,84,84	0
22	MG	A	1831	1/1	0.92	0.09	285,285,285,285	0
22	MG	A	1697	1/1	0.92	0.25	36,36,36,36	0
22	MG	A	1767	1/1	0.92	0.32	62,62,62,62	0
22	MG	A	1768	1/1	0.92	0.28	50,50,50,50	0
22	MG	A	1769	1/1	0.92	0.46	73,73,73,73	0
22	MG	A	1610	1/1	0.93	0.19	89,89,89,89	0
22	MG	A	1820	1/1	0.93	0.25	65,65,65,65	0
22	MG	A	1794	1/1	0.93	0.30	73,73,73,73	0
22	MG	A	1608	1/1	0.93	0.14	73,73,73,73	0
22	MG	A	1698	1/1	0.93	0.33	47,47,47,47	0
22	MG	A	1676	1/1	0.93	0.08	60,60,60,60	0
22	MG	A	1786	1/1	0.93	0.34	71,71,71,71	0
22	MG	A	1810	1/1	0.93	0.29	65,65,65,65	0
22	MG	A	1812	1/1	0.93	0.27	103,103,103,103	0
22	MG	A	1637	1/1	0.93	0.18	67,67,67,67	0
22	MG	A	1714	1/1	0.93	0.50	94,94,94,94	0
22	MG	A	1715	1/1	0.93	0.11	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
22	MG	A	1609	1/1	0.93	0.28	86,86,86,86	0
22	MG	B	302	1/1	0.93	0.36	84,84,84,84	0
22	MG	A	1690	1/1	0.93	0.40	70,70,70,70	0
22	MG	A	1670	1/1	0.94	0.21	57,57,57,57	0
22	MG	A	1704	1/1	0.94	0.24	60,60,60,60	0
22	MG	A	1635	1/1	0.94	0.34	41,41,41,41	0
22	MG	B	303	1/1	0.94	0.23	83,83,83,83	0
22	MG	A	1780	1/1	0.94	0.34	75,75,75,75	0
22	MG	A	1654	1/1	0.94	0.19	50,50,50,50	0
22	MG	A	1825	1/1	0.94	0.28	63,63,63,63	0
22	MG	A	1694	1/1	0.94	0.36	83,83,83,83	0
22	MG	A	1696	1/1	0.94	0.34	45,45,45,45	0
24	NMY	A	1832	42/42	0.94	0.13	54,85,153,163	0
22	MG	A	1606	1/1	0.94	0.82	72,72,72,72	0
23	K	A	1736	1/1	0.94	0.22	108,108,108,108	0
22	MG	A	1639	1/1	0.94	0.24	28,28,28,28	0
22	MG	A	1679	1/1	0.94	0.33	62,62,62,62	0
22	MG	A	1626	1/1	0.95	0.46	79,79,79,79	0
22	MG	A	1636	1/1	0.95	0.37	64,64,64,64	0
22	MG	A	1691	1/1	0.95	0.23	82,82,82,82	0
22	MG	A	1692	1/1	0.95	0.45	72,72,72,72	0
22	MG	P	101	1/1	0.95	0.27	68,68,68,68	0
22	MG	A	1612	1/1	0.95	0.64	93,93,93,93	0
22	MG	A	1811	1/1	0.95	0.18	79,79,79,79	0
22	MG	A	1716	1/1	0.95	0.10	49,49,49,49	0
22	MG	A	1717	1/1	0.95	0.14	66,66,66,66	0
22	MG	A	1638	1/1	0.95	0.08	64,64,64,64	0
22	MG	E	201	1/1	0.95	0.30	64,64,64,64	0
22	MG	A	1628	1/1	0.95	0.35	57,57,57,57	0
22	MG	A	1816	1/1	0.95	0.34	67,67,67,67	0
22	MG	A	1629	1/1	0.95	0.39	43,43,43,43	0
22	MG	A	1719	1/1	0.96	0.10	62,62,62,62	0
22	MG	A	1678	1/1	0.96	0.11	35,35,35,35	0
22	MG	A	1793	1/1	0.96	0.31	69,69,69,69	0
22	MG	A	1649	1/1	0.96	0.30	40,40,40,40	0
22	MG	A	1680	1/1	0.96	0.34	46,46,46,46	0
22	MG	A	1620	1/1	0.96	0.48	53,53,53,53	0
24	NMY	A	1833	42/42	0.96	0.10	55,78,103,105	0
22	MG	A	1677	1/1	0.96	0.45	63,63,63,63	0
22	MG	A	1703	1/1	0.96	0.20	51,51,51,51	0
22	MG	M	201	1/1	0.96	0.12	72,72,72,72	0
22	MG	A	1718	1/1	0.96	0.54	84,84,84,84	0

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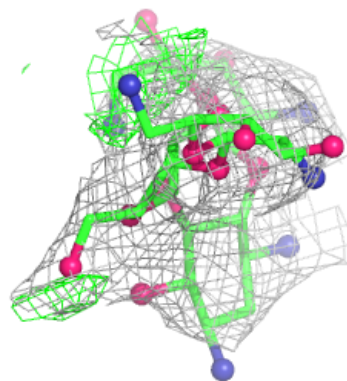
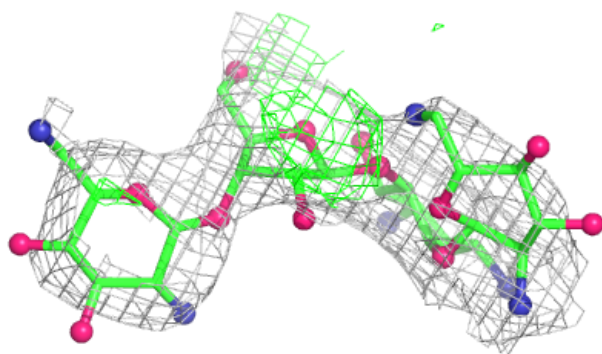
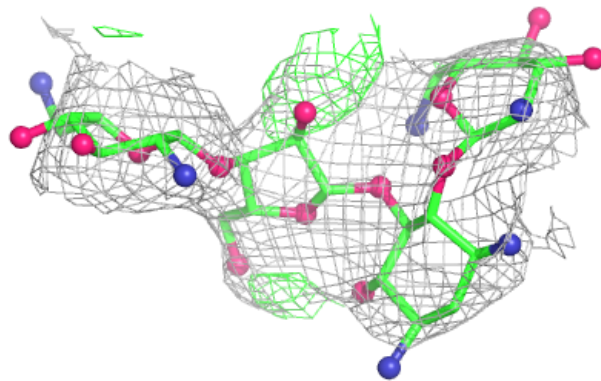
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
22	MG	A	1648	1/1	0.97	0.26	56,56,56,56	0
22	MG	A	1671	1/1	0.97	0.41	50,50,50,50	0
22	MG	A	1618	1/1	0.97	0.35	58,58,58,58	0
22	MG	A	1700	1/1	0.97	0.17	38,38,38,38	0
22	MG	A	1650	1/1	0.97	0.10	41,41,41,41	0
22	MG	A	1702	1/1	0.97	0.23	40,40,40,40	0
22	MG	A	1669	1/1	0.97	0.04	51,51,51,51	0
22	MG	A	1687	1/1	0.97	0.45	60,60,60,60	0
22	MG	A	1765	1/1	0.97	0.42	55,55,55,55	0
22	MG	A	1681	1/1	0.97	0.46	75,75,75,75	0
25	ZN	D	301	1/1	0.97	0.21	92,92,92,92	0
22	MG	A	1722	1/1	0.98	0.03	35,35,35,35	0
22	MG	A	1708	1/1	0.98	0.15	63,63,63,63	0
22	MG	A	1625	1/1	0.98	0.57	57,57,57,57	0
22	MG	A	1634	1/1	0.98	0.20	40,40,40,40	0
22	MG	A	1641	1/1	0.98	0.32	37,37,37,37	0
22	MG	A	1674	1/1	0.98	0.06	38,38,38,38	0
22	MG	A	1605	1/1	0.98	0.41	44,44,44,44	0
22	MG	A	1707	1/1	0.98	0.15	85,85,85,85	0
22	MG	A	1607	1/1	0.99	0.44	59,59,59,59	0
22	MG	A	1695	1/1	0.99	0.11	53,53,53,53	0
25	ZN	N	101	1/1	1.00	0.06	106,106,106,106	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.

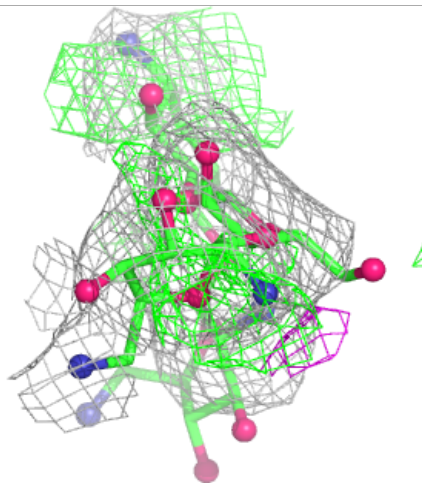
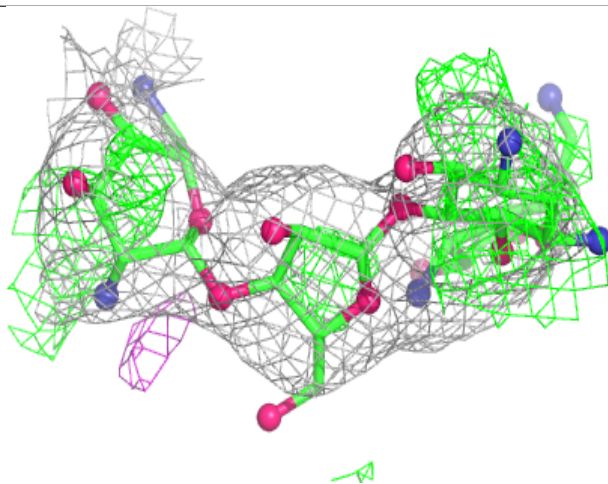
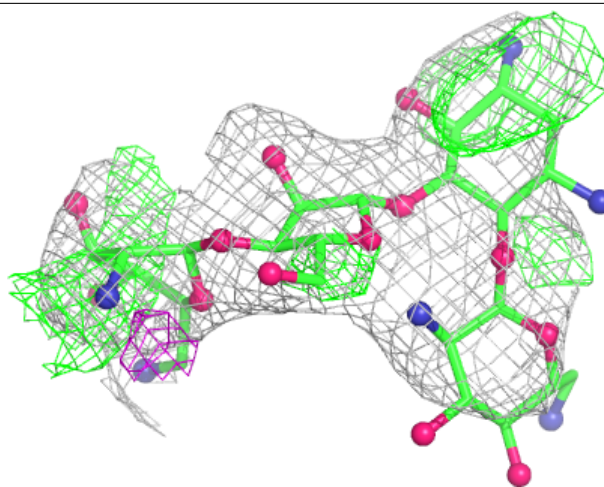
Electron density around NMY A 1837:

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



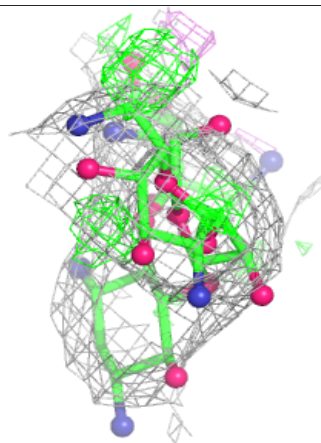
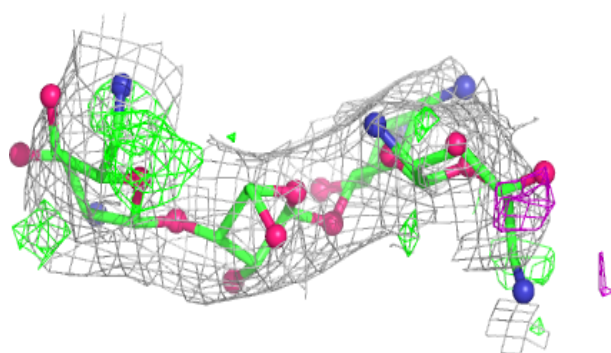
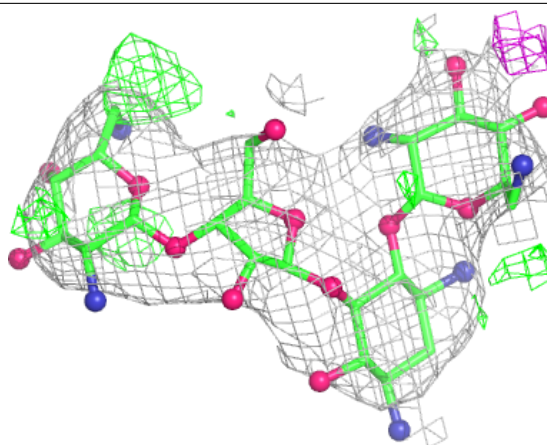
Electron density around NMY A 1834:

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



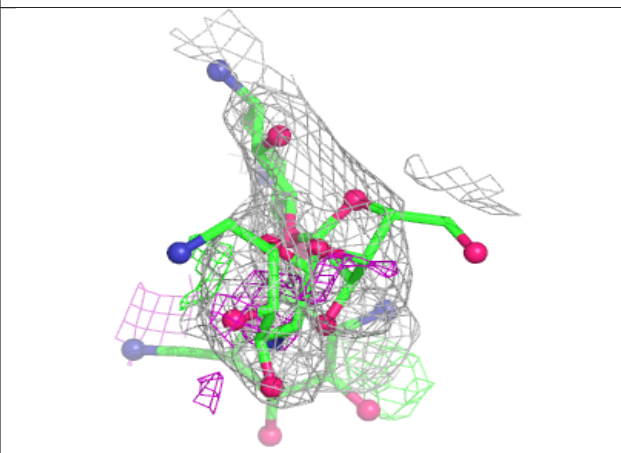
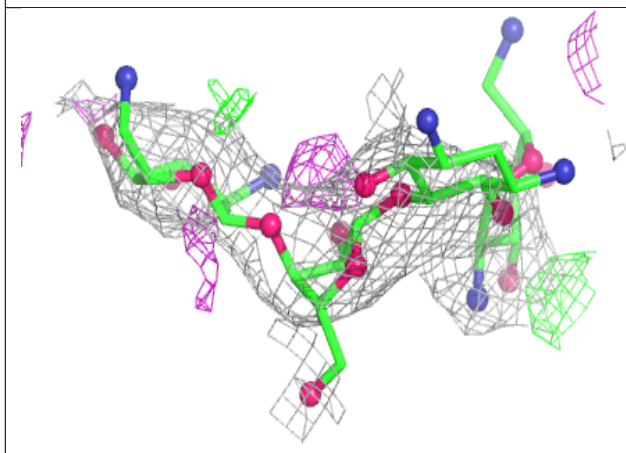
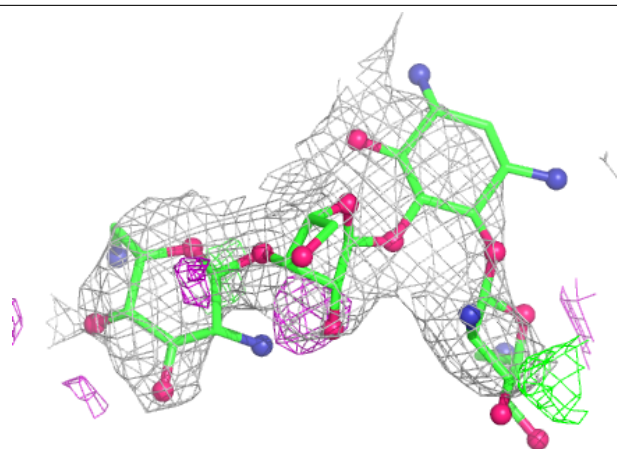
Electron density around NMY A 1835:

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

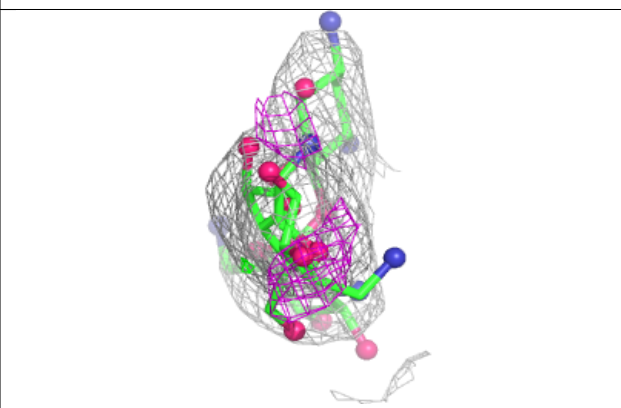
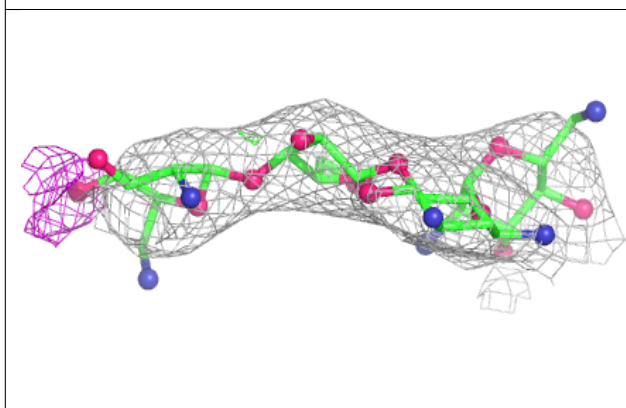
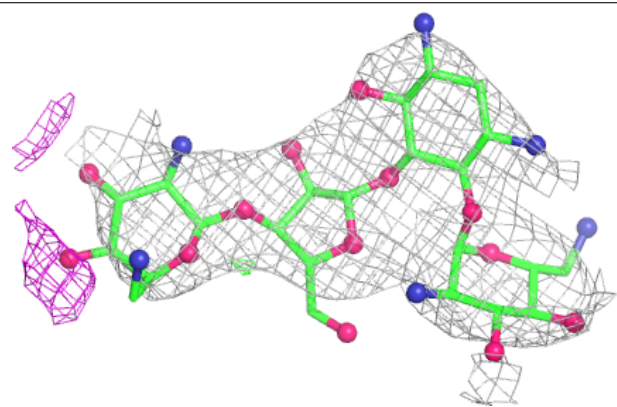


Electron density around NMY A 1836:

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

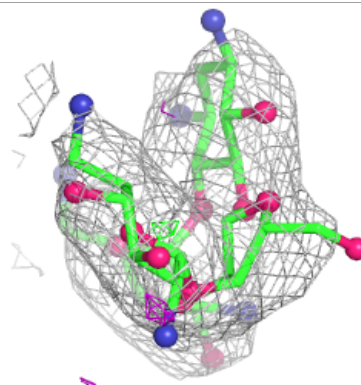
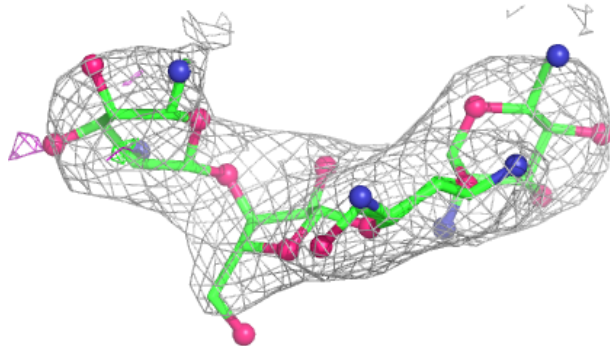
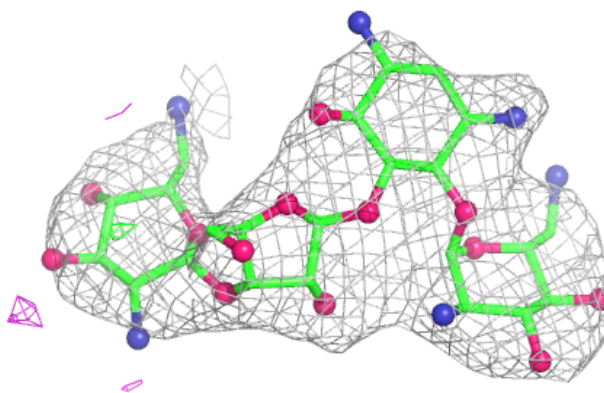
**Electron density around NMY A 1832:**

$2mF_o-DF_c$ (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.