



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:31 AM UTC

PDB ID : 4NXN / pdb_00004nxn
Title : Crystal Structure of the 30S ribosomal subunit from a GidB (RsmG) mutant of *Thermus thermophilus* (HB8), bound with streptomycin
Authors : Demirci, H.; Murphy IV, F.; Murphy, E.; Gregory, S.T.; Dahlberg, A.E.; Jogl, G.
Deposited on : 2013-12-09
Resolution : 3.54 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

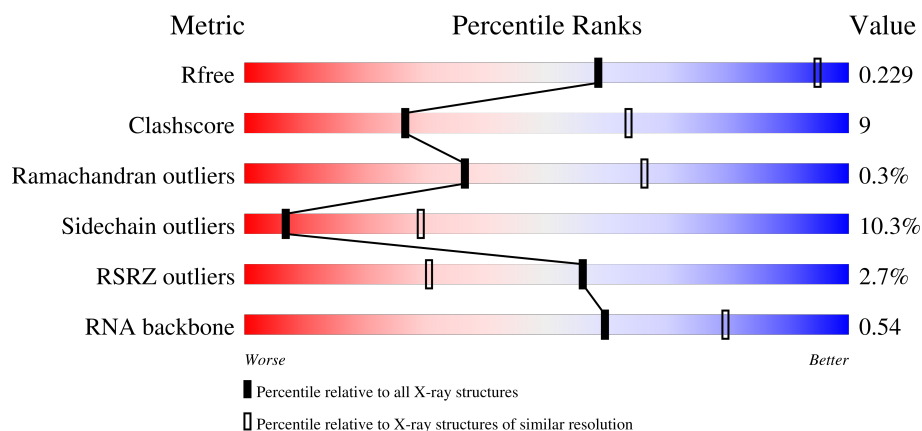
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.54 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	1008 (3.58-3.50)
Clashscore	190562	1062 (3.58-3.50)
Ramachandran outliers	187476	1033 (3.58-3.50)
Sidechain outliers	187428	1034 (3.58-3.50)
RSRZ outliers	180081	1007 (3.58-3.50)
RNA backbone	3983	1006 (4.02-3.06)

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	2% 55% 35% 9%
2	B	256	2% 58% 30% 9%
3	C	239	3% 56% 25% 5% 14%

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Mol	Chain	Length	Quality of chain
4	D	209	
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
23	MG	A	1726	-	-	-	X
23	MG	A	1740	-	-	-	X
23	MG	A	1751	-	-	-	X

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 52137 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1512	Total	C	N	O	P	0	0	0
			32506	14476	6011	10507	1512			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1534	C	A	SEE REMARK 999	GB M26923.1
A	1535	A	C	SEE REMARK 999	GB M26923.1

- Molecule 2 is a protein called ribosomal protein S2.

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

- Molecule 3 is a protein called ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	206	Total	C	N	O	S	0	0	0
			1612	1016	314	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	150	Total	C	N	O	S	0	0	0
			1146	724	217	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	98	Total	C	N	O	S	0	0	0
			792	498	156	137	1			

- Molecule 11 is a protein called ribosomal protein S11.

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

- Molecule 12 is a protein called ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	124	Total	C	N	O	S	0	0	0
			972	612	195	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	87	Total	C	N	O	S	0	0	0
			729	457	146	124	2			

- Molecule 16 is a protein called ribosomal protein S16.

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

- Molecule 17 is a protein called ribosomal protein S17.

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

- Molecule 18 is a protein called ribosomal protein S18.

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

- Molecule 19 is a protein called ribosomal protein S19.

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

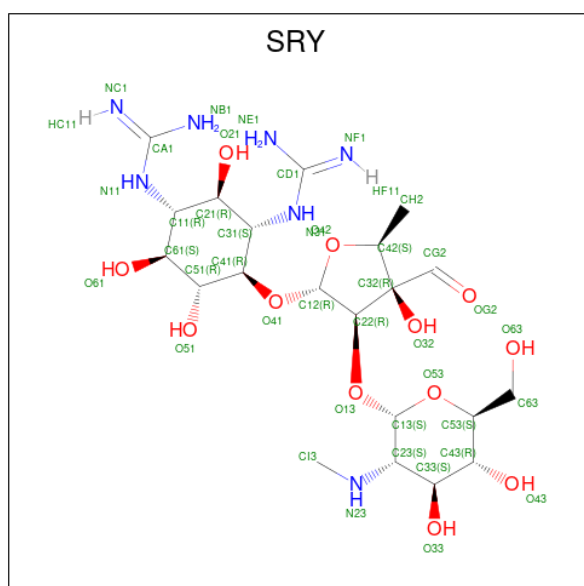
- Molecule 20 is a protein called ribosomal protein S20.

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	24	Total	C	N	O	0	0	0
			208	128	50	30			

- Molecule 22 is STREPTOMYCIN (CCD ID: SRY) (formula: $C_{21}H_{39}N_7O_{12}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
22	A	1	Total	C	N	O	0	0
			40	21	7	12		

- Molecule 23 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	A	227	Total	Mg	0	0
			227	227		
23	B	1	Total	Mg	0	0
			1	1		
23	D	1	Total	Mg	0	0
			1	1		
23	E	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	H	3	Total 3	Mg 3	0	0
23	M	1	Total 1	Mg 1	0	0
23	N	1	Total 1	Mg 1	0	0
23	P	2	Total 2	Mg 2	0	0
23	Q	2	Total 2	Mg 2	0	0
23	T	1	Total 1	Mg 1	0	0
23	U	1	Total 1	Mg 1	0	0

- Molecule 24 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

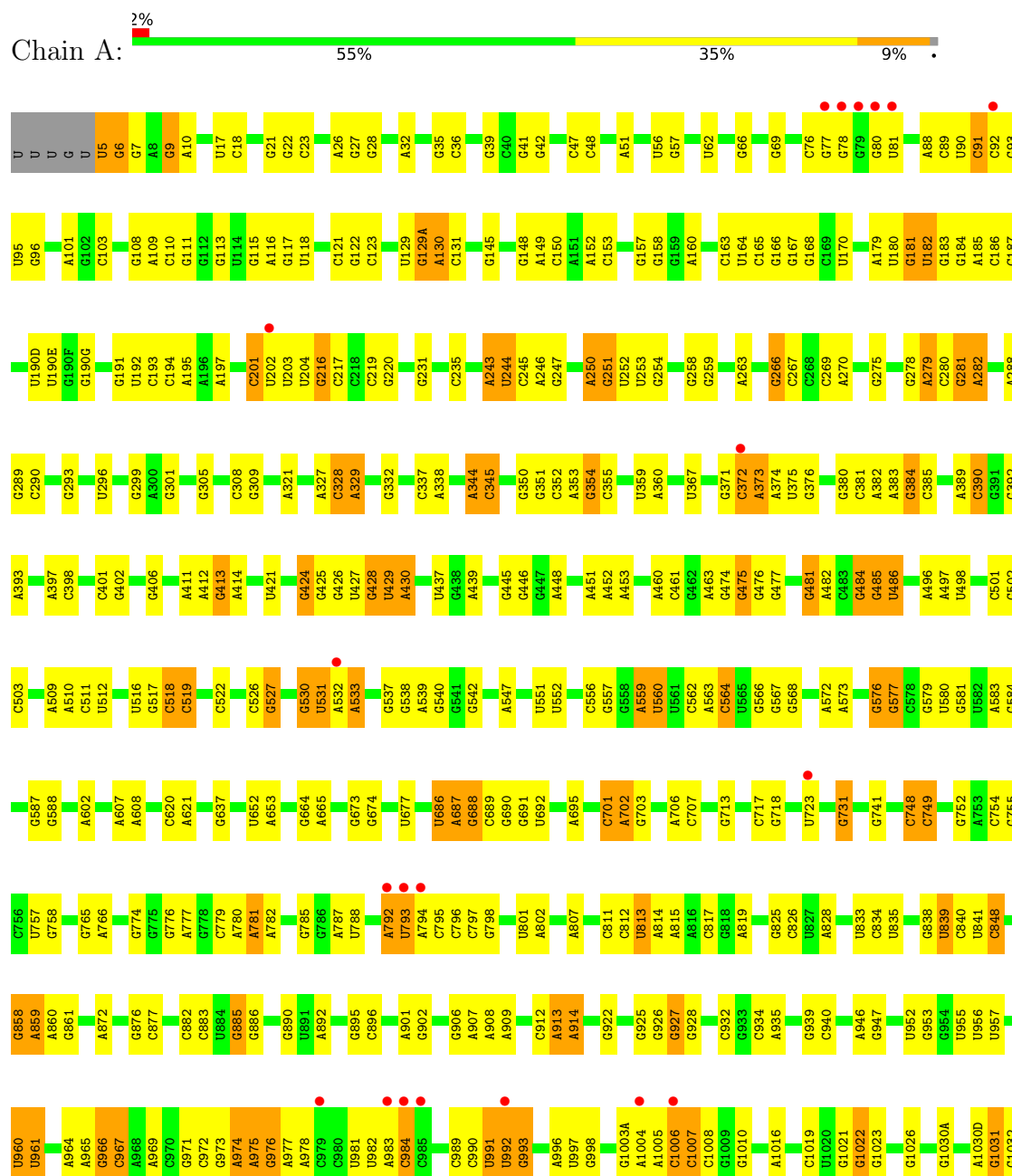
- Molecule 25 is water.

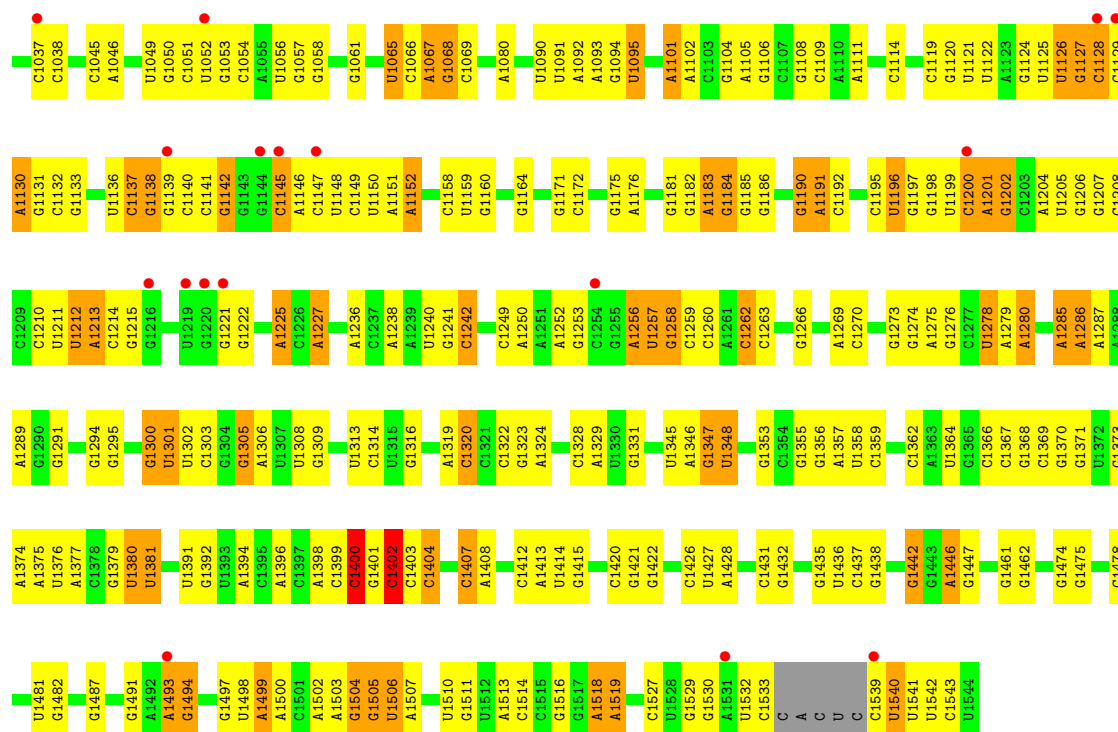
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	A	254	Total 254	O 254	0	0
25	D	1	Total 1	O 1	0	0
25	E	4	Total 4	O 4	0	0
25	L	1	Total 1	O 1	0	0

3 Residue-property plots [i](#)

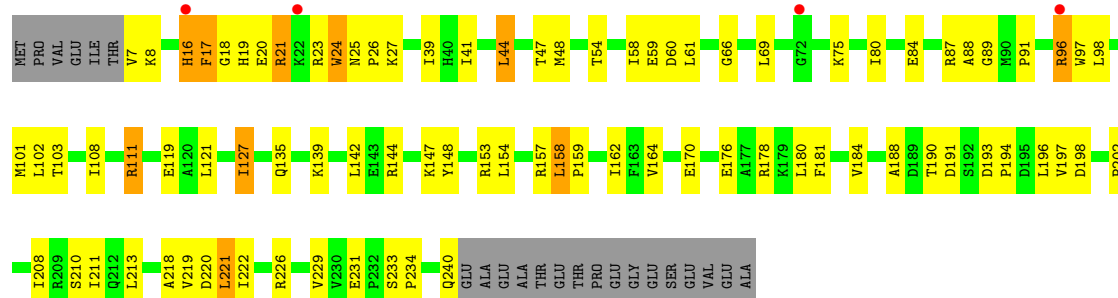
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: 16S rRNA

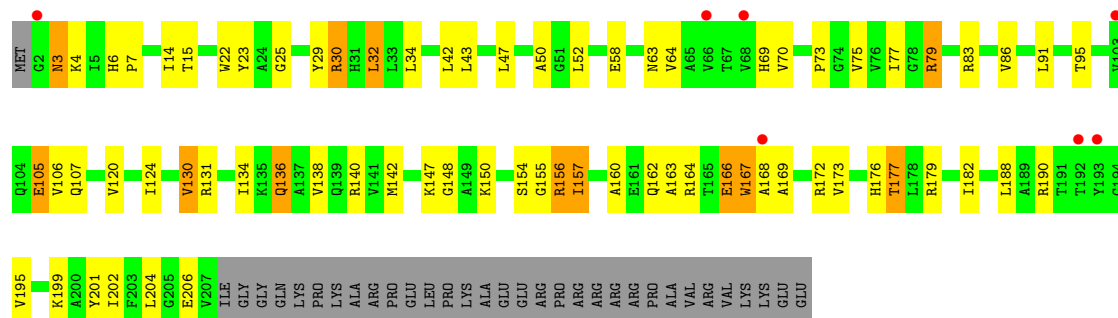




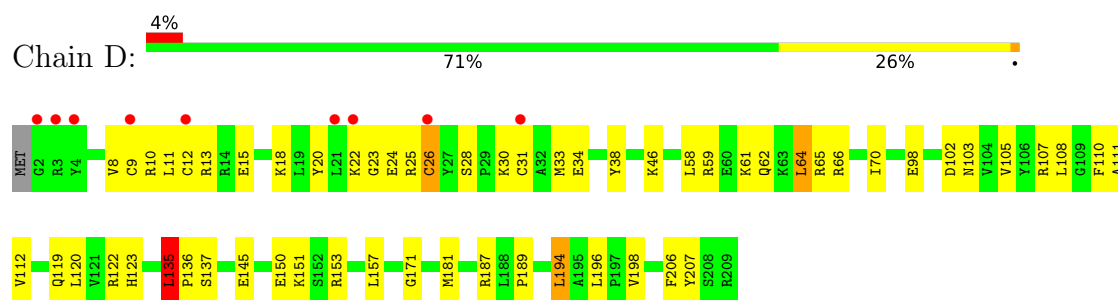
• Molecule 2: ribosomal protein S2



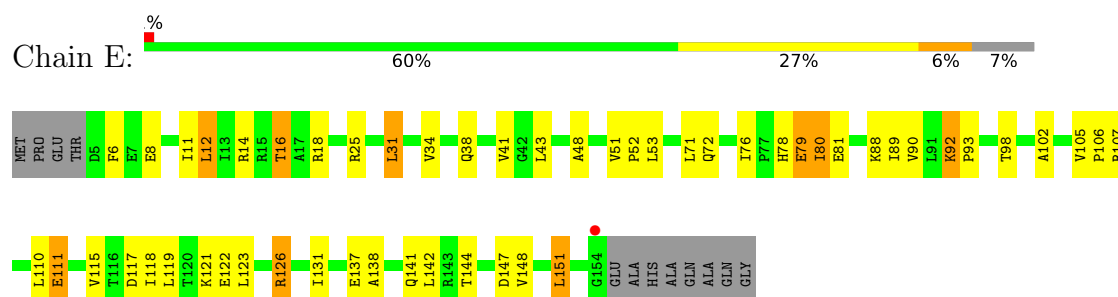
• Molecule 3: ribosomal protein S3



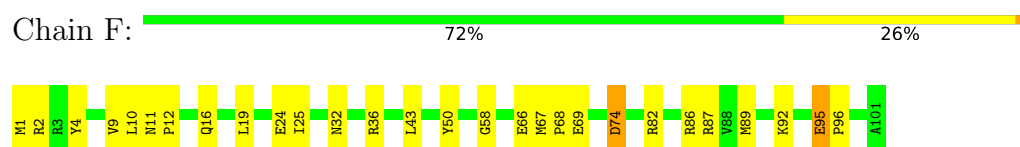
• Molecule 4: ribosomal protein S4



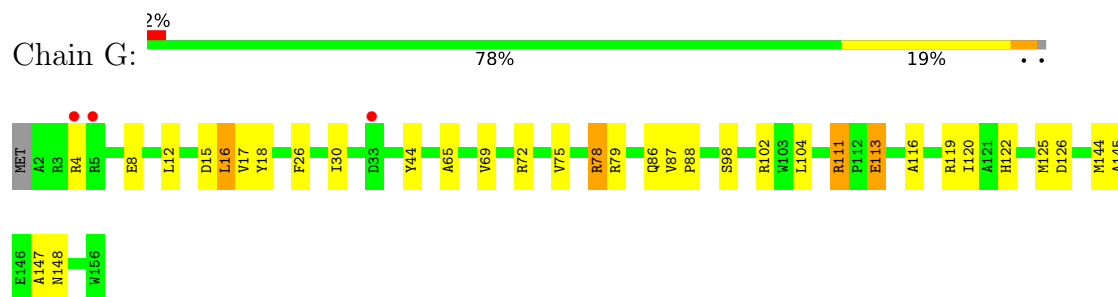
- Molecule 5: ribosomal protein S5



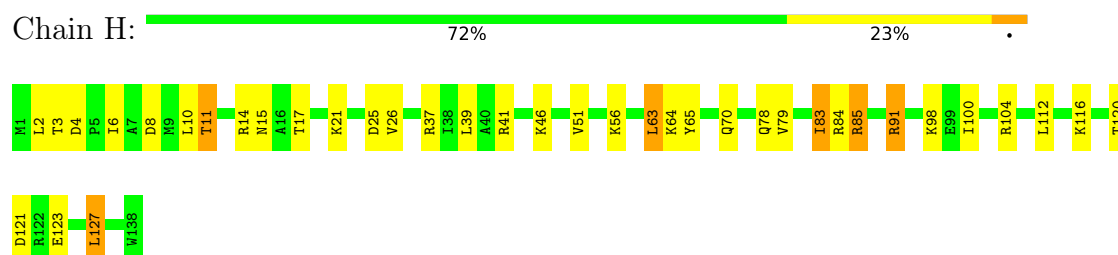
- Molecule 6: ribosomal protein S6



- Molecule 7: ribosomal protein S7

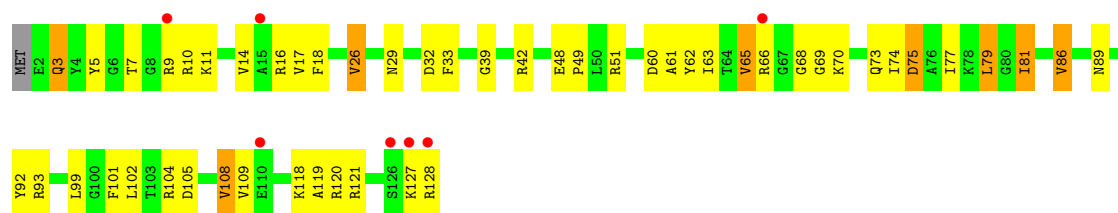


- Molecule 8: ribosomal protein S8

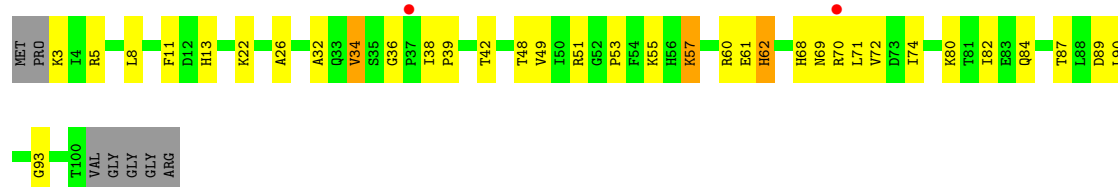


- Molecule 9: ribosomal protein S9

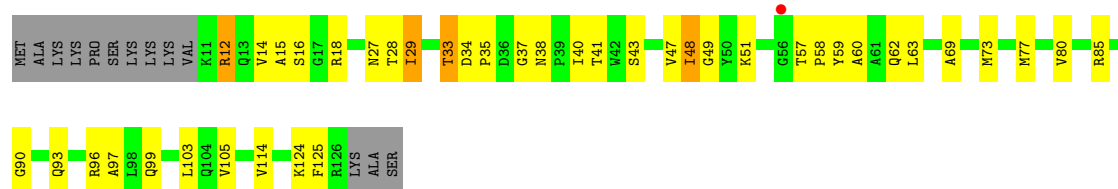




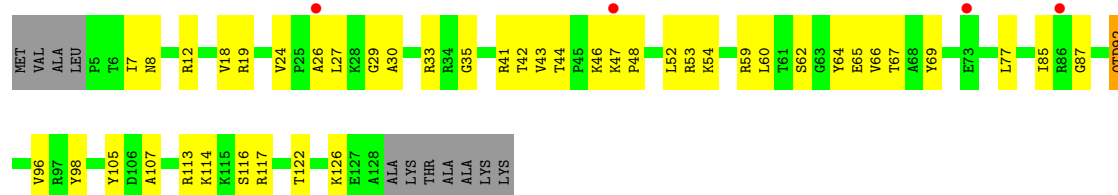
• Molecule 10: ribosomal protein S10



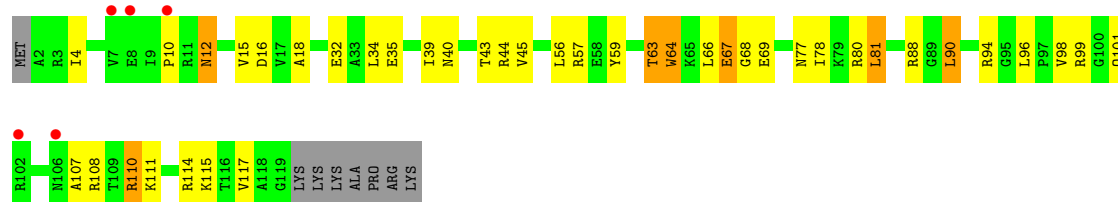
• Molecule 11: ribosomal protein S11



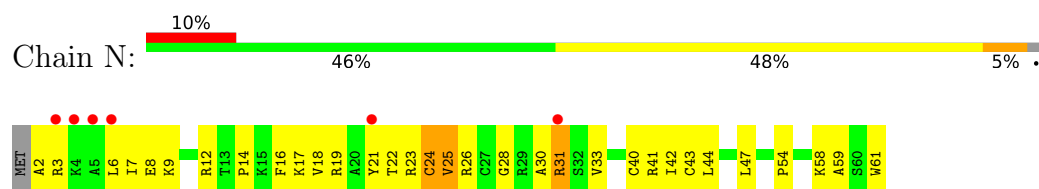
• Molecule 12: ribosomal protein S12



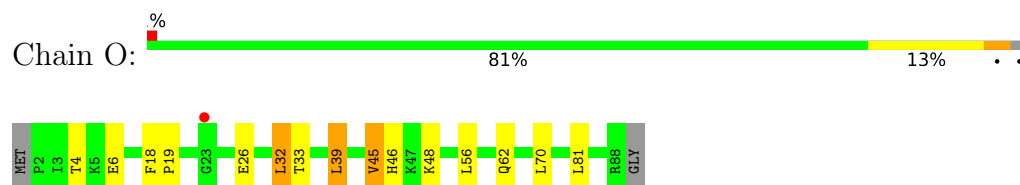
• Molecule 13: ribosomal protein S13



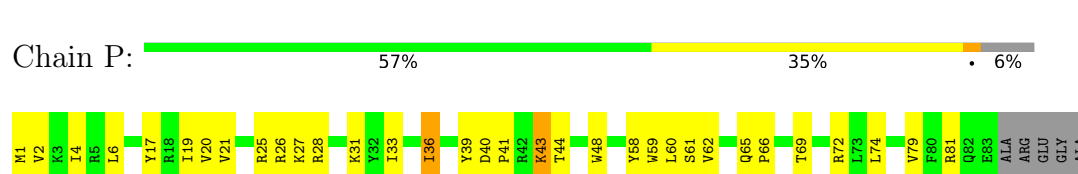
- Molecule 14: ribosomal protein S14



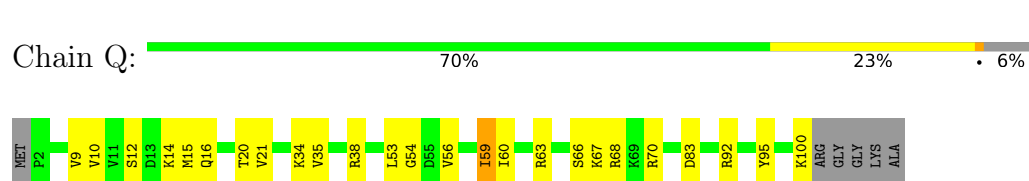
- Molecule 15: ribosomal protein S15



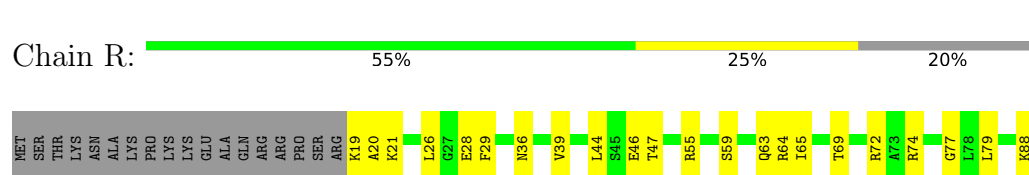
- Molecule 16: ribosomal protein S16



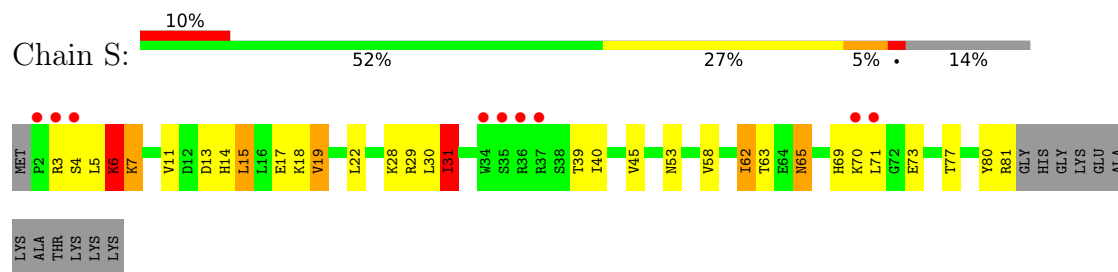
- Molecule 17: ribosomal protein S17



- Molecule 18: ribosomal protein S18

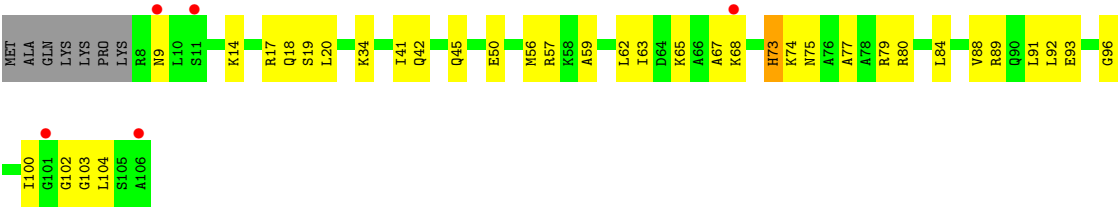


- Molecule 19: ribosomal protein S19



- 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	403.06Å 403.06Å 173.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.74 – 3.54 34.74 – 3.54	Depositor EDS
% Data completeness (in resolution range)	99.2 (34.74-3.54) 98.8 (34.74-3.54)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 3.56Å)	Xtriage
Refinement program	PHENIX dev_1555	Depositor
R, R_{free}	0.193 , 0.231 0.194 , 0.229	Depositor DCC
R_{free} test set	8518 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	124.9	Xtriage
Anisotropy	0.353	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 103.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	52137	wwPDB-VP
Average B, all atoms (Å ²)	148.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.90% 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: 2MG, MA6, MG, UR3, PSU, 5MC, ZN, SRY, 0TD, M2G, 4OC

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	0.26	0/36066	0.36	0/56284
2	B	0.47	0/1935	0.87	0/2609
3	C	0.36	0/1636	0.81	1/2205 (0.0%)
4	D	0.42	0/1733	0.84	5/2318 (0.2%)
5	E	0.55	0/1162	0.93	4/1564 (0.3%)
6	F	0.34	0/856	0.78	0/1154
7	G	0.35	0/1276	0.79	2/1709 (0.1%)
8	H	0.65	0/1136	0.91	2/1527 (0.1%)
9	I	0.36	0/1029	0.81	0/1379
10	J	0.35	0/805	0.89	2/1082 (0.2%)
11	K	0.48	0/879	0.83	2/1187 (0.2%)
12	L	0.49	0/977	0.97	4/1306 (0.3%)
13	M	0.38	0/947	0.84	1/1270 (0.1%)
14	N	0.35	0/501	0.85	2/664 (0.3%)
15	O	0.44	0/740	0.75	0/987
16	P	0.50	0/716	0.84	0/963
17	Q	0.53	0/836	0.89	0/1117
18	R	0.42	0/579	0.76	0/768
19	S	0.31	0/661	0.88	2/890 (0.2%)
20	T	0.50	0/765	0.81	0/1007
21	U	0.31	0/212	0.72	0/277
All	All	0.33	0/55447	0.56	27/82267 (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
3	C	0	1
20	T	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	2

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	26	ALA	N-CA-C	-8.58	101.87	111.82
12	L	30	ALA	CA-C-N	7.83	127.49	119.19
12	L	30	ALA	C-N-CA	7.83	127.49	119.19
4	D	171	GLY	CA-C-N	7.01	126.72	119.56
4	D	171	GLY	C-N-CA	7.01	126.72	119.56
4	D	26	CYS	N-CA-C	-7.00	104.70	113.18
19	S	6	LYS	CB-CA-C	-6.98	108.53	116.63
11	K	114	VAL	CA-C-N	-6.50	114.09	120.52
11	K	114	VAL	C-N-CA	-6.50	114.09	120.52
14	N	12	ARG	CB-CA-C	-6.42	109.18	116.63
3	C	167	TRP	N-CA-C	6.31	115.75	108.49
14	N	25	VAL	N-CA-C	6.03	116.69	110.36
13	M	67	GLU	CB-CA-C	-6.02	109.61	116.54
5	E	48	ALA	CA-C-N	5.89	126.30	119.47
5	E	48	ALA	C-N-CA	5.89	126.30	119.47
12	L	105	TYR	CB-CA-C	-5.76	109.94	116.63
19	S	30	LEU	CB-CA-C	-5.65	109.06	115.79
10	J	36	GLY	CA-C-N	5.62	126.87	119.84
10	J	36	GLY	C-N-CA	5.62	126.87	119.84
5	E	92	LYS	CA-C-N	5.50	125.41	119.85
5	E	92	LYS	C-N-CA	5.50	125.41	119.85
7	G	111	ARG	CA-C-N	5.40	124.73	118.85
7	G	111	ARG	C-N-CA	5.40	124.73	118.85
8	H	56	LYS	CA-C-N	5.08	125.31	119.83
8	H	56	LYS	C-N-CA	5.08	125.31	119.83
4	D	135	LEU	CA-C-N	5.06	124.84	119.28
4	D	135	LEU	C-N-CA	5.06	124.84	119.28

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	166	GLU	Peptide
20	T	93	GLU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32506	0	16426	411	0
2	B	1900	0	1951	53	0
3	C	1612	0	1677	41	0
4	D	1703	0	1763	37	0
5	E	1146	0	1207	34	0
6	F	843	0	857	14	0
7	G	1257	0	1296	19	0
8	H	1116	0	1177	25	0
9	I	1010	0	1037	44	0
10	J	792	0	835	23	0
11	K	864	0	881	23	0
12	L	972	0	1058	24	0
13	M	937	0	995	21	0
14	N	492	0	529	26	0
15	O	729	0	768	8	0
16	P	700	0	720	21	0
17	Q	823	0	891	18	0
18	R	574	0	644	13	0
19	S	647	0	673	23	0
20	T	763	0	861	20	0
21	U	208	0	221	6	0
22	A	40	0	36	4	0
23	A	227	0	0	0	0
23	B	1	0	0	0	0
23	D	1	0	0	0	0
23	E	1	0	0	0	0
23	H	3	0	0	0	0
23	M	1	0	0	0	0
23	N	1	0	0	0	0
23	P	2	0	0	0	0
23	Q	2	0	0	0	0
23	T	1	0	0	0	0
23	U	1	0	0	0	0
24	D	1	0	0	0	0
24	N	1	0	0	0	0
25	A	254	0	0	3	0
25	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	E	4	0	0	0	0
25	L	1	0	0	0	0
All	All	52137	0	36503	799	0

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

All (799) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:C:H5'	17:Q:70:ARG:HG2	1.55	0.89
1:A:80:G:H1	1:A:89:C:H42	1.15	0.87
1:A:664:G:H22	1:A:741:G:H1	1.25	0.82
1:A:1126:U:O4	1:A:1147:C:N4	2.14	0.81
1:A:1158:C:N3	1:A:1181:G:N2	2.29	0.80
1:A:984:C:H42	1:A:1221:G:H1	1.33	0.76
1:A:279:A:OP2	17:Q:95:TYR:OH	2.04	0.76
1:A:1057:G:H5''	3:C:154:SER:HB2	1.69	0.75
1:A:1125:U:H3	10:J:5:ARG:HH21	1.36	0.72
1:A:1058:G:OP1	3:C:199:LYS:NZ	2.23	0.71
1:A:1347:G:O6	9:I:10:ARG:NH2	2.23	0.71
8:H:21:LYS:O	8:H:65:TYR:OH	2.08	0.71
16:P:4:ILE:HG12	16:P:21:VAL:HG22	1.73	0.70
8:H:17:THR:O	8:H:78:GLN:NE2	2.23	0.69
3:C:156:ARG:NH1	3:C:160:ALA:O	2.24	0.69
3:C:73:PRO:HD3	3:C:105:GLU:HB2	1.74	0.69
1:A:974:A:OP2	14:N:41:ARG:NH1	2.26	0.69
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.73	0.69
1:A:166:G:H2'	1:A:167:G:H8	1.57	0.68
1:A:149:A:H2'	1:A:150:C:H6	1.58	0.68
2:B:111:ARG:HH11	2:B:111:ARG:HA	1.58	0.68
1:A:1192:C:O2	5:E:25:ARG:NH2	2.26	0.68
17:Q:12:SER:HB3	17:Q:20:THR:HB	1.76	0.68
8:H:46:LYS:HG3	8:H:64:LYS:HB3	1.76	0.68
1:A:1266:G:N2	1:A:1269:A:OP2	2.23	0.67
4:D:23:GLY:HA3	4:D:112:VAL:HG12	1.76	0.67
1:A:1147:C:HO2'	9:I:5:TYR:HH	1.39	0.67
4:D:22:LYS:HB2	4:D:26:CYS:SG	2.35	0.67
12:L:52:LEU:O	12:L:54:LYS:NZ	2.27	0.67
1:A:80:G:N2	1:A:89:C:N3	2.38	0.66
3:C:156:ARG:H	3:C:163:ALA:HA	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:16:PHE:HD1	14:N:19:ARG:HD2	1.60	0.66
1:A:1147:C:O2'	9:I:5:TYR:OH	2.12	0.66
13:M:90:LEU:HD22	13:M:94:ARG:HE	1.60	0.66
1:A:976:G:OP2	1:A:1358:U:H1'	1.96	0.66
1:A:537:G:OP1	12:L:113:ARG:NH2	2.29	0.66
1:A:1316:G:H5'	14:N:17:LYS:HE3	1.78	0.66
2:B:20:GLU:OE1	2:B:23:ARG:NH1	2.29	0.65
1:A:835:U:OP1	18:R:64:ARG:NH2	2.30	0.65
1:A:1128:C:OP1	9:I:66:ARG:NH2	2.30	0.65
1:A:564:C:O2'	8:H:91:ARG:NH2	2.30	0.64
8:H:10:LEU:HD22	8:H:83:ILE:HD11	1.77	0.64
1:A:103:C:OP1	20:T:17:ARG:NH1	2.30	0.64
1:A:201:C:N3	1:A:216:G:N2	2.38	0.64
7:G:69:VAL:HG21	7:G:104:LEU:HD21	1.80	0.64
1:A:1412:C:H2'	1:A:1413:A:C8	2.33	0.63
2:B:21:ARG:HA	2:B:39:ILE:HA	1.80	0.63
2:B:97:TRP:HZ2	2:B:102:LEU:HD13	1.63	0.63
1:A:559:A:OP1	5:E:126:ARG:NH1	2.31	0.63
1:A:269:C:H2'	1:A:270:A:C8	2.33	0.63
1:A:686:U:HO2'	1:A:687:A:H8	1.45	0.63
6:F:74:ASP:OD2	6:F:74:ASP:N	2.30	0.63
13:M:40:ASN:HD22	13:M:43:THR:HG23	1.64	0.63
1:A:974:A:H4'	1:A:975:A:H3'	1.81	0.63
4:D:102:ASP:OD1	4:D:103:ASN:N	2.32	0.63
1:A:235:C:N4	25:A:1989:HOH:O	2.31	0.62
18:R:20:ALA:O	18:R:55:ARG:NH1	2.32	0.62
1:A:390:C:H4'	16:P:28:ARG:HH21	1.64	0.62
1:A:153:C:H42	1:A:168:G:H1	1.45	0.62
20:T:50:GLU:HA	20:T:100:ILE:HG13	1.80	0.62
1:A:1030(A):G:N2	1:A:1030(D):A:OP2	2.32	0.62
1:A:991:U:O4	1:A:1212:U:O2'	2.17	0.62
1:A:1126:U:H3	1:A:1148:U:H3	1.48	0.62
8:H:116:LYS:HD3	8:H:127:LEU:HD12	1.82	0.62
1:A:838:G:H1	1:A:848:C:H42	1.48	0.62
1:A:973:G:H3'	1:A:974:A:H5''	1.82	0.62
12:L:53:ARG:NH1	12:L:92:0TD:OD2	2.28	0.62
1:A:1249:C:O2'	9:I:73:GLN:NE2	2.32	0.62
5:E:11:ILE:HD12	5:E:31:LEU:HD13	1.82	0.61
1:A:1195:C:H3'	1:A:1196:U:H5''	1.83	0.61
1:A:269:C:H2'	1:A:270:A:H8	1.66	0.61
1:A:263:A:OP2	20:T:79:ARG:NH1	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1516:G:N2	1:A:1519:MA6:OP2	2.30	0.61
1:A:427:U:OP1	4:D:13:ARG:NH2	2.34	0.60
5:E:102:ALA:O	5:E:107:ARG:NH1	2.33	0.60
10:J:34:VAL:HG13	10:J:74:ILE:HG12	1.83	0.60
1:A:501:C:H2'	1:A:502:G:C8	2.36	0.60
1:A:952:U:H2'	1:A:953:G:H8	1.66	0.60
3:C:155:GLY:HA2	3:C:164:ARG:H	1.66	0.60
10:J:49:VAL:HG13	14:N:41:ARG:HB3	1.83	0.60
2:B:23:ARG:O	2:B:24:TRP:HD1	1.84	0.60
1:A:953:G:H5'	1:A:965:A:H61	1.66	0.60
1:A:1125:U:OP2	1:A:1145:C:N4	2.34	0.60
1:A:1505:G:O2'	1:A:1506:U:OP2	2.15	0.60
1:A:9:G:OP2	5:E:121:LYS:NZ	2.24	0.60
2:B:87:ARG:HD3	2:B:234:PRO:HD2	1.83	0.60
14:N:3:ARG:HB2	14:N:6:LEU:HD23	1.82	0.60
3:C:148:GLY:HA3	3:C:172:ARG:O	2.02	0.60
12:L:27:LEU:C	12:L:29:GLY:H	2.10	0.59
2:B:91:PRO:HB3	2:B:154:LEU:HB2	1.85	0.59
1:A:517:G:N1	1:A:533:A:OP2	2.30	0.59
1:A:1124:G:H2'	1:A:1145:C:H41	1.66	0.59
1:A:250:A:H4'	1:A:251:G:O5'	2.03	0.59
2:B:59:GLU:HB2	2:B:221:LEU:HD11	1.83	0.59
10:J:22:LYS:HE3	10:J:90:LEU:HD12	1.85	0.59
11:K:57:THR:HG23	11:K:60:ALA:H	1.65	0.59
11:K:12:ARG:HH11	11:K:14:VAL:HG22	1.68	0.59
16:P:21:VAL:HG23	16:P:36:ILE:HD12	1.85	0.59
1:A:501:C:OP1	12:L:117:ARG:NH2	2.35	0.58
1:A:955:U:H1'	1:A:1227:A:H61	1.68	0.58
3:C:150:LYS:HB3	3:C:201:TYR:HB2	1.85	0.58
7:G:144:MET:O	7:G:148:ASN:ND2	2.35	0.58
1:A:1211:U:H4'	1:A:1213:A:H1'	1.85	0.58
1:A:1491:G:H5''	12:L:46:LYS:HG3	1.86	0.58
1:A:975:A:H4'	1:A:976:G:O5'	2.04	0.58
5:E:71:LEU:HD21	5:E:115:VAL:HG22	1.85	0.58
11:K:15:ALA:HA	11:K:77:MET:HA	1.85	0.58
17:Q:66:SER:O	17:Q:70:ARG:NH1	2.36	0.58
20:T:56:MET:HG3	20:T:88:VAL:HG21	1.85	0.58
1:A:673:G:H2'	1:A:674:G:C8	2.38	0.58
1:A:1061:G:H1	1:A:1195:C:H42	1.50	0.58
12:L:113:ARG:NH1	12:L:116:SER:H	2.01	0.58
17:Q:9:VAL:HG22	17:Q:56:VAL:HG22	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:24:TRP:HA	2:B:191:ASP:HA	1.86	0.58
13:M:64:TRP:HE3	13:M:66:LEU:HD11	1.67	0.58
17:Q:67:LYS:HA	17:Q:70:ARG:HH12	1.68	0.58
1:A:1130:A:O2'	9:I:3:GLN:NE2	2.36	0.57
1:A:1202:G:C4	14:N:42:ILE:HD13	2.39	0.57
3:C:25:GLY:O	3:C:29:TYR:HB2	2.04	0.57
1:A:776:G:N2	1:A:802:A:OP2	2.36	0.57
1:A:652:U:O4	1:A:752:G:O2'	2.18	0.57
1:A:1164:G:H1	1:A:1172:C:H42	1.50	0.57
1:A:372:C:H4'	1:A:373:A:O5'	2.04	0.57
1:A:946:A:H2'	1:A:947:G:C8	2.40	0.57
1:A:967:5MC:H4'	9:I:128:ARG:HE	1.70	0.57
1:A:1222:G:H5'	19:S:77:THR:HG21	1.86	0.57
12:L:41:ARG:HG2	12:L:42:THR:H	1.69	0.57
14:N:23:ARG:NH1	14:N:28:GLY:O	2.36	0.57
1:A:1345:U:OP1	9:I:120:ARG:NH1	2.37	0.57
3:C:52:LEU:HA	3:C:70:VAL:HG23	1.84	0.57
1:A:1308:U:OP2	13:M:99:ARG:HG3	2.05	0.57
12:L:113:ARG:HH11	12:L:116:SER:H	1.52	0.57
9:I:60:ASP:OD1	9:I:61:ALA:N	2.37	0.57
11:K:48:ILE:HD13	11:K:63:LEU:HB2	1.86	0.57
1:A:692:U:OP1	11:K:124:LYS:NZ	2.38	0.57
1:A:1257:U:H4'	1:A:1258:G:O5'	2.04	0.56
1:A:1305:G:N2	1:A:1331:G:H1'	2.20	0.56
4:D:20:TYR:HD2	4:D:26:CYS:HB3	1.70	0.56
1:A:1184:G:H2'	1:A:1185:G:H8	1.70	0.56
13:M:16:ASP:OD1	13:M:16:ASP:N	2.38	0.56
1:A:184:G:H2'	1:A:185:A:H8	1.69	0.56
19:S:22:LEU:HD13	19:S:28:LYS:HD3	1.85	0.56
1:A:1050:G:N2	1:A:1208:C:O2	2.34	0.56
1:A:1493:A:H2'	1:A:1494:G:C8	2.41	0.56
5:E:105:VAL:HB	5:E:106:PRO:HD3	1.86	0.56
1:A:191:G:N2	20:T:103:GLY:O	2.35	0.56
1:A:527:G:OP2	22:A:1601:SRY:O32	2.14	0.56
1:A:1355:G:H2'	1:A:1356:G:H8	1.71	0.56
1:A:1356:G:H2'	1:A:1357:A:C8	2.40	0.56
2:B:88:ALA:HB2	2:B:219:VAL:HG13	1.87	0.56
1:A:664:G:OP1	18:R:64:ARG:NH1	2.39	0.55
3:C:79:ARG:H	3:C:79:ARG:HD3	1.71	0.55
1:A:972:C:H4'	10:J:57:LYS:HG2	1.88	0.55
1:A:1101:A:OP2	2:B:96:ARG:NH2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:48:PRO:HD2	12:L:92:0TD:H3	1.87	0.55
16:P:43:LYS:HG3	16:P:48:TRP:CG	2.41	0.55
1:A:1003(A):G:O6	1:A:1038:C:N4	2.39	0.55
9:I:17:VAL:HG11	9:I:81:ILE:HA	1.88	0.55
4:D:26:CYS:HA	4:D:31:CYS:HB2	1.87	0.55
5:E:151:LEU:HD13	8:H:79:VAL:HG22	1.87	0.55
1:A:1150:U:O4	1:A:1151:A:N6	2.40	0.55
1:A:788:U:O2'	1:A:1539:C:O2	2.24	0.55
1:A:1426:C:H42	1:A:1474:G:H1	1.53	0.55
2:B:80:ILE:HD12	2:B:80:ILE:H	1.72	0.55
1:A:718:G:O6	18:R:74:ARG:NH1	2.40	0.55
2:B:103:THR:HA	2:B:180:LEU:HD11	1.88	0.55
11:K:40:ILE:HG22	11:K:41:THR:HG23	1.87	0.55
1:A:1474:G:H2'	1:A:1475:G:H8	1.72	0.55
5:E:12:LEU:HD13	5:E:31:LEU:HB2	1.88	0.55
5:E:76:ILE:HD11	5:E:118:ILE:HD11	1.89	0.54
1:A:1127:G:O2'	9:I:16:ARG:NH2	2.38	0.54
3:C:190:ARG:HG2	3:C:195:VAL:HG12	1.89	0.54
1:A:380:G:N2	1:A:383:A:OP2	2.39	0.54
1:A:686:U:O2'	1:A:687:A:H8	1.90	0.54
1:A:1278:U:H5''	1:A:1279:A:O4'	2.07	0.54
9:I:26:VAL:HB	9:I:33:PHE:HB2	1.89	0.54
1:A:1510:U:H2'	1:A:1511:G:C8	2.42	0.54
10:J:48:THR:HA	10:J:62:HIS:HB3	1.90	0.54
1:A:129:U:O3'	1:A:129(A):G:H3'	2.07	0.54
1:A:28:G:O2'	1:A:296:U:OP1	2.25	0.54
10:J:34:VAL:HG22	10:J:74:ILE:HG23	1.90	0.54
1:A:1141:C:H2'	1:A:1142:G:C8	2.43	0.54
17:Q:10:VAL:HG12	17:Q:21:VAL:HG22	1.89	0.54
1:A:522:C:OP2	12:L:69:TYR:OH	2.22	0.54
1:A:928:G:O2'	1:A:1533:C:OP1	2.26	0.54
13:M:63:THR:HG23	13:M:64:TRP:H	1.73	0.54
1:A:475:G:H2'	1:A:476:G:C8	2.42	0.54
12:L:77:LEU:HD21	12:L:107:ALA:HB2	1.89	0.54
1:A:691:G:H2'	1:A:692:U:C6	2.44	0.53
1:A:1316:G:H4'	14:N:18:VAL:HG11	1.90	0.53
1:A:1518:MA6:H93	1:A:1519:MA6:N1	2.24	0.53
11:K:99:GLN:HG2	11:K:105:VAL:HG21	1.91	0.53
1:A:932:C:H5'	7:G:4:ARG:HG2	1.90	0.53
1:A:1037:C:N3	1:A:1038:C:N4	2.57	0.53
1:A:1183:A:O2'	1:A:1184:G:OP1	2.26	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1250:A:H4'	9:I:68:GLY:N	2.23	0.53
11:K:90:GLY:HA2	11:K:93:GLN:HB2	1.91	0.53
11:K:18:ARG:HB2	11:K:33:THR:HG22	1.91	0.53
1:A:1442:G:N7	1:A:1446:A:N6	2.57	0.53
2:B:87:ARG:NH2	2:B:220:ASP:OD1	2.33	0.53
3:C:131:ARG:HA	3:C:134:ILE:HD12	1.90	0.53
1:A:542:G:OP1	4:D:10:ARG:NH2	2.41	0.53
1:A:1205:U:H4'	3:C:195:VAL:HG11	1.91	0.53
7:G:111:ARG:NH1	7:G:113:GLU:OE2	2.42	0.53
12:L:27:LEU:C	12:L:29:GLY:N	2.67	0.53
16:P:74:LEU:O	16:P:79:VAL:HG23	2.09	0.53
1:A:153:C:N4	1:A:168:G:H1	2.07	0.53
1:A:1210:C:O2'	1:A:1213:A:O2'	2.26	0.53
1:A:56:U:H2'	1:A:57:G:C8	2.43	0.52
1:A:983:A:O5'	14:N:3:ARG:NH2	2.42	0.52
11:K:80:VAL:HG21	11:K:103:LEU:HD13	1.91	0.52
19:S:18:LYS:O	19:S:22:LEU:HG	2.09	0.52
1:A:179:A:H2'	1:A:180:U:C6	2.44	0.52
1:A:216:G:H2'	1:A:217:C:C6	2.45	0.52
1:A:401:C:O2'	1:A:621:A:N3	2.38	0.52
1:A:782:A:C6	1:A:801:U:C2	2.97	0.52
3:C:150:LYS:HG3	3:C:169:ALA:HB2	1.91	0.52
4:D:65:ARG:HG3	4:D:70:ILE:HG22	1.91	0.52
4:D:150:GLU:HA	4:D:153:ARG:HG3	1.91	0.52
4:D:194:LEU:HB3	4:D:196:LEU:HG	1.91	0.52
1:A:122:G:C2	1:A:123:C:C2	2.97	0.52
1:A:677:U:H3	1:A:713:G:H22	1.58	0.52
1:A:706:A:O2'	11:K:29:ILE:HD11	2.10	0.52
12:L:47:LYS:HG3	12:L:48:PRO:HD3	1.91	0.52
1:A:89:C:H2'	1:A:90:U:O4'	2.08	0.52
1:A:1141:C:H2'	1:A:1142:G:H8	1.75	0.52
1:A:21:G:H2'	1:A:22:G:C8	2.43	0.52
1:A:149:A:H2'	1:A:150:C:C6	2.41	0.52
1:A:392:G:H2'	1:A:393:A:C8	2.44	0.52
1:A:990:C:H42	1:A:1215:G:H1	1.57	0.52
1:A:996:A:N1	1:A:1046:A:O2'	2.36	0.52
5:E:98:THR:N	5:E:117:ASP:OD1	2.43	0.52
9:I:108:VAL:HG12	9:I:109:VAL:H	1.75	0.52
1:A:113:G:H1'	1:A:354:G:H5'	1.92	0.52
1:A:512:U:OP1	4:D:46:LYS:NZ	2.37	0.52
1:A:620:C:C2	4:D:135:LEU:HD22	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:22:TRP:CZ2	3:C:32:LEU:HD22	2.45	0.52
14:N:24:CYS:HB3	14:N:33:VAL:HG22	1.92	0.52
1:A:186:C:H2'	1:A:187:C:C6	2.45	0.52
1:A:1420:C:H2'	1:A:1421:G:H8	1.74	0.52
1:A:707:C:OP1	11:K:85:ARG:NH1	2.40	0.52
4:D:61:LYS:HD2	4:D:207:TYR:OH	2.10	0.52
9:I:118:LYS:O	9:I:120:ARG:N	2.39	0.52
1:A:62:U:OP1	1:A:385:C:O2'	2.28	0.51
14:N:16:PHE:HB2	14:N:19:ARG:HG3	1.92	0.51
1:A:152:A:N6	1:A:170:U:C2	2.78	0.51
1:A:401:C:H2'	1:A:402:G:H8	1.75	0.51
1:A:1422:G:N2	1:A:1478:C:O2	2.43	0.51
2:B:119:GLU:HG3	2:B:142:LEU:HD21	1.91	0.51
2:B:184:VAL:HG12	2:B:197:VAL:HG13	1.92	0.51
5:E:107:ARG:O	5:E:111:GLU:HB2	2.10	0.51
1:A:538:G:H5''	12:L:114:LYS:HB2	1.92	0.51
1:A:1504:G:OP1	1:A:1507:A:H4'	2.10	0.51
2:B:18:GLY:HA3	2:B:41:ILE:HA	1.93	0.51
1:A:344:A:H5'	1:A:345:C:C5	2.45	0.51
1:A:978:A:O2'	1:A:1322:C:N3	2.43	0.51
8:H:63:LEU:H	8:H:63:LEU:HD22	1.76	0.51
6:F:50:TYR:CE1	18:R:77:GLY:HA2	2.46	0.51
9:I:99:LEU:HB3	9:I:101:PHE:HD1	1.76	0.51
1:A:1392:G:N2	1:A:1502:A:H8	2.09	0.51
13:M:4:ILE:HG23	13:M:57:ARG:HA	1.92	0.51
1:A:22:G:H2'	1:A:23:C:C6	2.46	0.51
1:A:530:G:H5'	1:A:531:U:H5''	1.93	0.51
3:C:30:ARG:HD3	3:C:30:ARG:H	1.76	0.51
6:F:4:TYR:CE1	6:F:92:LYS:HG2	2.46	0.51
4:D:105:VAL:HG13	4:D:110:PHE:HB2	1.91	0.51
1:A:1191:A:OP1	3:C:4:LYS:NZ	2.44	0.50
1:A:518:C:H4'	1:A:519:C:O5'	2.10	0.50
1:A:765:G:N2	1:A:813:U:OP2	2.45	0.50
1:A:1145:C:O2'	1:A:1146:A:O5'	2.29	0.50
1:A:1285:A:H4'	1:A:1286:A:O5'	2.10	0.50
12:L:35:GLY:HA3	12:L:60:LEU:HD13	1.93	0.50
20:T:45:GLN:HG3	20:T:91:LEU:HD13	1.92	0.50
1:A:110:C:H2'	1:A:111:G:O4'	2.11	0.50
1:A:448:A:OP2	1:A:485:G:N2	2.29	0.50
1:A:1435:G:H2'	1:A:1436:U:C6	2.47	0.50
2:B:84:GLU:OE2	2:B:233:SER:OG	2.23	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:18:LYS:HG3	4:D:33:MET:HG3	1.93	0.50
4:D:24:GLU:HG2	4:D:25:ARG:H	1.77	0.50
5:E:76:ILE:HG22	5:E:78:HIS:H	1.77	0.50
1:A:1391:U:H2'	1:A:1392:G:C8	2.47	0.50
17:Q:67:LYS:O	17:Q:68:ARG:HB2	2.11	0.50
1:A:563:A:N6	25:A:1936:HOH:O	2.44	0.50
2:B:16:HIS:CD2	2:B:210:SER:HB2	2.46	0.50
5:E:8:GLU:HG2	5:E:34:VAL:HG22	1.94	0.50
1:A:95:U:H2'	1:A:96:G:H8	1.76	0.50
1:A:110:C:O2'	16:P:25:ARG:O	2.27	0.50
1:A:258:G:H2'	1:A:259:G:H8	1.76	0.50
1:A:587:G:N2	1:A:754:C:OP2	2.44	0.50
7:G:17:VAL:HG12	7:G:18:TYR:CD1	2.47	0.50
1:A:452:A:O2'	1:A:453:A:O4'	2.30	0.50
1:A:1242:C:H42	1:A:1295:G:H1	1.58	0.50
6:F:1:MET:HE2	6:F:68:PRO:HD3	1.92	0.50
6:F:95:GLU:HG3	6:F:96:PRO:HD2	1.93	0.50
13:M:12:ASN:H	13:M:45:VAL:HB	1.77	0.50
6:F:2:ARG:CZ	6:F:69:GLU:HG2	2.41	0.50
1:A:1037:C:H2'	1:A:1038:C:C6	2.47	0.49
3:C:14:ILE:HG22	3:C:15:THR:HG23	1.94	0.49
10:J:32:ALA:O	10:J:34:VAL:HG23	2.12	0.49
1:A:430:A:P	4:D:8:VAL:H	2.35	0.49
1:A:781:A:C5	1:A:802:A:C2	3.01	0.49
1:A:1148:U:H2'	1:A:1149:C:O4'	2.12	0.49
2:B:89:GLY:H	2:B:226:ARG:HH22	1.59	0.49
5:E:11:ILE:HD13	5:E:105:VAL:HG13	1.93	0.49
6:F:9:VAL:HB	6:F:87:ARG:HB2	1.94	0.49
19:S:65:ASN:OD1	19:S:65:ASN:N	2.42	0.49
1:A:1256:A:H4'	1:A:1257:U:O5'	2.12	0.49
1:A:41:G:H2'	1:A:42:G:C8	2.47	0.49
1:A:1294:G:H2'	1:A:1295:G:H8	1.76	0.49
4:D:111:ALA:HB2	4:D:120:LEU:HD12	1.94	0.49
16:P:39:TYR:CE2	16:P:41:PRO:HG3	2.48	0.49
5:E:137:GLU:O	5:E:141:GLN:HG3	2.12	0.49
1:A:890:G:O2'	1:A:906:G:O6	2.30	0.49
1:A:1427:U:H2'	1:A:1428:A:C8	2.48	0.49
17:Q:12:SER:HB3	17:Q:20:THR:CB	2.41	0.49
1:A:877:C:O2	8:H:3:THR:HG21	2.12	0.49
1:A:1080:A:O3'	5:E:16:THR:OG1	2.30	0.49
1:A:1198:G:H2'	1:A:1199:U:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1391:U:H2'	1:A:1392:G:H8	1.78	0.49
3:C:50:ALA:HB2	3:C:75:VAL:HB	1.94	0.49
1:A:56:U:H2'	1:A:57:G:H8	1.76	0.49
1:A:78:G:O6	1:A:91:C:N4	2.46	0.49
1:A:1195:C:H3'	1:A:1196:U:C5'	2.42	0.49
1:A:1200:C:H1'	1:A:1204:A:N6	2.27	0.49
9:I:32:ASP:OD1	9:I:33:PHE:N	2.46	0.49
1:A:1300:G:H4'	1:A:1301:U:O5'	2.13	0.48
1:A:1532:U:H2'	1:A:1533:C:H3'	1.95	0.48
2:B:135:GLN:O	2:B:139:LYS:HB2	2.13	0.48
5:E:16:THR:OG1	5:E:16:THR:O	2.30	0.48
1:A:1371:G:O3'	9:I:69:GLY:HA3	2.13	0.48
1:A:130:A:OP2	1:A:190(E):U:O2'	2.19	0.48
1:A:501:C:H2'	1:A:502:G:H8	1.77	0.48
1:A:1348:U:H4'	9:I:120:ARG:HG3	1.95	0.48
2:B:25:ASN:O	2:B:27:LYS:N	2.46	0.48
1:A:355:C:H5'	1:A:389:A:OP2	2.13	0.48
10:J:53:PRO:HA	14:N:41:ARG:NH2	2.29	0.48
1:A:581:G:O6	1:A:758:G:C8	2.67	0.48
1:A:244:U:H4'	1:A:245:C:H5''	1.96	0.48
1:A:1101:A:H4'	1:A:1102:A:O5'	2.14	0.48
1:A:1437:C:H2'	1:A:1438:G:H8	1.77	0.48
2:B:17:PHE:CG	2:B:18:GLY:N	2.81	0.48
3:C:3:ASN:OD1	3:C:3:ASN:N	2.45	0.48
10:J:26:ALA:HB1	10:J:84:GLN:HB2	1.96	0.48
1:A:424:G:H2'	1:A:425:G:H8	1.78	0.48
1:A:757:U:H2'	1:A:758:G:O4'	2.14	0.48
1:A:118:U:H3'	1:A:288:A:H61	1.78	0.48
1:A:254:G:O2'	17:Q:16:GLN:O	2.32	0.48
1:A:860:A:H2'	1:A:861:G:O4'	2.13	0.48
1:A:1175:G:H2'	1:A:1176:A:C8	2.49	0.48
7:G:65:ALA:O	7:G:69:VAL:HG23	2.13	0.48
1:A:952:U:H2'	1:A:953:G:C8	2.47	0.48
1:A:1347:G:H1'	1:A:1348:U:H5	1.79	0.48
4:D:64:LEU:HD23	4:D:198:VAL:HG21	1.96	0.48
1:A:95:U:H2'	1:A:96:G:C8	2.48	0.48
1:A:123:C:O2'	1:A:290:C:O2	2.31	0.48
9:I:10:ARG:HD3	9:I:105:ASP:HB3	1.95	0.48
13:M:107:ALA:HB3	13:M:111:LYS:HE3	1.96	0.48
1:A:254:G:OP1	17:Q:66:SER:OG	2.31	0.47
1:A:748:C:H4'	1:A:749:C:O5'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1242:C:OP1	21:U:10:ARG:NH1	2.35	0.47
6:F:12:PRO:HG3	6:F:58:GLY:HA2	1.95	0.47
14:N:21:TYR:HE2	14:N:23:ARG:HE	1.62	0.47
16:P:36:ILE:HD13	16:P:36:ILE:H	1.79	0.47
1:A:1114:C:H42	1:A:1186:G:H1	1.61	0.47
2:B:147:LYS:HD2	2:B:148:TYR:CE2	2.48	0.47
5:E:80:ILE:HD13	5:E:138:ALA:HB1	1.95	0.47
8:H:2:LEU:HD21	8:H:8:ASP:HB2	1.97	0.47
1:A:275:G:H5'	17:Q:14:LYS:HD3	1.95	0.47
1:A:476:G:H2'	1:A:477:G:H8	1.80	0.47
1:A:1119:C:OP2	9:I:9:ARG:NH2	2.46	0.47
1:A:1109:C:OP2	3:C:176:HIS:ND1	2.47	0.47
4:D:24:GLU:C	4:D:26:CYS:H	2.23	0.47
5:E:88:LYS:HB3	5:E:123:LEU:HB2	1.95	0.47
16:P:21:VAL:HG12	16:P:33:ILE:HD12	1.95	0.47
1:A:481:G:O2'	1:A:482:A:H8	1.98	0.47
1:A:551:U:H2'	1:A:552:U:C6	2.50	0.47
1:A:695:A:H2	1:A:787:A:H1'	1.80	0.47
1:A:1291:G:H4'	9:I:39:GLY:HA3	1.97	0.47
1:A:1366:C:H2'	1:A:1367:C:C6	2.50	0.47
19:S:40:ILE:HG13	19:S:70:LYS:O	2.13	0.47
1:A:184:G:H2'	1:A:185:A:C8	2.48	0.47
1:A:384:G:H2'	1:A:385:C:C6	2.49	0.47
1:A:797:C:H2'	1:A:798:G:H8	1.80	0.47
1:A:992:U:O2	1:A:993:G:N2	2.48	0.47
1:A:1205:U:H2'	1:A:1206:G:C8	2.49	0.47
1:A:1258:G:H2'	1:A:1259:C:C6	2.50	0.47
2:B:54:THR:O	2:B:58:ILE:HG13	2.15	0.47
5:E:31:LEU:HD23	5:E:31:LEU:HA	1.76	0.47
8:H:25:ASP:N	8:H:25:ASP:OD1	2.47	0.47
19:S:31:ILE:HD13	19:S:31:ILE:HA	1.75	0.47
1:A:92:C:H2'	1:A:93:G:H8	1.79	0.47
1:A:1120:G:C6	1:A:1121:U:C4	3.02	0.47
10:J:8:LEU:HD12	10:J:70:ARG:HB2	1.97	0.47
19:S:15:LEU:HA	19:S:18:LYS:HB3	1.96	0.47
1:A:279:A:OP1	1:A:280:C:O2'	2.21	0.47
1:A:474:G:H5'	16:P:81:ARG:HB3	1.97	0.47
5:E:144:THR:O	5:E:148:VAL:HG23	2.15	0.47
8:H:41:ARG:NH2	8:H:123:GLU:OE2	2.48	0.47
18:R:36:ASN:OD1	18:R:39:VAL:HG12	2.14	0.47
1:A:281:G:H4'	1:A:282:A:O5'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1399:C:H4'	1:A:1400:5MC:H5''	1.97	0.46
2:B:24:TRP:CZ3	2:B:26:PRO:HA	2.51	0.46
2:B:162:ILE:HG22	2:B:164:VAL:HG23	1.95	0.46
9:I:18:PHE:CD1	9:I:62:TYR:HD2	2.33	0.46
13:M:108:ARG:NH2	13:M:114:ARG:HA	2.30	0.46
1:A:602:A:C2	1:A:637:G:C2	3.03	0.46
1:A:766:A:C8	1:A:814:A:N6	2.84	0.46
1:A:825:G:H21	8:H:11:THR:HG21	1.80	0.46
1:A:1513:A:H2'	1:A:1514:C:C6	2.50	0.46
10:J:42:THR:HG1	10:J:68:HIS:HD1	1.60	0.46
13:M:96:LEU:O	13:M:110:ARG:NH1	2.49	0.46
3:C:155:GLY:HA3	3:C:163:ALA:HB1	1.97	0.46
5:E:110:LEU:HD13	5:E:118:ILE:HD13	1.97	0.46
11:K:34:ASP:OD1	11:K:38:ASN:N	2.48	0.46
1:A:1329:A:OP2	21:U:7:ARG:NH2	2.49	0.46
9:I:48:GLU:N	9:I:49:PRO:HD2	2.30	0.46
1:A:164:U:H2'	1:A:165:C:C6	2.50	0.46
1:A:192:U:H2'	1:A:193:C:H6	1.81	0.46
11:K:69:ALA:O	11:K:73:MET:HG2	2.16	0.46
1:A:701:C:H4'	1:A:702:A:O5'	2.14	0.46
5:E:81:GLU:HG2	5:E:90:VAL:HG22	1.97	0.46
10:J:38:ILE:HD11	10:J:71:LEU:HD22	1.97	0.46
1:A:401:C:H2'	1:A:402:G:C8	2.50	0.46
1:A:960:U:H4'	1:A:961:U:C5'	2.46	0.46
1:A:1056:U:H5'	3:C:163:ALA:HB2	1.97	0.46
1:A:1323:G:OP2	19:S:3:ARG:NH1	2.48	0.46
4:D:98:GLU:HG2	4:D:189:PRO:HG3	1.98	0.46
5:E:11:ILE:HB	5:E:31:LEU:HB3	1.98	0.46
11:K:43:SER:HA	11:K:47:VAL:HG21	1.96	0.46
1:A:27:G:C6	1:A:557:G:C2	3.04	0.46
1:A:1474:G:H2'	1:A:1475:G:C8	2.51	0.46
2:B:19:HIS:CD2	2:B:20:GLU:HG2	2.51	0.46
4:D:9:CYS:O	4:D:12:CYS:HB2	2.16	0.46
1:A:359:U:H2'	1:A:360:A:C8	2.50	0.46
1:A:556:C:H2'	1:A:557:G:O4'	2.16	0.46
1:A:981:U:H5'	14:N:21:TYR:CZ	2.51	0.46
1:A:1262:C:H42	1:A:1273:G:H1	1.62	0.46
7:G:15:ASP:OD2	7:G:44:TYR:OH	2.33	0.46
1:A:1376:U:OP1	7:G:98:SER:OG	2.25	0.46
1:A:1407:5MC:O2'	1:A:1408:A:H5'	2.16	0.46
6:F:11:ASN:OD1	6:F:86:ARG:NH2	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:48:GLU:OE1	9:I:51:ARG:NH1	2.49	0.46
1:A:243:A:H4'	1:A:244:U:O5'	2.16	0.45
3:C:120:VAL:O	3:C:124:ILE:HG13	2.15	0.45
11:K:48:ILE:HG22	11:K:49:GLY:H	1.81	0.45
13:M:77:ASN:O	13:M:80:ARG:HB3	2.16	0.45
14:N:26:ARG:HB2	14:N:43:CYS:SG	2.57	0.45
15:O:45:VAL:HB	15:O:46:HIS:ND1	2.31	0.45
1:A:925:G:C2	1:A:927:G:C8	3.04	0.45
12:L:59:ARG:HD3	12:L:65:GLU:HG3	1.98	0.45
18:R:46:GLU:OE1	18:R:46:GLU:N	2.37	0.45
1:A:374:A:C6	1:A:375:U:C4	3.04	0.45
1:A:526:C:O3'	22:A:1601:SRV:HI31	2.16	0.45
1:A:1404:5MC:H1'	1:A:1499:A:C2	2.51	0.45
4:D:8:VAL:O	4:D:11:LEU:N	2.38	0.45
17:Q:100:LYS:HA	17:Q:100:LYS:HD3	1.71	0.45
1:A:1068:G:H8	1:A:1068:G:OP2	1.99	0.45
1:A:1121:U:H2'	1:A:1122:U:C6	2.51	0.45
9:I:89:ASN:HB3	9:I:92:TYR:CE1	2.51	0.45
9:I:99:LEU:HB3	9:I:101:PHE:CD1	2.52	0.45
20:T:57:ARG:HH12	20:T:100:ILE:HG21	1.82	0.45
1:A:157:G:H2'	1:A:158:G:C8	2.52	0.45
1:A:1105:A:H2'	1:A:1106:G:H8	1.81	0.45
2:B:158:LEU:HD23	2:B:159:PRO:HD2	1.98	0.45
3:C:130:VAL:HG11	3:C:157:ILE:HG23	1.97	0.45
9:I:118:LYS:C	9:I:120:ARG:H	2.24	0.45
19:S:22:LEU:HD22	19:S:28:LYS:HD2	1.98	0.45
1:A:35:G:H2'	1:A:36:C:C6	2.52	0.45
1:A:731:G:OP1	1:A:766:A:H1'	2.16	0.45
2:B:198:ASP:N	2:B:198:ASP:OD1	2.49	0.45
3:C:23:TYR:HA	10:J:11:PHE:CE1	2.52	0.45
3:C:83:ARG:HA	3:C:86:VAL:HB	1.99	0.45
8:H:6:ILE:O	8:H:10:LEU:HG	2.16	0.45
15:O:26:GLU:HA	15:O:81:LEU:HD11	1.98	0.45
1:A:858:G:O2'	1:A:859:A:H5''	2.17	0.45
1:A:1402:4OC:HM43	1:A:1500:A:H61	1.81	0.45
2:B:16:HIS:O	2:B:17:PHE:HD2	1.99	0.45
2:B:20:GLU:HB2	2:B:190:THR:HB	1.98	0.45
6:F:36:ARG:NH2	6:F:66:GLU:OE1	2.38	0.45
19:S:80:TYR:CG	19:S:81:ARG:N	2.84	0.45
1:A:76:C:H2'	1:A:77:G:C8	2.52	0.45
1:A:337:C:H2'	1:A:338:A:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:922:G:C2	1:A:1396:A:C6	3.05	0.45
1:A:1442:G:C5	1:A:1446:A:N6	2.85	0.45
5:E:79:GLU:OE1	8:H:104:ARG:NH1	2.50	0.45
16:P:74:LEU:HB3	16:P:79:VAL:HG21	1.98	0.45
1:A:1090:U:H2'	1:A:1091:U:C6	2.52	0.45
1:A:1542:U:H2'	1:A:1543:C:C6	2.51	0.45
3:C:155:GLY:HA2	3:C:164:ARG:O	2.17	0.45
9:I:99:LEU:HD22	9:I:101:PHE:HE1	1.81	0.45
11:K:59:TYR:CE2	11:K:63:LEU:HD11	2.52	0.45
15:O:81:LEU:HD23	15:O:81:LEU:HA	1.84	0.45
17:Q:68:ARG:H	17:Q:70:ARG:NH1	2.15	0.45
19:S:28:LYS:HE2	19:S:28:LYS:HB3	1.80	0.45
1:A:539:A:H2'	1:A:540:G:C8	2.52	0.45
1:A:1309:G:OP1	13:M:88:ARG:NH2	2.49	0.45
1:A:779:C:H2'	1:A:780:A:O4'	2.18	0.44
1:A:811:C:O2'	1:A:901:A:N1	2.43	0.44
2:B:96:ARG:HD2	2:B:97:TRP:H	1.83	0.44
9:I:48:GLU:CD	9:I:51:ARG:HD2	2.42	0.44
1:A:1031:G:H2'	1:A:1032:G:C8	2.52	0.44
1:A:1067:A:O2'	1:A:1093:A:O3'	2.33	0.44
1:A:1152:A:H5''	10:J:13:HIS:ND1	2.33	0.44
2:B:97:TRP:HH2	2:B:176:GLU:CD	2.25	0.44
2:B:98:LEU:O	2:B:101:MET:HG3	2.17	0.44
3:C:179:ARG:HD2	3:C:206:GLU:HG2	1.98	0.44
19:S:5:LEU:HD21	19:S:70:LYS:NZ	2.32	0.44
1:A:219:C:O2'	1:A:381:C:H5'	2.17	0.44
7:G:78:ARG:HD3	7:G:79:ARG:N	2.32	0.44
20:T:59:ALA:O	20:T:63:ILE:HG13	2.16	0.44
1:A:939:G:H2'	1:A:940:C:C6	2.52	0.44
1:A:1049:U:C5	14:N:2:ALA:HA	2.53	0.44
1:A:1127:G:N2	1:A:1145:C:O2	2.40	0.44
1:A:1414:U:H2'	1:A:1415:G:H8	1.82	0.44
2:B:181:PHE:CD2	8:H:70:GLN:HB3	2.53	0.44
4:D:61:LYS:HD3	4:D:206:PHE:CD2	2.53	0.44
5:E:72:GLN:HE21	5:E:144:THR:HG23	1.82	0.44
8:H:64:LYS:HG3	8:H:79:VAL:HG21	2.00	0.44
14:N:23:ARG:CZ	14:N:30:ALA:HB2	2.47	0.44
16:P:19:ILE:HD11	16:P:39:TYR:HB2	2.00	0.44
21:U:12:LYS:HB3	21:U:22:ARG:HG3	1.98	0.44
1:A:795:C:H5''	1:A:796:C:OP2	2.18	0.44
1:A:839:U:H2'	1:A:839:U:O2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1427:U:H2'	1:A:1428:A:H8	1.83	0.44
2:B:84:GLU:HB3	2:B:219:VAL:HG21	1.99	0.44
9:I:65:VAL:HG11	9:I:77:ILE:HD11	1.98	0.44
18:R:44:LEU:HD11	18:R:79:LEU:HD23	2.00	0.44
20:T:65:LYS:HA	20:T:68:LYS:HG3	1.98	0.44
1:A:1065:U:H5	1:A:1190:G:C4	2.36	0.44
5:E:92:LYS:HA	5:E:93:PRO:HD3	1.77	0.44
15:O:4:THR:OG1	15:O:6:GLU:OE2	2.36	0.44
20:T:14:LYS:O	20:T:18:GLN:HG3	2.18	0.44
1:A:243:A:C2	1:A:246:A:C8	3.05	0.44
1:A:371:G:O2'	1:A:372:C:H5'	2.18	0.44
1:A:372:C:H1'	1:A:373:A:OP2	2.17	0.44
1:A:381:C:H2'	1:A:382:A:O4'	2.18	0.44
1:A:620:C:H2'	1:A:621:A:O4'	2.18	0.44
1:A:908:A:C2	1:A:909:A:C5	3.06	0.44
1:A:946:A:H2'	1:A:947:G:H8	1.82	0.44
3:C:69:HIS:HB3	3:C:106:VAL:HG22	2.00	0.44
13:M:15:VAL:HG11	13:M:34:LEU:HD21	1.99	0.44
1:A:437:U:O2'	4:D:123:HIS:ND1	2.36	0.44
1:A:484:G:H4'	1:A:485:G:O5'	2.18	0.44
1:A:1007:C:H2'	1:A:1008:C:C6	2.52	0.44
1:A:1376:U:H2'	1:A:1377:A:C8	2.52	0.44
14:N:59:ALA:HB1	14:N:61:TRP:HZ3	1.83	0.44
16:P:26:ARG:HD2	16:P:31:LYS:O	2.17	0.44
16:P:40:ASP:OD1	16:P:44:THR:OG1	2.32	0.44
1:A:41:G:H2'	1:A:42:G:H8	1.82	0.44
1:A:278:G:C6	17:Q:95:TYR:HD2	2.36	0.44
1:A:1175:G:H2'	1:A:1176:A:H8	1.82	0.44
7:G:75:VAL:HG11	7:G:86:GLN:HB3	1.99	0.44
11:K:27:ASN:OD1	11:K:28:THR:N	2.49	0.44
1:A:1006:C:H2'	1:A:1007:C:O4'	2.18	0.43
1:A:1328:C:H2'	1:A:1329:A:H8	1.83	0.43
4:D:135:LEU:HA	4:D:136:PRO:HD3	1.82	0.43
5:E:142:LEU:HD23	5:E:142:LEU:HA	1.84	0.43
8:H:11:THR:HA	8:H:14:ARG:NH1	2.33	0.43
9:I:63:ILE:HG21	9:I:77:ILE:HG12	2.00	0.43
14:N:9:LYS:HG3	14:N:21:TYR:O	2.18	0.43
17:Q:21:VAL:HG21	17:Q:59:ILE:HD11	1.99	0.43
1:A:807:A:OP1	15:O:48:LYS:NZ	2.50	0.43
3:C:136:GLN:O	3:C:140:ARG:HG3	2.18	0.43
5:E:122:GLU:OE1	5:E:131:ILE:HG13	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:63:ILE:HD13	9:I:77:ILE:HG23	2.00	0.43
21:U:5:ASP:O	21:U:11:GLY:HA3	2.18	0.43
1:A:686:U:C2	1:A:687:A:N7	2.86	0.43
1:A:1095:U:OP1	1:A:1108:G:N2	2.42	0.43
1:A:1104:G:H4'	2:B:111:ARG:HH21	1.83	0.43
1:A:1240:U:OP1	7:G:119:ARG:NH2	2.20	0.43
1:A:1347:G:O2'	1:A:1348:U:P	2.76	0.43
4:D:98:GLU:OE2	4:D:107:ARG:NE	2.51	0.43
12:L:87:GLY:HA2	12:L:98:TYR:HA	1.99	0.43
16:P:59:TRP:HA	16:P:62:VAL:HG22	1.99	0.43
1:A:445:G:H2'	1:A:446:G:C8	2.53	0.43
1:A:1126:U:H3'	1:A:1127:G:C8	2.54	0.43
1:A:1320:C:OP2	19:S:70:LYS:NZ	2.50	0.43
1:A:1355:G:H2'	1:A:1356:G:C8	2.53	0.43
22:A:1601:SRY:O21	22:A:1601:SRY:NE1	2.52	0.43
2:B:218:ALA:O	2:B:222:ILE:HG13	2.18	0.43
6:F:89:MET:HE1	18:R:72:ARG:HG2	2.00	0.43
20:T:74:LYS:HA	20:T:74:LYS:HD3	1.75	0.43
1:A:476:G:H2'	1:A:477:G:C8	2.53	0.43
4:D:153:ARG:HD2	4:D:181:MET:SD	2.58	0.43
14:N:14:PRO:C	14:N:16:PHE:H	2.27	0.43
1:A:5:U:H4'	1:A:6:G:O5'	2.18	0.43
1:A:186:C:H2'	1:A:187:C:H6	1.83	0.43
1:A:885:G:C2	1:A:913:A:N1	2.86	0.43
1:A:1402:4OC:HM22	1:A:1403:C:O4'	2.18	0.43
3:C:6:HIS:HA	3:C:7:PRO:HD3	1.85	0.43
7:G:16:LEU:H	7:G:16:LEU:HD22	1.83	0.43
13:M:67:GLU:HB3	13:M:68:GLY:H	1.51	0.43
1:A:193:C:H2'	1:A:194:C:H6	1.84	0.43
1:A:580:U:H2'	1:A:581:G:O4'	2.18	0.43
1:A:956:U:H2'	1:A:957:U:O4'	2.19	0.43
1:A:1347:G:H3'	9:I:108:VAL:O	2.19	0.43
2:B:208:ILE:HA	2:B:211:ILE:HD12	2.01	0.43
11:K:124:LYS:HE3	11:K:125:PHE:CE2	2.53	0.43
15:O:39:LEU:HD13	15:O:56:LEU:HB2	2.00	0.43
19:S:18:LYS:HD3	19:S:31:ILE:HD11	2.00	0.43
1:A:960:U:C5	1:A:1225:A:H1'	2.54	0.43
2:B:101:MET:HA	2:B:108:ILE:HG13	1.99	0.43
8:H:121:ASP:OD1	8:H:121:ASP:N	2.51	0.43
1:A:1069:C:O2'	1:A:1192:C:H1'	2.19	0.43
1:A:1323:G:H2'	1:A:1324:A:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:10:ARG:HA	21:U:13:ILE:HD12	2.01	0.43
1:A:673:G:O3'	6:F:87:ARG:NH2	2.52	0.43
1:A:792:A:O2'	1:A:793:U:OP2	2.29	0.43
1:A:914:A:OP1	22:A:1601:SRV:HI33	2.18	0.43
1:A:1262:C:H2'	1:A:1263:C:C6	2.54	0.43
3:C:77:ILE:O	3:C:83:ARG:N	2.51	0.43
12:L:24:VAL:HG13	12:L:98:TYR:CE2	2.54	0.43
1:A:563:A:H2'	1:A:567:G:C8	2.54	0.42
1:A:1053:G:H4'	1:A:1054:C:H5'	2.00	0.42
1:A:1347:G:H2'	1:A:1373:G:H1	1.83	0.42
1:A:1374:A:H2'	1:A:1375:A:H8	1.84	0.42
3:C:22:TRP:HA	10:J:93:GLY:HA2	2.01	0.42
4:D:28:SER:O	4:D:30:LYS:N	2.47	0.42
13:M:90:LEU:HD13	13:M:94:ARG:HH21	1.84	0.42
1:A:109:A:C6	1:A:327:A:C6	3.08	0.42
1:A:251:G:C6	1:A:266:G:C6	3.07	0.42
1:A:293:G:C4	1:A:305:G:N2	2.87	0.42
1:A:1003(A):G:N1	1:A:1038:C:N3	2.67	0.42
1:A:1137:C:H5'	1:A:1138:G:C4	2.54	0.42
1:A:1313:U:OP2	19:S:6:LYS:HA	2.20	0.42
1:A:1320:C:H5''	19:S:3:ARG:NH2	2.34	0.42
2:B:61:LEU:HG	2:B:66:GLY:HA3	2.01	0.42
1:A:428:G:H4'	1:A:429:U:O5'	2.20	0.42
1:A:474:G:H2'	1:A:475:G:H8	1.84	0.42
1:A:833:U:H2'	1:A:834:C:C6	2.54	0.42
1:A:974:A:C8	14:N:31:ARG:HG2	2.54	0.42
3:C:134:ILE:O	3:C:138:VAL:HG23	2.19	0.42
9:I:9:ARG:HB3	9:I:14:VAL:HG12	1.99	0.42
8:H:100:ILE:HG23	8:H:112:LEU:HD11	2.01	0.42
12:L:92:0TD:H8	12:L:92:0TD:H4	1.88	0.42
13:M:101:GLN:N	13:M:101:GLN:OE1	2.52	0.42
21:U:5:ASP:HB3	21:U:8:THR:OG1	2.19	0.42
1:A:475:G:H2'	1:A:476:G:H8	1.85	0.42
1:A:886:G:C2	1:A:912:C:O2	2.72	0.42
1:A:1275:A:H2'	1:A:1276:G:O4'	2.20	0.42
1:A:1481:U:H2'	1:A:1482:G:O4'	2.20	0.42
5:E:51:VAL:HB	5:E:52:PRO:HD3	2.01	0.42
16:P:60:LEU:HD23	16:P:60:LEU:HA	1.80	0.42
19:S:7:LYS:HE3	19:S:7:LYS:HB2	1.73	0.42
19:S:45:VAL:HA	19:S:62:ILE:HD13	2.00	0.42
1:A:815:A:N3	1:A:1527:C:O2'	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1132:C:H2'	1:A:1133:G:H8	1.84	0.42
1:A:1461:G:H2'	1:A:1462:G:H8	1.85	0.42
2:B:196:LEU:HA	2:B:196:LEU:HD23	1.74	0.42
9:I:86:VAL:HG21	9:I:93:ARG:HG3	2.02	0.42
14:N:24:CYS:SG	14:N:40:CYS:HB3	2.59	0.42
16:P:58:TYR:O	16:P:61:SER:OG	2.27	0.42
20:T:20:LEU:HD23	20:T:20:LEU:HA	1.91	0.42
1:A:908:A:C2	1:A:909:A:C4	3.07	0.42
1:A:1347:G:HO2'	1:A:1348:U:P	2.42	0.42
1:A:1399:C:C2	1:A:1502:A:N6	2.88	0.42
1:A:1431:C:H2'	1:A:1432:G:O4'	2.20	0.42
4:D:9:CYS:HA	4:D:12:CYS:SG	2.60	0.42
9:I:79:LEU:HD23	9:I:101:PHE:O	2.20	0.42
11:K:62:GLN:HG3	11:K:97:ALA:HB2	2.01	0.42
14:N:26:ARG:HD2	14:N:47:LEU:HD11	2.02	0.42
1:A:560:U:H5'	1:A:566:G:N2	2.35	0.42
1:A:882:C:O2'	1:A:883:C:H5'	2.20	0.42
1:A:964:A:HO2'	10:J:55:LYS:HZ3	1.61	0.42
1:A:1221:G:H2'	1:A:1222:G:C8	2.55	0.42
1:A:1252:A:H2'	1:A:1253:G:O4'	2.20	0.42
1:A:1380:U:H1'	1:A:1381:U:OP2	2.18	0.42
2:B:231:GLU:CD	2:B:231:GLU:H	2.28	0.42
2:B:240:GLN:OE1	2:B:240:GLN:N	2.49	0.42
7:G:26:PHE:CE2	7:G:30:ILE:HD11	2.55	0.42
15:O:18:PHE:HB2	15:O:19:PRO:HD2	2.02	0.42
18:R:26:LEU:HD23	18:R:29:PHE:CE2	2.55	0.42
1:A:373:A:H1'	1:A:481:G:N3	2.35	0.42
1:A:559:A:H4'	1:A:560:U:O5'	2.20	0.42
1:A:583:A:H2'	1:A:584:G:O4'	2.19	0.42
1:A:1273:G:H2'	1:A:1274:G:O4'	2.20	0.42
3:C:167:TRP:HE3	3:C:168:ALA:N	2.18	0.42
4:D:62:GLN:O	4:D:66:ARG:HB2	2.20	0.42
1:A:997:U:H2'	1:A:998:G:C8	2.55	0.42
4:D:59:ARG:HH22	4:D:66:ARG:HH12	1.67	0.42
7:G:122:HIS:O	7:G:125:MET:HG3	2.19	0.42
11:K:33:THR:OG1	11:K:37:GLY:O	2.35	0.42
15:O:32:LEU:HD11	15:O:62:GLN:HB3	2.02	0.42
1:A:148:G:H2'	1:A:149:A:H8	1.85	0.41
1:A:1369:C:H2'	1:A:1370:G:C8	2.55	0.41
4:D:31:CYS:C	4:D:33:MET:H	2.28	0.41
4:D:58:LEU:HD12	4:D:59:ARG:HD2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:25:ILE:HG21	6:F:82:ARG:HD2	2.02	0.41
7:G:87:VAL:HA	7:G:88:PRO:HD3	1.82	0.41
9:I:42:ARG:NH2	9:I:75:ASP:OD2	2.34	0.41
9:I:104:ARG:NH1	9:I:105:ASP:O	2.44	0.41
1:A:1052:U:H2'	1:A:1200:C:H41	1.85	0.41
13:M:34:LEU:HD22	13:M:39:ILE:HB	2.01	0.41
19:S:11:VAL:HG22	19:S:39:THR:HB	2.01	0.41
20:T:74:LYS:HB3	20:T:75:ASN:H	1.64	0.41
20:T:92:LEU:O	20:T:96:GLY:HA2	2.20	0.41
1:A:485:G:O2'	1:A:486:U:P	2.78	0.41
1:A:939:G:H5''	7:G:102:ARG:NH2	2.35	0.41
9:I:5:TYR:HE2	9:I:7:THR:OG1	2.02	0.41
10:J:87:THR:HG23	10:J:89:ASP:OD1	2.20	0.41
16:P:6:LEU:HD23	16:P:17:TYR:CG	2.55	0.41
16:P:69:THR:O	16:P:72:ARG:HB3	2.20	0.41
1:A:426:G:OP1	4:D:38:TYR:OH	2.28	0.41
1:A:452:A:H2'	1:A:453:A:C8	2.55	0.41
1:A:826:C:O2	8:H:15:ASN:ND2	2.54	0.41
1:A:1294:G:H2'	1:A:1295:G:C8	2.56	0.41
1:A:1461:G:H2'	1:A:1462:G:C8	2.55	0.41
2:B:193:ASP:HA	2:B:194:PRO:HD2	1.93	0.41
3:C:43:LEU:O	3:C:47:LEU:HB2	2.21	0.41
6:F:11:ASN:HA	6:F:12:PRO:HD3	1.75	0.41
2:B:16:HIS:CE1	2:B:210:SER:HB2	2.55	0.41
3:C:29:TYR:OH	14:N:54:PRO:HG2	2.20	0.41
1:A:411:A:N3	1:A:413:G:O2'	2.46	0.41
1:A:413:G:H2'	1:A:428:G:N2	2.34	0.41
1:A:785:G:N2	1:A:798:G:C4	2.88	0.41
1:A:1126:U:H5'	25:A:2149:HOH:O	2.20	0.41
18:R:65:ILE:O	18:R:69:THR:OG1	2.32	0.41
20:T:67:ALA:HB2	20:T:77:ALA:HB2	2.02	0.41
20:T:100:ILE:HG22	20:T:102:GLY:N	2.34	0.41
1:A:308:C:H2'	1:A:309:G:H8	1.86	0.41
1:A:1402:4OC:HM43	1:A:1500:A:N6	2.35	0.41
1:A:1498:UR3:H6	1:A:1498:UR3:O5'	2.20	0.41
7:G:78:ARG:HD3	7:G:79:ARG:H	1.84	0.41
20:T:89:ARG:NH2	20:T:104:LEU:HB3	2.35	0.41
1:A:9:G:C2	1:A:26:A:N1	2.88	0.41
1:A:181:G:H4'	1:A:182:U:H5'	2.03	0.41
1:A:424:G:H2'	1:A:425:G:C8	2.56	0.41
1:A:1249:C:HO2'	9:I:73:GLN:HE22	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:44:LEU:O	2:B:47:THR:HB	2.20	0.41
8:H:4:ASP:CG	8:H:85:ARG:HH11	2.27	0.41
12:L:41:ARG:HG2	12:L:42:THR:N	2.35	0.41
16:P:65:GLN:HA	16:P:66:PRO:HD3	1.85	0.41
1:A:17:U:H2'	1:A:18:C:C6	2.56	0.41
1:A:130:A:H5'	17:Q:63:ARG:HE	1.86	0.41
1:A:328:C:H4'	1:A:329:A:O5'	2.20	0.41
1:A:451:A:N6	1:A:481:G:C4	2.89	0.41
1:A:463:A:H2'	1:A:474:G:O4'	2.20	0.41
1:A:607:A:C4	1:A:608:A:C8	3.09	0.41
1:A:689:C:H2'	1:A:690:G:O4'	2.21	0.41
1:A:892:A:C2	1:A:907:A:C4	3.09	0.41
1:A:996:A:C2	1:A:1046:A:H4'	2.55	0.41
1:A:1279:A:H5''	1:A:1280:A:OP1	2.20	0.41
1:A:1305:G:H22	1:A:1331:G:H1'	1.85	0.41
1:A:1314:C:C5	19:S:6:LYS:HD3	2.56	0.41
1:A:1437:C:H2'	1:A:1438:G:C8	2.55	0.41
3:C:182:ILE:HA	3:C:202:ILE:O	2.21	0.41
5:E:147:ASP:OD1	5:E:147:ASP:N	2.54	0.41
7:G:116:ALA:O	7:G:120:ILE:HG12	2.20	0.41
9:I:9:ARG:HD3	9:I:14:VAL:HG12	2.03	0.41
9:I:10:ARG:HE	9:I:11:LYS:HB2	1.86	0.41
9:I:70:LYS:O	9:I:74:ILE:HG13	2.21	0.41
11:K:58:PRO:HA	11:K:90:GLY:HA3	2.03	0.41
18:R:26:LEU:HD12	18:R:26:LEU:HA	1.78	0.41
18:R:59:SER:O	18:R:63:GLN:N	2.40	0.41
20:T:34:LYS:NZ	20:T:80:ARG:HH12	2.19	0.41
20:T:67:ALA:O	20:T:73:HIS:ND1	2.53	0.41
1:A:452:A:O2'	1:A:453:A:O5'	2.30	0.41
1:A:895:G:H2'	1:A:896:C:C6	2.56	0.41
1:A:1201:A:H1'	1:A:1202:G:OP2	2.20	0.41
12:L:7:ILE:HD13	12:L:7:ILE:HA	1.85	0.41
12:L:8:ASN:O	12:L:12:ARG:HG3	2.21	0.41
19:S:13:ASP:O	19:S:17:GLU:HG2	2.21	0.41
1:A:10:A:OP2	5:E:126:ARG:HG2	2.21	0.40
1:A:160:A:H1'	1:A:344:A:C5	2.56	0.40
1:A:181:G:H4'	1:A:182:U:C5'	2.51	0.40
1:A:1021:G:C2	1:A:1022:G:H1'	2.56	0.40
1:A:576:G:H3'	1:A:577:G:H5''	2.03	0.40
1:A:687:A:H4'	1:A:688:G:O5'	2.22	0.40
1:A:1126:U:H3'	1:A:1127:G:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:108:LEU:HD23	4:D:108:LEU:HA	1.88	0.40
7:G:145:ALA:C	7:G:147:ALA:H	2.30	0.40
10:J:8:LEU:O	10:J:69:ASN:HA	2.21	0.40
10:J:51:ARG:NH2	10:J:61:GLU:HB2	2.36	0.40
11:K:16:SER:O	11:K:35:PRO:HD3	2.21	0.40
1:A:376:G:N3	1:A:389:A:C2	2.89	0.40
1:A:502:G:H2'	1:A:503:C:O4'	2.21	0.40
1:A:1111:A:H61	3:C:177:THR:HG22	1.86	0.40
2:B:25:ASN:ND2	2:B:193:ASP:HB2	2.37	0.40
2:B:181:PHE:HD2	8:H:70:GLN:HB3	1.86	0.40
5:E:118:ILE:HG12	5:E:119:LEU:N	2.36	0.40
10:J:38:ILE:HA	10:J:39:PRO:HD3	1.85	0.40
10:J:48:THR:HG22	10:J:60:ARG:HG2	2.04	0.40
10:J:53:PRO:HA	14:N:41:ARG:HH22	1.86	0.40
13:M:77:ASN:O	13:M:81:LEU:HG	2.21	0.40
1:A:103:C:P	20:T:17:ARG:HH12	2.44	0.40
1:A:1412:C:H2'	1:A:1413:A:H8	1.82	0.40
2:B:102:LEU:HD21	2:B:162:ILE:HD11	2.04	0.40
2:B:188:ALA:O	2:B:202:PRO:HA	2.22	0.40
4:D:151:LYS:H	4:D:151:LYS:HD2	1.85	0.40
12:L:85:ILE:HG23	12:L:98:TYR:HB3	2.03	0.40
14:N:58:LYS:HE3	14:N:58:LYS:HB3	1.92	0.40
16:P:19:ILE:HG22	16:P:36:ILE:HD11	2.02	0.40
19:S:69:HIS:HB3	19:S:73:GLU:CD	2.46	0.40
2:B:127:ILE:H	2:B:127:ILE:HG13	1.54	0.40
8:H:4:ASP:OD1	8:H:85:ARG:NH1	2.54	0.40
8:H:120:THR:H	8:H:123:GLU:HB2	1.85	0.40
13:M:59:TYR:O	13:M:63:THR:HG22	2.22	0.40
17:Q:10:VAL:HG23	17:Q:54:GLY:H	1.86	0.40
19:S:19:VAL:HA	19:S:22:LEU:HB2	2.04	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	232/256 (91%)	209 (90%)	20 (9%)	3 (1%)	9	40
3	C	204/239 (85%)	178 (87%)	26 (13%)	0	100	100
4	D	206/209 (99%)	193 (94%)	13 (6%)	0	100	100
5	E	148/162 (91%)	141 (95%)	7 (5%)	0	100	100
6	F	99/101 (98%)	95 (96%)	4 (4%)	0	100	100
7	G	153/156 (98%)	143 (94%)	10 (6%)	0	100	100
8	H	136/138 (99%)	134 (98%)	2 (2%)	0	100	100
9	I	125/128 (98%)	117 (94%)	7 (6%)	1 (1%)	16	50
10	J	96/105 (91%)	79 (82%)	15 (16%)	2 (2%)	5	31
11	K	114/129 (88%)	104 (91%)	10 (9%)	0	100	100
12	L	121/135 (90%)	111 (92%)	10 (8%)	0	100	100
13	M	116/126 (92%)	106 (91%)	10 (9%)	0	100	100
14	N	58/61 (95%)	51 (88%)	7 (12%)	0	100	100
15	O	85/89 (96%)	78 (92%)	7 (8%)	0	100	100
16	P	81/88 (92%)	79 (98%)	2 (2%)	0	100	100
17	Q	97/105 (92%)	91 (94%)	6 (6%)	0	100	100
18	R	68/88 (77%)	64 (94%)	4 (6%)	0	100	100
19	S	78/93 (84%)	68 (87%)	8 (10%)	2 (3%)	4	27
20	T	97/106 (92%)	86 (89%)	11 (11%)	0	100	100
21	U	22/27 (82%)	19 (86%)	3 (14%)	0	100	100
All	All	2336/2541 (92%)	2146 (92%)	182 (8%)	8 (0%)	36	66

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	S	31	ILE
2	B	21	ARG
2	B	24	TRP
9	I	119	ALA
19	S	14	HIS
10	J	34	VAL
2	B	229	VAL
10	J	72	VAL

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	202/220 (92%)	181 (90%)	21 (10%)	7	29
3	C	160/188 (85%)	135 (84%)	25 (16%)	2	15
4	D	180/181 (99%)	169 (94%)	11 (6%)	17	44
5	E	115/123 (94%)	99 (86%)	16 (14%)	3	19
6	F	90/90 (100%)	81 (90%)	9 (10%)	7	30
7	G	126/127 (99%)	119 (94%)	7 (6%)	19	46
8	H	119/119 (100%)	107 (90%)	12 (10%)	7	29
9	I	98/99 (99%)	86 (88%)	12 (12%)	5	23
10	J	87/92 (95%)	82 (94%)	5 (6%)	18	46
11	K	88/99 (89%)	82 (93%)	6 (7%)	14	41
12	L	103/110 (94%)	91 (88%)	12 (12%)	5	25
13	M	94/101 (93%)	79 (84%)	15 (16%)	2	14
14	N	49/50 (98%)	42 (86%)	7 (14%)	3	18
15	O	79/80 (99%)	74 (94%)	5 (6%)	16	43
16	P	72/74 (97%)	66 (92%)	6 (8%)	10	35
17	Q	94/97 (97%)	85 (90%)	9 (10%)	8	31
18	R	61/77 (79%)	56 (92%)	5 (8%)	10	35
19	S	71/80 (89%)	58 (82%)	13 (18%)	2	10
20	T	76/82 (93%)	69 (91%)	7 (9%)	8	32
21	U	19/22 (86%)	17 (90%)	2 (10%)	6	28
All	All	1983/2111 (94%)	1778 (90%)	205 (10%)	7	29

All (205) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	7	VAL
2	B	8	LYS
2	B	16	HIS

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Mol	Chain	Res	Type
2	B	17	PHE
2	B	44	LEU
2	B	48	MET
2	B	60	ASP
2	B	69	LEU
2	B	75	LYS
2	B	96	ARG
2	B	111	ARG
2	B	121	LEU
2	B	127	ILE
2	B	144	ARG
2	B	153	ARG
2	B	157	ARG
2	B	158	LEU
2	B	170	GLU
2	B	178	ARG
2	B	213	LEU
2	B	221	LEU
3	C	3	ASN
3	C	30	ARG
3	C	32	LEU
3	C	34	LEU
3	C	42	LEU
3	C	58	GLU
3	C	63	ASN
3	C	64	VAL
3	C	79	ARG
3	C	91	LEU
3	C	95	THR
3	C	105	GLU
3	C	107	GLN
3	C	130	VAL
3	C	136	GLN
3	C	142	MET
3	C	147	LYS
3	C	156	ARG
3	C	157	ILE
3	C	162	GLN
3	C	166	GLU
3	C	173	VAL
3	C	177	THR
3	C	188	LEU

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Mol	Chain	Res	Type
3	C	204	LEU
4	D	15	GLU
4	D	34	GLU
4	D	64	LEU
4	D	119	GLN
4	D	122	ARG
4	D	135	LEU
4	D	137	SER
4	D	145	GLU
4	D	157	LEU
4	D	187	ARG
4	D	194	LEU
5	E	6	PHE
5	E	12	LEU
5	E	14	ARG
5	E	16	THR
5	E	18	ARG
5	E	31	LEU
5	E	38	GLN
5	E	41	VAL
5	E	43	LEU
5	E	53	LEU
5	E	79	GLU
5	E	80	ILE
5	E	89	ILE
5	E	111	GLU
5	E	126	ARG
5	E	151	LEU
6	F	10	LEU
6	F	16	GLN
6	F	19	LEU
6	F	24	GLU
6	F	32	ASN
6	F	43	LEU
6	F	67	MET
6	F	74	ASP
6	F	95	GLU
7	G	8	GLU
7	G	12	LEU
7	G	16	LEU
7	G	72	ARG
7	G	78	ARG

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Mol	Chain	Res	Type
7	G	113	GLU
7	G	126	ASP
8	H	11	THR
8	H	26	VAL
8	H	37	ARG
8	H	39	LEU
8	H	51	VAL
8	H	63	LEU
8	H	83	ILE
8	H	84	ARG
8	H	85	ARG
8	H	91	ARG
8	H	98	LYS
8	H	127	LEU
9	I	3	GLN
9	I	26	VAL
9	I	29	ASN
9	I	65	VAL
9	I	75	ASP
9	I	79	LEU
9	I	81	ILE
9	I	86	VAL
9	I	102	LEU
9	I	108	VAL
9	I	121	ARG
9	I	127	LYS
10	J	3	LYS
10	J	57	LYS
10	J	62	HIS
10	J	80	LYS
10	J	82	ILE
11	K	12	ARG
11	K	29	ILE
11	K	33	THR
11	K	48	ILE
11	K	51	LYS
11	K	96	ARG
12	L	18	VAL
12	L	19	ARG
12	L	33	ARG
12	L	43	VAL
12	L	44	THR

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Mol	Chain	Res	Type
12	L	62	SER
12	L	64	TYR
12	L	66	VAL
12	L	67	THR
12	L	96	VAL
12	L	122	THR
12	L	126	LYS
13	M	12	ASN
13	M	32	GLU
13	M	35	GLU
13	M	44	ARG
13	M	56	LEU
13	M	63	THR
13	M	64	TRP
13	M	69	GLU
13	M	78	ILE
13	M	81	LEU
13	M	90	LEU
13	M	98	VAL
13	M	110	ARG
13	M	115	LYS
13	M	117	VAL
14	N	7	ILE
14	N	8	GLU
14	N	22	THR
14	N	24	CYS
14	N	25	VAL
14	N	31	ARG
14	N	44	LEU
15	O	32	LEU
15	O	33	THR
15	O	39	LEU
15	O	45	VAL
15	O	70	LEU
16	P	1	MET
16	P	2	VAL
16	P	20	VAL
16	P	27	LYS
16	P	36	ILE
16	P	43	LYS
17	Q	15	MET
17	Q	34	LYS

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Mol	Chain	Res	Type
17	Q	35	VAL
17	Q	38	ARG
17	Q	53	LEU
17	Q	59	ILE
17	Q	60	ILE
17	Q	83	ASP
17	Q	92	ARG
18	R	19	LYS
18	R	21	LYS
18	R	28	GLU
18	R	47	THR
18	R	88	LYS
19	S	4	SER
19	S	6	LYS
19	S	7	LYS
19	S	15	LEU
19	S	19	VAL
19	S	29	ARG
19	S	31	ILE
19	S	53	ASN
19	S	58	VAL
19	S	62	ILE
19	S	63	THR
19	S	65	ASN
19	S	71	LEU
20	T	9	ASN
20	T	19	SER
20	T	41	ILE
20	T	42	GLN
20	T	62	LEU
20	T	73	HIS
20	T	84	LEU
21	U	15	ARG
21	U	22	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	204	ASN
2	B	224	GLN
3	C	6	HIS
3	C	102	ASN

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Mol	Chain	Res	Type
3	C	162	GLN
4	D	119	GLN
4	D	199	ASN
5	E	72	GLN
6	F	27	GLN
6	F	100	ASN
9	I	3	GLN
11	K	26	ASN
12	L	9	GLN
13	M	12	ASN
15	O	9	GLN
16	P	65	GLN
19	S	47	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1511/1522 (99%)	259 (17%)	45 (2%)

All (259) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	7	G
1	A	9	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	51	A
1	A	66	G
1	A	69	G
1	A	81	U
1	A	88	A
1	A	91	C
1	A	101	A
1	A	108	G
1	A	116	A
1	A	117	G
1	A	121	C
1	A	129(A)	G

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Mol	Chain	Res	Type
1	A	130	A
1	A	131	C
1	A	145	G
1	A	163	C
1	A	182	U
1	A	183	G
1	A	190(D)	U
1	A	190(G)	G
1	A	195	A
1	A	197	A
1	A	201	C
1	A	202	U
1	A	203	U
1	A	204	U
1	A	216	G
1	A	220	G
1	A	231	G
1	A	244	U
1	A	247	G
1	A	251	G
1	A	252	U
1	A	253	U
1	A	266	G
1	A	267	C
1	A	279	A
1	A	282	A
1	A	289	G
1	A	299	G
1	A	301	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	332	G
1	A	344	A
1	A	345	C
1	A	350	G
1	A	351	G
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	373	A

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Mol	Chain	Res	Type
1	A	384	G
1	A	390	C
1	A	397	A
1	A	398	C
1	A	406	G
1	A	412	A
1	A	413	G
1	A	414	A
1	A	421	U
1	A	424	G
1	A	429	U
1	A	430	A
1	A	439	A
1	A	460	A
1	A	461	C
1	A	475	G
1	A	481	G
1	A	485	G
1	A	486	U
1	A	497	A
1	A	498	U
1	A	509	A
1	A	510	A
1	A	511	C
1	A	518	C
1	A	519	C
1	A	527	G
1	A	530	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	547	A
1	A	559	A
1	A	560	U
1	A	562	C
1	A	564	C
1	A	568	G
1	A	572	A
1	A	573	A
1	A	576	G
1	A	577	G
1	A	579	G

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Mol	Chain	Res	Type
1	A	588	G
1	A	653	A
1	A	665	A
1	A	686	U
1	A	687	A
1	A	688	G
1	A	701	C
1	A	702	A
1	A	703	G
1	A	717	C
1	A	723	U
1	A	731	G
1	A	749	C
1	A	755	G
1	A	774	G
1	A	777	A
1	A	781	A
1	A	792	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	858	G
1	A	859	A
1	A	872	A
1	A	876	G
1	A	885	G
1	A	902	G
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	960	U
1	A	961	U
1	A	966	M2G

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Mol	Chain	Res	Type
1	A	969	A
1	A	971	G
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	982	U
1	A	984	C
1	A	989	C
1	A	991	U
1	A	992	U
1	A	993	G
1	A	1004	A
1	A	1005	A
1	A	1006	C
1	A	1007	C
1	A	1010	G
1	A	1016	A
1	A	1019	C
1	A	1022	G
1	A	1023	G
1	A	1026	G
1	A	1031	G
1	A	1045	C
1	A	1051	C
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1092	A
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1126	U
1	A	1127	G
1	A	1128	C
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1136	U
1	A	1137	C
1	A	1138	G
1	A	1139	G

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Mol	Chain	Res	Type
1	A	1140	C
1	A	1142	G
1	A	1145	C
1	A	1152	A
1	A	1159	U
1	A	1160	G
1	A	1171	G
1	A	1183	A
1	A	1184	G
1	A	1191	A
1	A	1196	U
1	A	1197	G
1	A	1200	C
1	A	1201	A
1	A	1202	G
1	A	1212	U
1	A	1213	A
1	A	1214	C
1	A	1225	A
1	A	1227	A
1	A	1236	A
1	A	1238	A
1	A	1241	G
1	A	1242	C
1	A	1256	A
1	A	1257	U
1	A	1258	G
1	A	1260	C
1	A	1262	C
1	A	1270	C
1	A	1278	U
1	A	1280	A
1	A	1286	A
1	A	1287	A
1	A	1289	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1303	C
1	A	1305	G
1	A	1306	A
1	A	1319	A

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Mol	Chain	Res	Type
1	A	1320	C
1	A	1346	A
1	A	1347	G
1	A	1348	U
1	A	1353	G
1	A	1359	C
1	A	1362	C
1	A	1364	U
1	A	1368	G
1	A	1379	G
1	A	1381	U
1	A	1394	A
1	A	1398	A
1	A	1400	5MC
1	A	1401	G
1	A	1402	4OC
1	A	1442	G
1	A	1446	A
1	A	1447	G
1	A	1487	G
1	A	1493	A
1	A	1494	G
1	A	1497	G
1	A	1499	A
1	A	1503	A
1	A	1504	G
1	A	1506	U
1	A	1529	G
1	A	1530	G
1	A	1540	PSU

All (45) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	5	U
1	A	115	G
1	A	129(A)	G
1	A	181	G
1	A	204	U
1	A	243	A
1	A	250	A
1	A	251	G

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Mol	Chain	Res	Type
1	A	281	G
1	A	328	C
1	A	372	C
1	A	428	G
1	A	429	U
1	A	484	G
1	A	485	G
1	A	496	A
1	A	509	A
1	A	518	C
1	A	559	A
1	A	687	A
1	A	701	C
1	A	748	C
1	A	792	A
1	A	812	C
1	A	913	A
1	A	960	U
1	A	975	A
1	A	992	U
1	A	1065	U
1	A	1067	A
1	A	1139	G
1	A	1182	G
1	A	1183	A
1	A	1190	G
1	A	1201	A
1	A	1256	A
1	A	1257	U
1	A	1285	A
1	A	1300	G
1	A	1301	U
1	A	1305	G
1	A	1346	A
1	A	1347	G
1	A	1380	U
1	A	1505	G

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MC	A	1404	1	19,22,23	0.96	1 (5%)	26,32,35	0.95	2 (7%)
1	M2G	A	966	1	24,27,28	1.19	4 (16%)	33,40,43	0.81	1 (3%)
1	4OC	A	1402	1	20,23,24	0.93	2 (10%)	25,32,35	0.86	1 (4%)
1	MA6	A	1518	1	23,26,27	1.17	2 (8%)	33,38,41	0.85	0
12	0TD	L	92	12	8,9,10	1.32	1 (12%)	6,11,13	2.39	3 (50%)
1	5MC	A	1407	1	19,22,23	0.98	1 (5%)	26,32,35	1.06	2 (7%)
1	2MG	A	1207	1	23,26,27	1.39	6 (26%)	33,38,41	1.14	5 (15%)
1	PSU	A	1541	1	18,21,22	1.13	1 (5%)	21,30,33	1.85	4 (19%)
1	PSU	A	516	23,1	18,21,22	1.13	1 (5%)	21,30,33	1.93	5 (23%)
1	PSU	A	1540	23,1	18,21,22	1.12	1 (5%)	21,30,33	1.81	4 (19%)
1	MA6	A	1519	1	23,26,27	1.22	3 (13%)	33,38,41	0.84	1 (3%)
1	UR3	A	1498	1	19,22,23	0.42	0	26,32,35	0.84	0
1	5MC	A	1400	1	19,22,23	1.10	3 (15%)	26,32,35	1.01	2 (7%)
1	5MC	A	967	1	19,22,23	0.97	1 (5%)	26,32,35	0.92	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	5MC	A	1404	1	-	0/7/25/26	0/2/2/2
1	M2G	A	966	1	-	3/11/29/30	0/3/3/3
1	4OC	A	1402	1	-	2/9/29/30	0/2/2/2
1	MA6	A	1518	1	-	3/11/29/30	0/3/3/3
12	0TD	L	92	12	-	2/7/12/14	-
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
1	2MG	A	1207	1	-	0/9/27/28	0/3/3/3
1	PSU	A	1541	1	-	0/7/25/26	0/2/2/2
1	PSU	A	516	23,1	-	0/7/25/26	0/2/2/2
1	PSU	A	1540	23,1	-	2/7/25/26	0/2/2/2
1	MA6	A	1519	1	-	3/11/29/30	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
1	5MC	A	1400	1	-	2/7/25/26	0/2/2/2
1	5MC	A	967	1	-	1/7/25/26	0/2/2/2

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1541	PSU	C6-C5	3.77	1.39	1.35
1	A	1540	PSU	C6-C5	3.71	1.39	1.35
1	A	516	PSU	C6-C5	3.63	1.39	1.35
1	A	1207	2MG	C2-N2	3.20	1.40	1.33
1	A	966	M2G	C2-N2	3.01	1.40	1.35
1	A	1207	2MG	C2-N1	2.86	1.41	1.36
1	A	1519	MA6	C5-C4	2.80	1.44	1.39
1	A	1518	MA6	C5-C4	2.73	1.44	1.39
1	A	1400	5MC	C2-N1	2.73	1.45	1.40
1	A	966	M2G	C4-N3	2.67	1.40	1.34
12	L	92	0TD	CB-CA	-2.62	1.53	1.54
1	A	1407	5MC	C2-N1	2.54	1.45	1.40
1	A	1519	MA6	C8-N9	2.46	1.41	1.37
1	A	1518	MA6	C8-N9	2.42	1.41	1.37
1	A	1207	2MG	C8-N9	2.41	1.42	1.37
1	A	1207	2MG	C4-N3	2.40	1.39	1.34
1	A	1402	4OC	C2-N3	2.39	1.41	1.36
1	A	967	5MC	C2-N3	2.32	1.41	1.36
1	A	966	M2G	C8-N9	2.29	1.42	1.37
1	A	1400	5MC	C6-C5	2.27	1.38	1.34
1	A	1402	4OC	C2-N1	2.22	1.44	1.40
1	A	1207	2MG	C6-N1	2.11	1.42	1.38
1	A	1400	5MC	C2-N3	2.08	1.40	1.36
1	A	966	M2G	C6-N1	2.08	1.42	1.38
1	A	1519	MA6	C2-N1	2.05	1.37	1.33
1	A	1404	5MC	C2-N1	2.05	1.44	1.40
1	A	1207	2MG	C2-N3	2.04	1.35	1.32

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	516	PSU	C4-N3-C2	-4.83	119.72	126.37
1	A	516	PSU	N1-C2-N3	4.82	120.25	115.17
1	A	1541	PSU	C4-N3-C2	-4.65	119.97	126.37
1	A	1541	PSU	N1-C2-N3	4.61	120.03	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1540	PSU	C4-N3-C2	-4.57	120.07	126.37
1	A	1540	PSU	N1-C2-N3	4.52	119.94	115.17
12	L	92	0TD	CSB-SB-CB	-4.47	94.32	102.36
1	A	1207	2MG	C5-C4-N3	-2.81	123.91	128.39
1	A	1541	PSU	O2-C2-N1	-2.77	119.93	122.79
1	A	1540	PSU	O2-C2-N1	-2.60	120.11	122.79
1	A	1540	PSU	C6-N1-C2	-2.57	120.31	122.69
1	A	1207	2MG	N9-C4-N3	2.53	131.01	125.95
1	A	1407	5MC	N4-C4-N3	-2.51	113.97	118.51
1	A	516	PSU	O2-C2-N1	-2.50	120.21	122.79
1	A	516	PSU	C6-N1-C2	-2.49	120.38	122.69
12	L	92	0TD	OD1-CG-CB	-2.44	117.33	122.44
1	A	1541	PSU	C6-N1-C2	-2.40	120.47	122.69
1	A	1404	5MC	N4-C4-N3	-2.37	114.21	118.51
1	A	1400	5MC	N4-C4-N3	-2.37	114.22	118.51
1	A	1207	2MG	O6-C6-N1	-2.34	115.71	120.11
1	A	1407	5MC	C5-C4-N3	2.33	124.15	121.75
1	A	967	5MC	N4-C4-N3	-2.25	114.44	118.51
1	A	1404	5MC	C5-C4-N3	2.23	124.05	121.75
12	L	92	0TD	O-C-CA	-2.16	119.20	124.77
1	A	516	PSU	O4'-C1'-C2'	2.15	108.13	105.15
1	A	966	M2G	C5-C4-N3	-2.14	124.99	128.39
1	A	967	5MC	C5-C4-N3	2.13	123.94	121.75
1	A	1207	2MG	C2-N1-C6	-2.13	121.97	124.55
1	A	1400	5MC	C5-C4-N3	2.12	123.93	121.75
1	A	1402	4OC	C5-C4-N4	-2.08	117.83	122.40
1	A	1519	MA6	C2-N1-C6	2.06	116.86	111.83
1	A	1207	2MG	C6-C5-N7	-2.00	126.65	130.29

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	966	M2G	N1-C2-N2-CM1
1	A	1400	5MC	O4'-C4'-C5'-O5'
1	A	1402	4OC	O4'-C4'-C5'-O5'
1	A	1518	MA6	C5-C6-N6-C9
1	A	1519	MA6	C5-C6-N6-C9
1	A	1402	4OC	C3'-C4'-C5'-O5'
1	A	1518	MA6	N1-C6-N6-C9
1	A	1519	MA6	N1-C6-N6-C9
1	A	1400	5MC	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
12	L	92	0TD	CG-CB-SB-CSB
1	A	1540	PSU	O4'-C4'-C5'-O5'
12	L	92	0TD	SB-CB-CG-OD1
1	A	1518	MA6	C5-C6-N6-C10
1	A	1519	MA6	C5-C6-N6-C10
1	A	966	M2G	N3-C2-N2-CM1
1	A	966	M2G	N1-C2-N2-CM2
1	A	967	5MC	O4'-C4'-C5'-O5'
1	A	1540	PSU	C4'-C5'-O5'-P

There are no ring outliers.

9 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1404	5MC	1	0
1	A	1402	4OC	3	0
1	A	1518	MA6	1	0
12	L	92	0TD	3	0
1	A	1407	5MC	1	0
1	A	1519	MA6	2	0
1	A	1498	UR3	1	0
1	A	1400	5MC	1	0
1	A	967	5MC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 244 ligands modelled in this entry, 243 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	SRY	A	1601	-	40,42,42	2.38	11 (27%)	49,63,63	1.85	9 (18%)

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
22	SRY	A	1601	-	-	3/20/87/87	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	A	1601	SRY	CD1-N31	8.65	1.48	1.33
22	A	1601	SRY	CA1-N11	7.08	1.45	1.33
22	A	1601	SRY	O53-C53	-3.79	1.35	1.44
22	A	1601	SRY	C23-N23	-2.95	1.42	1.47
22	A	1601	SRY	O32-C32	-2.89	1.39	1.44
22	A	1601	SRY	CA1-NB1	2.86	1.44	1.34
22	A	1601	SRY	CD1-NE1	2.77	1.44	1.34
22	A	1601	SRY	C32-CG2	-2.76	1.47	1.52
22	A	1601	SRY	C21-C11	-2.65	1.48	1.53
22	A	1601	SRY	O51-C51	-2.62	1.36	1.43
22	A	1601	SRY	O43-C43	-2.04	1.37	1.43

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	A	1601	SRY	C13-O13-C22	-5.58	106.77	116.26
22	A	1601	SRY	O13-C13-C23	4.99	116.17	108.07
22	A	1601	SRY	C12-O42-C42	-4.83	100.68	108.48
22	A	1601	SRY	CI3-N23-C23	-3.79	109.34	114.23
22	A	1601	SRY	O41-C12-O42	-3.62	107.67	111.37
22	A	1601	SRY	C12-O41-C41	-2.92	111.06	117.98
22	A	1601	SRY	C61-C11-N11	-2.71	105.63	110.62
22	A	1601	SRY	C13-O53-C53	-2.61	108.62	113.72
22	A	1601	SRY	OG2-CG2-C32	-2.16	119.21	124.17

There are no chirality outliers.

All (3) torsion outliers are listed below:

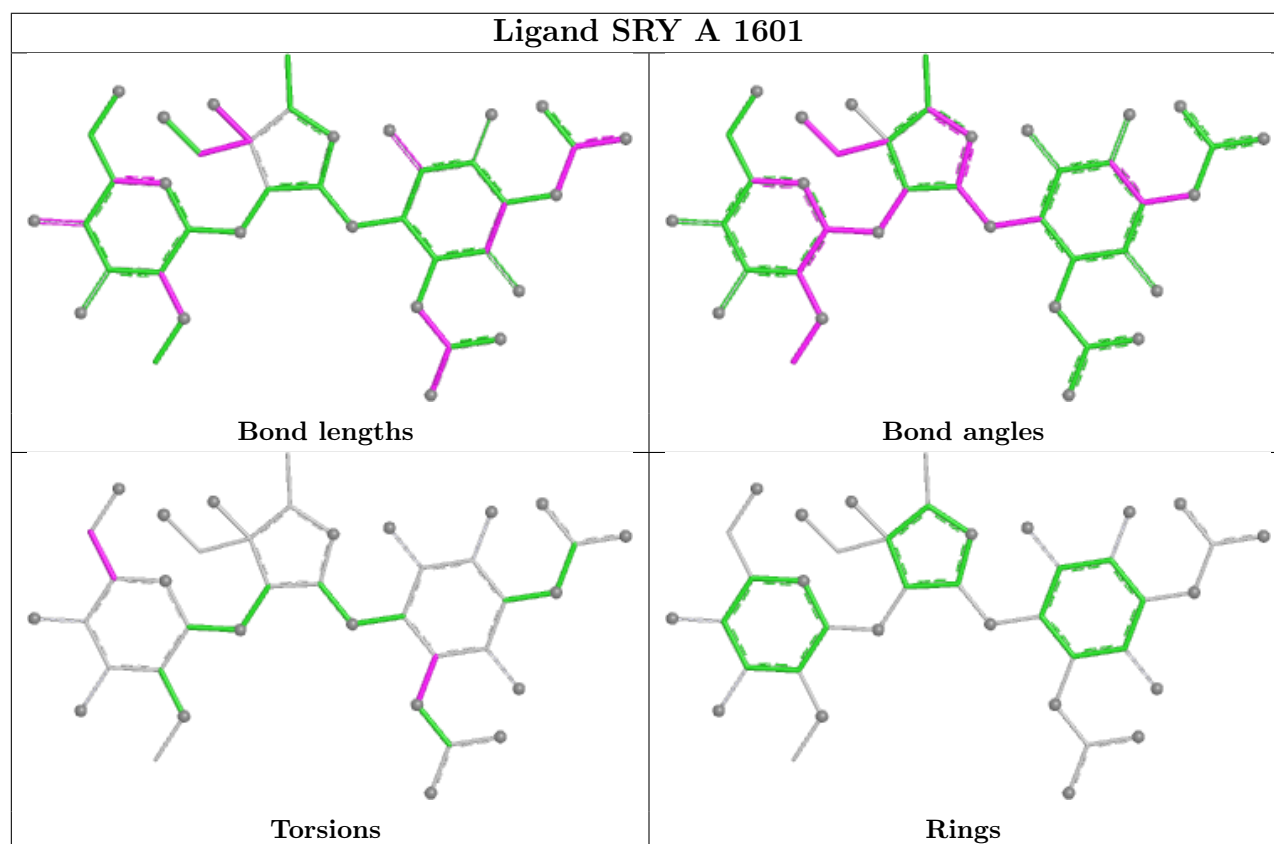
Mol	Chain	Res	Type	Atoms
22	A	1601	SRY	O53-C53-C63-O63
22	A	1601	SRY	C43-C53-C63-O63
22	A	1601	SRY	C21-C31-N31-CD1

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	A	1601	SRY	4	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	1499/1522 (98%)	0.02	37 (2%) 58 32	85, 130, 271, 382	0
2	B	234/256 (91%)	-0.17	4 (1%) 69 40	98, 143, 227, 240	0
3	C	206/239 (86%)	0.21	7 (3%) 48 26	148, 207, 271, 304	0
4	D	208/209 (99%)	0.05	9 (4%) 40 20	90, 127, 171, 259	0
5	E	150/162 (92%)	-0.25	1 (0%) 84 60	77, 106, 136, 201	0
6	F	101/101 (100%)	-0.45	0 100 100	119, 143, 167, 214	0
7	G	155/156 (99%)	-0.01	3 (1%) 66 38	135, 180, 230, 263	0
8	H	138/138 (100%)	-0.39	0 100 100	70, 93, 121, 166	0
9	I	127/128 (99%)	0.36	7 (5%) 30 16	136, 204, 249, 303	0
10	J	98/105 (93%)	0.46	2 (2%) 65 36	164, 247, 326, 391	0
11	K	116/129 (89%)	-0.03	1 (0%) 81 55	96, 124, 170, 203	0
12	L	123/135 (91%)	0.01	4 (3%) 49 26	75, 128, 151, 199	0
13	M	118/126 (93%)	0.03	5 (4%) 40 20	127, 156, 192, 327	0
14	N	60/61 (98%)	0.71	6 (10%) 12 8	165, 197, 252, 298	0
15	O	87/89 (97%)	-0.29	1 (1%) 78 51	85, 113, 150, 163	0
16	P	83/88 (94%)	-0.11	0 100 100	104, 124, 153, 198	0
17	Q	99/105 (94%)	-0.18	0 100 100	85, 104, 135, 167	0
18	R	70/88 (79%)	-0.32	0 100 100	96, 124, 170, 215	0
19	S	80/93 (86%)	0.68	9 (11%) 10 6	159, 221, 278, 327	0
20	T	99/106 (93%)	0.09	5 (5%) 33 18	103, 119, 155, 199	0
21	U	24/27 (88%)	0.89	4 (16%) 4 4	141, 172, 202, 216	0
All	All	3875/4063 (95%)	0.01	105 (2%) 56 30	70, 137, 253, 391	0

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	793	U	6.4
19	S	35	SER	5.9
4	D	9	CYS	5.5
9	I	9	ARG	5.4
4	D	2	GLY	5.0
4	D	31	CYS	5.0
1	A	1129	C	4.8
19	S	3	ARG	4.7
4	D	3	ARG	4.5
20	T	106	ALA	4.1
13	M	7	VAL	4.1
9	I	128	ARG	4.1
10	J	37	PRO	4.0
13	M	8	GLU	3.8
1	A	78	G	3.8
4	D	22	LYS	3.5
1	A	81	U	3.5
1	A	202	U	3.5
3	C	103	VAL	3.5
1	A	1220	G	3.5
4	D	26	CYS	3.5
1	A	792	A	3.4
2	B	96	ARG	3.4
1	A	983	A	3.3
9	I	15	ALA	3.2
1	A	1219	U	3.2
14	N	3	ARG	3.2
12	L	73	GLU	3.2
21	U	6	ARG	3.2
19	S	34	TRP	3.1
19	S	37	ARG	3.1
2	B	16	HIS	3.1
3	C	66	VAL	3.0
1	A	985	C	3.0
1	A	992	U	3.0
1	A	979	C	3.0
12	L	47	LYS	2.9
1	A	1145	C	2.9
4	D	4	TYR	2.9
1	A	794	A	2.9
1	A	1493	A	2.9
1	A	984	C	2.9
1	A	77	G	2.9

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Mol	Chain	Res	Type	RSRZ
4	D	21	LEU	2.8
9	I	127	LYS	2.8
19	S	2	PRO	2.8
3	C	193	TYR	2.8
1	A	79	G	2.8
21	U	18	TYR	2.8
1	A	80	G	2.7
9	I	66	ARG	2.7
19	S	36	ARG	2.7
3	C	68	VAL	2.7
4	D	12	CYS	2.7
14	N	6	LEU	2.7
20	T	11	SER	2.7
1	A	532	A	2.7
3	C	2	GLY	2.7
1	A	92	C	2.7
11	K	56	GLY	2.7
7	G	5	ARG	2.5
21	U	10	ARG	2.5
13	M	106	ASN	2.5
7	G	4	ARG	2.5
19	S	4	SER	2.5
1	A	1221	G	2.5
1	A	1539	C	2.4
1	A	1144	G	2.4
1	A	1531	A	2.4
21	U	25	LYS	2.4
1	A	372	C	2.3
3	C	192	THR	2.3
2	B	22	LYS	2.3
13	M	102	ARG	2.3
14	N	21	TYR	2.3
1	A	1052	U	2.3
10	J	70	ARG	2.3
12	L	26	ALA	2.3
1	A	1128	C	2.3
2	B	72	GLY	2.2
20	T	9	ASN	2.2
5	E	154	GLY	2.2
9	I	126	SER	2.2
1	A	1254	C	2.2
15	O	23	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1147	C	2.2
20	T	68	LYS	2.2
19	S	70	LYS	2.1
1	A	1004	A	2.1
14	N	5	ALA	2.1
1	A	1037	C	2.1
14	N	4	LYS	2.1
1	A	723	U	2.1
1	A	1216	G	2.1
12	L	86	ARG	2.1
14	N	31	ARG	2.1
3	C	168	ALA	2.1
1	A	1006	C	2.0
1	A	1200	C	2.0
1	A	1139	G	2.0
20	T	101	GLY	2.0
13	M	10	PRO	2.0
19	S	71	LEU	2.0
9	I	110	GLU	2.0
7	G	33	ASP	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($\text{\AA}^2$)	Q<0.9
1	PSU	A	1541	20/21	0.68	0.25	288,305,333,335	0
1	PSU	A	1540	20/21	0.85	0.17	279,294,305,305	0
12	0TD	L	92	10/11	0.92	0.15	122,125,128,294	0
1	MA6	A	1518	24/25	0.93	0.09	122,126,137,140	0
1	5MC	A	967	21/22	0.94	0.08	119,121,126,126	0
1	5MC	A	1407	21/22	0.94	0.09	132,139,146,152	0
1	M2G	A	966	25/26	0.95	0.09	123,127,159,162	0
1	UR3	A	1498	21/22	0.95	0.16	120,124,127,129	0
1	PSU	A	516	20/21	0.95	0.08	131,135,144,144	0
1	MA6	A	1519	24/25	0.95	0.10	118,122,123,128	0
1	2MG	A	1207	24/25	0.95	0.15	201,210,224,228	0
1	5MC	A	1400	21/22	0.95	0.10	116,122,125,126	0
1	5MC	A	1404	21/22	0.95	0.13	119,121,132,135	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	0.10	120,124,130,131	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
23	MG	A	1806	1/1	0.44	0.15	334,334,334,334	0
23	MG	A	1762	1/1	0.54	0.27	110,110,110,110	0
23	MG	A	1740	1/1	0.61	0.64	99,99,99,99	0
23	MG	A	1793	1/1	0.63	0.22	100,100,100,100	0
23	MG	N	102	1/1	0.63	0.14	96,96,96,96	0
23	MG	A	1760	1/1	0.67	0.18	128,128,128,128	0
23	MG	A	1713	1/1	0.70	0.28	121,121,121,121	0
23	MG	A	1795	1/1	0.70	0.30	108,108,108,108	0
23	MG	A	1789	1/1	0.71	0.20	81,81,81,81	0
23	MG	A	1805	1/1	0.71	0.24	108,108,108,108	0
23	MG	A	1667	1/1	0.72	0.10	141,141,141,141	0
23	MG	A	1726	1/1	0.73	0.44	106,106,106,106	0
23	MG	A	1680	1/1	0.75	0.29	139,139,139,139	0
23	MG	A	1670	1/1	0.77	0.10	170,170,170,170	0
23	MG	A	1751	1/1	0.77	0.41	94,94,94,94	0
23	MG	A	1823	1/1	0.77	0.20	127,127,127,127	0
23	MG	A	1783	1/1	0.77	0.09	129,129,129,129	0
23	MG	A	1741	1/1	0.78	0.14	96,96,96,96	0
23	MG	A	1821	1/1	0.78	0.19	106,106,106,106	0
23	MG	A	1785	1/1	0.78	0.13	304,304,304,304	0
23	MG	A	1732	1/1	0.78	0.12	73,73,73,73	0
23	MG	A	1752	1/1	0.79	0.28	110,110,110,110	0
23	MG	A	1779	1/1	0.79	0.12	139,139,139,139	0
23	MG	A	1727	1/1	0.79	0.37	92,92,92,92	0
23	MG	A	1747	1/1	0.80	0.23	89,89,89,89	0
23	MG	A	1776	1/1	0.80	0.32	106,106,106,106	0
23	MG	A	1812	1/1	0.80	0.18	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
23	MG	A	1688	1/1	0.81	0.14	135,135,135,135	0
23	MG	A	1815	1/1	0.81	0.10	108,108,108,108	0
23	MG	A	1678	1/1	0.81	0.12	91,91,91,91	0
23	MG	A	1718	1/1	0.81	0.11	90,90,90,90	0
23	MG	A	1735	1/1	0.81	0.08	74,74,74,74	0
23	MG	A	1811	1/1	0.82	0.12	122,122,122,122	0
23	MG	A	1822	1/1	0.82	0.34	104,104,104,104	0
23	MG	A	1772	1/1	0.82	0.28	107,107,107,107	0
23	MG	A	1708	1/1	0.82	0.14	111,111,111,111	0
23	MG	A	1723	1/1	0.83	0.20	72,72,72,72	0
23	MG	A	1807	1/1	0.83	0.08	222,222,222,222	0
23	MG	H	202	1/1	0.83	0.08	57,57,57,57	0
23	MG	H	203	1/1	0.83	0.11	76,76,76,76	0
23	MG	A	1730	1/1	0.83	0.17	148,148,148,148	0
23	MG	A	1627	1/1	0.84	0.10	76,76,76,76	0
23	MG	A	1707	1/1	0.84	0.09	120,120,120,120	0
23	MG	A	1640	1/1	0.84	0.32	102,102,102,102	0
23	MG	A	1602	1/1	0.84	0.10	112,112,112,112	0
23	MG	A	1729	1/1	0.84	0.36	124,124,124,124	0
23	MG	A	1774	1/1	0.85	0.21	79,79,79,79	0
23	MG	A	1620	1/1	0.85	0.14	85,85,85,85	0
23	MG	A	1797	1/1	0.85	0.23	75,75,75,75	0
23	MG	A	1603	1/1	0.85	0.12	90,90,90,90	0
23	MG	A	1675	1/1	0.85	0.17	119,119,119,119	0
23	MG	A	1628	1/1	0.85	0.09	99,99,99,99	0
23	MG	A	1810	1/1	0.85	0.10	433,433,433,433	0
23	MG	A	1611	1/1	0.85	0.14	104,104,104,104	0
23	MG	A	1706	1/1	0.86	0.56	114,114,114,114	0
23	MG	A	1764	1/1	0.86	0.21	146,146,146,146	0
23	MG	B	301	1/1	0.86	0.15	120,120,120,120	0
23	MG	A	1682	1/1	0.86	0.30	107,107,107,107	0
23	MG	A	1820	1/1	0.86	0.16	83,83,83,83	0
23	MG	A	1798	1/1	0.86	0.10	85,85,85,85	0
23	MG	P	102	1/1	0.86	0.08	80,80,80,80	0
23	MG	A	1698	1/1	0.87	0.11	85,85,85,85	0
23	MG	A	1771	1/1	0.87	0.12	76,76,76,76	0
23	MG	A	1715	1/1	0.87	0.14	110,110,110,110	0
23	MG	A	1676	1/1	0.87	0.07	157,157,157,157	0
23	MG	A	1721	1/1	0.87	0.14	100,100,100,100	0
23	MG	A	1709	1/1	0.87	0.15	172,172,172,172	0
23	MG	A	1816	1/1	0.87	0.13	132,132,132,132	0
23	MG	A	1710	1/1	0.87	0.07	168,168,168,168	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
23	MG	Q	202	1/1	0.87	0.08	55,55,55,55	0
23	MG	A	1630	1/1	0.88	0.12	79,79,79,79	0
23	MG	A	1637	1/1	0.88	0.32	81,81,81,81	0
23	MG	A	1618	1/1	0.88	0.25	73,73,73,73	0
23	MG	A	1781	1/1	0.88	0.07	119,119,119,119	0
23	MG	A	1683	1/1	0.88	0.24	91,91,91,91	0
23	MG	A	1742	1/1	0.88	0.22	97,97,97,97	0
23	MG	A	1769	1/1	0.88	0.11	102,102,102,102	0
23	MG	A	1790	1/1	0.88	0.33	78,78,78,78	0
23	MG	A	1746	1/1	0.88	0.10	100,100,100,100	0
23	MG	A	1649	1/1	0.88	0.09	67,67,67,67	0
23	MG	A	1763	1/1	0.89	0.33	106,106,106,106	0
23	MG	A	1800	1/1	0.89	0.18	131,131,131,131	0
23	MG	A	1719	1/1	0.89	0.59	95,95,95,95	0
23	MG	A	1767	1/1	0.89	0.15	104,104,104,104	0
23	MG	A	1824	1/1	0.89	0.12	104,104,104,104	0
23	MG	A	1827	1/1	0.89	0.08	74,74,74,74	0
23	MG	A	1768	1/1	0.89	0.11	79,79,79,79	0
23	MG	H	201	1/1	0.89	0.10	56,56,56,56	0
23	MG	A	1674	1/1	0.89	0.12	68,68,68,68	0
23	MG	A	1694	1/1	0.89	0.20	144,144,144,144	0
23	MG	A	1716	1/1	0.89	0.20	68,68,68,68	0
23	MG	A	1717	1/1	0.89	0.08	109,109,109,109	0
23	MG	A	1711	1/1	0.89	0.26	90,90,90,90	0
23	MG	A	1690	1/1	0.90	0.39	95,95,95,95	0
23	MG	A	1803	1/1	0.90	0.15	92,92,92,92	0
23	MG	A	1673	1/1	0.90	0.08	88,88,88,88	0
23	MG	A	1757	1/1	0.90	0.10	84,84,84,84	0
23	MG	A	1759	1/1	0.90	0.35	70,70,70,70	0
23	MG	A	1828	1/1	0.90	0.08	91,91,91,91	0
23	MG	A	1808	1/1	0.90	0.10	205,205,205,205	0
23	MG	E	201	1/1	0.90	0.09	83,83,83,83	0
23	MG	A	1714	1/1	0.90	0.09	110,110,110,110	0
23	MG	A	1679	1/1	0.90	0.06	121,121,121,121	0
23	MG	A	1655	1/1	0.90	0.15	116,116,116,116	0
23	MG	A	1777	1/1	0.90	0.15	83,83,83,83	0
23	MG	A	1733	1/1	0.90	0.14	82,82,82,82	0
23	MG	A	1799	1/1	0.90	0.22	79,79,79,79	0
23	MG	T	201	1/1	0.90	0.14	87,87,87,87	0
23	MG	A	1654	1/1	0.91	0.14	115,115,115,115	0
23	MG	A	1720	1/1	0.91	0.25	82,82,82,82	0
23	MG	A	1749	1/1	0.91	0.18	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
23	MG	A	1689	1/1	0.91	0.10	105,105,105,105	0
23	MG	A	1669	1/1	0.91	0.20	104,104,104,104	0
23	MG	A	1754	1/1	0.91	0.15	106,106,106,106	0
23	MG	A	1775	1/1	0.91	0.06	116,116,116,116	0
23	MG	A	1802	1/1	0.91	0.26	101,101,101,101	0
23	MG	A	1737	1/1	0.91	0.33	73,73,73,73	0
23	MG	A	1738	1/1	0.91	0.22	86,86,86,86	0
23	MG	A	1653	1/1	0.91	0.11	87,87,87,87	0
23	MG	A	1695	1/1	0.91	0.08	273,273,273,273	0
23	MG	A	1658	1/1	0.91	0.09	190,190,190,190	0
23	MG	A	1744	1/1	0.91	0.22	96,96,96,96	0
23	MG	A	1787	1/1	0.91	0.11	86,86,86,86	0
23	MG	A	1788	1/1	0.91	0.10	99,99,99,99	0
23	MG	A	1765	1/1	0.91	0.19	53,53,53,53	0
23	MG	A	1656	1/1	0.92	0.09	76,76,76,76	0
23	MG	A	1609	1/1	0.92	0.10	72,72,72,72	0
23	MG	A	1660	1/1	0.92	0.23	123,123,123,123	0
23	MG	A	1665	1/1	0.92	0.16	128,128,128,128	0
23	MG	A	1770	1/1	0.92	0.09	76,76,76,76	0
23	MG	D	302	1/1	0.92	0.11	92,92,92,92	0
23	MG	A	1645	1/1	0.92	0.11	164,164,164,164	0
23	MG	A	1629	1/1	0.92	0.19	180,180,180,180	0
23	MG	A	1625	1/1	0.92	0.27	137,137,137,137	0
23	MG	A	1739	1/1	0.92	0.14	55,55,55,55	0
23	MG	A	1671	1/1	0.92	0.15	73,73,73,73	0
23	MG	A	1633	1/1	0.92	0.10	130,130,130,130	0
23	MG	A	1712	1/1	0.92	0.16	83,83,83,83	0
23	MG	A	1610	1/1	0.92	0.11	102,102,102,102	0
23	MG	A	1662	1/1	0.93	0.14	89,89,89,89	0
23	MG	A	1792	1/1	0.93	0.18	98,98,98,98	0
23	MG	A	1696	1/1	0.93	0.10	105,105,105,105	0
23	MG	A	1794	1/1	0.93	0.14	56,56,56,56	0
23	MG	A	1773	1/1	0.93	0.07	75,75,75,75	0
23	MG	A	1632	1/1	0.93	0.13	95,95,95,95	0
23	MG	A	1700	1/1	0.93	0.11	136,136,136,136	0
23	MG	A	1825	1/1	0.93	0.12	96,96,96,96	0
23	MG	A	1761	1/1	0.93	0.05	89,89,89,89	0
23	MG	A	1607	1/1	0.93	0.23	91,91,91,91	0
23	MG	A	1778	1/1	0.93	0.06	149,149,149,149	0
23	MG	A	1692	1/1	0.93	0.04	143,143,143,143	0
23	MG	A	1687	1/1	0.93	0.20	76,76,76,76	0
23	MG	A	1748	1/1	0.93	0.15	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
23	MG	A	1736	1/1	0.93	0.08	114,114,114,114	0
23	MG	A	1786	1/1	0.93	0.14	180,180,180,180	0
23	MG	A	1724	1/1	0.93	0.14	57,57,57,57	0
23	MG	A	1725	1/1	0.93	0.12	74,74,74,74	0
23	MG	A	1753	1/1	0.93	0.13	51,51,51,51	0
23	MG	A	1813	1/1	0.93	0.05	81,81,81,81	0
23	MG	U	101	1/1	0.93	0.10	129,129,129,129	0
23	MG	A	1766	1/1	0.94	0.09	105,105,105,105	0
23	MG	A	1661	1/1	0.94	0.59	91,91,91,91	0
23	MG	A	1636	1/1	0.94	0.19	76,76,76,76	0
23	MG	A	1804	1/1	0.94	0.08	78,78,78,78	0
23	MG	A	1755	1/1	0.94	0.09	73,73,73,73	0
23	MG	A	1756	1/1	0.94	0.09	94,94,94,94	0
23	MG	A	1743	1/1	0.94	0.07	70,70,70,70	0
23	MG	A	1758	1/1	0.94	0.06	81,81,81,81	0
23	MG	A	1697	1/1	0.94	0.11	171,171,171,171	0
23	MG	A	1622	1/1	0.94	0.13	110,110,110,110	0
23	MG	A	1613	1/1	0.94	0.13	102,102,102,102	0
23	MG	A	1677	1/1	0.94	0.16	126,126,126,126	0
22	SRY	A	1601	40/40	0.94	0.11	86,104,124,135	0
23	MG	A	1605	1/1	0.94	0.08	75,75,75,75	0
23	MG	A	1819	1/1	0.94	0.06	68,68,68,68	0
23	MG	A	1650	1/1	0.94	0.10	77,77,77,77	0
23	MG	A	1780	1/1	0.94	0.08	84,84,84,84	0
23	MG	A	1643	1/1	0.95	0.07	81,81,81,81	0
23	MG	A	1691	1/1	0.95	0.13	186,186,186,186	0
23	MG	A	1635	1/1	0.95	0.09	61,61,61,61	0
23	MG	A	1612	1/1	0.95	0.05	101,101,101,101	0
23	MG	A	1745	1/1	0.95	0.07	53,53,53,53	0
23	MG	A	1616	1/1	0.95	0.11	54,54,54,54	0
23	MG	A	1826	1/1	0.95	0.08	119,119,119,119	0
23	MG	A	1728	1/1	0.95	0.11	97,97,97,97	0
23	MG	A	1638	1/1	0.95	0.08	156,156,156,156	0
23	MG	A	1684	1/1	0.95	0.18	168,168,168,168	0
23	MG	A	1685	1/1	0.95	0.17	72,72,72,72	0
23	MG	A	1639	1/1	0.95	0.11	44,44,44,44	0
23	MG	A	1809	1/1	0.95	0.12	187,187,187,187	0
23	MG	A	1701	1/1	0.95	0.16	93,93,93,93	0
23	MG	A	1703	1/1	0.95	0.15	79,79,79,79	0
23	MG	M	201	1/1	0.95	0.05	91,91,91,91	0
23	MG	A	1704	1/1	0.95	0.19	76,76,76,76	0
23	MG	P	101	1/1	0.95	0.10	52,52,52,52	0

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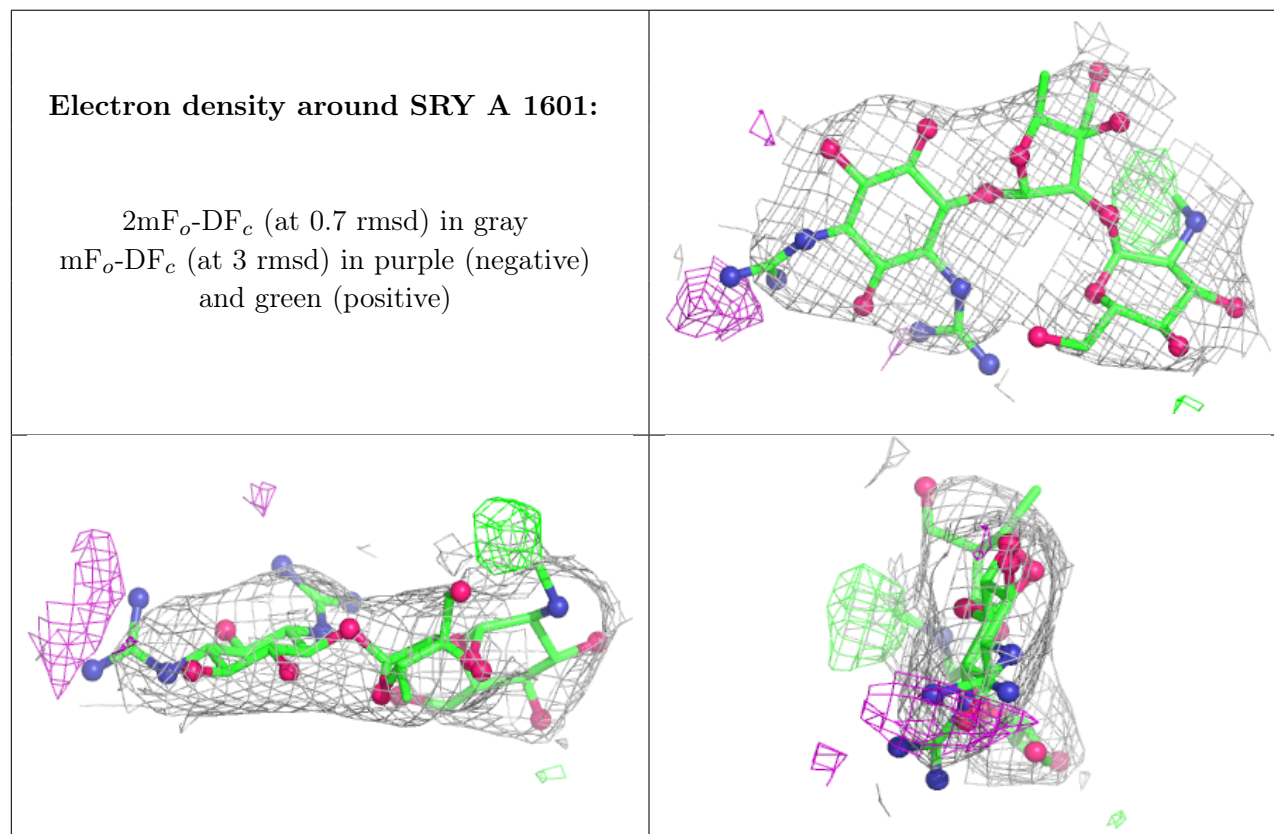
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
23	MG	A	1626	1/1	0.95	0.08	113,113,113,113	0
23	MG	A	1668	1/1	0.95	0.12	105,105,105,105	0
23	MG	A	1722	1/1	0.95	0.13	82,82,82,82	0
23	MG	A	1796	1/1	0.95	0.05	131,131,131,131	0
23	MG	A	1604	1/1	0.96	0.07	90,90,90,90	0
23	MG	A	1750	1/1	0.96	0.12	77,77,77,77	0
23	MG	A	1652	1/1	0.96	0.26	129,129,129,129	0
23	MG	A	1782	1/1	0.96	0.11	93,93,93,93	0
23	MG	A	1663	1/1	0.96	0.08	65,65,65,65	0
23	MG	A	1705	1/1	0.96	0.21	185,185,185,185	0
23	MG	A	1686	1/1	0.96	0.13	102,102,102,102	0
23	MG	A	1657	1/1	0.96	0.07	96,96,96,96	0
23	MG	A	1624	1/1	0.96	0.10	74,74,74,74	0
23	MG	Q	201	1/1	0.96	0.04	80,80,80,80	0
23	MG	A	1681	1/1	0.96	0.05	82,82,82,82	0
23	MG	A	1814	1/1	0.96	0.27	98,98,98,98	0
23	MG	A	1634	1/1	0.96	0.09	115,115,115,115	0
23	MG	A	1666	1/1	0.97	0.17	104,104,104,104	0
23	MG	A	1784	1/1	0.97	0.14	170,170,170,170	0
23	MG	A	1641	1/1	0.97	0.14	101,101,101,101	0
23	MG	A	1651	1/1	0.97	0.06	96,96,96,96	0
23	MG	A	1801	1/1	0.97	0.06	70,70,70,70	0
23	MG	A	1659	1/1	0.97	0.06	138,138,138,138	0
23	MG	A	1817	1/1	0.97	0.12	63,63,63,63	0
23	MG	A	1818	1/1	0.97	0.09	79,79,79,79	0
23	MG	A	1642	1/1	0.97	0.04	47,47,47,47	0
23	MG	A	1617	1/1	0.97	0.07	87,87,87,87	0
23	MG	A	1693	1/1	0.97	0.07	121,121,121,121	0
23	MG	A	1621	1/1	0.97	0.11	98,98,98,98	0
23	MG	A	1648	1/1	0.97	0.07	100,100,100,100	0
23	MG	A	1664	1/1	0.97	0.12	135,135,135,135	0
23	MG	A	1631	1/1	0.97	0.13	80,80,80,80	0
23	MG	A	1734	1/1	0.97	0.06	77,77,77,77	0
24	ZN	N	101	1/1	0.97	0.04	170,170,170,170	0
23	MG	A	1646	1/1	0.98	0.06	111,111,111,111	0
23	MG	A	1791	1/1	0.98	0.06	105,105,105,105	0
23	MG	A	1608	1/1	0.98	0.04	97,97,97,97	0
23	MG	A	1699	1/1	0.98	0.16	289,289,289,289	0
23	MG	A	1614	1/1	0.98	0.04	66,66,66,66	0
23	MG	A	1615	1/1	0.98	0.06	47,47,47,47	0
23	MG	A	1731	1/1	0.98	0.07	90,90,90,90	0
23	MG	A	1619	1/1	0.98	0.07	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
23	MG	A	1672	1/1	0.98	0.09	91,91,91,91	0
23	MG	A	1647	1/1	0.99	0.15	89,89,89,89	0
23	MG	A	1644	1/1	0.99	0.13	78,78,78,78	0
23	MG	A	1606	1/1	0.99	0.09	106,106,106,106	0
23	MG	A	1702	1/1	0.99	0.08	153,153,153,153	0
24	ZN	D	301	1/1	0.99	0.18	71,71,71,71	0
23	MG	A	1623	1/1	0.99	0.04	58,58,58,58	0

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



6.5 Other polymers ⓘ

There are no such residues in this entry.