



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 7, 2023 – 08:14 PM EDT

PDB ID : 6DTI
Title : Structure of the *Thermus thermophilus* 30S ribosomal subunit complexed with an unmodified anticodon stem loop (ASL) of *Escherichia coli* transfer RNA Arginine 2 (TRNAARG2) bound to an mRNA with an CGU-codon in the A-site and paromomycin
Authors : Cantara, W.A.; DeMirci, H.; Agris, P.F.
Deposited on : 2018-06-16
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](#) ①) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.35.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

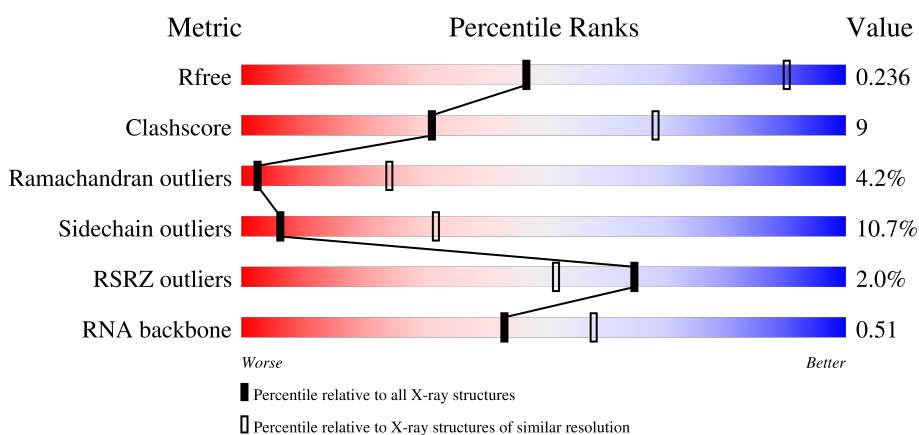
1 Overall quality at a glance

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}	130704	1028 (3.60-3.48)
Clashscore	141614	1109 (3.60-3.48)
Ramachandran outliers	138981	1073 (3.60-3.48)
Sidechain outliers	138945	1074 (3.60-3.48)
RSRZ outliers	127900	1079 (3.62-3.46)
RNA backbone	3102	1003 (4.02-3.00)

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	1507	
2	B	256	
3	C	239	
4	D	209	

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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	132	
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	V	27	
22	X	17	
23	W	6	

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
25	MG	A	1604	-	-	-	X
25	MG	A	1606	-	-	-	X
25	MG	A	1609	-	-	-	X
25	MG	A	1613	-	-	-	X
25	MG	A	1614	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	MG	A	1620	-	-	-	X
25	MG	A	1623	-	-	-	X
25	MG	A	1629	-	-	-	X
25	MG	A	1630	-	-	-	X
25	MG	A	1643	-	-	-	X
25	MG	A	1644	-	-	-	X
25	MG	A	1648	-	-	-	X
25	MG	A	1668	-	-	-	X
25	MG	A	1669	-	-	-	X
25	MG	A	1673	-	-	-	X
25	MG	A	1675	-	-	-	X
25	MG	A	1678	-	-	-	X
25	MG	A	1680	-	-	-	X
25	MG	A	1681	-	-	-	X
25	MG	A	1685	-	-	-	X
25	MG	A	1686	-	-	-	X
25	MG	A	1691	-	-	-	X
25	MG	E	201	-	-	-	X

2 Entry composition [i](#)

There are 25 unique types of molecules in this entry. The entry contains 52059 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	A	1507	32380	14414	5990	10470	1506	0	0	0

- Molecule 2 is a protein called 30S ribosomal protein S2.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	206	1612	1016	314	281	1	0	0	0

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	150	1146	724	217	201	4	0	0	0

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
9	I	127	1011	639	198	174	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	58	ARG	HIS	conflict	UNP P80374

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
10	J	98	792	498	156	137	1	0	0	0

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
12	L	124	970	611	195	163	1	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
13	M	125	997	617	207	171	2	0	0	0

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
17	Q	104	857	547	161	147	2	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	96	GLN	GLU	conflict	UNP P0DOY7

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
18	R	73	597	380	118	99	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	60	GLY	ALA	conflict	UNP Q5SLQ0

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

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

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
20	T	99	762	469	162	129	2	0	0	0

- Molecule 21 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
21	V	24	208	128	50	30	0	0	0

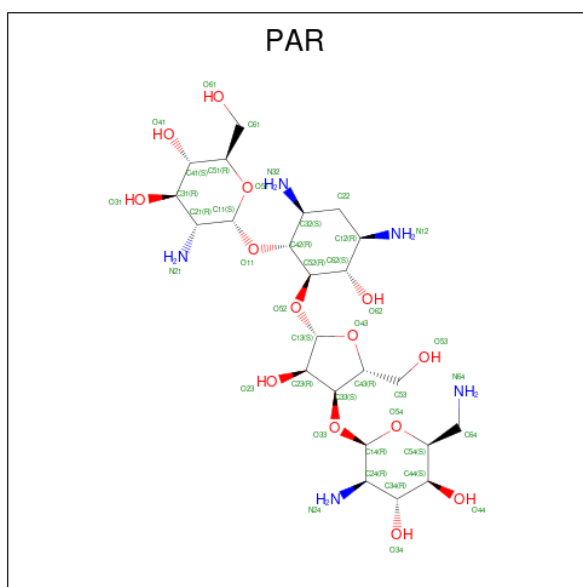
- Molecule 22 is a RNA chain called tRNA ASL Escherichia coli Arg2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
22	X	11	232	105	44	73	10	0	0	0

- Molecule 23 is a RNA chain called mRNA A-site fragment.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
23	W	4	82	38	15	26	3	0	0	0

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



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

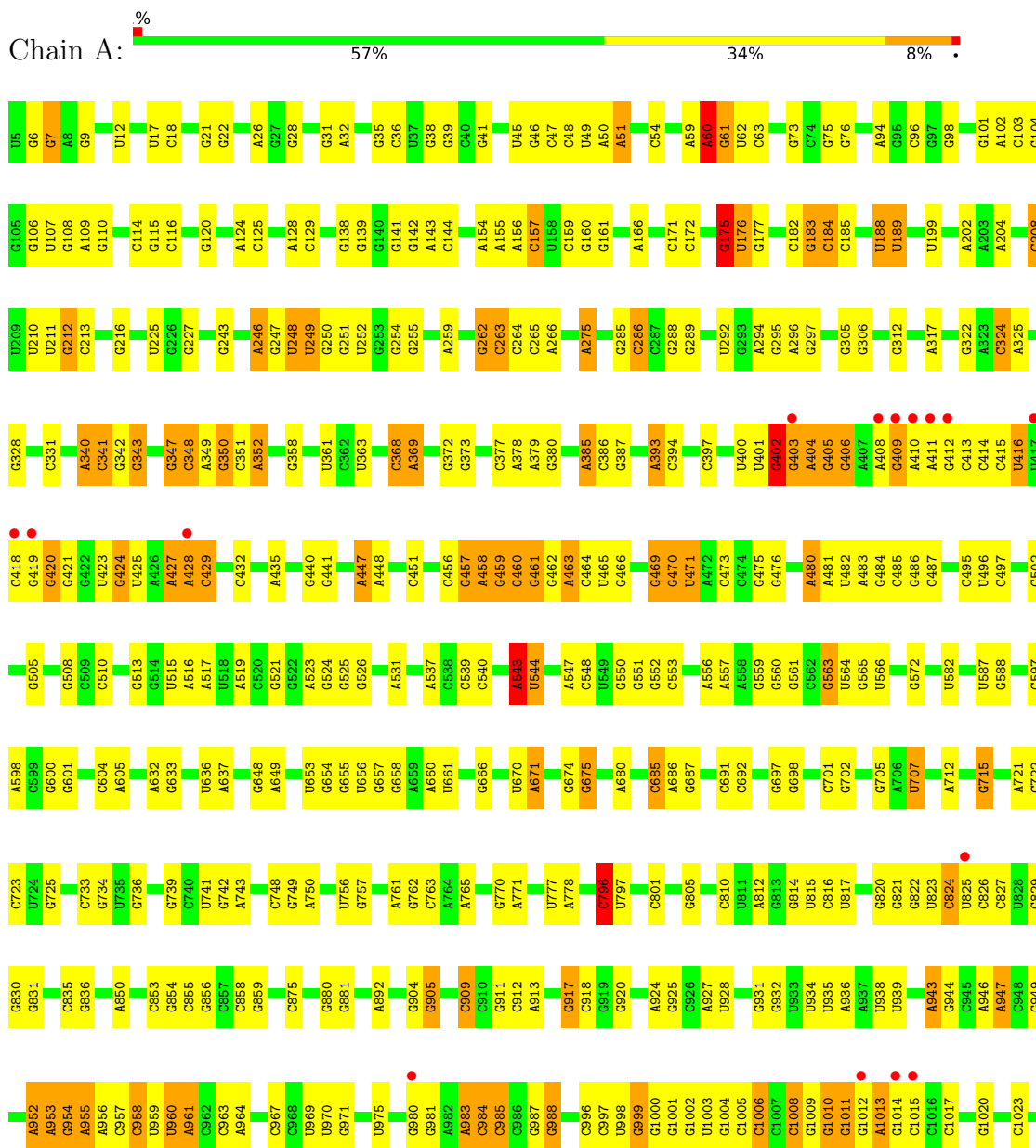
- Molecule 25 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

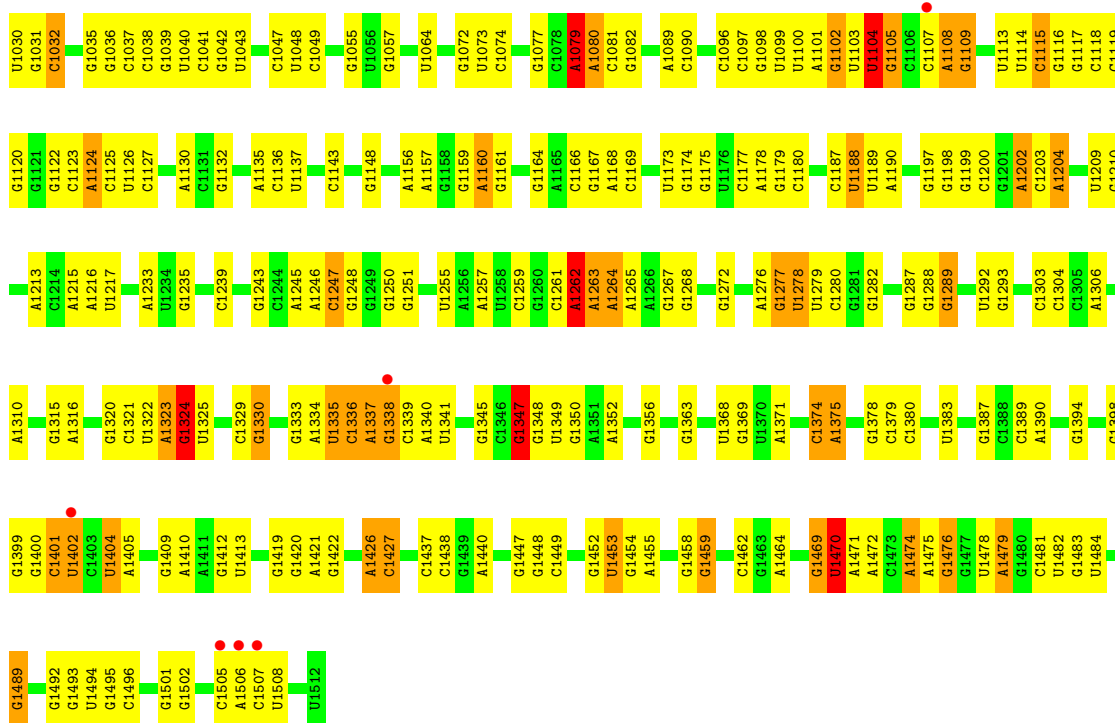
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
25	A	90	90	90	0	0
25	E	1	1	1	0	0
25	J	2	2	2	0	0
25	K	1	1	1	0	0

3 Residue-property plots [i](#)

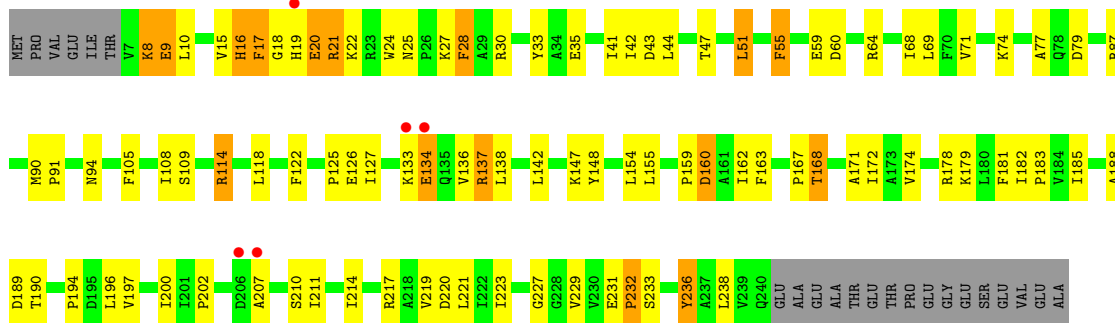
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: 16s rRNA

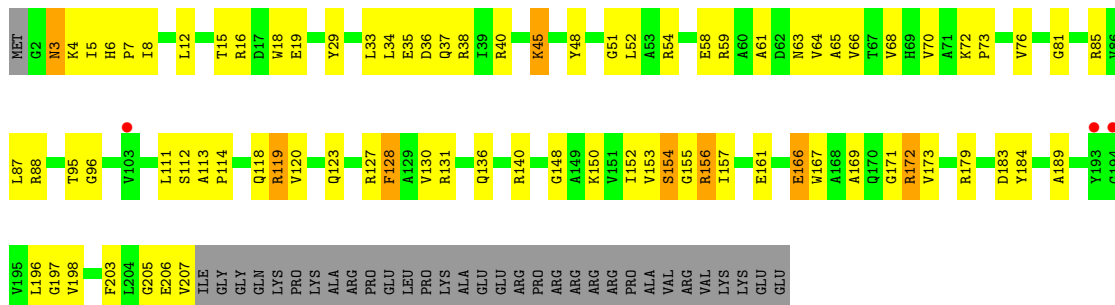




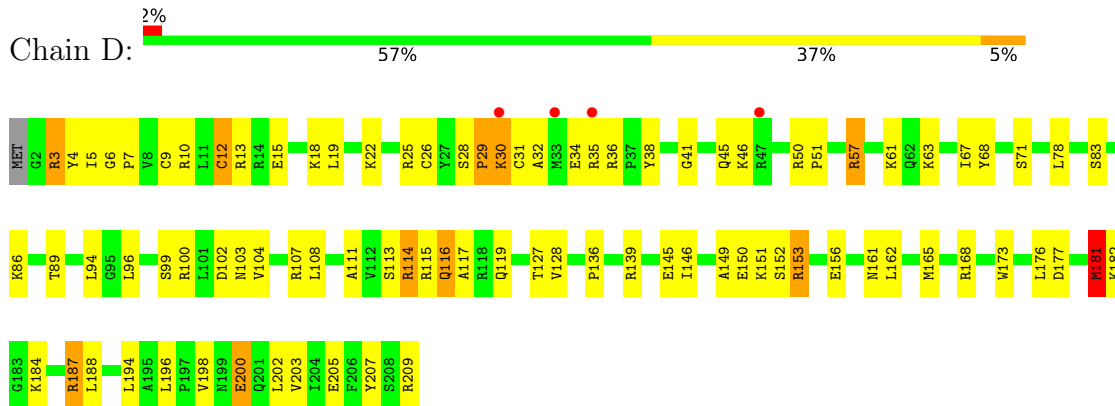
• Molecule 2: 30S ribosomal protein S2



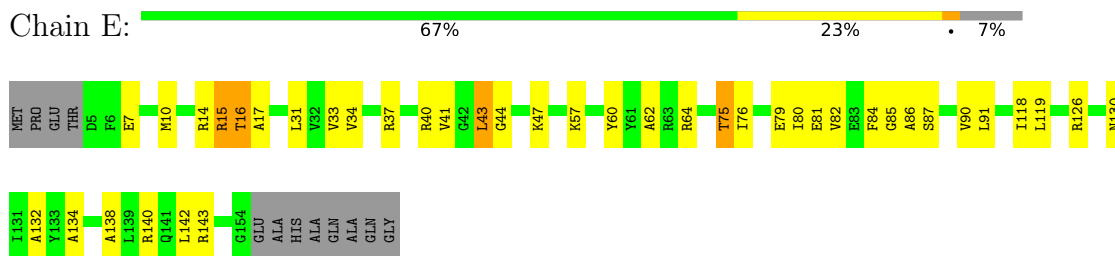
• Molecule 3: 30S ribosomal protein S3



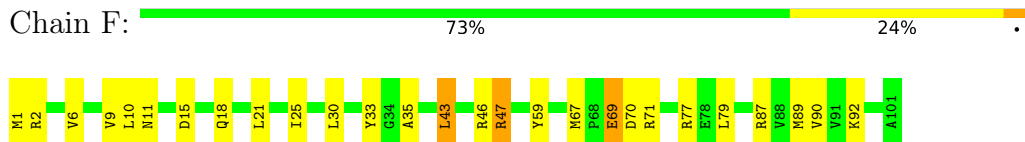
- Molecule 4: 30S ribosomal protein S4



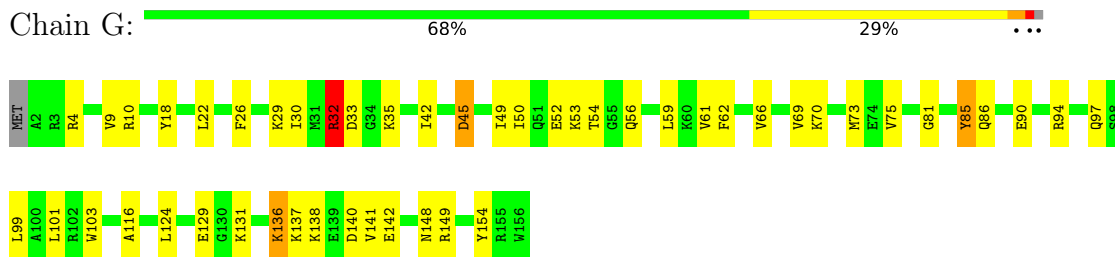
- Molecule 5: 30S ribosomal protein S5



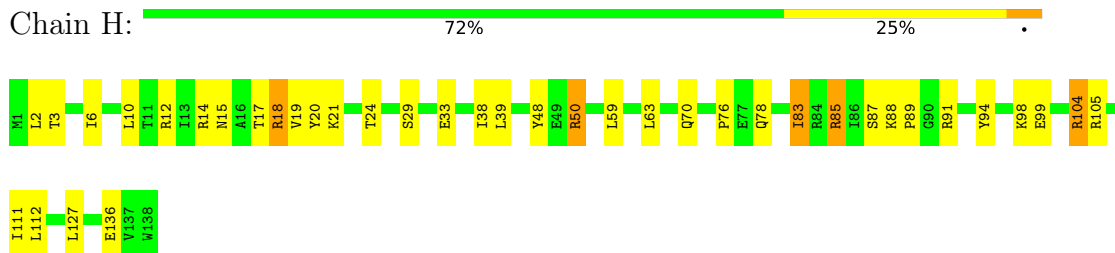
- Molecule 6: 30S ribosomal protein S6



- Molecule 7: 30S ribosomal protein S7



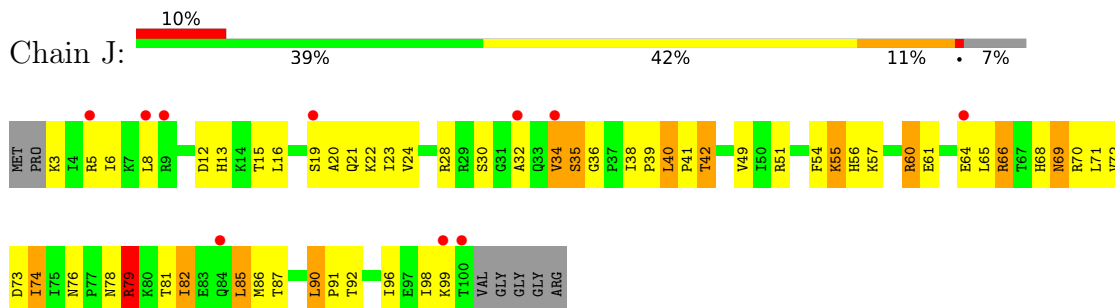
- Molecule 8: 30S ribosomal protein S8



- Molecule 9: 30S ribosomal protein S9



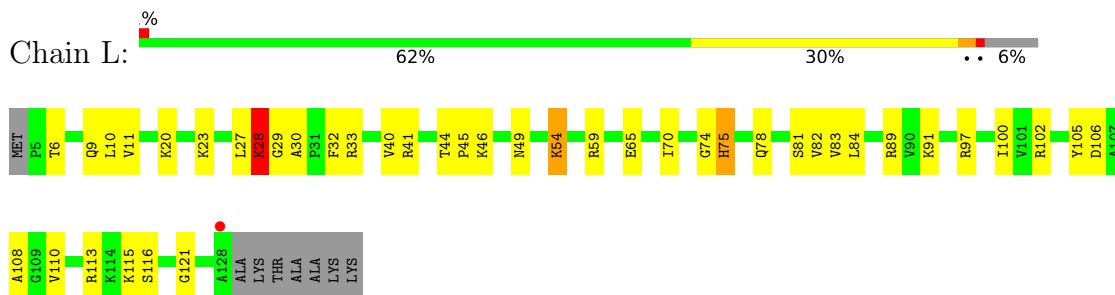
- Molecule 10: 30S ribosomal protein S10



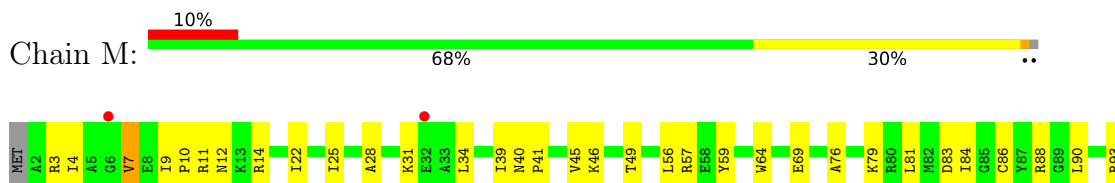
- Molecule 11: 30S ribosomal protein S11

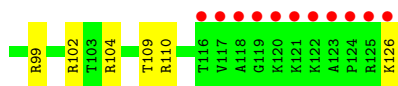


- Molecule 12: 30S ribosomal protein S12

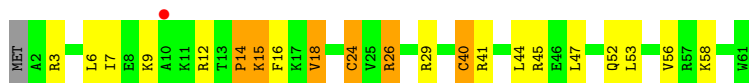


- Molecule 13: 30S ribosomal protein S13

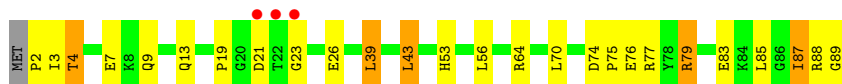




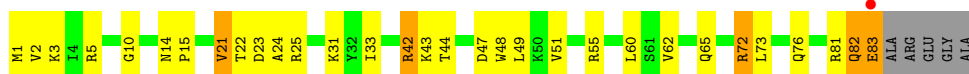
- Molecule 14: 30S ribosomal protein S14 type Z



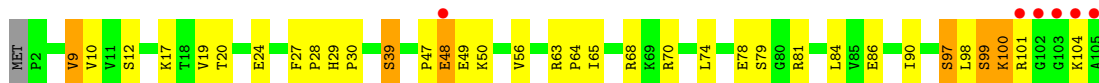
- Molecule 15: 30S ribosomal protein S15



- Molecule 16: 30S ribosomal protein S16



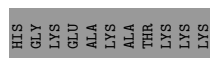
- Molecule 17: 30S ribosomal protein S17



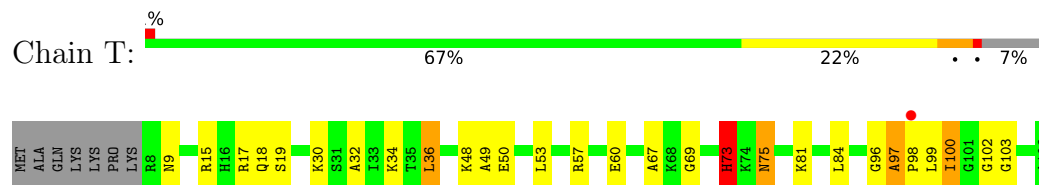
- Molecule 18: 30S ribosomal protein S18



- Molecule 19: 30S ribosomal protein S19



- Molecule 20: 30S ribosomal protein S20



- Molecule 21: 30S ribosomal protein Thx



- Molecule 22: tRNA ASL Escherichia coli Arg2



- Molecule 23: mRNA A-site fragment



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	404.54Å 404.54Å 176.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.34 – 3.54 49.34 – 3.54	Depositor EDS
% Data completeness (in resolution range)	90.4 (49.34-3.54) 92.1 (49.34-3.54)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 3.57Å)	Xtrriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.197 , 0.236 0.198 , 0.236	Depositor DCC
R_{free} test set	1894 reflections (1.16%)	wwPDB-VP
Wilson B-factor (Å ²)	138.8	Xtrriage
Anisotropy	0.010	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 101.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	52059	wwPDB-VP
Average B, all atoms (Å ²)	136.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.57% 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: PAR, MG

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	0.47	1/36244 (0.0%)	0.95	42/56567 (0.1%)
2	B	0.28	0/1935	0.50	0/2609
3	C	0.31	0/1636	0.47	0/2205
4	D	0.32	0/1733	0.49	0/2318
5	E	0.35	0/1162	0.54	0/1564
6	F	0.28	0/856	0.46	0/1154
7	G	0.28	0/1276	0.43	0/1709
8	H	0.34	0/1136	0.53	0/1527
9	I	0.29	0/1029	0.48	0/1378
10	J	0.30	0/805	0.85	2/1082 (0.2%)
11	K	0.33	0/900	0.50	0/1213
12	L	0.33	0/986	0.51	0/1320
13	M	0.28	0/1008	0.47	0/1347
14	N	0.32	0/501	0.51	0/664
15	O	0.31	0/745	0.47	0/992
16	P	0.33	0/716	0.47	0/963
17	Q	0.35	0/870	0.51	0/1159
18	R	0.30	0/603	0.47	0/799
19	S	0.26	0/661	0.49	0/890
20	T	0.32	0/764	0.48	0/1006
21	V	0.30	0/212	0.43	0/277
22	X	0.32	0/259	0.87	0/402
23	W	0.57	0/91	0.85	0/140
All	All	0.42	1/56128 (0.0%)	0.84	44/83285 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
10	J	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	275	A	N9-C4	-5.02	1.34	1.37

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	J	79	ARG	CD-NE-CZ	20.62	152.47	123.60
1	A	324	C	C6-N1-C2	-9.10	116.66	120.30
1	A	1347	G	C5-C6-N1	-7.62	107.69	111.50
1	A	402	G	C8-N9-C4	-6.93	103.63	106.40
1	A	183	G	N3-C4-N9	6.86	130.11	126.00
1	A	324	C	C5-C6-N1	6.68	124.34	121.00
1	A	1474	A	C5-N7-C8	-6.65	100.58	103.90
1	A	675	G	N1-C6-O6	6.39	123.73	119.90
1	A	1104	U	C5-C6-N1	6.37	125.89	122.70
1	A	324	C	C2-N1-C1'	6.35	125.78	118.80
1	A	1470	U	P-O3'-C3'	6.18	127.12	119.70
1	A	1474	A	C4-C5-N7	5.96	113.68	110.70
1	A	1079	A	P-O3'-C3'	5.82	126.68	119.70
1	A	324	C	N3-C2-O2	-5.72	117.89	121.90
1	A	183	G	N3-C4-C5	-5.69	125.76	128.60
1	A	110	G	N1-C6-O6	5.66	123.30	119.90
10	J	79	ARG	CB-CG-CD	-5.63	96.97	111.60
1	A	1032	C	C6-N1-C2	-5.62	118.05	120.30
1	A	404	A	C2-N3-C4	5.62	113.41	110.60
1	A	796	C	P-O3'-C3'	5.60	126.42	119.70
1	A	1323	A	P-O3'-C3'	5.56	126.37	119.70
1	A	1338	G	C4-N9-C1'	5.55	133.72	126.50
1	A	1474	A	N7-C8-N9	5.54	116.57	113.80
1	A	324	C	P-O3'-C3'	5.53	126.34	119.70
1	A	175	G	C4-N9-C1'	5.53	133.69	126.50
1	A	183	G	C4-N9-C1'	5.50	133.66	126.50
1	A	60	A	P-O3'-C3'	5.48	126.27	119.70
1	A	1032	C	C2-N1-C1'	5.46	124.81	118.80
1	A	275	A	C5-N7-C8	-5.46	101.17	103.90
1	A	324	C	N1-C2-O2	5.37	122.12	118.90
1	A	1136	C	C2-N1-C1'	5.34	124.67	118.80
1	A	1474	A	C6-C5-N7	-5.31	128.59	132.30
1	A	1262	A	P-O3'-C3'	5.30	126.06	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	543	A	C8-N9-C4	-5.28	103.69	105.80
1	A	1276	A	C6-C5-N7	-5.28	128.61	132.30
1	A	1347	G	C4-C5-C6	5.21	121.93	118.80
1	A	707	U	N1-C2-O2	5.16	126.41	122.80
1	A	424	G	P-O3'-C3'	5.12	125.85	119.70
1	A	175	G	N3-C4-C5	-5.12	126.04	128.60
1	A	685	C	P-O3'-C3'	5.09	125.81	119.70
1	A	1324	G	P-O3'-C3'	5.08	125.79	119.70
1	A	1276	A	N7-C8-N9	5.07	116.33	113.80
1	A	1474	A	N1-C6-N6	5.06	121.63	118.60
1	A	12	U	N3-C4-C5	-5.02	111.59	114.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	J	79	ARG	Sidechain

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	32380	0	16346	357	0
2	B	1900	0	1951	49	0
3	C	1612	0	1677	46	0
4	D	1703	0	1767	53	0
5	E	1146	0	1207	21	0
6	F	843	0	857	14	0
7	G	1257	0	1296	27	0
8	H	1116	0	1177	23	0
9	I	1011	0	1043	39	0
10	J	792	0	835	38	3
11	K	885	0	904	26	0
12	L	970	0	1057	26	0
13	M	997	0	1072	32	0
14	N	492	0	529	19	0
15	O	734	0	771	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	P	700	0	720	24	0
17	Q	857	0	930	16	0
18	R	597	0	668	10	0
19	S	647	0	673	20	0
20	T	762	0	856	15	0
21	V	208	0	221	6	0
22	X	232	0	122	3	0
23	W	82	0	44	2	0
24	A	42	0	45	0	0
25	A	90	0	0	0	0
25	E	1	0	0	0	0
25	J	2	0	0	0	0
25	K	1	0	0	0	0
All	All	52059	0	36768	785	3

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 (785) 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)
13:M:3:ARG:HE	13:M:7:VAL:HG13	1.36	0.91
1:A:403:G:O2'	1:A:427:A:OP1	1.92	0.86
4:D:18:LYS:HE3	4:D:31:CYS:HB3	1.58	0.85
1:A:405:G:H3'	1:A:427:A:H62	1.42	0.85
3:C:85:ARG:HA	3:C:88:ARG:HD3	1.59	0.85
1:A:648:G:H22	1:A:725:G:H1	1.27	0.82
3:C:58:GLU:HB3	10:J:92:THR:HG21	1.62	0.81
1:A:405:G:N2	1:A:429:C:OP1	2.13	0.80
1:A:208:C:H42	1:A:212:G:H1	1.31	0.78
3:C:33:LEU:HD21	14:N:53:LEU:HD22	1.64	0.78
8:H:10:LEU:HD22	8:H:83:ILE:HD11	1.68	0.76
13:M:3:ARG:HG3	13:M:7:VAL:HA	1.67	0.76
5:E:75:THR:OG1	5:E:76:ILE:N	2.19	0.76
4:D:13:ARG:NH1	4:D:38:TYR:O	2.20	0.74
1:A:1006:C:N4	1:A:1012:G:O6	2.20	0.74
1:A:1401:C:N3	1:A:1448:G:N1	2.31	0.73
1:A:931:G:N7	13:M:104:ARG:NH2	2.37	0.73
3:C:179:ARG:HD2	3:C:207:VAL:HG22	1.70	0.73
8:H:17:THR:HB	8:H:78:GLN:HE22	1.53	0.73
1:A:1064:U:H3	1:A:1077:G:H22	1.37	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1303:C:OP2	21:V:6:ARG:NH1	2.22	0.73
8:H:14:ARG:HG2	8:H:18:ARG:HH21	1.54	0.72
9:I:37:PHE:O	9:I:39:GLY:N	2.22	0.72
1:A:1166:C:OP1	10:J:51:ARG:NH2	2.22	0.72
3:C:58:GLU:H	3:C:65:ALA:HB3	1.54	0.72
1:A:661:U:H3	1:A:697:G:H22	1.39	0.71
1:A:953:A:H4'	1:A:954:G:H5''	1.73	0.71
5:E:43:LEU:HD11	5:E:132:ALA:HB1	1.73	0.71
7:G:54:THR:HG22	7:G:56:GLN:H	1.56	0.70
8:H:98:LYS:HG3	8:H:99:GLU:HG3	1.72	0.70
17:Q:48:GLU:O	17:Q:50:LYS:N	2.23	0.70
1:A:1369:G:H21	1:A:1474:A:H8	1.40	0.70
9:I:45:ALA:HA	9:I:48:GLU:HG2	1.74	0.69
10:J:38:ILE:HB	10:J:71:LEU:HB2	1.73	0.69
1:A:400:U:OP2	4:D:3:ARG:NH1	2.24	0.69
1:A:1008:C:OP1	1:A:1010:G:N2	2.26	0.69
1:A:952:A:OP2	14:N:29:ARG:NH2	2.25	0.69
2:B:114:ARG:HH12	2:B:138:LEU:HD11	1.58	0.69
11:K:65:ALA:HB1	11:K:98:LEU:HD13	1.75	0.68
9:I:43:ALA:O	9:I:45:ALA:N	2.25	0.68
17:Q:100:LYS:HE2	17:Q:101:ARG:HG2	1.75	0.68
1:A:932:G:H21	1:A:1204:A:H62	1.40	0.68
1:A:38:G:H22	1:A:393:A:H5'	1.58	0.68
1:A:1010:G:N7	1:A:1011:G:N2	2.41	0.68
1:A:521:G:OP1	12:L:113:ARG:NH2	2.26	0.67
4:D:63:LYS:HE3	4:D:198:VAL:HG12	1.75	0.67
6:F:15:ASP:HB3	6:F:18:GLN:HB2	1.75	0.67
1:A:526:G:OP1	4:D:10:ARG:NH2	2.28	0.67
4:D:28:SER:O	4:D:30:LYS:N	2.27	0.67
1:A:563:G:H5'	1:A:712:A:H1'	1.75	0.67
1:A:565:G:O3'	15:O:64:ARG:NH2	2.27	0.67
10:J:90:LEU:H	10:J:91:PRO:HD2	1.59	0.67
1:A:312:G:OP2	1:A:347:G:O2'	2.13	0.66
9:I:16:ARG:HE	9:I:64:THR:HB	1.59	0.66
20:T:75:ASN:OD1	20:T:75:ASN:N	2.27	0.66
1:A:1287:G:OP2	13:M:88:ARG:NH1	2.29	0.66
10:J:78:ASN:HB2	10:J:81:THR:HG23	1.77	0.66
2:B:87:ARG:NH2	2:B:220:ASP:OD1	2.26	0.65
1:A:1005:C:N4	1:A:1011:G:O6	2.30	0.65
2:B:16:HIS:CD2	2:B:210:SER:HB3	2.32	0.65
3:C:189:ALA:HB3	3:C:196:LEU:HB2	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:22:GLY:HA3	9:I:60:ASP:HB2	1.78	0.64
1:A:405:G:H3'	1:A:427:A:N6	2.10	0.64
15:O:39:LEU:HB3	15:O:56:LEU:HD12	1.80	0.64
3:C:131:ARG:NH2	3:C:166:GLU:OE2	2.31	0.64
4:D:29:PRO:O	4:D:35:ARG:NH2	2.30	0.64
10:J:16:LEU:HA	10:J:20:ALA:HB3	1.80	0.64
3:C:51:GLY:H	3:C:70:VAL:HG13	1.62	0.64
16:P:43:LYS:HG3	16:P:48:TRP:CD2	2.32	0.63
1:A:1245:A:N3	1:A:1303:C:O2'	2.29	0.63
7:G:138:LYS:NZ	7:G:142:GLU:OE1	2.31	0.63
1:A:1122:G:H21	1:A:1124:A:H62	1.46	0.63
12:L:74:GLY:O	12:L:102:ARG:NH2	2.31	0.63
19:S:28:LYS:HE3	19:S:47:HIS:HB3	1.79	0.63
1:A:155:A:N1	1:A:343:G:O2'	2.29	0.63
4:D:57:ARG:NH1	4:D:205:GLU:OE2	2.31	0.63
4:D:50:ARG:HE	4:D:51:PRO:HD2	1.64	0.62
9:I:79:LEU:HD22	9:I:83:ARG:HD2	1.80	0.62
10:J:57:LYS:O	10:J:60:ARG:NH1	2.32	0.62
1:A:405:G:N2	1:A:427:A:O2'	2.32	0.62
1:A:1000:G:H2'	1:A:1001:G:H8	1.65	0.62
12:L:28:LYS:HD3	12:L:33:ARG:HH22	1.64	0.62
20:T:50:GLU:HA	20:T:100:ILE:HD12	1.81	0.62
1:A:28:G:O2'	1:A:292:U:OP1	2.17	0.62
1:A:461:G:O6	1:A:464:C:N4	2.32	0.62
2:B:19:HIS:CD2	2:B:20:GLU:H	2.18	0.62
11:K:14:VAL:HG21	11:K:34:ASP:HB2	1.81	0.62
1:A:406:G:OP2	1:A:427:A:N6	2.33	0.61
16:P:10:GLY:HA3	16:P:14:ASN:O	2.00	0.61
10:J:65:LEU:HD23	14:N:56:VAL:HG22	1.80	0.61
1:A:458:A:H8	16:P:83:GLU:HG2	1.65	0.61
11:K:15:ALA:O	11:K:77:MET:HA	2.00	0.61
3:C:154:SER:OG	3:C:155:GLY:N	2.32	0.61
6:F:70:ASP:OD1	6:F:70:ASP:N	2.32	0.61
1:A:537:A:O2'	12:L:29:GLY:O	2.18	0.61
1:A:1400:G:N2	1:A:1449:C:O2	2.33	0.61
2:B:105:PHE:HA	2:B:108:ILE:HG22	1.82	0.61
2:B:91:PRO:HG2	2:B:155:LEU:HG	1.83	0.61
15:O:39:LEU:HD13	15:O:56:LEU:HB2	1.83	0.61
3:C:118:GLN:O	3:C:120:VAL:N	2.34	0.60
5:E:80:ILE:HG22	8:H:104:ARG:HH21	1.64	0.60
1:A:821:G:H1	1:A:827:C:H42	1.50	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:9:VAL:HG13	7:G:94:ARG:HH21	1.66	0.60
9:I:97:LYS:HA	9:I:102:LEU:HD11	1.82	0.60
10:J:61:GLU:OE2	14:N:45:ARG:NH1	2.31	0.60
18:R:32:ARG:HA	18:R:69:THR:HG21	1.81	0.60
1:A:722:C:OP2	6:F:92:LYS:NZ	2.25	0.60
1:A:1454:G:HO2'	1:A:1455:A:H8	1.49	0.60
2:B:43:ASP:O	2:B:47:THR:OG1	2.12	0.60
12:L:70:ILE:HG12	12:L:100:ILE:HD12	1.82	0.60
1:A:415:C:OP1	1:A:497:C:O2'	2.18	0.60
1:A:251:G:O3'	17:Q:17:LYS:NZ	2.33	0.60
1:A:1102:G:H3'	1:A:1123:C:N4	2.16	0.60
9:I:46:ALA:HB2	9:I:74:ILE:HG23	1.83	0.60
1:A:1383:U:O2	1:A:1489:G:N2	2.33	0.59
1:A:183:G:H21	1:A:184:C:H2'	1.67	0.59
1:A:1409:G:O2'	1:A:1440:A:N6	2.35	0.59
16:P:22:THR:HA	16:P:33:ILE:HD13	1.84	0.59
1:A:458:A:H1'	1:A:459:G:N2	2.16	0.59
2:B:18:GLY:HA3	2:B:41:ILE:HA	1.85	0.59
15:O:74:ASP:HB3	15:O:77:ARG:HG3	1.83	0.59
1:A:1043:U:C5	1:A:1167:G:H1'	2.37	0.59
1:A:1264:A:H2'	1:A:1265:A:C8	2.38	0.59
20:T:97:ALA:O	20:T:99:LEU:N	2.35	0.59
1:A:1109:G:OP1	9:I:3:GLN:NE2	2.35	0.59
11:K:17:GLY:HA2	11:K:35:PRO:HD3	1.84	0.58
21:V:13:ILE:HG22	21:V:22:ARG:CZ	2.33	0.58
1:A:405:G:H21	1:A:427:A:H8	1.51	0.58
10:J:6:ILE:HG13	10:J:98:ILE:HG23	1.85	0.58
13:M:4:ILE:HA	13:M:57:ARG:HG2	1.85	0.58
1:A:460:G:H2'	1:A:461:G:H4'	1.85	0.58
6:F:43:LEU:HD12	6:F:46:ARG:HD2	1.86	0.58
7:G:66:VAL:HG12	7:G:70:LYS:HE3	1.85	0.58
22:X:36:G:H1	23:W:1:C:H42	1.52	0.58
1:A:372:G:H5''	16:P:5:ARG:HB2	1.85	0.58
10:J:69:ASN:OD1	10:J:69:ASN:N	2.36	0.58
1:A:475:G:H2'	1:A:476:G:H8	1.67	0.58
1:A:1292:U:O2'	1:A:1337:A:N3	2.30	0.58
10:J:76:ASN:O	10:J:76:ASN:ND2	2.36	0.58
1:A:1398:G:H2'	1:A:1399:G:C8	2.39	0.58
11:K:54:ARG:O	11:K:57:THR:OG1	2.20	0.58
1:A:1042:G:H21	1:A:1167:G:H2'	1.69	0.58
1:A:1035:G:H2'	1:A:1036:G:O4'	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1101:A:H4'	10:J:36:GLY:HA3	1.86	0.57
10:J:32:ALA:HA	10:J:76:ASN:HD21	1.69	0.57
1:A:75:G:H2'	1:A:76:G:H8	1.69	0.57
1:A:1369:G:N2	1:A:1474:A:H8	2.02	0.57
3:C:153:VAL:HG23	3:C:198:VAL:HG12	1.86	0.57
1:A:1368:U:H2'	1:A:1369:G:C8	2.39	0.57
1:A:1100:U:O4	1:A:1101:A:N6	2.37	0.57
4:D:12:CYS:SG	4:D:31:CYS:SG	3.02	0.57
3:C:19:GLU:O	3:C:40:ARG:NH2	2.38	0.57
8:H:85:ARG:NE	8:H:87:SER:O	2.38	0.57
1:A:1119:C:H2'	1:A:1120:G:H8	1.69	0.57
5:E:81:GLU:HB2	5:E:90:VAL:HG22	1.85	0.57
1:A:225:U:O2'	16:P:23:ASP:OD2	2.22	0.56
1:A:403:G:H1	1:A:480:A:HO2'	1.53	0.56
1:A:1035:G:H5''	3:C:154:SER:HB2	1.86	0.56
4:D:113:SER:HB3	4:D:116:GLN:HB3	1.87	0.56
19:S:17:GLU:HA	19:S:20:LEU:HG	1.86	0.56
20:T:57:ARG:HH21	20:T:102:GLY:HA3	1.70	0.56
1:A:358:G:N2	1:A:361:U:OP2	2.38	0.56
5:E:84:PHE:O	5:E:86:ALA:N	2.38	0.56
5:E:82:VAL:HG21	5:E:138:ALA:HA	1.88	0.56
15:O:79:ARG:O	15:O:83:GLU:HG2	2.05	0.56
1:A:106:G:H1'	1:A:350:G:H5'	1.87	0.56
1:A:660:A:H1'	11:K:115:PRO:HB3	1.87	0.56
1:A:1261:C:H3'	1:A:1262:A:H8	1.70	0.56
1:A:1306:A:P	13:M:28:ALA:HB3	2.45	0.56
16:P:42:ARG:HB2	16:P:44:THR:HG23	1.88	0.56
2:B:134:GLU:O	2:B:138:LEU:N	2.39	0.56
10:J:30:SER:HB3	10:J:81:THR:HA	1.87	0.56
14:N:3:ARG:HH21	14:N:6:LEU:HD11	1.71	0.56
1:A:156:A:C5	1:A:157:C:H1'	2.40	0.56
4:D:187:ARG:NH1	4:D:188:LEU:H	2.04	0.56
7:G:129:GLU:HB2	7:G:131:LYS:HE2	1.87	0.56
1:A:1079:A:N7	2:B:172:ILE:HD11	2.21	0.56
1:A:936:A:N3	1:A:963:C:O2'	2.35	0.56
3:C:6:HIS:CE1	3:C:8:ILE:HB	2.42	0.55
3:C:153:VAL:HG22	3:C:196:LEU:HD12	1.88	0.55
6:F:9:VAL:HB	6:F:87:ARG:HB2	1.87	0.55
9:I:31:GLN:HB3	9:I:35:GLU:HB2	1.87	0.55
16:P:15:PRO:HD2	16:P:42:ARG:HD3	1.89	0.55
1:A:1119:C:H2'	1:A:1120:G:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:G:H2'	1:A:36:C:C6	2.42	0.55
3:C:150:LYS:HA	3:C:169:ALA:HB1	1.89	0.55
7:G:52:GLU:HG3	7:G:53:LYS:HG3	1.89	0.55
12:L:59:ARG:HG2	12:L:65:GLU:HB3	1.89	0.55
19:S:13:ASP:HA	19:S:16:LEU:HG	1.88	0.55
10:J:54:PHE:HD2	10:J:55:LYS:HG2	1.70	0.55
1:A:636:U:O4	1:A:736:G:O2'	2.24	0.55
11:K:87:THR:OG1	11:K:88:GLY:N	2.38	0.55
13:M:99:ARG:HH12	19:S:2:PRO:HG3	1.71	0.55
12:L:102:ARG:HH11	12:L:102:ARG:HB3	1.71	0.55
1:A:21:G:H2'	1:A:22:G:C8	2.42	0.54
1:A:1217:U:C2	7:G:32:ARG:HD3	2.41	0.54
9:I:9:ARG:HG2	9:I:14:VAL:HG22	1.88	0.54
1:A:1324:G:N2	1:A:1350:G:H2'	2.22	0.54
4:D:19:LEU:HD22	4:D:67:ILE:HD13	1.90	0.54
16:P:3:LYS:HG3	16:P:24:ALA:HB2	1.89	0.54
1:A:1293:G:H4'	14:N:18:VAL:HG11	1.89	0.54
2:B:174:VAL:O	2:B:178:ARG:HG2	2.07	0.54
6:F:6:VAL:HG22	6:F:90:VAL:HG22	1.89	0.54
2:B:233:SER:HB3	2:B:236:TYR:HB2	1.89	0.54
10:J:64:GLU:OE2	10:J:66:ARG:NH1	2.41	0.54
1:A:470:G:O2'	1:A:471:U:OP2	2.21	0.54
1:A:953:A:H5'	1:A:953:A:H8	1.73	0.54
1:A:1289:G:N7	19:S:3:ARG:HB2	2.22	0.54
9:I:32:ASP:O	9:I:34:ASN:N	2.41	0.54
11:K:32:ILE:HD13	11:K:68:ALA:HB1	1.89	0.54
4:D:149:ALA:HB3	4:D:152:SER:HB3	1.89	0.54
1:A:457:G:H1	16:P:82:GLN:HA	1.73	0.53
1:A:587:U:H2'	1:A:588:G:C8	2.43	0.53
2:B:231:GLU:HG2	2:B:232:PRO:HD2	1.90	0.53
1:A:404:A:N6	4:D:25:ARG:HH21	2.06	0.53
1:A:822:G:C6	1:A:824:C:H1'	2.43	0.53
2:B:160:ASP:N	2:B:160:ASP:OD1	2.41	0.53
3:C:123:GLN:O	3:C:128:PHE:HB2	2.09	0.53
17:Q:24:GLU:HG2	17:Q:39:SER:HB3	1.91	0.53
1:A:817:U:H3	1:A:831:G:H1	1.55	0.53
3:C:51:GLY:N	3:C:70:VAL:HG13	2.22	0.53
1:A:458:A:C8	16:P:83:GLU:HG2	2.43	0.53
1:A:459:G:H1	16:P:83:GLU:HB2	1.72	0.53
1:A:464:C:H2'	1:A:465:U:O4'	2.08	0.53
1:A:409:G:OP1	1:A:413:C:N4	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:7:PRO:HB2	4:D:10:ARG:HD2	1.91	0.53
1:A:295:G:H2'	1:A:296:A:C8	2.44	0.53
1:A:924:A:O2'	1:A:1310:A:N3	2.38	0.53
11:K:84:VAL:HG11	11:K:91:ARG:HD2	1.89	0.53
12:L:27:LEU:O	12:L:29:GLY:N	2.42	0.53
20:T:53:LEU:HD12	20:T:102:GLY:H	1.74	0.53
6:F:10:LEU:HD12	6:F:59:TYR:HB3	1.90	0.53
1:A:1104:U:H3	1:A:1105:G:N2	2.07	0.52
1:A:1374:C:H4'	1:A:1375:A:OP2	2.10	0.52
1:A:1412:G:H2'	1:A:1413:U:C6	2.44	0.52
3:C:37:GLN:NE2	14:N:52:GLN:OE1	2.31	0.52
4:D:108:LEU:HD22	4:D:176:LEU:HD13	1.91	0.52
4:D:150:GLU:HA	4:D:153:ARG:HH21	1.73	0.52
12:L:6:THR:OG1	12:L:9:GLN:HG3	2.10	0.52
6:F:30:LEU:HB3	6:F:35:ALA:HB3	1.91	0.52
14:N:24:CYS:HB3	14:N:29:ARG:H	1.73	0.52
1:A:928:U:OP2	13:M:102:ARG:HD2	2.09	0.52
1:A:1090:C:O2	3:C:179:ARG:HG2	2.10	0.52
2:B:168:THR:HA	2:B:171:ALA:HB2	1.90	0.52
19:S:36:ARG:NH2	19:S:75:ALA:O	2.43	0.52
1:A:427:A:O2'	1:A:428:A:H5'	2.10	0.52
4:D:103:ASN:OD1	4:D:114:ARG:NH2	2.42	0.52
1:A:414:C:H2'	1:A:415:C:C6	2.44	0.52
1:A:957:C:H3'	1:A:958:C:H5''	1.91	0.52
13:M:84:ILE:HG21	19:S:65:ASN:HD21	1.74	0.52
1:A:715:G:OP1	1:A:750:A:H1'	2.10	0.52
1:A:1495:G:OP1	11:K:123:LYS:NZ	2.30	0.52
8:H:6:ILE:HB	8:H:85:ARG:NH1	2.25	0.52
19:S:39:THR:HG22	19:S:70:LYS:HG2	1.92	0.52
1:A:451:C:H42	1:A:461:G:H1'	1.74	0.52
7:G:75:VAL:HG21	7:G:86:GLN:HG3	1.91	0.52
1:A:1097:C:H42	1:A:1132:G:H1	1.58	0.52
1:A:1404:U:H2'	1:A:1405:A:C8	2.44	0.52
1:A:564:U:H2'	1:A:565:G:O4'	2.09	0.51
1:A:1203:C:N4	13:M:104:ARG:HG2	2.25	0.51
3:C:52:LEU:HD13	3:C:68:VAL:HG13	1.92	0.51
10:J:19:SER:HB3	10:J:91:PRO:HD3	1.92	0.51
11:K:85:ARG:HD2	11:K:111:ASP:O	2.10	0.51
1:A:1482:U:H2'	1:A:1483:G:C8	2.46	0.51
4:D:100:ARG:O	4:D:104:VAL:HG23	2.11	0.51
1:A:475:G:H2'	1:A:476:G:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:43:LEU:HD11	15:O:53:HIS:HB2	1.92	0.51
17:Q:86:GLU:O	17:Q:90:ILE:HG12	2.11	0.51
1:A:188:U:O2'	1:A:189:U:H5'	2.11	0.51
1:A:1389:C:H2'	1:A:1390:A:C8	2.45	0.51
1:A:75:G:H2'	1:A:76:G:C8	2.45	0.51
1:A:523:A:H2'	1:A:524:G:C8	2.46	0.51
1:A:1315:G:C6	1:A:1316:A:C6	2.99	0.51
2:B:18:GLY:HA2	2:B:42:ILE:HG13	1.93	0.51
1:A:1250:G:C2	1:A:1251:G:H1'	2.46	0.50
1:A:1458:G:H2'	1:A:1459:G:O4'	2.11	0.50
1:A:934:U:H2'	1:A:935:U:O4'	2.10	0.50
11:K:21:ILE:HG12	11:K:30:VAL:HG12	1.93	0.50
1:A:397:C:O2'	1:A:605:A:N3	2.38	0.50
1:A:632:A:H2'	1:A:633:G:O4'	2.11	0.50
1:A:856:G:H5'	8:H:89:PRO:HG2	1.94	0.50
1:A:1042:G:N2	1:A:1167:G:H2'	2.26	0.50
1:A:160:G:H2'	1:A:161:G:H8	1.76	0.50
1:A:368:C:H1'	1:A:369:A:OP2	2.12	0.50
1:A:470:G:HO2'	1:A:471:U:P	2.34	0.50
1:A:954:G:OP2	1:A:1335:U:O2'	2.27	0.50
5:E:7:GLU:OE2	5:E:37:ARG:NE	2.40	0.50
11:K:72:ALA:HB1	11:K:77:MET:HG3	1.92	0.50
18:R:58:LEU:HD23	18:R:62:GLU:HB3	1.94	0.50
1:A:988:G:O6	1:A:999:G:N2	2.45	0.50
7:G:42:ILE:HD11	7:G:116:ALA:HB3	1.94	0.50
7:G:62:PHE:HD1	7:G:124:LEU:HD21	1.76	0.50
12:L:27:LEU:C	12:L:29:GLY:H	2.15	0.50
13:M:76:ALA:HA	13:M:79:LYS:HE2	1.92	0.50
1:A:447:A:HO2'	1:A:448:A:H8	1.60	0.50
1:A:924:A:H2'	1:A:925:G:C8	2.47	0.50
2:B:25:ASN:OD1	2:B:27:LYS:HB2	2.12	0.50
4:D:145:GLU:HA	4:D:184:LYS:HA	1.92	0.50
19:S:17:GLU:O	19:S:21:GLU:HB2	2.12	0.50
20:T:67:ALA:HA	20:T:73:HIS:H	1.76	0.50
7:G:99:LEU:HD22	7:G:103:TRP:CZ2	2.46	0.50
1:A:368:C:H4'	1:A:369:A:O5'	2.11	0.50
1:A:954:G:N7	1:A:1336:C:H1'	2.27	0.50
4:D:102:ASP:HB3	4:D:136:PRO:HB3	1.93	0.49
5:E:84:PHE:HB2	5:E:134:ALA:HB2	1.93	0.49
1:A:1035:G:H1	1:A:1180:C:H42	1.59	0.49
1:A:175:G:H4'	1:A:176:U:H5'	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:733:C:H2'	1:A:734:G:H8	1.77	0.49
1:A:597:C:H2'	1:A:598:A:C8	2.48	0.49
10:J:5:ARG:HE	10:J:99:LYS:HD2	1.77	0.49
11:K:33:THR:HA	11:K:39:PRO:HA	1.94	0.49
20:T:53:LEU:HB2	20:T:100:ILE:HD13	1.95	0.49
1:A:62:U:H2'	1:A:63:C:C6	2.48	0.49
1:A:1469:G:H2'	1:A:1470:U:H5'	1.94	0.49
4:D:6:GLY:H	4:D:115:ARG:HH22	1.61	0.49
12:L:75:HIS:HA	12:L:102:ARG:NH2	2.28	0.49
1:A:377:C:H2'	1:A:378:A:O4'	2.13	0.49
1:A:1469:G:C2'	1:A:1470:U:H5'	2.43	0.49
4:D:83:SER:HA	4:D:89:THR:OG1	2.13	0.49
13:M:99:ARG:NH1	19:S:2:PRO:HG3	2.27	0.49
1:A:262:G:H5''	1:A:263:C:H5	1.78	0.49
2:B:91:PRO:HG3	2:B:154:LEU:HB2	1.94	0.49
7:G:22:LEU:HD11	7:G:101:LEU:HD21	1.95	0.49
21:V:3:LYS:HA	21:V:11:GLY:HA2	1.95	0.49
1:A:1233:A:N6	1:A:1255:U:O4'	2.44	0.49
4:D:111:ALA:HB3	4:D:117:ALA:HB2	1.94	0.49
7:G:85:TYR:HD2	7:G:154:TYR:HE2	1.61	0.49
1:A:657:G:H2'	1:A:658:G:C8	2.48	0.48
1:A:670:U:HO2'	1:A:671:A:H8	1.59	0.48
20:T:60:GLU:HG3	20:T:81:LYS:HD3	1.95	0.48
1:A:138:G:H1	1:A:172:C:H42	1.61	0.48
1:A:262:G:H5'	1:A:264:C:H41	1.78	0.48
1:A:955:A:H2'	1:A:956:A:H5''	1.94	0.48
7:G:136:LYS:O	7:G:140:ASP:N	2.45	0.48
8:H:19:VAL:HG13	8:H:21:LYS:HG2	1.94	0.48
10:J:8:LEU:O	10:J:70:ARG:N	2.46	0.48
11:K:18:ARG:HH21	11:K:37:GLY:HA2	1.77	0.48
15:O:87:ILE:O	15:O:89:GLY:N	2.45	0.48
1:A:587:U:H2'	1:A:588:G:H8	1.78	0.48
1:A:45:U:H2'	1:A:46:G:C8	2.49	0.48
1:A:288:G:C5	1:A:289:G:H1'	2.48	0.48
1:A:405:G:H2'	1:A:405:G:N3	2.27	0.48
1:A:470:G:O2'	1:A:471:U:P	2.72	0.48
8:H:17:THR:HB	8:H:78:GLN:NE2	2.25	0.48
1:A:26:A:O2'	4:D:209:ARG:NH1	2.46	0.48
1:A:116:C:O2'	1:A:286:C:O2	2.29	0.48
1:A:544:U:H5'	1:A:550:G:N2	2.29	0.48
1:A:820:G:C6	1:A:829:G:C6	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:15:GLU:HB3	4:D:63:LYS:HG2	1.95	0.48
4:D:61:LYS:HG3	4:D:203:VAL:HG13	1.96	0.48
1:A:17:U:H2'	1:A:18:C:C6	2.49	0.48
1:A:1108:A:OP2	1:A:1109:G:H8	1.97	0.48
9:I:20:ARG:HG3	9:I:60:ASP:HB3	1.95	0.48
1:A:60:A:H4'	1:A:61:G:O5'	2.14	0.48
1:A:958:C:H5'	1:A:959:U:C5	2.49	0.48
10:J:55:LYS:HB2	10:J:56:HIS:H	1.52	0.48
12:L:11:VAL:HG23	17:Q:29:HIS:CD2	2.49	0.48
1:A:513:G:O6	12:L:49:ASN:ND2	2.47	0.48
1:A:953:A:H5'	1:A:953:A:C8	2.48	0.48
1:A:1265:A:N3	1:A:1329:C:O2'	2.38	0.48
6:F:21:LEU:O	6:F:25:ILE:HG12	2.13	0.48
9:I:100:GLY:O	9:I:102:LEU:N	2.47	0.48
10:J:12:ASP:HB3	10:J:15:THR:HG22	1.96	0.48
12:L:32:PHE:HB3	12:L:84:LEU:HD11	1.95	0.48
17:Q:100:LYS:H	17:Q:100:LYS:HD3	1.79	0.48
1:A:457:G:C2	16:P:82:GLN:HB3	2.49	0.47
3:C:148:GLY:HA3	3:C:172:ARG:H	1.78	0.47
4:D:9:CYS:HB3	4:D:32:ALA:HB2	1.96	0.47
7:G:73:MET:SD	7:G:90:GLU:HA	2.53	0.47
9:I:48:GLU:N	9:I:49:PRO:HD2	2.28	0.47
19:S:53:ASN:HD21	19:S:55:LYS:HB3	1.78	0.47
2:B:27:LYS:HB3	2:B:194:PRO:HD2	1.96	0.47
12:L:54:LYS:HD2	12:L:54:LYS:N	2.29	0.47
3:C:4:LYS:HA	3:C:4:LYS:HD3	1.68	0.47
20:T:32:ALA:O	20:T:36:LEU:HB2	2.14	0.47
1:A:691:C:H2'	1:A:692:C:C6	2.49	0.47
1:A:1320:G:H2'	1:A:1321:C:C6	2.49	0.47
7:G:18:TYR:CD2	7:G:59:LEU:HB2	2.49	0.47
7:G:26:PHE:CE2	7:G:30:ILE:HD11	2.50	0.47
1:A:1001:G:H2'	1:A:1002:G:H5'	1.96	0.47
1:A:1380:C:H1'	1:A:1472:A:N1	2.30	0.47
2:B:147:LYS:HE3	2:B:148:TYR:CE1	2.49	0.47
1:A:1167:G:H5''	3:C:3:ASN:HB2	1.96	0.47
9:I:36:TYR:OH	9:I:73:GLN:NE2	2.45	0.47
18:R:52:PRO:O	18:R:56:THR:HG23	2.14	0.47
1:A:697:G:H2'	1:A:698:G:C8	2.49	0.47
1:A:702:G:H5'	11:K:117:ASN:HB2	1.97	0.47
1:A:796:C:OP1	1:A:881:G:H1'	2.15	0.47
1:A:1243:G:N2	1:A:1246:A:OP2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1030:U:H2'	1:A:1177:C:H41	1.79	0.47
2:B:17:PHE:HB3	2:B:44:LEU:HD21	1.96	0.47
11:K:30:VAL:HG21	11:K:65:ALA:HA	1.96	0.47
18:R:38:GLU:H	18:R:38:GLU:HG3	1.47	0.47
1:A:96:C:P	20:T:17:ARG:HH21	2.38	0.46
1:A:853:C:H1'	8:H:15:ASN:HD21	1.78	0.46
1:A:909:C:H42	1:A:1363:G:H1	1.63	0.46
1:A:1042:G:O2'	1:A:1167:G:N2	2.47	0.46
7:G:50:ILE:HG21	7:G:61:VAL:HG11	1.96	0.46
9:I:34:ASN:N	9:I:34:ASN:OD1	2.48	0.46
10:J:82:ILE:HG22	10:J:86:MET:HB2	1.97	0.46
19:S:13:ASP:OD1	19:S:13:ASP:N	2.48	0.46
1:A:103:C:H2'	1:A:104:G:O4'	2.16	0.46
1:A:154:A:H2'	1:A:155:A:O4'	2.15	0.46
1:A:252:U:H5'	17:Q:17:LYS:NZ	2.31	0.46
1:A:1000:G:H2'	1:A:1001:G:C8	2.48	0.46
1:A:1481:C:H2'	1:A:1482:U:O4'	2.16	0.46
2:B:159:PRO:HG2	2:B:162:ILE:HD11	1.98	0.46
10:J:74:ILE:HD13	10:J:74:ILE:H	1.80	0.46
1:A:403:G:N1	1:A:480:A:O2'	2.44	0.46
1:A:1079:A:H4'	1:A:1080:A:O5'	2.15	0.46
10:J:22:LYS:C	10:J:24:VAL:H	2.19	0.46
13:M:22:ILE:HB	13:M:25:ILE:HB	1.97	0.46
15:O:85:LEU:HD23	15:O:87:ILE:HD12	1.97	0.46
1:A:835:C:H2'	1:A:836:G:O4'	2.15	0.46
1:A:1426:A:H5'	1:A:1427:C:H5	1.79	0.46
11:K:20:TYR:CZ	11:K:83:ILE:HD12	2.51	0.46
13:M:79:LYS:O	13:M:83:ASP:HB2	2.16	0.46
1:A:1125:C:O2	9:I:16:ARG:NH1	2.49	0.46
1:A:1245:A:H2'	1:A:1246:A:C8	2.50	0.46
4:D:30:LYS:HB3	4:D:35:ARG:HH22	1.79	0.46
21:V:15:ARG:HA	21:V:15:ARG:HD3	1.72	0.46
1:A:51:A:N7	1:A:107:U:O2'	2.42	0.46
1:A:98:G:OP2	20:T:18:GLN:NE2	2.48	0.46
1:A:143:A:H2'	1:A:144:C:C6	2.49	0.46
1:A:1055:G:H1	5:E:47:LYS:NZ	2.14	0.46
4:D:61:LYS:HD2	4:D:207:TYR:OH	2.16	0.46
1:A:1496:C:OP1	11:K:120:ARG:NH2	2.49	0.46
3:C:73:PRO:O	3:C:76:VAL:HG22	2.15	0.46
1:A:810:C:H4'	8:H:12:ARG:HG3	1.98	0.46
1:A:959:U:H5	1:A:960:U:HO2'	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1104:U:O2'	1:A:1105:G:OP1	2.32	0.46
1:A:1277:G:O2'	1:A:1278:U:P	2.74	0.46
5:E:140:ARG:O	5:E:143:ARG:NH2	2.49	0.46
1:A:486:G:H2'	1:A:487:C:O4'	2.16	0.46
1:A:1390:A:H2	1:A:1459:G:H22	1.61	0.46
4:D:9:CYS:HA	4:D:12:CYS:HB2	1.98	0.46
4:D:187:ARG:CZ	4:D:188:LEU:H	2.29	0.46
1:A:485:C:H2'	1:A:486:G:C8	2.51	0.46
9:I:18:PHE:O	9:I:61:ALA:HA	2.16	0.46
1:A:457:G:N3	1:A:457:G:H2'	2.31	0.45
1:A:543:A:OP1	5:E:126:ARG:NH2	2.48	0.45
1:A:1057:G:O3'	5:E:14:ARG:NH2	2.49	0.45
2:B:181:PHE:HD2	8:H:70:GLN:HB3	1.81	0.45
3:C:59:ARG:HG3	3:C:63:ASN:O	2.16	0.45
3:C:130:VAL:HG21	3:C:157:ILE:HG23	1.98	0.45
9:I:53:VAL:HG21	9:I:85:LEU:HD21	1.97	0.45
12:L:33:ARG:HA	12:L:33:ARG:HD3	1.75	0.45
19:S:50:ALA:HB1	19:S:57:HIS:HB3	1.98	0.45
1:A:35:G:H2'	1:A:36:C:H6	1.82	0.45
1:A:1262:A:H4'	1:A:1263:A:O5'	2.16	0.45
1:A:1483:G:H2'	1:A:1484:U:O4'	2.16	0.45
8:H:24:THR:HG22	8:H:63:LEU:HD21	1.98	0.45
10:J:16:LEU:HD13	10:J:70:ARG:HG2	1.98	0.45
1:A:386:C:H2'	1:A:387:G:C8	2.51	0.45
9:I:17:VAL:HG11	9:I:81:ILE:HG12	1.98	0.45
12:L:89:ARG:HH21	12:L:97:ARG:HD2	1.82	0.45
1:A:1209:U:OP1	9:I:126:SER:OG	2.34	0.45
8:H:20:TYR:CE1	8:H:76:PRO:HD2	2.50	0.45
1:A:128:A:N6	16:P:25:ARG:HH21	2.14	0.45
1:A:458:A:H1'	1:A:459:G:H22	1.79	0.45
2:B:8:LYS:HD3	2:B:9:GLU:HG3	1.98	0.45
7:G:85:TYR:HB3	7:G:86:GLN:H	1.59	0.45
11:K:48:ILE:HA	11:K:48:ILE:HD13	1.77	0.45
14:N:40:CYS:O	14:N:44:LEU:HB2	2.16	0.45
1:A:1387:G:H1	1:A:1462:C:H42	1.62	0.45
10:J:12:ASP:OD1	10:J:13:HIS:N	2.49	0.45
19:S:22:LEU:HD22	19:S:28:LYS:HZ3	1.82	0.45
1:A:262:G:H5''	1:A:263:C:C5	2.51	0.45
12:L:82:VAL:N	12:L:106:ASP:OD2	2.46	0.45
1:A:254:G:H2'	1:A:255:G:H8	1.82	0.45
19:S:28:LYS:HG2	19:S:47:HIS:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:373:G:OP1	16:P:3:LYS:HD3	2.16	0.45
1:A:636:U:C2	1:A:736:G:N2	2.85	0.45
1:A:855:C:H5''	8:H:88:LYS:HD2	1.99	0.45
1:A:1036:G:H2'	1:A:1037:C:O4'	2.17	0.45
1:A:1394:G:O2'	1:A:1455:A:N6	2.50	0.45
7:G:26:PHE:HD1	7:G:101:LEU:HD22	1.82	0.45
1:A:402:G:C8	1:A:480:A:C6	3.04	0.45
1:A:405:G:C2	1:A:429:C:H5'	2.52	0.45
1:A:653:U:H2'	1:A:654:G:C8	2.52	0.45
1:A:654:G:H2'	1:A:655:G:O4'	2.17	0.45
1:A:680:A:N3	1:A:770:G:O2'	2.46	0.45
1:A:1476:G:OP1	1:A:1479:A:H4'	2.17	0.45
2:B:87:ARG:HB2	2:B:219:VAL:HG11	1.99	0.45
6:F:33:TYR:HA	6:F:71:ARG:NH2	2.32	0.45
1:A:762:G:O5'	1:A:762:G:H8	2.00	0.44
1:A:762:G:H2'	1:A:763:C:O4'	2.17	0.44
1:A:1089:A:O2'	2:B:133:LYS:NZ	2.35	0.44
1:A:1209:U:P	9:I:126:SER:HG	2.40	0.44
11:K:98:LEU:HD12	11:K:98:LEU:HA	1.76	0.44
16:P:47:ASP:OD2	16:P:47:ASP:N	2.50	0.44
1:A:124:A:H1'	1:A:259:A:O2'	2.17	0.44
1:A:1116:G:C8	1:A:1118:C:H1'	2.53	0.44
1:A:1261:C:H3'	1:A:1262:A:C8	2.51	0.44
2:B:8:LYS:HB2	2:B:9:GLU:H	1.51	0.44
2:B:68:ILE:O	2:B:90:MET:HB3	2.17	0.44
2:B:118:LEU:HD21	2:B:138:LEU:HG	1.99	0.44
17:Q:27:PHE:HA	17:Q:28:PRO:HD3	1.79	0.44
4:D:177:ASP:HB3	4:D:182:LYS:HG3	1.99	0.44
18:R:86:VAL:HB	18:R:87:ARG:H	1.49	0.44
19:S:40:ILE:HG23	19:S:44:MET:HE2	1.98	0.44
1:A:1126:U:H2'	1:A:1127:C:O4'	2.18	0.44
2:B:90:MET:HA	2:B:91:PRO:HD3	1.87	0.44
1:A:469:G:H4'	1:A:470:G:O5'	2.17	0.44
1:A:1246:A:H5'	21:V:19:GLY:HA2	1.99	0.44
1:A:1347:G:H2'	1:A:1348:G:H8	1.82	0.44
3:C:45:LYS:HD2	3:C:45:LYS:HA	1.78	0.44
4:D:30:LYS:HB3	4:D:35:ARG:HH12	1.82	0.44
9:I:85:LEU:HD12	9:I:85:LEU:HA	1.76	0.44
19:S:31:ILE:HB	19:S:49:ILE:HG23	1.99	0.44
3:C:35:GLU:HA	3:C:38:ARG:HB2	1.99	0.44
3:C:196:LEU:HB3	3:C:197:GLY:H	1.62	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:45:GLN:O	4:D:46:LYS:HG3	2.18	0.44
4:D:176:LEU:HD12	4:D:182:LYS:O	2.17	0.44
5:E:142:LEU:HD23	5:E:142:LEU:HA	1.83	0.44
14:N:24:CYS:HB2	14:N:40:CYS:HB3	1.87	0.44
17:Q:12:SER:HB3	17:Q:20:THR:HB	2.00	0.44
18:R:53:ARG:NH2	18:R:60:GLY:HA2	2.32	0.44
1:A:400:U:H2'	1:A:401:U:H6	1.82	0.44
1:A:1102:G:H5'	10:J:35:SER:O	2.18	0.44
1:A:1159:G:H4'	1:A:1160:A:H5'	1.99	0.44
1:A:1166:C:H5''	3:C:5:ILE:HD13	2.00	0.44
2:B:223:ILE:O	2:B:227:GLY:N	2.50	0.44
13:M:110:ARG:HE	13:M:110:ARG:HB2	1.50	0.44
1:A:1040:U:H2'	1:A:1041:C:C6	2.53	0.44
1:A:1401:C:H5'	1:A:1402:U:OP2	2.17	0.44
4:D:57:ARG:HD2	4:D:202:LEU:HD22	1.98	0.44
6:F:2:ARG:NE	6:F:69:GLU:HG2	2.33	0.44
13:M:3:ARG:N	13:M:9:ILE:HG12	2.32	0.44
2:B:219:VAL:C	2:B:221:LEU:H	2.20	0.44
3:C:7:PRO:HG2	3:C:184:TYR:HB2	1.99	0.44
12:L:82:VAL:HG13	12:L:105:TYR:HB3	1.99	0.44
14:N:26:ARG:HG3	14:N:47:LEU:HD11	2.00	0.44
1:A:182:C:C2	1:A:183:G:H8	2.36	0.43
1:A:741:U:H2'	1:A:742:G:O4'	2.16	0.43
1:A:829:G:H2'	1:A:830:G:C8	2.53	0.43
7:G:26:PHE:O	7:G:30:ILE:HG13	2.18	0.43
9:I:55:ALA:O	9:I:58:ARG:HB2	2.17	0.43
13:M:3:ARG:NE	13:M:7:VAL:HG13	2.17	0.43
13:M:34:LEU:HD13	13:M:41:PRO:HA	2.00	0.43
13:M:90:LEU:HD12	13:M:93:ARG:HD2	2.00	0.43
1:A:905:G:N2	1:A:1368:U:H1'	2.33	0.43
1:A:999:G:H2'	1:A:1000:G:H8	1.83	0.43
1:A:1400:G:C2	1:A:1401:C:H1'	2.53	0.43
14:N:7:ILE:HG22	14:N:9:LYS:HG2	2.00	0.43
19:S:44:MET:HG3	19:S:62:ILE:HD12	2.00	0.43
1:A:510:C:OP2	12:L:91:LYS:HE2	2.19	0.43
1:A:1452:G:C6	1:A:1453:U:C4	3.07	0.43
3:C:29:TYR:HE1	3:C:33:LEU:HD22	1.83	0.43
9:I:89:ASN:O	9:I:92:TYR:HB2	2.18	0.43
1:A:7:G:H5'	1:A:294:A:O4'	2.18	0.43
1:A:1404:U:H2'	1:A:1405:A:H8	1.82	0.43
4:D:162:LEU:HD21	4:D:181:MET:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:127:LYS:HD3	13:M:126:LYS:HE3	2.01	0.43
14:N:12:ARG:O	14:N:14:PRO:HD3	2.19	0.43
1:A:159:C:H2'	1:A:160:G:H8	1.83	0.43
1:A:539:C:H2'	1:A:540:C:C6	2.53	0.43
1:A:547:A:O2'	1:A:550:G:O2'	2.25	0.43
1:A:756:U:H2'	1:A:757:G:C8	2.53	0.43
1:A:796:C:H6	1:A:796:C:H2'	1.58	0.43
11:K:70:LYS:HA	11:K:73:MET:HG2	2.00	0.43
16:P:72:ARG:O	16:P:76:GLN:HB2	2.18	0.43
1:A:604:C:H2'	1:A:605:A:O4'	2.19	0.43
1:A:1272:G:O2'	13:M:14:ARG:NH1	2.52	0.43
2:B:9:GLU:OE2	2:B:217:ARG:NH2	2.51	0.43
4:D:128:VAL:HG22	4:D:146:ILE:HG12	2.01	0.43
13:M:11:ARG:HA	13:M:45:VAL:HB	2.00	0.43
16:P:43:LYS:HG3	16:P:48:TRP:CE2	2.53	0.43
1:A:1200:C:P	19:S:78:ARG:HH21	2.42	0.43
1:A:1400:G:N2	1:A:1401:C:H1'	2.34	0.43
2:B:122:PHE:HA	2:B:127:ILE:HG22	2.00	0.43
3:C:16:ARG:NH2	3:C:183:ASP:OD1	2.52	0.43
13:M:12:ASN:HA	13:M:46:LYS:HB2	2.01	0.43
3:C:136:GLN:HG3	3:C:140:ARG:HH12	1.84	0.43
1:A:340:A:H5'	1:A:341:C:C5	2.54	0.43
1:A:547:A:H2'	1:A:551:G:C8	2.54	0.43
1:A:1263:A:H2'	1:A:1264:A:H4'	2.01	0.43
1:A:1329:C:H2'	1:A:1330:G:C8	2.54	0.43
1:A:1493:G:H2'	1:A:1494:U:O4'	2.19	0.43
2:B:167:PRO:HG3	2:B:188:ALA:HB2	2.01	0.43
4:D:194:LEU:HD23	4:D:196:LEU:HD12	2.01	0.43
17:Q:104:LYS:HA	17:Q:104:LYS:HD2	1.75	0.43
1:A:96:C:O2'	1:A:166:A:N1	2.40	0.43
3:C:150:LYS:HA	3:C:169:ALA:CB	2.49	0.43
12:L:44:THR:HA	12:L:45:PRO:HD3	1.77	0.43
13:M:4:ILE:HG23	13:M:57:ARG:HA	1.99	0.43
15:O:2:PRO:HB2	15:O:3:ILE:H	1.65	0.43
15:O:75:PRO:O	15:O:79:ARG:HB2	2.19	0.43
1:A:249:U:H2'	1:A:250:G:C8	2.54	0.42
1:A:996:C:H2'	1:A:997:C:O4'	2.19	0.42
1:A:1098:G:H2'	1:A:1099:U:C6	2.54	0.42
7:G:32:ARG:HB3	7:G:33:ASP:H	1.49	0.42
8:H:38:ILE:HD12	8:H:111:ILE:HG23	2.01	0.42
16:P:5:ARG:NH2	16:P:24:ALA:HA	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:378:A:H2'	1:A:379:A:C8	2.54	0.42
1:A:440:G:H2'	1:A:441:G:H8	1.83	0.42
1:A:722:C:H2'	1:A:723:C:H6	1.84	0.42
1:A:1038:C:P	14:N:45:ARG:HH22	2.41	0.42
4:D:94:LEU:HD11	4:D:200:GLU:HG2	2.01	0.42
10:J:42:THR:HB	10:J:68:HIS:HA	2.00	0.42
3:C:12:LEU:HD13	3:C:18:TRP:NE1	2.34	0.42
9:I:116:LYS:HA	9:I:123:PRO:HD3	2.00	0.42
12:L:28:LYS:HB3	12:L:30:ALA:HB2	2.02	0.42
18:R:19:LYS:HE2	18:R:19:LYS:HB3	1.93	0.42
1:A:305:G:H2'	1:A:306:G:H8	1.84	0.42
1:A:653:U:H2'	1:A:654:G:H8	1.84	0.42
1:A:1398:G:H1'	1:A:1452:G:N2	2.34	0.42
5:E:31:LEU:HD12	5:E:44:GLY:O	2.20	0.42
11:K:99:GLN:HG2	11:K:105:VAL:HG21	2.02	0.42
17:Q:63:ARG:HG2	17:Q:64:PRO:HD2	2.00	0.42
1:A:199:U:O4'	20:T:103:GLY:HA2	2.20	0.42
1:A:351:C:H2'	1:A:352:A:O4'	2.20	0.42
1:A:963:C:H2'	1:A:964:A:C8	2.54	0.42
1:A:999:G:H2'	1:A:1000:G:C8	2.53	0.42
1:A:1333:G:H2'	1:A:1334:A:C8	2.55	0.42
4:D:207:TYR:C	4:D:209:ARG:H	2.22	0.42
8:H:6:ILE:HB	8:H:85:ARG:HH12	1.85	0.42
9:I:16:ARG:NE	9:I:64:THR:HB	2.32	0.42
10:J:86:MET:HE3	10:J:87:THR:H	1.85	0.42
16:P:42:ARG:H	16:P:42:ARG:HG2	1.43	0.42
1:A:526:G:H5'	4:D:41:GLY:HA3	2.02	0.42
1:A:1401:C:H3'	1:A:1402:U:O4'	2.19	0.42
1:A:348:C:O2	1:A:351:C:N4	2.50	0.42
1:A:815:U:H2'	1:A:816:C:C6	2.55	0.42
1:A:1038:C:H2'	1:A:1039:G:H8	1.84	0.42
2:B:189:ASP:N	2:B:189:ASP:OD2	2.53	0.42
3:C:111:LEU:HD23	3:C:111:LEU:HA	1.83	0.42
5:E:40:ARG:HE	5:E:40:ARG:HB3	1.67	0.42
17:Q:10:VAL:HG13	17:Q:19:VAL:HB	2.01	0.42
7:G:45:ASP:O	7:G:49:ILE:HG12	2.20	0.42
9:I:32:ASP:H	9:I:35:GLU:HB2	1.85	0.42
10:J:34:VAL:HG12	10:J:36:GLY:H	1.85	0.42
12:L:89:ARG:HH21	12:L:97:ARG:CD	2.33	0.42
14:N:7:ILE:HG23	14:N:9:LYS:HE3	2.01	0.42
14:N:58:LYS:HD2	14:N:58:LYS:HA	1.86	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:48:LYS:HA	20:T:48:LYS:HD2	1.90	0.42
1:A:858:C:H2'	1:A:859:G:H8	1.85	0.42
1:A:999:G:N2	1:A:1000:G:O6	2.52	0.42
3:C:203:PHE:O	3:C:205:GLY:N	2.49	0.42
8:H:48:TYR:HD1	8:H:59:LEU:HD22	1.85	0.42
9:I:127:LYS:HD3	13:M:126:LYS:HG3	2.01	0.42
17:Q:97:SER:O	17:Q:99:SER:N	2.53	0.42
1:A:378:A:H2'	1:A:379:A:H8	1.85	0.42
1:A:1010:G:H2'	1:A:1011:G:O4'	2.20	0.42
1:A:1239:C:H42	1:A:1250:G:H1	1.68	0.42
4:D:22:LYS:HB2	4:D:26:CYS:SG	2.60	0.42
8:H:33:GLU:CD	8:H:50:ARG:HH21	2.23	0.42
10:J:49:VAL:O	10:J:60:ARG:HA	2.19	0.42
20:T:48:LYS:O	20:T:50:GLU:N	2.53	0.42
1:A:129:C:O2	16:P:1:MET:HB2	2.19	0.41
1:A:331:C:O2'	1:A:1410:A:N3	2.47	0.41
1:A:340:A:H5'	1:A:341:C:H5	1.84	0.41
1:A:423:U:OP2	4:D:36:ARG:NH1	2.51	0.41
2:B:196:LEU:HD23	2:B:196:LEU:HA	1.84	0.41
3:C:36:ASP:HB2	3:C:59:ARG:NH2	2.35	0.41
1:A:432:C:H4'	4:D:156:GLU:HG2	2.01	0.41
1:A:544:U:H5'	1:A:550:G:C2	2.54	0.41
1:A:943:A:H5'	1:A:947:A:O4'	2.19	0.41
1:A:961:A:N1	1:A:1199:G:N2	2.66	0.41
1:A:983:A:H5''	1:A:984:C:C6	2.55	0.41
4:D:173:TRP:HB2	4:D:187:ARG:O	2.20	0.41
6:F:67:MET:HE2	6:F:67:MET:HB3	1.95	0.41
9:I:7:THR:HB	9:I:8:GLY:H	1.65	0.41
11:K:92:GLU:O	11:K:96:ARG:HG3	2.19	0.41
13:M:57:ARG:C	13:M:59:TYR:H	2.23	0.41
15:O:9:GLN:O	15:O:13:GLN:HG2	2.20	0.41
18:R:79:LEU:HD12	18:R:79:LEU:HA	1.79	0.41
1:A:141:G:C2	1:A:142:G:C8	3.08	0.41
1:A:1324:G:O6	9:I:10:ARG:NH2	2.52	0.41
3:C:120:VAL:HG23	3:C:198:VAL:HG21	2.00	0.41
4:D:7:PRO:O	4:D:10:ARG:HG2	2.20	0.41
5:E:60:TYR:O	5:E:64:ARG:HG3	2.20	0.41
5:E:87:SER:OG	5:E:130:ASN:HB3	2.20	0.41
10:J:54:PHE:CD2	10:J:55:LYS:HG2	2.53	0.41
10:J:61:GLU:OE2	14:N:45:ARG:HD2	2.20	0.41
1:A:351:C:H5'	1:A:385:A:OP2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:925:G:O3'	13:M:109:THR:OG1	2.38	0.41
1:A:1115:C:H4'	1:A:1116:G:N3	2.35	0.41
2:B:114:ARG:HH22	2:B:138:LEU:HD21	1.85	0.41
10:J:24:VAL:HG12	10:J:28:ARG:HD2	2.02	0.41
11:K:112:THR:HA	11:K:113:PRO:HD3	1.89	0.41
18:R:53:ARG:HD3	18:R:58:LEU:O	2.20	0.41
1:A:246:A:H1'	1:A:248:U:C5	2.55	0.41
1:A:985:C:N3	1:A:1000:G:N2	2.65	0.41
1:A:1288:G:H5''	19:S:3:ARG:HD2	2.02	0.41
3:C:148:GLY:HA2	3:C:171:GLY:HA3	2.02	0.41
4:D:22:LYS:O	4:D:25:ARG:HD3	2.19	0.41
1:A:459:G:N1	16:P:83:GLU:HB2	2.35	0.41
1:A:524:G:C6	1:A:525:G:C5	3.08	0.41
1:A:1247:C:H2'	1:A:1248:G:C8	2.56	0.41
1:A:1324:G:H3'	9:I:108:VAL:O	2.21	0.41
1:A:1349:U:H2'	1:A:1350:G:O4'	2.20	0.41
1:A:1398:G:H2'	1:A:1399:G:H8	1.82	0.41
3:C:70:VAL:HG12	3:C:72:LYS:H	1.84	0.41
12:L:102:ARG:HB3	12:L:102:ARG:NH1	2.35	0.41
14:N:15:LYS:HB3	14:N:16:PHE:H	1.76	0.41
15:O:4:THR:HB	15:O:7:GLU:HB2	2.03	0.41
3:C:19:GLU:HG2	3:C:54:ARG:HE	1.86	0.41
4:D:34:GLU:O	4:D:36:ARG:N	2.51	0.41
4:D:67:ILE:HG23	4:D:68:TYR:CD1	2.56	0.41
5:E:15:ARG:HD3	5:E:16:THR:O	2.20	0.41
10:J:71:LEU:HD23	10:J:71:LEU:HA	1.87	0.41
13:M:3:ARG:H	13:M:9:ILE:HG12	1.85	0.41
16:P:3:LYS:O	16:P:21:VAL:HA	2.21	0.41
1:A:139:G:H1	1:A:171:C:H42	1.67	0.41
1:A:721:A:H2'	1:A:722:C:C6	2.55	0.41
1:A:1037:C:O3'	14:N:45:ARG:NH2	2.53	0.41
1:A:1399:G:H2'	1:A:1400:G:H8	1.85	0.41
2:B:125:PRO:O	2:B:127:ILE:N	2.50	0.41
7:G:42:ILE:HD12	7:G:42:ILE:HA	1.87	0.41
9:I:25:LYS:HB2	9:I:60:ASP:OD1	2.20	0.41
9:I:56:LEU:HB3	9:I:57:GLY:H	1.60	0.41
20:T:36:LEU:HD23	20:T:36:LEU:HA	1.87	0.41
1:A:416:U:C5	1:A:420:G:H8	2.39	0.41
1:A:469:G:H5'	1:A:471:U:O4'	2.21	0.41
1:A:715:G:H5'	1:A:750:A:H4'	2.01	0.41
1:A:814:G:H2'	1:A:815:U:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1013:A:C8	1:A:1014:G:C8	3.09	0.41
1:A:1096:C:OP1	9:I:9:ARG:HD2	2.21	0.41
1:A:1135:A:C6	1:A:1157:A:C6	3.08	0.41
1:A:1187:C:N4	1:A:1188:U:O4	2.54	0.41
1:A:1437:C:H2'	1:A:1438:C:O4'	2.21	0.41
2:B:22:LYS:NZ	2:B:35:GLU:OE1	2.53	0.41
2:B:28:PHE:CD2	2:B:190:THR:HA	2.55	0.41
2:B:35:GLU:H	2:B:35:GLU:HG2	1.65	0.41
2:B:47:THR:HG23	2:B:202:PRO:HG2	2.03	0.41
2:B:137:ARG:NH2	2:B:138:LEU:HD13	2.35	0.41
2:B:182:ILE:HA	2:B:183:PRO:HD2	1.78	0.41
4:D:150:GLU:O	4:D:153:ARG:HB2	2.20	0.41
5:E:118:ILE:HG12	5:E:119:LEU:N	2.36	0.41
6:F:47:ARG:CZ	6:F:47:ARG:H	2.33	0.41
13:M:40:ASN:HA	13:M:41:PRO:HD2	1.92	0.41
22:X:36:G:H1	23:W:1:C:N4	2.19	0.41
22:X:36:G:H2'	22:X:37:A:H8	1.85	0.41
1:A:582:U:H4'	8:H:94:TYR:CG	2.55	0.41
1:A:1047:C:O2'	1:A:1169:C:H1'	2.21	0.41
1:A:1080:A:H2'	1:A:1081:C:C6	2.56	0.41
2:B:55:PHE:HD2	2:B:55:PHE:HA	1.67	0.41
8:H:6:ILE:HD12	8:H:6:ILE:H	1.85	0.41
10:J:8:LEU:HD21	10:J:20:ALA:HB1	2.03	0.41
12:L:10:LEU:HD23	12:L:10:LEU:HA	1.85	0.41
16:P:49:LEU:HD22	16:P:73:LEU:HD22	2.02	0.41
17:Q:81:ARG:NE	17:Q:84:LEU:HD23	2.36	0.41
1:A:1038:C:O2	1:A:1175:G:C2	2.74	0.40
1:A:1096:C:H1'	1:A:1156:A:C4	2.56	0.40
1:A:1277:G:O2'	1:A:1280:C:N4	2.54	0.40
1:A:1378:G:C2	1:A:1379:C:H1'	2.56	0.40
3:C:113:ALA:N	3:C:114:PRO:HD2	2.36	0.40
3:C:156:ARG:NH2	3:C:161:GLU:HA	2.36	0.40
11:K:73:MET:HE1	11:K:103:LEU:N	2.36	0.40
13:M:34:LEU:HD22	13:M:39:ILE:HB	2.03	0.40
18:R:23:LYS:HD2	18:R:57:GLY:O	2.21	0.40
1:A:115:G:N2	1:A:116:C:H1'	2.37	0.40
1:A:674:G:H2'	1:A:675:G:O4'	2.21	0.40
1:A:927:A:C2	1:A:1210:G:N3	2.89	0.40
1:A:1203:C:C4	13:M:104:ARG:HG2	2.56	0.40
2:B:105:PHE:O	2:B:109:SER:OG	2.29	0.40
6:F:1:MET:HA	6:F:67:MET:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:90:GLU:H	7:G:90:GLU:HG2	1.77	0.40
7:G:137:LYS:O	7:G:141:VAL:HG23	2.21	0.40
8:H:127:LEU:HD23	8:H:127:LEU:HA	1.93	0.40
1:A:102:A:H2'	1:A:322:G:N2	2.36	0.40
1:A:265:C:H2'	1:A:266:A:C8	2.56	0.40
1:A:463:A:OP1	1:A:463:A:H4'	2.21	0.40
1:A:955:A:C2'	1:A:956:A:H5''	2.51	0.40
1:A:1197:G:H2'	1:A:1198:G:C8	2.57	0.40
2:B:51:LEU:HD11	2:B:214:ILE:HD11	2.02	0.40
2:B:69:LEU:HB3	2:B:162:ILE:CD1	2.51	0.40
5:E:34:VAL:HG12	5:E:62:ALA:HB1	2.03	0.40
12:L:102:ARG:NH1	12:L:108:ALA:O	2.53	0.40
13:M:3:ARG:O	13:M:57:ARG:HD3	2.21	0.40
17:Q:9:VAL:HG13	17:Q:56:VAL:HG22	2.02	0.40
21:V:18:TYR:CD1	21:V:24:ARG:HG2	2.57	0.40
1:A:917:G:C6	1:A:918:C:N4	2.90	0.40
1:A:1114:U:H5''	1:A:1115:C:C5	2.56	0.40
1:A:1268:G:O2'	9:I:38:GLN:O	2.31	0.40
5:E:91:LEU:HB3	5:E:118:ILE:HD11	2.02	0.40
1:A:552:G:C6	1:A:553:C:N4	2.89	0.40
1:A:566:U:OP2	1:A:742:G:N1	2.47	0.40
1:A:748:C:H2'	1:A:749:G:O4'	2.22	0.40
1:A:829:G:H2'	1:A:830:G:H8	1.85	0.40
1:A:1202:A:H2'	1:A:1202:A:N3	2.37	0.40
1:A:1352:A:H4'	7:G:29:LYS:HE2	2.03	0.40
9:I:43:ALA:HA	9:I:74:ILE:HD13	2.02	0.40
10:J:40:LEU:HA	10:J:41:PRO:HD3	1.96	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:79:ARG:CD	10:J:79:ARG:NE[8_665]	1.46	0.74
10:J:79:ARG:CG	10:J:79:ARG:CD[8_665]	1.53	0.67
10:J:79:ARG:CG	10:J:79:ARG:CG[8_665]	2.05	0.15

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%)	176 (76%)	44 (19%)	12 (5%)	2	20
3	C	204/239 (85%)	166 (81%)	27 (13%)	11 (5%)	2	19
4	D	206/209 (99%)	178 (86%)	22 (11%)	6 (3%)	4	33
5	E	148/162 (91%)	134 (90%)	11 (7%)	3 (2%)	7	42
6	F	99/101 (98%)	89 (90%)	10 (10%)	0	100	100
7	G	153/156 (98%)	137 (90%)	13 (8%)	3 (2%)	7	42
8	H	136/138 (99%)	124 (91%)	11 (8%)	1 (1%)	22	62
9	I	125/128 (98%)	98 (78%)	16 (13%)	11 (9%)	1	9
10	J	96/105 (91%)	65 (68%)	21 (22%)	10 (10%)	0	7
11	K	117/129 (91%)	98 (84%)	17 (14%)	2 (2%)	9	45
12	L	122/132 (92%)	98 (80%)	18 (15%)	6 (5%)	2	21
13	M	123/126 (98%)	91 (74%)	29 (24%)	3 (2%)	6	37
14	N	58/61 (95%)	45 (78%)	9 (16%)	4 (7%)	1	14
15	O	86/89 (97%)	79 (92%)	3 (4%)	4 (5%)	2	22
16	P	81/88 (92%)	71 (88%)	9 (11%)	1 (1%)	13	52
17	Q	102/105 (97%)	84 (82%)	11 (11%)	7 (7%)	1	14
18	R	71/88 (81%)	62 (87%)	6 (8%)	3 (4%)	3	24
19	S	78/93 (84%)	55 (70%)	19 (24%)	4 (5%)	2	20
20	T	97/106 (92%)	81 (84%)	9 (9%)	7 (7%)	1	14
21	V	22/27 (82%)	21 (96%)	1 (4%)	0	100	100
All	All	2356/2538 (93%)	1952 (83%)	306 (13%)	98 (4%)	3	24

All (98) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	232	PRO

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Mol	Chain	Res	Type
2	B	236	TYR
8	H	91	ARG
9	I	38	GLN
9	I	43	ALA
10	J	85	LEU
14	N	14	PRO
17	Q	47	PRO
17	Q	49	GLU
17	Q	79	SER
2	B	21	ARG
2	B	74	LYS
2	B	137	ARG
3	C	3	ASN
3	C	119	ARG
3	C	154	SER
3	C	167	TRP
4	D	4	TYR
4	D	29	PRO
5	E	85	GLY
7	G	4	ARG
9	I	39	GLY
9	I	101	PHE
9	I	121	ARG
10	J	23	ILE
10	J	72	VAL
10	J	73	ASP
10	J	90	LEU
12	L	116	SER
12	L	121	GLY
13	M	86	CYS
15	O	21	ASP
15	O	88	ARG
16	P	31	LYS
18	R	86	VAL
19	S	6	LYS
20	T	49	ALA
2	B	9	GLU
2	B	126	GLU
2	B	207	ALA
2	B	238	LEU
3	C	61	ALA
3	C	66	VAL

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Mol	Chain	Res	Type
3	C	156	ARG
3	C	206	GLU
4	D	30	LYS
4	D	153	ARG
4	D	181	MET
7	G	32	ARG
9	I	33	PHE
9	I	88	TYR
9	I	117	HIS
10	J	34	VAL
11	K	117	ASN
12	L	28	LYS
12	L	46	LYS
12	L	115	LYS
17	Q	98	LEU
19	S	23	ASN
20	T	73	HIS
20	T	98	PRO
2	B	77	ALA
3	C	96	GLY
5	E	16	THR
5	E	17	ALA
9	I	118	LYS
10	J	40	LEU
10	J	55	LYS
10	J	60	ARG
11	K	126	ARG
12	L	78	GLN
13	M	10	PRO
15	O	19	PRO
15	O	23	GLY
17	Q	97	SER
18	R	21	LYS
19	S	30	LEU
20	T	96	GLY
20	T	97	ALA
2	B	20	GLU
3	C	15	THR
9	I	7	THR
14	N	15	LYS
17	Q	99	SER
2	B	136	VAL

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Mol	Chain	Res	Type
14	N	24	CYS
17	Q	30	PRO
18	R	87	ARG
19	S	26	GLY
20	T	9	ASN
7	G	81	GLY
9	I	44	VAL
4	D	5	ILE
13	M	7	VAL
14	N	18	VAL
20	T	69	GLY
3	C	81	GLY
10	J	39	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	B	202/220 (92%)	172 (85%)	30 (15%)	3 19
3	C	160/188 (85%)	146 (91%)	14 (9%)	10 39
4	D	180/181 (99%)	159 (88%)	21 (12%)	5 28
5	E	115/123 (94%)	107 (93%)	8 (7%)	15 47
6	F	90/90 (100%)	83 (92%)	7 (8%)	12 43
7	G	126/127 (99%)	116 (92%)	10 (8%)	12 43
8	H	119/119 (100%)	107 (90%)	12 (10%)	7 34
9	I	98/99 (99%)	82 (84%)	16 (16%)	2 14
10	J	87/92 (95%)	76 (87%)	11 (13%)	4 24
11	K	90/99 (91%)	77 (86%)	13 (14%)	3 20
12	L	104/109 (95%)	94 (90%)	10 (10%)	8 36
13	M	100/101 (99%)	94 (94%)	6 (6%)	19 53
14	N	49/50 (98%)	46 (94%)	3 (6%)	18 53
15	O	79/80 (99%)	71 (90%)	8 (10%)	7 34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	P	72/74 (97%)	60 (83%)	12 (17%)	2	13
17	Q	96/97 (99%)	87 (91%)	9 (9%)	8	37
18	R	64/77 (83%)	57 (89%)	7 (11%)	6	31
19	S	71/80 (89%)	64 (90%)	7 (10%)	8	35
20	T	75/82 (92%)	66 (88%)	9 (12%)	5	27
21	V	19/22 (86%)	18 (95%)	1 (5%)	22	57
All	All	1996/2110 (95%)	1782 (89%)	214 (11%)	6	32

All (214) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	8	LYS
2	B	10	LEU
2	B	15	VAL
2	B	16	HIS
2	B	17	PHE
2	B	21	ARG
2	B	24	TRP
2	B	28	PHE
2	B	30	ARG
2	B	33	TYR
2	B	51	LEU
2	B	55	PHE
2	B	59	GLU
2	B	60	ASP
2	B	64	ARG
2	B	71	VAL
2	B	79	ASP
2	B	94	ASN
2	B	114	ARG
2	B	134	GLU
2	B	142	LEU
2	B	160	ASP
2	B	163	PHE
2	B	168	THR
2	B	179	LYS
2	B	185	ILE
2	B	197	VAL
2	B	200	ILE
2	B	211	ILE

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Mol	Chain	Res	Type
2	B	229	VAL
3	C	34	LEU
3	C	45	LYS
3	C	48	TYR
3	C	64	VAL
3	C	87	LEU
3	C	95	THR
3	C	112	SER
3	C	119	ARG
3	C	127	ARG
3	C	128	PHE
3	C	152	ILE
3	C	166	GLU
3	C	172	ARG
3	C	173	VAL
4	D	3	ARG
4	D	12	CYS
4	D	57	ARG
4	D	71	SER
4	D	78	LEU
4	D	86	LYS
4	D	96	LEU
4	D	99	SER
4	D	107	ARG
4	D	114	ARG
4	D	116	GLN
4	D	119	GLN
4	D	127	THR
4	D	139	ARG
4	D	151	LYS
4	D	161	ASN
4	D	165	MET
4	D	168	ARG
4	D	181	MET
4	D	187	ARG
4	D	200	GLU
5	E	10	MET
5	E	15	ARG
5	E	33	VAL
5	E	41	VAL
5	E	43	LEU
5	E	57	LYS

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Mol	Chain	Res	Type
5	E	75	THR
5	E	79	GLU
6	F	11	ASN
6	F	43	LEU
6	F	47	ARG
6	F	69	GLU
6	F	77	ARG
6	F	79	LEU
6	F	89	MET
7	G	10	ARG
7	G	32	ARG
7	G	35	LYS
7	G	45	ASP
7	G	69	VAL
7	G	85	TYR
7	G	97	GLN
7	G	136	LYS
7	G	148	ASN
7	G	149	ARG
8	H	2	LEU
8	H	3	THR
8	H	18	ARG
8	H	29	SER
8	H	39	LEU
8	H	50	ARG
8	H	83	ILE
8	H	85	ARG
8	H	104	ARG
8	H	105	ARG
8	H	112	LEU
8	H	136	GLU
9	I	7	THR
9	I	16	ARG
9	I	23	ASN
9	I	34	ASN
9	I	40	LEU
9	I	47	LEU
9	I	51	ARG
9	I	54	ASP
9	I	58	ARG
9	I	70	LYS
9	I	79	LEU

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Mol	Chain	Res	Type
9	I	92	TYR
9	I	102	LEU
9	I	104	ARG
9	I	114	TYR
9	I	128	ARG
10	J	3	LYS
10	J	21	GLN
10	J	35	SER
10	J	42	THR
10	J	66	ARG
10	J	69	ASN
10	J	74	ILE
10	J	79	ARG
10	J	82	ILE
10	J	85	LEU
10	J	96	ILE
11	K	29	ILE
11	K	34	ASP
11	K	40	ILE
11	K	48	ILE
11	K	57	THR
11	K	81	ASP
11	K	85	ARG
11	K	98	LEU
11	K	104	GLN
11	K	109	VAL
11	K	110	ASP
11	K	117	ASN
11	K	123	LYS
12	L	20	LYS
12	L	23	LYS
12	L	28	LYS
12	L	40	VAL
12	L	41	ARG
12	L	54	LYS
12	L	75	HIS
12	L	81	SER
12	L	83	VAL
12	L	110	VAL
13	M	31	LYS
13	M	49	THR
13	M	56	LEU

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Mol	Chain	Res	Type
13	M	64	TRP
13	M	69	GLU
13	M	81	LEU
14	N	26	ARG
14	N	40	CYS
14	N	41	ARG
15	O	4	THR
15	O	26	GLU
15	O	39	LEU
15	O	43	LEU
15	O	70	LEU
15	O	76	GLU
15	O	79	ARG
15	O	87	ILE
16	P	2	VAL
16	P	21	VAL
16	P	42	ARG
16	P	51	VAL
16	P	55	ARG
16	P	60	LEU
16	P	62	VAL
16	P	65	GLN
16	P	72	ARG
16	P	81	ARG
16	P	82	GLN
16	P	83	GLU
17	Q	9	VAL
17	Q	39	SER
17	Q	48	GLU
17	Q	65	ILE
17	Q	68	ARG
17	Q	70	ARG
17	Q	74	LEU
17	Q	78	GLU
17	Q	100	LYS
18	R	38	GLU
18	R	41	LYS
18	R	47	THR
18	R	66	LEU
18	R	75	ILE
18	R	79	LEU
18	R	86	VAL

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Mol	Chain	Res	Type
19	S	7	LYS
19	S	15	LEU
19	S	35	SER
19	S	36	ARG
19	S	37	ARG
19	S	51	VAL
19	S	77	THR
20	T	15	ARG
20	T	19	SER
20	T	30	LYS
20	T	34	LYS
20	T	36	LEU
20	T	73	HIS
20	T	75	ASN
20	T	84	LEU
20	T	100	ILE
21	V	9	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	16	HIS
2	B	19	HIS
12	L	49	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1506/1507 (99%)	300 (19%)	25 (1%)
22	X	10/17 (58%)	0	0
23	W	3/6 (50%)	0	0
All	All	1519/1530 (99%)	300 (19%)	25 (1%)

All (300) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	7	G
1	A	9	G
1	A	31	G

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Mol	Chain	Res	Type
1	A	32	A
1	A	39	G
1	A	41	G
1	A	47	C
1	A	48	C
1	A	49	U
1	A	50	A
1	A	51	A
1	A	54	C
1	A	59	A
1	A	61	G
1	A	73	G
1	A	94	A
1	A	101	G
1	A	109	A
1	A	114	C
1	A	120	G
1	A	125	C
1	A	157	C
1	A	176	U
1	A	177	G
1	A	184	C
1	A	185	C
1	A	188	U
1	A	189	U
1	A	202	A
1	A	204	A
1	A	208	C
1	A	210	U
1	A	211	U
1	A	212	G
1	A	213	C
1	A	216	G
1	A	227	G
1	A	243	G
1	A	246	A
1	A	247	G
1	A	248	U
1	A	249	U
1	A	263	C
1	A	275	A
1	A	285	G

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Mol	Chain	Res	Type
1	A	286	C
1	A	297	G
1	A	317	A
1	A	324	C
1	A	325	A
1	A	328	G
1	A	340	A
1	A	341	C
1	A	342	G
1	A	343	G
1	A	347	G
1	A	348	C
1	A	349	A
1	A	350	G
1	A	352	A
1	A	363	U
1	A	369	A
1	A	380	G
1	A	385	A
1	A	393	A
1	A	394	C
1	A	402	G
1	A	403	G
1	A	405	G
1	A	406	G
1	A	408	A
1	A	409	G
1	A	410	A
1	A	411	A
1	A	412	G
1	A	416	U
1	A	418	C
1	A	419	G
1	A	420	G
1	A	421	G
1	A	425	U
1	A	427	A
1	A	428	A
1	A	429	C
1	A	435	A
1	A	447	A
1	A	456	C

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Mol	Chain	Res	Type
1	A	457	G
1	A	458	A
1	A	459	G
1	A	460	G
1	A	461	G
1	A	462	G
1	A	463	A
1	A	466	G
1	A	470	G
1	A	471	U
1	A	473	C
1	A	480	A
1	A	481	A
1	A	482	U
1	A	483	A
1	A	484	G
1	A	495	C
1	A	496	U
1	A	502	C
1	A	505	G
1	A	508	G
1	A	515	U
1	A	516	A
1	A	517	A
1	A	519	A
1	A	531	A
1	A	543	A
1	A	544	U
1	A	548	C
1	A	556	A
1	A	557	A
1	A	559	G
1	A	560	G
1	A	561	G
1	A	563	G
1	A	572	G
1	A	600	G
1	A	601	G
1	A	637	A
1	A	649	A
1	A	656	U
1	A	666	G

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Mol	Chain	Res	Type
1	A	671	A
1	A	686	A
1	A	687	G
1	A	701	C
1	A	705	G
1	A	707	U
1	A	715	G
1	A	739	G
1	A	743	A
1	A	761	A
1	A	765	A
1	A	771	A
1	A	777	U
1	A	778	A
1	A	797	U
1	A	801	C
1	A	805	G
1	A	812	A
1	A	823	U
1	A	824	C
1	A	825	U
1	A	826	C
1	A	850	A
1	A	854	G
1	A	875	C
1	A	880	G
1	A	892	A
1	A	904	G
1	A	905	G
1	A	909	C
1	A	911	G
1	A	912	C
1	A	913	A
1	A	917	G
1	A	920	G
1	A	938	U
1	A	939	U
1	A	944	G
1	A	946	A
1	A	947	A
1	A	949	G
1	A	952	A

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Mol	Chain	Res	Type
1	A	953	A
1	A	954	G
1	A	955	A
1	A	958	C
1	A	960	U
1	A	961	A
1	A	967	C
1	A	969	U
1	A	970	U
1	A	971	G
1	A	975	U
1	A	980	G
1	A	981	G
1	A	983	A
1	A	984	C
1	A	985	C
1	A	987	G
1	A	988	G
1	A	998	U
1	A	999	G
1	A	1003	U
1	A	1004	G
1	A	1006	C
1	A	1008	C
1	A	1009	G
1	A	1010	G
1	A	1011	G
1	A	1013	A
1	A	1015	C
1	A	1017	C
1	A	1020	G
1	A	1023	C
1	A	1031	G
1	A	1032	C
1	A	1048	U
1	A	1049	C
1	A	1072	G
1	A	1073	U
1	A	1074	C
1	A	1079	A
1	A	1080	A
1	A	1082	G

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Mol	Chain	Res	Type
1	A	1102	G
1	A	1103	U
1	A	1104	U
1	A	1105	G
1	A	1107	C
1	A	1108	A
1	A	1109	G
1	A	1113	U
1	A	1115	C
1	A	1117	G
1	A	1124	A
1	A	1130	A
1	A	1137	U
1	A	1143	C
1	A	1148	G
1	A	1160	A
1	A	1161	G
1	A	1164	G
1	A	1168	A
1	A	1173	U
1	A	1174	G
1	A	1178	A
1	A	1179	G
1	A	1188	U
1	A	1189	U
1	A	1190	A
1	A	1202	A
1	A	1204	A
1	A	1213	A
1	A	1215	A
1	A	1216	A
1	A	1235	G
1	A	1247	C
1	A	1257	A
1	A	1259	C
1	A	1263	A
1	A	1264	A
1	A	1267	G
1	A	1278	U
1	A	1279	U
1	A	1282	G
1	A	1289	G

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Mol	Chain	Res	Type
1	A	1304	C
1	A	1322	U
1	A	1323	A
1	A	1324	G
1	A	1325	U
1	A	1330	G
1	A	1336	C
1	A	1337	A
1	A	1338	G
1	A	1339	C
1	A	1340	A
1	A	1341	U
1	A	1345	G
1	A	1347	G
1	A	1356	G
1	A	1371	A
1	A	1375	A
1	A	1401	C
1	A	1402	U
1	A	1404	U
1	A	1419	G
1	A	1420	G
1	A	1421	A
1	A	1422	G
1	A	1426	A
1	A	1427	C
1	A	1447	G
1	A	1453	U
1	A	1459	G
1	A	1464	A
1	A	1469	G
1	A	1471	A
1	A	1475	A
1	A	1476	G
1	A	1478	U
1	A	1479	A
1	A	1489	G
1	A	1492	G
1	A	1501	G
1	A	1502	G
1	A	1505	C
1	A	1506	A

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Mol	Chain	Res	Type
1	A	1507	C
1	A	1508	U

All (25) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	60	A
1	A	108	G
1	A	175	G
1	A	247	G
1	A	262	G
1	A	324	C
1	A	368	C
1	A	424	G
1	A	469	G
1	A	470	G
1	A	543	A
1	A	685	C
1	A	796	C
1	A	943	A
1	A	1079	A
1	A	1104	U
1	A	1160	A
1	A	1178	A
1	A	1262	A
1	A	1277	G
1	A	1323	A
1	A	1324	G
1	A	1335	U
1	A	1374	C
1	A	1470	U

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 95 ligands modelled in this entry, 94 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
24	PAR	A	1601	-	45,45,45	1.38	8 (17%)	64,67,67	1.66	12 (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
24	PAR	A	1601	-	-	2/18/94/94	0/4/4/4

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1601	PAR	C52-C42	3.93	1.60	1.52
24	A	1601	PAR	C64-C54	3.25	1.56	1.52
24	A	1601	PAR	C13-C23	2.45	1.56	1.52
24	A	1601	PAR	C62-C52	2.36	1.58	1.52
24	A	1601	PAR	O54-C14	2.18	1.47	1.41
24	A	1601	PAR	C44-C54	2.12	1.57	1.53
24	A	1601	PAR	O54-C54	2.08	1.49	1.44
24	A	1601	PAR	O43-C13	2.04	1.45	1.41

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1601	PAR	O33-C14-C24	6.11	118.73	108.22
24	A	1601	PAR	O54-C54-C44	3.63	116.30	109.69
24	A	1601	PAR	O52-C13-C23	3.43	115.07	107.96
24	A	1601	PAR	C34-C24-N24	-3.25	104.40	111.05
24	A	1601	PAR	O34-C34-C44	-2.77	103.95	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1601	PAR	O11-C11-O51	2.76	118.39	110.67
24	A	1601	PAR	C14-O33-C33	-2.65	111.41	117.96
24	A	1601	PAR	O52-C13-O43	-2.51	108.72	111.43
24	A	1601	PAR	C13-O52-C52	-2.32	112.21	117.96
24	A	1601	PAR	O51-C51-C61	2.24	112.01	106.44
24	A	1601	PAR	C11-O51-C51	2.09	117.78	113.69
24	A	1601	PAR	C13-C23-C33	2.00	104.51	102.10

There are no chirality outliers.

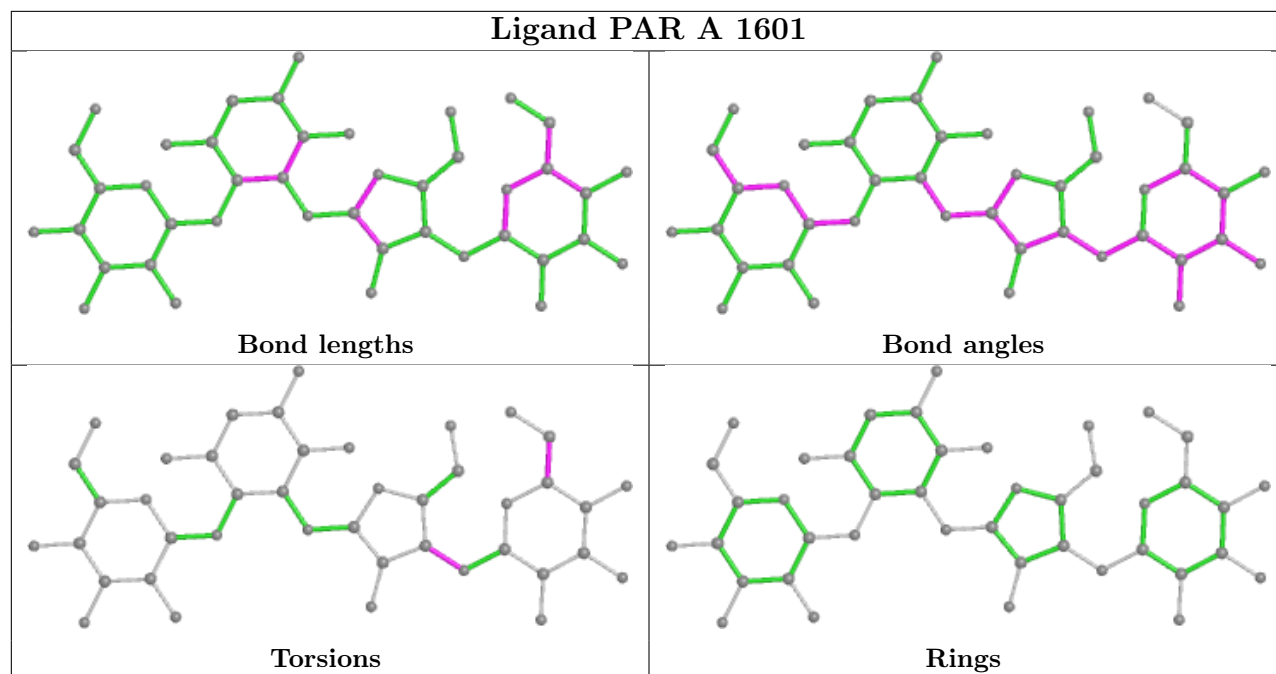
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	A	1601	PAR	C44-C54-C64-N64
24	A	1601	PAR	C43-C33-O33-C14

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data i

6.1 Protein, DNA and RNA chains i

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1507/1507 (100%)	0.03	21 (1%) 75 62	76, 119, 225, 386	0
2	B	234/256 (91%)	-0.09	5 (2%) 63 50	101, 165, 229, 356	0
3	C	206/239 (86%)	-0.15	3 (1%) 73 61	95, 155, 226, 290	0
4	D	208/209 (99%)	-0.12	4 (1%) 66 53	92, 136, 202, 274	0
5	E	150/162 (92%)	-0.30	0 100 100	74, 112, 161, 210	0
6	F	101/101 (100%)	-0.29	0 100 100	105, 146, 195, 230	0
7	G	155/156 (99%)	-0.31	0 100 100	99, 148, 210, 278	0
8	H	138/138 (100%)	-0.24	0 100 100	70, 106, 154, 190	0
9	I	127/128 (99%)	0.01	0 100 100	93, 155, 204, 254	0
10	J	98/105 (93%)	0.55	10 (10%) 6 6	97, 180, 276, 318	0
11	K	119/129 (92%)	-0.06	4 (3%) 45 33	82, 125, 189, 228	0
12	L	124/132 (93%)	0.04	1 (0%) 86 75	73, 122, 194, 210	0
13	M	125/126 (99%)	0.63	13 (10%) 6 6	108, 155, 230, 324	0
14	N	60/61 (98%)	-0.21	1 (1%) 70 57	107, 141, 201, 294	0
15	O	88/89 (98%)	0.06	3 (3%) 45 33	79, 128, 189, 237	0
16	P	83/88 (94%)	0.40	1 (1%) 79 67	78, 110, 153, 255	0
17	Q	104/105 (99%)	0.24	6 (5%) 23 16	78, 111, 205, 265	0
18	R	73/88 (82%)	-0.08	1 (1%) 75 62	90, 131, 224, 248	0
19	S	80/93 (86%)	0.00	2 (2%) 57 43	114, 175, 217, 294	0
20	T	99/106 (93%)	-0.08	1 (1%) 82 71	86, 117, 190, 214	0
21	V	24/27 (88%)	0.02	0 100 100	107, 141, 190, 211	0
22	X	11/17 (64%)	0.24	1 (9%) 9 7	135, 159, 256, 288	0
23	W	4/6 (66%)	0.72	0 100 100	126, 126, 148, 152	0
All	All	3918/4068 (96%)	-0.00	77 (1%) 65 52	70, 131, 220, 386	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	412	G	12.1
1	A	418	C	11.6
1	A	1107	C	11.4
13	M	123	ALA	11.2
1	A	409	G	9.8
10	J	100	THR	9.6
1	A	1506	A	9.3
13	M	124	PRO	9.1
1	A	410	A	8.8
1	A	408	A	7.2
1	A	1507	C	6.6
13	M	121	LYS	6.5
1	A	1505	C	6.5
11	K	129	SER	6.5
1	A	411	A	6.2
17	Q	105	ALA	6.0
17	Q	104	LYS	5.9
10	J	19	SER	5.6
2	B	134	GLU	5.5
1	A	428	A	5.3
1	A	417	U	4.4
13	M	125	ARG	4.3
13	M	122	LYS	4.1
13	M	120	LYS	4.0
1	A	403	G	3.9
17	Q	101	ARG	3.9
3	C	194	GLY	3.8
17	Q	103	GLY	3.5
13	M	126	LYS	3.5
1	A	980	G	3.5
15	O	22	THR	3.3
18	R	17	SER	3.1
13	M	119	GLY	3.1
4	D	35	ARG	2.9
10	J	99	LYS	2.9
1	A	1338	G	2.9
10	J	5	ARG	2.9
3	C	103	VAL	2.9
2	B	207	ALA	2.8
11	K	128	ALA	2.8
2	B	133	LYS	2.7
13	M	32	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
10	J	32	ALA	2.7
1	A	1015	C	2.7
1	A	1012	G	2.6
10	J	64	GLU	2.6
11	K	11	LYS	2.6
3	C	193	TYR	2.5
1	A	419	G	2.5
4	D	30	LYS	2.4
10	J	8	LEU	2.4
4	D	47	ARG	2.4
22	X	33	U	2.4
19	S	3	ARG	2.3
2	B	206	ASP	2.3
13	M	117	VAL	2.3
19	S	69	HIS	2.3
16	P	83	GLU	2.3
14	N	10	ALA	2.2
13	M	6	GLY	2.2
11	K	12	ARG	2.2
20	T	98	PRO	2.2
1	A	1014	G	2.2
1	A	1402	U	2.2
10	J	84	GLN	2.2
15	O	21	ASP	2.2
12	L	128	ALA	2.2
13	M	118	ALA	2.1
17	Q	102	GLY	2.1
17	Q	48	GLU	2.1
13	M	116	THR	2.1
15	O	23	GLY	2.1
4	D	33	MET	2.1
10	J	34	VAL	2.1
1	A	825	U	2.1
2	B	19	HIS	2.0
10	J	9	ARG	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
25	MG	A	1609	1/1	0.25	0.58	93,93,93,93	0
25	MG	A	1620	1/1	0.29	0.73	89,89,89,89	0
25	MG	A	1681	1/1	0.37	0.81	100,100,100,100	0
25	MG	A	1673	1/1	0.38	0.55	104,104,104,104	0
25	MG	A	1691	1/1	0.45	1.40	104,104,104,104	0
25	MG	A	1685	1/1	0.46	1.25	96,96,96,96	0
25	MG	A	1648	1/1	0.50	0.43	97,97,97,97	0
25	MG	A	1668	1/1	0.51	0.41	89,89,89,89	0
25	MG	A	1669	1/1	0.51	0.43	91,91,91,91	0
25	MG	A	1638	1/1	0.54	0.28	100,100,100,100	0
25	MG	A	1630	1/1	0.66	1.07	86,86,86,86	0
25	MG	A	1613	1/1	0.67	1.26	108,108,108,108	0
25	MG	A	1680	1/1	0.69	0.60	88,88,88,88	0
25	MG	A	1606	1/1	0.69	1.18	81,81,81,81	0
25	MG	A	1604	1/1	0.71	0.52	86,86,86,86	0
25	MG	A	1675	1/1	0.73	0.79	106,106,106,106	0
25	MG	A	1678	1/1	0.73	0.74	114,114,114,114	0
25	MG	A	1686	1/1	0.73	0.55	90,90,90,90	0
25	MG	A	1643	1/1	0.73	0.50	67,67,67,67	0
25	MG	A	1614	1/1	0.74	1.54	84,84,84,84	0
25	MG	A	1629	1/1	0.74	1.24	86,86,86,86	0
25	MG	A	1623	1/1	0.77	0.60	87,87,87,87	0
25	MG	A	1644	1/1	0.78	0.98	73,73,73,73	0
25	MG	E	201	1/1	0.78	1.12	69,69,69,69	0
25	MG	A	1602	1/1	0.79	0.36	105,105,105,105	0
25	MG	J	202	1/1	0.81	0.43	97,97,97,97	0
25	MG	A	1666	1/1	0.82	1.45	109,109,109,109	0
25	MG	A	1665	1/1	0.83	0.52	71,71,71,71	0
25	MG	A	1664	1/1	0.83	0.39	95,95,95,95	0
25	MG	A	1605	1/1	0.84	0.37	115,115,115,115	0
25	MG	A	1672	1/1	0.84	0.16	89,89,89,89	0

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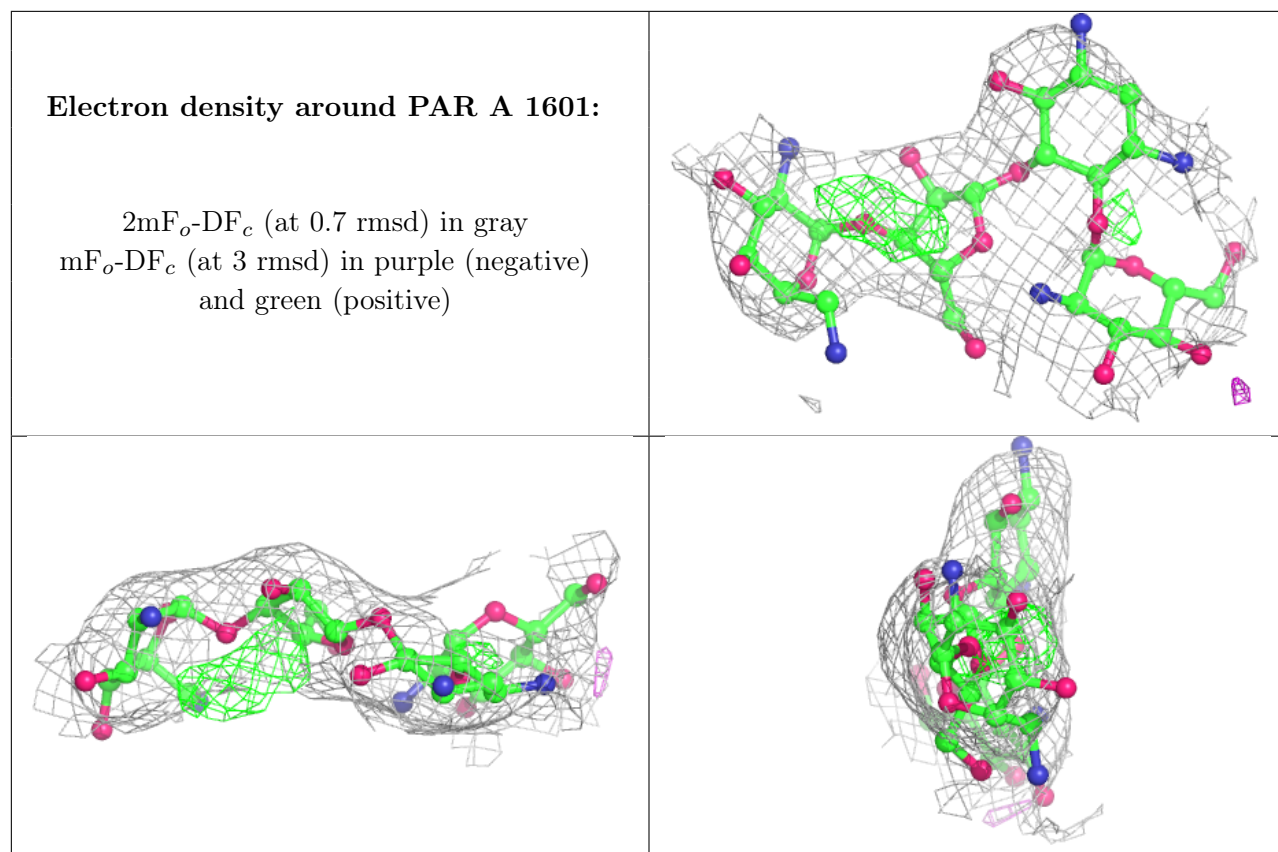
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
25	MG	A	1652	1/1	0.84	1.01	72,72,72,72	0
25	MG	A	1632	1/1	0.85	1.48	116,116,116,116	0
25	MG	A	1690	1/1	0.86	0.15	83,83,83,83	0
25	MG	A	1663	1/1	0.87	0.25	91,91,91,91	0
25	MG	A	1618	1/1	0.88	0.46	71,71,71,71	0
25	MG	A	1636	1/1	0.89	0.86	83,83,83,83	0
25	MG	A	1687	1/1	0.89	0.42	93,93,93,93	0
25	MG	K	201	1/1	0.89	0.49	89,89,89,89	0
25	MG	A	1603	1/1	0.90	1.18	96,96,96,96	0
25	MG	A	1670	1/1	0.90	0.20	111,111,111,111	0
25	MG	A	1667	1/1	0.91	0.30	140,140,140,140	0
25	MG	A	1626	1/1	0.91	0.23	73,73,73,73	0
25	MG	A	1662	1/1	0.91	0.13	105,105,105,105	0
25	MG	A	1658	1/1	0.92	0.36	110,110,110,110	0
25	MG	A	1671	1/1	0.92	0.34	102,102,102,102	0
25	MG	A	1628	1/1	0.92	0.28	100,100,100,100	0
25	MG	A	1657	1/1	0.92	0.48	105,105,105,105	0
25	MG	A	1619	1/1	0.93	0.54	66,66,66,66	0
25	MG	A	1682	1/1	0.93	0.28	85,85,85,85	0
25	MG	A	1610	1/1	0.93	0.21	99,99,99,99	0
25	MG	A	1615	1/1	0.93	0.18	93,93,93,93	0
25	MG	A	1625	1/1	0.93	0.10	85,85,85,85	0
25	MG	A	1635	1/1	0.93	0.37	89,89,89,89	0
25	MG	A	1676	1/1	0.93	0.39	123,123,123,123	0
25	MG	A	1607	1/1	0.93	0.31	95,95,95,95	0
25	MG	A	1679	1/1	0.93	0.36	87,87,87,87	0
25	MG	A	1627	1/1	0.93	0.53	85,85,85,85	0
25	MG	A	1654	1/1	0.94	0.44	110,110,110,110	0
25	MG	A	1608	1/1	0.94	0.22	89,89,89,89	0
25	MG	A	1634	1/1	0.94	0.38	85,85,85,85	0
25	MG	A	1683	1/1	0.94	0.22	78,78,78,78	0
25	MG	A	1659	1/1	0.94	0.19	77,77,77,77	0
24	PAR	A	1601	42/42	0.94	0.21	101,107,113,115	0
25	MG	A	1642	1/1	0.95	0.34	89,89,89,89	0
25	MG	A	1660	1/1	0.95	0.23	86,86,86,86	0
25	MG	A	1633	1/1	0.95	0.52	87,87,87,87	0
25	MG	A	1655	1/1	0.95	0.39	67,67,67,67	0
25	MG	A	1639	1/1	0.95	0.60	94,94,94,94	0
25	MG	A	1641	1/1	0.95	0.35	109,109,109,109	0
25	MG	A	1645	1/1	0.96	0.26	73,73,73,73	0
25	MG	A	1624	1/1	0.96	0.51	67,67,67,67	0
25	MG	A	1661	1/1	0.96	0.28	107,107,107,107	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
25	MG	A	1656	1/1	0.96	0.98	80,80,80,80	0
25	MG	A	1616	1/1	0.96	0.41	68,68,68,68	0
25	MG	A	1684	1/1	0.96	0.15	107,107,107,107	0
25	MG	A	1653	1/1	0.96	0.18	84,84,84,84	0
25	MG	A	1651	1/1	0.97	0.43	79,79,79,79	0
25	MG	A	1640	1/1	0.97	0.21	99,99,99,99	0
25	MG	A	1617	1/1	0.97	0.49	69,69,69,69	0
25	MG	A	1622	1/1	0.97	0.62	67,67,67,67	0
25	MG	A	1631	1/1	0.97	0.48	89,89,89,89	0
25	MG	A	1637	1/1	0.97	0.26	66,66,66,66	0
25	MG	A	1611	1/1	0.97	0.31	94,94,94,94	0
25	MG	A	1612	1/1	0.97	0.63	101,101,101,101	0
25	MG	A	1649	1/1	0.97	0.22	88,88,88,88	0
25	MG	A	1650	1/1	0.97	0.16	69,69,69,69	0
25	MG	A	1689	1/1	0.98	0.16	111,111,111,111	0
25	MG	A	1647	1/1	0.98	0.16	69,69,69,69	0
25	MG	A	1677	1/1	0.98	0.25	88,88,88,88	0
25	MG	A	1674	1/1	0.98	0.40	99,99,99,99	0
25	MG	J	201	1/1	0.98	0.44	96,96,96,96	0
25	MG	A	1646	1/1	0.98	0.22	70,70,70,70	0
25	MG	A	1688	1/1	0.98	0.33	80,80,80,80	0
25	MG	A	1621	1/1	0.99	0.30	81,81,81,81	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 [i](#)

There are no such residues in this entry.