Full wwPDB X-ray Structure Validation Report ⓘ

Apr 28, 2024 – 06:53 pm BST

PDB ID	:	6G63
Title	:	RNase E in complex with sRNA RrpA
Authors	:	Bandyra, K.B.; Luisi, B.F.
Deposited on	:	2018-03-31
Resolution	:	3.95 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:

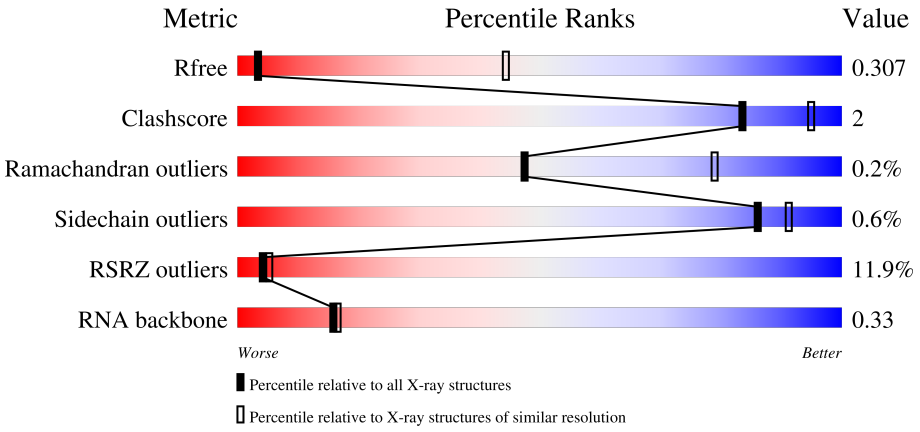
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.95 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	1025 (4.22-3.70)
Clashscore	141614	1085 (4.22-3.70)
Ramachandran outliers	138981	1047 (4.22-3.70)
Sidechain outliers	138945	1039 (4.22-3.70)
RSRZ outliers	127900	1013 (4.28-3.64)
RNA backbone	3102	1041 (4.84-3.00)

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 <=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	510	17% 92% 5%
1	G	510	11% 94%
1	L	510	10% 93%
1	N	510	8% 90% 6%

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Mol	Chain	Length	Quality of chain
2	B	27	30% 41% 15% 15%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 31975 atoms, of which 15827 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 protein called Ribonuclease E.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	494	Total	C	H	N	O	S	0	0	0
			7851	2443	3939	721	737	11			
1	G	493	Total	C	H	N	O	S	0	0	0
			7846	2435	3944	723	732	12			
1	L	493	Total	C	H	N	O	S	0	0	0
			7872	2447	3962	720	731	12			
1	N	494	Total	C	H	N	O	S	0	0	0
			7889	2452	3971	721	733	12			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	303	ARG	ASP	engineered mutation	UNP P21513
A	346	ARG	ASP	engineered mutation	UNP P21513
G	303	ARG	ASP	engineered mutation	UNP P21513
G	346	ARG	ASP	engineered mutation	UNP P21513
L	303	ARG	ASP	engineered mutation	UNP P21513
L	346	ARG	ASP	engineered mutation	UNP P21513
N	303	ARG	ASP	engineered mutation	UNP P21513
N	346	ARG	ASP	engineered mutation	UNP P21513

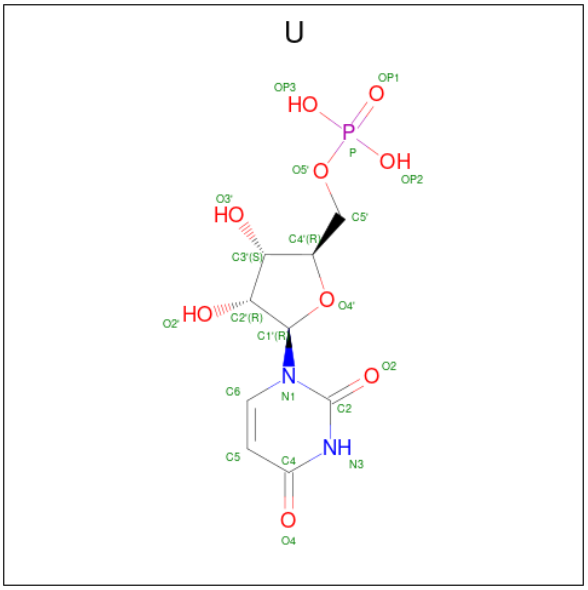
- Molecule 2 is a RNA chain called RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	23	Total	C	N	O	P	0	0	0
			484	219	82	160	23			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Zn 1 1	0	0
3	L	1	Total Zn 1 1	0	0

- Molecule 4 is URIDINE-5'-MONOPHOSPHATE (three-letter code: U) (formula: $C_9H_{13}N_2O_9P$).



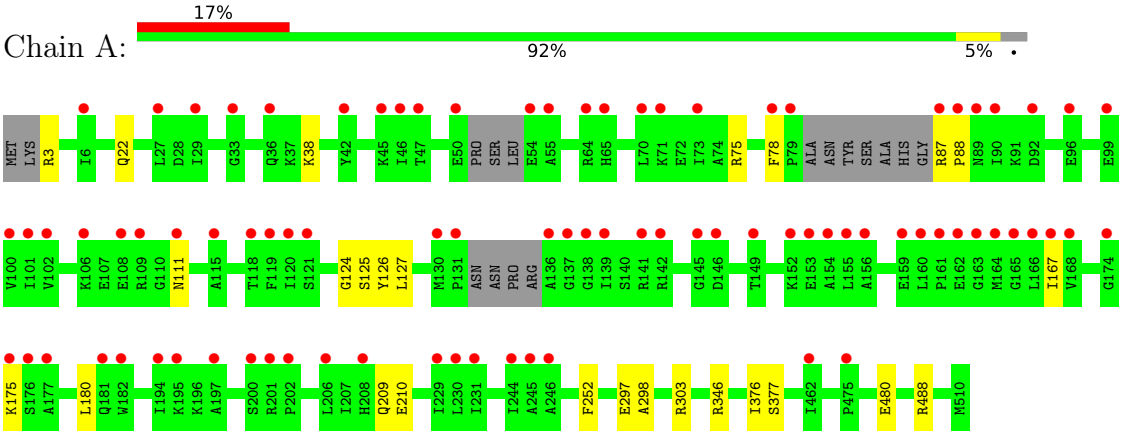
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	N	1	Total C H N O P 31 9 11 2 8 1	0	0

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.

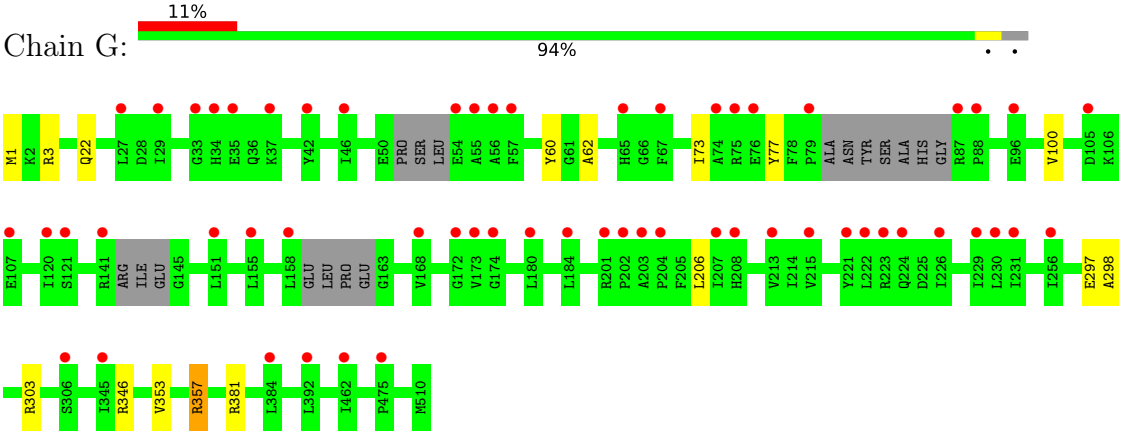
• Molecule 1: Ribonuclease E

Chain A:



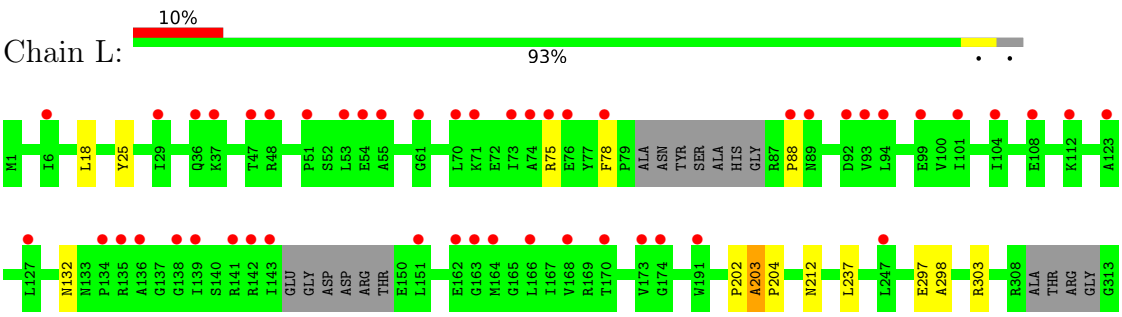
• Molecule 1: Ribonuclease E

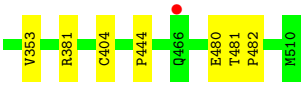
Chain G:



• Molecule 1: Ribonuclease E

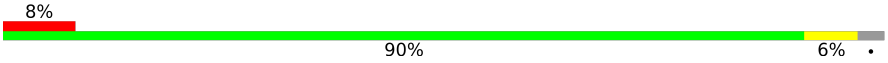
Chain L:

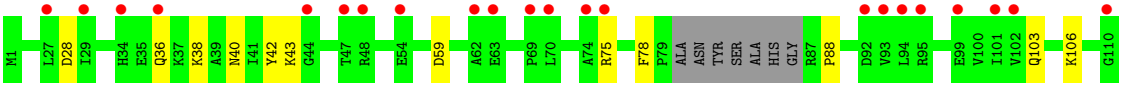


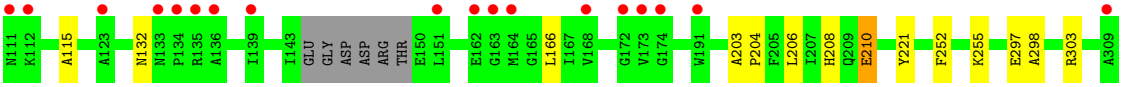


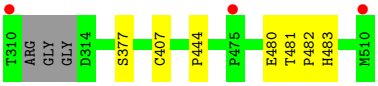
• Molecule 1: Ribonuclease E

Chain N:



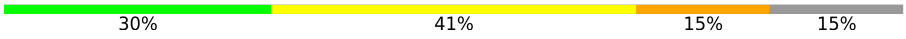


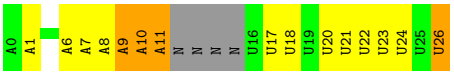




• Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α, β, γ	110.63Å 110.63Å 466.02Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.95 – 3.95 19.95 – 3.95	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.95-3.95) 100.0 (19.95-3.95)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.67 (at 3.94Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.275 , 0.296 0.288 , 0.307	Depositor DCC
R_{free} test set	1372 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å^2)	145.0	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 114.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.24$	Xtriage
Estimated twinning fraction	0.389 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	31975	wwPDB-VP
Average B, all atoms (Å^2)	189.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.41% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: ZN

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	0.29	0/3971	0.59	0/5354
1	G	0.31	0/3960	0.63	3/5336 (0.1%)
1	L	0.33	1/3971 (0.0%)	0.60	0/5355
1	N	0.30	0/3979	0.60	0/5367
2	B	0.33	0/540	0.94	0/834
All	All	0.31	1/16421 (0.0%)	0.62	3/22246 (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
1	L	0	1
1	N	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	353	VAL	CB-CG1	-7.41	1.37	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	G	357	ARG	CG-CD-NE	-6.24	98.70	111.80
1	G	381	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	G	381	ARG	CG-CD-NE	5.55	123.46	111.80

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	L	212	ASN	Peptide
1	N	210	GLU	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3912	3939	3950	28	4
1	G	3902	3944	3946	26	0
1	L	3910	3962	3965	16	0
1	N	3918	3971	3974	21	0
2	B	484	0	244	15	4
3	A	1	0	0	0	0
3	L	1	0	0	0	0
4	N	20	11	11	0	0
All	All	16148	15827	16090	77	4

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 2.

All (77) 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:303:ARG:HD2	1:G:298:ALA:HB2	1.23	1.12
1:L:303:ARG:HD2	1:N:298:ALA:HB2	1.38	1.05
1:A:111:ASN:HB2	1:G:303:ARG:NH2	1.78	0.98
1:A:298:ALA:HB1	1:G:346:ARG:NH1	1.85	0.92
1:A:111:ASN:HB2	1:G:303:ARG:HH22	1.43	0.83
1:A:298:ALA:HB1	1:G:346:ARG:HH11	1.41	0.82
1:L:303:ARG:HD3	1:N:297:GLU:HG3	1.65	0.78
1:A:298:ALA:HB2	1:G:303:ARG:HD2	1.68	0.74
1:A:303:ARG:HD3	1:G:297:GLU:HG3	1.72	0.71
1:G:77:TYR:OH	1:G:100:VAL:HG21	1.92	0.70
1:L:298:ALA:HB2	1:N:303:ARG:HD2	1.75	0.67
2:B:7:A:H2'	2:B:8:A:C8	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3:ARG:HH12	2:B:10:A:H4'	1.63	0.63
1:L:303:ARG:HD3	1:N:297:GLU:CG	2.29	0.62
1:G:73:ILE:HG23	1:G:77:TYR:CD2	2.34	0.62
1:A:488:ARG:NH1	2:B:23:U:OP1	2.33	0.61
1:N:203:ALA:HB3	1:N:204:PRO:HD3	1.82	0.60
1:G:1:MET:N	2:B:11:A:OP1	2.35	0.60
1:L:203:ALA:HB3	1:L:204:PRO:HD3	1.84	0.59
1:L:203:ALA:HB3	1:L:204:PRO:CD	2.33	0.59
2:B:20:U:H2'	2:B:21:U:H6	1.68	0.59
2:B:8:A:H2'	2:B:9:A:C8	2.39	0.58
1:A:298:ALA:HB2	1:G:303:ARG:NH1	2.19	0.57
1:A:298:ALA:CB	1:G:303:ARG:HD2	2.34	0.57
1:A:125:SER:OG	1:A:180:LEU:HD22	2.06	0.56
2:B:22:U:H2'	2:B:23:U:C6	2.41	0.55
1:L:18:LEU:HD22	1:L:25:TYR:CD1	2.42	0.55
1:N:444:PRO:HG3	1:N:480:GLU:O	2.06	0.54
1:N:28:ASP:OD1	1:N:221:TYR:OH	2.18	0.54
1:G:353:VAL:CG1	1:G:357:ARG:NH2	2.71	0.53
1:N:106:LYS:HB2	1:N:115:ALA:HB3	1.89	0.53
2:B:22:U:H2'	2:B:23:U:H6	1.74	0.53
1:A:346:ARG:HH11	1:G:298:ALA:HB1	1.74	0.53
1:A:210:GLU:O	1:A:210:GLU:HG3	2.09	0.52
1:A:111:ASN:HB2	1:G:303:ARG:HH21	1.72	0.52
1:A:298:ALA:HB2	1:G:303:ARG:CZ	2.40	0.51
1:A:303:ARG:CD	1:G:298:ALA:HB2	2.16	0.51
2:B:21:U:H2'	2:B:22:U:H6	1.77	0.50
1:A:298:ALA:HB2	1:G:303:ARG:CD	2.38	0.49
2:B:20:U:H2'	2:B:21:U:C6	2.46	0.49
1:L:444:PRO:HG3	1:L:480:GLU:O	2.13	0.48
1:A:297:GLU:O	1:G:303:ARG:NH1	2.47	0.48
2:B:21:U:H2'	2:B:22:U:C6	2.49	0.48
2:B:9:A:H2'	2:B:10:A:C8	2.49	0.48
1:N:444:PRO:CG	1:N:480:GLU:O	2.63	0.47
1:L:297:GLU:HG3	1:N:303:ARG:HD3	1.96	0.46
1:A:175:LYS:HB3	1:A:180:LEU:HD11	1.97	0.46
1:A:124:GLY:N	1:A:127:LEU:O	2.38	0.46
1:L:404:CYS:SG	1:N:407:CYS:HB3	2.56	0.46
1:A:38:LYS:NZ	1:A:209:GLN:O	2.39	0.45
1:N:38:LYS:CB	1:N:210:GLU:OE1	2.65	0.45
1:N:42:TYR:CE1	1:N:206:LEU:HD13	2.52	0.45
1:N:481:THR:OG1	1:N:482:PRO:HD3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3:ARG:NH1	2:B:10:A:H4'	2.30	0.44
1:L:75:ARG:HA	1:L:78:PHE:CD1	2.53	0.43
1:N:40:ASN:O	1:N:103:GLN:HA	2.17	0.43
1:A:210:GLU:O	1:A:210:GLU:CG	2.66	0.43
1:L:203:ALA:CB	1:L:204:PRO:CD	2.96	0.42
1:N:43:LYS:HB3	1:N:203:ALA:O	2.20	0.42
1:L:481:THR:OG1	1:L:482:PRO:CD	2.67	0.42
1:G:22:GLN:NE2	2:B:10:A:C8	2.88	0.42
1:G:353:VAL:HG13	1:G:357:ARG:NH2	2.34	0.42
1:A:75:ARG:HA	1:A:78:PHE:CD1	2.54	0.42
2:B:8:A:C6	2:B:9:A:N6	2.88	0.42
1:L:481:THR:OG1	1:L:482:PRO:HD3	2.20	0.42
1:A:87:ARG:N	1:A:88:PRO:CD	2.83	0.41
1:A:376:ILE:HG22	1:A:377:SER:O	2.20	0.41
1:A:127:LEU:HA	1:A:167:ILE:O	2.21	0.41
1:A:126:TYR:CZ	1:A:180:LEU:HD12	2.55	0.41
1:L:297:GLU:CG	1:N:303:ARG:HD3	2.51	0.41
1:G:353:VAL:HG11	1:G:357:ARG:NH2	2.36	0.41
1:N:36:GLN:HG2	1:N:210:GLU:HB3	2.02	0.41
1:G:60:TYR:CE2	1:G:62:ALA:HB2	2.56	0.41
1:L:381:ARG:NH2	1:N:377:SER:HA	2.36	0.41
1:N:252:PHE:CE1	1:N:255:LYS:HD2	2.56	0.40
1:N:75:ARG:HA	1:N:78:PHE:CD1	2.57	0.40
1:A:303:ARG:HD3	1:G:297:GLU:CG	2.45	0.40

All (4) 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)
1:A:3:ARG:NH2	2:B:26:U:OP1[5_554]	1.91	0.29
1:A:22:GLN:NE2	2:B:24:U:O2'[5_554]	1.97	0.23
1:A:3:ARG:HH22	2:B:26:U:OP1[5_554]	1.38	0.22
1:A:3:ARG:N	2:B:26:U:O3'[5_554]	2.10	0.10

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
1	A	486/510 (95%)	464 (96%)	22 (4%)	0	100 100
1	G	483/510 (95%)	468 (97%)	15 (3%)	0	100 100
1	L	485/510 (95%)	464 (96%)	18 (4%)	3 (1%)	25 63
1	N	486/510 (95%)	470 (97%)	15 (3%)	1 (0%)	47 79
All	All	1940/2040 (95%)	1866 (96%)	70 (4%)	4 (0%)	47 79

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	88	PRO
1	L	202	PRO
1	N	88	PRO
1	L	203	ALA

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
1	A	419/434 (96%)	417 (100%)	2 (0%)	88 93
1	G	418/434 (96%)	417 (100%)	1 (0%)	93 96
1	L	421/434 (97%)	419 (100%)	2 (0%)	88 93
1	N	422/434 (97%)	417 (99%)	5 (1%)	71 83
All	All	1680/1736 (97%)	1670 (99%)	10 (1%)	86 91

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	252	PHE
1	A	480	GLU

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Mol	Chain	Res	Type
1	G	206	LEU
1	L	132	ASN
1	L	237	LEU
1	N	59	ASP
1	N	132	ASN
1	N	166	LEU
1	N	208	HIS
1	N	483	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	485	HIS
1	G	506	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	21/27 (77%)	8 (38%)	0

All (8) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	1	A
2	B	6	A
2	B	9	A
2	B	10	A
2	B	11	A
2	B	17	U
2	B	18	U
2	B	26	U

There are no RNA pucker outliers to report.

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 (i)

Of 3 ligands modelled in this entry, 2 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	$\#\|Z\| > 2$
4	U	N	601	-	18,21,22	0.36	0	26,30,33	0.40	0

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
4	U	N	601	-	-	3/7/25/26	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	N	601	U	O4'-C4'-C5'-O5'
4	N	601	U	C3'-C4'-C5'-O5'
4	N	601	U	C4'-C5'-O5'-P

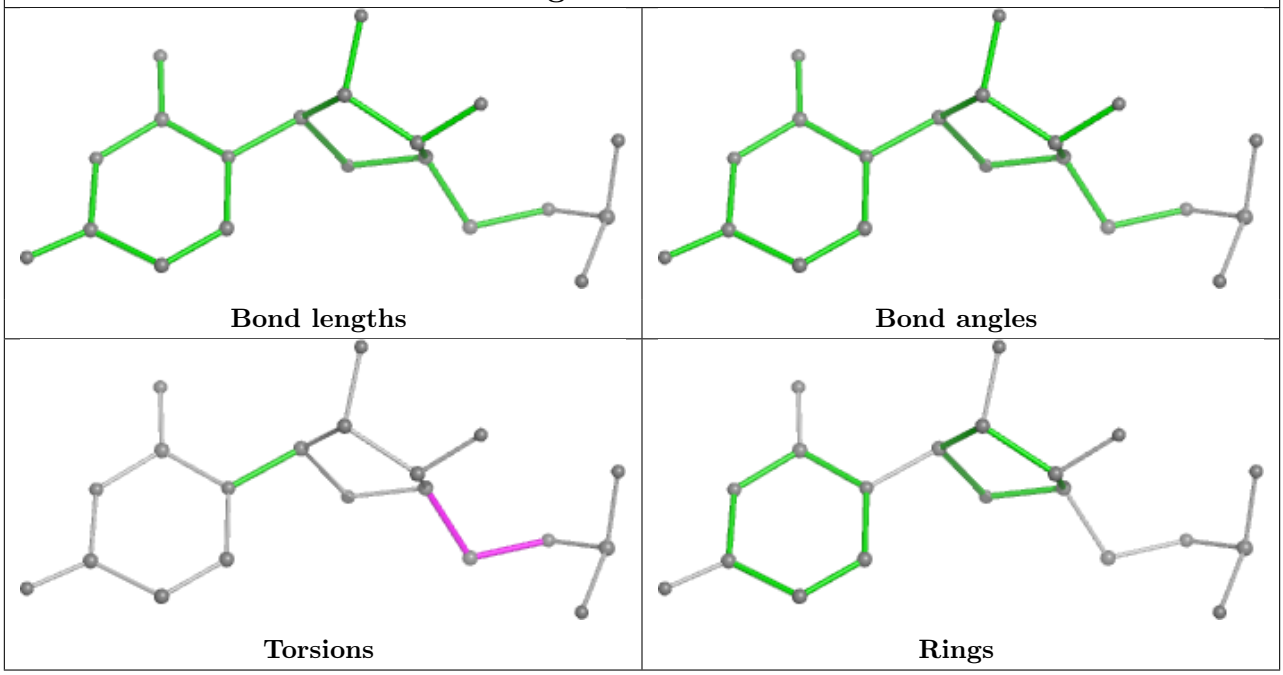
There are no ring outliers.

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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand U N 601



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, 95^{th} 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	494/510 (96%)	1.11	86 (17%) 1 2	71, 211, 429, 466	0
1	G	493/510 (96%)	0.59	58 (11%) 4 5	73, 223, 399, 438	0
1	L	493/510 (96%)	0.56	50 (10%) 7 7	69, 188, 365, 409	0
1	N	494/510 (96%)	0.46	43 (8%) 10 9	70, 193, 341, 356	0
2	B	23/27 (85%)	0.23	0 100 100	218, 244, 296, 334	0
All	All	1997/2067 (96%)	0.67	237 (11%) 4 5	69, 205, 399, 466	0

All (237) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	138	GLY	28.7
1	A	88	PRO	16.9
1	A	164	MET	11.6
1	L	74	ALA	10.6
1	A	165	GLY	10.4
1	A	131	PRO	10.2
1	A	54	GLU	10.1
1	A	137	GLY	10.0
1	A	136	ALA	9.8
1	A	163	GLY	9.7
1	A	87	ARG	8.9
1	A	166	LEU	8.9
1	G	202	PRO	8.7
1	A	194	ILE	8.2
1	A	145	GLY	7.9
1	A	154	ALA	7.7
1	A	89	ASN	7.6
1	A	161	PRO	7.3
1	A	167	ILE	7.0
1	A	78	PHE	6.8

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Mol	Chain	Res	Type	RSRZ
1	A	155	LEU	6.7
1	L	75	ARG	6.6
1	L	37	LYS	6.5
1	A	146	ASP	6.3
1	A	120	ILE	6.2
1	G	79	PRO	6.1
1	G	173	VAL	5.9
1	A	71	LYS	5.8
1	A	130	MET	5.6
1	L	36	GLN	5.6
1	G	172	GLY	5.5
1	G	155	LEU	5.5
1	A	90	ILE	5.5
1	A	246	ALA	5.4
1	A	79	PRO	5.4
1	A	42	TYR	5.3
1	A	139	ILE	5.3
1	A	100	VAL	5.2
1	A	160	LEU	5.1
1	L	168	VAL	5.1
1	A	153	GLU	4.9
1	L	70	LEU	4.9
1	A	162	GLU	4.9
1	L	78	PHE	4.8
1	G	230	LEU	4.8
1	G	180	LEU	4.8
1	G	42	TYR	4.7
1	N	151	LEU	4.6
1	L	173	VAL	4.6
1	A	159	GLU	4.6
1	N	174	GLY	4.5
1	G	37	LYS	4.5
1	G	65	HIS	4.5
1	G	34	HIS	4.4
1	G	208	HIS	4.4
1	L	139	ILE	4.4
1	N	164	MET	4.4
1	L	135	ARG	4.3
1	A	27	LEU	4.3
1	L	166	LEU	4.3
1	A	149	THR	4.2
1	L	143	ILE	4.2

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Mol	Chain	Res	Type	RSRZ
1	N	163	GLY	4.2
1	L	191	TRP	4.2
1	G	75	ARG	4.2
1	A	229	ILE	4.1
1	A	181	GLN	4.1
1	L	53	LEU	4.1
1	G	74	ALA	4.0
1	G	223	ARG	4.0
1	A	168	VAL	4.0
1	G	120	ILE	4.0
1	A	230	LEU	4.0
1	G	87	ARG	4.0
1	L	92	ASP	4.0
1	A	70	LEU	3.9
1	N	111	ASN	3.9
1	A	121	SER	3.8
1	A	102	VAL	3.8
1	G	221	TYR	3.8
1	A	152	LYS	3.8
1	A	175	LYS	3.8
1	G	33	GLY	3.7
1	A	119	PHE	3.7
1	G	229	ILE	3.7
1	L	138	GLY	3.7
1	A	197	ALA	3.7
1	G	201	ARG	3.6
1	N	62	ALA	3.6
1	N	94	LEU	3.6
1	G	88	PRO	3.6
1	N	134	PRO	3.6
1	N	70	LEU	3.5
1	L	136	ALA	3.5
1	N	139	ILE	3.5
1	A	142	ARG	3.5
1	A	65	HIS	3.5
1	L	174	GLY	3.4
1	N	75	ARG	3.4
1	N	162	GLU	3.4
1	G	141	ARG	3.4
1	N	191	TRP	3.4
1	G	184	LEU	3.4
1	G	174	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	206	LEU	3.4
1	A	73	ILE	3.4
1	L	47	THR	3.3
1	N	168	VAL	3.3
1	L	54	GLU	3.3
1	G	231	ILE	3.3
1	N	101	ILE	3.2
1	L	55	ALA	3.2
1	L	29	ILE	3.2
1	G	56	ALA	3.2
1	L	71	LYS	3.2
1	G	345	ILE	3.2
1	G	204	PRO	3.1
1	N	92	ASP	3.1
1	N	34	HIS	3.1
1	G	203	ALA	3.1
1	G	256	ILE	3.1
1	A	55	ALA	3.1
1	N	310	THR	3.1
1	A	177	ALA	3.0
1	G	57	PHE	3.0
1	N	102	VAL	2.9
1	N	173	VAL	2.9
1	A	101	ILE	2.9
1	L	94	LEU	2.9
1	L	170	THR	2.9
1	G	207	ILE	2.9
1	A	50	GLU	2.9
1	A	200	SER	2.9
1	L	141	ARG	2.9
1	N	44	GLY	2.8
1	L	51	PRO	2.8
1	N	510	MET	2.8
1	N	54	GLU	2.8
1	A	46	ILE	2.8
1	A	92	ASP	2.8
1	L	104	ILE	2.8
1	L	466	GLN	2.8
1	N	123	ALA	2.8
1	G	158	LEU	2.7
1	A	118	THR	2.7
1	N	36	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
1	N	133	ASN	2.7
1	G	105	ASP	2.7
1	G	215	VAL	2.6
1	A	45	LYS	2.6
1	L	101	ILE	2.6
1	A	231	ILE	2.6
1	N	110	GLY	2.6
1	G	121	SER	2.6
1	A	156	ALA	2.5
1	L	164	MET	2.5
1	L	151	LEU	2.5
1	A	182	TRP	2.5
1	A	109	ARG	2.5
1	G	29	ILE	2.5
1	L	73	ILE	2.5
1	N	135	ARG	2.5
1	A	208	HIS	2.5
1	G	213	VAL	2.5
1	L	76	GLU	2.5
1	A	47	THR	2.5
1	G	35	GLU	2.4
1	A	106	LYS	2.4
1	N	99	GLU	2.4
1	A	462	ILE	2.4
1	A	245	ALA	2.4
1	N	74	ALA	2.4
1	G	67	PHE	2.4
1	L	134	PRO	2.4
1	N	112	LYS	2.4
1	A	36	GLN	2.4
1	L	163	GLY	2.4
1	A	111	ASN	2.4
1	G	76	GLU	2.4
1	L	127	LEU	2.4
1	G	55	ALA	2.3
1	A	244	ILE	2.3
1	A	176	SER	2.3
1	N	95	ARG	2.3
1	G	462	ILE	2.3
1	L	93	VAL	2.3
1	G	392	LEU	2.3
1	A	108	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	L	112	LYS	2.3
1	A	33	GLY	2.3
1	A	201	ARG	2.3
1	G	222	LEU	2.3
1	L	247	LEU	2.3
1	A	99	GLU	2.2
1	L	88	PRO	2.2
1	A	195	LYS	2.2
1	L	99	GLU	2.2
1	N	69	PRO	2.2
1	G	224	GLN	2.2
1	N	29	ILE	2.2
1	G	168	VAL	2.2
1	L	89	ASN	2.2
1	N	47	THR	2.2
1	A	141	ARG	2.2
1	A	475	PRO	2.2
1	L	6	ILE	2.2
1	N	48	ARG	2.2
1	G	27	LEU	2.2
1	L	162	GLU	2.2
1	A	202	PRO	2.1
1	G	54	GLU	2.1
1	L	108	GLU	2.1
1	A	64	ARG	2.1
1	N	93	VAL	2.1
1	L	61	GLY	2.1
1	L	142	ARG	2.1
1	G	46	ILE	2.1
1	N	63	GLU	2.1
1	A	96	GLU	2.1
1	A	115	ALA	2.1
1	G	306	SER	2.1
1	A	29	ILE	2.1
1	A	6	ILE	2.1
1	G	96	GLU	2.1
1	N	136	ALA	2.1
1	N	309	ALA	2.1
1	L	123	ALA	2.1
1	N	475	PRO	2.1
1	G	107	GLU	2.1
1	G	384	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	N	172	GLY	2.1
1	G	226	ILE	2.0
1	G	151	LEU	2.0
1	N	27	LEU	2.0
1	A	174	GLY	2.0
1	G	475	PRO	2.0
1	L	48	ARG	2.0

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

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)

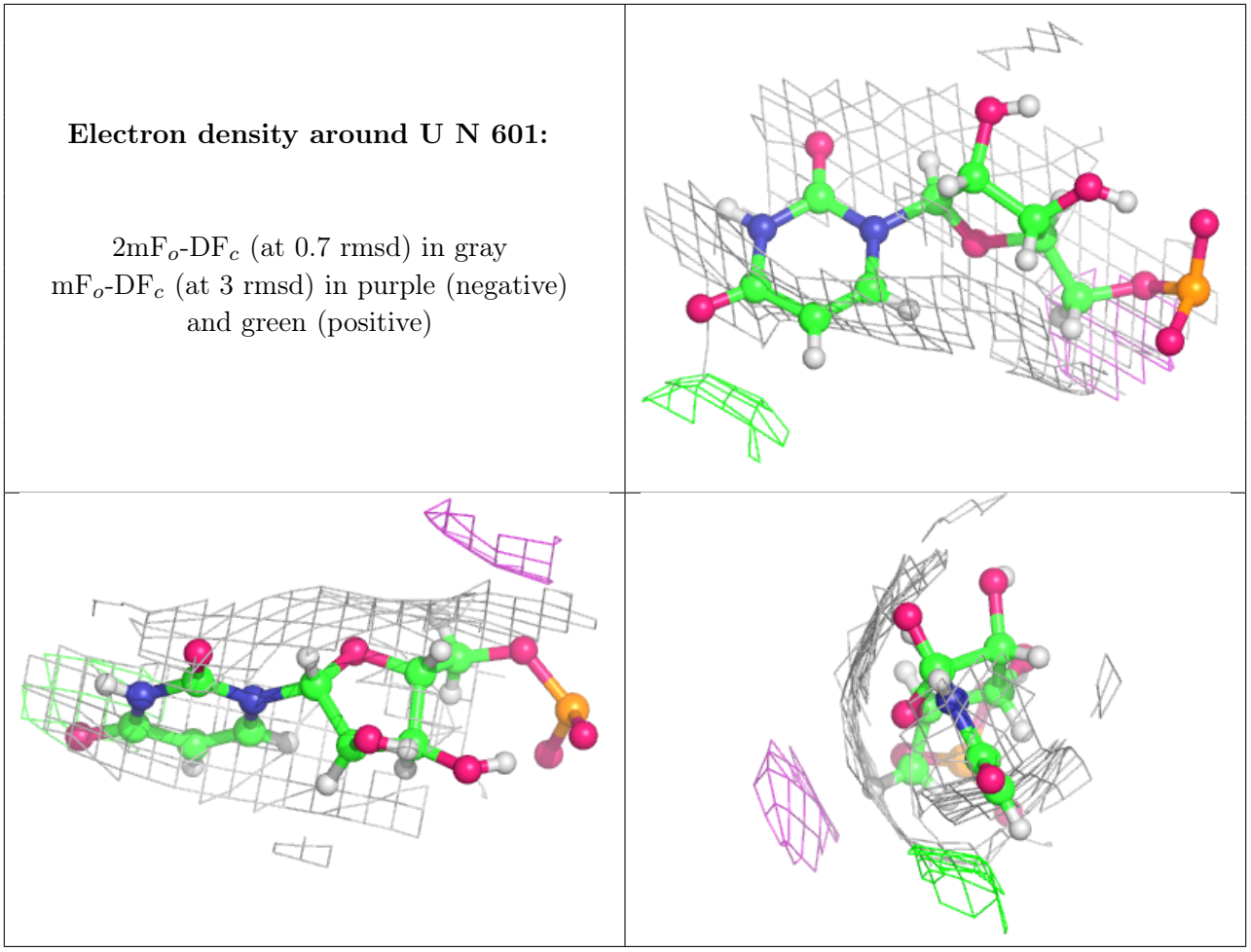
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
4	U	N	601	20/21	0.74	0.23	137,296,297,297	0
3	ZN	L	601	1/1	0.98	0.37	115,115,115,115	0
3	ZN	A	601	1/1	0.98	0.39	118,118,118,118	0

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

Electron density around U N 601:

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



6.5 Other polymers

There are no such residues in this entry.