



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 10, 2021 – 07:26 PM EDT

PDB ID : 3ERC  
Title : Crystal structure of the heterodimeric vaccinia virus mRNA polyadenylate polymerase with three fragments of RNA and 3'-deoxy ATP  
Authors : Li, C.; Li, H.; Zhou, S.; Poulos, T.L.; Gershon, P.D.  
Deposited on : 2008-10-01  
Resolution : 3.21 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
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)	:	2.23.2

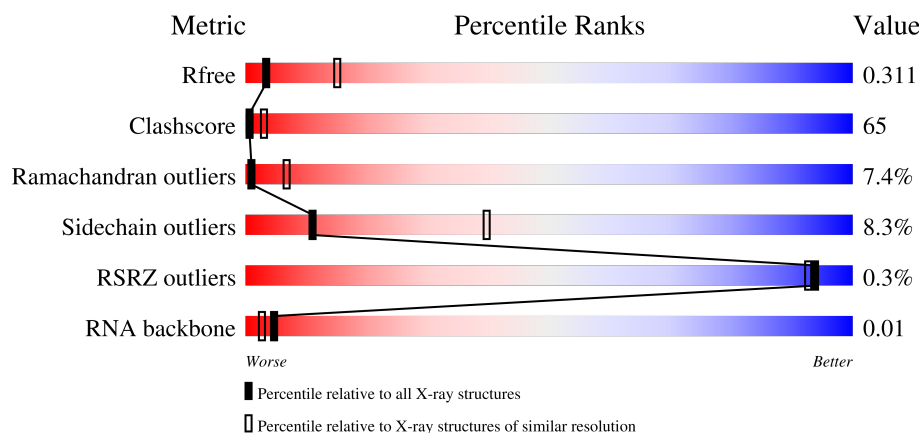
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

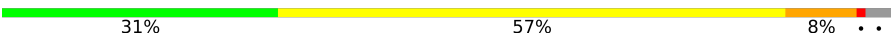
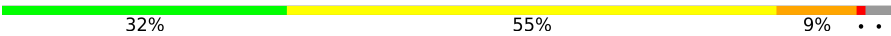
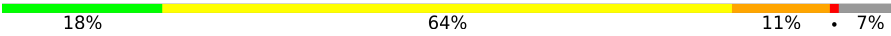
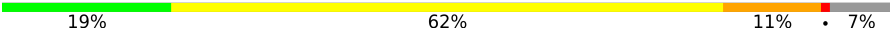
The reported resolution of this entry is 3.21 Å.

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	1335 (3.24-3.20)
Clashscore	141614	1460 (3.24-3.20)
Ramachandran outliers	138981	1437 (3.24-3.20)
Sidechain outliers	138945	1436 (3.24-3.20)
RSRZ outliers	127900	1291 (3.24-3.20)
RNA backbone	3102	1023 (3.54-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	297	
1	B	297	
2	C	479	
2	D	479	

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Mol	Chain	Length	Quality of chain
3	E	5	<div><div></div><div>40%</div><div>40%</div><div>20%</div></div>
3	F	5	<div><div></div><div>40%</div><div>40%</div><div>20%</div></div>
4	G	4	<div><div></div><div>25%</div><div>50%</div><div>25%</div></div>
5	I	5	<div><div></div><div>80%</div><div>20%</div></div>

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 12480 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 protein called Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	288	Total	C	N	O	S	0	0	0
			2382	1552	394	424	12			
1	B	288	Total	C	N	O	S	0	0	0
			2382	1552	394	424	12			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	140	ALA	ARG	engineered mutation	UNP P07617
A	142	ALA	LYS	engineered mutation	UNP P07617
A	143	ALA	ARG	engineered mutation	UNP P07617
B	140	ALA	ARG	engineered mutation	UNP P07617
B	142	ALA	LYS	engineered mutation	UNP P07617
B	143	ALA	ARG	engineered mutation	UNP P07617

- Molecule 2 is a protein called Poly(A) polymerase catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	445	Total	C	N	O	S	0	0	0
			3627	2318	605	680	24			
2	D	445	Total	C	N	O	S	0	0	0
			3627	2318	605	680	24			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	36	SER	LEU	engineered mutation	UNP P23371
D	36	SER	LEU	engineered mutation	UNP P23371

- Molecule 3 is a RNA chain called RNA/DNA chimera (5'-D(CP\*)R(UP\*UP\*)D(CP\*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	5	Total	C	N	O	P	0	0	0
			94	45	13	32	4			
3	F	5	Total	C	N	O	P	0	0	0
			94	45	13	32	4			

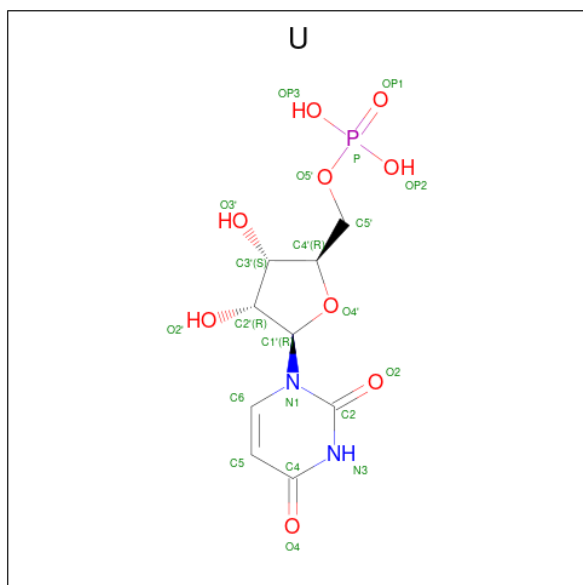
- Molecule 4 is a RNA chain called RNA/DNA chimera (5'-D(CP\*)R(UP\*UP\*)-D(C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	4	Total	C	N	O	P	0	0	0
			75	36	10	26	3			

- Molecule 5 is a RNA chain called RNA/DNA chimera (5'-D(CP\*CP\*)R(UP\*UP\*)D(C)-3').

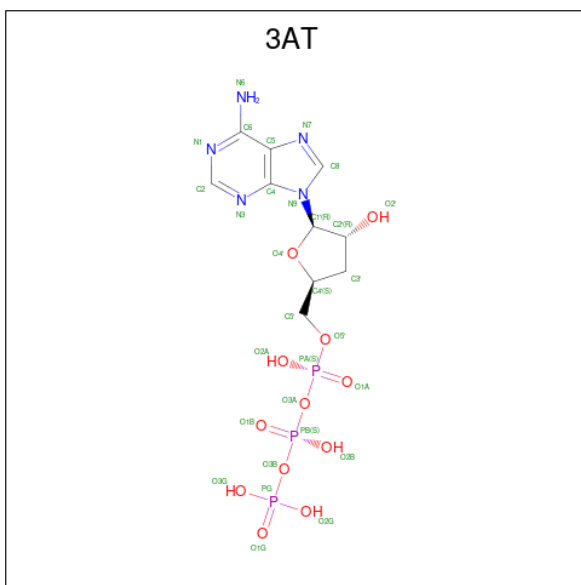
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	I	5	Total	C	N	O	P	0	0	0
			94	45	13	32	4			

- Molecule 6 is URIDINE-5'-MONOPHOSPHATE (three-letter code: U) (formula: C<sub>9</sub>H<sub>13</sub>N<sub>2</sub>O<sub>9</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	C	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
6	D	1	Total	C	N	O	P	0	0
			20	9	2	8	1		

- Molecule 7 is 3'-DEOXYADENOSINE-5'-TRIPHOSPHATE (three-letter code: 3AT) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>12</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	C	1	Total 30	C 10	N 5	O 12	P 3	0	0
7	D	1	Total 30	C 10	N 5	O 12	P 3	0	0

- Molecule 8 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	C	2	Total Ca 2 2	0	0
8	D	2	Total Ca 2 2	0	0

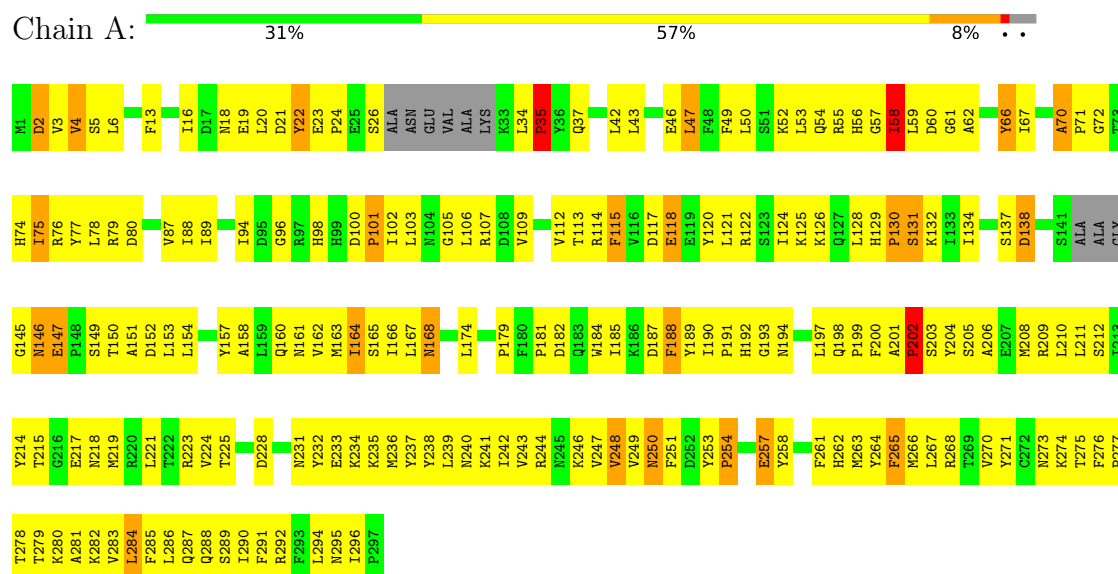
- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	C	1	Total O 1 1	0	0

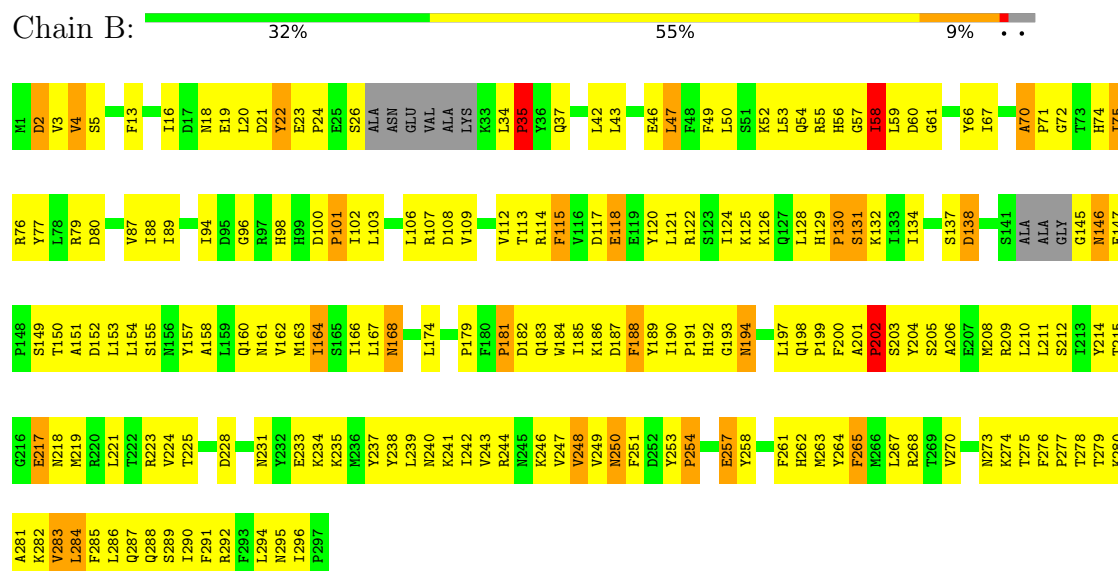
### 3 Residue-property plots

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

#### • Molecule 1: Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase

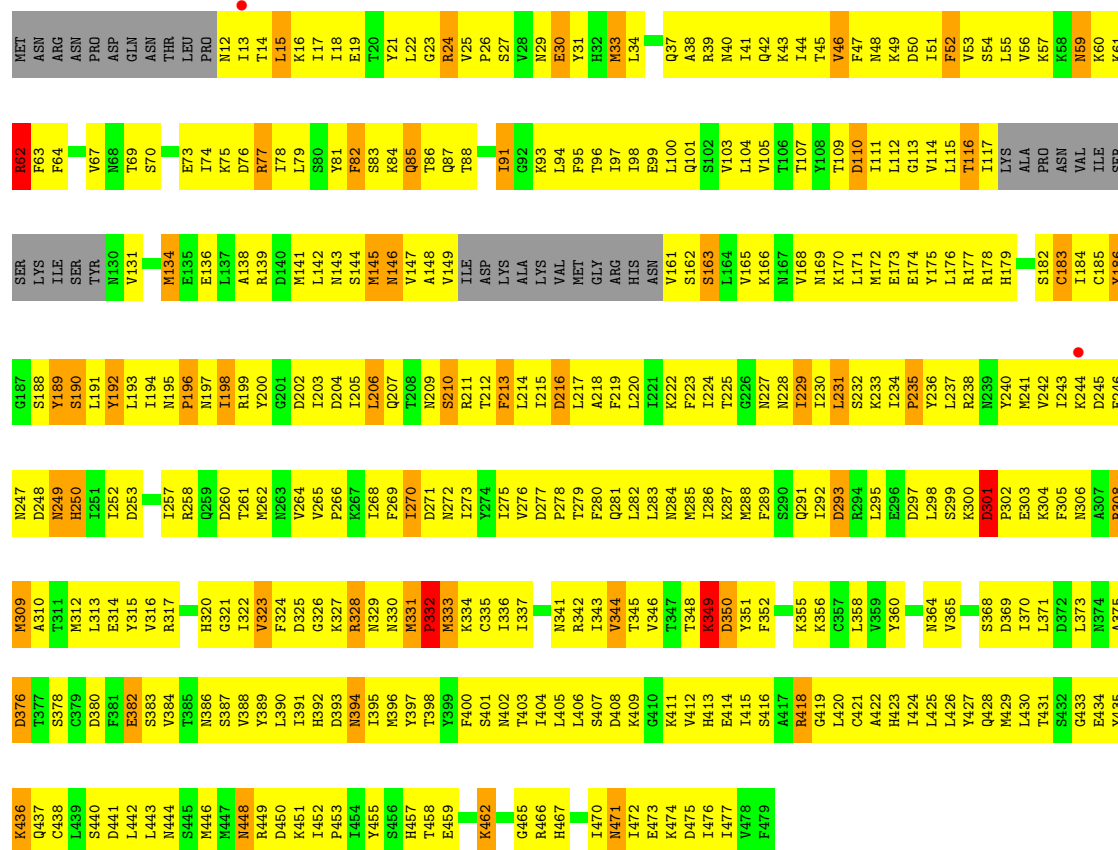


#### • Molecule 1: Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase



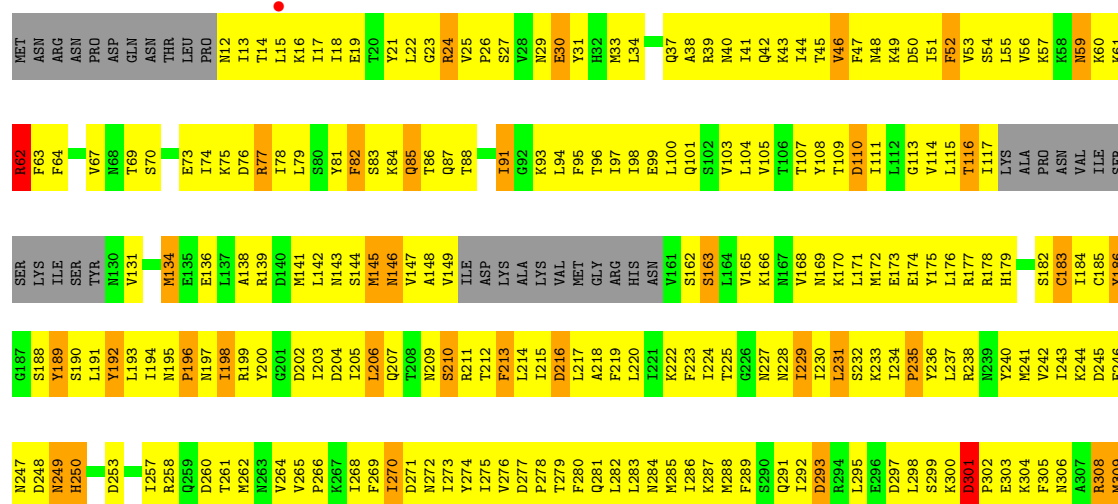
- Molecule 2: Poly(A) polymerase catalytic subunit

Chain C:  18% 64% 11% 7%

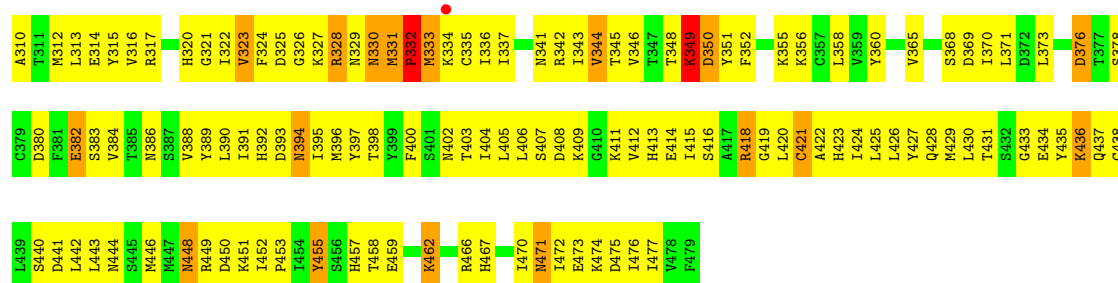


- Molecule 2: Poly(A) polymerase catalytic subunit

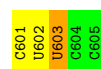
Chain D:  19% 62% 11% 7%



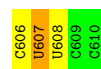




- Molecule 3: RNA/DNA chimera (5'-D(CP\*)R(UP\*UP\*)D(CP\*C)-3')



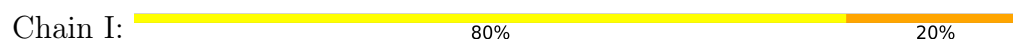
- Molecule 3: RNA/DNA chimera (5'-D(CP\*)R(UP\*UP\*)D(CP\*C)-3')



- Molecule 4: RNA/DNA chimera (5'-D(CP\*)R(UP\*UP\*)-D(C)-3')



- Molecule 5: RNA/DNA chimera (5'-D(CP\*CP\*)R(UP\*UP\*)D(C)-3')



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.92Å 77.15Å 108.03Å 89.52° 73.45° 63.76°	Depositor
Resolution (Å)	38.55 – 3.21 38.55 – 3.16	Depositor EDS
% Data completeness (in resolution range)	93.8 (38.55-3.21) 91.4 (38.55-3.16)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.13 (at 3.18Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.245 , 0.309 0.242 , 0.311	Depositor DCC
$R_{free}$ test set	1453 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	78.7	Xtriage
Anisotropy	0.318	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 73.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.056 for h,h-k,h-l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	12480	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.62% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 3AT, CA

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	0.48	0/2444	0.69	0/3308
1	B	0.49	0/2444	0.69	0/3308
2	C	0.48	0/3686	0.70	0/4972
2	D	0.48	0/3686	0.70	0/4972
3	E	1.01	0/103	0.96	0/156
3	F	0.76	0/103	0.74	0/156
4	G	0.92	0/82	0.78	0/124
5	I	0.75	0/103	0.71	0/156
All	All	0.50	0/12651	0.70	0/17152

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
2	D	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	455	TYR	Sidechain

## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2382	0	2389	223	0
1	B	2382	0	2389	229	0
2	C	3627	0	3689	595	0
2	D	3627	0	3689	600	0
3	E	94	0	55	7	0
3	F	94	0	55	14	0
4	G	75	0	44	5	0
5	I	94	0	55	11	0
6	C	20	0	11	3	0
6	D	20	0	11	2	0
7	C	30	0	12	3	0
7	D	30	0	12	4	0
8	C	2	0	0	0	0
8	D	2	0	0	0	0
9	C	1	0	0	2	0
All	All	12480	0	12411	1620	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 65.

The worst 5 of 1620 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)
2:C:168:VAL:HA	2:C:171:LEU:HD12	1.23	1.11
2:D:168:VAL:HA	2:D:171:LEU:HD12	1.22	1.10
1:A:219:MET:HE3	1:A:221:LEU:HD11	1.32	1.10
2:C:86:THR:HB	2:C:87:GLN:HE22	1.20	1.06
2:C:91:ILE:HD13	2:C:91:ILE:H	1.21	1.06

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	282/297 (95%)	207 (73%)	57 (20%)	18 (6%)	1	9
1	B	282/297 (95%)	203 (72%)	61 (22%)	18 (6%)	1	9
2	C	439/479 (92%)	293 (67%)	110 (25%)	36 (8%)	1	5
2	D	439/479 (92%)	295 (67%)	109 (25%)	35 (8%)	1	5
All	All	1442/1552 (93%)	998 (69%)	337 (23%)	107 (7%)	1	7

5 of 107 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	ASP
1	A	146	ASN
1	A	147	GLU
1	A	277	PRO
1	B	2	ASP

### 5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	266/270 (98%)	241 (91%)	25 (9%)	8	32
1	B	266/270 (98%)	241 (91%)	25 (9%)	8	32
2	C	422/453 (93%)	390 (92%)	32 (8%)	13	44
2	D	422/453 (93%)	390 (92%)	32 (8%)	13	44
All	All	1376/1446 (95%)	1262 (92%)	114 (8%)	11	40

5 of 114 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	110	ASP
2	D	418	ARG
2	C	328	ARG
2	D	394	ASN
2	D	264	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	227	ASN
2	C	392	HIS
2	D	444	ASN
2	D	330	ASN
2	C	228	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	E	1/5 (20%)	1 (100%)	0
3	F	2/5 (40%)	1 (50%)	0
4	G	2/4 (50%)	1 (50%)	0
5	I	2/5 (40%)	1 (50%)	0
All	All	7/19 (36%)	4 (57%)	0

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	E	603	U
3	F	607	U
4	G	502	U
5	I	703	U

There are no RNA pucker outliers to report.

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

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 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	$\# Z  > 2$
7	3AT	D	800	8	25,32,32	1.95	7 (28%)	28,50,50	2.16	4 (14%)
6	U	D	602	-	14,21,22	1.42	2 (14%)	14,30,33	1.27	2 (14%)
7	3AT	C	801	8	25,32,32	1.61	5 (20%)	28,50,50	2.18	6 (21%)
6	U	C	600	-	14,21,22	1.42	2 (14%)	14,30,33	1.35	2 (14%)

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
7	3AT	D	800	8	-	6/18/34/34	0/3/3/3
6	U	D	602	-	-	1/5/25/26	0/2/2/2
7	3AT	C	801	8	-	6/18/34/34	0/3/3/3
6	U	C	600	-	-	3/5/25/26	0/2/2/2

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	D	800	3AT	PG-O1G	3.83	1.62	1.50
6	D	602	U	C4-N3	3.72	1.39	1.33
6	C	600	U	C4-N3	3.71	1.39	1.33
7	D	800	3AT	C4-N3	3.63	1.40	1.35
7	D	800	3AT	C2'-C1'	3.37	1.57	1.54

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	D	800	3AT	N3-C2-N1	-6.35	118.75	128.68
7	C	801	3AT	N3-C2-N1	-6.31	118.82	128.68
7	D	800	3AT	PA-O3A-PB	-5.96	112.38	132.83
7	C	801	3AT	PA-O3A-PB	-5.18	115.05	132.83
7	C	801	3AT	PB-O3B-PG	-4.94	115.87	132.83

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	600	U	C4'-C5'-O5'-P
6	C	600	U	O4'-C1'-N1-C6
6	C	600	U	C2'-C1'-N1-C6
6	D	602	U	O4'-C1'-N1-C6
7	C	801	3AT	PB-O3B-PG-O3G

There are no ring outliers.

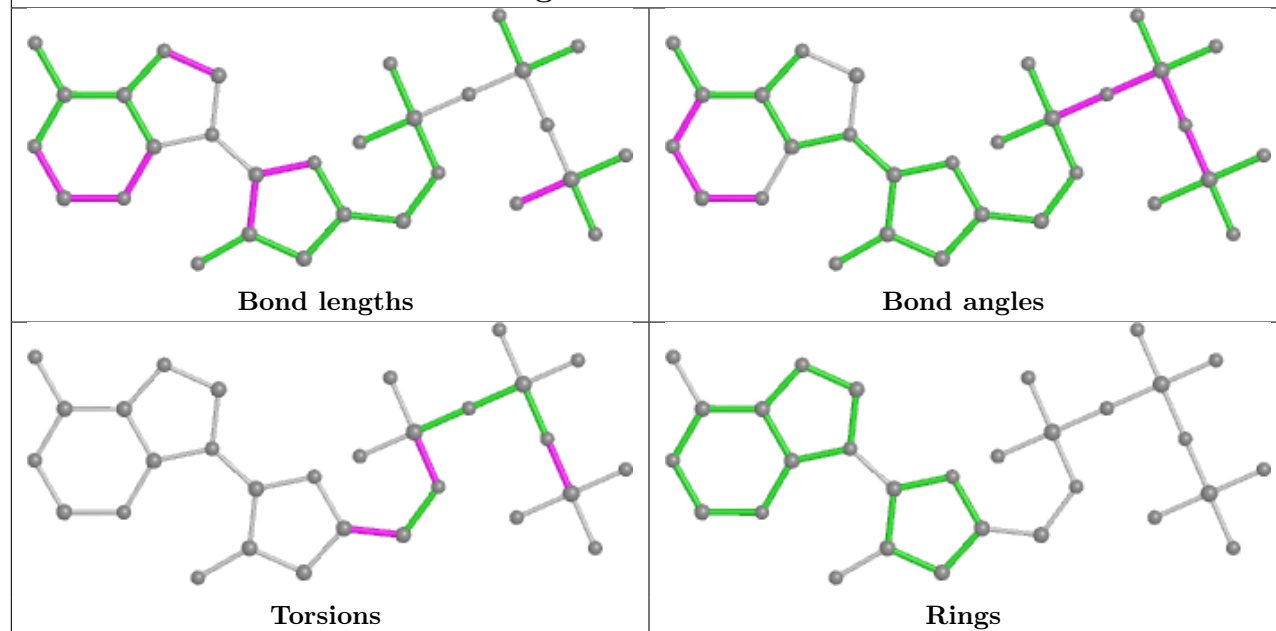
4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	D	800	3AT	4	0
6	D	602	U	2	0
7	C	801	3AT	3	0
6	C	600	U	3	0

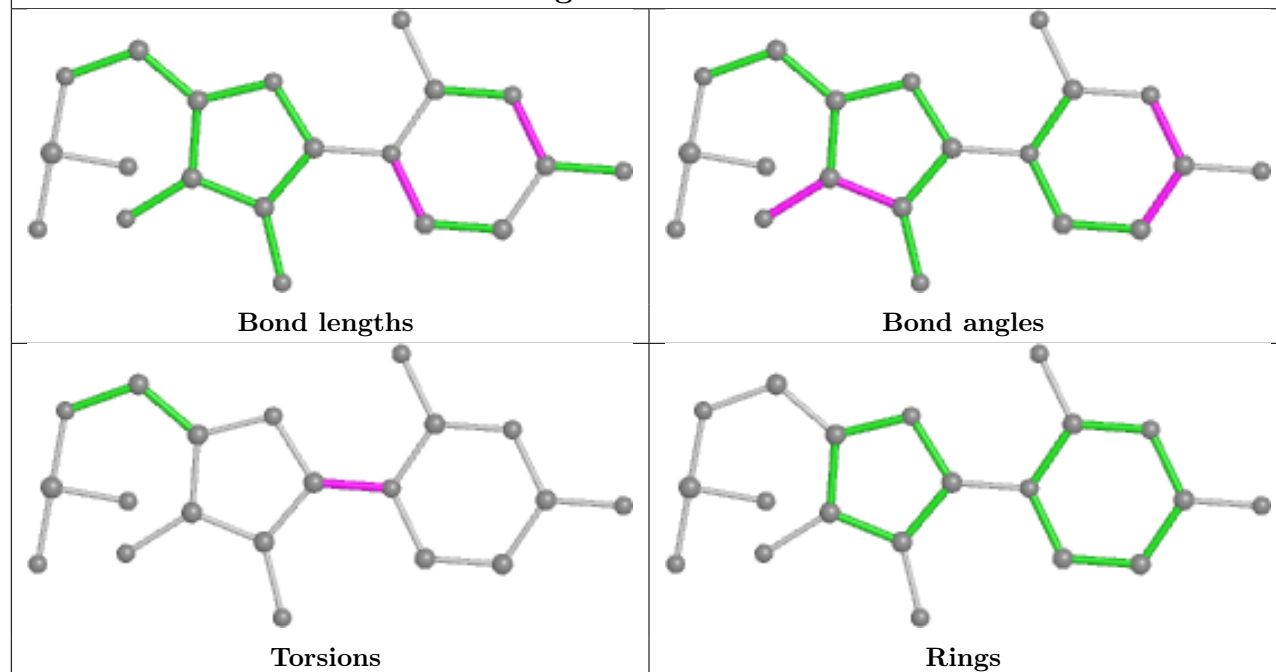
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

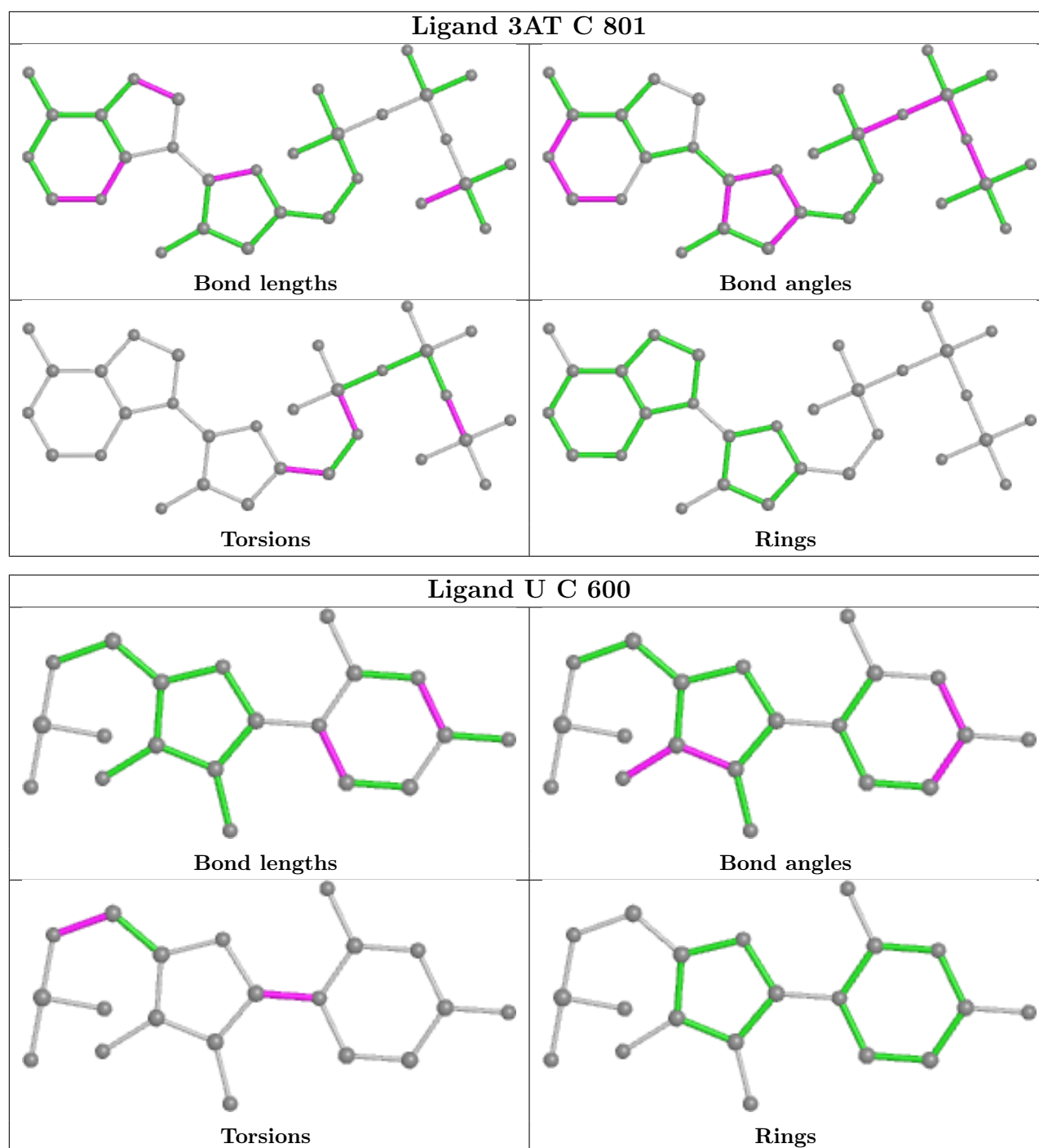


## Ligand 3AT D 800



## Ligand U D 602





## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	288/297 (96%)	-0.47	0 100 100	41, 68, 94, 133	0
1	B	288/297 (96%)	-0.49	0 100 100	41, 66, 93, 124	0
2	C	445/479 (92%)	-0.24	2 (0%) 92 89	47, 90, 123, 156	0
2	D	445/479 (92%)	-0.16	2 (0%) 92 89	41, 94, 130, 162	0
3	E	5/5 (100%)	0.36	0 100 100	101, 102, 150, 157	0
3	F	5/5 (100%)	0.37	0 100 100	97, 100, 138, 157	0
4	G	4/4 (100%)	-0.36	0 100 100	81, 97, 119, 122	0
5	I	5/5 (100%)	-0.24	0 100 100	95, 101, 116, 116	0
All	All	1485/1571 (94%)	-0.31	4 (0%) 94 92	41, 82, 122, 162	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	13	ILE	3.2
2	D	334	LYS	3.1
2	D	15	LEU	2.1
2	C	244	LYS	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

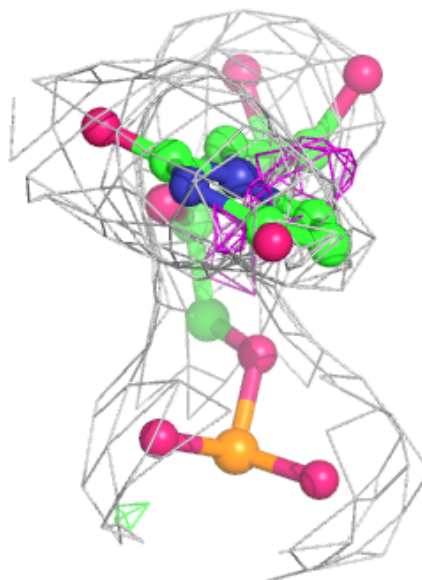
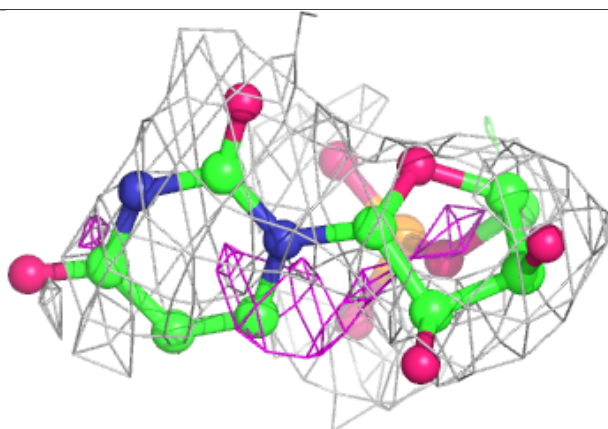
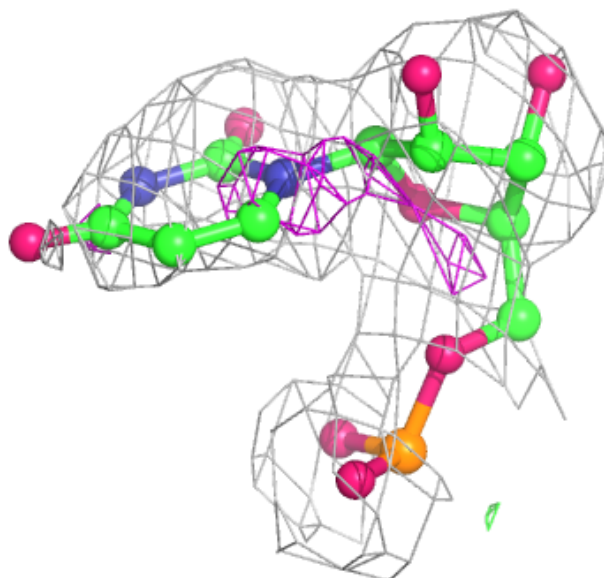
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
6	U	D	602	20/21	0.83	0.30	79,79,79,79	0
6	U	C	600	20/21	0.86	0.17	79,79,79,79	0
8	CA	C	901	1/1	0.91	0.19	79,79,79,79	0
7	3AT	D	800	30/30	0.93	0.25	79,108,108,108	0
8	CA	C	902	1/1	0.94	0.13	79,79,79,79	0
8	CA	D	903	1/1	0.94	0.13	79,79,79,79	0
8	CA	D	904	1/1	0.94	0.15	79,79,79,79	0
7	3AT	C	801	30/30	0.95	0.21	79,93,97,97	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.

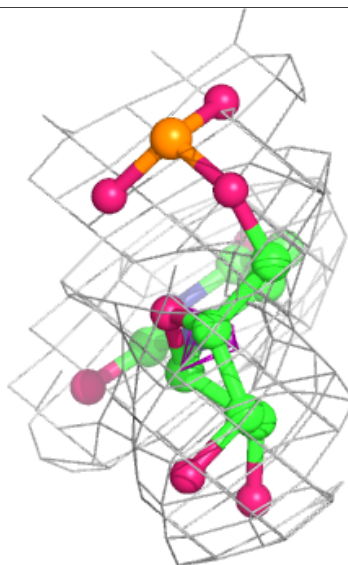
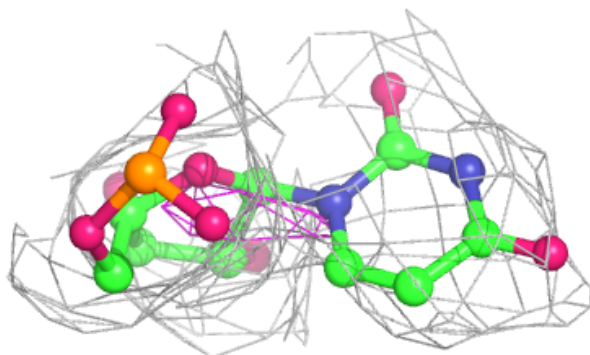
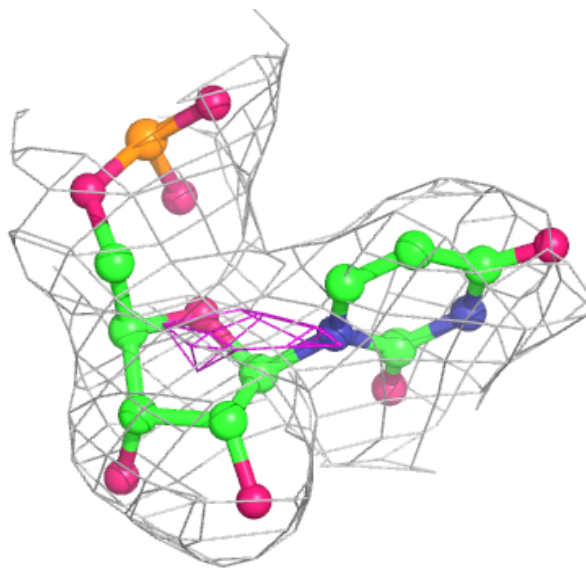
**Electron density around U D 602:**

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



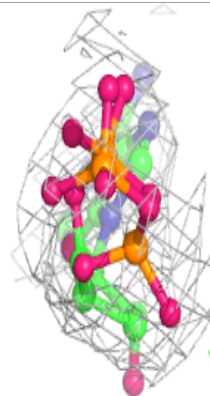
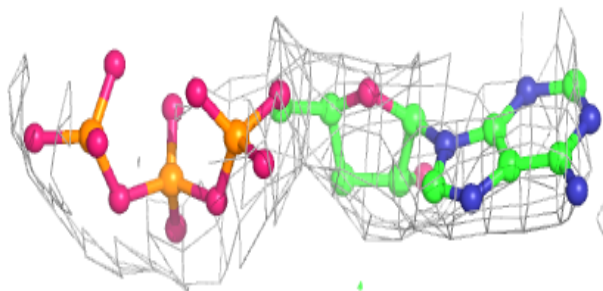
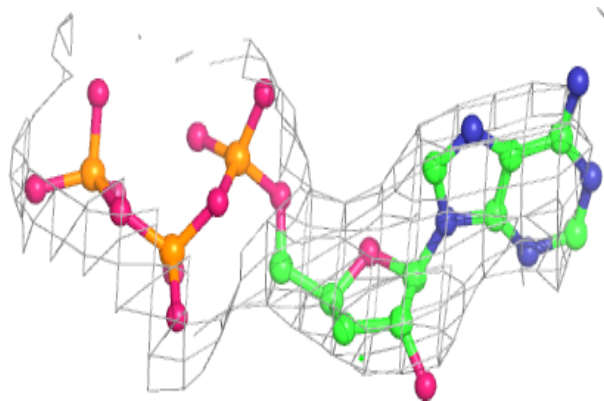
**Electron density around U C 600:**

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

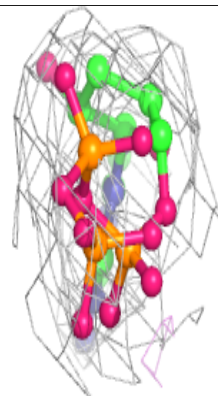
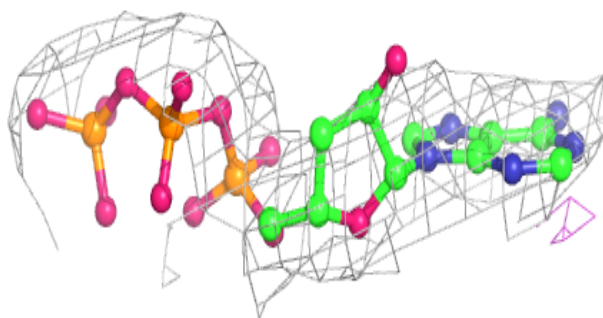
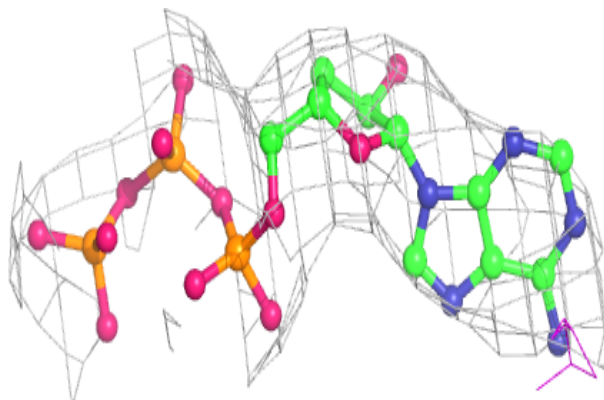


**Electron density around 3AT D 800:**

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

**Electron density around 3AT C 801:**

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.