



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 09:46 AM UTC

PDB ID : 8GJH / pdb_00008gjh
Title : Salmonella ArnA
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Deposited on : 2023-03-15
Resolution : 3.60 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

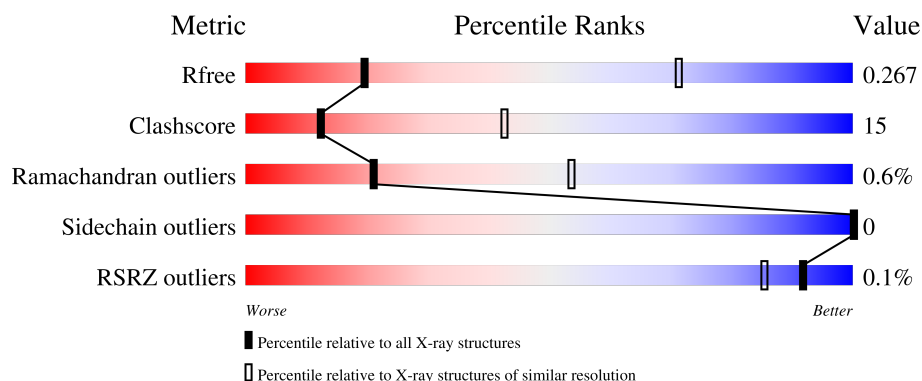
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1747 (3.70-3.50)
Clashscore	190562	1827 (3.70-3.50)
Ramachandran outliers	187476	1773 (3.70-3.50)
Sidechain outliers	187428	1772 (3.70-3.50)
RSRZ outliers	180081	1745 (3.70-3.50)

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	660	
1	B	660	
1	C	660	
1	D	660	
1	E	660	

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Mol	Chain	Length	Quality of chain
1	F	660	 A horizontal bar chart showing the quality of the chain. The bar is divided into three segments: a green segment on the left labeled '62%', a yellow segment in the middle labeled '34%', and a small grey segment on the right labeled with two dots '• •'.

2 Entry composition [i](#)

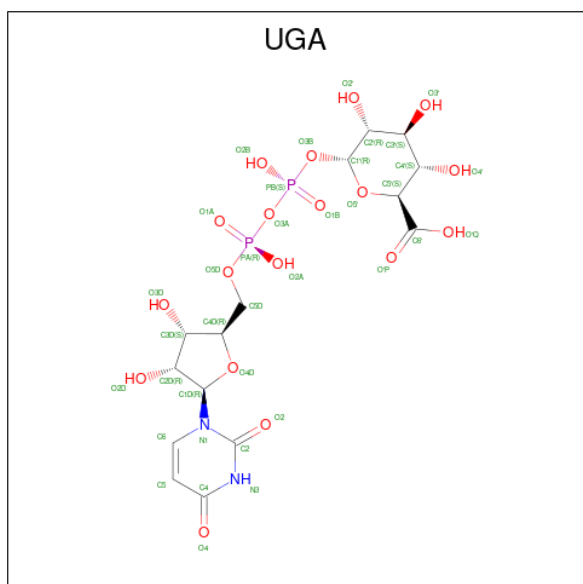
There are 2 unique types of molecules in this entry. The entry contains 30375 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Bifunctional polymyxin resistance protein ArnA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	639	Total	C	N	O	S	0	0	0
			5028	3196	893	918	21			
1	B	638	Total	C	N	O	S	0	0	0
			5023	3193	892	917	21			
1	C	639	Total	C	N	O	S	0	0	0
			5028	3196	893	918	21			
1	D	638	Total	C	N	O	S	0	0	0
			5023	3193	892	917	21			
1	E	638	Total	C	N	O	S	0	0	0
			5023	3193	892	917	21			
1	F	639	Total	C	N	O	S	0	0	0
			5028	3196	893	918	21			

- Molecule 2 is URIDINE-5'-DIPHOSPHATE-GLUCURONIC ACID (CCD ID: UGA) (formula: C₁₅H₂₂N₂O₁₈P₂) (labeled as "Ligand of Interest" by depositor).

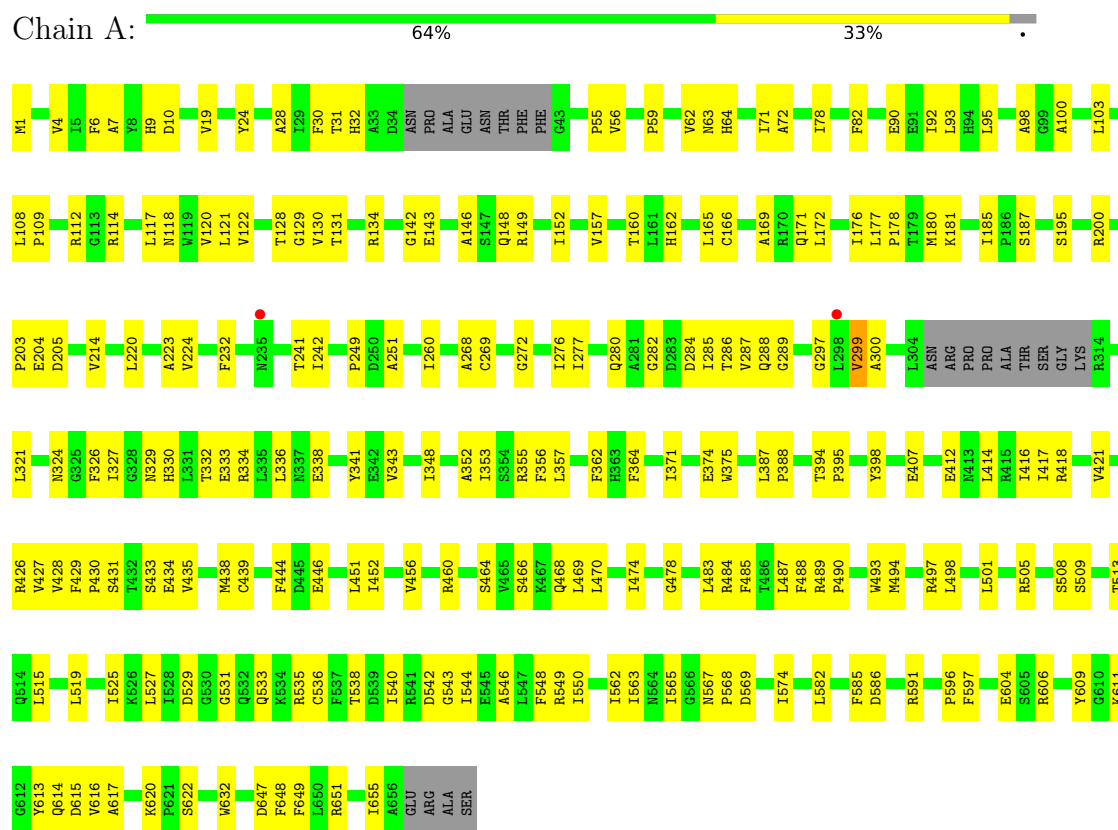


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			37	15	2	18	2		
2	B	1	Total	C	N	O	P	0	0
			37	15	2	18	2		
2	C	1	Total	C	N	O	P	0	0
			37	15	2	18	2		
2	D	1	Total	C	N	O	P	0	0
			37	15	2	18	2		
2	E	1	Total	C	N	O	P	0	0
			37	15	2	18	2		
2	F	1	Total	C	N	O	P	0	0
			37	15	2	18	2		

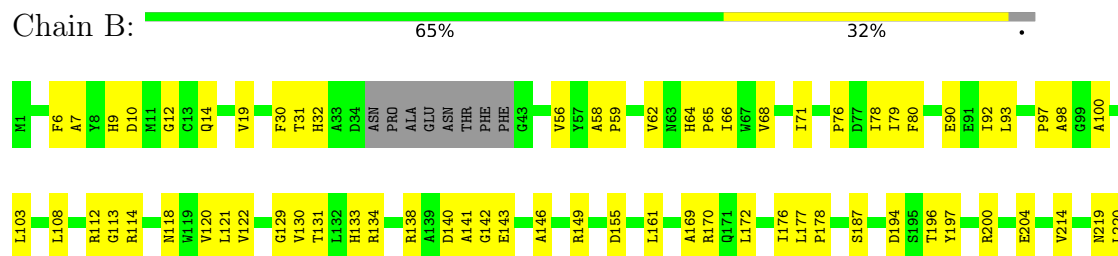
3 Residue-property plots

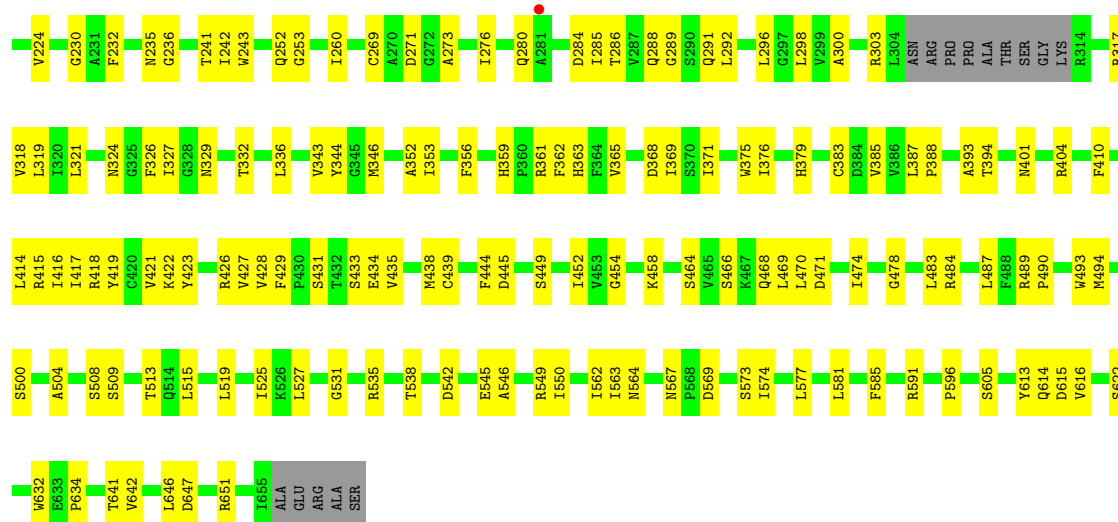
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Bifunctional polymyxin resistance protein ArnA



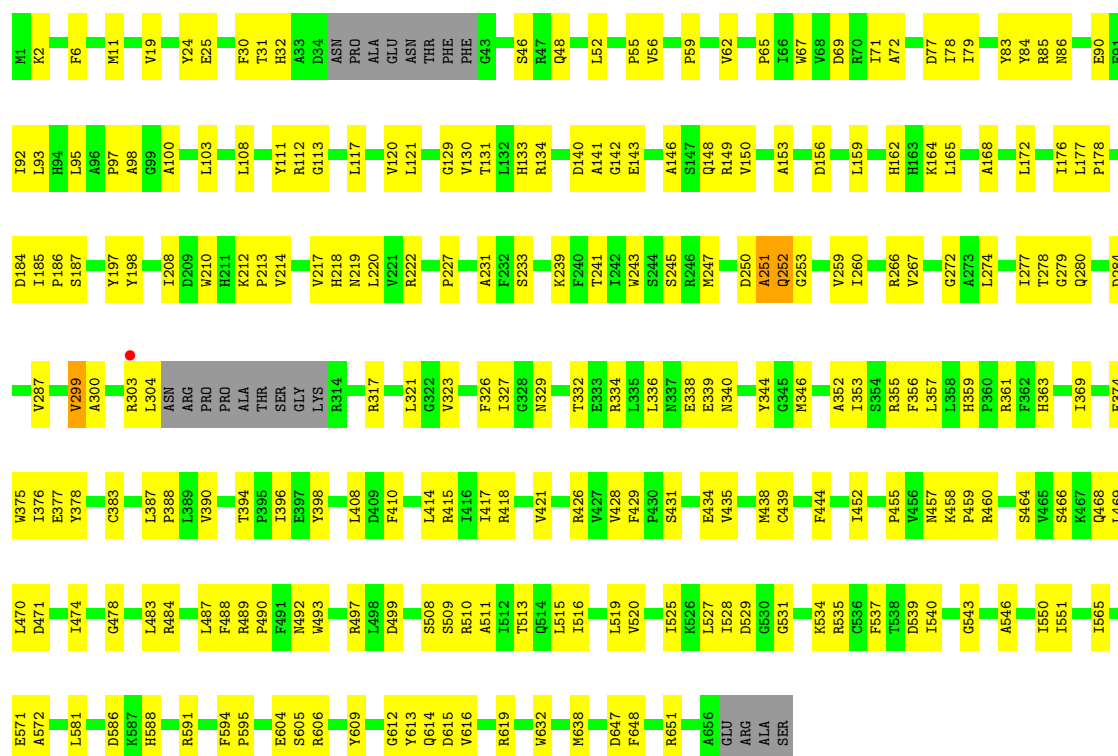
- Molecule 1: Bifunctional polymyxin resistance protein ArnA





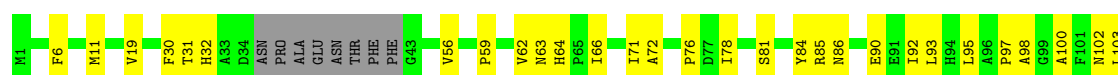
• Molecule 1: Bifunctional polymyxin resistance protein ArnA

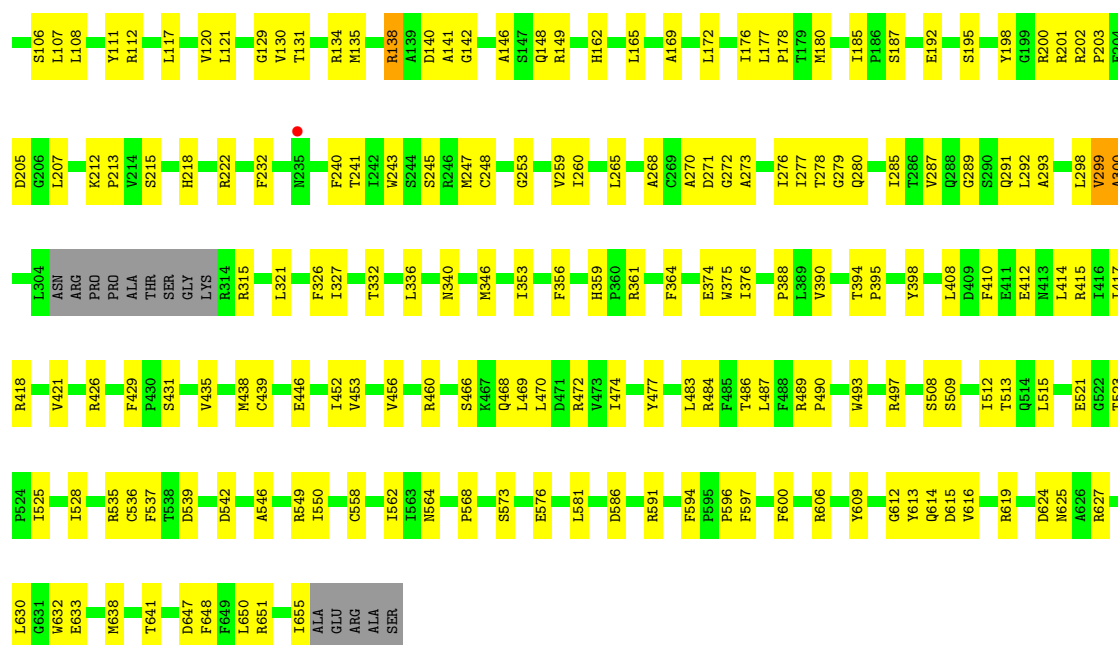
Chain C: 62% 35%



• Molecule 1: Bifunctional polymyxin resistance protein ArnA

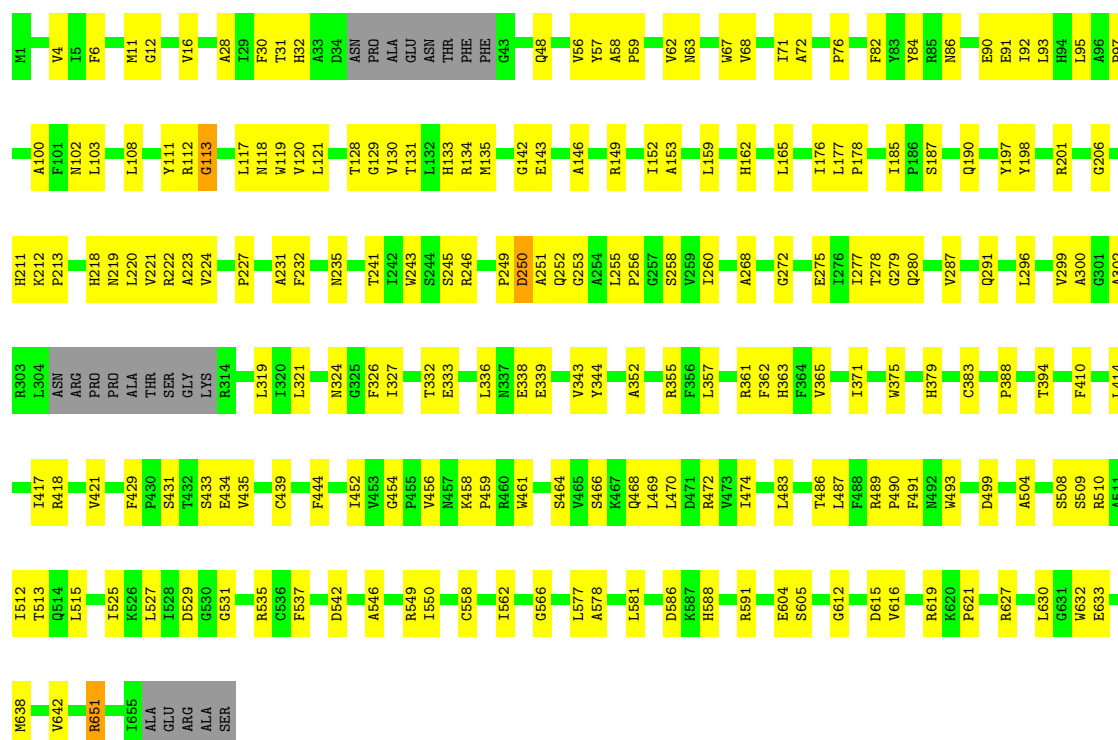
Chain D: 65% 31%





- Molecule 1: Bifunctional polymyxin resistance protein ArnA

Chain E: 65% 31% .



- Molecule 1: Bifunctional polymyxin resistance protein ArnA

Chain F: 62% 34% . .

R619	W493	L389	L304	E192	E90	K1
W620	M494	V390	ASN	S195	E91	K2
P621		T394	ARG		I92	A3
	L498	L408	PRO		L93	V4
L630	D499	L408	PRO	Y198		I5
G631	S500		ALA	G199	A96	F6
W632	G631		THR	R200	P97	A7
E633		L414	SER		A98	Y8
P634	A503	R415	GLY	K212	G99	H9
	A504	T416	LYS	P213	A100	D10
		R418	R314	V214	F101	M11
W638	S508			R222	L103	G12
R639	S509	V421	L319	A223		I29
V642	R510		I320	R223	S106	F30
	A511		L321		L107	T31
L650	I512	R426	N324	F232	L108	H32
	L527	V427	G325	S233		A33
A656		F429	F326	Y234	Y111	D34
GLU	G531	P430	I327	N235		ASN
ARG		S431			R112	PRO
ALA	K534	T432	L331	T241	G113	
SER	R535	S433	T332	I242	R114	ALA
	C536	E434	E333	W243		GLU
	F537	V435	R334	S244	L117	ASN
			R334	S245		THR
			L335	R246	V120	PHE
			L336	M247	L121	PHE
	D542	M438	N337	C248		G43
	G543	C439	E338	P249	G129	
	I544	I452		D250	V130	S46
	A546	V453	Y344	A251	T131	R47
L547	E546	G454		Q252		Q48
F548		P455	A352		R134	A49
R549		V456	I353	I260		
I550		N457	S354		G142	V56
I551		K458	R355	R266	Y57	
		P459	F356	A146	A58	
	I563	R460	L357	G272	P59	
W562		W461		A273		
I565			F362	L274	R149	V62
G566	S464		H363		D155	M63
N567	V465		F364	I277	D156	
P568	S466			T278	V157	P65
	K467		D368	G279	I66	
E571	Q468		I369	Q280	T160	W67
A572	L469		S370		L161	V68
	L470		I371	I285	H162	D69
L580			H372	T286		R70
L581	I474			V287	C166	I71
			W375			
H588	G478		I376	Q291	I176	D77
P589			E377		L177	I78
	L483		Y378	L296	P178	I79
R606	R484		H379	G297	F80	
	F485		V380	L298	G183	
	T486		K381	V299	I184	S81
G612	L487			A300	D185	
W613				G301	I185	Y84
Q614	F488		V386		P186	R85
D615	R489		L387	R302	S187	N86
V616	P490		P388	A303		

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	90.83Å 129.44Å 140.19Å 62.99° 71.66° 77.76°	Depositor
Resolution (Å)	29.83 – 3.60 29.83 – 3.60	Depositor EDS
% Data completeness (in resolution range)	95.0 (29.83-3.60) 95.0 (29.83-3.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 3.56Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.218 , 0.267 0.218 , 0.267	Depositor DCC
R_{free} test set	2000 reflections (3.20%)	wwPDB-VP
Wilson B-factor (Å ²)	108.4	Xtriage
Anisotropy	0.214	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 67.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	30375	wwPDB-VP
Average B, all atoms (Å ²)	111.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% 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: UGA

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	0.15	0/5143	0.38	0/6984
1	B	0.14	0/5138	0.37	0/6977
1	C	0.17	0/5143	0.40	0/6984
1	D	0.17	0/5138	0.40	0/6977
1	E	0.16	0/5138	0.39	0/6977
1	F	0.16	0/5143	0.39	0/6984
All	All	0.16	0/30843	0.39	0/41883

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	D	0	1
1	E	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	138	ARG	Sidechain
1	E	651	ARG	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	5028	0	4994	163	0
1	B	5023	0	4989	156	0
1	C	5028	0	4994	175	0
1	D	5023	0	4989	155	0
1	E	5023	0	4989	159	0
1	F	5028	0	4994	166	0
2	A	37	0	19	2	0
2	B	37	0	19	4	0
2	C	37	0	19	5	0
2	D	37	0	19	3	0
2	E	37	0	19	2	0
2	F	37	0	19	3	0
All	All	30375	0	30063	930	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 15.

The worst 5 of 930 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:1:MET:SD	1:A:181:LYS:NZ	2.16	1.17
1:A:129:GLY:HA3	1:A:149:ARG:HA	1.52	0.91
1:E:299:VAL:HG23	1:E:300:ALA:H	1.37	0.88
1:C:129:GLY:HA3	1:C:149:ARG:HA	1.55	0.86
1:A:582:LEU:HD11	1:A:597:PHE:CE2	2.10	0.85

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	633/660 (96%)	578 (91%)	52 (8%)	3 (0%)	24	57
1	B	632/660 (96%)	574 (91%)	55 (9%)	3 (0%)	24	57
1	C	633/660 (96%)	568 (90%)	61 (10%)	4 (1%)	21	54
1	D	632/660 (96%)	564 (89%)	64 (10%)	4 (1%)	21	54
1	E	632/660 (96%)	571 (90%)	57 (9%)	4 (1%)	21	54
1	F	633/660 (96%)	567 (90%)	60 (10%)	6 (1%)	14	46
All	All	3795/3960 (96%)	3422 (90%)	349 (9%)	24 (1%)	21	54

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	253	GLY
1	E	250	ASP
1	F	251	ALA
1	F	300	ALA
1	A	63	ASN

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	538/555 (97%)	538 (100%)	0	100	100
1	B	538/555 (97%)	538 (100%)	0	100	100
1	C	538/555 (97%)	538 (100%)	0	100	100
1	D	538/555 (97%)	538 (100%)	0	100	100
1	E	538/555 (97%)	538 (100%)	0	100	100
1	F	538/555 (97%)	538 (100%)	0	100	100
All	All	3228/3330 (97%)	3228 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 59 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	518	ASN
1	F	450	ASN
1	D	614	GLN
1	F	372	HIS
1	E	601	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	UGA	E	1100	-	38,39,39	1.48	7 (18%)	56,60,60	1.75	8 (14%)
2	UGA	D	1100	-	38,39,39	1.46	7 (18%)	56,60,60	1.85	8 (14%)
2	UGA	A	1100	-	38,39,39	1.48	7 (18%)	56,60,60	1.84	9 (16%)
2	UGA	B	1100	-	38,39,39	1.51	7 (18%)	56,60,60	1.90	9 (16%)
2	UGA	F	1100	-	38,39,39	1.45	6 (15%)	56,60,60	1.80	9 (16%)
2	UGA	C	1100	-	38,39,39	1.48	7 (18%)	56,60,60	1.77	9 (16%)

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
2	UGA	E	1100	-	-	1/25/61/61	0/3/3/3
2	UGA	D	1100	-	-	3/25/61/61	0/3/3/3
2	UGA	A	1100	-	-	6/25/61/61	0/3/3/3
2	UGA	B	1100	-	-	0/25/61/61	0/3/3/3
2	UGA	F	1100	-	-	6/25/61/61	0/3/3/3
2	UGA	C	1100	-	-	6/25/61/61	0/3/3/3

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1100	UGA	C5-C4	-2.83	1.37	1.43
2	B	1100	UGA	C4-N3	-2.82	1.33	1.38
2	D	1100	UGA	C4-N3	-2.80	1.33	1.38
2	C	1100	UGA	C5-C4	-2.79	1.37	1.43
2	F	1100	UGA	C5-C4	-2.79	1.37	1.43

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1100	UGA	O'Q-C6'-O'P	7.55	141.21	124.08
2	E	1100	UGA	O'Q-C6'-O'P	7.47	141.03	124.08
2	A	1100	UGA	O'Q-C6'-O'P	7.41	140.88	124.08
2	B	1100	UGA	O'Q-C6'-O'P	7.40	140.87	124.08
2	C	1100	UGA	O'Q-C6'-O'P	7.34	140.74	124.08

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

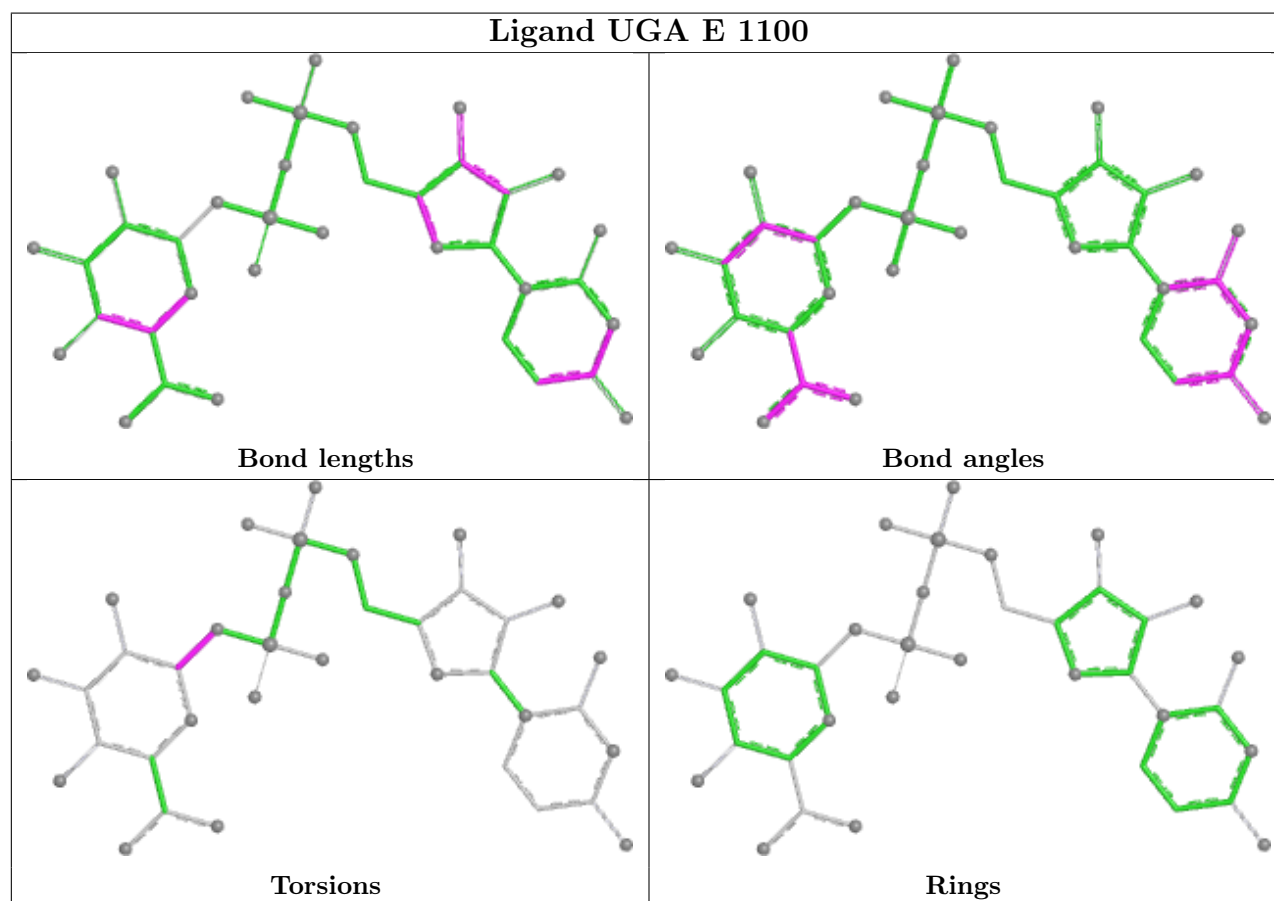
Mol	Chain	Res	Type	Atoms
2	C	1100	UGA	C5D-O5D-PA-O3A
2	C	1100	UGA	C5D-O5D-PA-O2A
2	F	1100	UGA	C1'-O3B-PB-O3A
2	F	1100	UGA	C5D-O5D-PA-O3A
2	F	1100	UGA	C5D-O5D-PA-O1A

There are no ring outliers.

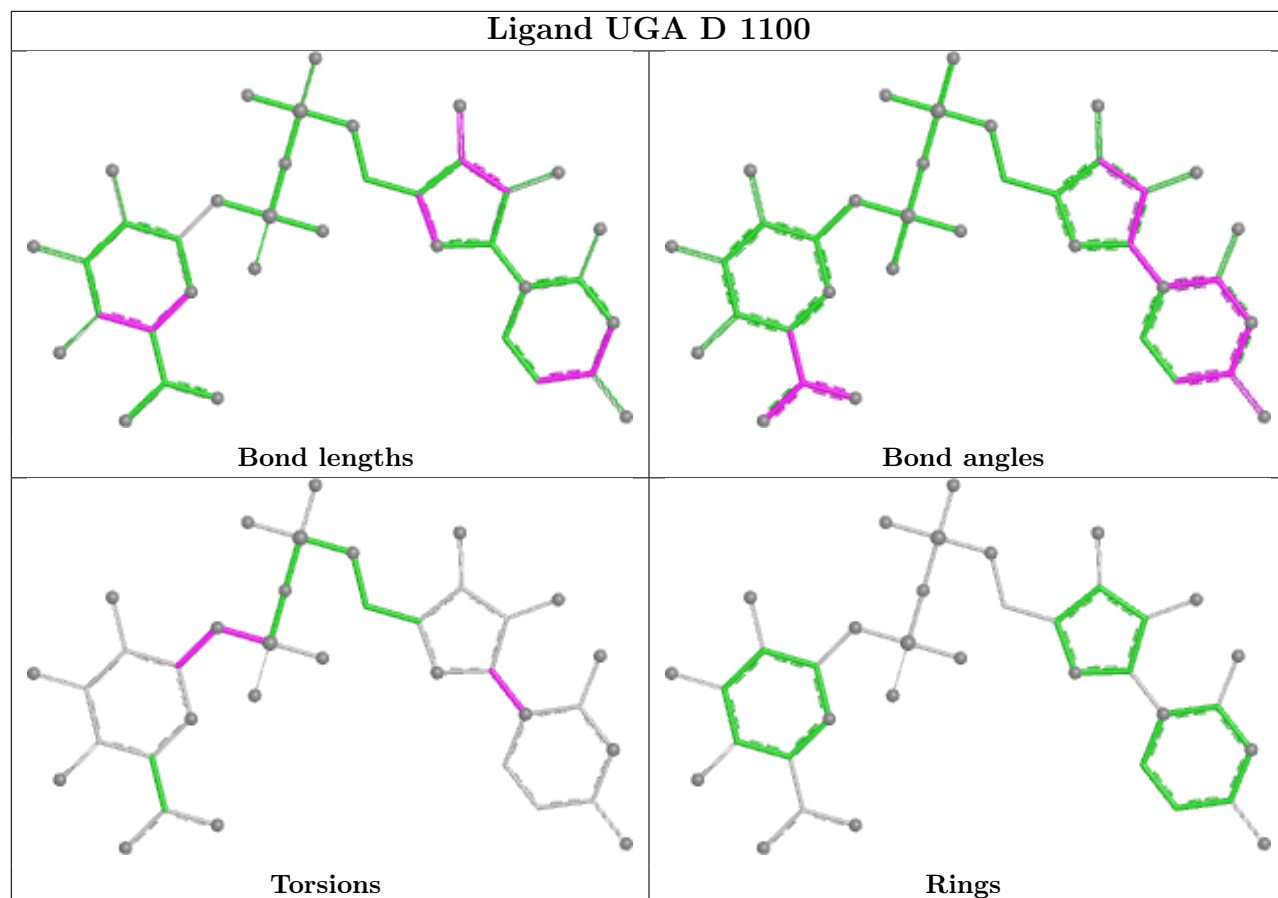
6 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1100	UGA	2	0
2	D	1100	UGA	3	0
2	A	1100	UGA	2	0
2	B	1100	UGA	4	0
2	F	1100	UGA	3	0
2	C	1100	UGA	5	0

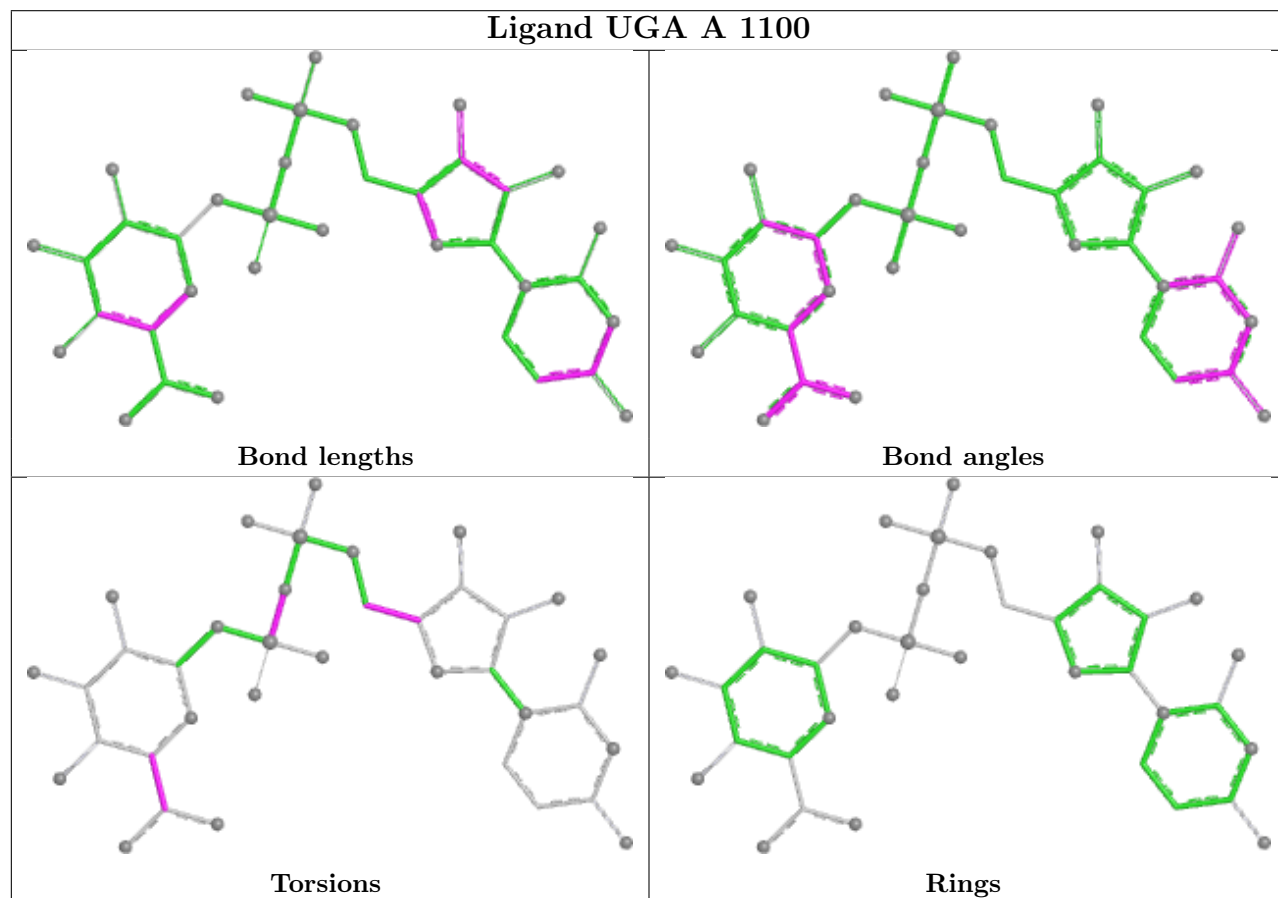
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



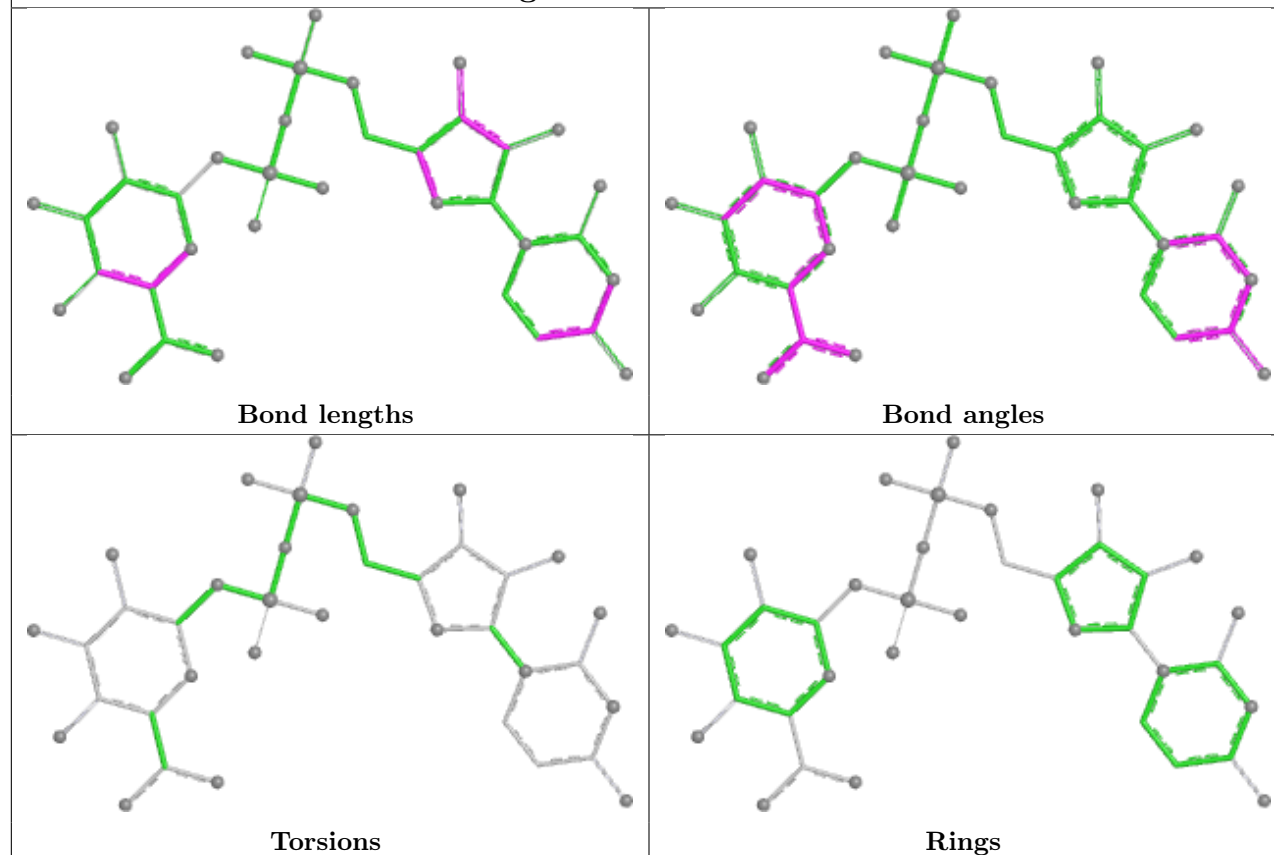
Ligand UGA D 1100



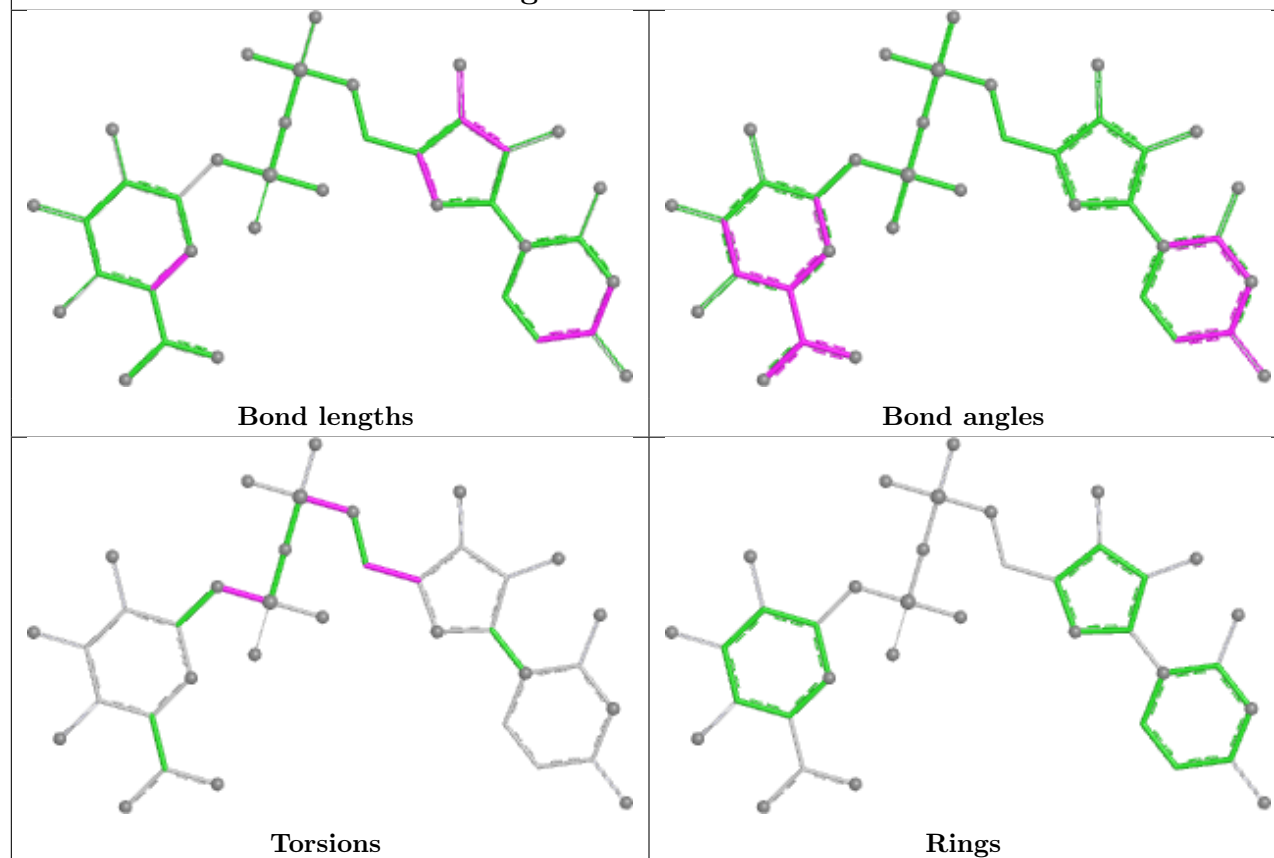
Ligand UGA A 1100

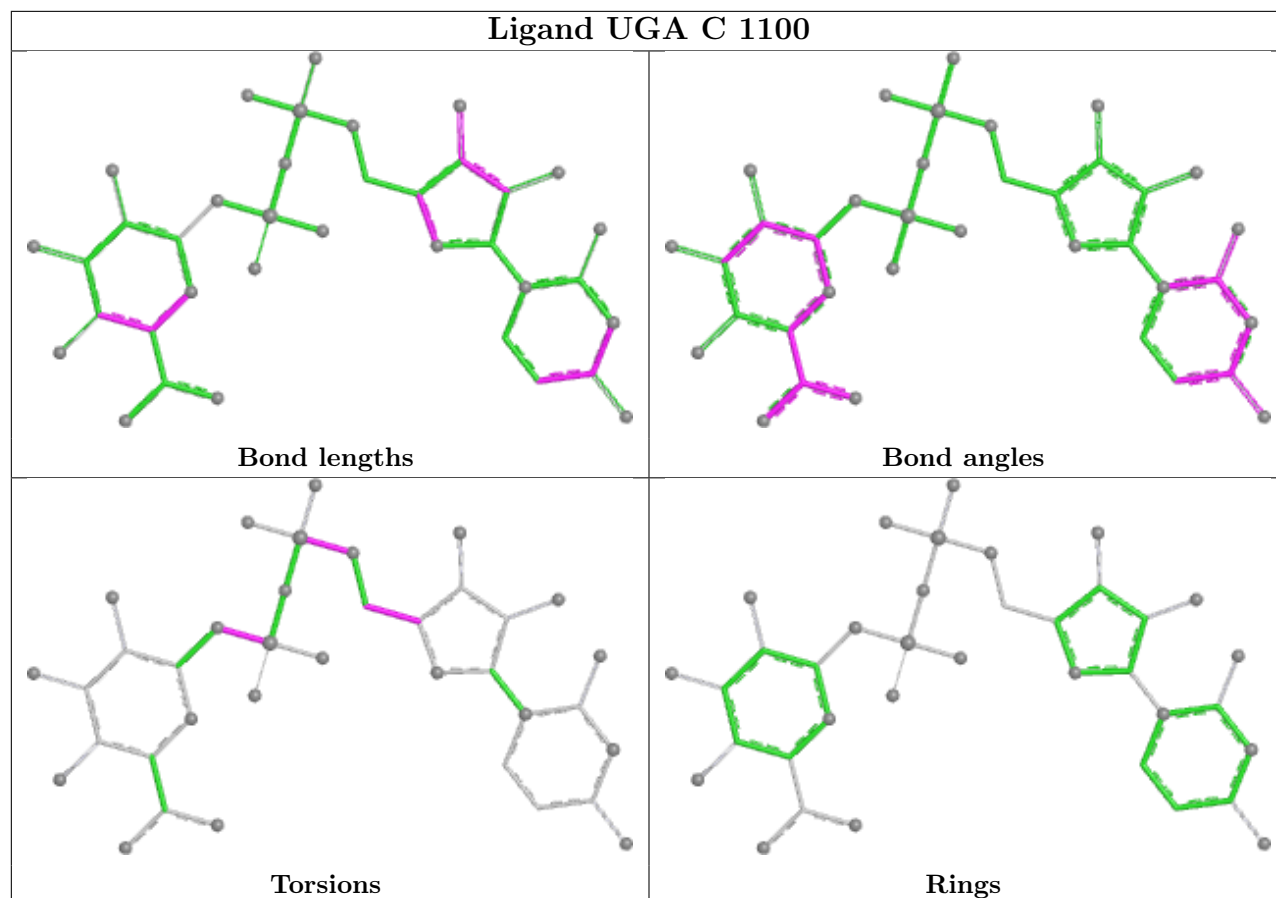


Ligand UGA B 1100



Ligand UGA F 1100





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	639/660 (96%)	-0.24	2 (0%) 90 75	63, 124, 164, 193	0
1	B	638/660 (96%)	-0.26	1 (0%) 91 80	61, 116, 158, 177	0
1	C	639/660 (96%)	-0.28	1 (0%) 91 80	61, 108, 162, 176	0
1	D	638/660 (96%)	-0.27	1 (0%) 91 80	66, 110, 140, 181	0
1	E	638/660 (96%)	-0.28	0 100 100	60, 106, 136, 158	0
1	F	639/660 (96%)	-0.27	0 100 100	60, 106, 136, 171	0
All	All	3831/3960 (96%)	-0.27	5 (0%) 92 85	60, 111, 155, 193	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	281	ALA	3.0
1	D	235	ASN	2.6
1	C	303	ARG	2.4
1	A	235	ASN	2.1
1	A	298	LEU	2.1

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](#)

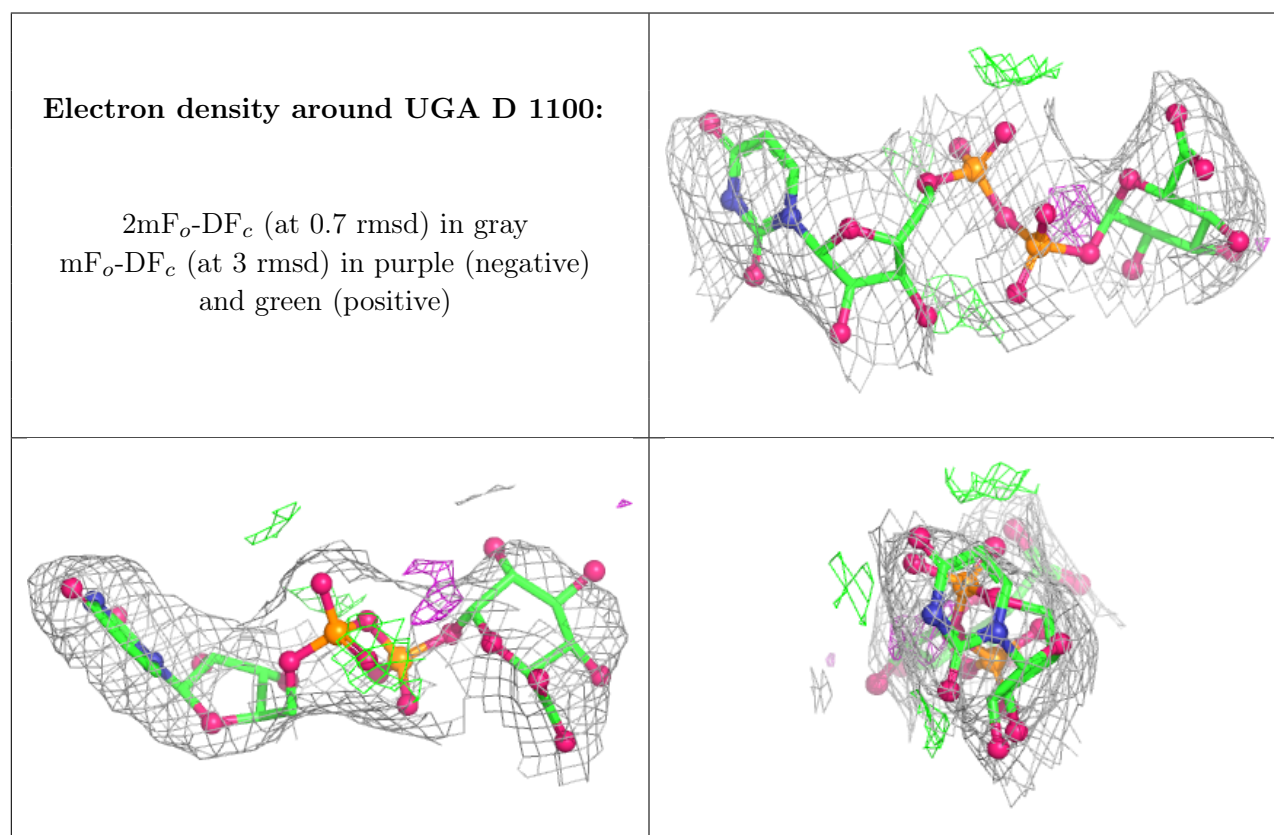
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

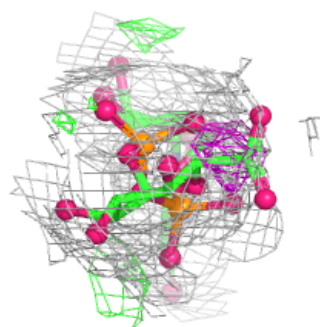
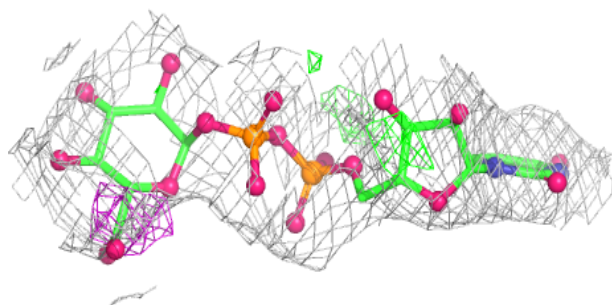
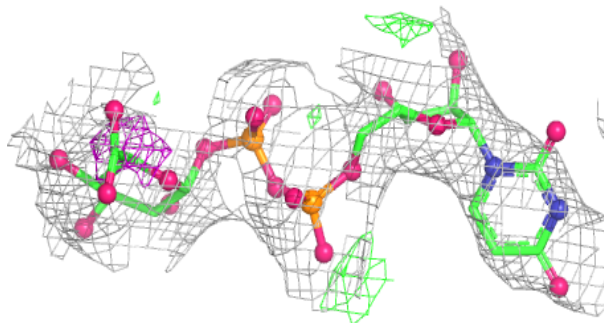
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	UGA	D	1100	37/37	0.87	0.10	98,111,129,138	0
2	UGA	C	1100	37/37	0.89	0.10	84,94,107,110	0
2	UGA	E	1100	37/37	0.89	0.10	87,100,112,115	0
2	UGA	F	1100	37/37	0.89	0.09	101,114,123,130	0
2	UGA	B	1100	37/37	0.91	0.08	95,105,114,119	0
2	UGA	A	1100	37/37	0.93	0.09	102,109,128,132	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.

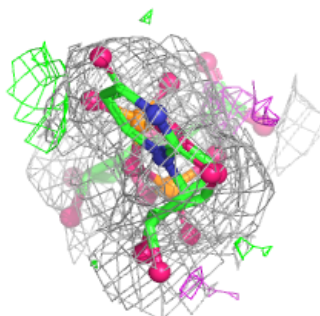
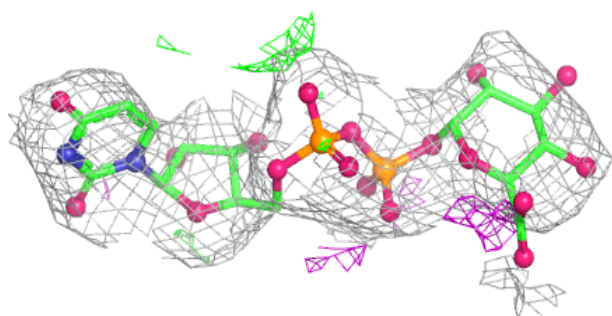
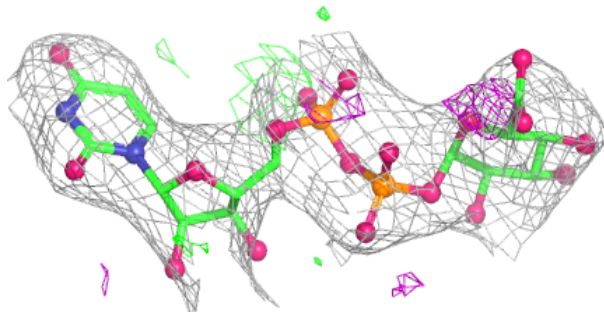


Electron density around UGA C 1100:

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

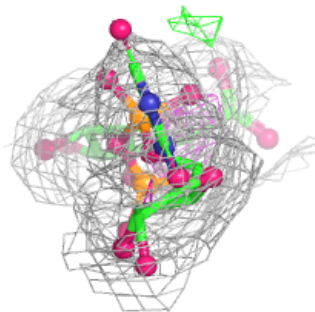
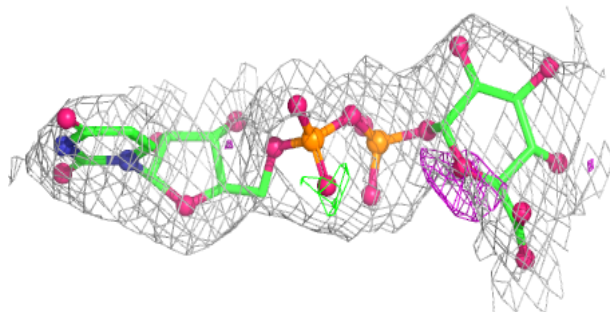
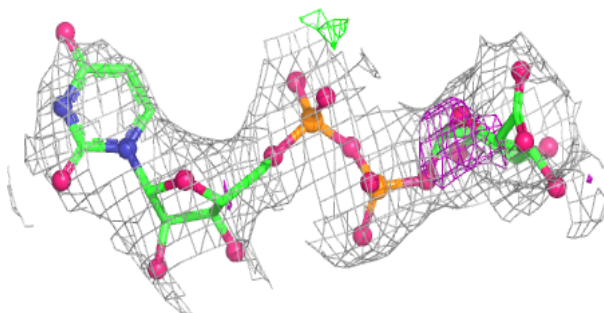
**Electron density around UGA E 1100:**

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

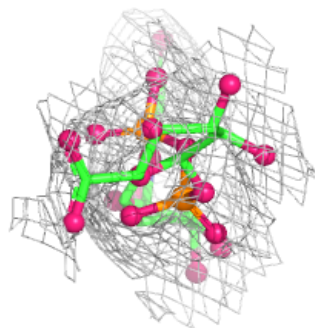
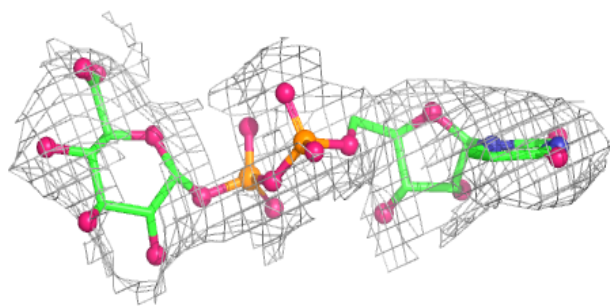
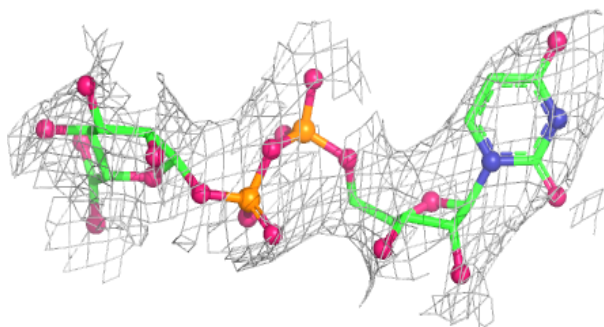


Electron density around UGA F 1100:

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

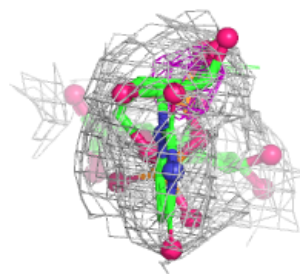
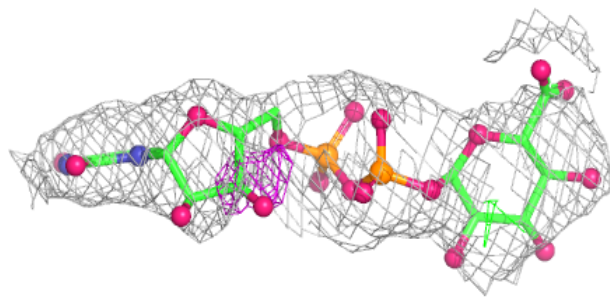
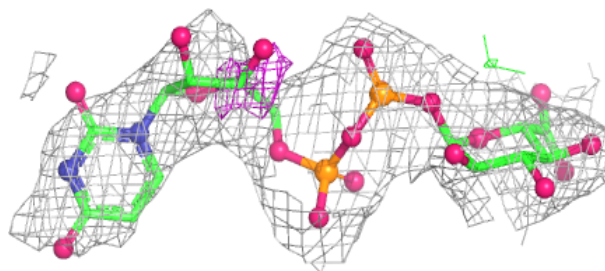
**Electron density around UGA B 1100:**

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



Electron density around UGA A 1100:

$2mF_o - DF_c$ (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.