



# Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 12:29 pm BST

PDB ID : 2Y0E  
Title : BceC and the final step of UGDs reaction  
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Deposited on : 2010-12-02  
Resolution : 1.75 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](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 : 2.11  
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) : 2.11

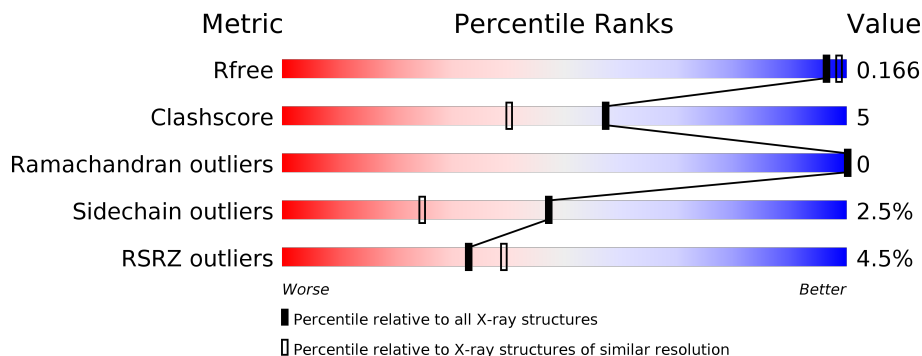
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.75 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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 on 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	478	 3% 87% 9% • •
1	B	478	 3% 83% 11% 6%
1	C	478	 9% 86% 9% • 5%
1	D	478	 2% 84% 10% • 5%

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	GOL	A	1466	-	-	X	-

## 2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 16024 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 UDP-GLUCOSE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	461	Total 3624	C 2277	N 645	O 687	S 15	0	19	0
1	B	451	Total 3578	C 2248	N 643	O 672	S 15	0	22	0
1	C	455	Total 3563	C 2238	N 632	O 678	S 15	0	14	0
1	D	454	Total 3616	C 2262	N 657	O 679	S 18	0	30	0

There are 32 discrepancies between the modelled and reference sequences:

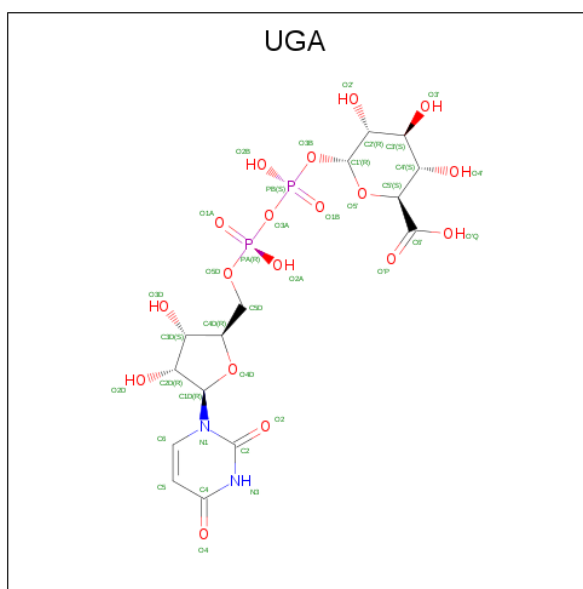
Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	HIS	-	expression tag	UNP C9E261
A	-7	HIS	-	expression tag	UNP C9E261
A	-6	HIS	-	expression tag	UNP C9E261
A	-5	HIS	-	expression tag	UNP C9E261
A	-4	HIS	-	expression tag	UNP C9E261
A	-3	HIS	-	expression tag	UNP C9E261
A	-2	GLY	-	expression tag	UNP C9E261
A	-1	SER	-	expression tag	UNP C9E261
B	-8	HIS	-	expression tag	UNP C9E261
B	-7	HIS	-	expression tag	UNP C9E261
B	-6	HIS	-	expression tag	UNP C9E261
B	-5	HIS	-	expression tag	UNP C9E261
B	-4	HIS	-	expression tag	UNP C9E261
B	-3	HIS	-	expression tag	UNP C9E261
B	-2	GLY	-	expression tag	UNP C9E261
B	-1	SER	-	expression tag	UNP C9E261
C	-8	HIS	-	expression tag	UNP C9E261
C	-7	HIS	-	expression tag	UNP C9E261
C	-6	HIS	-	expression tag	UNP C9E261
C	-5	HIS	-	expression tag	UNP C9E261
C	-4	HIS	-	expression tag	UNP C9E261

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	HIS	-	expression tag	UNP C9E261
C	-2	GLY	-	expression tag	UNP C9E261
C	-1	SER	-	expression tag	UNP C9E261
D	-8	HIS	-	expression tag	UNP C9E261
D	-7	HIS	-	expression tag	UNP C9E261
D	-6	HIS	-	expression tag	UNP C9E261
D	-5	HIS	-	expression tag	UNP C9E261
D	-4	HIS	-	expression tag	UNP C9E261
D	-3	HIS	-	expression tag	UNP C9E261
D	-2	GLY	-	expression tag	UNP C9E261
D	-1	SER	-	expression tag	UNP C9E261

- Molecule 2 is URIDINE-5'-DIPHOSPHATE-GLUCURONIC ACID (three-letter code: UGA) (formula:  $C_{15}H_{22}N_2O_{18}P_2$ ).



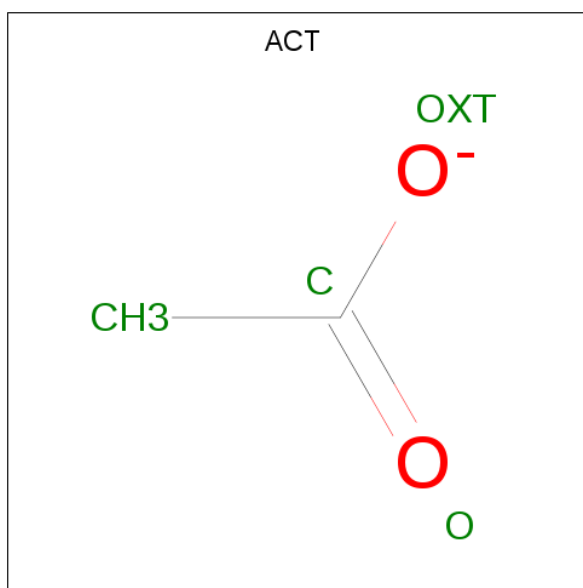
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
2	A	1	Total	C	N	O	P	0	0
			37	15	2	18	2		
2	B	1	Total	C	N	O	P	0	0
			37	15	2	18	2		
2	C	1	Total	C	N	O	P	0	0
			37	15	2	18	2		
2	D	1	Total	C	N	O	P	0	0
			37	15	2	18	2		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



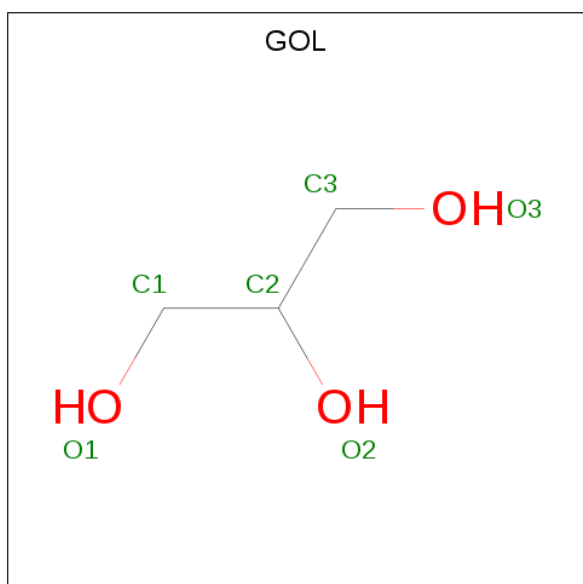
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	C	1	Total C O 6 3 3	0	0
5	C	1	Total C O 6 3 3	0	0
5	D	1	Total C O 6 3 3	0	0

- Molecule 6 is water.

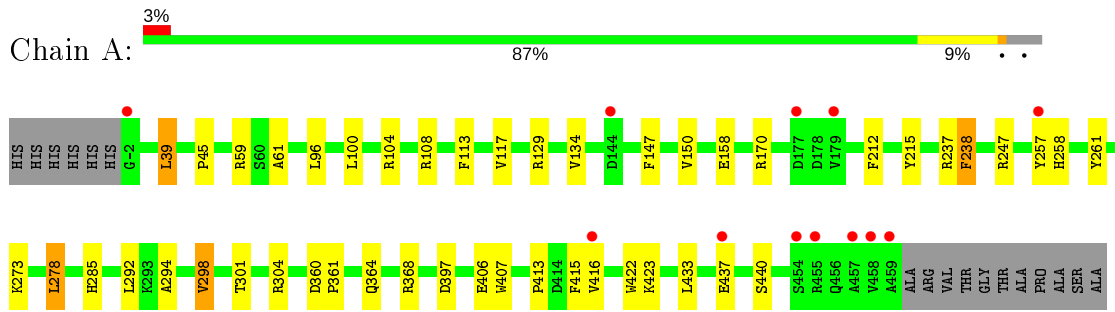
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	380	Total O 380 380	0	0
6	B	330	Total O 330 330	0	0
6	C	289	Total O 289 289	0	0
6	D	374	Total O 374 374	0	0



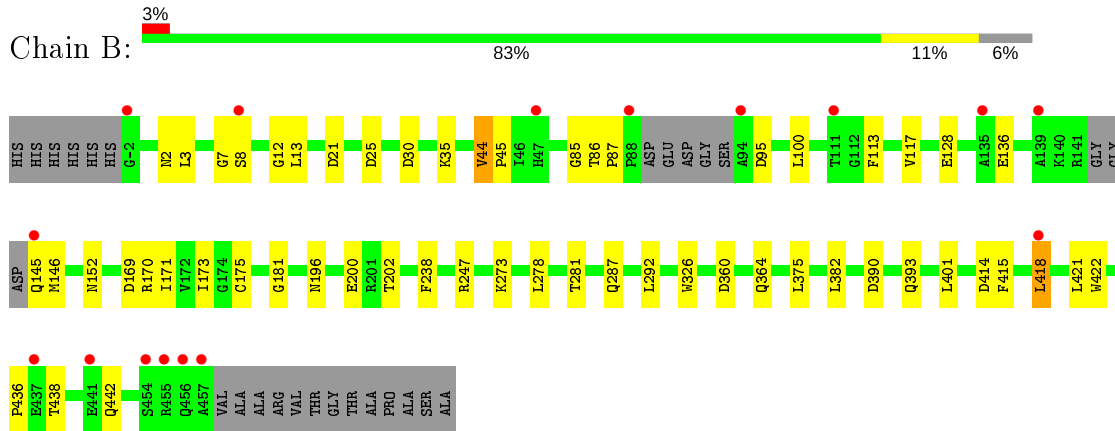
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

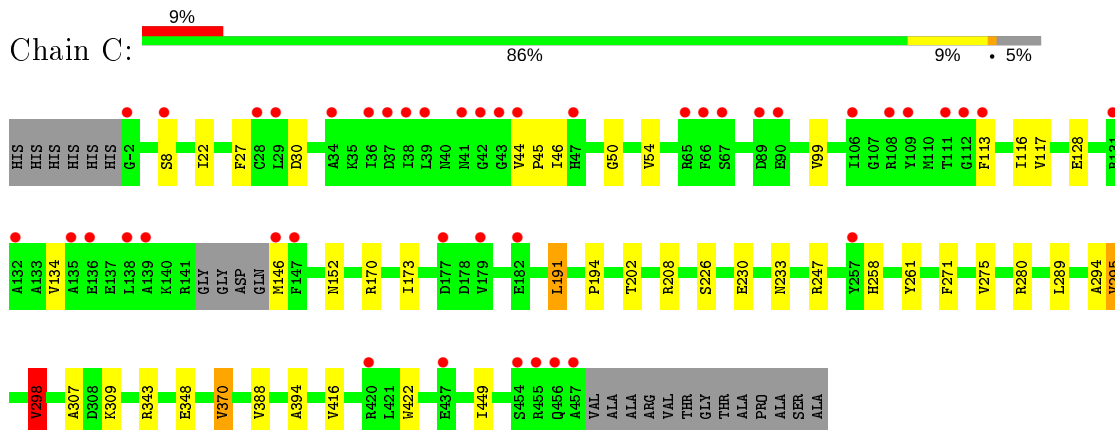
• Molecule 1: UDP-GLUCOSE DEHYDROGENASE



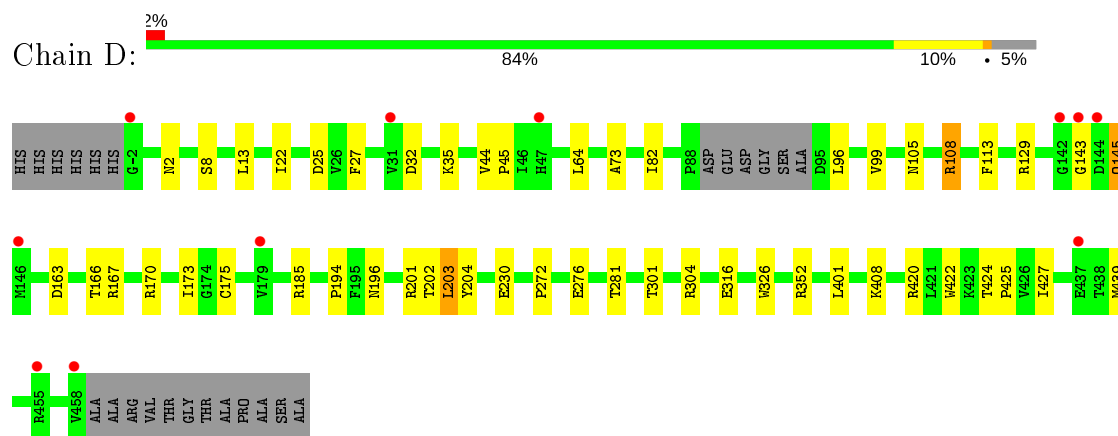
• Molecule 1: UDP-GLUCOSE DEHYDROGENASE



• Molecule 1: UDP-GLUCOSE DEHYDROGENASE



- Molecule 1: UDP-GLUCOSE DEHYDROGENASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	97.63Å 108.93Å 187.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.69 – 1.75 47.42 – 1.75	Depositor EDS
% Data completeness (in resolution range)	98.2 (35.69-1.75) 98.2 (47.42-1.75)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.41 (at 1.75Å)	Xtrriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.163 , 0.197 0.164 , 0.166	Depositor DCC
$R_{free}$ test set	9969 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.3	Xtrriage
Anisotropy	0.027	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 51.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	16024	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.78% 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: GOL, UGA, SO4, ACT

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	0.58	0/3784	0.67	0/5123
1	B	0.56	0/3740	0.68	1/5062 (0.0%)
1	C	0.55	0/3693	0.66	1/5000 (0.0%)
1	D	0.58	0/3842	0.68	0/5192
All	All	0.57	0/15059	0.67	2/20377 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	418	LEU	CA-CB-CG	8.57	135.00	115.30
1	C	298	VAL	CG1-CB-CG2	5.75	120.10	110.90

There are no chirality outliers.

There are no planarity outliers.

### 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	3624	0	3595	34	0
1	B	3578	0	3552	45	0
1	C	3563	0	3523	29	0
1	D	3616	0	3572	41	0
2	A	37	0	19	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	37	0	19	0	0
2	C	37	0	19	0	0
2	D	37	0	19	0	0
3	A	15	0	0	0	0
3	B	25	0	0	0	0
3	C	15	0	0	0	0
3	D	15	0	0	0	0
4	A	4	0	3	0	0
4	B	4	0	3	0	0
4	C	4	0	3	0	0
4	D	4	0	3	0	0
5	A	18	0	24	6	0
5	C	12	0	16	4	0
5	D	6	0	8	3	0
6	A	380	0	0	5	0
6	B	330	0	0	4	0
6	C	289	0	0	6	0
6	D	374	0	0	3	0
All	All	16024	0	14378	144	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 5.

All (144) 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:59[B]:ARG:HD2	6:A:2068:HOH:O	1.72	0.88
1:D:427:ILE:HD12	1:D:439[B]:MET:HE1	1.57	0.85
1:A:258:HIS:HA	5:A:1466:GOL:H32	1.63	0.81
1:A:360:ASP:H	1:A:364[B]:GLN:HE21	1.29	0.79
1:D:113:PHE:H	5:D:1463:GOL:H31	1.50	0.77
1:D:143:GLY:HA3	1:D:145[A]:GLN:HE22	1.50	0.76
1:A:261:TYR:CE2	5:A:1466:GOL:H31	2.22	0.75
1:A:261:TYR:HE2	5:A:1466:GOL:H31	1.55	0.72
1:B:390:ASP:CG	1:B:393[B]:GLN:HE21	1.93	0.72
1:B:86[A]:THR:O	1:B:273:LYS:HD2	1.90	0.71
1:B:360:ASP:H	1:B:364[A]:GLN:HE21	1.39	0.69
1:A:397:ASP:O	1:A:423[A]:LYS:HE3	1.93	0.69
1:C:307:ALA:HB1	1:C:348[B]:GLU:HG2	1.75	0.68
1:D:316[B]:GLU:HG3	1:D:352:ARG:HH12	1.58	0.68
1:B:8:SER:HB3	1:B:13[B]:LEU:HD21	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:87[B]:PRO:O	1:B:95:ASP:HB3	1.94	0.66
1:D:105:ASN:HA	1:D:108[B]:ARG:HG2	1.76	0.66
1:A:301:THR:HG22	1:A:304:ARG:NH2	2.11	0.65
1:C:307:ALA:CB	1:C:348[B]:GLU:HG2	2.27	0.65
1:D:196:ASN:ND2	1:D:201:ARG:H	1.95	0.65
1:D:230[B]:GLU:HG3	6:D:2206:HOH:O	1.97	0.64
1:C:247:ARG:NH2	6:C:2125:HOH:O	2.32	0.61
1:A:134:VAL:HG22	1:A:147:PHE:CZ	2.35	0.61
5:C:1463:GOL:H32	6:C:2265:HOH:O	1.99	0.61
1:C:22:ILE:HD12	1:C:194:PRO:HG2	1.83	0.60
1:D:32:ASP:OD2	1:D:35:LYS:HE3	2.02	0.60
1:C:233[A]:ASN:ND2	6:C:2116:HOH:O	2.35	0.59
1:C:271:PHE:O	1:C:275:VAL:HG13	2.02	0.59
1:D:96:LEU:HD22	1:D:129[B]:ARG:NH1	2.18	0.59
1:C:8:SER:OG	1:C:30:ASP:HB2	2.03	0.58
1:D:301[B]:THR:HG22	1:D:304:ARG:NH2	2.19	0.58
1:A:39:LEU:HD13	1:A:45[A]:PRO:HD3	1.86	0.57
1:D:143:GLY:HA3	1:D:145[A]:GLN:NE2	2.18	0.57
1:C:230:GLU:HG3	1:C:298:VAL:HG11	1.88	0.56
1:D:420[A]:ARG:HH11	1:D:420[A]:ARG:HG2	1.70	0.56
1:D:316[B]:GLU:HG3	1:D:352:ARG:NH1	2.21	0.55
1:B:414:ASP:O	1:B:418:LEU:HD23	2.06	0.55
1:B:8:SER:HB3	1:B:13[B]:LEU:CD2	2.37	0.55
1:A:247:ARG:NH2	6:A:2232:HOH:O	2.39	0.55
1:D:113:PHE:N	5:D:1463:GOL:H31	2.21	0.55
1:A:285:HIS:NE2	5:A:1465:GOL:H2	2.23	0.54
1:B:200:GLU:OE2	1:B:202[B]:THR:OG1	2.23	0.54
1:B:173[A]:ILE:HD12	1:B:202[A]:THR:HG21	1.89	0.54
1:B:8:SER:HB2	1:B:35:LYS:NZ	2.24	0.53
1:D:272:PRO:O	1:D:276[B]:GLU:HG2	2.09	0.53
1:A:237:ARG:HD2	1:B:287:GLN:HE21	1.72	0.53
1:B:438:THR:O	1:B:442:GLN:HG3	2.08	0.53
1:A:215:TYR:HB3	1:A:278:LEU:HG	1.90	0.52
1:B:169:ASP:HB2	6:B:2123:HOH:O	2.08	0.52
1:D:175[B]:CYS:SG	1:D:185[B]:ARG:HG3	2.50	0.52
1:B:196:ASN:HD21	1:B:202[B]:THR:HG23	1.75	0.51
1:B:173[A]:ILE:HD12	1:B:202[A]:THR:CG2	2.40	0.51
1:B:171:ILE:HB	1:B:202[B]:THR:HG22	1.92	0.51
1:D:173:ILE:HD12	1:D:202[B]:THR:CG2	2.40	0.51
1:A:96:LEU:HD12	1:A:129:ARG:NH1	2.25	0.51
1:D:173:ILE:HD12	1:D:202[B]:THR:HG21	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59[B]:ARG:NH2	6:A:2059:HOH:O	2.43	0.50
1:D:2:ASN:HD22	1:D:25:ASP:HB3	1.76	0.50
1:B:2:ASN:HD22	1:B:25:ASP:HB3	1.75	0.50
1:B:86[B]:THR:HG22	6:B:2062:HOH:O	2.12	0.50
1:A:158:GLU:HB2	6:A:2013:HOH:O	2.12	0.50
1:D:301[B]:THR:HG22	1:D:304:ARG:HH22	1.76	0.50
1:A:117:VAL:HG22	1:A:150[B]:VAL:CG2	2.42	0.50
1:A:437:GLU:O	1:A:440:SER:HB2	2.12	0.50
1:B:86[B]:THR:HB	1:B:95:ASP:O	2.12	0.49
1:B:21:ASP:OD2	1:D:408:LYS:HE2	2.11	0.49
1:C:50:GLY:O	1:C:54:VAL:HG23	2.12	0.49
1:A:258:HIS:ND1	5:A:1466:GOL:H12	2.28	0.49
1:C:173:ILE:HD12	1:C:202:THR:HG21	1.95	0.49
1:D:163:ASP:HA	1:D:166[B]:THR:HG22	1.94	0.48
1:C:294:ALA:O	1:C:298:VAL:HG13	2.13	0.48
1:D:202[B]:THR:HG21	1:D:204:TYR:CZ	2.48	0.48
1:D:427:ILE:HD12	1:D:439[B]:MET:CE	2.38	0.48
1:B:390:ASP:OD1	1:B:393[B]:GLN:HG3	2.14	0.48
1:B:87[B]:PRO:O	1:B:95:ASP:CB	2.62	0.48
1:C:343:ARG:CZ	1:C:370:VAL:HG13	2.44	0.48
1:D:203[A]:LEU:HD22	6:D:2194:HOH:O	2.13	0.47
1:C:388:VAL:HG21	1:C:394:ALA:HB2	1.97	0.47
1:B:375:LEU:HB2	1:B:382:LEU:HD21	1.97	0.47
1:C:226:SER:HB2	1:C:295:VAL:HB	1.96	0.47
1:A:294:ALA:O	1:A:298:VAL:HG13	2.15	0.47
1:C:261:TYR:HE2	5:C:1462:GOL:H2	1.80	0.47
1:D:22:ILE:HD12	1:D:194:PRO:HG2	1.97	0.47
1:C:116:ILE:HD13	1:C:134:VAL:HG21	1.97	0.46
1:D:96:LEU:HD12	1:D:96:LEU:N	2.31	0.46
1:A:104[A]:ARG:NH2	6:A:2113:HOH:O	2.44	0.46
1:A:113:PHE:HB2	5:A:1464:GOL:H2	1.97	0.45
1:B:175[B]:CYS:SG	1:B:181:GLY:O	2.75	0.45
1:B:113:PHE:HA	1:B:146:MET:O	2.17	0.45
1:B:415:PHE:HA	1:B:418:LEU:HD23	1.98	0.45
1:B:8:SER:HB2	1:B:35:LYS:CE	2.47	0.45
1:C:289:LEU:HD22	1:D:230[B]:GLU:HG2	1.99	0.45
1:B:128:GLU:HG3	6:B:2145:HOH:O	2.15	0.45
5:C:1463:GOL:C3	6:C:2265:HOH:O	2.62	0.44
1:B:7:GLY:HA2	1:B:30:ASP:OD1	2.18	0.44
1:C:191:LEU:HD12	1:C:191:LEU:O	2.17	0.44
1:D:44:VAL:HA	1:D:45:PRO:HD3	1.80	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:247[B]:ARG:NE	6:B:2163:HOH:O	2.49	0.43
1:A:237:ARG:HH11	1:B:287:GLN:NE2	2.17	0.43
1:A:292:LEU:HA	1:A:292:LEU:HD23	1.86	0.43
1:A:238[B]:PHE:CZ	1:B:281:THR:CG2	3.01	0.43
1:A:238[B]:PHE:CZ	1:B:281:THR:HG22	2.53	0.43
1:C:230:GLU:CG	1:C:298:VAL:HG11	2.50	0.42
1:B:44:VAL:HA	1:B:45[B]:PRO:HD3	1.61	0.42
1:C:117:VAL:CG1	1:C:152:ASN:HB3	2.49	0.42
1:A:61:ALA:HA	1:C:416:VAL:HG21	2.01	0.42
1:B:8:SER:HB2	1:B:35:LYS:HZ1	1.83	0.42
1:C:309:LYS:HE3	1:C:449:ILE:HD13	2.01	0.42
1:A:257[B]:TYR:CE1	1:A:258:HIS:CE1	3.08	0.42
1:C:128[B]:GLU:CD	1:C:208:ARG:HH21	2.23	0.42
1:A:361:PRO:HG2	1:A:407:TRP:CD2	2.55	0.42
1:D:196:ASN:HD22	1:D:201:ARG:H	1.64	0.42
1:C:233[B]:ASN:ND2	6:C:2118:HOH:O	2.52	0.42
1:B:7:GLY:O	1:B:12:GLY:HA3	2.20	0.41
1:B:8:SER:HB2	1:B:35:LYS:HE3	2.02	0.41
1:B:8:SER:C	1:B:35:LYS:HZ2	2.23	0.41
1:B:86[B]:THR:N	1:B:87[B]:PRO:HD3	2.35	0.41
1:C:44:VAL:HG12	1:C:46:ILE:H	1.86	0.41
1:D:326:TRP:CG	1:D:401:LEU:HD11	2.55	0.41
1:A:117:VAL:HG22	1:A:150[B]:VAL:HG21	2.03	0.41
1:B:292:LEU:HA	1:B:292:LEU:HD23	1.81	0.41
1:D:281[B]:THR:HG21	6:D:2116:HOH:O	2.20	0.41
1:C:128[B]:GLU:HG3	6:C:2051:HOH:O	2.21	0.41
1:C:44:VAL:HA	1:C:45:PRO:HD3	1.78	0.41
1:D:82:ILE:HG21	1:D:99:VAL:HB	2.03	0.41
1:B:117:VAL:CG1	1:B:152:ASN:HB3	2.50	0.41
1:D:8:SER:O	1:D:13:LEU:HG	2.21	0.41
1:C:113:PHE:HA	1:C:146:MET:O	2.21	0.41
1:A:100:LEU:O	1:A:104[B]:ARG:HG3	2.21	0.41
1:B:390:ASP:N	1:B:393[B]:GLN:NE2	2.69	0.41
1:B:85[A]:GLY:C	1:B:87[A]:PRO:HD3	2.42	0.41
1:D:27:PHE:CE1	1:D:73:ALA:HB2	2.56	0.41
1:D:424:THR:HA	1:D:425[A]:PRO:HD3	1.89	0.41
1:B:326:TRP:CG	1:B:401:LEU:HD11	2.56	0.40
1:D:113:PHE:H	5:D:1463:GOL:C3	2.25	0.40
1:A:406:GLU:HB2	1:A:433:LEU:HD21	2.02	0.40
1:A:413:PRO:HG2	1:A:415:PHE:CE2	2.57	0.40
1:C:258:HIS:ND1	5:C:1462:GOL:H12	2.37	0.40



There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	479/478 (100%)	474 (99%)	5 (1%)	0	100	100
1	B	467/478 (98%)	456 (98%)	11 (2%)	0	100	100
1	C	465/478 (97%)	461 (99%)	4 (1%)	0	100	100
1	D	481/478 (101%)	471 (98%)	10 (2%)	0	100	100
All	All	1892/1912 (99%)	1862 (98%)	30 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	385/377 (102%)	374 (97%)	11 (3%)	42	19
1	B	381/377 (101%)	371 (97%)	10 (3%)	46	23
1	C	376/377 (100%)	367 (98%)	9 (2%)	49	26
1	D	392/377 (104%)	382 (97%)	10 (3%)	46	23
All	All	1534/1508 (102%)	1494 (97%)	40 (3%)	47	23

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	LEU
1	A	108	ARG
1	A	170	ARG
1	A	212	PHE
1	A	238[A]	PHE
1	A	238[B]	PHE
1	A	273	LYS
1	A	278	LEU
1	A	298	VAL
1	A	416	VAL
1	A	422	TRP
1	B	3	LEU
1	B	44	VAL
1	B	100	LEU
1	B	136	GLU
1	B	145	GLN
1	B	170	ARG
1	B	238	PHE
1	B	278	LEU
1	B	421	LEU
1	B	422	TRP
1	C	27	PHE
1	C	99	VAL
1	C	170	ARG
1	C	191	LEU
1	C	280	ARG
1	C	295	VAL
1	C	298	VAL
1	C	370	VAL
1	C	422	TRP
1	D	64	LEU
1	D	108[A]	ARG
1	D	108[B]	ARG
1	D	145[A]	GLN
1	D	145[B]	GLN
1	D	167	ARG
1	D	170	ARG
1	D	203[A]	LEU
1	D	203[B]	LEU
1	D	422	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	152	ASN
1	A	287	GLN
1	B	2	ASN
1	B	33	GLN
1	B	40	ASN
1	B	287	GLN
1	B	333	ASN
1	C	40	ASN
1	C	97	GLN
1	C	105	ASN
1	D	2	ASN
1	D	33	GLN
1	D	40	ASN
1	D	97	GLN
1	D	196	ASN
1	D	233	ASN
1	D	442	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

28 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
3	SO4	B	1459	-	4,4,4	0.27	0	6,6,6	0.45	0
4	ACT	A	1463	-	1,3,3	0.46	0	0,3,3	0.00	-
2	UGA	C	501	-	33,39,39	1.62	3 (9%)	46,60,60	1.96	8 (17%)
3	SO4	A	1462	-	4,4,4	0.14	0	6,6,6	0.12	0
2	UGA	B	501	-	33,39,39	1.78	3 (9%)	46,60,60	1.75	6 (13%)
4	ACT	B	1463	-	1,3,3	0.67	0	0,3,3	0.00	-
5	GOL	A	1465	-	5,5,5	0.31	0	5,5,5	0.50	0
3	SO4	C	1459	-	4,4,4	0.13	0	6,6,6	0.25	0
3	SO4	A	1460	-	4,4,4	0.16	0	6,6,6	0.41	0
3	SO4	D	1460	-	4,4,4	0.13	0	6,6,6	0.19	0
3	SO4	C	1458	-	4,4,4	0.19	0	6,6,6	0.25	0
2	UGA	D	501	-	33,39,39	1.66	3 (9%)	46,60,60	1.80	9 (19%)
4	ACT	D	1462	-	1,3,3	0.52	0	0,3,3	0.00	-
5	GOL	C	1462	-	5,5,5	0.35	0	5,5,5	0.44	0
5	GOL	A	1466	-	5,5,5	0.16	0	5,5,5	0.64	0
5	GOL	D	1463	-	5,5,5	0.17	0	5,5,5	0.42	0
3	SO4	B	1460	-	4,4,4	0.14	0	6,6,6	0.08	0
3	SO4	A	1461	-	4,4,4	0.12	0	6,6,6	0.16	0
5	GOL	A	1464	-	5,5,5	0.23	0	5,5,5	0.29	0
3	SO4	D	1461	-	4,4,4	0.13	0	6,6,6	0.09	0
3	SO4	B	1458	-	4,4,4	0.15	0	6,6,6	0.16	0
4	ACT	C	1461	-	1,3,3	1.41	0	0,3,3	0.00	-
3	SO4	B	1461	-	4,4,4	0.15	0	6,6,6	0.10	0
3	SO4	C	1460	-	4,4,4	0.14	0	6,6,6	0.13	0
5	GOL	C	1463	-	5,5,5	0.36	0	5,5,5	0.34	0
3	SO4	D	1459	-	4,4,4	0.22	0	6,6,6	0.39	0
3	SO4	B	1462	-	4,4,4	0.14	0	6,6,6	0.15	0
2	UGA	A	501	-	33,39,39	1.79	3 (9%)	46,60,60	1.80	10 (21%)

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
5	GOL	D	1463	-	-	2/4/4/4	-
5	GOL	A	1465	-	-	3/4/4/4	-
5	GOL	C	1462	-	-	2/4/4/4	-
2	UGA	B	501	-	-	3/21/61/61	0/3/3/3
5	GOL	A	1466	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	C	1463	-	-	2/4/4/4	-
2	UGA	C	501	-	-	3/21/61/61	0/3/3/3
2	UGA	A	501	-	-	4/21/61/61	0/3/3/3
2	UGA	D	501	-	-	4/21/61/61	0/3/3/3
5	GOL	A	1464	-	-	2/4/4/4	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	UGA	C6-N1	-7.27	1.34	1.47
2	B	501	UGA	C6-N1	-6.92	1.34	1.47
2	C	501	UGA	C6-N1	-6.05	1.36	1.47
2	D	501	UGA	C6-N1	-6.00	1.36	1.47
2	B	501	UGA	C6-C5	-5.09	1.38	1.52
2	A	501	UGA	C5-C4	-4.64	1.39	1.50
2	C	501	UGA	C6-C5	-4.58	1.40	1.52
2	D	501	UGA	C6-C5	-4.47	1.40	1.52
2	D	501	UGA	C5-C4	-4.35	1.40	1.50
2	C	501	UGA	C5-C4	-4.35	1.40	1.50
2	A	501	UGA	C6-C5	-4.34	1.40	1.52
2	B	501	UGA	C5-C4	-3.93	1.40	1.50

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	501	UGA	C4-N3-C2	-8.46	118.77	125.79
2	B	501	UGA	C4-N3-C2	-7.17	119.84	125.79
2	A	501	UGA	C4-N3-C2	-6.80	120.15	125.79
2	D	501	UGA	C4-N3-C2	-6.49	120.40	125.79
2	C	501	UGA	N3-C2-N1	4.34	121.24	116.65
2	D	501	UGA	N3-C2-N1	4.32	121.22	116.65
2	C	501	UGA	C5-C4-N3	4.17	121.33	116.65
2	A	501	UGA	N3-C2-N1	4.12	121.01	116.65
2	B	501	UGA	N3-C2-N1	3.87	120.75	116.65
2	C	501	UGA	C6'-C5'-C4'	-3.52	104.23	113.04
2	B	501	UGA	C5-C4-N3	3.48	120.56	116.65
2	B	501	UGA	C6'-C5'-C4'	-3.45	104.41	113.04
2	D	501	UGA	C5-C4-N3	3.39	120.45	116.65
2	D	501	UGA	C6'-C5'-C4'	-3.37	104.61	113.04
2	A	501	UGA	C5-C4-N3	2.84	119.83	116.65
2	C	501	UGA	O4D-C1D-N1	-2.75	105.55	109.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	UGA	C5-C6-N1	2.73	120.61	111.61
2	D	501	UGA	C1'-O5'-C5'	2.67	116.56	112.24
2	B	501	UGA	C1'-O5'-C5'	2.63	116.49	112.24
2	A	501	UGA	O2B-PB-O1B	2.63	125.23	112.24
2	D	501	UGA	O5'-C1'-C2'	-2.62	104.81	110.35
2	B	501	UGA	C5-C6-N1	2.62	120.24	111.61
2	A	501	UGA	PA-O3A-PB	2.61	141.78	132.83
2	D	501	UGA	C5-C6-N1	2.56	120.06	111.61
2	A	501	UGA	O3D-C3D-C4D	-2.54	103.71	111.05
2	C	501	UGA	C1'-O5'-C5'	2.49	116.26	112.24
2	D	501	UGA	O2-C2-N3	-2.44	116.96	121.50
2	A	501	UGA	C6'-C5'-C4'	-2.42	106.98	113.04
2	A	501	UGA	C4'-C3'-C2'	-2.37	106.69	110.82
2	C	501	UGA	C5-C6-N1	2.22	118.93	111.61
2	A	501	UGA	O2-C2-N3	-2.21	117.38	121.50
2	C	501	UGA	O2-C2-N3	-2.21	117.39	121.50
2	D	501	UGA	O3B-PB-O1B	-2.10	101.58	109.47

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	501	UGA	C1'-O3B-PB-O2B
2	B	501	UGA	C1'-O3B-PB-O2B
2	B	501	UGA	PA-O3A-PB-O3B
5	A	1465	GOL	C1-C2-C3-O3
2	D	501	UGA	C1'-O3B-PB-O2B
5	A	1466	GOL	O1-C1-C2-C3
5	A	1464	GOL	O2-C2-C3-O3
5	D	1463	GOL	C1-C2-C3-O3
5	C	1463	GOL	C1-C2-C3-O3
5	C	1462	GOL	O1-C1-C2-C3
5	A	1464	GOL	C1-C2-C3-O3
5	A	1465	GOL	O2-C2-C3-O3
5	D	1463	GOL	O2-C2-C3-O3
2	C	501	UGA	C1'-O3B-PB-O3A
2	B	501	UGA	C1'-O3B-PB-O3A
2	D	501	UGA	C1'-O3B-PB-O3A
5	C	1463	GOL	O2-C2-C3-O3
2	A	501	UGA	C1'-O3B-PB-O3A
5	C	1462	GOL	O1-C1-C2-O2
2	C	501	UGA	PA-O3A-PB-O3B

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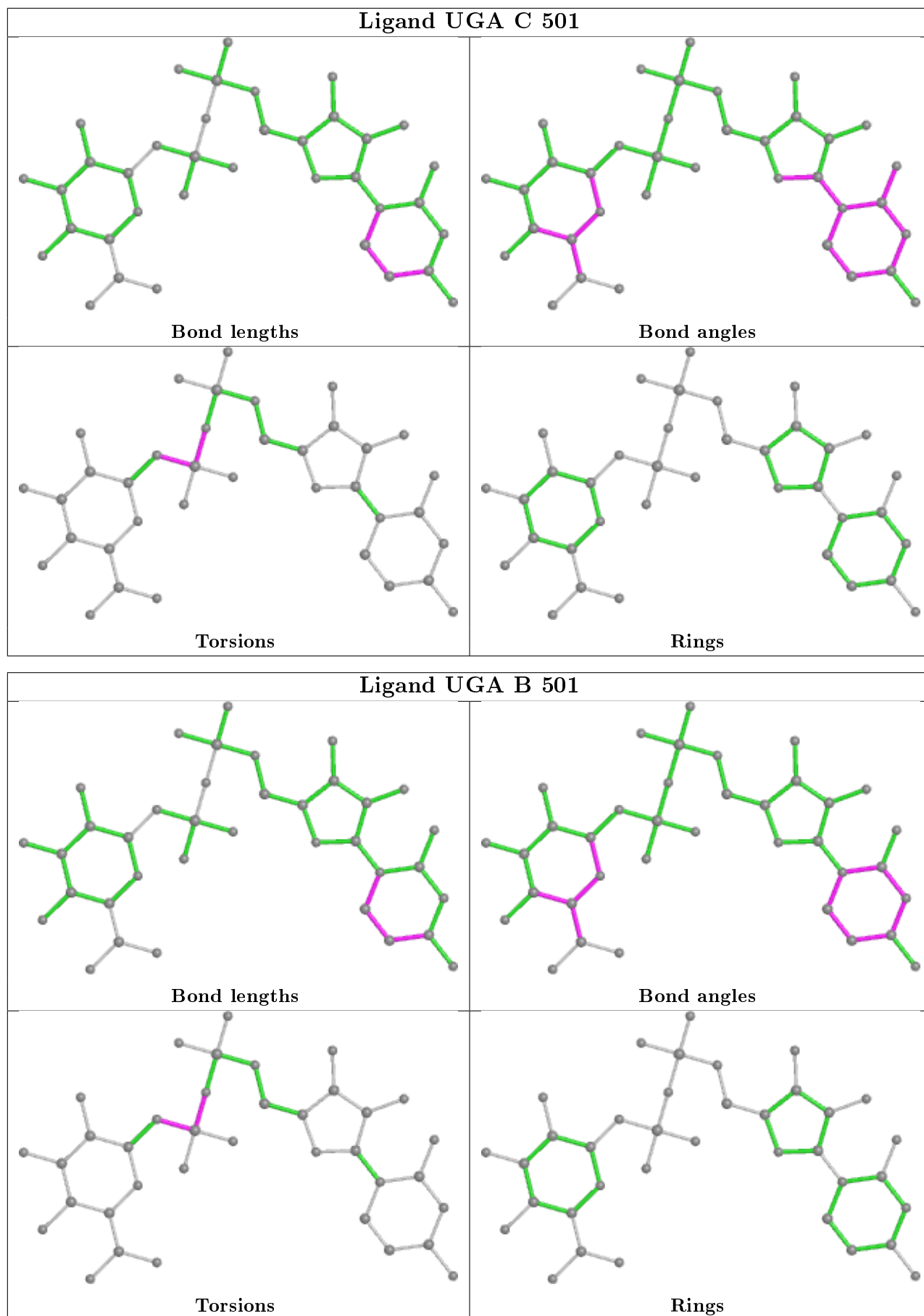
Mol	Chain	Res	Type	Atoms
2	A	501	UGA	PA-O3A-PB-O3B
5	A	1465	GOL	O1-C1-C2-O2
5	A	1466	GOL	O1-C1-C2-O2
2	D	501	UGA	C1'-O3B-PB-O1B
2	A	501	UGA	PB-O3A-PA-O2A
2	D	501	UGA	PA-O3A-PB-O3B
2	A	501	UGA	PB-O3A-PA-O1A

There are no ring outliers.

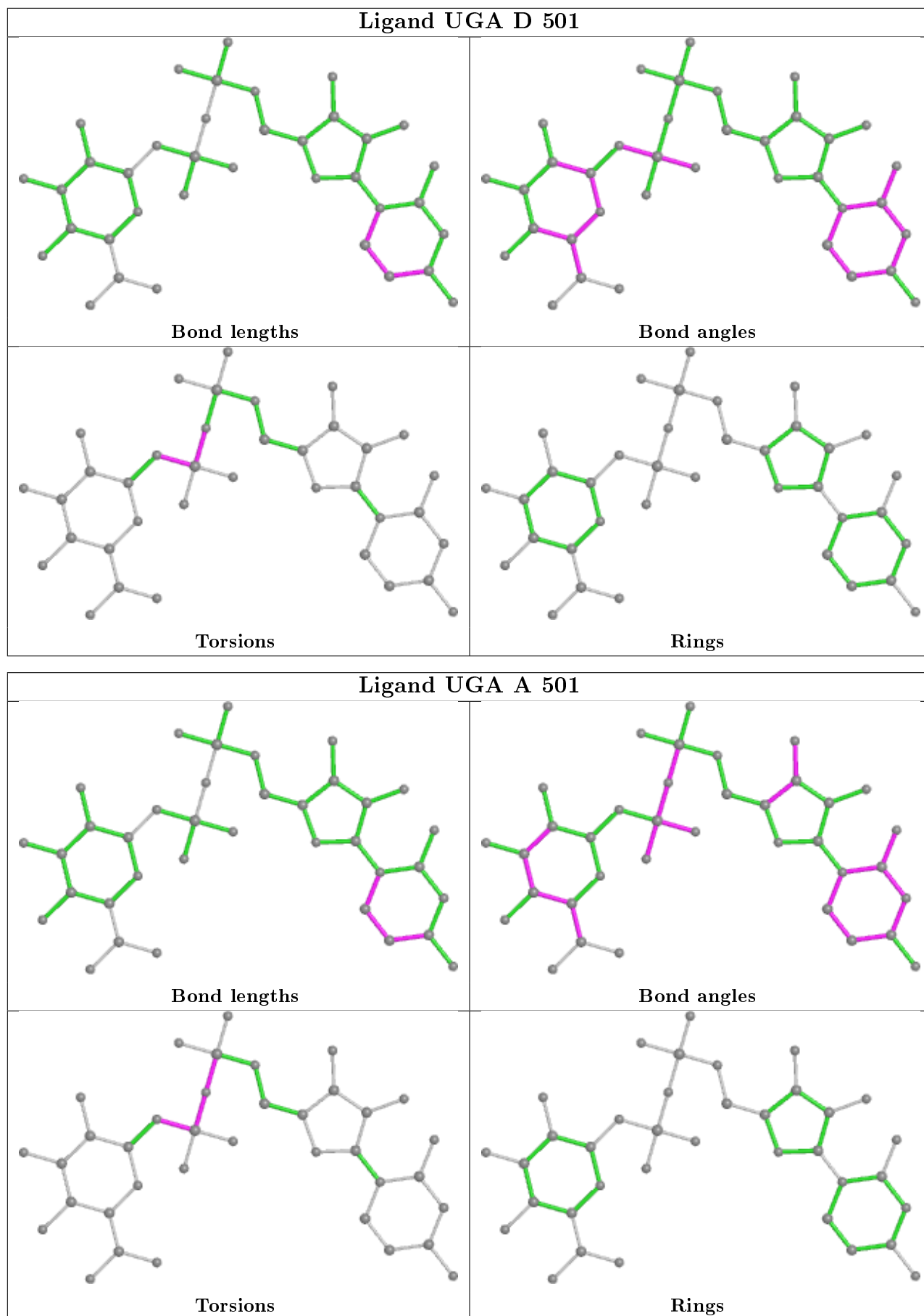
6 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1465	GOL	1	0
5	C	1462	GOL	2	0
5	A	1466	GOL	4	0
5	D	1463	GOL	3	0
5	A	1464	GOL	1	0
5	C	1463	GOL	2	0

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







## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [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	461/478 (96%)	-0.11	12 (2%) 56 62	9, 19, 36, 68	0
1	B	451/478 (94%)	0.01	16 (3%) 44 50	8, 20, 45, 66	0
1	C	455/478 (95%)	0.36	43 (9%) 8 11	8, 24, 63, 91	0
1	D	454/478 (94%)	-0.06	11 (2%) 59 65	7, 19, 40, 75	0
All	All	1821/1912 (95%)	0.05	82 (4%) 33 39	7, 20, 47, 91	0

All (82) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	143	GLY	5.2
1	C	38	ILE	5.1
1	B	94	ALA	5.1
1	C	139	ALA	4.8
1	C	44	VAL	4.7
1	C	257[A]	TYR	4.6
1	A	455	ARG	4.5
1	A	257[A]	TYR	4.4
1	B	455	ARG	4.4
1	C	113	PHE	4.2
1	C	455	ARG	4.1
1	A	144	ASP	4.0
1	C	112	GLY	3.9
1	B	47	HIS	3.7
1	C	146	MET	3.7
1	D	31	VAL	3.7
1	A	458	VAL	3.5
1	A	459	ALA	3.5
1	C	39	LEU	3.5
1	B	457	ALA	3.4
1	C	147	PHE	3.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	139	ALA	3.3
1	B	88[A]	PRO	3.3
1	C	29	LEU	3.3
1	C	34	ALA	3.3
1	D	455[A]	ARG	3.2
1	C	131	ARG	3.1
1	B	-2	GLY	3.0
1	C	111	THR	3.0
1	C	138	LEU	3.0
1	D	144	ASP	2.9
1	B	454	SER	2.9
1	C	182	GLU	2.9
1	A	416	VAL	2.8
1	B	456	GLN	2.8
1	C	65	ARG	2.7
1	B	135	ALA	2.7
1	C	42	GLY	2.7
1	C	41	ASN	2.7
1	C	36	ILE	2.7
1	C	8	SER	2.7
1	D	146[A]	MET	2.6
1	C	-2	GLY	2.6
1	A	-2	GLY	2.5
1	D	-2	GLY	2.5
1	B	418	LEU	2.5
1	C	454	SER	2.5
1	C	37	ASP	2.5
1	B	145	GLN	2.4
1	D	437	GLU	2.4
1	A	457	ALA	2.4
1	C	177	ASP	2.4
1	D	142	GLY	2.4
1	C	136	GLU	2.3
1	C	135	ALA	2.3
1	C	456	GLN	2.3
1	B	441	GLU	2.3
1	C	67	SER	2.3
1	C	47	HIS	2.3
1	C	89	ASP	2.3
1	C	420	ARG	2.3
1	C	109	TYR	2.3
1	C	108	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	177	ASP	2.3
1	D	458	VAL	2.3
1	C	90	GLU	2.3
1	A	179	VAL	2.2
1	C	66	PHE	2.2
1	A	454	SER	2.2
1	C	132	ALA	2.2
1	C	106	ILE	2.2
1	B	437	GLU	2.2
1	C	28[A]	CYS	2.2
1	C	179	VAL	2.2
1	C	437	GLU	2.1
1	D	179	VAL	2.1
1	D	47	HIS	2.1
1	A	437	GLU	2.1
1	B	8	SER	2.1
1	B	111	THR	2.0
1	C	43	GLY	2.0
1	C	457	ALA	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 carbohydrates 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<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( $\text{\AA}^2$ )	Q<0.9
5	GOL	C	1463	6/6	0.79	0.18	46,55,57,57	0
5	GOL	A	1465	6/6	0.80	0.14	57,58,60,60	0
3	SO4	B	1461	5/5	0.82	0.21	93,94,94,95	0
3	SO4	C	1460	5/5	0.84	0.28	87,87,88,89	0

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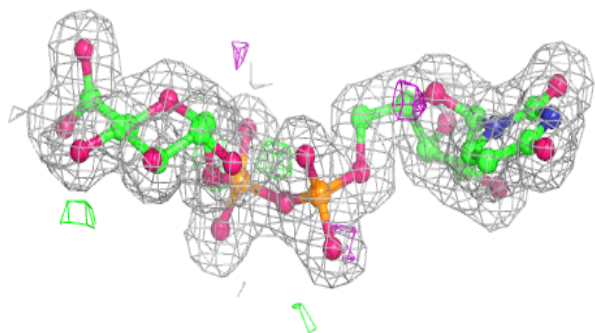
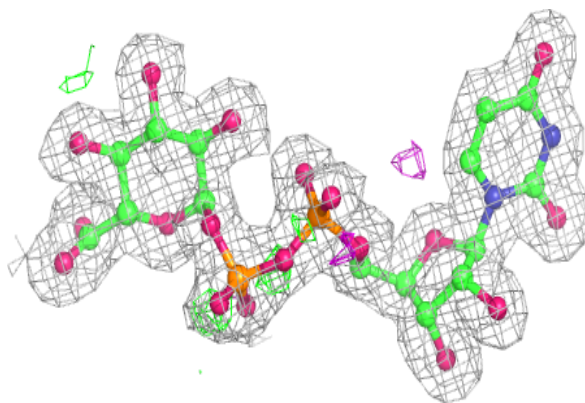
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	SO4	D	1461	5/5	0.85	0.28	93,94,94,94	0
3	SO4	B	1462	5/5	0.86	0.18	73,75,75,76	0
3	SO4	A	1462	5/5	0.87	0.23	88,89,89,89	0
3	SO4	D	1460	5/5	0.87	0.22	69,71,71,72	0
3	SO4	C	1459	5/5	0.88	0.28	41,53,56,56	0
5	GOL	A	1464	6/6	0.90	0.23	44,46,48,48	0
5	GOL	A	1466	6/6	0.91	0.18	21,40,47,49	0
5	GOL	D	1463	6/6	0.91	0.16	41,44,47,50	0
3	SO4	B	1460	5/5	0.91	0.20	72,72,73,75	0
4	ACT	B	1463	4/4	0.93	0.17	23,24,25,29	0
5	GOL	C	1462	6/6	0.94	0.14	18,37,42,47	0
3	SO4	A	1461	5/5	0.94	0.11	59,60,63,65	0
3	SO4	B	1459	5/5	0.95	0.11	31,38,39,45	0
3	SO4	D	1459	5/5	0.95	0.10	32,38,40,41	0
4	ACT	D	1462	4/4	0.95	0.10	23,24,24,28	0
3	SO4	A	1460	5/5	0.96	0.12	44,48,51,51	0
3	SO4	C	1458	5/5	0.97	0.11	44,45,49,49	0
4	ACT	C	1461	4/4	0.97	0.12	26,26,26,29	0
4	ACT	A	1463	4/4	0.98	0.08	16,18,20,21	0
2	UGA	A	501	37/37	0.98	0.08	7,11,16,21	0
2	UGA	B	501	37/37	0.99	0.09	7,10,14,17	0
3	SO4	B	1458	5/5	0.99	0.07	19,22,25,26	0
2	UGA	D	501	37/37	0.99	0.08	6,10,15,20	0
2	UGA	C	501	37/37	0.99	0.08	8,11,17,19	0

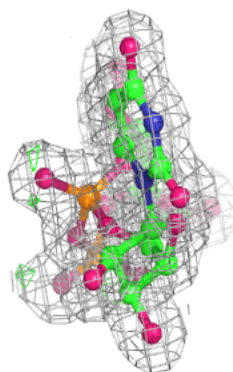
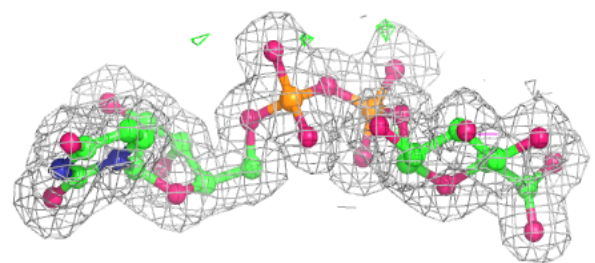
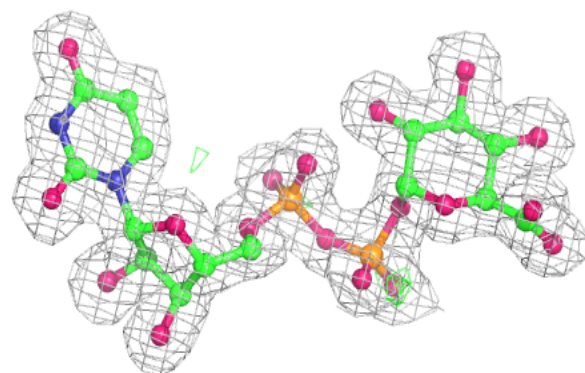
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around UGA A 501:**

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

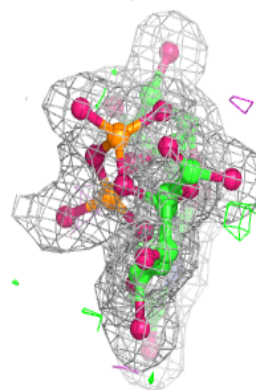
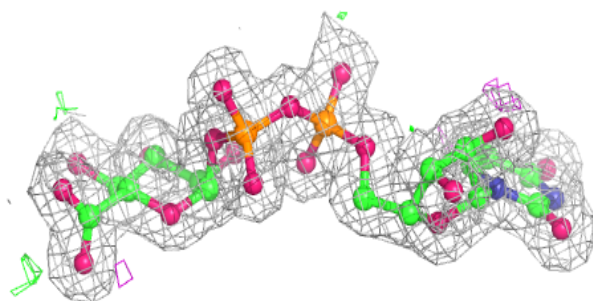
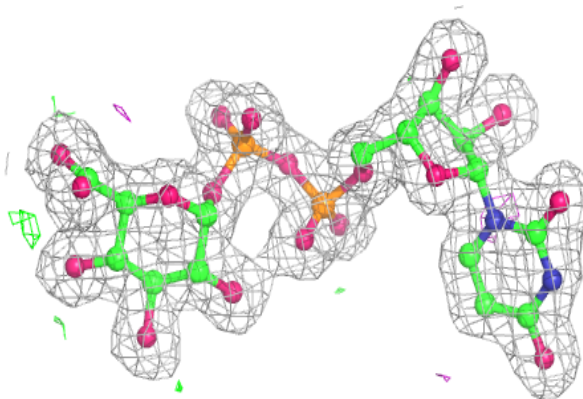
**Electron density around UGA B 501:**

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

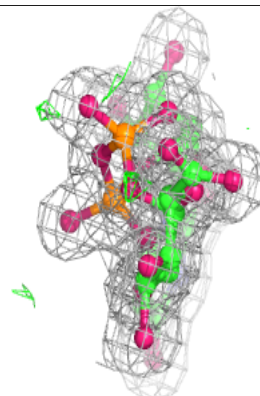
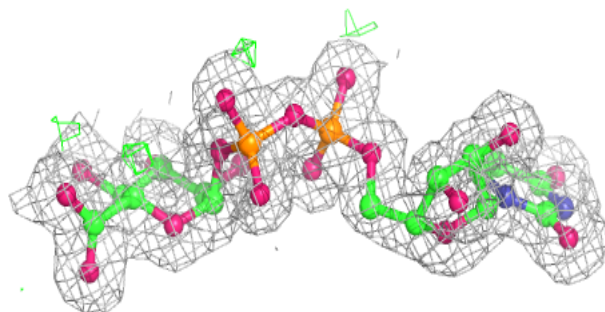
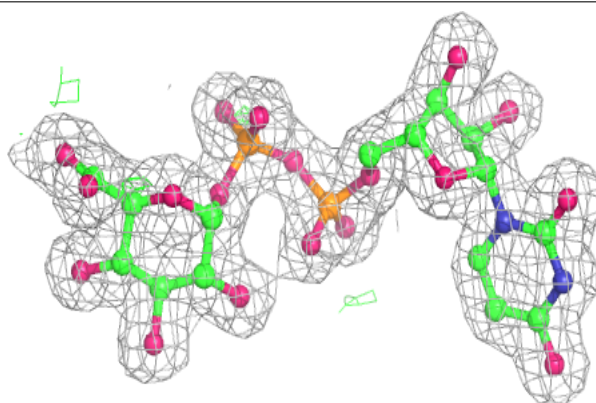


**Electron density around UGA D 501:**

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

**Electron density around UGA C 501:**

$2mF_o-DF_c$  (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.