



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2021 – 12:31 PM JST

PDB ID : 7C0R  
Title : Crystal structure of a dinucleotide-binding protein (F79A) of ABC transporter endogenously bound to uridylyl-3'-5'-phospho-guanosine (Form I)  
Authors : Kanaujia, S.P.; Chandravanshi, M.; Samanta, R.  
Deposited on : 2020-05-01  
Resolution : 1.77 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 : 2.23.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.23.1

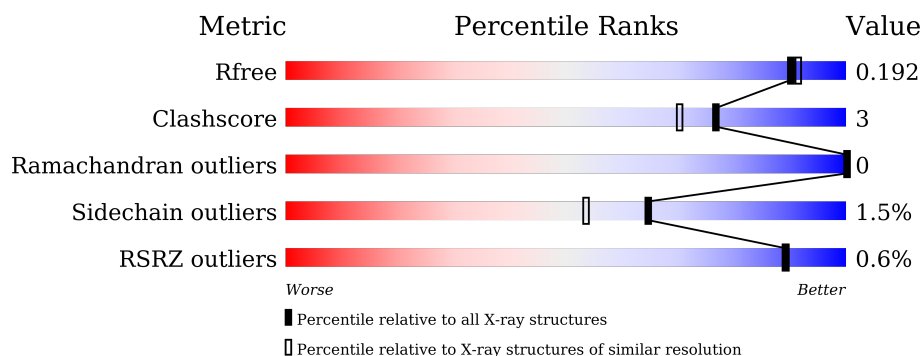
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*



The reported resolution of this entry is 1.77 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	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

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 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	406	 88% 9% ..
1	B	406	 88% 9% .

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6984 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 Sugar ABC transporter, periplasmic sugar-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	397	Total	C	N	O	S	0	1	0
			3058	1975	517	562	4			
1	B	396	Total	C	N	O	S	0	4	0
			3062	1979	513	566	4			

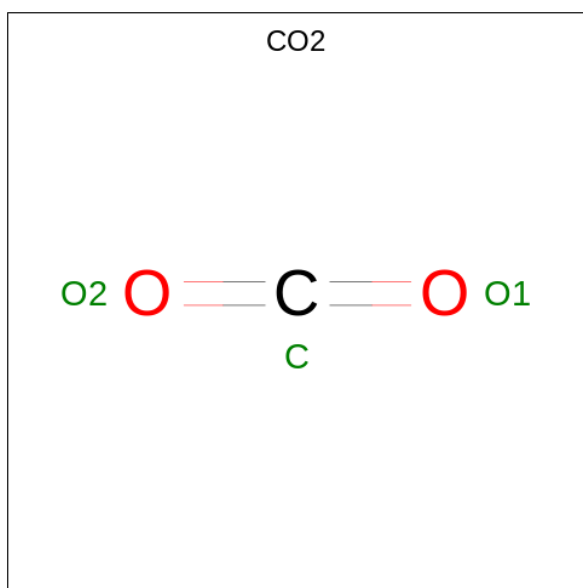
There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	initiating methionine	UNP Q5SLB4
A	0	MET	-	expression tag	UNP Q5SLB4
A	79	ALA	PHE	engineered mutation	UNP Q5SLB4
A	399	HIS	-	expression tag	UNP Q5SLB4
A	400	HIS	-	expression tag	UNP Q5SLB4
A	401	HIS	-	expression tag	UNP Q5SLB4
A	402	HIS	-	expression tag	UNP Q5SLB4
A	403	HIS	-	expression tag	UNP Q5SLB4
A	404	HIS	-	expression tag	UNP Q5SLB4
B	-1	MET	-	initiating methionine	UNP Q5SLB4
B	0	MET	-	expression tag	UNP Q5SLB4
B	79	ALA	PHE	engineered mutation	UNP Q5SLB4
B	399	HIS	-	expression tag	UNP Q5SLB4
B	400	HIS	-	expression tag	UNP Q5SLB4
B	401	HIS	-	expression tag	UNP Q5SLB4
B	402	HIS	-	expression tag	UNP Q5SLB4
B	403	HIS	-	expression tag	UNP Q5SLB4
B	404	HIS	-	expression tag	UNP Q5SLB4

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

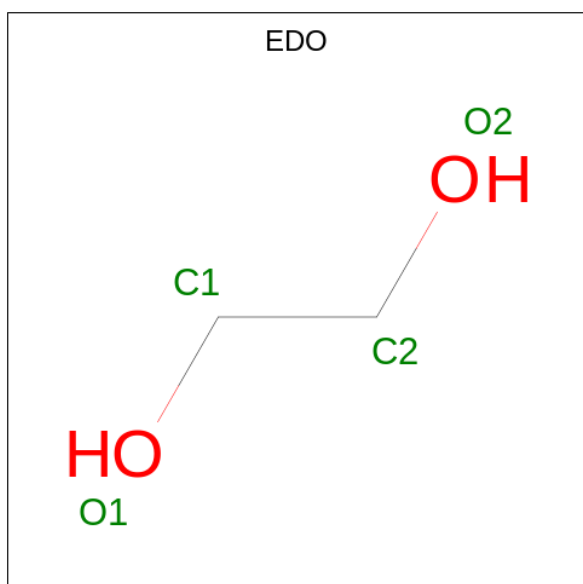
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Cl	0	0
			2	2		

- Molecule 3 is CARBON DIOXIDE (three-letter code: CO<sub>2</sub>) (formula: CO<sub>2</sub>).



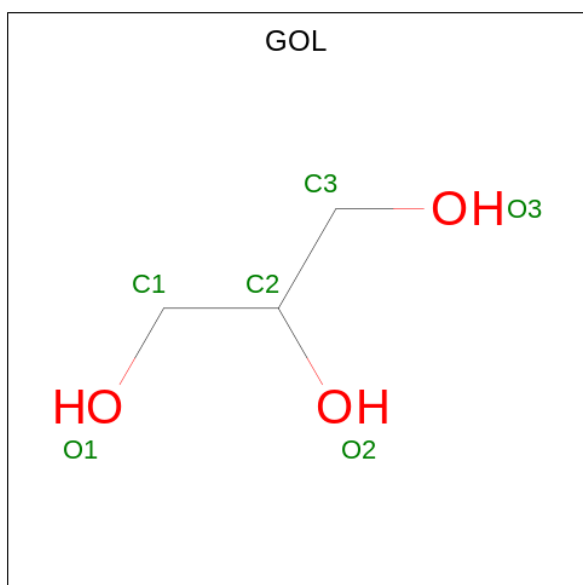
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			3	1	2		
3	A	1	Total	C	O	0	0
			3	1	2		
3	A	1	Total	C	O	0	0
			3	1	2		
3	B	1	Total	C	O	0	0
			3	1	2		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

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



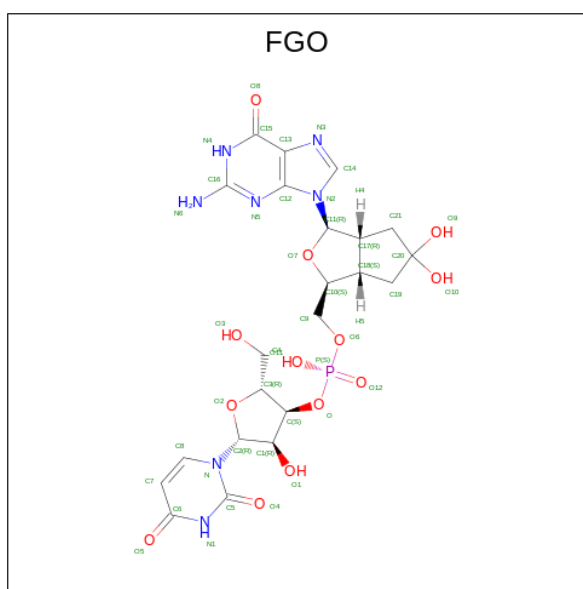
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0

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

- Molecule 6 is [(1S,3R,3aR,6aS)-3-(2-azanyl-6-oxidanylidene-1H-purin-9-yl)-5,5-bis(oxidanyl)-1,3,3a,4,6,6a-hexahydrocyclopenta[c]furan-1-yl]methyl [(2R,3S,4R,5R)-5-[2,4-bis(oxidanylidene)pyrimidin-1-yl]-2-(hydroxymethyl)-4-oxidanyl-oxolan-3-yl]hydrogen phosphate (three-letter code: FGO) (formula: C<sub>22</sub>H<sub>28</sub>N<sub>7</sub>O<sub>13</sub>P) (labeled as "Ligand of Interest" by depositor).



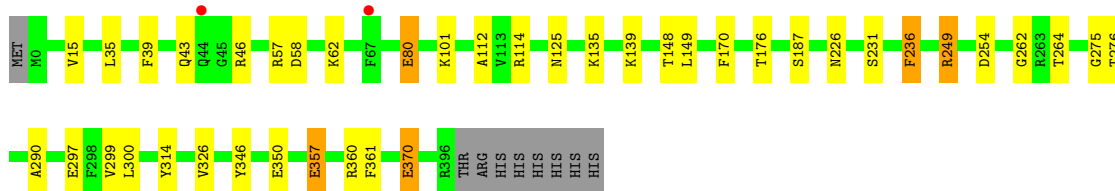
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	P	0	0
			43	22	7	13	1		
6	B	1	Total	C	N	O	P	0	0
			43	22	7	13	1		

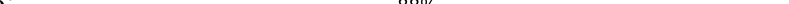
- Molecule 7 is water.

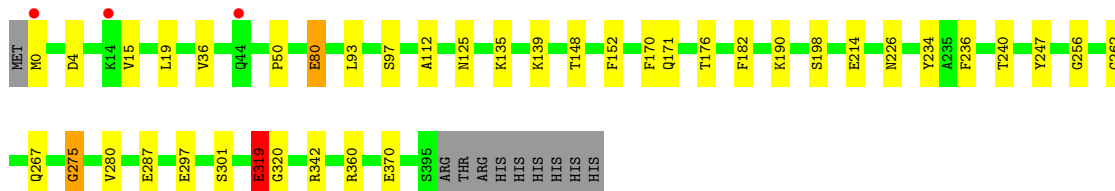
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	342	Total	O	0	0
			342	342		
7	B	358	Total	O	0	0
			358	358		



- Molecule 1: Sugar ABC transporter, periplasmic sugar-binding protein.



- Chain B:  88% 9% .



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	58.39Å 121.58Å 66.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	60.79 – 1.77 60.79 – 1.77	Depositor EDS
% Data completeness (in resolution range)	95.1 (60.79-1.77) 95.1 (60.79-1.77)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.18 (at 1.77Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.143 , 0.182 0.151 , 0.192	Depositor DCC
$R_{free}$ test set	4254 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.9	Xtriage
Anisotropy	0.457	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 29.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.389 for h,-k,-l	Xtriage
Reported twinning fraction	0.633 for H, K, L 0.367 for -h,-k,l	Depositor
Outliers	0 of 85004 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6984	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.73% 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: FGO, CL, GOL, CO2, EDO

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	1.13	10/3130 (0.3%)	1.11	5/4246 (0.1%)
1	B	1.13	10/3143 (0.3%)	1.16	5/4264 (0.1%)
All	All	1.13	20/6273 (0.3%)	1.13	10/8510 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	297	GLU	CD-OE2	16.61	1.44	1.25
1	A	80	GLU	CD-OE2	10.89	1.37	1.25
1	B	297	GLU	CD-OE2	9.78	1.36	1.25
1	B	80	GLU	CD-OE2	9.55	1.36	1.25
1	B	319	GLU	CD-OE2	8.27	1.34	1.25

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	360	ARG	NE-CZ-NH1	7.45	124.02	120.30
1	A	46	ARG	NE-CZ-NH1	6.66	123.63	120.30
1	B	360	ARG	NE-CZ-NH1	6.29	123.45	120.30
1	A	297	GLU	OE1-CD-OE2	6.21	130.75	123.30
1	A	114	ARG	NE-CZ-NH2	-6.03	117.28	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	236	PHE	Mainchain
1	A	346	TYR	Mainchain

## 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	3058	0	3092	17	0
1	B	3062	0	3096	15	0
2	A	2	0	0	1	0
3	A	9	0	0	0	0
3	B	3	0	0	0	0
4	A	8	0	12	0	0
4	B	32	0	48	6	0
5	A	12	0	16	2	0
5	B	12	0	16	1	0
6	A	43	0	0	1	0
6	B	43	0	0	0	0
7	A	342	0	0	7	0
7	B	358	0	0	3	0
All	All	6984	0	6280	38	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 3.

The worst 5 of 38 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:357:GLU:OE2	6:A:510:FGO:N6	2.08	0.86
4:B:506:EDO:C1	7:B:741:HOH:O	2.37	0.72
1:B:93:LEU:HD12	1:B:280:VAL:HG12	1.79	0.65
1:A:58:ASP:O	1:A:62:LYS:HG3	1.98	0.62
2:A:501:CL:CL	7:A:735:HOH:O	2.53	0.61

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	396/406 (98%)	392 (99%)	4 (1%)	0	100	100
1	B	398/406 (98%)	393 (99%)	5 (1%)	0	100	100
All	All	794/812 (98%)	785 (99%)	9 (1%)	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	310/318 (98%)	305 (98%)	5 (2%)	62	51
1	B	312/318 (98%)	308 (99%)	4 (1%)	69	59
All	All	622/636 (98%)	613 (99%)	9 (1%)	65	56

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	226	ASN
1	B	319	GLU
1	A	249	ARG
1	A	264	THR
1	B	15	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 22 ligands modelled in this entry, 2 are monoatomic - leaving 20 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
5	GOL	B	510	-	5,5,5	0.10	0	5,5,5	0.43	0
4	EDO	B	507	-	3,3,3	0.32	0	2,2,2	0.43	0
5	GOL	B	511	-	5,5,5	0.17	0	5,5,5	0.46	0
5	GOL	A	508	-	5,5,5	0.19	0	5,5,5	0.45	0
4	EDO	A	507	-	3,3,3	0.22	0	2,2,2	0.08	0
5	GOL	A	509	-	5,5,5	0.16	0	5,5,5	0.67	0
3	CO2	A	504	-	2,2,2	0.01	0	1,1,1	0.89	0
6	FGO	A	510	-	40,48,48	1.71	7 (17%)	39,75,75	2.13	12 (30%)
4	EDO	B	509	-	3,3,3	0.13	0	2,2,2	0.76	0
4	EDO	B	503	-	3,3,3	0.22	0	2,2,2	0.09	0
4	EDO	A	506	-	3,3,3	0.33	0	2,2,2	0.14	0
4	EDO	B	506	-	3,3,3	0.41	0	2,2,2	0.29	0
4	EDO	B	505	-	3,3,3	0.18	0	2,2,2	0.06	0
3	CO2	B	501	-	2,2,2	0.42	0	1,1,1	1.58	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	EDO	B	508	-	3,3,3	0.37	0	2,2,2	1.15	0
4	EDO	B	504	-	3,3,3	0.28	0	2,2,2	0.56	0
4	EDO	B	502	-	3,3,3	0.17	0	2,2,2	0.32	0
3	CO2	A	505	-	2,2,2	0.44	0	1,1,1	1.41	0
6	FGO	B	512	-	40,48,48	1.48	6 (15%)	39,75,75	2.23	13 (33%)
3	CO2	A	503	-	2,2,2	0.38	0	1,1,1	0.79	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	EDO	A	506	-	-	1/1/1/1	-
5	GOL	A	509	-	-	4/4/4/4	-
4	EDO	B	506	-	-	1/1/1/1	-
4	EDO	B	505	-	-	0/1/1/1	-
4	EDO	B	502	-	-	1/1/1/1	-
4	EDO	B	507	-	-	1/1/1/1	-
5	GOL	B	510	-	-	1/4/4/4	-
6	FGO	A	510	-	-	2/15/63/63	0/6/6/6
4	EDO	B	509	-	-	0/1/1/1	-
4	EDO	B	503	-	-	0/1/1/1	-
5	GOL	B	511	-	-	2/4/4/4	-
4	EDO	B	508	-	-	1/1/1/1	-
6	FGO	B	512	-	-	1/15/63/63	0/6/6/6
4	EDO	B	504	-	-	0/1/1/1	-
5	GOL	A	508	-	-	4/4/4/4	-
4	EDO	A	507	-	-	1/1/1/1	-

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	510	FGO	C19-C18	-5.62	1.44	1.53
6	A	510	FGO	C8-N	4.55	1.41	1.35
6	B	512	FGO	C19-C18	-3.19	1.48	1.53
6	B	512	FGO	O5-C6	2.97	1.32	1.24
6	B	512	FGO	C21-C20	2.91	1.58	1.52

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	512	FGO	C17-C18-C10	5.96	114.89	103.72
6	A	510	FGO	C17-C18-C10	5.17	113.40	103.72
6	B	512	FGO	C15-C13-C12	-4.83	116.19	120.80
6	B	512	FGO	C11-N2-C12	-4.62	118.53	126.64
6	B	512	FGO	O7-C10-C18	-4.46	96.81	104.89

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

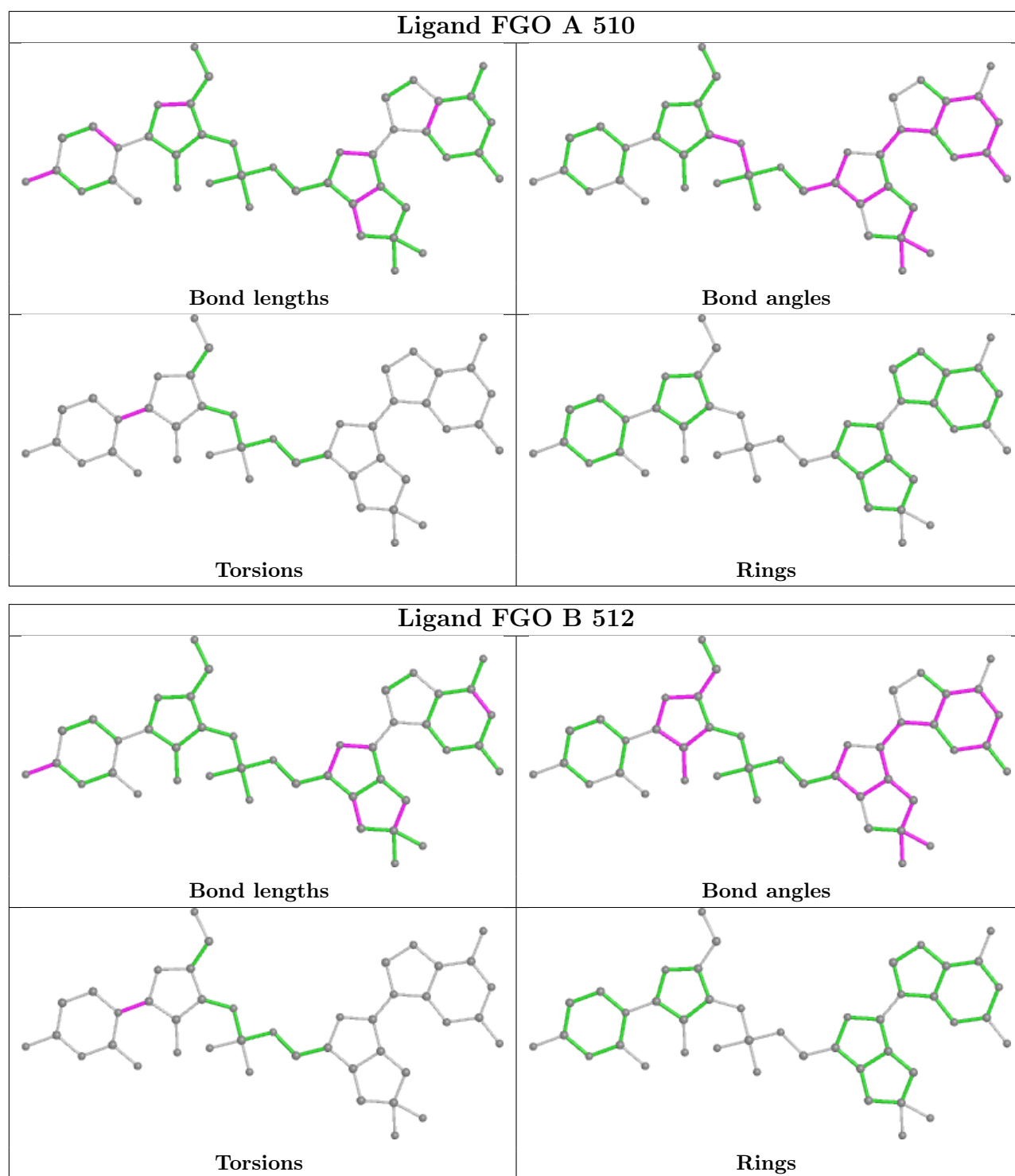
Mol	Chain	Res	Type	Atoms
5	A	508	GOL	O1-C1-C2-C3
5	A	508	GOL	C1-C2-C3-O3
5	A	509	GOL	O1-C1-C2-C3
6	A	510	FGO	O2-C2-N-C8
6	A	510	FGO	C1-C2-N-C8

There are no ring outliers.

7 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	510	GOL	1	0
4	B	507	EDO	1	0
5	A	508	GOL	2	0
6	A	510	FGO	1	0
4	B	506	EDO	3	0
4	B	505	EDO	1	0
4	B	508	EDO	1	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 ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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	397/406 (97%)	-0.49	2 (0%) 91 91	10, 17, 33, 53	0
1	B	396/406 (97%)	-0.48	3 (0%) 86 86	8, 17, 32, 70	0
All	All	793/812 (97%)	-0.49	5 (0%) 89 89	8, 17, 33, 70	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	67	PHE	3.5
1	B	44	GLN	2.7
1	A	44	GLN	2.5
1	B	14	LYS	2.4
1	B	0	MET	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](#)

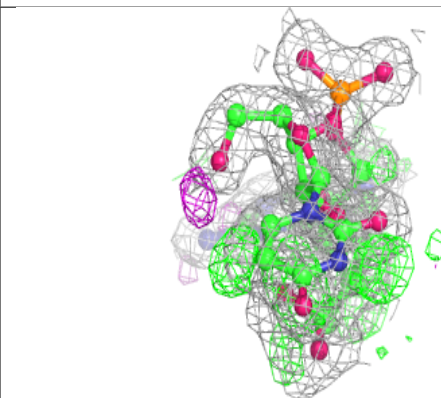
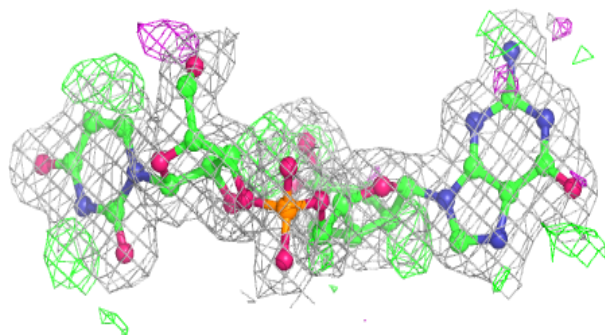
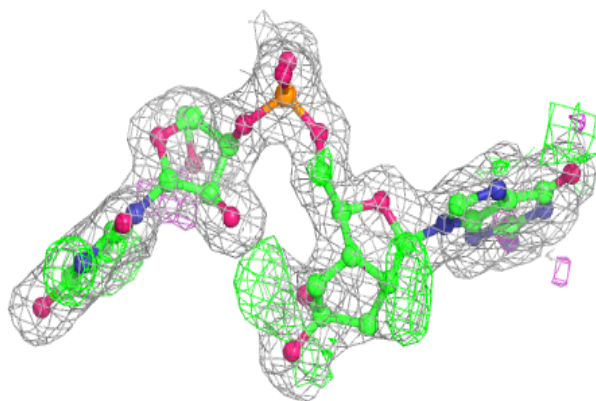
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 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
3	CO2	A	503	3/3	0.85	0.11	37,37,46,48	0
5	GOL	A	508	6/6	0.88	0.18	30,38,41,43	0
4	EDO	B	505	4/4	0.89	0.14	39,42,42,46	0
4	EDO	B	508	4/4	0.91	0.18	21,21,27,29	0
3	CO2	A	504	3/3	0.92	0.09	41,41,45,45	0
4	EDO	B	507	4/4	0.92	0.10	30,33,34,36	0
4	EDO	A	507	4/4	0.93	0.08	27,28,29,34	0
4	EDO	B	502	4/4	0.94	0.07	32,41,42,42	0
4	EDO	B	504	4/4	0.94	0.10	20,20,24,25	0
4	EDO	A	506	4/4	0.94	0.15	22,25,27,31	0
4	EDO	B	509	4/4	0.95	0.14	27,30,32,37	0
3	CO2	A	505	3/3	0.95	0.09	22,22,28,37	0
4	EDO	B	503	4/4	0.96	0.07	23,30,30,32	0
4	EDO	B	506	4/4	0.96	0.13	22,29,32,39	0
3	CO2	B	501	3/3	0.96	0.17	23,23,23,35	0
5	GOL	B	510	6/6	0.96	0.09	19,25,27,30	0
5	GOL	B	511	6/6	0.96	0.09	16,19,21,27	0
6	FGO	A	510	43/43	0.96	0.09	10,19,29,34	0
6	FGO	B	512	43/43	0.96	0.09	10,19,29,38	0
5	GOL	A	509	6/6	0.97	0.10	20,25,29,35	0
2	CL	A	502	1/1	0.98	0.06	33,33,33,33	0
2	CL	A	501	1/1	0.99	0.07	33,33,33,33	0

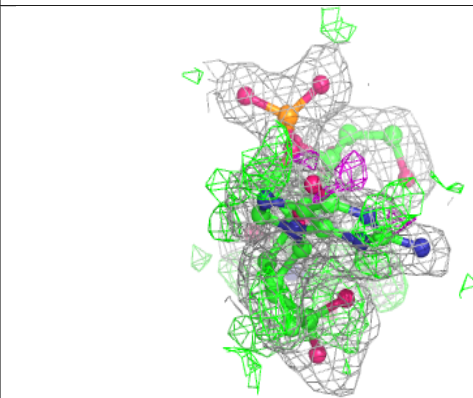
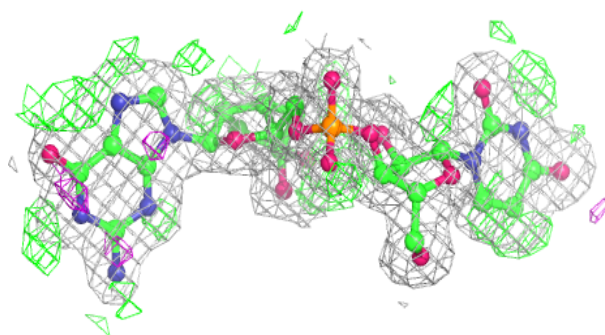
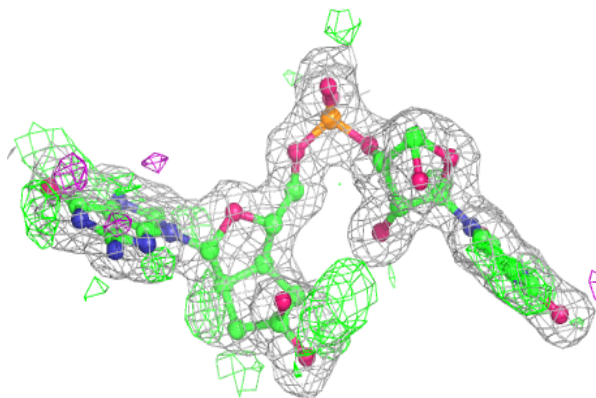
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around FGO A 510:**

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

**Electron density around FGO B 512:**

$2mF_o-DF_c$  (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.