



# Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 03:31 pm BST

PDB ID : 3TAX  
Title : A Neutral Diphosphate Mimic Crosslinks the Active Site of Human O-GlcNAc Transferase  
Authors : Lazarus, M.B.; Jiang, J.; Pasquina, L.; Sliz, P.; Walker, S.  
Deposited on : 2011-08-04  
Resolution : 1.88 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

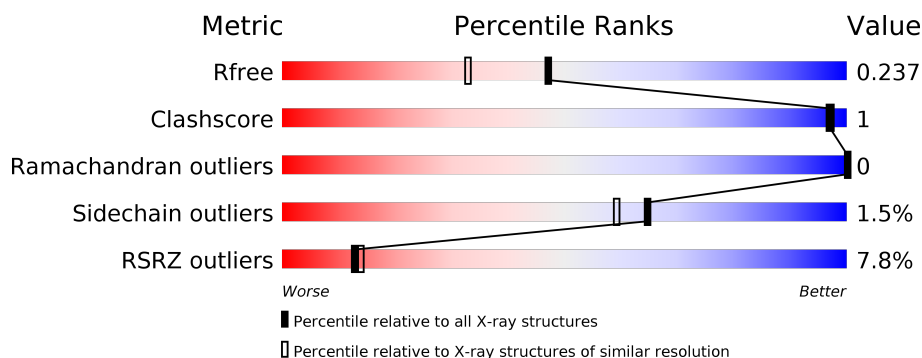
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.88 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	9470 (1.90-1.86)
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

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	723	<div> <div>7%</div> <div> <div></div> <div>93%</div> <div></div> </div> <div></div> </div>
1	C	723	<div> <div>8%</div> <div> <div></div> <div>93%</div> <div></div> </div> <div></div> </div>
2	B	14	<div> <div></div> <div> <div>79%</div> <div>21%</div> </div> </div>
2	D	14	<div> <div></div> <div> <div>86%</div> <div>14%</div> </div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12326 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-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	695	Total	C	N	O	S	0	5	0
			5522	3505	964	1016	37			
1	C	695	Total	C	N	O	S	0	5	0
			5522	3505	964	1016	37			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	309	GLY	-	EXPRESSION TAG	UNP O15294
A	310	PRO	-	EXPRESSION TAG	UNP O15294
A	311	GLY	-	EXPRESSION TAG	UNP O15294
A	312	SER	-	EXPRESSION TAG	UNP O15294
C	309	GLY	-	EXPRESSION TAG	UNP O15294
C	310	PRO	-	EXPRESSION TAG	UNP O15294
C	311	GLY	-	EXPRESSION TAG	UNP O15294
C	312	SER	-	EXPRESSION TAG	UNP O15294

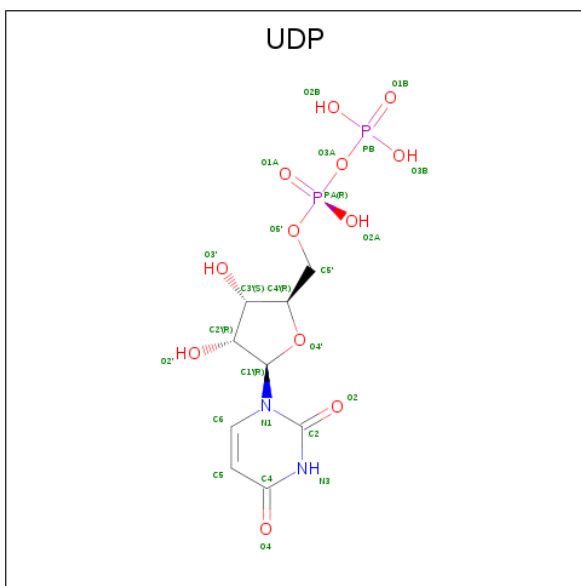
- Molecule 2 is a protein called Casein kinase II subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	14	Total	C	N	O	S	0	0	0
			95	58	15	20	2			
2	D	14	Total	C	N	O	S	0	0	0
			95	58	15	20	2			

There are 2 discrepancies between the modelled and reference sequences:

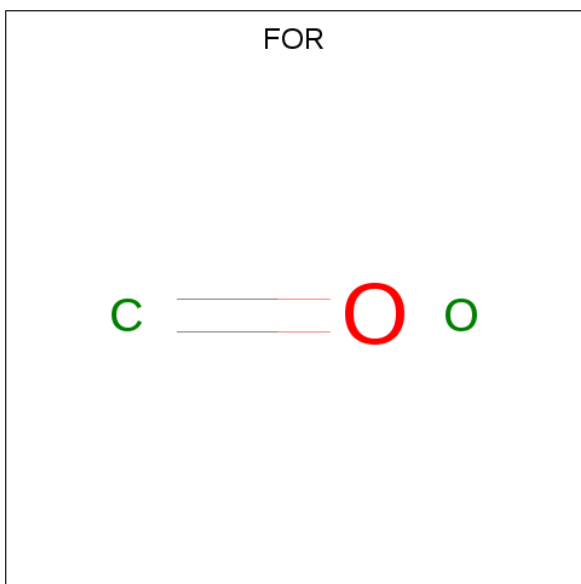
Chain	Residue	Modelled	Actual	Comment	Reference
B	13	TYR	-	EXPRESSION TAG	UNP P68400
D	13	TYR	-	EXPRESSION TAG	UNP P68400

- Molecule 3 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula:  $C_9H_{14}N_2O_{12}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
3	C	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

- Molecule 4 is FORMYL GROUP (three-letter code: FOR) (formula:  $CH_2O$ ).



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

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

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

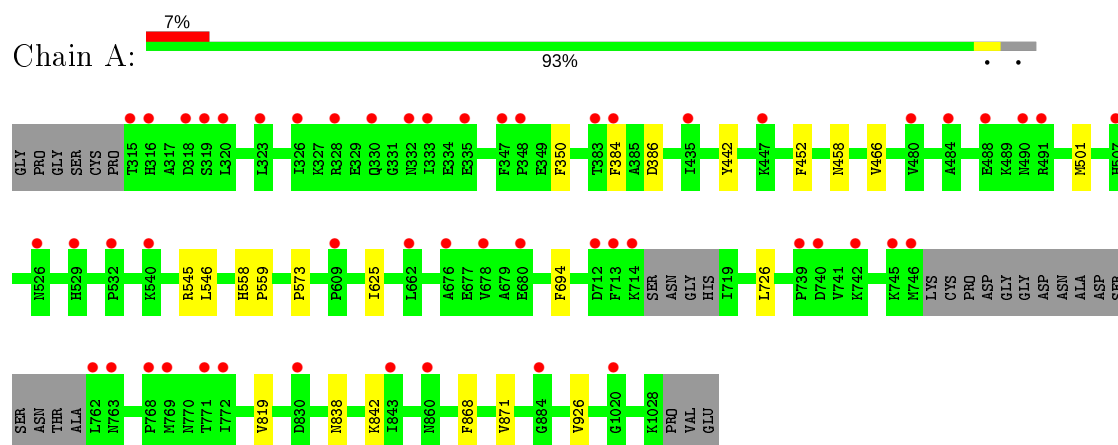
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	492	Total	O	0	0
			492	492		
6	B	17	Total	O	0	0
			17	17		
6	C	497	Total	O	0	0
			497	497		
6	D	12	Total	O	0	0
			12	12		

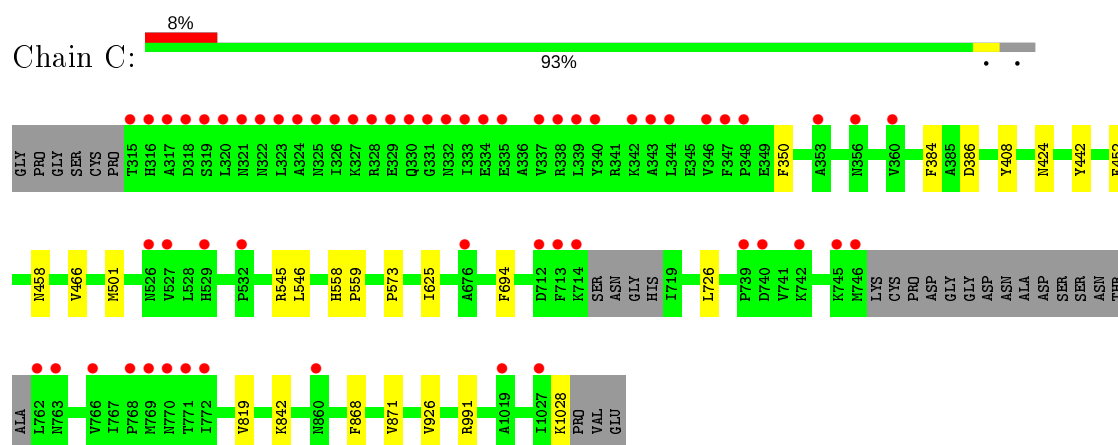
### 3 Residue-property plots

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.

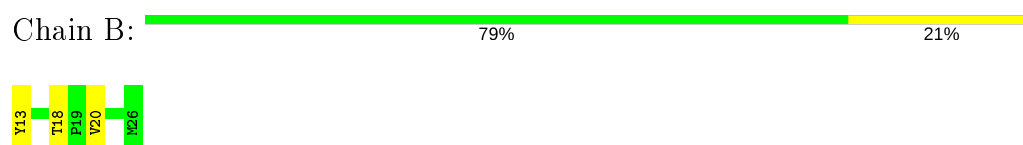
- Molecule 1: UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit




- Molecule 1: UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit



- Molecule 2: Casein kinase II subunit alpha



- Molecule 2: Casein kinase II subunit alpha

Chain D:  86% 14%



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	98.60Å 136.64Å 153.32Å 90.00° 103.02° 90.00°	Depositor
Resolution (Å)	37.60 – 1.88 43.57 – 1.88	Depositor EDS
% Data completeness (in resolution range)	99.2 (37.60-1.88) 99.1 (43.57-1.88)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.12 (at 1.88Å)	Xtriage
Refinement program	BUSTER 2.11.1	Depositor
R, $R_{free}$	0.219 , 0.237 0.217 , 0.237	Depositor DCC
$R_{free}$ test set	8002 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.2	Xtriage
Anisotropy	0.259	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 49.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	12326	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 26.40 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.6522e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: UDP, SO4, FOR

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	0.46	0/5657	0.59	0/7670
1	C	0.46	0/5657	0.59	0/7670
2	B	0.42	0/97	0.58	0/131
2	D	0.41	0/97	0.56	0/131
All	All	0.46	0/11508	0.59	0/15602

There are no bond length outliers.

There are no bond angle outliers.

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	5522	0	5501	9	0
1	C	5522	0	5501	9	0
2	B	95	0	88	2	0
2	D	95	0	88	1	0
3	A	25	0	11	1	0
3	C	25	0	11	0	0
4	A	2	0	0	1	0
4	C	2	0	0	1	0
5	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	5	0	0	0	0
5	C	5	0	0	0	0
5	D	5	0	0	0	0
6	A	492	0	0	0	0
6	B	17	0	0	0	0
6	C	497	0	0	0	0
6	D	12	0	0	0	0
All	All	12326	0	11200	21	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 1.

All (21) 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:B:13:TYR:N	2:B:18:THR:HG1	1.94	0.65
2:D:13:TYR:N	2:D:18:THR:HG1	1.96	0.64
1:A:545:ARG:HD3	1:A:573:PRO:O	2.04	0.57
1:C:545:ARG:HD3	1:C:573:PRO:O	2.05	0.57
1:C:842[B]:LYS:HE2	4:C:1250:FOR:C	2.33	0.49
1:A:726:LEU:HD23	1:A:819:VAL:HG22	1.96	0.48
1:C:726:LEU:HD23	1:C:819:VAL:HG22	1.96	0.47
1:A:842[B]:LYS:HE2	4:A:1250:FOR:C	2.36	0.46
1:C:726:LEU:CD2	1:C:819:VAL:HG22	2.46	0.46
1:A:726:LEU:CD2	1:A:819:VAL:HG22	2.47	0.44
1:A:838:ASN:HB3	1:A:842[B]:LYS:HD2	1.99	0.43
3:A:1212:UDP:H5'1	2:B:20:VAL:HG12	2.01	0.43
1:C:546:LEU:HD21	1:C:625:ILE:HD12	2.01	0.43
1:C:408:TYR:CZ	1:C:424:ASN:HB3	2.54	0.43
1:A:546:LEU:HD21	1:A:625:ILE:HD12	2.01	0.42
1:C:466:VAL:HG12	1:C:871:VAL:HG23	2.02	0.41
1:A:442:TYR:CZ	1:A:458:ASN:HB3	2.55	0.41
1:C:558:HIS:CG	1:C:559:PRO:HD2	2.56	0.41
1:A:558:HIS:CG	1:A:559:PRO:HD2	2.55	0.40
1:A:466:VAL:HG12	1:A:871:VAL:HG23	2.04	0.40
1:C:442:TYR:CZ	1:C:458:ASN:HB3	2.57	0.40

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	694/723 (96%)	680 (98%)	14 (2%)	0	100	100
1	C	694/723 (96%)	680 (98%)	14 (2%)	0	100	100
2	B	12/14 (86%)	12 (100%)	0	0	100	100
2	D	12/14 (86%)	12 (100%)	0	0	100	100
All	All	1412/1474 (96%)	1384 (98%)	28 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	602/618 (97%)	594 (99%)	8 (1%)	69	64
1	C	602/618 (97%)	592 (98%)	10 (2%)	60	54
2	B	11/11 (100%)	11 (100%)	0	100	100
2	D	11/11 (100%)	11 (100%)	0	100	100
All	All	1226/1258 (98%)	1208 (98%)	18 (2%)	65	59

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	350	PHE
1	A	384	PHE

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Mol	Chain	Res	Type
1	A	386	ASP
1	A	452	PHE
1	A	501	MET
1	A	694	PHE
1	A	868	PHE
1	A	926	VAL
1	C	350	PHE
1	C	384	PHE
1	C	386	ASP
1	C	452	PHE
1	C	501	MET
1	C	694	PHE
1	C	868	PHE
1	C	926	VAL
1	C	991	ARG
1	C	1028	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	406	GLN
1	A	681	GLN
1	C	406	GLN
1	C	681	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 carbohydrates in this entry.

## 5.6 Ligand geometry

8 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	UDP	A	1212	-	20,26,26	2.19	7 (35%)	25,40,40	1.38	5 (20%)
5	SO4	A	3	-	4,4,4	0.28	0	6,6,6	0.10	0
5	SO4	C	4	-	4,4,4	0.16	0	6,6,6	0.11	0
5	SO4	D	2	-	4,4,4	0.39	0	6,6,6	0.27	0
5	SO4	B	1	-	4,4,4	0.32	0	6,6,6	0.22	0
4	FOR	C	1250	1	0,1,1	0.00	-	-	-	-
3	UDP	C	1212	-	20,26,26	2.11	8 (40%)	25,40,40	1.35	3 (12%)
4	FOR	A	1250	1	0,1,1	0.00	-	-	-	-

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
3	UDP	A	1212	-	-	3/14/32/32	0/2/2/2
3	UDP	C	1212	-	-	4/14/32/32	0/2/2/2

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1212	UDP	O4'-C1'	5.33	1.48	1.41
3	A	1212	UDP	C6-N1	4.90	1.41	1.35
3	A	1212	UDP	C4-N3	4.41	1.40	1.33
3	A	1212	UDP	O4'-C1'	4.12	1.46	1.41
3	C	1212	UDP	C4-N3	4.01	1.40	1.33
3	A	1212	UDP	O3'-C3'	2.81	1.49	1.43
3	C	1212	UDP	O3'-C3'	2.59	1.49	1.43
3	C	1212	UDP	C2-N3	-2.54	1.33	1.38
3	A	1212	UDP	C2-N3	-2.49	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1212	UDP	C6-N1	2.37	1.38	1.35
3	C	1212	UDP	O4-C4	-2.31	1.18	1.24
3	C	1212	UDP	C3'-C4'	2.23	1.58	1.53
3	A	1212	UDP	C3'-C2'	2.17	1.59	1.53
3	C	1212	UDP	PA-O1A	-2.06	1.43	1.50
3	A	1212	UDP	C3'-C4'	2.00	1.58	1.53

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1212	UDP	O2B-PB-O3A	3.43	116.14	104.64
3	A	1212	UDP	PA-O3A-PB	-3.04	122.38	132.83
3	C	1212	UDP	PA-O3A-PB	-2.81	123.19	132.83
3	A	1212	UDP	O2B-PB-O3A	2.58	113.28	104.64
3	C	1212	UDP	O3A-PB-O1B	-2.34	98.24	111.19
3	A	1212	UDP	O3A-PB-O1B	-2.33	98.26	111.19
3	A	1212	UDP	O3B-PB-O3A	2.25	112.17	104.64
3	A	1212	UDP	C5-C4-N3	-2.03	118.84	123.31

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1212	UDP	C2'-C1'-N1-C6
3	A	1212	UDP	O4'-C1'-N1-C6
3	C	1212	UDP	C2'-C1'-N1-C6
3	C	1212	UDP	O4'-C1'-N1-C6
3	C	1212	UDP	O4'-C4'-C5'-O5'
3	A	1212	UDP	O4'-C4'-C5'-O5'
3	C	1212	UDP	C3'-C4'-C5'-O5'

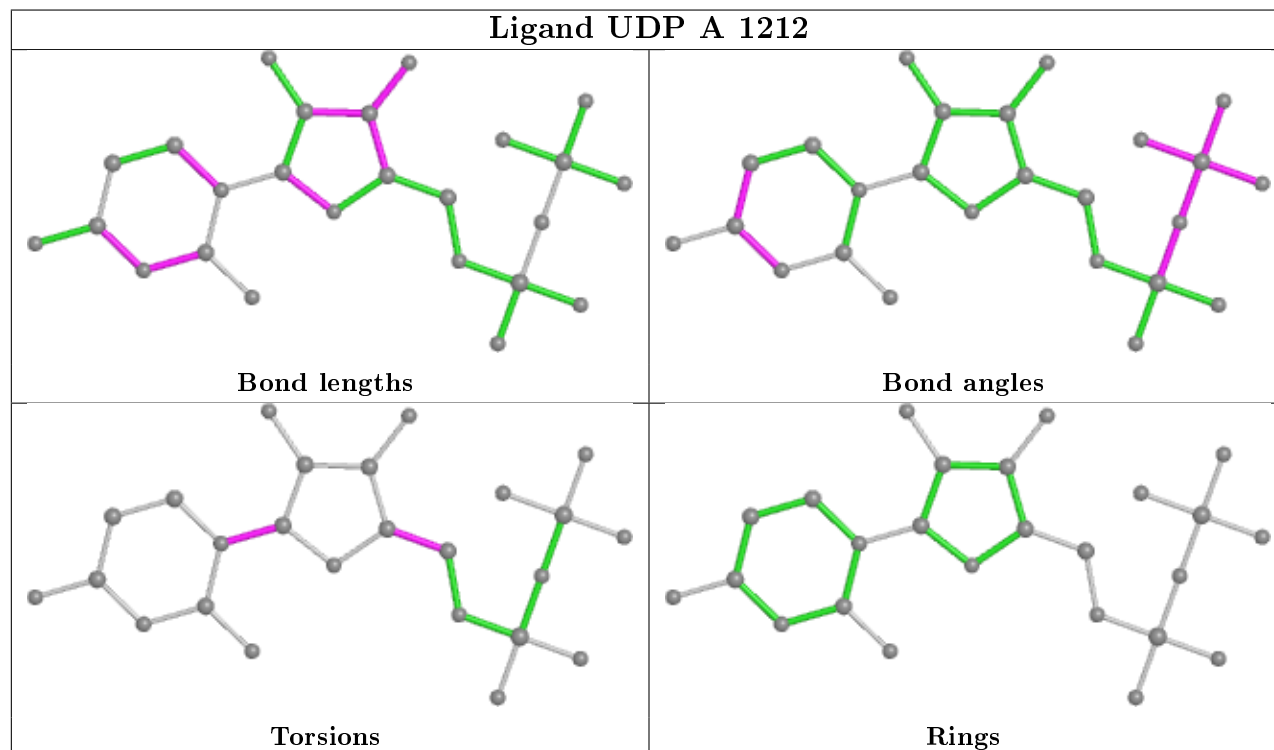
There are no ring outliers.

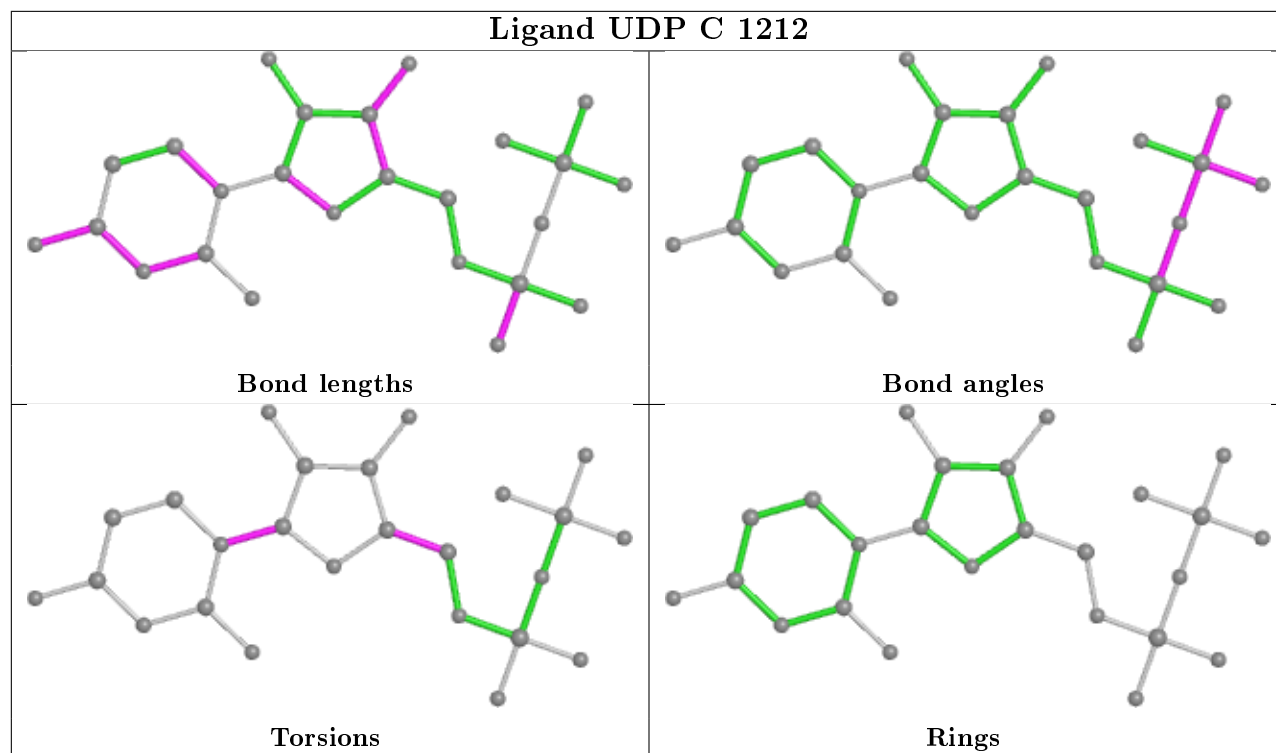
3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1212	UDP	1	0
4	C	1250	FOR	1	0
4	A	1250	FOR	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 [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.



## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<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	695/723 (96%)	0.39	52 (7%) 14 15	12, 24, 49, 87	0
1	C	695/723 (96%)	0.44	58 (8%) 11 12	11, 23, 57, 89	0
2	B	14/14 (100%)	0.09	0 100 100	14, 21, 40, 50	0
2	D	14/14 (100%)	0.24	0 100 100	15, 21, 41, 51	0
All	All	1418/1474 (96%)	0.41	110 (7%) 13 14	11, 23, 52, 89	0

All (110) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	326	ILE	10.3
1	C	323	LEU	8.5
1	C	333	ILE	8.4
1	C	335	GLU	7.7
1	C	746	MET	7.5
1	A	746	MET	7.3
1	A	713	PHE	6.8
1	C	315	THR	6.7
1	C	316	HIS	6.5
1	C	317	ALA	6.5
1	C	769	MET	6.2
1	C	318	ASP	6.1
1	A	714	LYS	5.9
1	C	324	ALA	5.6
1	C	713	PHE	5.6
1	C	319[A]	SER	5.5
1	C	331	GLY	5.2
1	C	327	LYS	5.2
1	C	339	LEU	5.0
1	C	320	LEU	4.8
1	C	347	PHE	4.8

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Mol	Chain	Res	Type	RSRZ
1	C	328	ARG	4.8
1	A	739	PRO	4.8
1	C	330	GLN	4.7
1	A	772	ILE	4.6
1	A	769	MET	4.5
1	A	768	PRO	4.4
1	C	714	LYS	4.3
1	C	338	ARG	4.3
1	A	335	GLU	4.2
1	A	315	THR	4.2
1	A	745	LYS	4.2
1	C	745	LYS	4.2
1	C	739	PRO	4.2
1	A	316	HIS	4.1
1	C	321	ASN	4.1
1	A	526	ASN	4.1
1	C	768	PRO	4.1
1	C	526	ASN	3.9
1	A	771	THR	3.9
1	C	740	ASP	3.9
1	C	346	VAL	3.9
1	A	740	ASP	3.8
1	C	742	LYS	3.8
1	C	325	ASN	3.8
1	A	347	PHE	3.7
1	C	762	LEU	3.6
1	C	348	PRO	3.6
1	C	763	ASN	3.4
1	A	490	ASN	3.4
1	C	332	ASN	3.4
1	C	860	ASN	3.4
1	A	662	LEU	3.4
1	A	491	ARG	3.3
1	A	532	PRO	3.3
1	A	333	ILE	3.3
1	A	323	LEU	3.3
1	A	762	LEU	3.3
1	A	712	ASP	3.2
1	C	712	ASP	3.2
1	A	507	HIS	3.2
1	C	334	GLU	3.2
1	C	344	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	532	PRO	3.1
1	C	340	TYR	3.0
1	A	488	GLU	2.9
1	C	772	ILE	2.9
1	C	353	ALA	2.9
1	A	860	ASN	2.8
1	A	763	ASN	2.8
1	C	329	GLU	2.7
1	C	770	ASN	2.6
1	A	676	ALA	2.6
1	A	319[A]	SER	2.5
1	A	742	LYS	2.5
1	A	332	ASN	2.5
1	C	322	ASN	2.5
1	C	771	THR	2.5
1	A	529	HIS	2.4
1	C	676	ALA	2.4
1	A	484	ALA	2.4
1	C	1019	ALA	2.4
1	A	435	ILE	2.4
1	C	529	HIS	2.3
1	C	766	VAL	2.3
1	C	342	LYS	2.3
1	A	348	PRO	2.3
1	C	343	ALA	2.3
1	C	527	VAL	2.2
1	C	337	VAL	2.2
1	C	360	VAL	2.2
1	A	678	VAL	2.2
1	A	383	THR	2.2
1	A	540	LYS	2.2
1	A	480	VAL	2.2
1	A	609	PRO	2.1
1	A	326	ILE	2.1
1	A	843	ILE	2.1
1	A	1020	GLY	2.1
1	C	1027	ILE	2.1
1	A	884	GLY	2.1
1	A	318	ASP	2.1
1	A	328	ARG	2.1
1	A	680	GLU	2.0
1	A	384	PHE	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	330	GLN	2.0
1	A	830	ASP	2.0
1	A	320	LEU	2.0
1	C	356	ASN	2.0
1	A	447	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 carbohydrates in this entry.

## 6.4 Ligands [i](#)

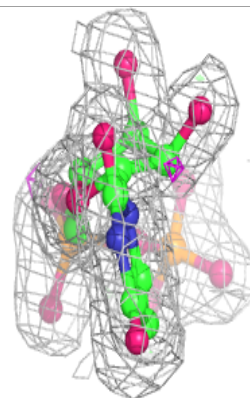
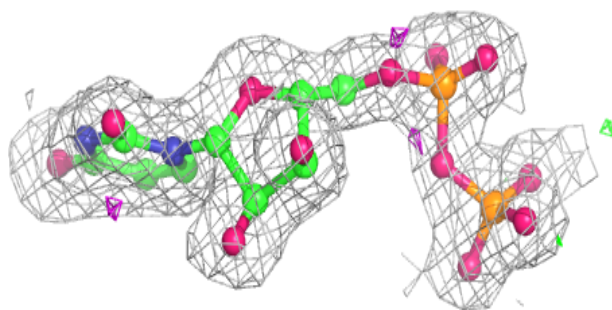
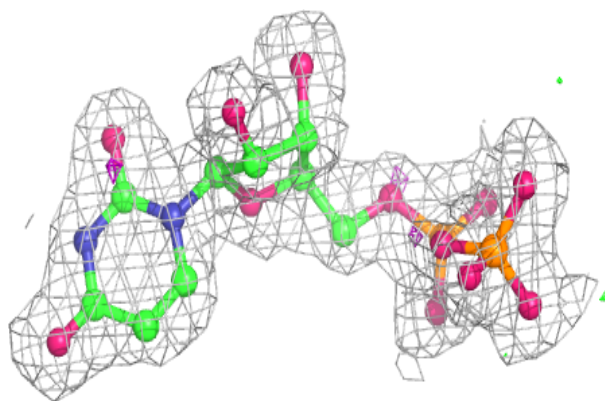
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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	SO4	A	3	5/5	0.93	0.18	49,54,55,55	5
4	FOR	A	1250	2/2	0.94	0.31	29,29,29,31	2
4	FOR	C	1250	2/2	0.95	0.32	31,31,31,33	2
5	SO4	C	4	5/5	0.96	0.12	47,51,52,53	5
3	UDP	C	1212	25/25	0.97	0.11	12,13,19,19	0
3	UDP	A	1212	25/25	0.97	0.12	12,13,19,20	0
5	SO4	B	1	5/5	0.98	0.12	28,31,34,35	5
5	SO4	D	2	5/5	0.98	0.10	30,34,35,35	5

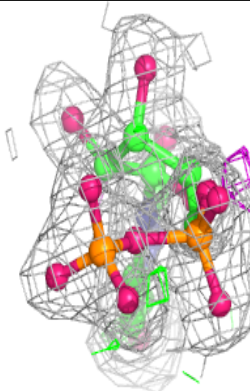
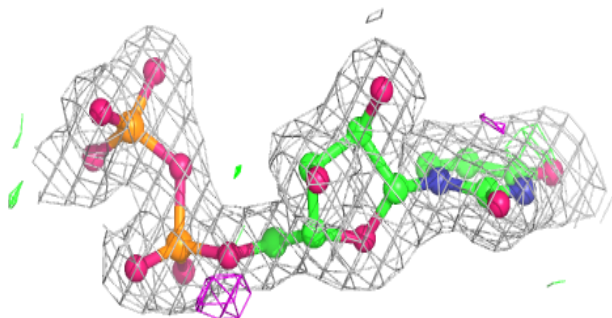
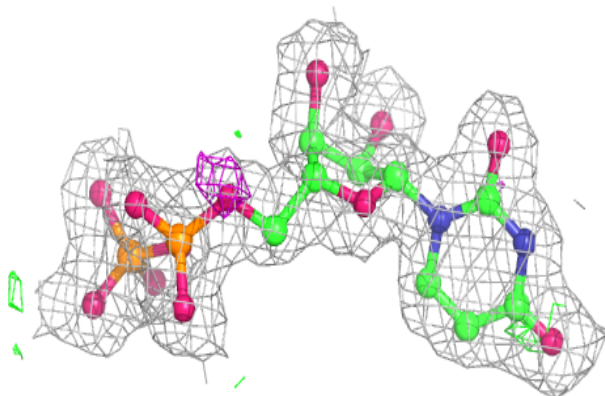
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around UDP C 1212:**

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

**Electron density around UDP A 1212:**

$2mF_o-DF_c$  (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.