



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 12:44 pm BST

PDB ID : 4N3C  
Title : Crystal Structure of human O-GlcNAc Transferase bound to a peptide from HCF-1 pro-repeat2(1-26) and UDP-GlcNAc  
Authors : Lazarus, M.B.; Herr, W.; Walker, S.  
Deposited on : 2013-10-06  
Resolution : 2.55 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

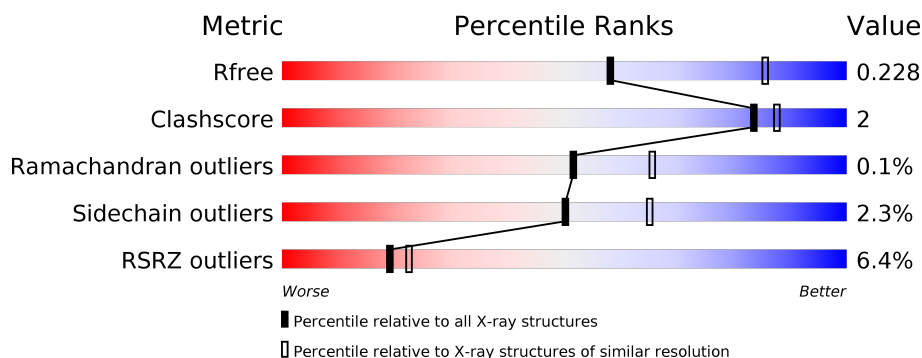
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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>6%</div> <div>89%</div> <div>7%</div> <div>.</div> </div>
2	B	26	<div> <div>12%</div> <div>62%</div> <div>15%</div> <div>23%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5804 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	697	Total	C	N	O	S	0	3	0
			5523	3507	964	1014	38			

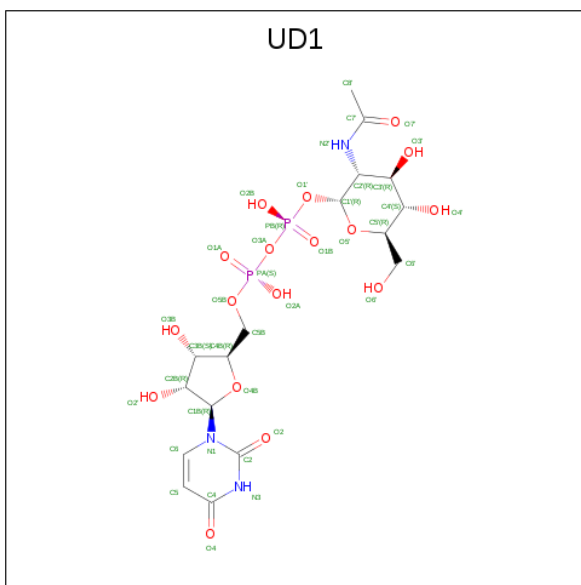
There are 4 discrepancies between the modelled and reference sequences:

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

- Molecule 2 is a protein called Host cell factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	20	Total	C	N	O	S	0	0	0
			140	80	24	35	1			

- Molecule 3 is URIDINE-DIPHOSPHATE-N-ACETYLGLUCOSAMINE (three-letter code: UD1) (formula: C<sub>17</sub>H<sub>27</sub>N<sub>3</sub>O<sub>17</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			39	17	3	17	2		

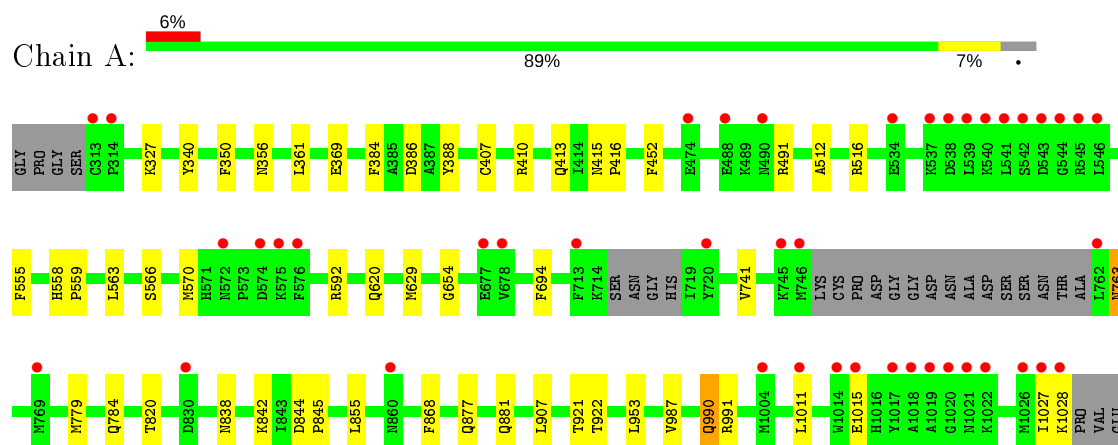
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	97	Total O 97 97	0	0
4	B	5	Total O 5 5	0	0

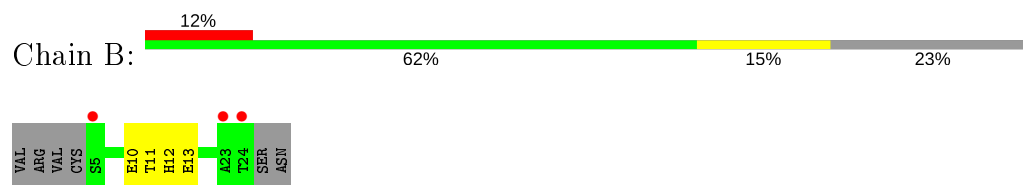
### 3 Residue-property plots [i](#)

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-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit



- Molecule 2: Host cell factor 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	98.88 Å 98.88 Å 365.93 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	62.52 – 2.55 62.52 – 2.55	Depositor EDS
% Data completeness (in resolution range)	95.0 (62.52-2.55) 95.0 (62.52-2.55)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.15	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.91 (at 2.55 Å)	Xtriage
Refinement program	PHENIX 1.8.1_1168	Depositor
R, $R_{free}$	0.184 , 0.226 0.184 , 0.228	Depositor DCC
$R_{free}$ test set	1692 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.0	Xtriage
Anisotropy	0.331	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 44.7	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	0.95	EDS
Total number of atoms	5804	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.11% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UD1

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	0.23	0/5656	0.41	0/7671
2	B	0.25	0/142	0.49	0/197
All	All	0.23	0/5798	0.41	0/7868

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

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	5523	0	5506	25	0
2	B	140	0	123	1	0
3	A	39	0	25	4	0
4	A	97	0	0	0	0
4	B	5	0	0	0	0
All	All	5804	0	5654	27	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 2.

All (27) 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:559:PRO:HB2	3:A:1201:UD1:H6'2	1.66	0.77
1:A:838:ASN:HB3	1:A:842:LYS:HD2	1.87	0.56
1:A:953:LEU:O	1:A:990:GLN:HG2	2.07	0.55
1:A:779:MET:HG3	1:A:784:GLN:HB2	1.91	0.52
3:A:1201:UD1:H2'	2:B:10:GLU:OE1	2.10	0.52
1:A:921:THR:N	3:A:1201:UD1:O2B	2.44	0.51
1:A:629:MET:O	1:A:654:GLY:HA3	2.12	0.50
1:A:877:GLN:O	1:A:881:GLN:NE2	2.45	0.49
1:A:1011:LEU:O	1:A:1015:GLU:HG2	2.14	0.48
1:A:361:LEU:HD13	1:A:369:GLU:HG2	1.95	0.47
1:A:763:ASN:OD1	1:A:763:ASN:N	2.47	0.47
1:A:340:TYR:CZ	1:A:356:ASN:HB3	2.50	0.47
3:A:1201:UD1:H1'	3:A:1201:UD1:O1A	2.15	0.46
1:A:559:PRO:O	1:A:563:LEU:HG	2.16	0.46
1:A:558:HIS:CG	1:A:559:PRO:HD2	2.51	0.45
1:A:410:ARG:NH1	1:A:413:GLN:OE1	2.46	0.45
1:A:987:VAL:O	1:A:991:ARG:HG3	2.17	0.45
1:A:512:ALA:O	1:A:516:ARG:HG2	2.18	0.43
1:A:820:THR:HG22	1:A:907:LEU:HD11	2.01	0.43
1:A:327:LYS:HA	1:A:327:LYS:HD3	1.83	0.42
1:A:384:PHE:CE1	1:A:386:ASP:HB2	2.55	0.42
1:A:415:ASN:HA	1:A:416:PRO:HD2	1.92	0.42
1:A:844:ASP:HB2	1:A:845:PRO:HD2	2.02	0.42
1:A:1028:LYS:HA	1:A:1028:LYS:HD2	1.91	0.41
1:A:555:PHE:O	1:A:592:ARG:HD3	2.21	0.41
1:A:388:TYR:O	1:A:407:CYS:HB3	2.21	0.40
1:A:566:SER:O	1:A:570:MET:HG2	2.21	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	694/723 (96%)	682 (98%)	11 (2%)	1 (0%)	51	65
2	B	18/26 (69%)	18 (100%)	0	0	100	100
All	All	712/749 (95%)	700 (98%)	11 (2%)	1 (0%)	51	65

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1027	ILE

### 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%)	591 (98%)	11 (2%)	59	74
2	B	17/23 (74%)	14 (82%)	3 (18%)	2	2
All	All	619/641 (97%)	605 (98%)	14 (2%)	50	65

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	350	PHE
1	A	452	PHE
1	A	491	ARG
1	A	620	GLN
1	A	694	PHE
1	A	741	VAL
1	A	763	ASN
1	A	855	LEU
1	A	868	PHE
1	A	922	THR
1	A	990	GLN
2	B	11	THR
2	B	12	HIS
2	B	13	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	881	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](#)

1 ligand is 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	UD1	A	1201	-	34,41,41	1.86	7 (20%)	45,62,62	1.36	6 (13%)

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	UD1	A	1201	-	-	6/24/63/63	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1201	UD1	PB-O1'	6.65	1.77	1.60
3	A	1201	UD1	O4-C4	3.92	1.34	1.24
3	A	1201	UD1	PA-O5B	3.61	1.73	1.59
3	A	1201	UD1	C4'-C5'	2.45	1.58	1.53
3	A	1201	UD1	O5B-C5B	-2.29	1.35	1.44
3	A	1201	UD1	O4B-C1B	-2.26	1.37	1.41
3	A	1201	UD1	C1'-C2'	2.01	1.56	1.53

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1201	UD1	PB-O3A-PA	3.50	144.85	132.83
3	A	1201	UD1	O2A-PA-O1A	2.67	125.46	112.24
3	A	1201	UD1	O1'-C1'-C2'	2.57	113.05	108.40
3	A	1201	UD1	O3A-PB-O1'	-2.43	97.58	102.48
3	A	1201	UD1	O5B-PA-O1A	-2.14	100.71	109.07
3	A	1201	UD1	O5'-C1'-C2'	-2.12	106.43	110.58

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1201	UD1	O5'-C1'-O1'-PB
3	A	1201	UD1	C2B-C1B-N1-C6
3	A	1201	UD1	O4B-C1B-N1-C6
3	A	1201	UD1	O4B-C4B-C5B-O5B
3	A	1201	UD1	C3B-C4B-C5B-O5B
3	A	1201	UD1	C3'-C2'-N2'-C7'

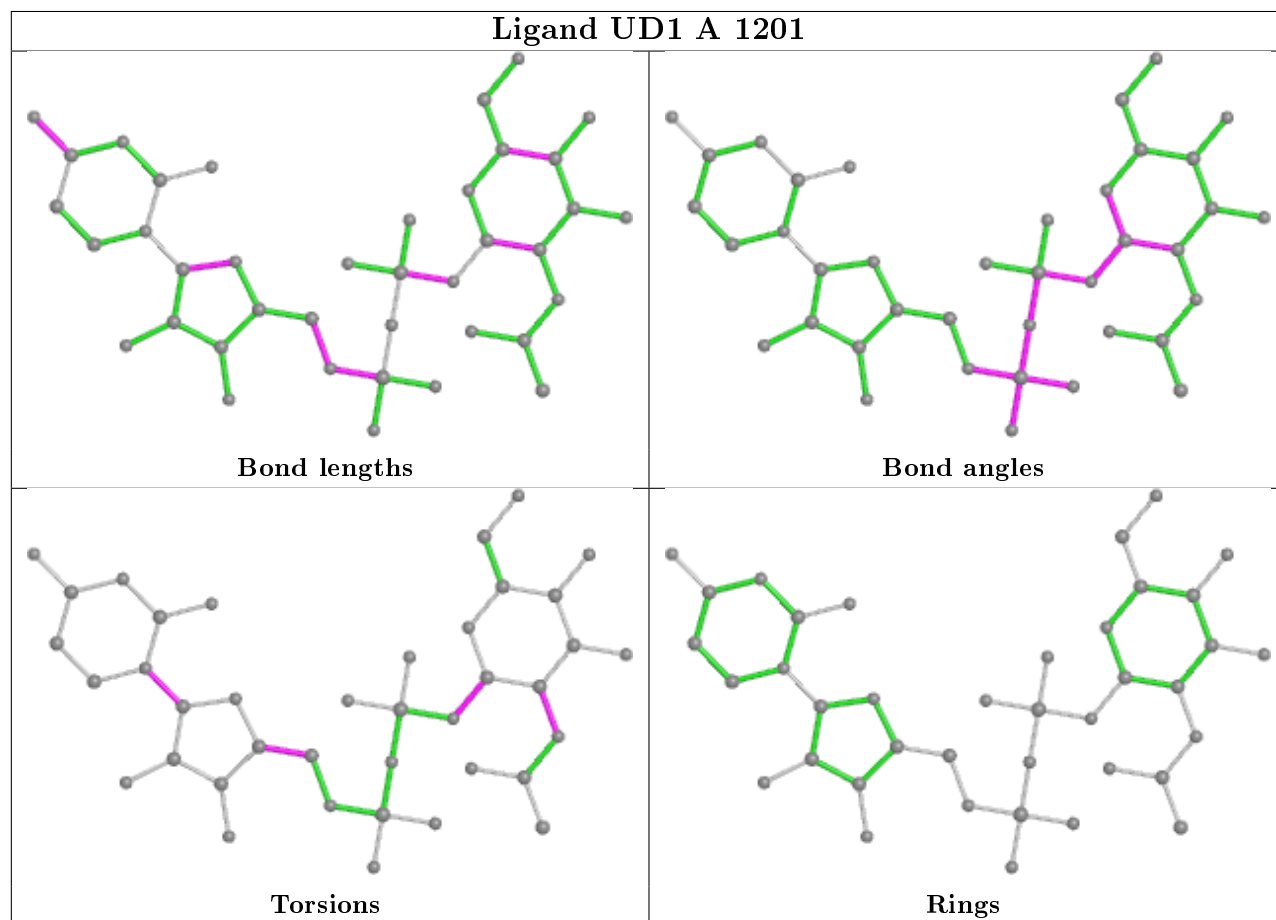
There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1201	UD1	4	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

### 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	697/723 (96%)	0.35	43 (6%) 20 24	29, 46, 75, 101	0
2	B	20/26 (76%)	1.22	3 (15%) 2 2	38, 61, 87, 96	0
All	All	717/749 (95%)	0.37	46 (6%) 19 22	29, 46, 76, 101	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	313	CYS	8.2
2	B	5	SER	6.0
2	B	24	THR	5.5
1	A	541	LEU	4.2
1	A	746	MET	4.1
1	A	540	LYS	3.9
1	A	860	ASN	3.9
1	A	544	GLY	3.8
1	A	713	PHE	3.7
1	A	830	ASP	3.7
1	A	314	PRO	3.6
1	A	762	LEU	3.6
1	A	1019	ALA	3.5
1	A	1018	ALA	3.5
1	A	1026	MET	3.4
1	A	538	ASP	3.4
1	A	1014	TRP	3.4
1	A	769	MET	3.3
1	A	546	LEU	3.3
1	A	575	LYS	3.3
1	A	1015	GLU	3.2
1	A	677	GLU	3.2
1	A	539	LEU	3.1
1	A	537	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	1028	LYS	3.1
1	A	542	SER	3.1
1	A	1021	ASN	2.9
1	A	576	PHE	2.9
1	A	1011	LEU	2.9
1	A	545	ARG	2.8
1	A	745	LYS	2.8
1	A	574	ASP	2.8
1	A	1027	ILE	2.7
1	A	572	ASN	2.7
1	A	720	TYR	2.6
1	A	543	ASP	2.5
1	A	1004	MET	2.5
1	A	534	GLU	2.5
2	B	23	ALA	2.5
1	A	490	ASN	2.3
1	A	1017	TYR	2.3
1	A	488	GLU	2.3
1	A	678	VAL	2.1
1	A	1022	LYS	2.1
1	A	474	GLU	2.1
1	A	1020	GLY	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](#)

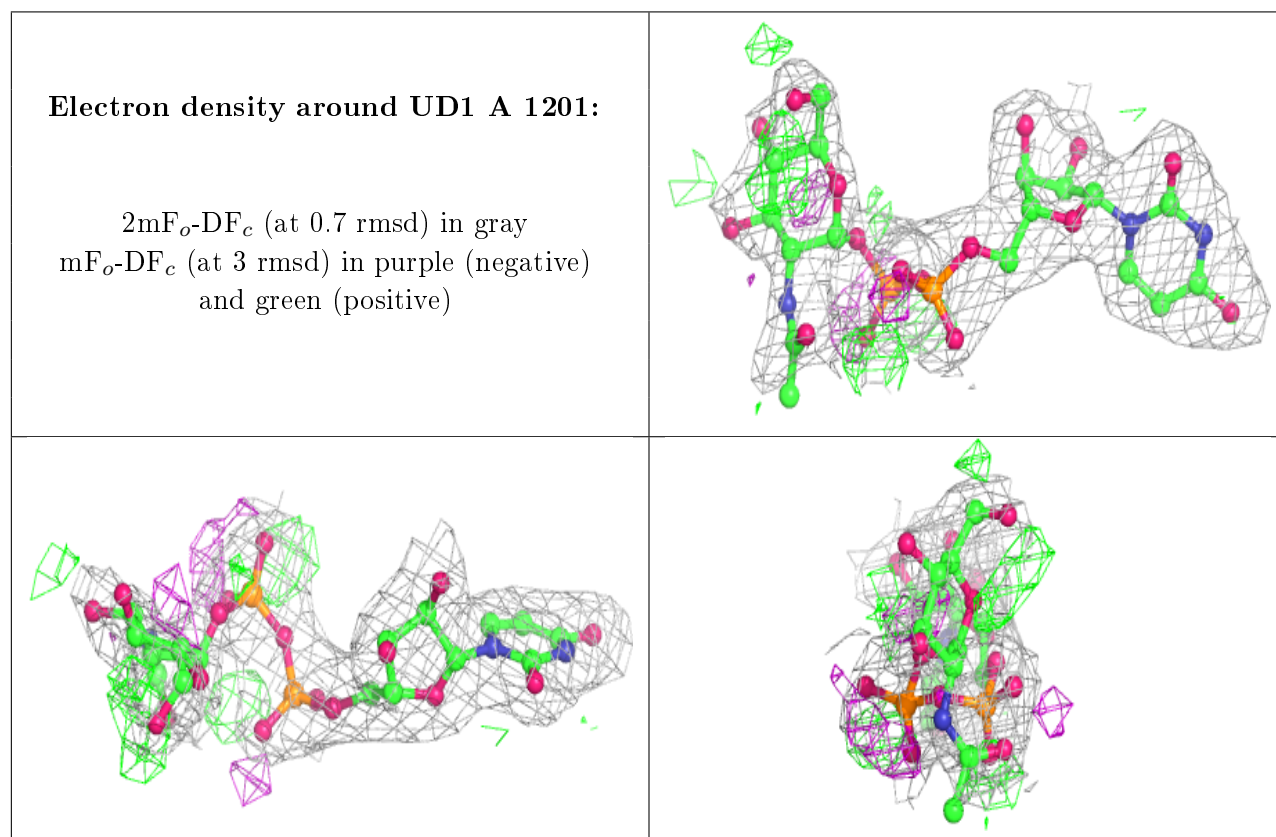
There are no carbohydrates in this entry.

## 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
3	UD1	A	1201	39/39	0.97	0.21	28,37,97,97	0

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.