

# Full wwPDB X-ray Structure Validation Report (i)

#### Aug 21, 2023 – 02:55 PM EDT

PDB ID : 2PFH

Title : Complex of Aldose Reductase with NADP+ and simultaneously bound com-

petetive inhibitors Fidarestat and IDD594. Concentration of Fidarestat in

soaking solution is less than concentration of IDD594.

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Deposited on : 2007-04-05

Resolution : 0.85 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
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

 $Mol Probity \quad : \quad 4.02b\text{--}467$ 

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS: 2.35

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) : 2.35

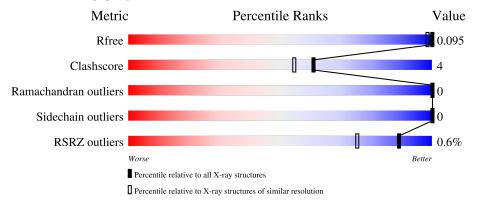


## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 0.85 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar \ resolution} \\ (\#{\rm Entries, \ resolution \ range(\AA)}) \end{array}$		
$R_{free}$	130704	1071 (1.04-0.70)		
Clashscore	141614	1143 (1.04-0.68)		
Ramachandran outliers	138981	1065 (1.04-0.68)		
Sidechain outliers	138945	1066 (1.04-0.68)		
RSRZ outliers	127900	1038 (1.04-0.70)		

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	Α	316	82%	16%	•••		



## 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 3919 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 Aldose reductase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Λ	914	Total	С	N	О	S	7	105	1
1	A	314	3098	1992	518	571	17	1	105	1

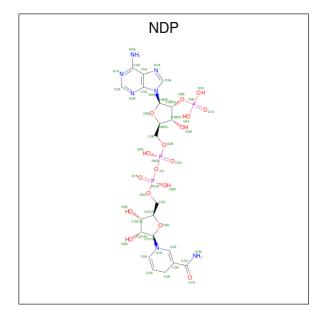
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4	ILE	LEU	SEE REMARK 999	UNP P15121

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cl 1 1	0	1

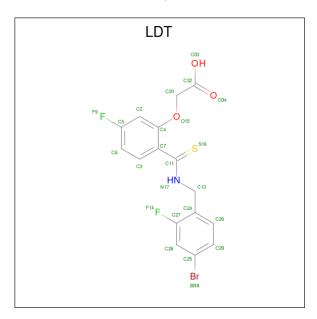
• Molecule 3 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C<sub>21</sub>H<sub>30</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).





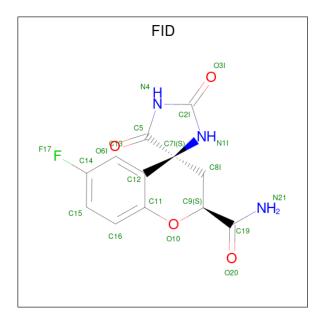
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
9	Λ	1	Total	С	N	О	Р	0	0
3	A	1	48	21	7	17	3	U	U

 $\bullet$  Molecule 4 is IDD594 (three-letter code: LDT) (formula:  $\rm C_{16}H_{12}BrF_2NO_3S).$ 



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf		
4	٨	1	Total	Br	С	F	N	О	S	0	1
4	A	1	24	1	16	2	1	3	1	0	1

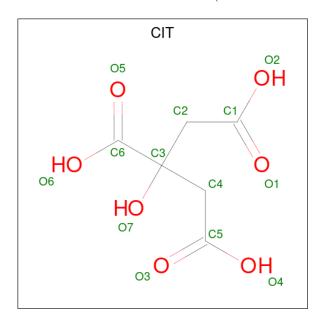
• Molecule 5 is (2S,4S)-2-AMINOFORMYL-6-FLUORO-SPIRO[CHROMAN-4,4'-IMIDAZO LIDINE]-2',5'-DIONE (three-letter code: FID) (formula:  $C_{12}H_{10}FN_3O_4$ ).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
E	Λ	1	Total	С	F	N	О	0	1
5	А	1	20	12	1	3	4	U	1

 $\bullet$  Molecule 6 is CITRIC ACID (three-letter code: CIT) (formula:  $\mathrm{C_6H_8O_7}).$ 



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 13 6 7	0	1
6	A	1	Total C O 13 6 7	0	1

• Molecule 7 is water.

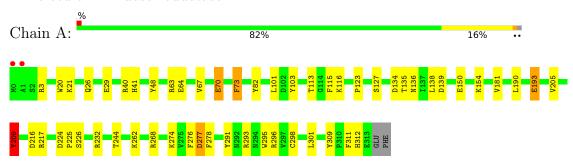
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	656	Total O 702 702	0	305



# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.







# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	49.15Å 66.55Å 47.24Å	D
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $92.31^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	50.00 - 0.85	Depositor
Resolution (A)	34.74 - 0.85	EDS
% Data completeness	95.4 (50.00-0.85)	Depositor
(in resolution range)	95.4 (34.74-0.85)	EDS
$R_{merge}$	0.08	Depositor
$R_{sum}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	5.02 (at 0.85Å)	Xtriage
Refinement program	SHELXL-97	Depositor
D D	0.082 , $0.095$	Depositor
$R, R_{free}$	0.094 , $0.095$	DCC
$R_{free}$ test set	12783 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	5.3	Xtriage
Anisotropy	0.096	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.27 , 72.6	EDS
L-test for twinning <sup>2</sup>	$< L >=0.50, < L^2>=0.33$	Xtriage
	0.002 for -l,k,h	
Estimated twinning fraction	0.018  for  -h,-k,l	Xtriage
	0.015  for  l,-k,h	
$F_o, F_c$ correlation	0.99	EDS
Total number of atoms	3919	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	8.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.99% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

## 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: FID, CL, CIT, LDT, NDP

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).

Mal	Chain	Bo	nd lengths	Bond angles		
IVIOI	Mol Chain		# Z  > 5	RMSZ $ $ # $ Z  > 5$		
1	A	6.18	$17/3368 \; (0.5\%)$	2.58	60/4566 (1.3%)	

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	1

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
1	A	312[A]	HIS	CG-CD2	178.57	4.39	1.35
1	A	312[B]	HIS	CG-CD2	178.57	4.39	1.35
1	A	312[A]	HIS	CG-ND1	124.21	4.12	1.38
1	A	312[B]	HIS	CG-ND1	124.21	4.12	1.38
1	A	26[A]	GLN	CD-NE2	90.05	3.58	1.32
1	A	26[B]	GLN	CD-NE2	90.05	3.58	1.32
1	A	26[A]	GLN	CD-OE1	77.60	2.94	1.24
1	A	26[B]	GLN	CD-OE1	77.60	2.94	1.24
1	A	293[A]	ARG	CB-CG	-7.41	1.32	1.52
1	A	293[B]	ARG	CB-CG	-7.41	1.32	1.52
1	A	29[A]	GLU	CD-OE1	-6.96	1.18	1.25
1	A	29[B]	GLU	CD-OE1	-6.96	1.18	1.25
1	A	64[A]	GLU	CD-OE1	-5.65	1.19	1.25
1	A	64[B]	GLU	CD-OE1	-5.65	1.19	1.25
1	A	150	GLU	CD-OE2	-5.45	1.19	1.25
1	A	40[A]	ARG	CZ-NH2	5.21	1.39	1.33
1	A	40[B]	ARG	CZ-NH2	5.21	1.39	1.33



All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	312[A]	HIS	ND1-CG-CD2	-54.82	29.25	106.00
1	A	312[B]	HIS	ND1-CG-CD2	-54.82	29.25	106.00
1	A	26[A]	GLN	CG-CD-OE1	-40.72	40.15	121.60
1	A	26[B]	GLN	CG-CD-OE1	-40.72	40.15	121.60
1	A	26[A]	GLN	OE1-CD-NE2	-36.71	37.48	121.90
1	A	26[B]	GLN	OE1-CD-NE2	-36.71	37.48	121.90
1	A	26[A]	GLN	CG-CD-NE2	-34.63	33.59	116.70
1	A	26[B]	GLN	CG-CD-NE2	-34.63	33.59	116.70
1	A	312[A]	HIS	CG-ND1-CE1	32.17	153.24	108.20
1	A	312[B]	HIS	CG-ND1-CE1	32.17	153.24	108.20
1	A	312[A]	HIS	CB-CG-ND1	-20.63	71.63	123.20
1	A	312[B]	HIS	CB-CG-ND1	-20.63	71.63	123.20
1	A	3	ARG	NE-CZ-NH2	-15.92	112.34	120.30
1	A	312[A]	HIS	CG-CD2-NE2	14.98	137.65	109.20
1	A	312[B]	HIS	CG-CD2-NE2	14.98	137.65	109.20
1	A	232	ARG	NE-CZ-NH1	11.01	125.80	120.30
1	A	293[A]	ARG	NE-CZ-NH1	-10.57	115.01	120.30
1	A	293[B]	ARG	NE-CZ-NH1	-10.57	115.01	120.30
1	A	276[A]	PHE	CB-CG-CD1	10.03	127.82	120.80
1	A	276[B]	PHE	CB-CG-CD1	10.03	127.82	120.80
1	A	312[A]	HIS	CB-CG-CD2	-9.74	100.59	130.80
1	A	312[B]	HIS	CB-CG-CD2	-9.74	100.59	130.80
1	A	217[A]	ARG	NE-CZ-NH2	-9.21	115.69	120.30
1	A	217[B]	ARG	NE-CZ-NH2	-9.21	115.69	120.30
1	A	217[A]	ARG	NE-CZ-NH1	8.29	124.44	120.30
1	A	217[B]	ARG	NE-CZ-NH1	8.29	124.44	120.30
1	A	268	ARG	NE-CZ-NH1	7.89	124.25	120.30
1	A	224	ASP	CB-CG-OD1	7.62	125.16	118.30
1	A	63[A]	ARG	NE-CZ-NH2	-7.59	116.51	120.30
1	A	216	ASP	CB-CG-OD2	-7.04	111.96	118.30
1	A	276[A]	PHE	CB-CG-CD2	-6.66	116.14	120.80
1	A	276[B]	PHE	CB-CG-CD2	-6.66	116.14	120.80
1	A	3	ARG	NH1-CZ-NH2	6.59	126.66	119.40
1	A	134[A]	ASP	CB-CG-OD2	-6.59	112.36	118.30
1	A	134[B]	ASP	CB-CG-OD2	-6.59	112.36	118.30
1	A	82	TYR	CB-CG-CD1	6.43	124.86	121.00
1	A	296[A]	ARG	NE-CZ-NH2	-5.96	117.32	120.30
1	A	296[B]	ARG	NE-CZ-NH2	-5.96	117.32	120.30
1	A	277[A]	ASP	CB-CG-OD2	-5.87	113.01	118.30
1	A	277[B]	ASP	CB-CG-OD2	-5.87	113.01	118.30
1	A	278[A]	PHE	CB-CG-CD1	5.82	124.87	120.80
1	A	278[B]	PHE	CB-CG-CD1	5.82	124.87	120.80

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Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	103	TYR	CB-CG-CD1	5.73	124.44	121.00
1	A	193[A]	GLU	CB-CA-C	-5.69	99.01	110.40
1	A	193[B]	GLU	CB-CA-C	-5.69	99.01	110.40
1	A	135[A]	THR	O-C-N	-5.62	113.72	122.70
1	A	135[B]	THR	O-C-N	-5.62	113.72	122.70
1	A	135[C]	THR	O-C-N	-5.62	113.72	122.70
1	A	291	TYR	CD1-CE1-CZ	5.59	124.83	119.80
1	A	73	PHE	CB-CG-CD1	5.48	124.64	120.80
1	A	67[A]	VAL	CB-CA-C	-5.41	101.12	111.40
1	A	67[B]	VAL	CB-CA-C	-5.41	101.12	111.40
1	A	232	ARG	NH1-CZ-NH2	-5.32	113.54	119.40
1	A	291	TYR	CB-CG-CD2	5.19	124.12	121.00
1	A	209	TYR	CA-CB-CG	5.16	123.21	113.40
1	A	70[A]	GLU	CB-CG-CD	5.06	127.85	114.20
1	A	70[B]	GLU	CB-CG-CD	5.06	127.85	114.20
1	A	115	PHE	CB-CG-CD2	-5.05	117.27	120.80
1	A	127[A]	SER	O-C-N	-5.02	114.67	123.20
1	A	127[B]	SER	O-C-N	-5.02	114.67	123.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	$\operatorname{Res}$	Type	Group
1	A	209	TYR	Sidechain

### 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	3098	0	3002	28	0
2	A	1	0	0	0	0
3	A	48	0	26	4	0
4	A	24	0	11	1	0
5	A	20	0	10	3	0
6	A	26	0	10	0	0
7	A	702	0	0	13	0
All	All	3919	0	3059	29	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 4.

All (29) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
	* A 901[D] DID H010	distance (Å)	overlap (Å)
1:A:298[B]:CYS:SG	5:A:321[B]:FID:H8I2	2.13	0.89
1:A:295[A]:TRP:CZ3	7:A:3675[A]:HOH:O	2.29	0.84
1:A:274:LYS:HE3	7:A:3509[A]:HOH:O	1.83	0.78
3:A:318:NDP:H42N	5:A:321[B]:FID:C2I	2.28	0.64
1:A:209:TYR:CE1	3:A:318:NDP:H41N	2.34	0.62
1:A:209:TYR:CZ	3:A:318:NDP:H41N	2.36	0.60
1:A:244[B]:THR:HG22	7:A:3120:HOH:O	2.01	0.59
1:A:181:VAL:HA	1:A:205:VAL:O	2.03	0.57
1:A:136[C]:ASN:O	1:A:139:ASP:HB2	2.04	0.56
1:A:225:PRO:HG2	1:A:295[B]:TRP:CD2	2.44	0.52
1:A:225:PRO:HG2	1:A:295[B]:TRP:CE2	2.44	0.52
1:A:262:LYS:O	3:A:318:NDP:H8A	2.11	0.50
1:A:70[A]:GLU:HG2	7:A:3350:HOH:O	2.12	0.50
1:A:41:HIS:HA	1:A:73:PHE:O	2.15	0.47
1:A:20:TRP:CE3	1:A:21:LYS:HE3	2.49	0.47
1:A:138:LEU:HG	7:A:3701[B]:HOH:O	2.15	0.47
1:A:309[B]:TYR:CE2	1:A:311[B]:PHE:HB2	2.51	0.46
1:A:301[B]:LEU:HD11	7:A:3260:HOH:O	2.16	0.45
1:A:193[A]:GLU:HG3	7:A:3503[A]:HOH:O	2.17	0.45
1:A:226:SER:N	7:A:3634[B]:HOH:O	2.45	0.45
1:A:154[B]:LYS:HD3	7:A:3334:HOH:O	2.18	0.44
1:A:116[A]:LYS:HZ3	1:A:123:PRO:HB2	1.83	0.43
1:A:101:LEU:HD23	7:A:3533[A]:HOH:O	2.19	0.43
1:A:116[A]:LYS:NZ	7:A:3267:HOH:O	2.48	0.42
1:A:136[A]:ASN:HB2	7:A:3076:HOH:O	2.20	0.42
1:A:113:THR:OG1	4:A:320[A]:LDT:BR8	2.85	0.42
1:A:277[B]:ASP:HB3	7:A:3250:HOH:O	2.20	0.40
1:A:48:TYR:OH	5:A:321[B]:FID:O3I	2.35	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	408/316 (129%)	404 (99%)	4 (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	Analysed Rotameric Outlie			
1	A	368/281 (131%)	368 (100%)	0	100 100	

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

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

Mol	Chain	Res	Type
1	A	129	ASN

#### 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 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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	Tuno	Chain	Res	Link	Во	ond leng	ths	В	ond ang	gles
MIOI	Type		nes	Link	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	CIT	A	450[A]	-	12,12,12	1.02	1 (8%)	17,17,17	1.99	3 (17%)
3	NDP	A	318	-	45,52,52	1.79	8 (17%)	53,80,80	1.20	7 (13%)
4	LDT	A	320[A]	-	25,25,25	1.41	2 (8%)	34,34,34	1.50	7 (20%)
5	FID	A	321[B]	-	21,22,22	0.83	1 (4%)	23,34,34	3.04	11 (47%)
6	CIT	A	400[A]	-	12,12,12	1.97	5 (41%)	17,17,17	3.06	4 (23%)

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
6	CIT	A	450[A]	_	-	0/16/16/16	-
3	NDP	A	318	-	-	5/30/77/77	0/5/5/5
4	LDT	A	320[A]	-	-	3/14/14/14	0/2/2/2
5	FID	A	321[B]	-	-	0/4/34/34	0/3/3/3
6	CIT	A	400[A]	-	-	0/16/16/16	-

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$Ideal(\AA)$
3	A	318	NDP	C4N-C3N	-6.28	1.37	1.49
3	A	318	NDP	C6N-C5N	4.46	1.41	1.33
3	A	318	NDP	C4N-C5N	-3.70	1.39	1.48
4	A	320[A]	LDT	C6-C5	3.15	1.43	1.37
3	A	318	NDP	O4B-C1B	3.12	1.45	1.41
6	A	400[A]	CIT	O1-C1	3.12	1.32	1.22
6	A	400[A]	CIT	O3-C5	2.98	1.32	1.22
3	A	318	NDP	C1D-N1N	2.83	1.54	1.46
6	A	400[A]	CIT	O5-C6	2.80	1.31	1.22

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Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}( ext{\AA})$
6	A	400[A]	CIT	O4-C5	-2.72	1.21	1.30
6	A	400[A]	CIT	C3-C6	2.71	1.56	1.53
3	A	318	NDP	C2N-C3N	2.54	1.42	1.34
3	A	318	NDP	C4A-N3A	-2.52	1.32	1.35
3	A	318	NDP	C3B-C2B	2.26	1.58	1.52
4	A	320[A]	LDT	O34-C32	2.24	1.29	1.22
5	A	321[B]	FID	O3I-C2I	2.14	1.27	1.23
6	A	450[A]	CIT	O2-C1	-2.06	1.23	1.30

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
6	A	400[A]	CIT	O5-C6-C3	-9.64	108.60	122.25
5	A	321[B]	FID	C7I-C5-N4	-7.27	103.38	107.89
5	A	321[B]	FID	O6I-C5-N4	5.64	133.79	126.17
6	A	450[A]	CIT	O6-C6-C3	5.19	122.06	113.05
5	A	321[B]	FID	O10-C11-C12	4.98	128.91	122.59
6	A	400[A]	CIT	O6-C6-C3	4.78	121.35	113.05
6	A	450[A]	CIT	O5-C6-C3	-4.56	115.79	122.25
5	A	321[B]	FID	C8I-C7I-N1I	4.53	119.98	112.08
6	A	400[A]	CIT	O7-C3-C6	4.14	114.68	108.86
5	A	321[B]	FID	O6I-C5-C7I	-3.97	122.59	125.81
3	A	318	NDP	C5A-C6A-N6A	3.84	126.19	120.35
5	A	321[B]	FID	N4-C2I-N1I	-3.57	103.55	107.55
5	A	321[B]	FID	C5-N4-C2I	3.54	115.40	111.69
5	A	321[B]	FID	C7I-C12-C11	-3.33	117.57	120.95
4	A	320[A]	LDT	F9-C5-C2	-3.04	113.90	118.25
3	A	318	NDP	C5A-C6A-N1A	-2.99	113.58	120.35
6	A	400[A]	CIT	C4-C3-C6	-2.82	104.05	110.11
5	A	321[B]	FID	C13-C12-C11	2.74	120.70	116.78
5	A	321[B]	FID	O10-C9-C8I	-2.73	106.09	111.78
6	A	450[A]	CIT	O7-C3-C6	-2.51	105.34	108.86
5	A	321[B]	FID	O10-C11-C16	-2.46	111.91	116.29
3	A	318	NDP	O2D-C2D-C3D	-2.41	104.01	111.82
4	A	320[A]	LDT	C28-C27-C24	2.38	127.09	123.98
4	A	320[A]	LDT	C13-N17-C11	-2.35	121.59	124.86
4	A	320[A]	LDT	C26-C29-C25	2.33	122.22	119.19
4	A	320[A]	LDT	O33-C32-O34	2.30	129.04	123.30
3	A	318	NDP	N3A-C2A-N1A	2.16	132.06	128.68
4	A	320[A]	LDT	O15-C4-C2	-2.13	118.68	123.58
3	A	318	NDP	C3N-C7N-N7N	-2.13	113.89	117.67
3	A	318	NDP	PN-O3-PA	2.11	140.07	132.83
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Mol	Chain	Res	Type	pe Atoms		$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
4	A	320[A]	LDT	C3-C7-C4	2.09	120.95	118.21
3	A	318	NDP	C1B-N9A-C4A	2.09	130.31	126.64

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	318	NDP	O4D-C1D-N1N-C2N
3	A	318	NDP	PA-O3-PN-O1N
3	A	318	NDP	C4D-C5D-O5D-PN
3	A	318	NDP	PA-O3-PN-O5D
4	A	320[A]	LDT	N17-C11-C7-C4
4	A	320[A]	LDT	N17-C11-C7-C3
3	A	318	NDP	C2B-O2B-P2B-O2X
4	A	320[A]	LDT	S16-C11-C7-C4

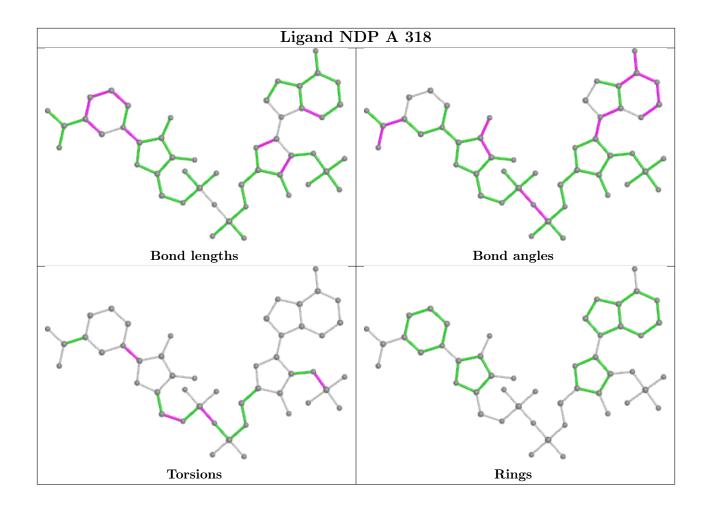
There are no ring outliers.

3 monomers are involved in 7 short contacts:

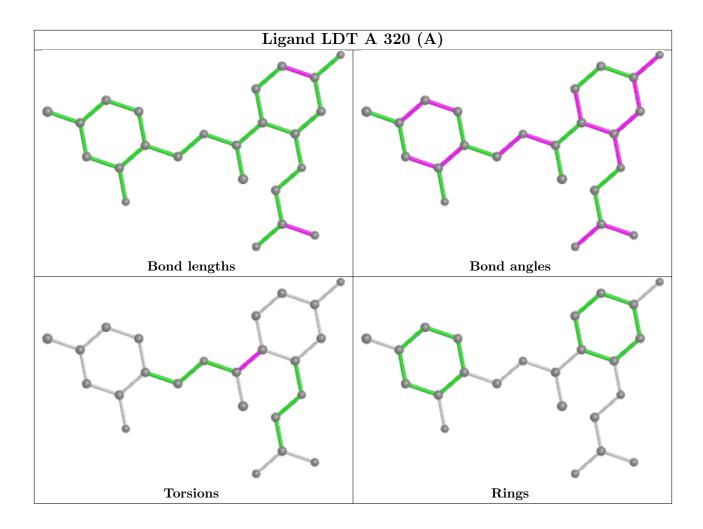
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	318	NDP	4	0
4	A	320[A]	LDT	1	0
5	A	321[B]	FID	3	0

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 then 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.

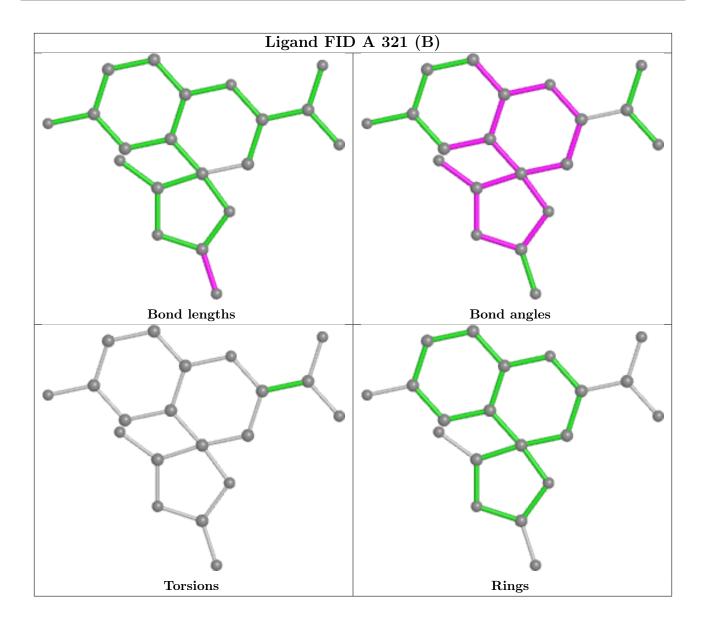












# 5.7 Other polymers (i)

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,  $95^{th}$  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.

N	<b>I</b> ol	Chain	Analysed	<rsrz></rsrz>	$\#\mathrm{RSRZ}{>}2$		$OWAB(Å^2)$	Q<0.9	
	1	A	314/316 (99%)	-0.74	2 (0%)	89	75	3, 6, 13, 27	26 (8%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	0[A]	MET	6.0
1	A	1	ALA	3.3

#### 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.

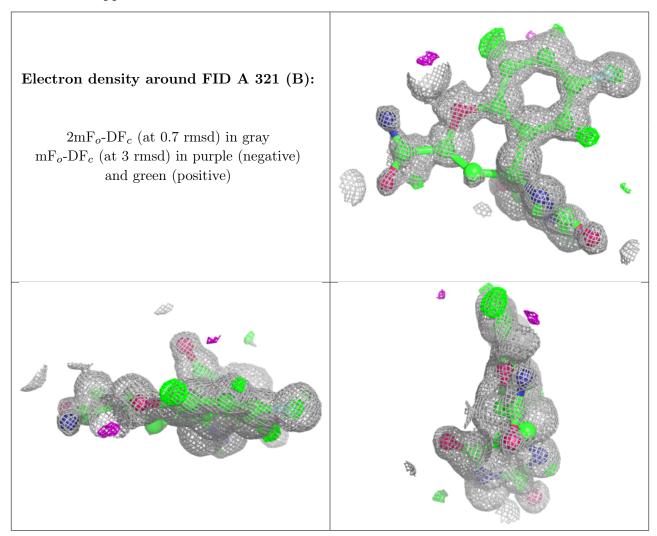
### 6.4 Ligands (i)

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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathring{\mathbf{A}}^2)$	Q < 0.9
6	CIT	A	450[A]	13/13	0.88	0.23	1,6,7,8	13
6	CIT	A	400[A]	13/13	0.98	0.10	7,10,12,16	13
5	FID	A	321[B]	20/20	0.99	0.05	3,4,7,9	20
2	CL	A	2000[A]	1/1	1.00	0.03	5,5,5,5	1
3	NDP	A	318	48/48	1.00	0.03	2,3,5,6	0
4	LDT	A	320[A]	24/24	1.00	0.03	3,4,5,5	24



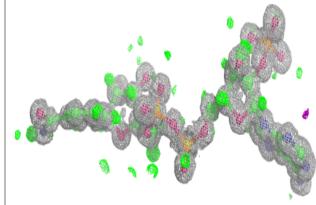
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

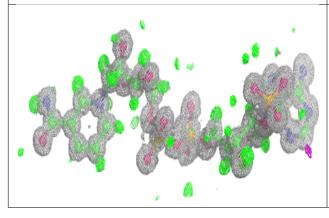


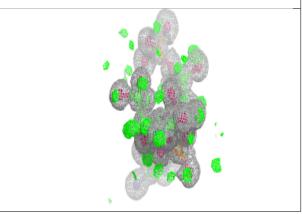


#### Electron density around NDP A 318:

 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$  (at 0.7 rmsd) in gray  $\mathrm{mF}_o\text{-}\mathrm{DF}_c$  (at 3 rmsd) in purple (negative) and green (positive)

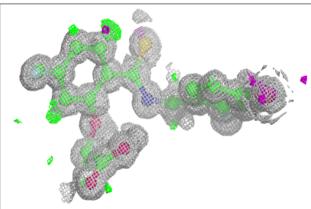


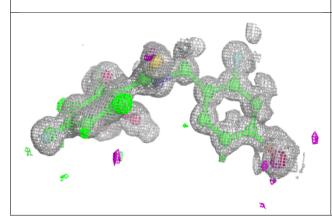


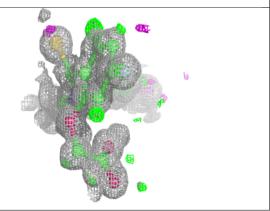


#### Electron density around LDT A 320 (A):

 $2 {
m mF}_o {
m -DF}_c$  (at 0.7 rmsd) in gray  ${
m mF}_o {
m -DF}_c$  (at 3 rmsd) in purple (negative) and green (positive)









## 6.5 Other polymers (i)

There are no such residues in this entry.

