

Full wwPDB X-ray Structure Validation Report (i)

Aug 21, 2023 – 09:48 PM EDT

PDB ID : 2PD9

Title: Human aldose reductase mutant V47I complexed with fidarestat.

Authors: Steuber, H.; Heine, A.; Klebe, G.

Deposited on : 2007-03-31

Resolution : 1.55 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
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:

MolProbity : 4.02b-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)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

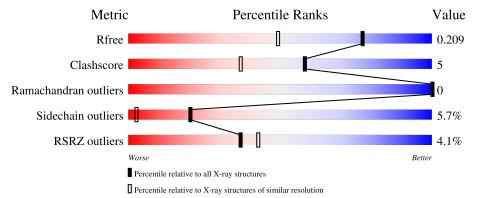
Validation Pipeline (wwPDB-VP) : 2.35

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 1.55 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{A})}) \end{array}$
R_{free}	130704	1483 (1.56-1.56)
Clashscore	141614	1529 (1.56-1.56)
Ramachandran outliers	138981	1498 (1.56-1.56)
Sidechain outliers	138945	1495 (1.56-1.56)
RSRZ outliers	127900	1465 (1.56-1.56)

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		
			4%		
1	A	316	81%	17%	•



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3011 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.

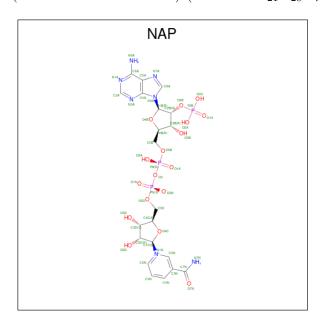
• Molecule 1 is a protein called Aldose reductase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	315	Total	С	N	O	S	0	7	0
1	A	310	2547	1640	425	470	12	U	1	

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4	ILE	LEU	$\operatorname{conflict}$	UNP P15121
A	47	ILE	VAL	engineered mutation	UNP P15121

• Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).

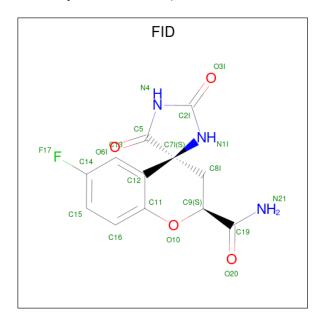


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
2	A	1	Total 48	C 21	N 7	O 17	P 3	0	0

• Molecule 3 is (2S,4S)-2-AMINOFORMYL-6-FLUORO-SPIRO[CHROMAN-4,4'-IMIDAZO



 $\label{eq:liding} LIDINE]\mbox{-}2', \mbox{5'-DIONE (three-letter code: FID) (formula: $C_{12}H_{10}FN_3O_4)$.}$



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
9	Λ	1	Total	С	F	N	О	0	0
)	A	1	20	12	1	3	4	U	0

• Molecule 4 is water.

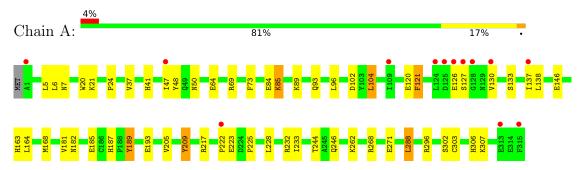
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	396	Total O 396 396	0	0



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	49.42Å 66.91Å 47.31Å	D === == :4 ===
a, b, c, α , β , γ	90.00° 92.11° 90.00°	Depositor
Resolution (Å)	30.00 - 1.55	Depositor
Resolution (A)	18.78 - 1.55	EDS
% Data completeness	94.9 (30.00-1.55)	Depositor
(in resolution range)	95.9 (18.78-1.55)	EDS
R_{merge}	0.03	Depositor
R_{sum}	0.03	Depositor
$< I/\sigma(I) > 1$	18.66 (at 1.55Å)	Xtriage
Refinement program	SHELXL-97	Depositor
υ .	0.155 , 0.204	Depositor
R, R_{free}	0.162 , 0.209	DCC
R_{free} test set	2166 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	11.0	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.31 , 51.7	EDS
L-test for twinning ²	$< L > = 0.49, < L^2> = 0.32$	Xtriage
	0.000 for -l,k,h	
Estimated twinning fraction	0.025 for -h,-k,l	Xtriage
	0.018 for l,-k,h	
F_o, F_c correlation	0.96	EDS
Total number of atoms	3011	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.40% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities 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, NAP

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		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.55	0/2631	1.34	19/3573~(0.5%)	

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}(^{o})$
1	A	217	ARG	NE-CZ-NH1	11.72	126.16	120.30
1	A	69	ARG	NE-CZ-NH1	10.95	125.77	120.30
1	A	209	TYR	CA-CB-CG	7.97	128.54	113.40
1	A	209	TYR	CG-CD1-CE1	7.43	127.25	121.30
1	A	296	ARG	NE-CZ-NH1	7.12	123.86	120.30
1	A	288	LEU	CA-CB-CG	7.04	131.49	115.30
1	A	232	ARG	NE-CZ-NH1	6.69	123.64	120.30
1	A	306	HIS	CG-ND1-CE1	6.62	117.47	108.20
1	A	102[A]	ASP	CB-CG-OD1	6.60	124.24	118.30
1	A	102[B]	ASP	CB-CG-OD1	6.60	124.24	118.30
1	A	121	PHE	CB-CG-CD1	6.22	125.15	120.80
1	A	48	TYR	CD1-CE1-CZ	5.95	125.15	119.80
1	A	209	TYR	CB-CG-CD1	5.85	124.51	121.00
1	A	120	GLU	O-C-N	-5.58	113.77	122.70
1	A	296	ARG	CB-CA-C	-5.28	99.85	110.40
1	A	268	ARG	NE-CZ-NH2	-5.20	117.70	120.30
1	A	193	GLU	OE1-CD-OE2	5.13	129.45	123.30
1	A	64	GLU	CA-CB-CG	5.11	124.63	113.40
1	A	189	TYR	CB-CG-CD1	5.00	124.00	121.00

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	2547	0	2578	25	0
2	A	48	0	25	1	0
3	A	20	0	10	1	0
4	A	396	0	0	6	0
All	All	3011	0	2613	25	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (25) 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:130[B]:VAL:HG21	1:A:303:CYS:SG	2.17	0.85
1:A:89:LYS:O	1:A:93:GLN:HG3	1.84	0.77
1:A:130[B]:VAL:HG22	1:A:302:SER:O	1.95	0.66
1:A:222:PRO:HG2	1:A:223:GLU:OE1	2.01	0.61
1:A:189:TYR:CE2	1:A:225:PRO:HB2	2.37	0.59
1:A:185:GLU:OE2	1:A:187:HIS:HE1	1.90	0.55
1:A:85:LYS:HD2	4:A:976:HOH:O	2.10	0.50
1:A:47[A]:ILE:HG13	1:A:121:PHE:CD2	2.47	0.49
1:A:181:VAL:HA	1:A:205:VAL:O	2.13	0.49
1:A:47[B]:ILE:HD12	3:A:600:FID:C14	2.44	0.47
1:A:246:GLN:NE2	1:A:271[B]:GLU:HG2	2.30	0.46
1:A:41:HIS:HA	1:A:73:PHE:O	2.16	0.46
1:A:244[A]:THR:HG23	4:A:752:HOH:O	2.15	0.45
1:A:262:LYS:O	2:A:500:NAP:H8A	2.17	0.45
1:A:96:LEU:CD2	1:A:104:LEU:HD13	2.47	0.45
1:A:85:LYS:HG3	4:A:976:HOH:O	2.18	0.44
1:A:20:TRP:CE3	1:A:21:LYS:HE3	2.53	0.44
1:A:84:GLU:OE2	1:A:84:GLU:N	2.50	0.44
1:A:24:PRO:HG3	4:A:952:HOH:O	2.19	0.42
1:A:233:ILE:HG22	1:A:244[B]:THR:HG23	2.00	0.42
1:A:37:VAL:HG12	1:A:37:VAL:O	2.19	0.41
1:A:146:GLU:HG2	4:A:806:HOH:O	2.19	0.41
1:A:96:LEU:HD23	1:A:104:LEU:HD13	2.02	0.41

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Atom-1 Atom-2		$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:A:164:LEU:O	1:A:168:MET:HG2	2.21	0.41
1:A:133[A]:SER:HB2	4:A:848:HOH:O	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	Perce	entiles
1	A	320/316 (101%)	317 (99%)	3 (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		Percentiles		
1	A	287/281 (102%)	271 (94%)	16 (6%)	21 3		

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	6	LEU
1	A	7	ASN
1	A	50	ASN

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Mol	Chain	Res	Type
1	A	85	LYS
1	A	104	LEU
1	A	126	GLU
1	A	127	SER
1	A	137	ILE
1	A	138	LEU
1	A	163	HIS
1	A	182	ASN
1	A	209	TYR
1	A	228	LEU
1	A	288	LEU
1	A	307	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	50	ASN
1	A	93	GLN
1	A	129	ASN
1	A	182	ASN
1	A	187	HIS
1	A	241	ASN
1	A	283	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 monosaccharides in this entry.



5.6 Ligand geometry (i)

2 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		hain Bos		В	ond leng	gths	В	ond ang	gles
WIOI	туре	Chain	nes	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2		
2	NAP	A	500	-	45,52,52	1.53	10 (22%)	56,80,80	1.59	11 (19%)		
3	FID	A	600	-	21,22,22	0.91	0	23,34,34	2.22	8 (34%)		

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.

\mathbf{Mol}	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAP	A	500	-	-	5/31/67/67	0/5/5/5
3	FID	A	600	-	-	0/4/34/34	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	Ideal(A)
2	A	500	NAP	C2N-N1N	4.32	1.40	1.35
2	A	500	NAP	C2A-N3A	3.12	1.37	1.32
2	A	500	NAP	O4D-C1D	3.00	1.45	1.41
2	A	500	NAP	C6N-N1N	2.61	1.41	1.35
2	A	500	NAP	P2B-O2B	2.46	1.63	1.59
2	A	500	NAP	C2A-N1A	2.27	1.38	1.33
2	A	500	NAP	C4A-N3A	2.17	1.38	1.35
2	A	500	NAP	C8A-N7A	-2.15	1.30	1.34
2	A	500	NAP	C5B-C4B	2.02	1.57	1.51
2	A	500	NAP	C4N-C3N	2.01	1.42	1.39

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}(^{o})$
3	A	600	FID	C7I-C5-N4	5.13	111.08	107.89

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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	A	500	NAP	C5A-C6A-N6A	4.53	127.23	120.35
3	A	600	FID	N4-C2I-N1I	4.46	112.54	107.55
2	A	500	NAP	C3N-C2N-N1N	-4.22	116.30	120.43
3	A	600	FID	C5-N4-C2I	-4.17	107.33	111.69
2	A	500	NAP	N3A-C2A-N1A	-4.05	122.35	128.68
3	A	600	FID	O3I-C2I-N1I	-3.82	120.84	126.62
2	A	500	NAP	C2N-C3N-C4N	3.20	121.88	118.26
3	A	600	FID	C11-O10-C9	2.73	122.66	115.43
2	A	500	NAP	C3N-C7N-N7N	-2.66	114.56	117.75
3	A	600	FID	C8I-C7I-N1I	2.37	116.21	112.08
2	A	500	NAP	O2A-PA-O1A	2.34	123.79	112.24
2	A	500	NAP	C6N-N1N-C2N	2.31	124.08	121.97
2	A	500	NAP	PN-O3-PA	2.27	140.62	132.83
2	A	500	NAP	C5A-C6A-N1A	-2.23	115.30	120.35
2	A	500	NAP	O3D-C3D-C4D	2.17	117.33	111.05
3	A	600	FID	C7I-C12-C11	-2.11	118.81	120.95
3	A	600	FID	O6I-C5-C7I	-2.05	124.15	125.81
2	A	500	NAP	C2A-N1A-C6A	2.01	122.20	118.75

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500	NAP	C4D-C5D-O5D-PN
2	A	500	NAP	PA-O3-PN-O5D
2	A	500	NAP	C2B-O2B-P2B-O1X
2	A	500	NAP	C2B-O2B-P2B-O3X
2	A	500	NAP	PA-O3-PN-O2N

There are no ring outliers.

2 monomers are involved in 2 short contacts:

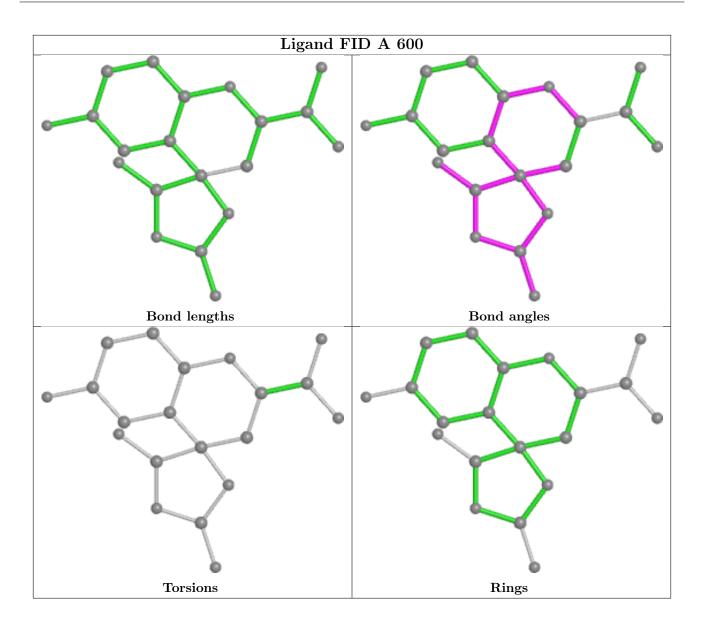
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	NAP	1	0
3	A	600	FID	1	0

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 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.

Mol	Chain	Analysed	<RSRZ $>$	$\# \mathrm{RSRZ}{>}2$		$OWAB(Å^2)$	Q<0.9
1	A	315/316 (99%)	0.54	13 (4%)	37 43	7, 12, 26, 51	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res Type		RSRZ	
1	A	126	GLU	5.5	
1	A	124	LEU	4.5	
1	A	128	GLY	4.2	
1	A	315	PHE	4.2	
1	A	222	PRO	3.5	
1	A	137	ILE	3.3	
1	A	127	SER	3.1	
1	A	313	GLU	3.1	
1	A	47[A]	ILE	2.8	
1	A	130[A]	VAL	2.7	
1	A	1	ALA	2.4	
1	A	125	ASP	2.1	
1	A	109	ILE	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.

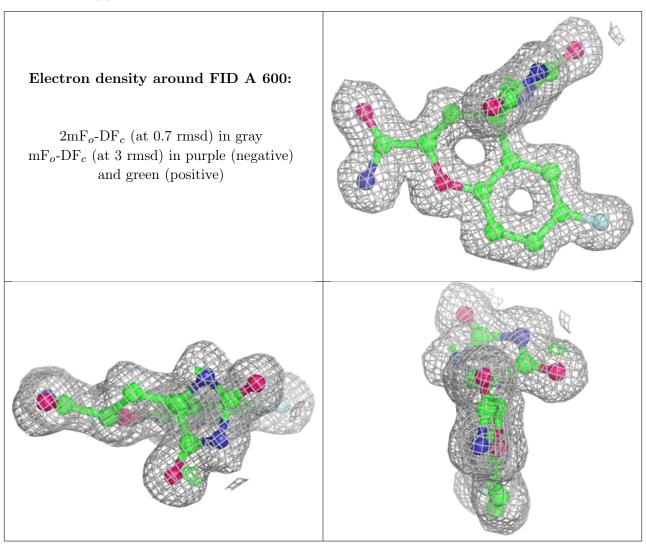


6.4 Ligands (i)

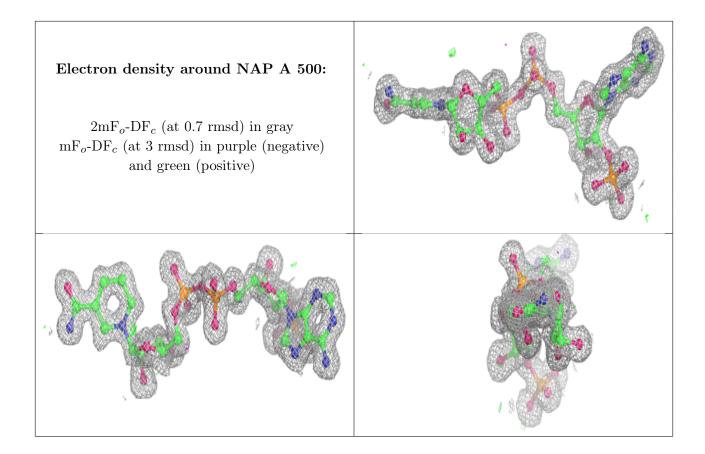
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
3	FID	A	600	20/20	0.96	0.09	7,10,15,16	0
2	NAP	A	500	48/48	0.97	0.08	5,8,12,14	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.

