



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:06 PM UTC

PDB ID : 2PDX / pdb\_00002pdx  
Title : Human aldose reductase double mutant S302R-C303D complexed with zopolrestat.  
Authors : Steuber, H.; Heine, A.; Klebe, G.  
Deposited on : 2007-04-01  
Resolution : 1.65 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.

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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

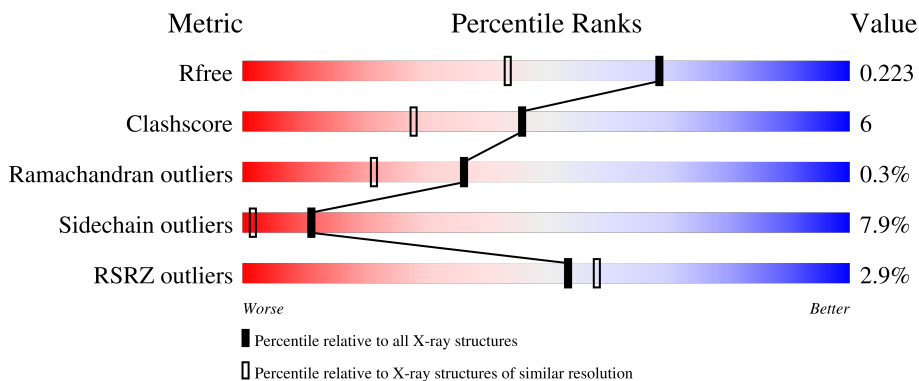
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

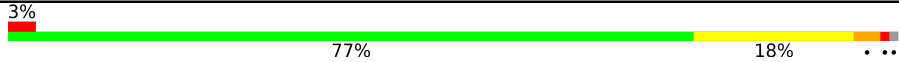
The reported resolution of this entry is 1.65 Å.

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))
$R_{free}$	180053	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

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	316	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2865 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.

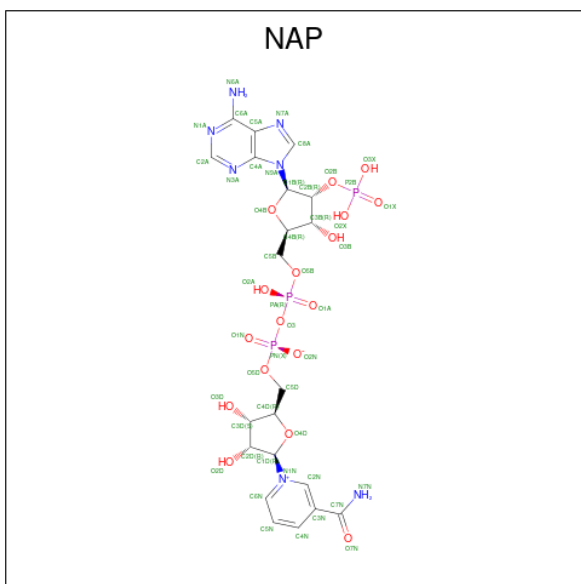
- Molecule 1 is a protein called Aldose reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	312	2513	1614	426	461	12	0	4	0

There are 3 discrepancies between the modelled and reference sequences:

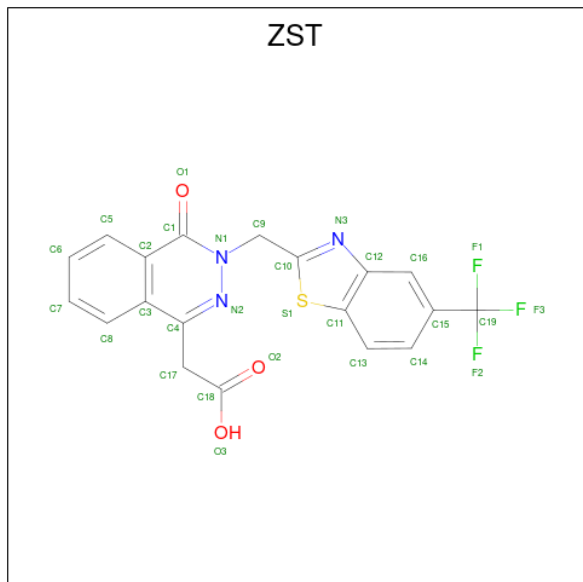
Chain	Residue	Modelled	Actual	Comment	Reference
A	4	ILE	LEU	conflict	UNP P15121
A	302	ARG	SER	engineered mutation	UNP P15121
A	303	ASP	CYS	engineered mutation	UNP P15121

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula:  $C_{21}H_{28}N_7O_{17}P_3$ ).



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

- Molecule 3 is 3,4-DIHYDRO-4-OXO-3-((5-TRIFLUOROMETHYL-2-BENZOTHIAZOLYL)METHYL)-1-PHTHALAZINE ACETIC ACID (CCD ID: ZST) (formula: C<sub>19</sub>H<sub>12</sub>F<sub>3</sub>N<sub>3</sub>O<sub>3</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	F	N	O			S
3	A	1	29	19	3	3	3	1	0	0

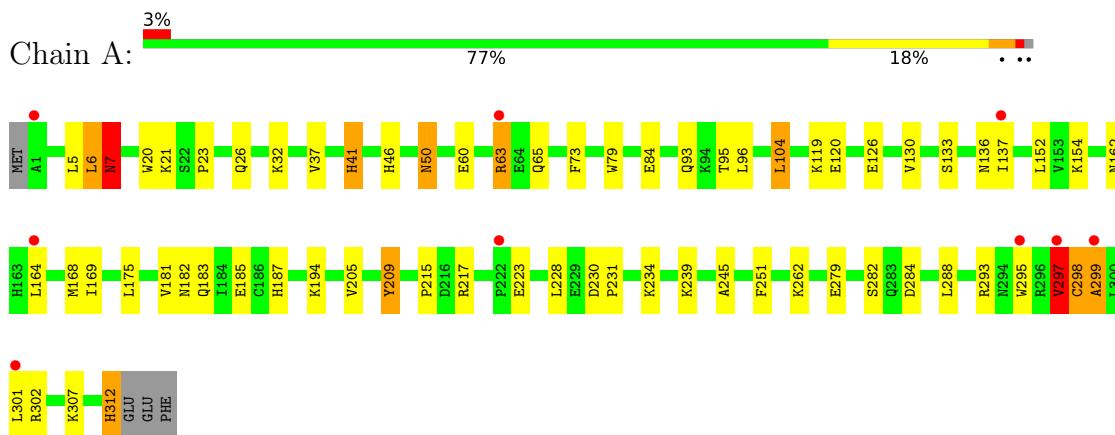
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	275	Total	O	0	0
			275	275		

### 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.

- Molecule 1: Aldose reductase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	49.29Å 67.26Å 47.80Å 90.00° 91.40° 90.00°	Depositor
Resolution (Å)	30.00 – 1.65 30.00 – 1.65	Depositor EDS
% Data completeness (in resolution range)	85.9 (30.00-1.65) 90.6 (30.00-1.65)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.92 (at 1.65Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, $R_{free}$	0.174 , 0.222 0.186 , 0.223	Depositor DCC
$R_{free}$ test set	1692 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.6	Xtriage
Anisotropy	0.144	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 50.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.009 for -l,k,h 0.036 for -h,-k,l 0.027 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	2865	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.84% 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: ZST, 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	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.54	0/2590	1.47	22/3517 (0.6%)

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	282	SER	CA-C-O	8.75	129.99	120.10
1	A	209	TYR	CA-CB-CG	8.72	129.59	113.90
1	A	307	LYS	CA-C-N	7.41	134.51	122.65
1	A	307	LYS	C-N-CA	7.41	134.51	122.65
1	A	46	HIS	CA-C-O	7.33	128.32	120.55
1	A	312	HIS	CA-CB-CG	-6.51	107.28	113.80
1	A	7	ASN	CA-CB-CG	6.40	119.00	112.60
1	A	162	ASN	CA-CB-CG	6.30	118.90	112.60
1	A	79	TRP	CA-C-N	6.27	129.53	120.38
1	A	79	TRP	C-N-CA	6.27	129.53	120.38
1	A	41	HIS	CA-CB-CG	6.16	119.96	113.80
1	A	245	ALA	CA-C-N	6.12	128.48	120.28
1	A	245	ALA	C-N-CA	6.12	128.48	120.28
1	A	284	ASP	CA-CB-CG	6.01	118.61	112.60
1	A	120	GLU	CA-C-N	5.87	129.24	120.31
1	A	120	GLU	C-N-CA	5.87	129.24	120.31
1	A	182	ASN	CA-CB-CG	5.72	118.32	112.60
1	A	50	ASN	OD1-CG-ND2	-5.46	117.14	122.60
1	A	50	ASN	CA-CB-CG	5.45	118.05	112.60
1	A	297	VAL	CA-C-O	5.38	126.06	120.25
1	A	251	PHE	O-C-N	-5.35	116.16	120.38
1	A	298	CYS	CA-C-O	5.04	126.92	120.57

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	2513	0	2532	30	0
2	A	48	0	25	3	0
3	A	29	0	11	0	0
4	A	275	0	0	7	0
All	All	2865	0	2568	30	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 6.

All (30) 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:32:LYS:HE3	1:A:60[A]:GLU:OE1	1.85	0.77
1:A:164:LEU:O	1:A:168[B]:MET:HG2	1.87	0.74
1:A:136:ASN:HB2	4:A:817:HOH:O	1.96	0.64
1:A:230:ASP:O	1:A:234:LYS:HG3	2.02	0.60
1:A:60[B]:GLU:OE2	1:A:63:ARG:HD3	2.02	0.60
1:A:312:HIS:HD2	4:A:723:HOH:O	1.87	0.57
1:A:185:GLU:OE2	1:A:187:HIS:HE1	1.88	0.56
1:A:217:ARG:CZ	1:A:297:VAL:HG22	2.37	0.54
1:A:84:GLU:OE2	1:A:133:SER:HB2	2.08	0.53
1:A:20:TRP:CE3	1:A:21:LYS:HE3	2.45	0.52
1:A:5:LEU:HD13	1:A:6:LEU:O	2.11	0.51
1:A:279:GLU:HG3	4:A:798:HOH:O	2.12	0.50
1:A:23:PRO:HG2	1:A:26:GLN:OE1	2.12	0.49
1:A:215:PRO:HD2	2:A:500:NAP:H4B	1.94	0.49
1:A:194:LYS:HG2	4:A:841:HOH:O	2.14	0.47
1:A:183:GLN:OE1	2:A:500:NAP:H2N	2.15	0.46
1:A:217:ARG:CD	1:A:297:VAL:HG13	2.46	0.46
1:A:302:ARG:HG3	4:A:678:HOH:O	2.14	0.46
1:A:181:VAL:HA	1:A:205:VAL:O	2.17	0.45
1:A:7:ASN:ND2	4:A:647:HOH:O	2.49	0.45

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93[A]:GLN:NE2	4:A:845:HOH:O	2.50	0.45
1:A:231:PRO:O	1:A:234:LYS:HB2	2.17	0.45
1:A:298:CYS:O	1:A:299:ALA:HB2	2.18	0.43
1:A:41:HIS:HA	1:A:73:PHE:O	2.19	0.43
1:A:96:LEU:HD23	1:A:104:LEU:HD13	2.03	0.41
1:A:130:VAL:HG21	1:A:301:LEU:CD1	2.51	0.41
1:A:130:VAL:HG21	1:A:301:LEU:HD13	2.02	0.41
1:A:295:TRP:CH2	1:A:297:VAL:HG23	2.55	0.41
1:A:96:LEU:CD2	1:A:104:LEU:HD13	2.50	0.41
1:A:262:LYS:O	2:A:500:NAP:H8A	2.22	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	314/316 (99%)	308 (98%)	5 (2%)	1 (0%)	36 21

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	299	ALA

### 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	281/281 (100%)	259 (92%)	22 (8%)	11 2

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LEU
1	A	7	ASN
1	A	37	VAL
1	A	50	ASN
1	A	63	ARG
1	A	65	GLN
1	A	95	THR
1	A	104	LEU
1	A	119	LYS
1	A	126	GLU
1	A	137	ILE
1	A	152	LEU
1	A	154	LYS
1	A	169	ILE
1	A	175	LEU
1	A	209	TYR
1	A	223	GLU
1	A	228	LEU
1	A	239	LYS
1	A	288	LEU
1	A	293	ARG
1	A	297	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	50	ASN
1	A	163	HIS
1	A	187	HIS
1	A	200	GLN
1	A	283	GLN
1	A	312	HIS

### 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 oligosaccharides 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	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAP	A	500	-	50,52,52	1.60	10 (20%)	71,80,80	1.72	14 (19%)
3	ZST	A	600	-	32,32,32	0.98	1 (3%)	43,48,48	2.83	15 (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.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAP	A	500	-	-	4/35/67/67	0/5/5/5
3	ZST	A	600	-	-	0/14/14/14	0/4/4/4

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	NAP	O4D-C1D	4.67	1.47	1.40

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	NAP	C6N-N1N	3.55	1.43	1.35
2	A	500	NAP	C2N-N1N	3.44	1.38	1.35
2	A	500	NAP	C2A-N1A	3.21	1.39	1.33
3	A	600	ZST	C9-C10	2.91	1.55	1.50
2	A	500	NAP	C4N-C3N	2.67	1.43	1.39
2	A	500	NAP	P2B-O2B	2.50	1.63	1.59
2	A	500	NAP	C3N-C7N	2.19	1.53	1.50
2	A	500	NAP	C5N-C4N	2.12	1.42	1.38
2	A	500	NAP	C3B-C2B	2.05	1.57	1.53
2	A	500	NAP	C6N-C5N	2.00	1.42	1.38

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	600	ZST	C10-C9-N1	-13.21	101.71	112.10
3	A	600	ZST	O1-C1-N1	6.87	126.32	120.55
2	A	500	NAP	C6A-C5A-C4A	5.09	124.13	117.18
2	A	500	NAP	C2N-C3N-C4N	4.67	123.69	118.26
2	A	500	NAP	O7N-C7N-C3N	-4.37	114.25	119.60
2	A	500	NAP	C5A-C4A-N3A	-4.35	120.73	126.72
2	A	500	NAP	O7N-C7N-N7N	3.75	128.03	122.62
3	A	600	ZST	C11-S1-C10	3.29	91.77	89.06
2	A	500	NAP	C6A-C5A-N7A	-3.12	126.07	132.09
3	A	600	ZST	C8-C3-C4	3.07	125.44	121.20
2	A	500	NAP	N3A-C2A-N1A	-3.00	124.03	128.58
3	A	600	ZST	C14-C15-C16	2.86	123.37	117.86
3	A	600	ZST	C14-C15-C19	-2.73	115.57	119.96
3	A	600	ZST	C18-C17-C4	-2.72	109.00	113.28
3	A	600	ZST	C9-N1-N2	-2.63	110.88	114.27
3	A	600	ZST	S1-C10-N3	-2.62	112.96	116.34
3	A	600	ZST	C9-C10-S1	2.54	124.14	120.55
2	A	500	NAP	O3X-P2B-O2X	2.53	117.31	107.80
2	A	500	NAP	O2A-PA-O1A	2.52	124.17	112.44
3	A	600	ZST	C17-C4-N2	-2.51	110.81	116.46
2	A	500	NAP	C3N-C7N-N7N	-2.51	114.65	117.74
2	A	500	NAP	C5A-C4A-N9A	2.41	108.44	105.81
2	A	500	NAP	O3B-C3B-C4B	-2.26	104.58	111.08
3	A	600	ZST	O1-C1-C2	-2.25	117.33	123.11
3	A	600	ZST	C3-C2-C1	-2.17	118.40	120.95
3	A	600	ZST	C16-C12-C11	-2.16	117.75	120.08
2	A	500	NAP	N3A-C4A-N9A	2.16	130.83	127.17
3	A	600	ZST	C5-C2-C3	2.10	121.61	119.26

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	NAP	C6N-N1N-C2N	2.04	123.61	121.88

There are no chirality outliers.

All (4) torsion outliers are listed below:

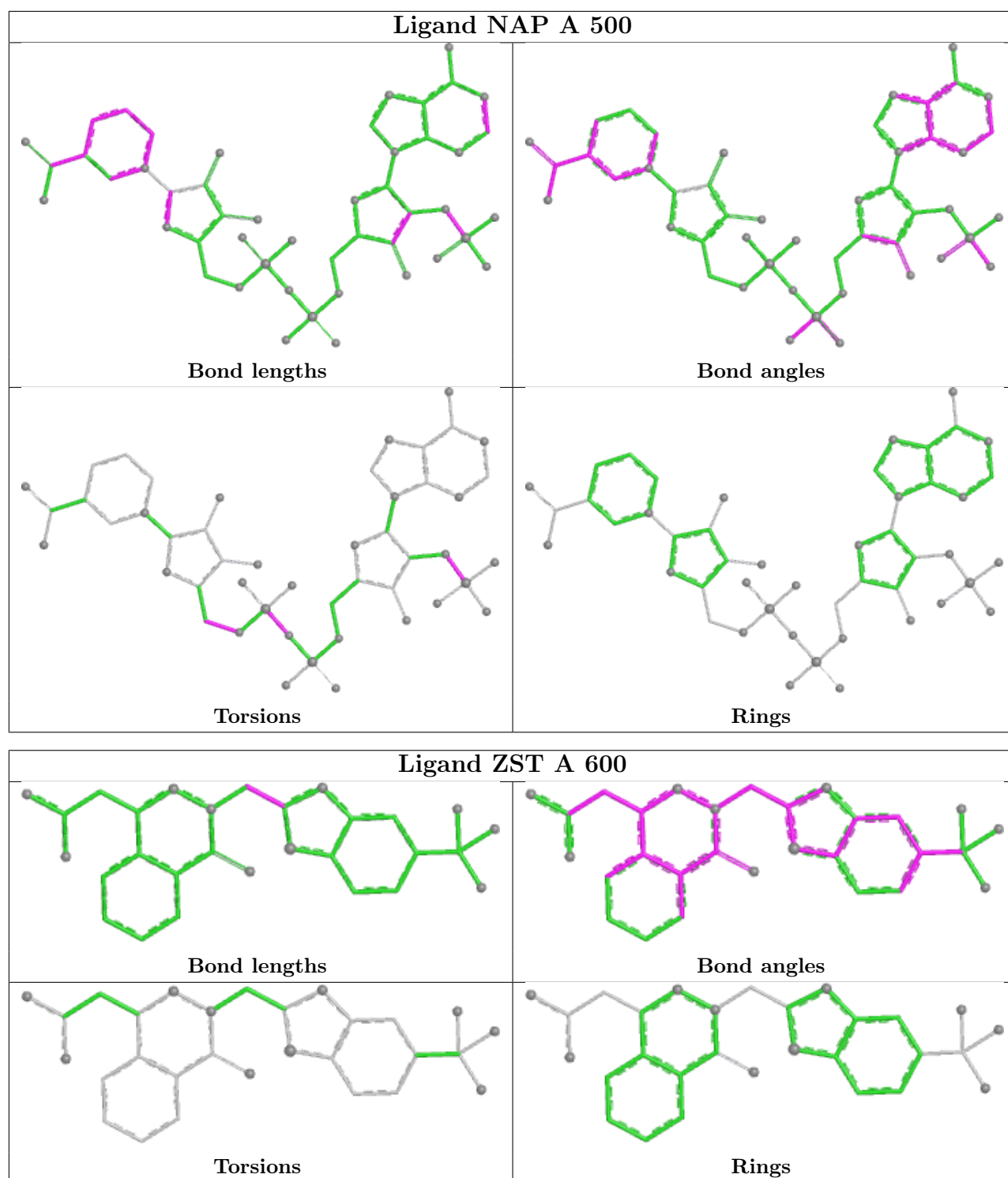
Mol	Chain	Res	Type	Atoms
2	A	500	NAP	C4D-C5D-O5D-PN
2	A	500	NAP	C2B-O2B-P2B-O1X
2	A	500	NAP	PA-O3-PN-O5D
2	A	500	NAP	PA-O3-PN-O2N

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	NAP	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 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

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	312/316 (98%)	-0.10	9 (2%) 53 58	7, 14, 31, 51	4 (1%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	222	PRO	3.7
1	A	297	VAL	3.3
1	A	295	TRP	3.2
1	A	164	LEU	3.0
1	A	299	ALA	2.7
1	A	137	ILE	2.5
1	A	301	LEU	2.5
1	A	63	ARG	2.3
1	A	1	ALA	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](#)

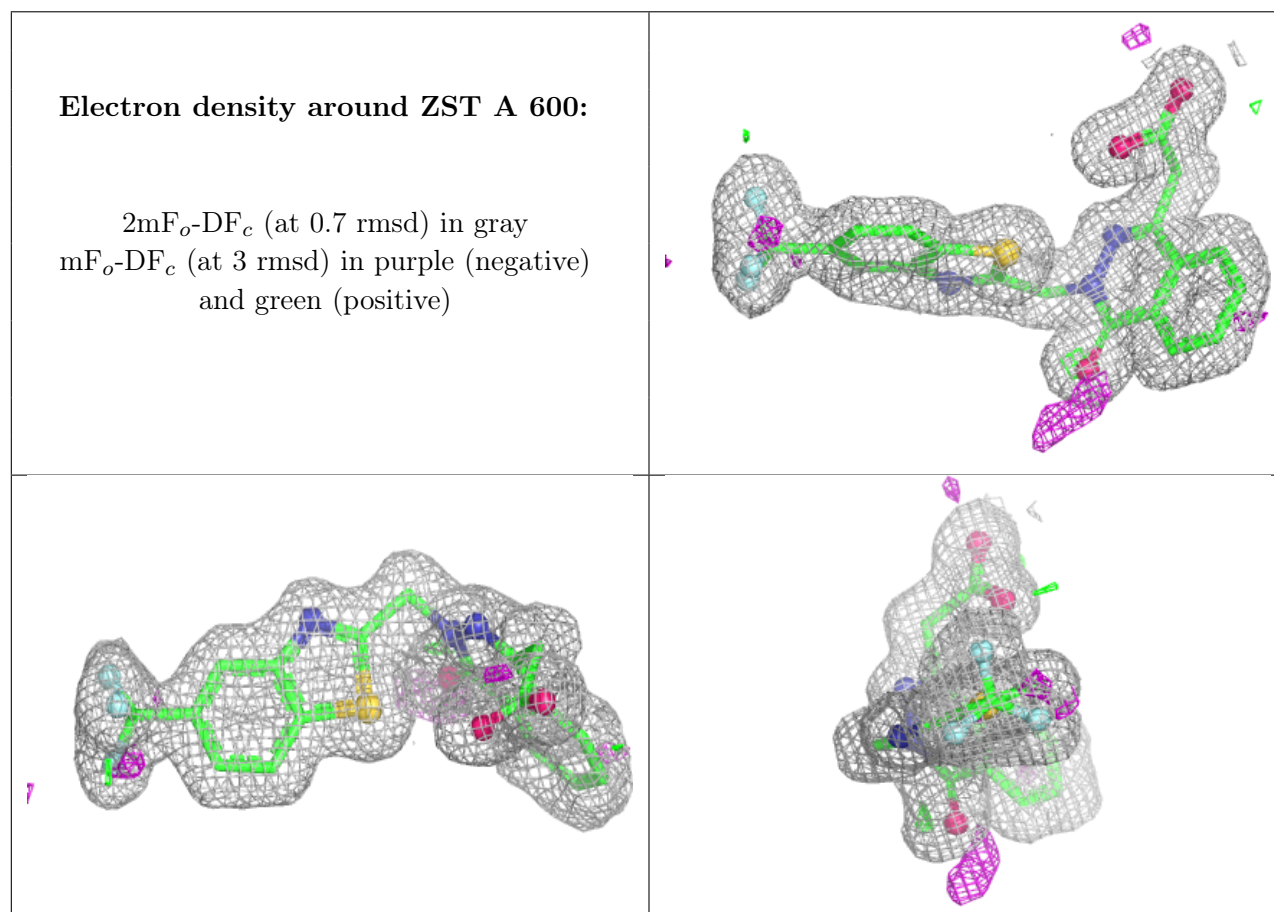
There are no oligosaccharides in this entry.

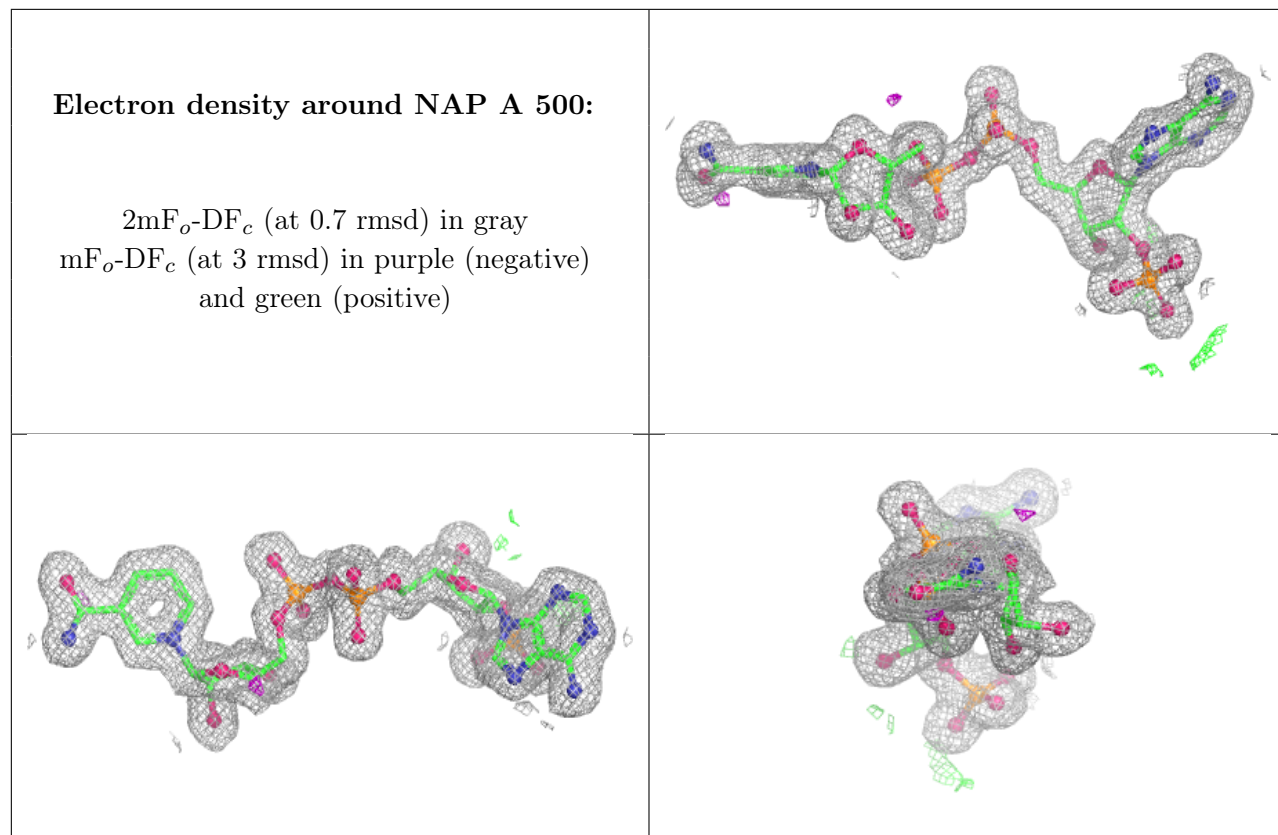
### 6.4 Ligands [i](#)

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	ZST	A	600	29/29	0.96	0.06	6,10,23,35	0
2	NAP	A	500	48/48	0.98	0.04	5,9,13,17	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.