

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

#### Sep 15, 2022 - 03:47 pm BST

PDB ID	:	7PPX
Title	:	ATAD2 in complex with FragLite3
Authors	:	Turberville, S.; Martin, M.P.; Hope, I.; Wood, D.J.; Ng, Y.M.; Heath, R.;
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Deposited on		
Resolution	:	1.35  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:

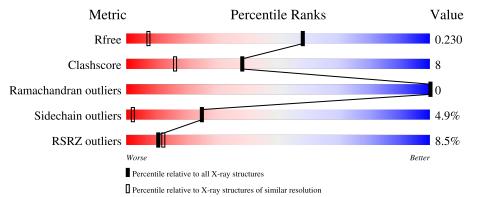
MolProbity		4 02b-467
5		
Mogul	:	1.8.4, CSD as $541be(2020)$
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.30
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.30

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 1.35 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	1509(1.38-1.34)
Clashscore	141614	1551 (1.38-1.34)
Ramachandran outliers	138981	1530 (1.38-1.34)
Sidechain outliers	138945	1530 (1.38-1.34)
RSRZ outliers	127900	1487 (1.38-1.34)

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		
			8%		
1	AAA	130	85%	15%	•

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	7ZX	AAA	1203	-	-	Х	-



#### 7 PPX

# 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 1343 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.

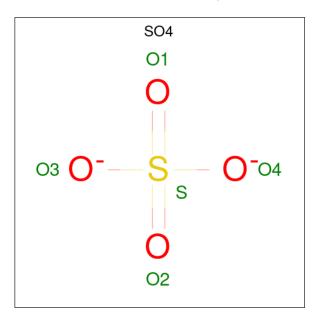
• Molecule 1 is a protein called ATPase family AAA domain-containing protein 2.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	AAA	130	Total 1115	C 697	N 196	O 217	${ m S}{ m 5}$	0	4	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	979	SER	-	expression tag	UNP Q6PL18
AAA	980	MET	-	expression tag	UNP Q6PL18

• Molecule 2 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



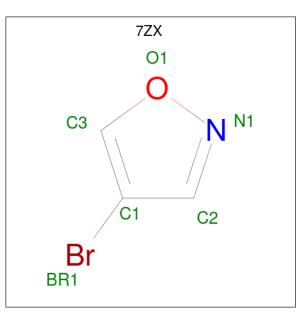
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	AAA	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	AAA	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0



• Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	AAA	1	Total Cl 1 1	0	0

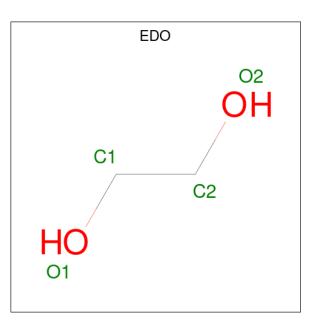
• Molecule 4 is 4-bromanyl-1,2-oxazole (three-letter code: 7ZX) (formula:  $C_3H_2BrNO$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf
4	ΛΛΛ	1	Total	Br	С	Ν	Ο	0	0
4	ЛЛА	1	6	1	3	1	1		0

• Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	AAA	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
5	AAA	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
5	AAA	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
5	AAA	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
5	AAA	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
5	AAA	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
5	AAA	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
5	AAA	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
5	AAA	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
5	AAA	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
5	AAA	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
5	AAA	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 6 is water.



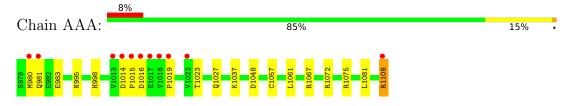
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	AAA	163	Total O 163 163	0	0



## 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.

• Molecule 1: ATPase family AAA domain-containing protein 2





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants	79.20Å 79.20Å 137.91Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	68.69 - 1.35	Depositor
Resolution (A)	68.59 - 1.35	EDS
% Data completeness	99.6 (68.69-1.35)	Depositor
(in resolution range)	99.6~(68.59-1.35)	EDS
R <sub>merge</sub>	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.14 (at 1.35 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
B B.	0.211 , $0.231$	Depositor
$R, R_{free}$	0.211 , $0.230$	DCC
$R_{free}$ test set	2935 reflections $(5.19%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	21.4	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning <sup>2</sup>	$ L  > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	1343	wwPDB-VP
Average B, all atoms $(Å^2)$	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.79% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<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: SO4, EDO, CL,  $7\mathrm{ZX}$ 

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	Mol Chain	Bond	lengths	Bond	angles
		RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	AAA	0.78	0/1133	1.13	0/1528

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	AAA	1115	0	1102	15	0
2	AAA	10	0	0	0	0
3	AAA	1	0	0	1	0
4	AAA	6	0	0	3	0
5	AAA	48	0	72	6	0
6	AAA	163	0	0	4	0
All	All	1343	0	1174	18	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 8.

All (18) 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:AAA:998:HIS:HD2	5:AAA:1205:EDO:H11	1.30	0.97
1:AAA:998:HIS:CD2	5:AAA:1205:EDO:H11	2.10	0.86
5:AAA:1212:EDO:O2	5:AAA:1213:EDO:H22	1.89	0.72
3:AAA:1202:CL:CL	6:AAA:1384:HOH:O	2.47	0.70
1:AAA:995:ASN:ND2	6:AAA:1303:HOH:O	2.34	0.60
1:AAA:998:HIS:HD2	5:AAA:1205:EDO:C1	2.09	0.58
1:AAA:1075:ARG:HH21	5:AAA:1208:EDO:H21	1.76	0.51
1:AAA:1081[B]:LEU:C	1:AAA:1081[B]:LEU:HD23	2.31	0.50
1:AAA:1037:LYS:HZ1	4:AAA:1203:7ZX:C3	2.27	0.48
1:AAA:1027:GLN:HG2	6:AAA:1335:HOH:O	2.15	0.46
1:AAA:1037:LYS:NZ	4:AAA:1203:7ZX:C3	2.78	0.46
5:AAA:1210:EDO:H21	6:AAA:1302:HOH:O	2.17	0.44
1:AAA:1016:ASP:O	1:AAA:1019:PRO:HD3	2.18	0.44
1:AAA:1048:ASP:O	4:AAA:1203:7ZX:BR1	2.90	0.44
1:AAA:1014:ASP:OD1	1:AAA:1015:PRO:HD2	2.18	0.43
1:AAA:1072:ARG:HG2	1:AAA:1075:ARG:NH2	2.35	0.42
1:AAA:1057:CYS:O	1:AAA:1061:LEU:HG	2.20	0.42
1:AAA:1108:ARG:HH21	1:AAA:1108:ARG:HD3	1.68	0.41

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	AAA	132/130~(102%)	131~(99%)	1 (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 Out		Percentiles
1	AAA	127/123~(103%)	120 (94%)	7~(6%)	21 1

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	980	MET
1	AAA	981	GLN
1	AAA	983	GLU
1	AAA	1023	THR
1	AAA	1067[A]	ARG
1	AAA	1067[B]	ARG
1	AAA	1108	ARG

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. There are no such side chains identified.

#### 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 16 ligands modelled in this entry, 1 is monoatomic - leaving 15 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



N/ -1	<b>T</b> a	Chain	Dec	T : 1-	В	ond leng	gths	В	ond ang	gles
Mol	Type	Chain	$\operatorname{Res}$	Link	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2
4	7ZX	AAA	1203	-	$4,\!6,\!6$	1.38	0	$3,\!7,\!7$	1.14	0
2	SO4	AAA	1216	-	4,4,4	0.37	0	$6,\!6,\!6$	0.07	0
5	EDO	AAA	1205	-	3,3,3	0.27	0	$2,\!2,\!2$	0.18	0
5	EDO	AAA	1207	-	3,3,3	0.29	0	$2,\!2,\!2$	0.56	0
5	EDO	AAA	1208	-	3,3,3	0.12	0	$2,\!2,\!2$	0.20	0
5	EDO	AAA	1211	-	3,3,3	0.14	0	$2,\!2,\!2$	0.25	0
5	EDO	AAA	1213	-	3,3,3	0.13	0	$2,\!2,\!2$	0.35	0
5	EDO	AAA	1206	-	3,3,3	0.25	0	$2,\!2,\!2$	0.69	0
5	EDO	AAA	1214	-	3,3,3	0.23	0	$2,\!2,\!2$	0.34	0
5	EDO	AAA	1215	-	3,3,3	0.13	0	$2,\!2,\!2$	0.25	0
5	EDO	AAA	1204	-	3,3,3	0.61	0	$2,\!2,\!2$	0.11	0
5	EDO	AAA	1209	-	3,3,3	0.11	0	$2,\!2,\!2$	0.43	0
5	EDO	AAA	1210	-	3,3,3	0.07	0	$2,\!2,\!2$	0.27	0
2	SO4	AAA	1201	-	4,4,4	0.79	0	$6,\!6,\!6$	0.65	0
5	EDO	AAA	1212	-	3, 3, 3	0.34	0	$2,\!2,\!2$	0.52	0

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).

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
4	7ZX	AAA	1203	-	-	-	0/1/1/1
5	EDO	AAA	1205	-	-	1/1/1/1	-
5	EDO	AAA	1207	-	-	1/1/1/1	-
5	EDO	AAA	1208	-	-	1/1/1/1	-
5	EDO	AAA	1211	-	-	0/1/1/1	-
5	EDO	AAA	1213	-	-	0/1/1/1	-
5	EDO	AAA	1206	-	-	0/1/1/1	-
5	EDO	AAA	1214	-	-	0/1/1/1	-
5	EDO	AAA	1215	-	-	0/1/1/1	-
5	EDO	AAA	1209	-	-	1/1/1/1	-
5	EDO	AAA	1210	-	-	1/1/1/1	-
5	EDO	AAA	1204	-	-	0/1/1/1	-
5	EDO	AAA	1212	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.



Mol	Chain	Res	Type	Atoms
5	AAA	1205	EDO	O1-C1-C2-O2
5	AAA	1210	EDO	O1-C1-C2-O2
5	AAA	1212	EDO	O1-C1-C2-O2
5	AAA	1208	EDO	O1-C1-C2-O2
5	AAA	1207	EDO	O1-C1-C2-O2
5	AAA	1209	EDO	O1-C1-C2-O2

All (6) torsion outliers are listed below:

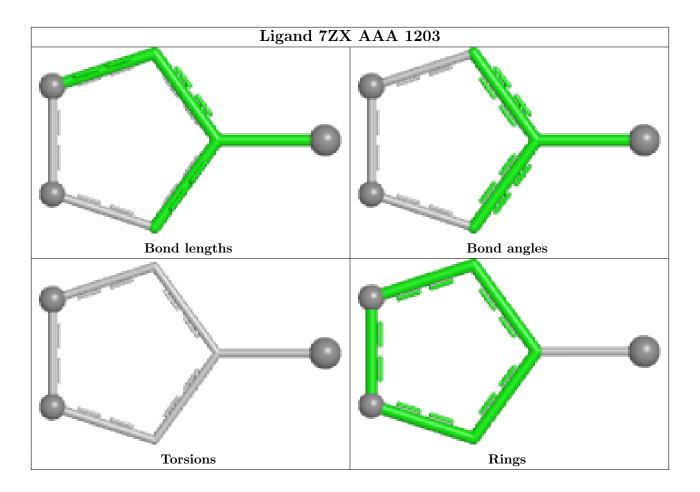
There are no ring outliers.

6 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	AAA	1203	7ZX	3	0
5	AAA	1205	EDO	3	0
5	AAA	1208	EDO	1	0
5	AAA	1213	EDO	1	0
5	AAA	1210	EDO	1	0
5	AAA	1212	EDO	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 $>$	#RSRZ>2	$OWAB(Å^2)$	Q < 0.9
1	AAA	130/130~(100%)	0.61	11 (8%) 10 12	15, 24, 60, 89	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	980	MET	5.9
1	AAA	1015	PRO	3.9
1	AAA	1014	ASP	3.7
1	AAA	1018	VAL	3.4
1	AAA	1013	VAL	3.1
1	AAA	981	GLN	2.6
1	AAA	1108	ARG	2.5
1	AAA	1017	GLU	2.4
1	AAA	1022	VAL	2.4
1	AAA	1019	PRO	2.4
1	AAA	1016	ASP	2.3

## 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,

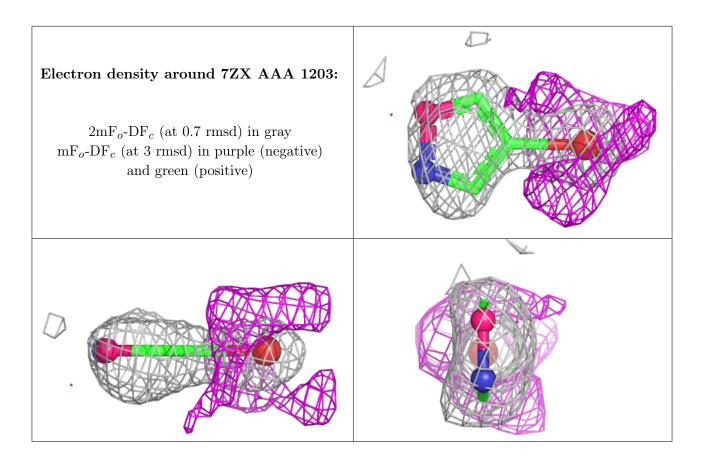


Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B$ -factors( $Å^2$ )	Q<0.9
5	EDO	AAA	1210	4/4	0.53	0.25	68,70,74,78	0
5	EDO	AAA	1215	4/4	0.63	0.23	$55,\!55,\!59,\!67$	0
5	EDO	AAA	1205	4/4	0.68	0.22	$55,\!57,\!63,\!63$	0
4	7ZX	AAA	1203	6/6	0.73	0.24	72,78,87,128	0
5	EDO	AAA	1208	4/4	0.79	0.13	62,69,71,77	0
5	EDO	AAA	1214	4/4	0.82	0.22	54,60,61,64	0
2	SO4	AAA	1216	5/5	0.82	0.13	99,99,99,106	5
5	EDO	AAA	1207	4/4	0.86	0.14	42,46,47,50	0
5	EDO	AAA	1211	4/4	0.87	0.18	$53,\!55,\!56,\!58$	0
5	EDO	AAA	1212	4/4	0.87	0.32	54,62,68,70	0
5	EDO	AAA	1213	4/4	0.88	0.27	$52,\!57,\!58,\!59$	0
5	EDO	AAA	1209	4/4	0.92	0.25	44,45,53,61	0
5	EDO	AAA	1206	4/4	0.93	0.12	45,46,48,54	0
3	CL	AAA	1202	1/1	0.95	0.12	69,69,69,69	0
5	EDO	AAA	1204	4/4	0.98	0.07	19,20,24,25	0
2	SO4	AAA	1201	5/5	0.98	0.08	27,28,31,32	0

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.

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.

