Full wwPDB X-ray Structure Validation Report ⓘ

Nov 30, 2020 – 10:04 AM GMT

PDB ID	:	6YHR
Title	:	Crystal structure of Werner syndrome helicase
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Deposited on	:	2020-03-30
Resolution	:	2.20 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 ⓘ symbol.

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

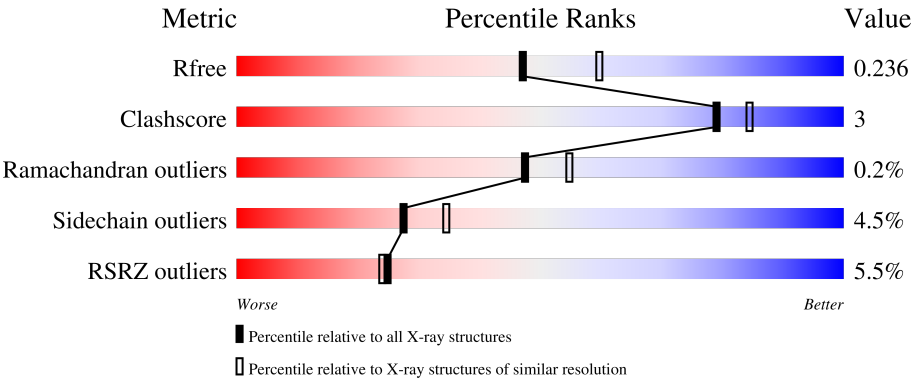
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.14.6
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.14.6

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 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 >=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	A	585	5% 82% 9% · 8%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4519 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.

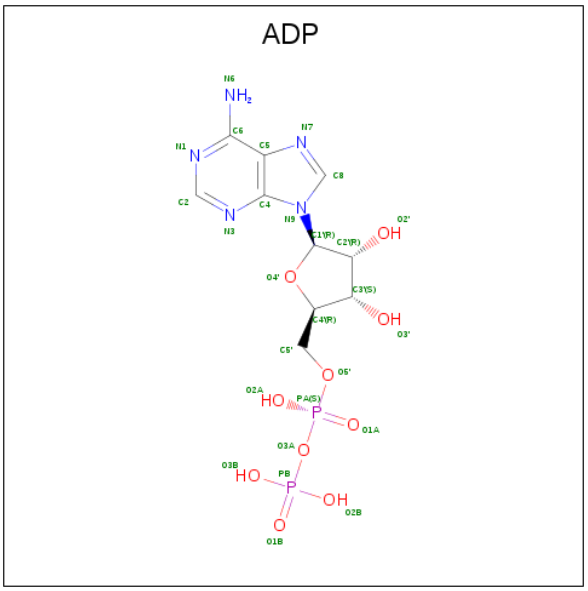
- Molecule 1 is a protein called Werner syndrome ATP-dependent helicase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	541	Total	C	N	O	S	0	2	0
			4295	2728	759	774	34			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	516	MET	-	initiating methionine	UNP Q14191
A	1074	PHE	LEU	variant	UNP Q14191
A	1094	ALA	VAL	expression tag	UNP Q14191
A	1095	GLU	-	expression tag	UNP Q14191
A	1096	ASN	-	expression tag	UNP Q14191
A	1097	LEU	-	expression tag	UNP Q14191
A	1098	TYR	-	expression tag	UNP Q14191
A	1099	PHE	-	expression tag	UNP Q14191
A	1100	GLN	-	expression tag	UNP Q14191

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Zn	0	0
			2	2		

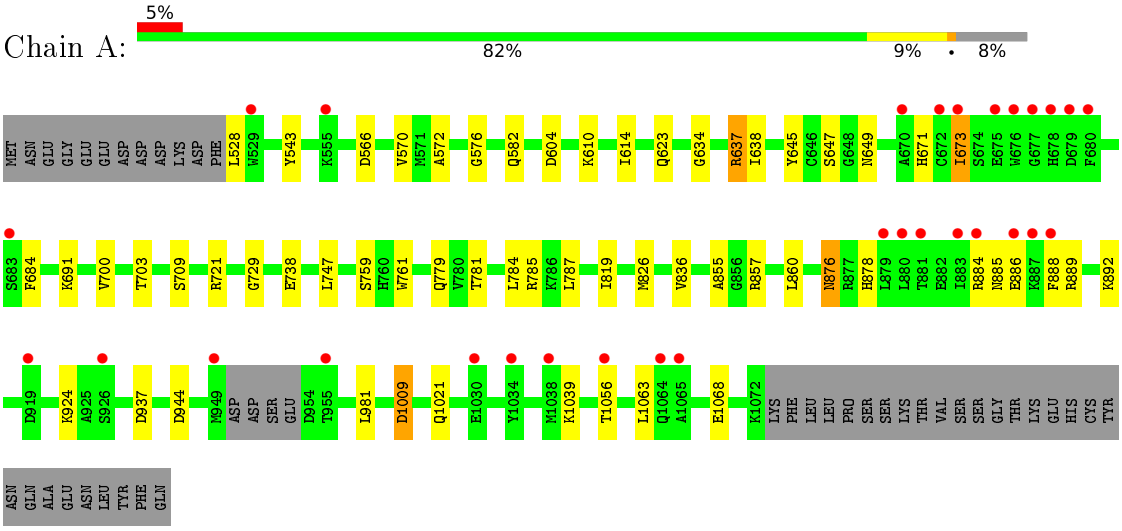
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	195	Total	O	0	0
			195	195		

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: Werner syndrome ATP-dependent helicase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	54.59Å 90.63Å 138.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	69.12 – 2.20 69.12 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.4 (69.12-2.20) 98.4 (69.12-2.20)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.28 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.197 , 0.236 0.197 , 0.236	Depositor DCC
R_{free} test set	1659 reflections (4.73%)	wwPDB-VP
Wilson B-factor (Å^2)	53.5	Xtriage
Anisotropy	0.473	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 52.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4519	wwPDB-VP
Average B, all atoms (Å^2)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] 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.

5 Model quality

5.1 Standard geometry

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

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	0.24	0/4385	0.42	0/5919

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	4295	0	4283	24	0
2	A	27	0	12	1	0
3	A	2	0	0	0	0
4	A	195	0	0	3	0
All	All	4519	0	4295	24	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 3.

All (24) 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:885:ASN:HB3	1:A:888:PHE:HB3	1.80	0.62
1:A:857[A]:ARG:HH11	2:A:1201:ADP:H5'2	1.69	0.58
1:A:645:TYR:O	1:A:649:ASN:ND2	2.32	0.54
1:A:779:GLN:NE2	4:A:1312:HOH:O	2.42	0.52
1:A:836:VAL:HG23	1:A:855:ALA:HB2	1.91	0.52
1:A:673:ILE:HG12	1:A:684:PHE:HB3	1.94	0.50
1:A:886:GLU:OE1	1:A:889:ARG:NH2	2.45	0.49
1:A:634:GLY:O	1:A:637:ARG:NH1	2.40	0.47
1:A:570:VAL:HG22	1:A:703:THR:HG23	1.95	0.47
1:A:566:ASP:OD1	1:A:691:LYS:NZ	2.43	0.47
1:A:543:TYR:HB3	1:A:614:ILE:HD11	1.97	0.47
1:A:604:ASP:HB3	1:A:826:MET:HG3	1.99	0.45
1:A:738:GLU:HG3	1:A:937:ASP:HB3	1.99	0.45
1:A:857[A]:ARG:NH2	4:A:1304:HOH:O	2.36	0.45
1:A:747:LEU:HA	1:A:747:LEU:HD12	1.85	0.44
1:A:1039:LYS:NZ	4:A:1306:HOH:O	2.37	0.44
1:A:572:ALA:HB2	1:A:729:GLY:O	2.18	0.44
1:A:761:TRP:CD1	1:A:787:LEU:HG	2.53	0.44
1:A:1021:GLN:HB3	1:A:1063:LEU:HD21	1.99	0.43
1:A:876:ASN:ND2	1:A:878:HIS:H	2.18	0.42
1:A:1009:ASP:N	1:A:1009:ASP:OD1	2.48	0.42
1:A:582:GLN:HG2	1:A:638:ILE:HD13	2.02	0.42
1:A:784:LEU:HD12	1:A:819:ILE:HD11	2.02	0.41
1:A:781:THR:O	1:A:785:ARG:HG2	2.21	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	A	539/585 (92%)	525 (97%)	13 (2%)	1 (0%)	47 55

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	576	GLY

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	466/518 (90%)	445 (96%)	21 (4%)	27 34

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	528	LEU
1	A	610	LYS
1	A	623	GLN
1	A	637	ARG
1	A	647	SER
1	A	671	HIS
1	A	673	ILE
1	A	700	VAL
1	A	709	SER
1	A	721	ARG
1	A	759	SER
1	A	860	LEU
1	A	876	ASN
1	A	884	ARG
1	A	892	LYS
1	A	924	LYS
1	A	944	ASP
1	A	981	LEU
1	A	1009	ASP
1	A	1056	THR
1	A	1068	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	876	ASN
1	A	945	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	ADP	A	1201	-	24,29,29	0.95	1 (4%)	29,45,45	1.41	4 (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
2	ADP	A	1201	-	-	0/12/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1201	ADP	C5-C4	2.50	1.47	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1201	ADP	PA-O3A-PB	-3.28	121.56	132.83
2	A	1201	ADP	N3-C2-N1	-3.25	123.60	128.68
2	A	1201	ADP	C4-C5-N7	-2.84	106.44	109.40
2	A	1201	ADP	C3'-C2'-C1'	2.22	104.33	100.98

There are no chirality outliers.

There are no torsion outliers.

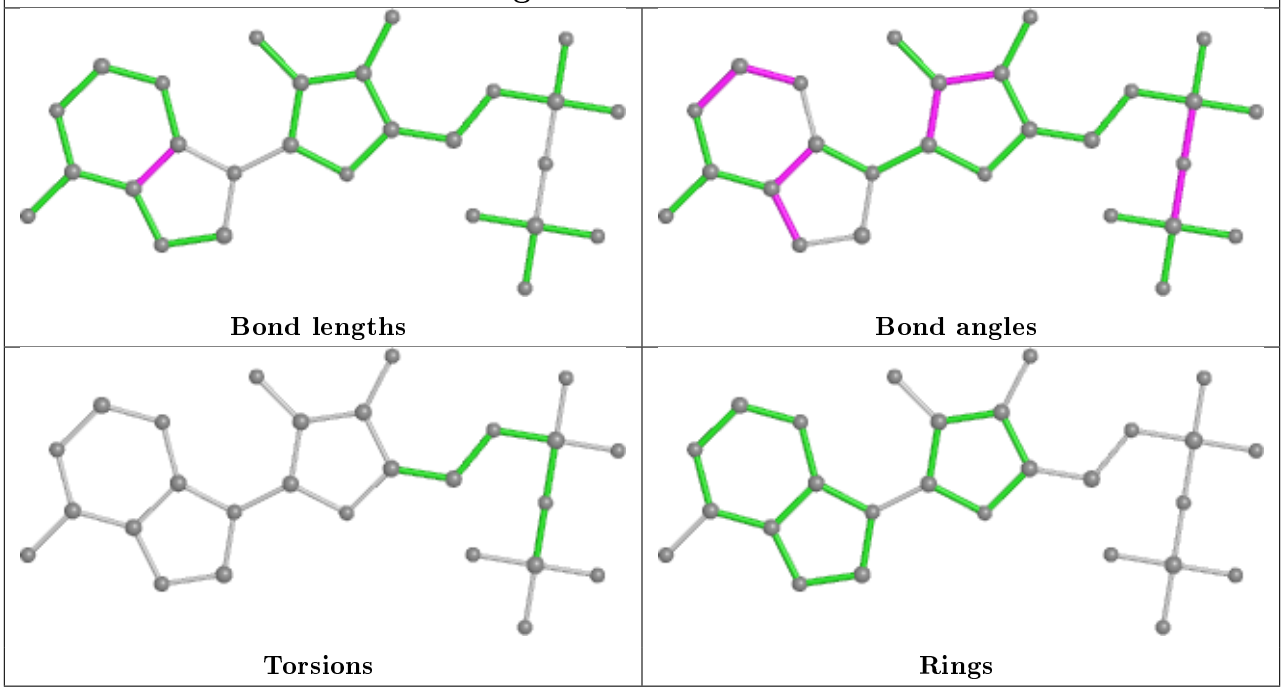
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1201	ADP	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.

Ligand ADP A 1201



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^{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	A	541/585 (92%)	0.33	30 (5%)	25	24	41, 65, 112, 137	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	884	ARG	7.1
1	A	676	TRP	6.8
1	A	678	HIS	5.8
1	A	883	ILE	5.2
1	A	679	ASP	5.1
1	A	949	MET	5.1
1	A	677	GLY	4.9
1	A	888	PHE	4.6
1	A	881	THR	4.3
1	A	879	LEU	4.0
1	A	955	THR	3.6
1	A	880	LEU	3.5
1	A	673	ILE	3.3
1	A	1038	MET	3.3
1	A	886	GLU	3.1
1	A	670	ALA	3.1
1	A	1034	TYR	3.0
1	A	887	LYS	3.0
1	A	672	CYS	2.9
1	A	1064	GLN	2.8
1	A	529	TRP	2.5
1	A	926	SER	2.4
1	A	1065	ALA	2.4
1	A	683	SER	2.4
1	A	919	ASP	2.3
1	A	555	LYS	2.3
1	A	675	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	1030	GLU	2.1
1	A	1056	THR	2.0
1	A	680	PHE	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)

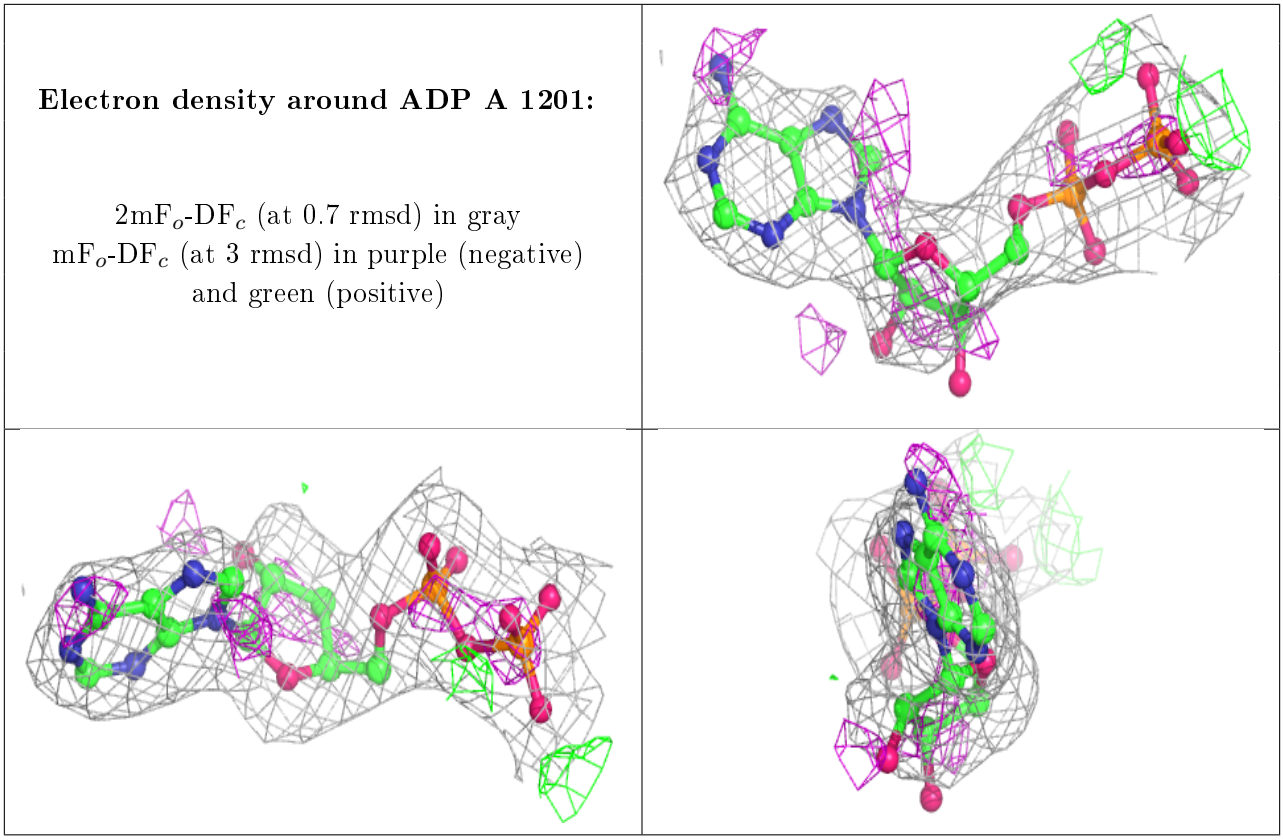
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	ADP	A	1201	27/27	0.91	0.14	54,75,95,120	0
3	ZN	A	1202	1/1	0.99	0.20	57,57,57,57	0
3	ZN	A	1203	1/1	1.00	0.19	48,48,48,48	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.

Electron density around ADP A 1201:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers

There are no such residues in this entry.