



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 17, 2025 – 03:16 pm GMT

PDB ID : 9T99 / pdb\_00009t99  
Title : Structure of C. elegans Dicer-related helicase 1 (DRH1) bound to blunt end 5'P-dsRNA  
Authors : Cusack, S.; Uchikawa, E.  
Deposited on : 2025-11-14  
Resolution : 2.18 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>.

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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	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
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)	:	2.46

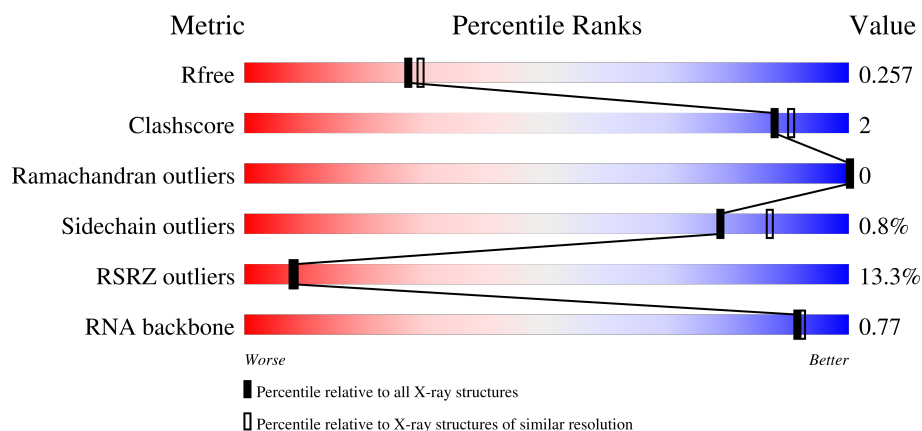
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.18 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))
$R_{free}$	164625	8336 (2.20-2.16)
Clashscore	180529	9404 (2.20-2.16)
Ramachandran outliers	177936	9297 (2.20-2.16)
Sidechain outliers	177891	9297 (2.20-2.16)
RSRZ outliers	164620	8337 (2.20-2.16)
RNA backbone	3690	1035 (2.50-1.86)

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	728	
2	S	11	
3	X	12	
3	Y	12	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12502 atoms, of which 6032 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 Dicer-related helicase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	700	Total	C	H	N	O	S	0	6	0
			11253	3501	5639	994	1079	40			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	290	GLY	-	expression tag	UNP G5EDI8
A	431	GLN	GLU	engineered mutation	UNP G5EDI8

- Molecule 2 is a RNA chain called RNA (5'-R(P\*GP\*GP\*UP\*AP\*GP\*UP\*CP\*UP\*AP\*CP\*C)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	S	11	Total	C	H	N	O	P	0	0	0
			353	104	119	40	79	11			

- Molecule 3 is a RNA chain called RNA (5'-R(P\*GP\*GP\*UP\*AP\*GP\*CP\*GP\*CP\*UP\*AP\*CP\*C)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	X	12	Total	C	H	N	O	P	0	0	0
			388	114	131	46	85	12			
3	Y	12	Total	C	H	N	O	P	0	0	0
			388	114	131	46	85	12			

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		

- Molecule 5 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
5	A	1	Total	C	H	N	O	P	0	0
			39	10	12	5	10	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	61	Total	O	0	0
			61	61		
6	X	9	Total	O	0	0
			9	9		
6	Y	10	Total	O	0	0
			10	10		



- Molecule 1: Dicer-related helicase





## 4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	134.35Å 134.35Å 221.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	72.08 – 2.18 72.08 – 2.18	Depositor EDS
% Data completeness (in resolution range)	84.2 (72.08-2.18) 84.2 (72.08-2.18)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.71 (at 2.18Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, $R_{free}$	0.218 , 0.257 0.218 , 0.257	Depositor DCC
$R_{free}$ test set	2278 reflections (4.30%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	57.1	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 48.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	12502	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% 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: 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	0.13	0/5722	0.26	0/7723
2	S	0.08	0/260	0.17	0/401
3	X	0.16	0/286	0.21	0/442
3	Y	0.15	0/286	0.23	0/442
All	All	0.13	0/6554	0.26	0/9008

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	A	5614	5639	5612	24	0
2	S	234	119	119	0	1
3	X	257	131	131	0	0
3	Y	257	131	131	1	0
4	A	1	0	0	0	0
5	A	27	12	12	0	0
6	A	61	0	0	0	0
6	X	9	0	0	0	0
6	Y	10	0	0	0	0
All	All	6470	6032	6005	24	1



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 2.

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:604:SER:O	1:A:983:ARG:NH1	2.17	0.78
1:A:386:ILE:HG22	1:A:392:ILE:HD12	1.74	0.68
1:A:799:ALA:O	1:A:803:ARG:N	2.25	0.68
1:A:473:LEU:HD22	1:A:491:LEU:CD2	2.26	0.66
1:A:876:LYS:NZ	1:A:994:ASP:OD1	2.31	0.63
1:A:473:LEU:HD22	1:A:491:LEU:HD23	1.81	0.61
1:A:293:LEU:HD23	1:A:298:GLU:CG	2.33	0.59
1:A:795:THR:OG1	1:A:803:ARG:NH2	2.39	0.55
1:A:293:LEU:HD23	1:A:298:GLU:HG2	1.89	0.54
1:A:409:SER:N	1:A:1001:GLU:OE2	2.38	0.53
1:A:352:MET:HE1	1:A:780:LEU:HD21	1.92	0.50
1:A:473:LEU:HD22	1:A:491:LEU:HD21	1.93	0.50
1:A:293:LEU:HD23	1:A:298:GLU:HG3	1.94	0.48
1:A:638:HIS:HB2	1:A:639:PRO:HD2	1.98	0.46
1:A:366:ASP:OD1	1:A:367:HIS:N	2.49	0.46
1:A:895:GLU:OE2	1:A:983:ARG:NH2	2.52	0.43
1:A:995:LYS:NZ	3:Y:16:A:OP1	2.51	0.42
1:A:522:LEU:HD21	1:A:685:LYS:HD3	2.02	0.42
1:A:372:GLN:HG2	1:A:385:VAL:HG12	2.02	0.42
1:A:758:LYS:HA	1:A:761:MET:HE3	2.01	0.41
1:A:984:ILE:HG21	1:A:996:TYR:CZ	2.55	0.41
1:A:498:LYS:HD3	1:A:852:ARG:CZ	2.51	0.40
1:A:554:LEU:HD12	1:A:561:ILE:HD11	2.04	0.40
1:A:384:ASN:OD1	1:A:384:ASN:N	2.54	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:3:U:O4	2:S:9:A:H61[15_555]	1.51	0.09

## 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	698/728 (96%)	678 (97%)	20 (3%)	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	Rotameric	Outliers	Percentiles	
1	A	642/659 (97%)	637 (99%)	5 (1%)	79	87

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	320	LYS
1	A	417	ASP
1	A	626	GLU
1	A	685	LYS
1	A	823	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	367	HIS
1	A	694	ASN
1	A	800	HIS

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Mol	Chain	Res	Type
1	A	908	ASN
1	A	956	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	S	10/11 (90%)	0	0
3	X	11/12 (91%)	0	0
3	Y	11/12 (91%)	0	0
All	All	32/35 (91%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

## 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 oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 1 is 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	$\# Z  > 2$
5	ADP	A	1102	-	24,29,29	0.99	2 (8%)	29,45,45	1.41	3 (10%)

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
5	ADP	A	1102	-	-	2/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1102	ADP	O4'-C1'	2.42	1.44	1.41
5	A	1102	ADP	C5-C4	2.35	1.47	1.40

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1102	ADP	N3-C2-N1	-3.80	122.74	128.68
5	A	1102	ADP	PA-O3A-PB	-3.33	121.40	132.83
5	A	1102	ADP	C4-C5-N7	-2.54	106.76	109.40

There are no chirality outliers.

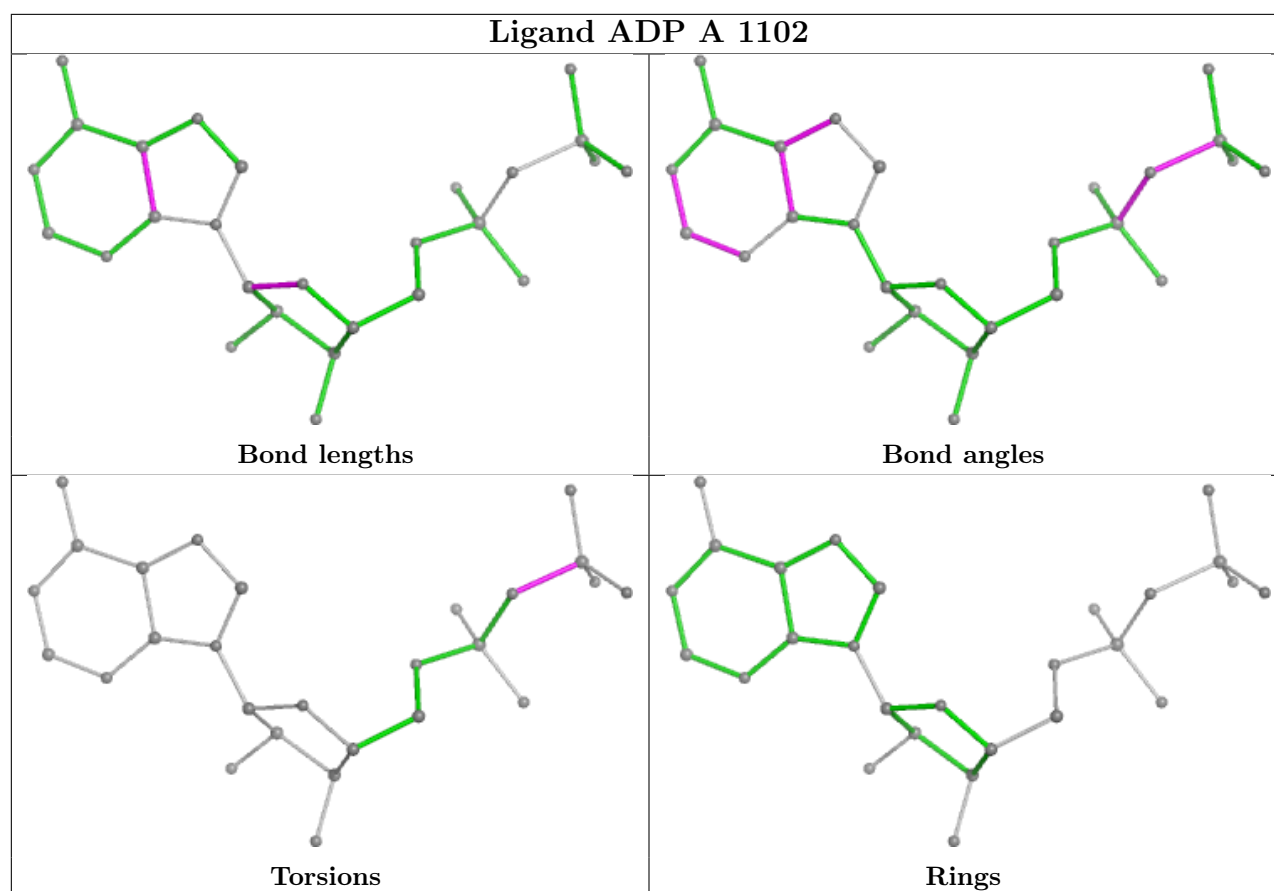
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1102	ADP	PA-O3A-PB-O3B
5	A	1102	ADP	PA-O3A-PB-O1B

There are no ring outliers.

No monomer is involved in short contacts.

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 [i](#)

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<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	700/728 (96%)	0.81	98 (14%) <b>7</b> <b>7</b>	23, 85, 165, 259	3 (0%)
2	S	11/11 (100%)	0.76	0 <b>100</b> <b>100</b>	133, 154, 161, 162	0
3	X	12/12 (100%)	-0.63	0 <b>100</b> <b>100</b>	47, 58, 95, 112	0
3	Y	12/12 (100%)	-0.47	0 <b>100</b> <b>100</b>	46, 56, 114, 130	0
All	All	735/763 (96%)	0.77	98 (13%) <b>8</b> <b>8</b>	23, 85, 163, 259	3 (0%)

All (98) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	617	ILE	4.8
1	A	603	VAL	4.8
1	A	986	VAL	4.6
1	A	787	LEU	4.3
1	A	801	VAL	4.2
1	A	794	ALA	4.2
1	A	798	ILE	4.1
1	A	643	LEU	4.0
1	A	795	THR	3.9
1	A	518	PRO	3.8
1	A	672	LEU	3.8
1	A	290	GLY	3.8
1	A	805	GLY	3.8
1	A	703	ILE	3.5
1	A	751	SER	3.5
1	A	759	LEU	3.5
1	A	776	ALA	3.5
1	A	608	PHE	3.5
1	A	814	CYS	3.4
1	A	550	ILE	3.2
1	A	673	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	386	ILE	3.1
1	A	473	LEU	3.1
1	A	793	TYR	3.1
1	A	604	SER	3.1
1	A	654	THR	3.0
1	A	554	LEU	3.0
1	A	769	ILE	2.9
1	A	675	THR	2.9
1	A	676	GLY	2.9
1	A	782	VAL	2.9
1	A	529	ASP	2.9
1	A	665	TRP	2.9
1	A	655	PRO	2.9
1	A	780	LEU	2.9
1	A	580	PHE	2.8
1	A	388	SER	2.8
1	A	796	ASN	2.8
1	A	632	SER	2.8
1	A	797	GLU	2.8
1	A	987	LYS	2.8
1	A	779	GLY	2.8
1	A	621	LEU	2.8
1	A	415	ARG	2.7
1	A	960	VAL	2.7
1	A	674	GLY	2.7
1	A	559	ILE	2.6
1	A	982	LYS	2.6
1	A	638	HIS	2.6
1	A	980	THR	2.6
1	A	291	LEU	2.6
1	A	988	LYS	2.6
1	A	909	THR	2.6
1	A	763	ALA	2.5
1	A	705	PHE	2.5
1	A	823	LEU	2.5
1	A	662	ILE	2.5
1	A	800	HIS	2.5
1	A	646	LEU	2.5
1	A	812	SER	2.4
1	A	698	ALA	2.4
1	A	958	ILE	2.4
1	A	728	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	352	MET	2.4
1	A	516	ILE	2.4
1	A	292	CYS	2.3
1	A	932	GLN	2.3
1	A	520	LYS	2.3
1	A	380	VAL	2.3
1	A	789	ILE	2.3
1	A	689	TYR	2.3
1	A	695	LEU	2.3
1	A	770	LEU	2.3
1	A	661	MET	2.3
1	A	807	GLY	2.2
1	A	669	HIS	2.2
1	A	364	TYR	2.2
1	A	678	ALA	2.2
1	A	815	VAL	2.2
1	A	664	ILE	2.2
1	A	491	LEU	2.2
1	A	765	GLY	2.2
1	A	735	MET	2.2
1	A	788	VAL	2.2
1	A	578	SER	2.1
1	A	946[A]	ARG	2.1
1	A	781	ASP	2.1
1	A	605	GLY	2.1
1	A	546	VAL	2.1
1	A	597	CYS	2.1
1	A	691	VAL	2.1
1	A	361	ILE	2.1
1	A	612	GLY	2.0
1	A	754	LYS	2.0
1	A	808	ARG	2.0
1	A	637	PHE	2.0
1	A	730	ILE	2.0
1	A	727	MET	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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



## 6.3 Carbohydrates [i](#)

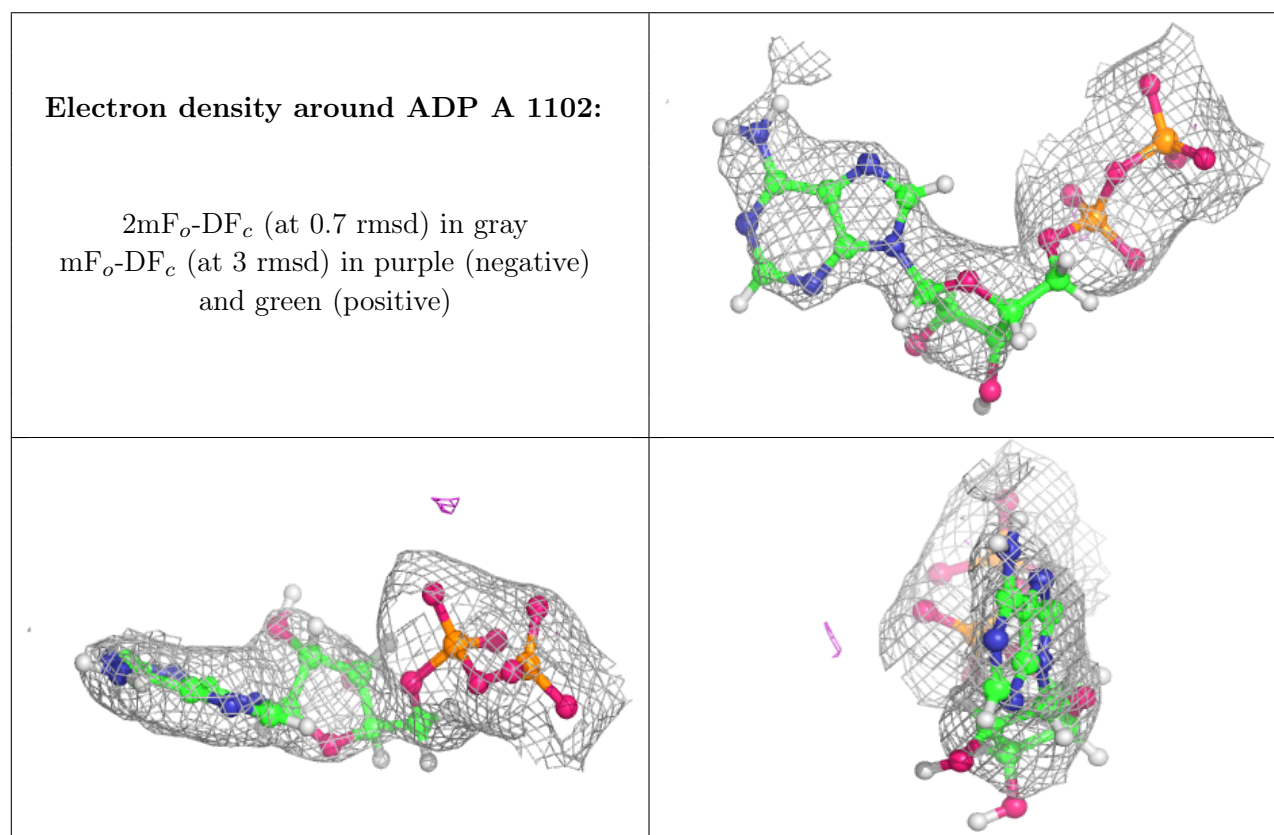
There are no oligosaccharides in this entry.

## 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.

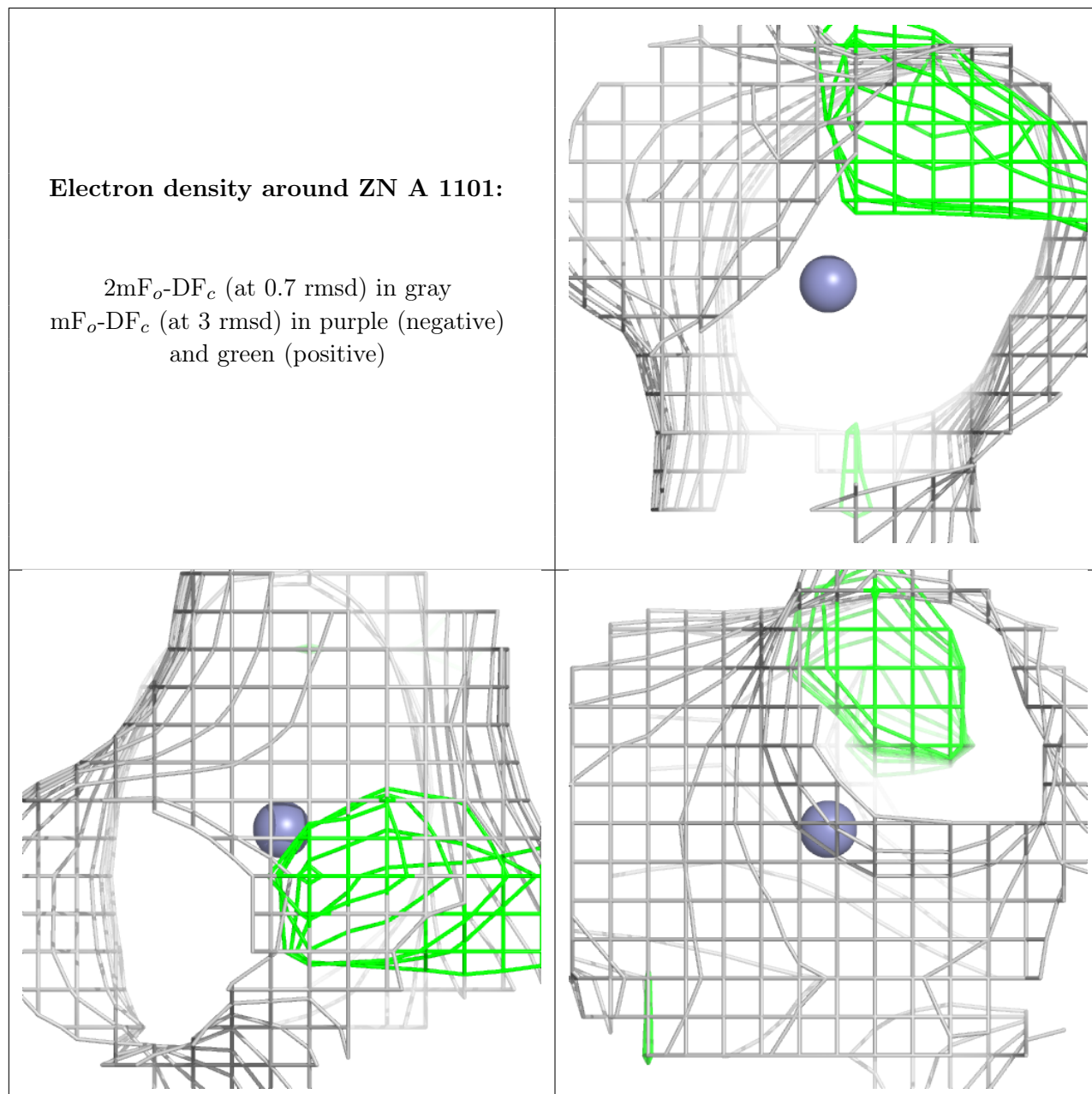
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	ADP	A	1102	27/27	0.88	0.10	72,110,133,136	0
4	ZN	A	1101	1/1	0.98	0.04	70,70,70,70	0

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 ZN A 1101:**

$2mF_o-DF_c$  (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.