



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 06:48 AM UTC

PDB ID : 3CWT / pdb\_00003cwt  
Title : Crystal Structure of an AlkA Host/Guest Complex 2'-fluoro-2'-deoxyinosine:  
Adenine Base Pair  
Authors : Bowman, B.R.; Lee, S.; Wang, S.; Verdine, G.L.  
Deposited on : 2008-04-22  
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
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

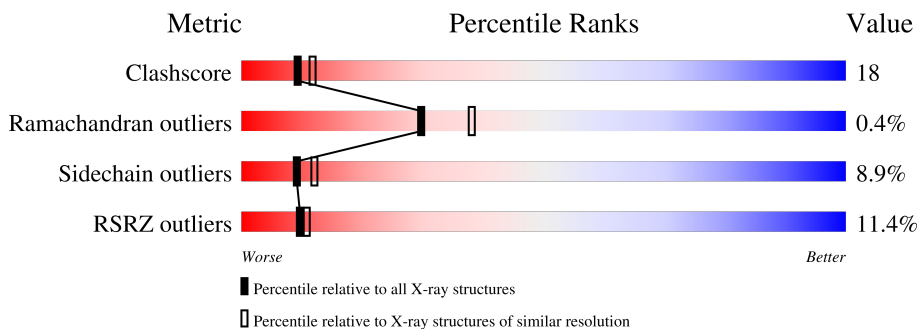
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	282	<div style="display: flex; align-items: center;"> <div style="width: 10%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 63%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 32%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: orange;"></div> </div>
1	B	282	<div style="display: flex; align-items: center;"> <div style="width: 10%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 67%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 27%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: orange;"></div> </div>
1	C	282	<div style="display: flex; align-items: center;"> <div style="width: 9%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 66%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 31%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 4%; height: 10px; background-color: orange;"></div> </div>
1	D	282	<div style="display: flex; align-items: center;"> <div style="width: 13%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 65%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 29%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 6%; height: 10px; background-color: orange;"></div> </div>
2	E	12	<div style="display: flex; align-items: center;"> <div style="width: 58%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 75%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 17%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 8%; height: 10px; background-color: orange;"></div> </div>
2	G	12	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 67%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 33%; height: 10px; background-color: yellow; margin-right: 5px;"></div> </div>
3	F	12	<div style="display: flex; align-items: center;"> <div style="width: 17%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 75%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 83%; height: 10px; background-color: yellow; margin-right: 5px;"></div> </div>

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
3	H	12	 67% 33%

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9948 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 DNA-3-methyladenine glycosylase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	282	Total	C	N	O	S	0	0	0
			2215	1427	387	389	12			
1	B	281	Total	C	N	O	S	0	0	0
			2209	1424	386	387	12			
1	C	282	Total	C	N	O	S	0	0	0
			2215	1427	387	389	12			
1	D	281	Total	C	N	O	S	0	0	0
			2209	1424	386	387	12			

- Molecule 2 is a DNA chain called DNA (5'-D(\*DGP\*DAP\*DCP\*DAP\*DTP\*DGP\*DAP\*(2FI)P\*DTP\*DGP\*DCP\*DC)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	F	N	O				P
2	E	12	Total	C	F	N	O	P	0	0	0
			245	117	1	47	69	11			
2	G	12	Total	C	F	N	O	P	0	0	0
			245	117	1	47	69	11			

- Molecule 3 is a DNA chain called DNA (5'-D(\*DGP\*DGP\*DCP\*DAP\*DAP\*DTP\*DCP\*DAP\*DTP\*DGP\*DTP\*DC)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	F	12	Total	C	N	O	P	0	0	0
			243	117	45	70	11			
3	H	12	Total	C	N	O	P	0	0	0
			243	117	45	70	11			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	30	Total O 30 30	0	0

*Continued on next page...*

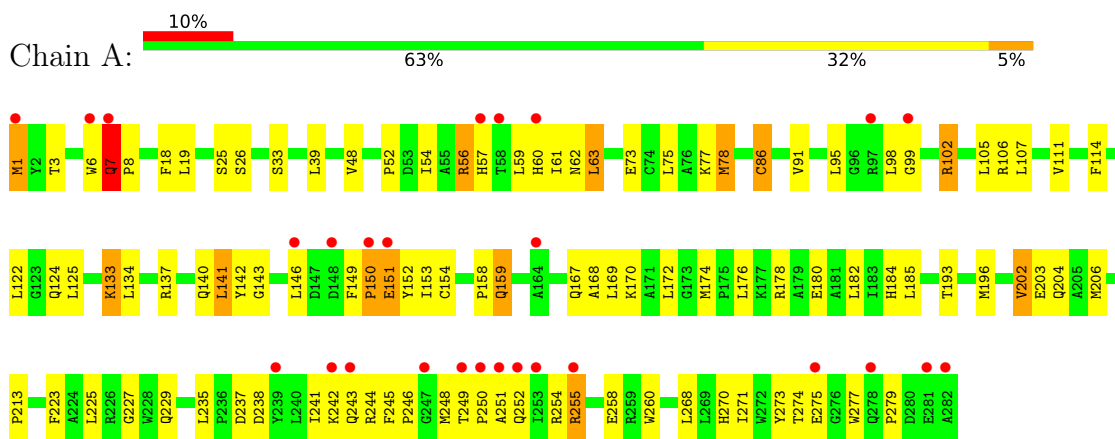
*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
4	B	27	Total O 27 27	0	0
4	C	30	Total O 30 30	0	0
4	D	34	Total O 34 34	0	0
4	E	1	Total O 1 1	0	0
4	H	2	Total O 2 2	0	0

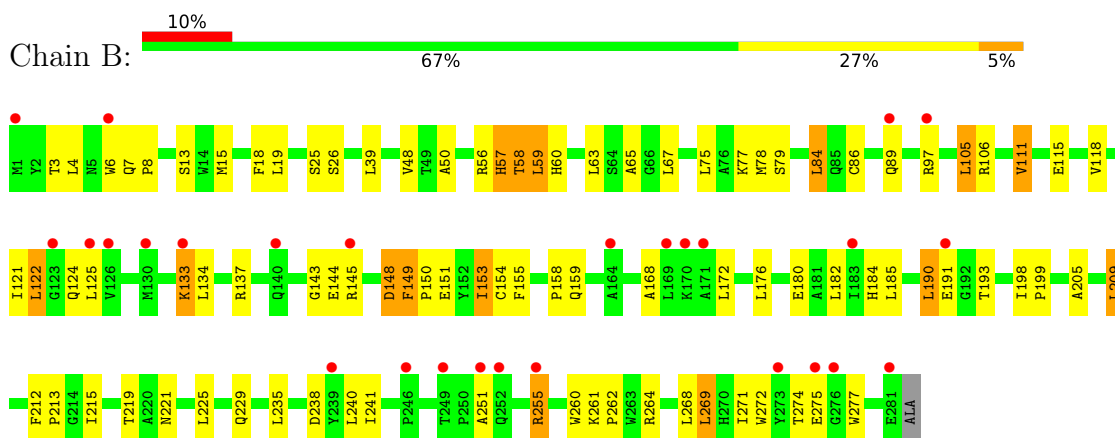
### 3 Residue-property plots [i](#)

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.

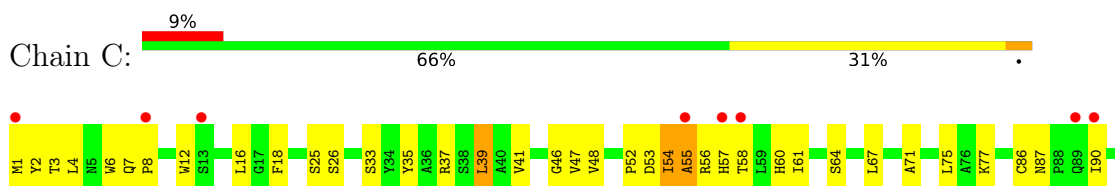
- Molecule 1: DNA-3-methyladenine glycosylase 2

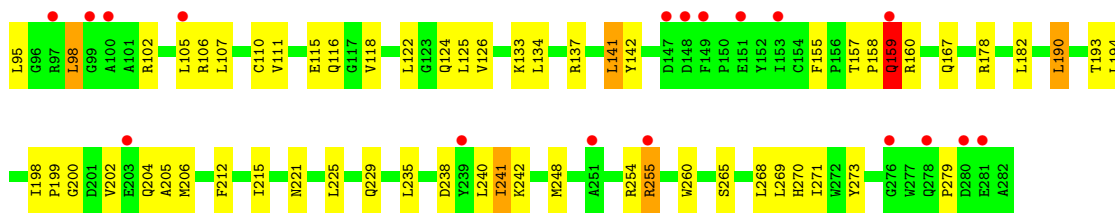


- Molecule 1: DNA-3-methyladenine glycosylase 2

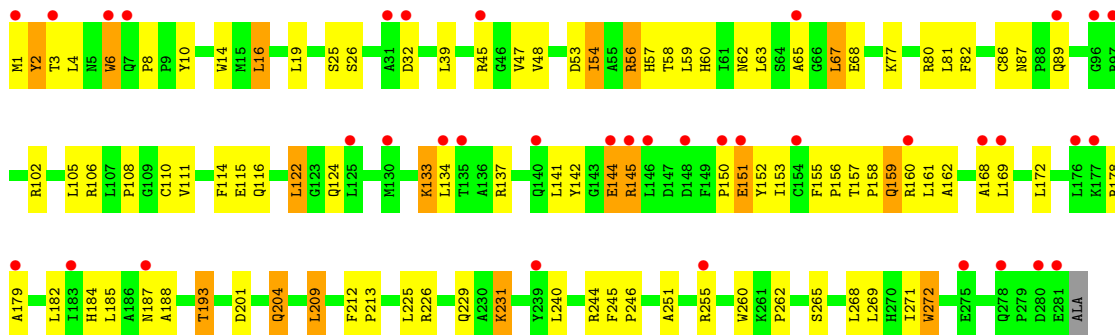


- Molecule 1: DNA-3-methyladenine glycosylase 2

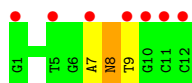
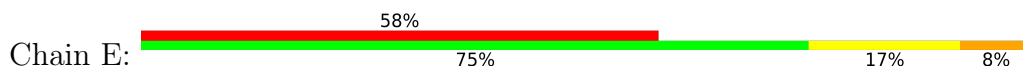




● Molecule 1: DNA-3-methyladenine glycosylase 2



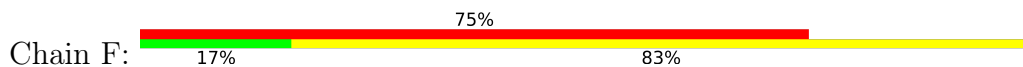
● Molecule 2: DNA (5'-D(\*DGP\*DAP\*DCP\*DAP\*DTP\*DGP\*DAP\*(2FI)P\*DTP\*DGP\*DCP\*DC)-3')



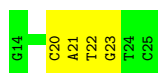
● Molecule 2: DNA (5'-D(\*DGP\*DGP\*DCP\*DAP\*DAP\*DTP\*DCP\*DAP\*DTP\*DGP\*DCP\*DC)-3')



● Molecule 3: DNA (5'-D(\*DGP\*DGP\*DCP\*DAP\*DAP\*DTP\*DCP\*DAP\*DTP\*DGP\*DTP\*D C)-3')



● Molecule 3: DNA (5'-D(\*DGP\*DGP\*DCP\*DAP\*DAP\*DTP\*DCP\*DAP\*DTP\*DGP\*DTP\*D C)-3')



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.75Å 101.48Å 103.11Å 90.00° 93.72° 90.00°	Depositor
Resolution (Å)	50.00 – 2.30 50.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	93.2 (50.00-2.30) 93.2 (50.00-2.30)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.83 (at 2.10Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.239 , 0.280 0.238 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.1	Xtrriage
Anisotropy	0.264	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 31.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	9948	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% 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: 2FI

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	0.50	0/2277	0.99	15/3104 (0.5%)
1	B	0.48	0/2271	0.94	6/3097 (0.2%)
1	C	0.46	0/2277	0.88	5/3104 (0.2%)
1	D	0.50	0/2271	0.92	5/3097 (0.2%)
2	E	0.28	0/249	0.73	0/380
2	G	0.31	0/249	0.78	0/380
3	F	0.30	0/272	0.73	0/418
3	H	0.30	0/272	0.79	0/418
All	All	0.47	0/10138	0.91	31/13998 (0.2%)

There are no bond length outliers.

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	2	TYR	N-CA-C	-7.82	98.02	110.14
1	A	255	ARG	N-CA-C	-7.37	103.23	111.71
1	A	275	GLU	N-CA-C	7.12	119.66	111.11
1	A	7	GLN	CA-C-N	7.04	124.73	119.66
1	A	7	GLN	C-N-CA	7.04	124.73	119.66

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	2215	0	2209	77	0
1	B	2209	0	2204	80	0
1	C	2215	0	2209	77	0
1	D	2209	0	2204	89	0
2	E	245	0	134	5	0
2	G	245	0	134	7	0
3	F	243	0	137	17	0
3	H	243	0	137	3	0
4	A	30	0	0	0	0
4	B	27	0	0	0	0
4	C	30	0	0	0	0
4	D	34	0	0	0	0
4	E	1	0	0	0	0
4	H	2	0	0	0	0
All	All	9948	0	9368	347	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 18.

The worst 5 of 347 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:3:THR:HG22	1:A:60:HIS:HD2	1.04	1.12
1:B:133:LYS:HE3	1:B:137:ARG:HH21	1.09	1.08
1:B:143:GLY:HA3	1:B:153:ILE:HD11	1.21	1.07
1:D:54:ILE:HD12	1:D:54:ILE:H	1.19	1.05
1:B:121:ILE:HA	1:B:124:GLN:HE21	1.23	1.03

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	280/282 (99%)	269 (96%)	11 (4%)	0	100	100
1	B	279/282 (99%)	270 (97%)	8 (3%)	1 (0%)	30	38
1	C	280/282 (99%)	266 (95%)	11 (4%)	3 (1%)	11	13
1	D	279/282 (99%)	267 (96%)	12 (4%)	0	100	100
All	All	1118/1128 (99%)	1072 (96%)	42 (4%)	4 (0%)	30	38

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	275	GLU
1	C	55	ALA
1	C	57	HIS
1	C	126	VAL

### 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	222/222 (100%)	202 (91%)	20 (9%)	9	12
1	B	222/222 (100%)	199 (90%)	23 (10%)	7	8
1	C	222/222 (100%)	208 (94%)	14 (6%)	16	23
1	D	222/222 (100%)	200 (90%)	22 (10%)	7	9
All	All	888/888 (100%)	809 (91%)	79 (9%)	9	12

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	4	LEU
1	D	159	GLN
1	D	16	LEU
1	D	68	GLU
1	D	209	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37

such sidechains are listed below:

Mol	Chain	Res	Type
1	D	7	GLN
1	D	210	GLN
1	D	60	HIS
1	D	140	GLN
1	B	187	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

2 non-standard protein/DNA/RNA residues 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	2FI	E	8	2	21,24,25	1.59	5 (23%)	30,35,38	0.85	1 (3%)
2	2FI	G	8	2	21,24,25	1.35	3 (14%)	30,35,38	1.12	2 (6%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	2FI	E	8	2	-	1/7/25/26	0/3/3/3
2	2FI	G	8	2	-	0/7/25/26	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	8	2FI	C2-N3	3.65	1.37	1.30
2	G	8	2FI	C2-N3	3.44	1.36	1.30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	8	2FI	C2-N1	2.83	1.40	1.35
2	G	8	2FI	O6-C6	2.66	1.28	1.23
2	G	8	2FI	C2-N1	2.54	1.40	1.35

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	8	2FI	C2'-C1'-N9	3.63	119.85	114.27
2	G	8	2FI	O4'-C1'-C2'	-2.12	103.60	105.84
2	E	8	2FI	N1-C2-N3	-2.04	123.15	125.50

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	8	2FI	C4'-C5'-O5'-P

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	8	2FI	5	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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<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	282/282 (100%)	0.64	27 (9%) 13 15	22, 41, 76, 101	0
1	B	281/282 (99%)	0.75	27 (9%) 13 15	26, 42, 70, 111	0
1	C	282/282 (100%)	0.71	26 (9%) 14 16	27, 44, 76, 139	0
1	D	281/282 (99%)	0.88	37 (13%) 7 8	25, 42, 67, 125	0
2	E	11/12 (91%)	2.42	7 (63%) 0 0	47, 76, 132, 142	0
2	G	11/12 (91%)	1.15	1 (9%) 15 16	47, 65, 82, 94	0
3	F	12/12 (100%)	2.50	9 (75%) 0 0	57, 119, 131, 141	0
3	H	12/12 (100%)	0.60	0 100 100	41, 57, 91, 102	0
All	All	1172/1176 (99%)	0.78	134 (11%) 10 11	22, 43, 79, 142	0

The worst 5 of 134 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	130	MET	5.7
1	D	6	TRP	5.5
2	E	9	DT	4.9
1	D	183	ILE	4.4
1	B	130	MET	4.4

### 6.2 Non-standard residues in protein, DNA, RNA chains [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(Å <sup>2</sup> )	Q<0.9
2	2FI	E	8	22/23	0.87	0.27	20,20,21,22	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	2FI	G	8	22/23	0.93	0.20	20,20,20,22	0

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.