



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:19 AM GMT

PDB ID : 2GL0  
Title : Structure of PAE2307 in complex with adenosine  
Authors : Lott, J.S.; Paget, B.; Johnston, J.M.; Baker, E.N.  
Deposited on : 2006-04-04  
Resolution : 2.25 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

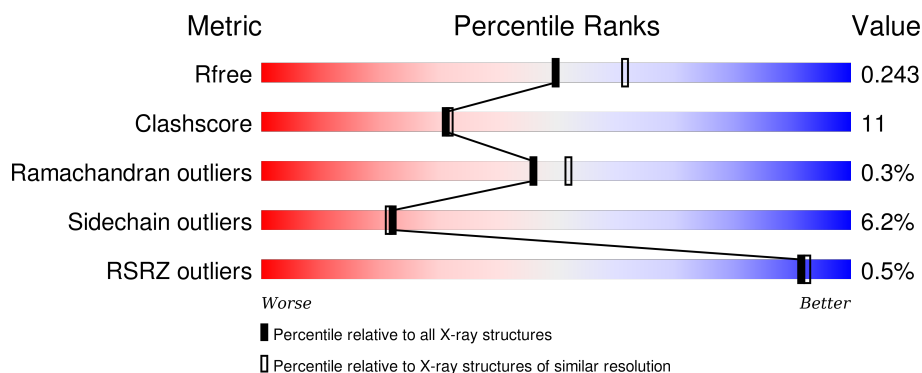
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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))
$R_{free}$	91344	1640 (2.28-2.24)
Clashscore	102246	1095 (2.26-2.26)
Ramachandran outliers	100387	1063 (2.26-2.26)
Sidechain outliers	100360	1063 (2.26-2.26)
RSRZ outliers	91569	1647 (2.28-2.24)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	167	<div> <div>%</div> <div> <div></div> <div>77%</div> <div>19%</div> <div>...</div> </div> </div>
1	B	167	<div> <div>%</div> <div> <div></div> <div>72%</div> <div>22%</div> <div>...</div> </div> </div>
1	C	167	<div> <div></div> <div> <div></div> <div>71%</div> <div>22%</div> <div>...</div> </div> </div>
1	D	167	<div> <div></div> <div> <div></div> <div>77%</div> <div>17%</div> <div>...</div> </div> </div>
1	E	167	<div> <div></div> <div> <div></div> <div>75%</div> <div>19%</div> <div>...</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	167	<div> <div></div> <div>%</div> <div>71%</div> <div>21%</div> <div>5%</div> <div></div> </div>

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
2	PO4	C	502	-	-	X	X
2	PO4	D	501	-	-	X	-

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8217 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 conserved hypothetical protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	163	Total	C	N	O	S	0	0	0
			1283	826	225	230	2			
1	B	163	Total	C	N	O	S	0	0	0
			1283	826	225	230	2			
1	C	162	Total	C	N	O	S	0	0	0
			1277	823	224	228	2			
1	D	163	Total	C	N	O	S	0	0	0
			1283	826	225	230	2			
1	E	163	Total	C	N	O	S	0	0	0
			1283	826	225	230	2			
1	F	162	Total	C	N	O	S	0	0	0
			1277	823	224	228	2			

There are 18 discrepancies between the modelled and reference sequences:

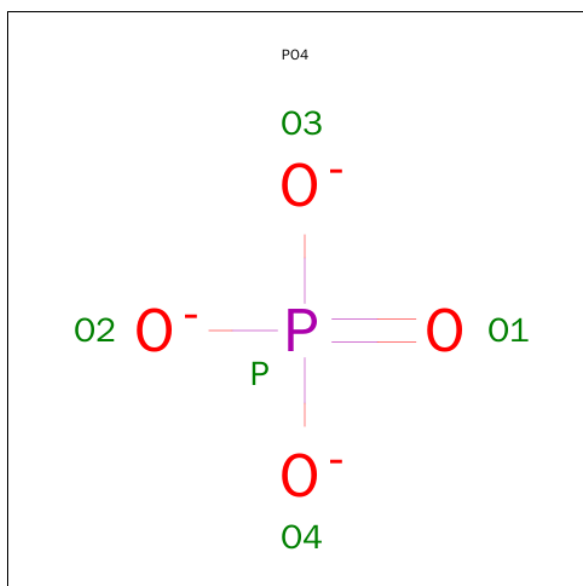
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	CLONING ARTIFACT	UNP Q8ZVF7
A	2	THR	-	CLONING ARTIFACT	UNP Q8ZVF7
A	3	ASP	-	CLONING ARTIFACT	UNP Q8ZVF7
B	1	MET	-	CLONING ARTIFACT	UNP Q8ZVF7
B	2	THR	-	CLONING ARTIFACT	UNP Q8ZVF7
B	3	ASP	-	CLONING ARTIFACT	UNP Q8ZVF7
C	1	MET	-	CLONING ARTIFACT	UNP Q8ZVF7
C	2	THR	-	CLONING ARTIFACT	UNP Q8ZVF7
C	3	ASP	-	CLONING ARTIFACT	UNP Q8ZVF7
D	1	MET	-	CLONING ARTIFACT	UNP Q8ZVF7
D	2	THR	-	CLONING ARTIFACT	UNP Q8ZVF7
D	3	ASP	-	CLONING ARTIFACT	UNP Q8ZVF7
E	1	MET	-	CLONING ARTIFACT	UNP Q8ZVF7
E	2	THR	-	CLONING ARTIFACT	UNP Q8ZVF7
E	3	ASP	-	CLONING ARTIFACT	UNP Q8ZVF7
F	1	MET	-	CLONING ARTIFACT	UNP Q8ZVF7
F	2	THR	-	CLONING ARTIFACT	UNP Q8ZVF7

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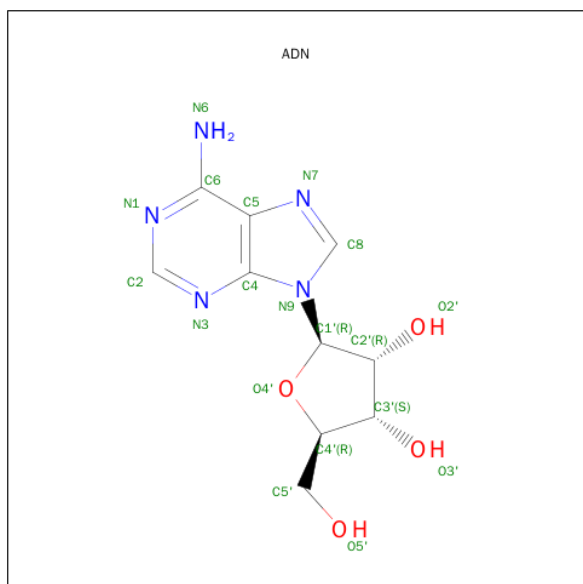
Chain	Residue	Modelled	Actual	Comment	Reference
F	3	ASP	-	CLONING ARTIFACT	UNP Q8ZVF7

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total O P 5 4 1	0	0
2	C	1	Total O P 5 4 1	0	0

- Molecule 3 is ADENOSINE (three-letter code: ADN) (formula: C<sub>10</sub>H<sub>13</sub>N<sub>5</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			19	10	5	4		
3	B	1	Total	C	N	O	0	0
			19	10	5	4		
3	C	1	Total	C	N	O	0	0
			19	10	5	4		
3	D	1	Total	C	N	O	0	0
			19	10	5	4		
3	E	1	Total	C	N	O	0	0
			19	10	5	4		
3	F	1	Total	C	N	O	0	0
			19	10	5	4		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	70	Total	O	0	0
			70	70		
4	B	72	Total	O	0	0
			72	72		
4	C	81	Total	O	0	0
			81	81		
4	D	60	Total	O	0	0
			60	60		
4	E	53	Total	O	0	0
			53	53		
4	F	71	Total	O	0	0
			71	71		



- Molecule 1: conserved hypothetical protein





- Molecule 1: conserved hypothetical protein

Chain E: 75% 19% . . .



- Molecule 1: conserved hypothetical protein

Chain F: % 71% 21% 5% .





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.86 Å 109.83 Å 112.48 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.33 – 2.25 45.39 – 2.25	Depositor EDS
% Data completeness (in resolution range)	98.1 (49.33-2.25) 98.1 (45.39-2.25)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.19 (at 2.24 Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.170 , 0.245 0.170 , 0.243	Depositor DCC
$R_{free}$ test set	2271 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	28.9	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 44.5	EDS
Estimated twinning fraction	0.026 for -h,l,k	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 45058 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8217	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 31.51 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.0942e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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, 0.375 respectively for untwinned datasets, and 0.333, 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: ADN, PO4

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	1.32	3/1306 (0.2%)	1.09	4/1768 (0.2%)
1	B	1.18	1/1306 (0.1%)	1.11	4/1768 (0.2%)
1	C	1.35	6/1300 (0.5%)	1.15	7/1760 (0.4%)
1	D	1.25	3/1306 (0.2%)	1.16	6/1768 (0.3%)
1	E	1.15	1/1306 (0.1%)	1.05	1/1768 (0.1%)
1	F	1.28	2/1300 (0.2%)	1.11	2/1760 (0.1%)
All	All	1.25	16/7824 (0.2%)	1.11	24/10592 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	158	PHE	C-N	-17.48	0.93	1.34
1	C	157	LYS	C-N	-12.78	1.04	1.34
1	A	110	VAL	CB-CG2	-6.34	1.39	1.52
1	F	109	VAL	CB-CG2	6.32	1.66	1.52
1	E	90	TYR	CD1-CE1	6.10	1.48	1.39

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	111	ARG	NE-CZ-NH2	-13.18	113.71	120.30
1	F	111	ARG	NE-CZ-NH2	-12.64	113.98	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	158	PHE	O-C-N	-10.34	106.16	122.70
1	F	111	ARG	NE-CZ-NH1	9.36	124.98	120.30
1	A	155	ARG	NE-CZ-NH1	7.57	124.08	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	158	PHE	Mainchain

## 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	1283	0	1335	32	0
1	B	1283	0	1335	34	0
1	C	1277	0	1328	35	0
1	D	1283	0	1335	28	0
1	E	1283	0	1335	39	0
1	F	1277	0	1330	29	0
2	C	5	0	0	2	0
2	D	5	0	0	7	0
3	A	19	0	13	0	0
3	B	19	0	13	1	0
3	C	19	0	13	0	0
3	D	19	0	13	1	0
3	E	19	0	13	0	0
3	F	19	0	13	1	0
4	A	70	0	0	3	1
4	B	72	0	0	4	1
4	C	81	0	0	3	0
4	D	60	0	0	4	0
4	E	53	0	0	7	0
4	F	71	0	0	5	0
All	All	8217	0	8076	171	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 11.

The worst 5 of 171 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:E:157:LYS:HB2	1:E:157:LYS:NZ	1.46	1.17
1:A:121:LYS:HE3	4:C:967:HOH:O	1.47	1.15
4:A:971:HOH:O	1:B:163:VAL:HG12	1.59	1.01
1:C:131:ARG:HG2	1:C:131:ARG:HH11	1.22	1.00
1:E:126:GLU:CB	4:E:957:HOH:O	2.10	0.98

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)
4:A:942:HOH:O	4:B:971:HOH:O[2_555]	1.94	0.26

## 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	161/167 (96%)	154 (96%)	7 (4%)	0	100	100
1	B	161/167 (96%)	151 (94%)	10 (6%)	0	100	100
1	C	160/167 (96%)	151 (94%)	8 (5%)	1 (1%)	30	30
1	D	161/167 (96%)	155 (96%)	6 (4%)	0	100	100
1	E	161/167 (96%)	150 (93%)	11 (7%)	0	100	100
1	F	160/167 (96%)	154 (96%)	4 (2%)	2 (1%)	15	10
All	All	964/1002 (96%)	915 (95%)	46 (5%)	3 (0%)	46	52

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	28	PHE
1	C	28	PHE
1	F	46	VAL

### 5.3.2 Protein sidechains ⓘ

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	139/143 (97%)	134 (96%)	5 (4%)	42	51
1	B	139/143 (97%)	130 (94%)	9 (6%)	21	20
1	C	138/143 (96%)	130 (94%)	8 (6%)	25	25
1	D	139/143 (97%)	133 (96%)	6 (4%)	35	41
1	E	139/143 (97%)	131 (94%)	8 (6%)	25	25
1	F	138/143 (96%)	122 (88%)	16 (12%)	7	4
All	All	832/858 (97%)	780 (94%)	52 (6%)	22	21

5 of 52 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	12	ASP
1	E	47	LYS
1	F	149	GLU
1	D	50	ILE
1	D	137	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	20	ASN
1	D	98	ASN
1	F	17	GLN
1	C	98	ASN
1	E	105	ASN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

8 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$
3	ADN	A	901	-	16,21,21	1.40	2 (12%)	16,31,31	2.29	8 (50%)
3	ADN	B	902	-	16,21,21	1.38	2 (12%)	16,31,31	2.51	4 (25%)
2	PO4	C	502	-	4,4,4	0.76	0	6,6,6	0.27	0
3	ADN	C	903	-	16,21,21	1.63	2 (12%)	16,31,31	2.81	7 (43%)
2	PO4	D	501	-	4,4,4	1.18	0	6,6,6	0.29	0
3	ADN	D	904	-	16,21,21	1.59	3 (18%)	16,31,31	2.46	5 (31%)
3	ADN	E	905	-	16,21,21	1.28	2 (12%)	16,31,31	2.09	5 (31%)
3	ADN	F	906	-	16,21,21	1.14	2 (12%)	16,31,31	1.61	3 (18%)

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
3	ADN	A	901	-	-	0/2/22/22	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ADN	B	902	-	-	0/2/22/22	0/3/3/3
2	PO4	C	502	-	-	0/0/0/0	0/0/0/0
3	ADN	C	903	-	-	0/2/22/22	0/3/3/3
2	PO4	D	501	-	-	0/0/0/0	0/0/0/0
3	ADN	D	904	-	-	0/2/22/22	0/3/3/3
3	ADN	E	905	-	-	0/2/22/22	0/3/3/3
3	ADN	F	906	-	-	0/2/22/22	0/3/3/3

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	903	ADN	C3'-C4'	-2.66	1.45	1.53
3	F	906	ADN	C2-N3	2.09	1.35	1.32
3	E	905	ADN	C2-N3	2.11	1.35	1.32
3	A	901	ADN	O4'-C1'	2.44	1.44	1.41
3	D	904	ADN	C4-N3	2.63	1.39	1.35

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	904	ADN	N3-C2-N1	-7.78	122.94	128.89
3	C	903	ADN	C5'-C4'-C3'	-7.74	96.77	115.08
3	B	902	ADN	N3-C2-N1	-7.33	123.28	128.89
3	C	903	ADN	C4-C5-N7	-4.56	105.28	109.48
3	E	905	ADN	N3-C2-N1	-4.31	125.59	128.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	902	ADN	1	0
2	C	502	PO4	2	0
2	D	501	PO4	7	0
3	D	904	ADN	1	0
3	F	906	ADN	1	0

## 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	163/167 (97%)	-0.38	2 (1%) 81 83	8, 15, 22, 28	0
1	B	163/167 (97%)	-0.37	1 (0%) 90 91	9, 15, 22, 29	0
1	C	162/167 (97%)	-0.26	0 100 100	13, 20, 27, 31	0
1	D	163/167 (97%)	-0.34	0 100 100	11, 17, 24, 29	0
1	E	163/167 (97%)	-0.19	0 100 100	11, 19, 27, 30	0
1	F	162/167 (97%)	-0.22	2 (1%) 81 83	9, 15, 22, 27	0
All	All	976/1002 (97%)	-0.29	5 (0%) 91 92	8, 17, 25, 31	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	145	GLY	3.5
1	F	144	LEU	2.3
1	A	103	ILE	2.2
1	A	102	ALA	2.2
1	B	148	THR	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	PO4	C	502	5/5	0.94	0.30	5.72	54,55,56,56	5
2	PO4	D	501	5/5	0.96	0.18	1.12	27,31,32,34	5
3	ADN	E	905	19/19	0.94	0.10	-0.03	29,36,40,42	0
3	ADN	B	902	19/19	0.95	0.11	-0.11	33,37,41,46	0
3	ADN	A	901	19/19	0.96	0.10	-0.23	22,30,33,34	0
3	ADN	C	903	19/19	0.96	0.10	-0.24	22,25,35,37	0
3	ADN	D	904	19/19	0.94	0.10	-0.36	29,40,43,44	0
3	ADN	F	906	19/19	0.97	0.08	-1.07	24,26,30,30	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.