

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

#### Aug 15, 2023 – 09:47 PM EDT

PDB ID : 1THN

Title : Crystal Structures of the ADP and ATP bound forms of the Bacillus Anti-

sigma factor SpoIIAB in complex with the Anti-anti-sigma SpoIIAA: in-

hibitory complex with ADP, crystal form I

Authors: Masuda, S.; Murakami, K.S.; Wang, S.; Olson, C.A.; Donigan, J.; Leon, F.;

Darst, S.A.; Campbell, E.A.

Deposited on : 2004-06-01

Resolution : 2.50 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
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:

 $Mol Probity \quad : \quad 4.02b\text{--}467$ 

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS: 2.35

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) : 2.35

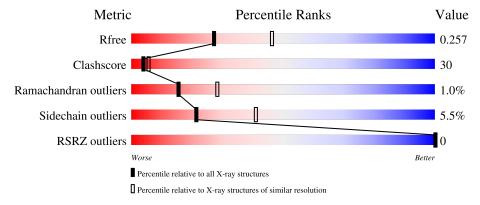


## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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						
1	A	145	45%	43%	6% 6%				
1	С	145	37%	53%	• 6%				
2	В	116	65%	30%					
2	D	116	50%	46%	• •				

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	DMF	A	201	-	-	X	-



## 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4004 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 Anti-sigma F factor.

$\mathbf{Mol}$	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	136	Total 1060	C 663	11	O 214	S 5	42	0	0
1	С	136	Total 1060	C 663		O 214	S 5	20	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	34	MET	THR	SEE REMARK 999	UNP O32727
A	137	HIS	-	insertion	UNP O32727
A	138	GLY	-	insertion	UNP O32727
A	139	ILE	-	insertion	UNP O32727
A	140	HIS	-	insertion	UNP O32727
A	141	HIS	-	insertion	UNP O32727
A	142	HIS	-	insertion	UNP O32727
A	143	HIS	-	insertion	UNP O32727
A	144	HIS	-	insertion	UNP O32727
A	145	HIS	-	insertion	UNP O32727
С	34	MET	THR	SEE REMARK 999	UNP O32727
С	137	HIS	-	insertion	UNP O32727
С	138	GLY	-	insertion	UNP O32727
С	139	ILE	-	insertion	UNP O32727
С	140	HIS	-	insertion	UNP O32727
С	141	HIS	-	insertion	UNP O32727
С	142	HIS	-	insertion	UNP O32727
С	143	HIS	-	insertion	UNP O32727
С	144	HIS	-	insertion	UNP O32727
С	145	HIS	_	insertion	UNP O32727

• Molecule 2 is a protein called Anti-sigma F factor antagonist.



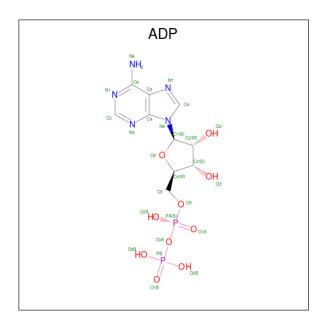
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	R	114	Total	С	N	О	S	10	0	0
	D	114	883	559	156	164	4	15		0
2	D	115	Total	С	N	О	S	10	0	0
	ע	115	889	562	157	166	4	10	0	

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	13	VAL	GLU	SEE REMARK 999	UNP O32726
В	29	GLU	ASN	SEE REMARK 999	UNP O32726
В	30	LEU	CYS	SEE REMARK 999	UNP O32726
В	31	ARG	MET	SEE REMARK 999	UNP O32726
В	32	GLU	ASN	SEE REMARK 999	UNP O32726
В	33	GLN	LYS	SEE REMARK 999	UNP O32726
В	34	VAL	CYS	SEE REMARK 999	UNP O32726
В	35	THR	ARG	SEE REMARK 999	UNP O32726
В	36	ASP	MET	SEE REMARK 999	UNP O32726
В	37	VAL	CYS	SEE REMARK 999	UNP O32726
В	40	ASN	LYS	SEE REMARK 999	UNP O32726
D	13	VAL	GLU	SEE REMARK 999	UNP O32726
D	29	GLU	ASN	SEE REMARK 999	UNP O32726
D	30	LEU	CYS	SEE REMARK 999	UNP O32726
D	31	ARG	MET	SEE REMARK 999	UNP O32726
D	32	GLU	ASN	SEE REMARK 999	UNP O32726
D	33	GLN	LYS	SEE REMARK 999	UNP O32726
D	34	VAL	CYS	SEE REMARK 999	UNP O32726
D	35	THR	ARG	SEE REMARK 999	UNP O32726
D	36	ASP	MET	SEE REMARK 999	UNP O32726
D	37	VAL	CYS	SEE REMARK 999	UNP O32726
D	40	ASN	LYS	SEE REMARK 999	UNP O32726

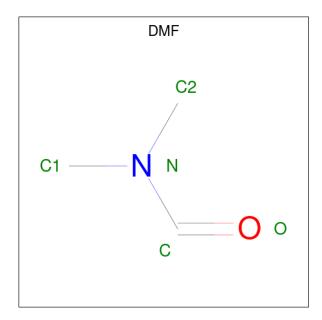
• Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
2	Λ	1	Total	С	N	О	Р	0	0	
3	3 A	1	27	10	5	10	2	U		
9	C	1	Total	С	N	О	Р	0	0	
3	3  C	1	27	10	5	10	2	U		

 $\bullet$  Molecule 4 is DIMETHYLFORMAMIDE (three-letter code: DMF) (formula:  $\mathrm{C_3H_7NO}).$ 



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 5	C 3	N 1	O 1	0	0

 $\bullet$  Molecule 5 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	22	Total O 22 22	0	0
5	В	10	Total O 10 10	0	0
5	С	13	Total O 13 13	0	0
5	D	8	Total O 8 8	0	0



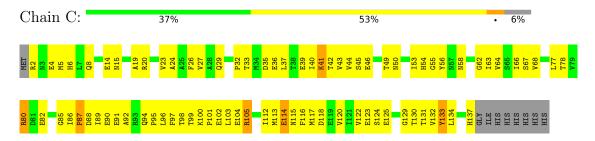
## 3 Residue-property plots (i)

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.

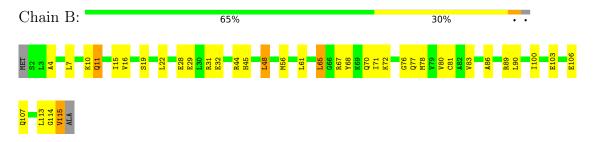
• Molecule 1: Anti-sigma F factor



• Molecule 1: Anti-sigma F factor



• Molecule 2: Anti-sigma F factor antagonist



• Molecule 2: Anti-sigma F factor antagonist









# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41	Depositor
Cell constants	49.06Å 49.06Å 265.67Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	30.00 - 2.50	Depositor
rtesolution (A)	27.50 - 2.37	EDS
% Data completeness	98.1 (30.00-2.50)	Depositor
(in resolution range)	97.5 (27.50-2.37)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.03	Depositor
$< I/\sigma(I) > 1$	$9.02 \; (at \; 2.36 \text{Å})$	Xtriage
Refinement program	CNS	Depositor
$R, R_{free}$	0.224 , $0.265$	Depositor
It, Itfree	0.216 , $0.257$	DCC
$R_{free}$ test set	1118 reflections $(4.53\%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.9	Xtriage
Anisotropy	0.485	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.31, 24.8	EDS
L-test for twinning <sup>2</sup>	$< L >=0.50, < L^2>=0.34$	Xtriage
Estimated twinning fraction	0.499 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4004	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.36% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



<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: ADP, DMF

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			
IVIOI	Chain	RMSZ	77 1 1		# Z  > 5		
1	A	0.45	0/1076	0.75	0/1459		
1	С	0.43	0/1076	0.69	0/1459		
2	В	0.46	0/891	0.77	1/1200 (0.1%)		
2	D	0.45	0/897	0.72	0/1207		
All	All	0.44	0/3940	0.73	1/5325 (0.0%)		

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	48	LEU	CA-CB-CG	8.48	134.81	115.30

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	1060	0	1041	75	0
1	С	1060	0	1041	77	1
2	В	883	0	918	29	1
2	D	889	0	923	63	0
3	A	27	0	12	2	0
3	С	27	0	12	1	0

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	J	1	1

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	5	0	7	5	0
5	A	22	0	0	1	0
5	В	10	0	0	1	0
5	С	13	0	0	0	0
5	D	8	0	0	2	0
All	All	4004	0	3954	233	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 30.

The worst 5 of 233 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
2:D:101:ARG:HH12	2:D:112:ALA:HB1	1.05	1.19
1:A:45:SER:O	1:A:49:THR:HG22	1.55	1.06
2:D:5:ILE:HD12	2:D:33:GLN:NE2	1.76	1.00
1:C:85:GLY:HA2	1:C:130:THR:HG23	1.41	1.00
1:A:29:GLN:HB3	4:A:201:DMF:H11	1.42	0.99

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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned} \operatorname{Clash} \ \operatorname{overlap}\ (\mathring{\mathbf{A}}) \end{aligned}$
2:B:103:GLU:OE2	1:C:90:GLU:OE1[4_564]	2.12	0.08

### 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	P	erce	entiles
1	A	134/145~(92%)	123 (92%)	10 (8%)	1 (1%)		22	39
1	С	134/145 (92%)	115 (86%)	17 (13%)	2 (2%)		10	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perc	entiles
2	В	112/116 (97%)	103 (92%)	8 (7%)	1 (1%)	17	31
2	D	113/116 (97%)	105 (93%)	7 (6%)	1 (1%)	17	31
All	All	493/522 (94%)	446 (90%)	42 (8%)	5 (1%)	15	28

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	В	11	GLN
2	D	55	PHE
1	A	3	ASN
1	С	55	GLY
1	С	87	PRO

#### 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	120/128 (94%)	112 (93%)	8 (7%)	16 31
1	С	120/128 (94%)	113 (94%)	7 (6%)	20 38
2	В	97/98 (99%)	92 (95%)	5 (5%)	23 44
2	D	97/98~(99%)	93 (96%)	4 (4%)	30 55
All	All	$434/452 \ (96\%)$	410 (94%)	24 (6%)	21 41

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	С	41	LYS
1	С	114	GLU
1	С	105	ARG
1	С	115	ASN
1	A	74	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:



Mol	Chain	Res	Type
1	A	115	ASN
2	В	107	GLN
2	D	33	GLN
1	С	58	ASN
1	A	94	GLN

#### 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)

3 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	Tuno	Chain	Res	Link	Bo	nd leng	ths	В	ond ang	les
MIOI	Iol Type Chain Res		nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	ADP	С	201	-	24,29,29	1.37	2 (8%)	29,45,45	0.88	0
3	ADP	A	200	-	24,29,29	1.46	5 (20%)	29,45,45	0.95	1 (3%)
4	DMF	A	201	-	4,4,4	0.71	0	4,4,4	0.36	0

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	ADP	С	201	-	-	0/12/32/32	0/3/3/3
3	ADP	A	200	_	-	0/12/32/32	0/3/3/3
4	DMF	A	201	-	-	2/2/2/2	-

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
3	С	201	ADP	C8-N7	-3.36	1.28	1.34
3	A	200	ADP	C8-N7	-2.98	1.29	1.34
3	A	200	ADP	O4'-C1'	2.80	1.45	1.41
3	С	201	ADP	O4'-C1'	2.67	1.44	1.41
3	A	200	ADP	C2'-C1'	2.23	1.57	1.53

#### All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
3	A	200	ADP	C5-C6-N6	2.16	123.64	120.35

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	201	DMF	O-C-N-C2
4	A	201	DMF	O-C-N-C1

There are no ring outliers.

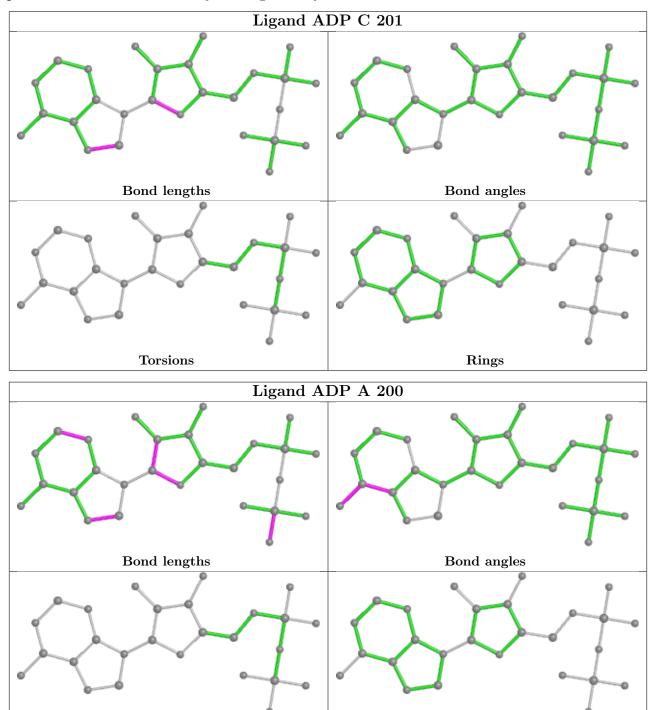
3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	С	201	ADP	1	0
3	A	200	ADP	2	0
4	A	201	DMF	5	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.

**Torsions** 



Rings

# 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 $>$	#	∤RSR	$\mathbf{Z}>2$	$OWAB(A^2)$	Q<0.9
1	A	136/145~(93%)	-0.44	0	100	100	25, 39, 54, 61	12 (8%)
1	С	136/145 (93%)	-0.39	0	100	100	27, 41, 52, 56	5 (3%)
2	В	114/116 (98%)	-0.62	0	100	100	17, 32, 43, 47	6 (5%)
2	D	115/116 (99%)	-0.66	0	100	100	13, 32, 48, 54	2 (1%)
All	All	501/522~(95%)	-0.52	0	100	100	13, 36, 51, 61	25 (4%)

There are no RSRZ outliers to report.

### 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.

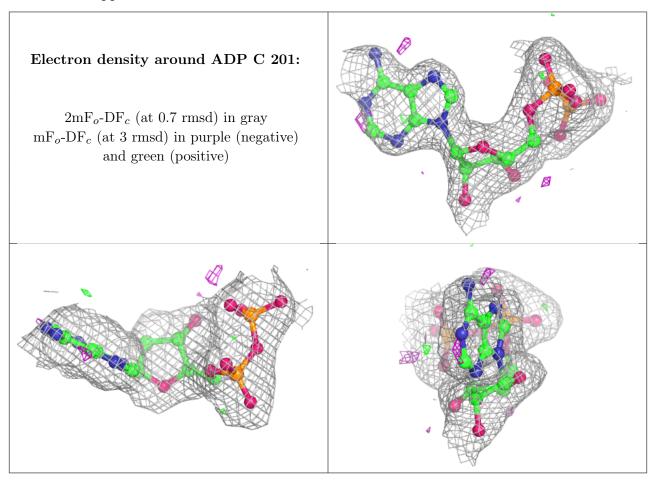
### 6.4 Ligands (i)

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.

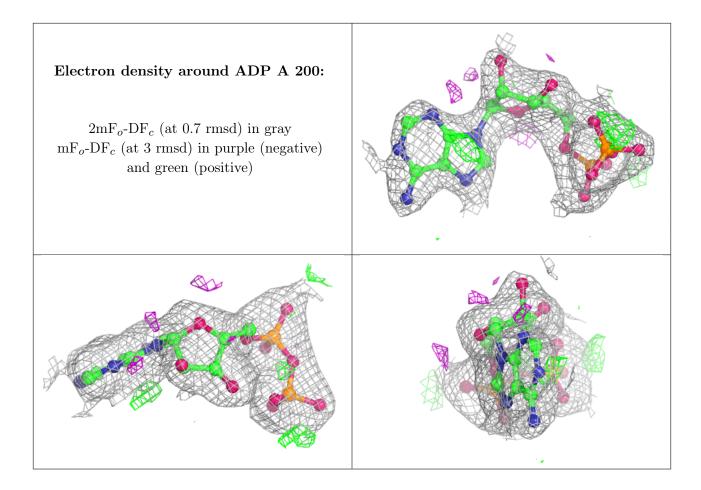
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
4	DMF	A	201	5/5	0.82	0.25	42,45,47,47	0
3	ADP	С	201	27/27	0.96	0.15	36,49,59,61	0
3	ADP	A	200	27/27	0.96	0.15	29,43,54,55	0



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.







## 6.5 Other polymers (i)

There are no such residues in this entry.

