

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

#### Feb 6, 2023 – 12:16 pm GMT

PDB ID	:	7R30
Title	:	Carbon regulatory PII-like protein SbtB from Synechocystis sp. 6803 in com-
		plex with ADP and AMP resulting from ADP soak
Authors	:	Selim, K.A.; Albrecht, R.; Hartmann, M.D.
Deposited on		
Resolution	:	1.90  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 (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

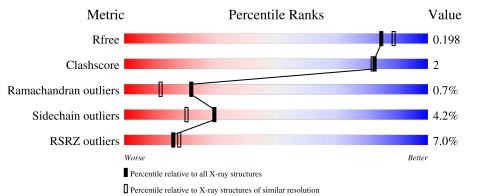
The following versions of software and data (see references (1)) were used in the production of this report:

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 1.90 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	А	120	8%	9%		18%
1	В	120	5% 81%		•	15%
1	С	120	4%	8%	•	15%



# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2492 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.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	98	Total	С	Ν	Ο	$\mathbf{S}$	0	2	0
	Π	30	754	483	121	145	5	0		0
1	В	102	Total	С	Ν	Ο	$\mathbf{S}$	0	1	0
	D	102	782	501	126	150	5	0		
1	C	102	Total	С	Ν	0	S	0	1	0
	U	0 102	787	502	130	150	5		1	0

• Molecule 1 is a protein called Membrane-associated protein slr1513.

Chain	Residue	Modelled	Actual	Comment	Reference
А	111	SER	-	expression tag	UNP P73954
А	112	ALA	-	expression tag	UNP P73954
А	113	TRP	-	expression tag	UNP P73954
А	114	SER	-	expression tag	UNP P73954
А	115	HIS	-	expression tag	UNP P73954
A	116	PRO	-	expression tag	UNP P73954
А	117	GLN	-	expression tag	UNP P73954
А	118	PHE	-	expression tag	UNP P73954
А	119	GLU	-	expression tag	UNP P73954
А	120	LYS	-	expression tag	UNP P73954
В	111	SER	-	expression tag	UNP P73954
В	112	ALA	-	expression tag	UNP P73954
В	113	TRP	-	expression tag	UNP P73954
В	114	SER	-	expression tag	UNP P73954
В	115	HIS	-	expression tag	UNP P73954
В	116	PRO	-	expression tag	UNP P73954
В	117	GLN	-	expression tag	UNP P73954
В	118	PHE	-	expression tag	UNP P73954
В	119	GLU	-	expression tag	UNP P73954
В	120	LYS	-	expression tag	UNP P73954
С	111	SER	-	expression tag	UNP P73954
С	112	ALA	-	expression tag	UNP P73954
С	113	TRP	-	expression tag	UNP P73954
				$\alpha$ $\cdot$ 1	on nort nado

There are 30 discrepancies between the modelled and reference sequences:

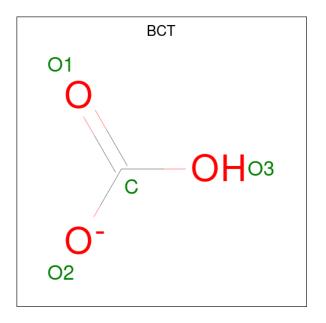
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Chain	Residue	Modelled	Actual	Comment	Reference
С	114	SER	-	expression tag	UNP P73954
С	115	HIS	-	expression tag	UNP P73954
С	116	PRO	-	expression tag	UNP P73954
С	117	GLN	-	expression tag	UNP P73954
С	118	PHE	-	expression tag	UNP P73954
С	119	GLU	-	expression tag	UNP P73954
C	120	LYS	-	expression tag	UNP P73954

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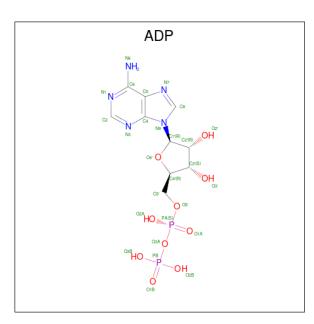
• Molecule 2 is BICARBONATE ION (three-letter code: BCT) (formula: CHO<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	А	1	Total 4	С 1	O 3	0	0

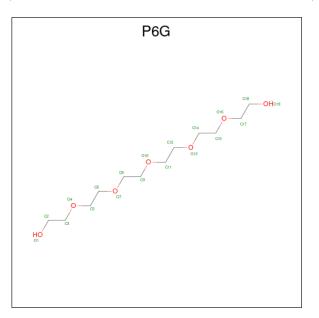
• Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
3	3 B	1	Total	С	Ν	0	Р	0	0	
0		L	23	10	5	7	1	0	0	
3	В	1	Total	С	Ν	Ο	Р	0	0	
0	9 D	1	23	10	5	7	1	0	0	
3	С	C 1	Total	С	N	Ō	Р	0	0	
3			27	10	5	10	2	0	U	

• Molecule 4 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula:  $C_{12}H_{26}O_7$ ) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	С	1	Total 19	C 12	0 7	0	0

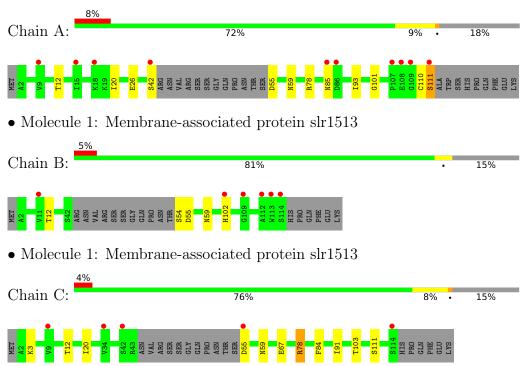
• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	14	Total O 14 14	0	0
5	В	34	Total O 34 34	0	0
5	С	25	TotalO2525	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.



 $\bullet$  Molecule 1: Membrane-associated protein slr1513



# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants	63.64Å 63.64Å 82.21Å	Deperitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	32.95 - 1.90	Depositor
Resolution (A)	32.95 - 1.90	EDS
% Data completeness	100.0 (32.95-1.90)	Depositor
(in resolution range)	100.0 (32.95 - 1.90)	EDS
R <sub>merge</sub>	0.06	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.02 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
D D	0.171 , $0.195$	Depositor
$R, R_{free}$	0.179 , $0.198$	DCC
$R_{free}$ test set	1467 reflections $(4.98\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	44.3	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.36, $49.0$	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.49, < L^2 > = 0.32$	Xtriage
	0.013 for -h,-k,l	
Estimated twinning fraction	0.050 for h,-h-k,-l	Xtriage
	0.029 for -k,-h,-l	
$\mathbf{F}_o, \mathbf{F}_c$ correlation	0.97	EDS
Total number of atoms	2492	wwPDB-VP
Average B, all atoms $(Å^2)$	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.60% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<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: BCT, ADP, P6G

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		
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.88	0/766	0.89	0/1029	
1	В	1.02	0/793	0.93	0/1067	
1	С	1.00	0/798	0.98	0/1073	
All	All	0.97	0/2357	0.94	0/3169	

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	А	754	0	769	5	0
1	В	782	0	789	1	0
1	С	787	0	792	5	0
2	А	4	0	0	0	0
3	В	46	0	24	0	0
3	С	27	0	12	0	0
4	С	19	0	26	1	0
5	А	14	0	0	0	0
5	В	34	0	0	0	0
5	С	25	0	0	1	0
All	All	2492	0	2412	12	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 2.

All (12) 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:C:12:THR:O	1:C:59[A]:ASN:HB2	1.84	0.75
1:A:12:THR:O	1:A:59:ASN:HB2	1.96	0.65
4:C:202:P6G:H91	5:C:321:HOH:O	2.05	0.56
1:B:12:THR:O	1:B:59:ASN:HB2	2.08	0.53
1:A:26:GLU:OE1	1:A:78:ARG:NH2	2.44	0.49
1:C:12:THR:HG21	1:C:20:ILE:CD1	2.47	0.44
1:A:110:CYS:O	1:A:111:SER:HB2	2.18	0.44
1:A:12:THR:HG21	1:A:20:ILE:CD1	2.49	0.43
1:C:84:PHE:HE2	1:C:91:ILE:HG13	1.84	0.42
1:A:93:ILE:HD13	1:A:93:ILE:HG21	1.90	0.42
1:C:78:ARG:HE	1:C:78:ARG:HB2	1.60	0.41
1:C:3:LYS:CE	1:C:67:GLU:HG3	2.52	0.40

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	А	96/120~(80%)	95~(99%)	0	1 (1%)	15 6
1	В	99/120~(82%)	97~(98%)	2(2%)	0	100 100
1	С	99/120~(82%)	95~(96%)	3~(3%)	1 (1%)	15 6
All	All	294/360~(82%)	287~(98%)	5(2%)	2(1%)	22 12

All (2) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	С	111	SER
1	А	101	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	А	80/99~(81%)	76~(95%)	4(5%)	24 15
1	В	82/99~(83%)	79~(96%)	3~(4%)	34 25
1	С	82/99~(83%)	79~(96%)	3~(4%)	34 25
All	All	244/297~(82%)	234 (96%)	10 (4%)	30 21

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	42	SER
1	А	55	ASP
1	А	85	ASN
1	А	111	SER
1	В	54	SER
1	В	55	ASP
1	В	102	HIS
1	С	55	ASP
1	С	78	ARG
1	С	103	THR

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

Mol	Chain	Res	Type
1	А	36	ASN
1	А	102	HIS



#### 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)

5 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	Bo	ond leng	ths	В	ond ang	les
	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
3	ADP	В	202	-	22,25,29	1.10	2 (9%)	$25,\!38,\!45$	1.57	6 (24%)
3	ADP	В	201	-	22,25,29	0.88	0	$25,\!38,\!45$	1.59	6 (24%)
3	ADP	С	201	-	24,29,29	1.34	4 (16%)	29,45,45	1.68	7 (24%)
4	P6G	С	202	-	18,18,18	0.79	0	17,17,17	1.31	2 (11%)
2	BCT	А	201	-	2,3,3	0.71	0	2,3,3	1.37	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	-	-	1/12/32/32	0/3/3/3
3	ADP	В	202	-	-	1/6/26/32	0/3/3/3
3	ADP	В	201	-	-	0/6/26/32	0/3/3/3
4	P6G	С	202	-	-	9/16/16/16	-



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	В	202	ADP	PA-O3A	2.86	1.65	1.54
3	С	201	ADP	C2-N3	2.73	1.36	1.32
3	С	201	ADP	C4-N3	-2.42	1.32	1.35
3	С	201	ADP	O2'-C2'	2.31	1.48	1.43
3	С	201	ADP	C5-C4	2.18	1.46	1.40
3	В	202	ADP	PA-O1A	2.06	1.57	1.50

All (6) bond length outliers are listed below:

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	В	202	ADP	N3-C2-N1	-3.68	122.92	128.68
3	В	201	ADP	N3-C2-N1	-3.45	123.28	128.68
3	С	201	ADP	N3-C2-N1	-3.22	123.64	128.68
3	С	201	ADP	N6-C6-N1	3.18	125.17	118.57
3	С	201	ADP	C3'-C2'-C1'	2.87	105.31	100.98
3	В	201	ADP	O2A-PA-O1A	2.85	121.83	110.68
3	В	201	ADP	C1'-N9-C4	-2.84	121.64	126.64
3	В	201	ADP	C2-N1-C6	2.74	123.44	118.75
3	В	201	ADP	N6-C6-N1	2.68	124.14	118.57
3	В	202	ADP	O2'-C2'-C1'	-2.61	101.22	110.85
3	С	201	ADP	O3B-PB-O1B	2.50	120.46	110.68
4	С	202	P6G	C11-O10-C9	2.48	124.06	113.29
3	В	201	ADP	O2A-PA-O5'	-2.47	100.17	106.73
3	В	202	ADP	C3'-C2'-C1'	2.40	104.59	100.98
3	В	202	ADP	C4-C5-N7	-2.31	106.99	109.40
3	С	201	ADP	C5-C6-N6	-2.30	116.86	120.35
3	С	201	ADP	O3B-PB-O2B	2.25	116.25	107.64
3	С	201	ADP	C2'-C3'-C4'	-2.23	98.31	102.64
3	В	202	ADP	O2A-PA-O5'	-2.09	101.17	106.73
4	С	202	P6G	O13-C12-C11	2.08	119.75	110.39
3	В	202	ADP	C1'-N9-C4	-2.00	123.12	126.64

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	С	202	P6G	O16-C17-C18-O19
4	С	202	P6G	O13-C14-C15-O16
4	С	202	P6G	O10-C11-C12-O13
4	С	202	P6G	O4-C5-C6-O7
4	С	202	P6G	O7-C8-C9-O10

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Mol	Chain	Res	Type	Atoms
4	С	202	P6G	C6-C5-O4-C3
4	С	202	P6G	C18-C17-O16-C15
4	С	202	P6G	C5-C6-O7-C8
4	С	202	P6G	С12-С11-О10-С9
3	В	202	ADP	C5'-O5'-PA-O1A
3	С	201	ADP	C5'-O5'-PA-O1A

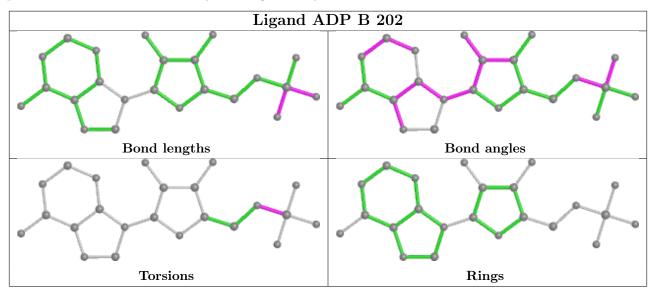
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There are no ring outliers.

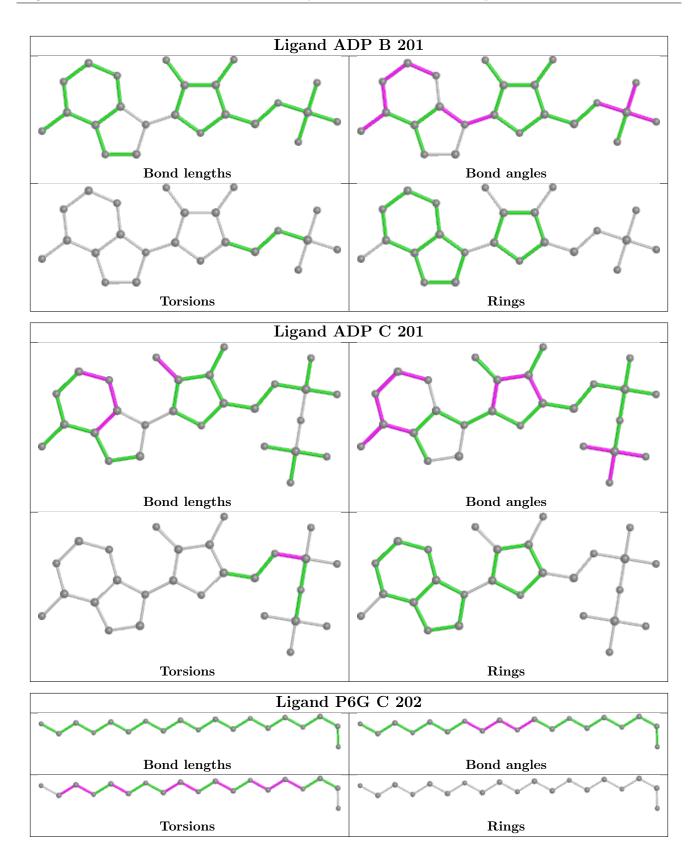
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	202	P6G	1	0

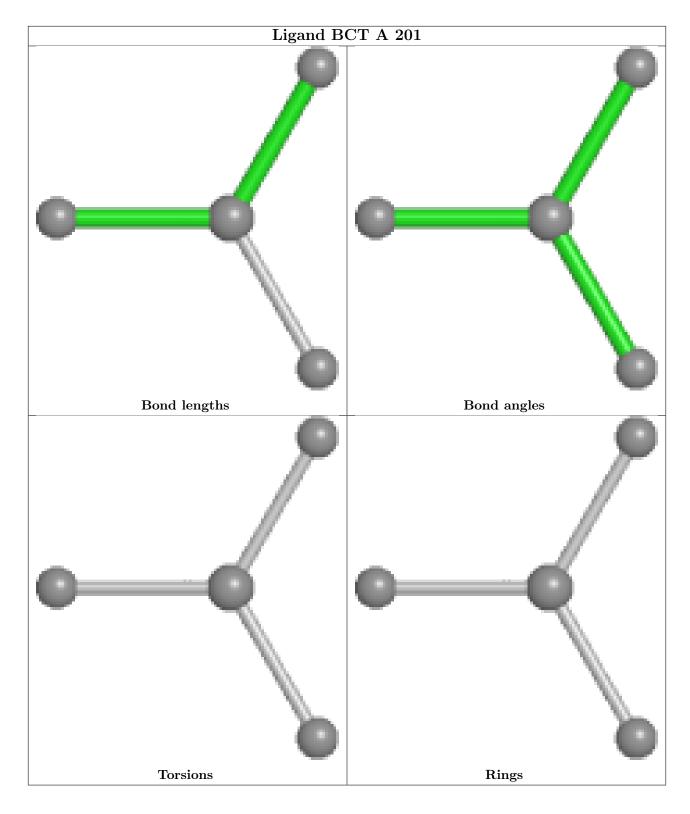
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.











## 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,  $95^{th}$  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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	98/120~(81%)	0.59	10 (10%) 6 8	37, 51, 74, 84	0
1	В	102/120~(85%)	0.34	6 (5%) 22 25	32, 46, 82, 115	0
1	С	102/120~(85%)	0.22	5 (4%) 29 33	34, 46, 70, 94	0
All	All	302/360~(83%)	0.38	21 (6%) 16 18	32, 48, 77, 115	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	109	GLY	4.3
1	С	55	ASP	4.2
1	В	113	TRP	3.5
1	В	112	ALA	3.5
1	А	86	ASP	3.4
1	А	107	PRO	3.2
1	В	109	GLY	3.2
1	А	15	ILE	3.1
1	А	9	VAL	2.9
1	В	102	HIS	2.6
1	А	108	GLU	2.6
1	В	114	SER	2.5
1	А	85	ASN	2.4
1	А	42	SER	2.4
1	А	111	SER	2.3
1	С	114	SER	2.3
1	С	34	VAL	2.2
1	А	18	LYS	2.2
1	С	42	SER	2.1
1	В	11	VAL	2.1
1	С	9	VAL	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.

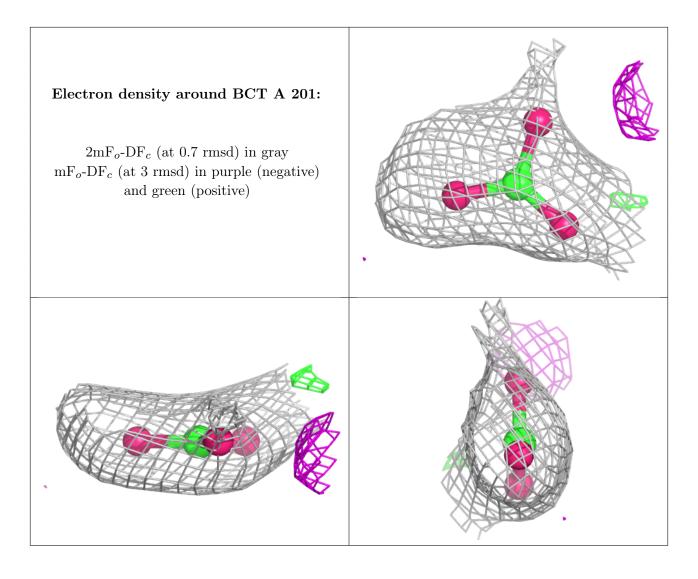
### 6.4 Ligands (i)

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.

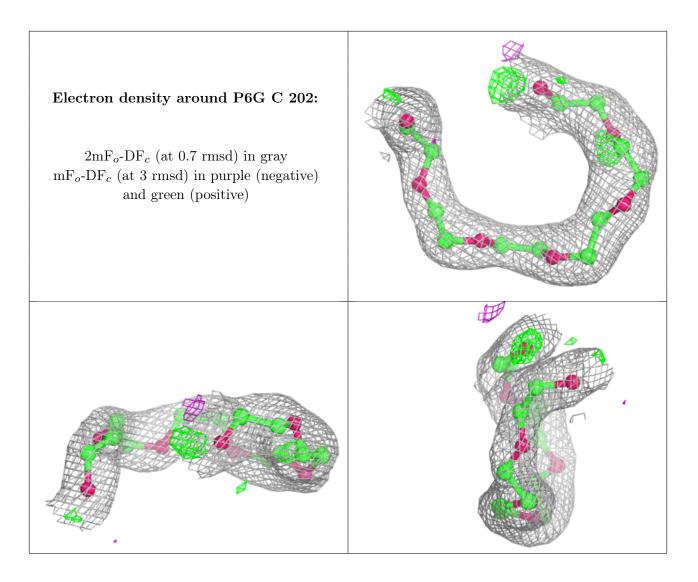
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
2	BCT	А	201	4/4	0.76	0.18	$62,\!68,\!73,\!80$	0
4	P6G	С	202	19/19	0.88	0.23	45,59,73,74	0
3	ADP	С	201	27/27	0.95	0.08	$36,\!40,\!56,\!58$	0
3	ADP	В	201	23/27	0.96	0.07	38,44,61,65	0
3	ADP	В	202	23/27	0.96	0.09	34,37,54,61	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.

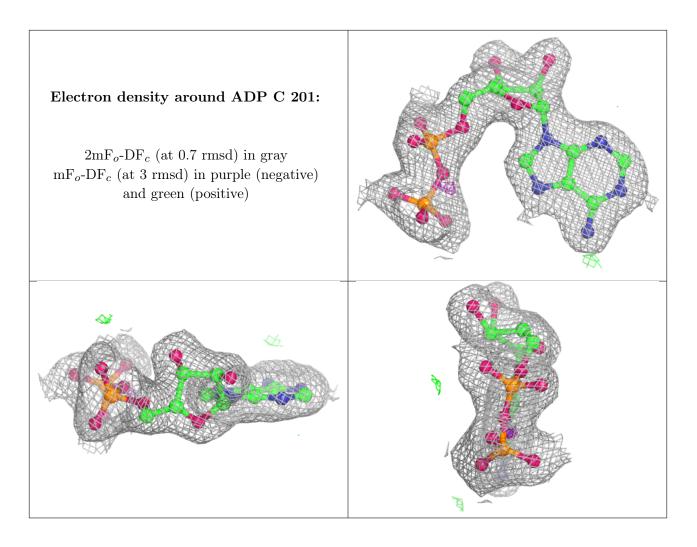




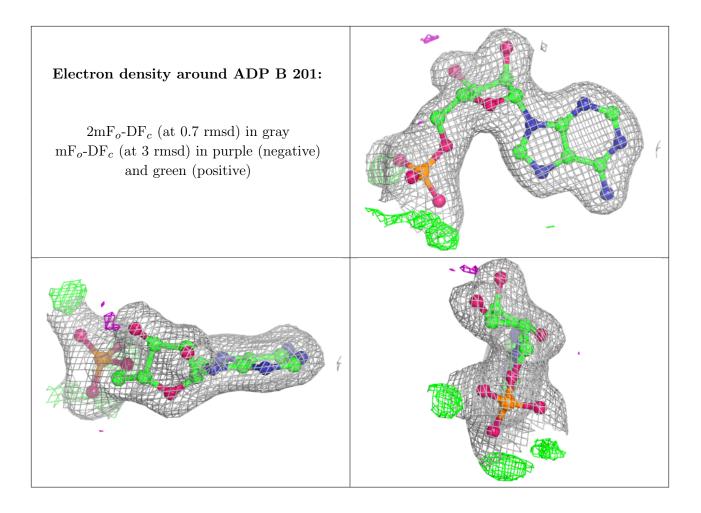




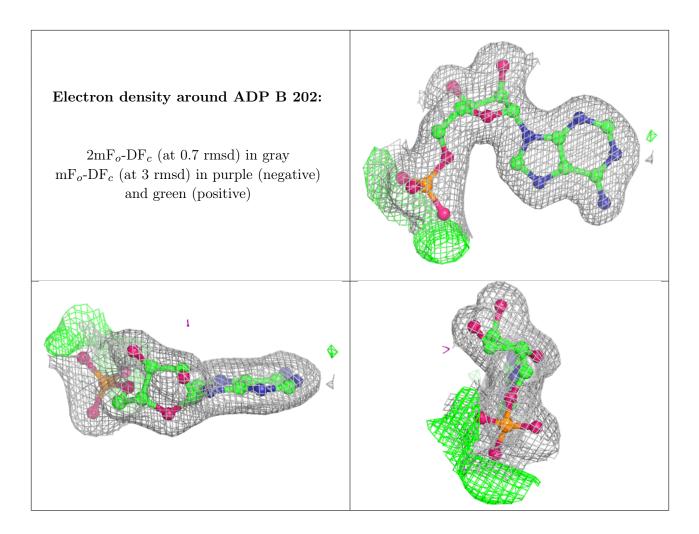












## 6.5 Other polymers (i)

There are no such residues in this entry.

