

Full wwPDB X-ray Structure Validation Report (i)

Sep 6, 2023 – 02:38 PM EDT

:	4FRN
:	Crystal structure of the cobalamin riboswitch regulatory element
:	Reyes, F.E.; Johnson, J.E.; Polaski, J.T.; Batey, R.T.
	2012-06-26
:	3.43 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:

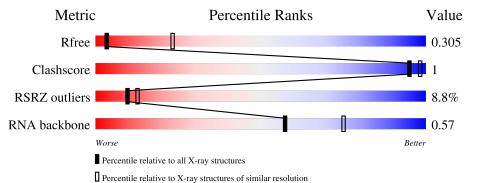
Xtriage (Phenix) EDS buster-report	: : :	4.02b-467 1.8.5 (274361), CSD as541be (2020) 1.13 2.35 1.1.7 (2018) 20191225.v01 (using entries in the PDB archive December 25th 2019)
	: :	0

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 3.43 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	1278 (3.50-3.38)
Clashscore	141614	1361 (3.50-3.38)
RSRZ outliers	127900	1192 (3.50-3.38)
RNA backbone	3102	1024 (3.92-2.96)

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	102	73%	24%					
1	В	102	8%	23%	•				

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	I2A	А	201	Х	-	-	-



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Mo	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	I2A	В	201	X	-	-	-



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2 Entry composition (i)

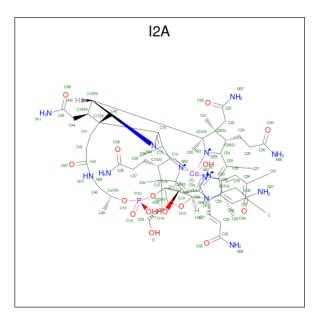
There are 3 unique types of molecules in this entry. The entry contains 4560 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 RNA chain called Cobalamin riboswitch aptamer domain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Λ	102	Total	С	Ν	0	Р	0	0	0
	Л	102	2182	976	400	704	102	0	0	
1	В	102	Total	С	Ν	0	Р	0	0	0
	D	102	2182	976	400	704	102	0	0	0

• Molecule 2 is Hydroxocobalamin (three-letter code: I2A) (formula: $C_{62}H_{88}CoN_{13}O_{15}P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
9	Λ	1	Total	С	Co	Ν	Ο	Р	0	0
	A	1	92	62	1	13	15	1	0	0
0	р	1	Total	С	Co	Ν	Ο	Р	0	0
	D	1	92	62	1	13	15	1	0	0

• Molecule 3 is BARIUM ION (three-letter code: BA) (formula: Ba).



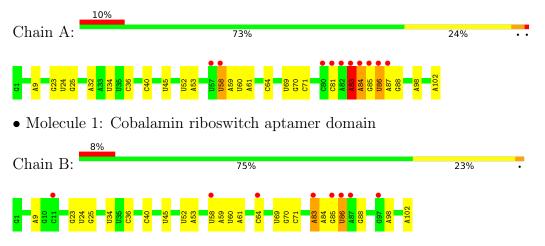
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	6	Total Ba 6 6	0	0
3	В	6	Total Ba 6 6	0	0



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: Cobalamin riboswitch aptamer domain





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	55.60Å 81.83Å 147.72Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.83 - 3.43	Depositor
Resolution (A)	54.83 - 3.43	EDS
% Data completeness	99.0(54.83-3.43)	Depositor
(in resolution range)	99.1(54.83-3.43)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	0.08	Depositor
$< I/\sigma(I) > 1$	$3.82 (at 3.40 \text{\AA})$	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
B B.	0.251 , 0.273	Depositor
R, R_{free}	0.274 , 0.305	DCC
R_{free} test set	450 reflections $(4.77%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	77.5	Xtriage
Anisotropy	0.964	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.24 , 19.7	EDS
L-test for twinning ²	$ < L >=0.44, < L^2>=0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4560	wwPDB-VP
Average B, all atoms $(Å^2)$	101.0	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 27.91 % 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 2.0215e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

²Theoretical 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.



¹Intensities 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: BA, I2A

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	Bo	nd lengths	Bond angles		
	Unam	RMSZ	RMSZ	# Z > 5		
1	А	0.92	2/2443~(0.1%)	0.79	0/3806	
1	В	0.92	1/2443~(0.0%)	0.79	0/3806	
All	All	0.92	3/4886~(0.1%)	0.79	0/7612	

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
1	В	83	А	C3'-O3'	5.89	1.50	1.42
1	А	86	U	C3'-O3'	5.12	1.49	1.42
1	А	83	А	C3'-O3'	5.04	1.49	1.42

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	2182	0	1101	3	0
1	В	2182	0	1101	2	0
2	А	92	0	86	2	0
2	В	92	0	86	1	0
3	А	6	0	0	0	0
3	В	6	0	0	0	0



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4560	0	2374	8	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 1.

All (8) 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:B:85:G:H3'	1:B:86:U:H5"	1.69	0.74
1:A:52:U:H5"	1:A:53:A:H5'	1.85	0.57
1:B:52:U:H5"	1:B:53:A:H5'	1.86	0.57
2:A:201:I2A:H84	2:A:201:I2A:H80	1.90	0.54
2:B:201:I2A:H80	2:B:201:I2A:H84	1.91	0.53
1:A:83:A:H4'	1:A:84:A:OP2	2.10	0.51
2:A:201:I2A:H57	2:A:201:I2A:H66	1.86	0.40
1:A:32:A:H1'	1:A:58:U:H2'	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein molecules in this entry.

5.3.2 Protein sidechains (i)

There are no protein molecules in this entry.

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	А	101/102~(99%)	25 (24%)	2 (1%)
1	В	101/102~(99%)	22 (21%)	1 (0%)
All	All	202/204~(99%)	47 (23%)	3 (1%)

All (47) RNA backbone outliers are listed below:



Mol	Chain	Res	Type
1	А	9	А
1	А	23	G
1	А	24	U
1	А	24 25	G
	А	34 36	U
1	А	36	С
1	А	40	С
1	А	45	U
1	А	45 58 59	U
1	А	59	А
1	А	60	U
1	А	61	А
1	А	64	С
1	A B B B B B	60 61 64 69 70 71 81 83 84	Type A G U G U C U A U A U A U A C U A C Q C A C Q A G U A G U A G U A G A G A G A A G U A G U A G U A G U
1	А	70	G
1	А	71	С
1	А	81	С
1 1 1 1	А	83	А
1	А	84	А
1	А	85 86	G
1	А	86	U
1	А	87	А
1	А	88	G
1	А	98	А
1	А	102	А
1	В	9	А
1	В	23	G
1	В	23 24	U
1	В	25	G
1	В	34	U
1	В	36	С
1	В	40	U C C U
1	В	45	U
1	В	58	U
1	В	59	A
1	В	60	U
1	В	61	A
1	В	64	С
1	В	69	U
1	В	70	G
1	В	71	С
1	В	83	U A U A C U G C A
1	В	84	А
L			ext page



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Mol	Chain	Res	Type
1	В	86	U
1	В	88	G
1	В	98	А
1	В	102	А

All (3)	RNA	pucker	outliers	are	listed	below:
· · · · · (\mathbf{U}_{j}	101111	pucker	outifiers	arc	moucu	DC10W.

Mol	Chain	Res	Type
1	А	83	А
1	А	86	U
1	В	83	А

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)

Of 14 ligands modelled in this entry, 12 are monoatomic - leaving 2 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	Turne	Chain Res		Link	Boi	nd lengt	hs	Boi	nd angle	s
IVIOI	Type	Chain	Res	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
2	I2A	В	201	-	93,103,103	1.54	6 (6%)	133,177,177	1.24	10 (7%)
2	I2A	А	201	-	93,103,103	1.55	6 (6%)	133,177,177	1.27	10 (7%)

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.



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	I2A	В	201	-	1/1/42/49	8/52/277/277	-
2	I2A	А	201	-	1/1/42/49	12/52/277/277	-

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

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
2	А	201	I2A	C32-C31	9.45	1.54	1.32
2	В	201	I2A	C32-C31	9.43	1.54	1.32
2	В	201	I2A	C35-C12	-6.73	1.39	1.54
2	А	201	I2A	C35-C12	-6.69	1.39	1.54
2	В	201	I2A	C33-N08	-3.33	1.24	1.33
2	А	201	I2A	C33-N08	-3.32	1.24	1.33
2	А	201	I2A	O05-C33	2.99	1.32	1.24
2	В	201	I2A	O05-C33	2.97	1.32	1.24
2	А	201	I2A	C08-C31	2.80	1.54	1.50
2	В	201	I2A	C08-C31	2.72	1.54	1.50
2	А	201	I2A	O03-C26	2.10	1.30	1.24
2	В	201	I2A	O03-C26	2.09	1.30	1.24

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	201	I2A	C34-C12-C35	-4.97	100.96	109.35
2	А	201	I2A	C36-C13-C12	4.91	130.38	116.63
2	В	201	I2A	C34-C12-C35	-4.70	101.40	109.35
2	В	201	I2A	C36-C13-C12	4.70	129.79	116.63
2	В	201	I2A	C12-C11-N03	-3.43	107.73	111.50
2	А	201	I2A	C10-C09-N02	-3.20	122.05	125.73
2	А	201	I2A	C12-C11-N03	-3.00	108.21	111.50
2	В	201	I2A	C10-C09-N02	-2.93	122.35	125.73
2	А	201	I2A	C12-C13-C14	-2.82	98.14	101.86
2	В	201	I2A	C42-C41-C17	2.70	120.72	115.52
2	А	201	I2A	C01-C19-N04	2.66	110.55	106.33
2	В	201	I2A	C01-C19-N04	2.61	110.46	106.33
2	А	201	I2A	C42-C41-C17	2.60	120.52	115.52
2	А	201	I2A	C12-C11-C10	2.50	125.83	123.54
2	А	201	I2A	C24-C03-C02	2.22	123.79	119.09
2	В	201	I2A	C05-C06-N02	-2.20	120.51	123.86
2	В	201	I2A	C12-C11-C10	2.18	125.53	123.54
2	В	201	I2A	C12-C13-C14	-2.15	99.02	101.86
2	В	201	I2A	C24-C03-C02	2.13	123.60	119.09



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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	201	I2A	C05-C06-N02	-2.11	120.65	123.86

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	А	201	I2A	N04
2	В	201	I2A	N04

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	А	201	I2A	C08-C31-C32-C33
2	А	201	I2A	C07-C08-C31-C32
2	А	201	I2A	C09-C08-C31-C32
2	В	201	I2A	C08-C31-C32-C33
2	В	201	I2A	C07-C08-C31-C32
2	В	201	I2A	C09-C08-C31-C32
2	В	201	I2A	C31-C32-C33-N08
2	В	201	I2A	C31-C32-C33-O05
2	А	201	I2A	O13-C52-C53-O
2	А	201	I2A	C51-C52-C53-O
2	А	201	I2A	C31-C32-C33-N08
2	А	201	I2A	C31-C32-C33-O05
2	В	201	I2A	C04-C03-C24-C25
2	В	201	I2A	C17-C18-C44-C45
2	А	201	I2A	C17-C18-C44-C45
2	А	201	I2A	C19-C18-C44-C45
2	А	201	I2A	C03-C24-C25-C26
2	А	201	I2A	N10-C46-C47-O10
2	А	201	I2A	N10-C46-C47-C48
2	В	201	I2A	C21-C02-C22-C23

There are no ring outliers.

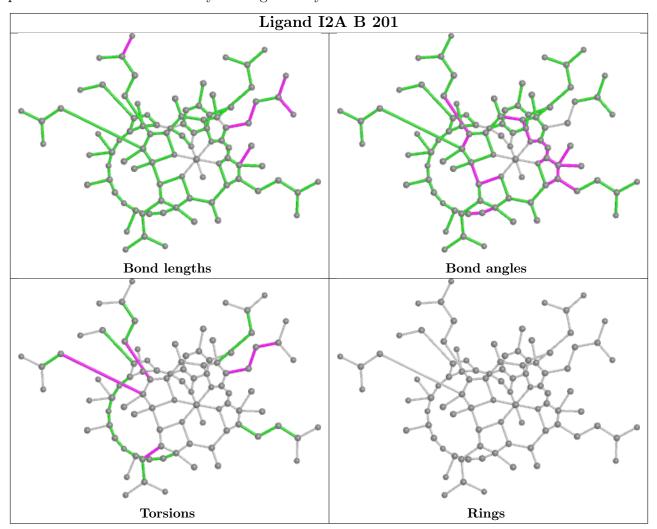
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	201	I2A	1	0
2	А	201	I2A	2	0

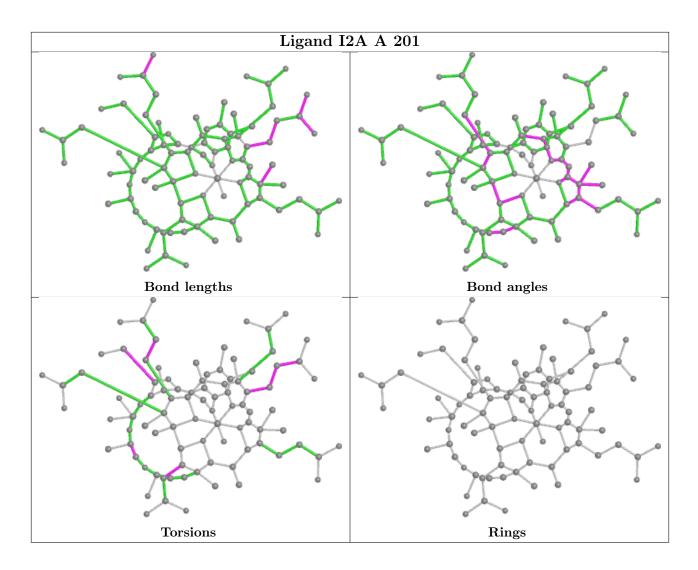
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will



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 similar 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	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q < 0.9
1	А	102/102~(100%)	0.90	10 (9%) 7 10	67, 97, 172, 201	0
1	В	102/102~(100%)	0.87	8 (7%) 13 16	58, 92, 145, 157	0
All	All	204/204~(100%)	0.88	18 (8%) 10 13	58, 94, 161, 201	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	87	А	6.3
1	В	58	U	6.0
1	А	83	А	5.3
1	А	58	U	4.2
1	В	83	А	3.5
1	В	86	U	3.2
1	А	80	С	3.2
1	А	87	А	2.7
1	А	84	А	2.6
1	В	97	G	2.4
1	А	85	G	2.4
1	А	81	С	2.3
1	А	82	А	2.3
1	В	85	G	2.2
1	В	11	С	2.2
1	А	86	U	2.1
1	В	64	С	2.1
1	А	57	U	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 monosaccharides in this entry.

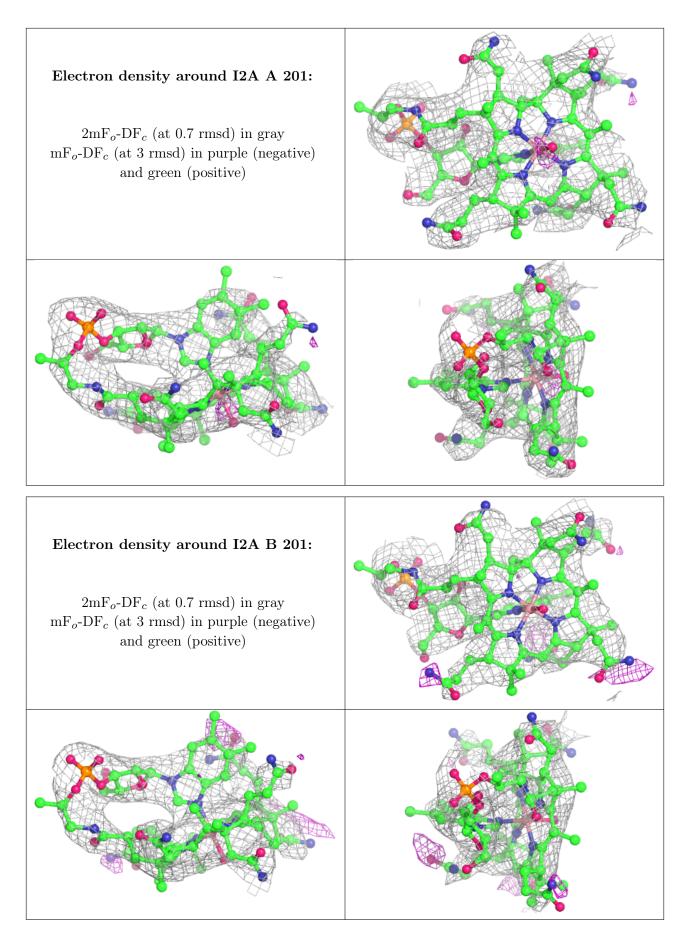
6.4 Ligands (i)

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	B-factors(Å ²)	Q<0.9
3	BA	А	202	1/1	0.23	0.20	184,184,184,184	0
3	BA	А	203	1/1	0.66	0.26	199,199,199,199	0
3	BA	В	202	1/1	0.70	0.17	181,181,181,181	0
3	BA	В	205	1/1	0.71	0.23	218,218,218,218	0
3	BA	В	206	1/1	0.71	0.16	222,222,222,222	0
3	BA	В	207	1/1	0.77	0.16	197,197,197,197	0
3	BA	А	206	1/1	0.83	0.22	209,209,209,209	0
3	BA	А	207	1/1	0.85	0.19	171,171,171,171	0
3	BA	В	204	1/1	0.87	0.09	174,174,174,174	0
2	I2A	А	201	92/92	0.91	0.32	54,55,56,56	0
3	BA	А	205	1/1	0.92	0.07	188,188,188,188	0
2	I2A	В	201	92/92	0.92	0.38	52,53,55,56	0
3	BA	А	204	1/1	0.93	0.26	204,204,204,204	0
3	BA	В	203	1/1	0.94	0.26	202,202,202,202	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.

