

wwPDB X-ray Structure Validation Summary Report (i)

Mar 11, 2024 - 06:08 pm GMT

PDB ID	:	8S8X
Title	:	SARS-CoV-2 nsp10-16 methyltransferase in complex with Toyocamycin and
		m7GpppA-RNA (Cap0-RNA)
Authors	:	Kremling, V.; Sprenger, J.; Oberthuer, D.; Scheer, T.E.S.
Deposited on		
Resolution	:	1.99 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:

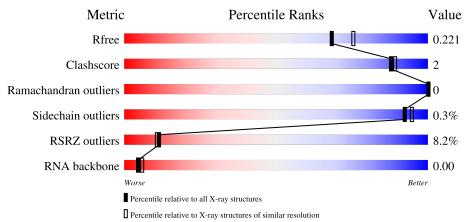
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.99 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)
RNA backbone	3102	1079 (2.50-1.50)

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	А	304	3% 95%		• •
2	В	140	18%	6%	19%
3	С	3	67%	339	%

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
8	GTA	С	1	Х	-	-	-



8S8X

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 6858 atoms, of which 3250 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 2'-O-methyltransferase nsp16.

Mol	Chain	Residues			Atom	s	ZeroOcc	AltConf	Trace		
1	A	301	Total 4782	C 1531	Н 2381	N 403	O 450	S 17	0	5	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	7097	GLU	-	expression tag	UNP P0DTD1
А	7098	ASN	-	expression tag	UNP P0DTD1
А	7099	LEU	-	expression tag	UNP P0DTD1
A	7100	TYR	-	expression tag	UNP P0DTD1
А	7101	PHE	-	expression tag	UNP P0DTD1
А	7102	GLN	_	expression tag	UNP P0DTD1

• Molecule 2 is a protein called Non-structural protein 10.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	В	114	Total 1651	C 526	Н 805	N 142	0 163	S 15	0	2	0

There is a discrepancy between the modelled and reference sequences:

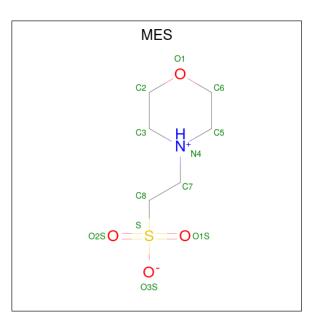
Chain	Residue	Modelled	Actual	Comment	Reference
В	4253	GLY	-	expression tag	UNP P0DTD1

• Molecule 3 is a RNA chain called m7GpppA-RNA (Cap0-RNA).

Mol	Chain	Residues		A	Atom	ıs			ZeroOcc	AltConf	Trace
3	С	2	Total 37		H 12	N 2	0 11	Р 2	0	0	0
			57	10	1Z	2	11	\angle			

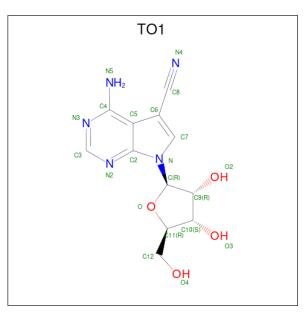
• Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).





Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	А	1	Total 25	-	Н 13	N 1	0 4	S 1	0	0

• Molecule 5 is 4-amino-7-(beta-D-ribofuranosyl)-7H-pyrrolo[2,3-d]pyrimidine-5-carbon itrile (three-letter code: TO1) (formula: $C_{12}H_{13}N_5O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues		Ate	\mathbf{oms}		ZeroOcc	AltConf	
5	Δ	1	Total	С	Η	Ν	0	0	0
0		1	34	12	13	5	4	0	U

• Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

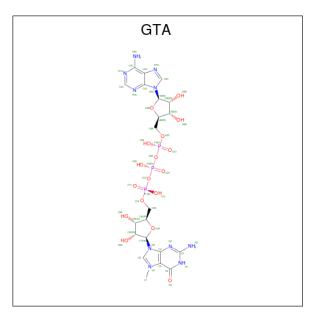


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	1	Total Mg 1 1	0	0

• Molecule 7 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	В	2	Total 2	Zn 2	0	0

• Molecule 8 is P1-7-METHYLGUANOSINE-P3-ADENOSINE-5', 5'-TRIPHOSPHAT E (three-letter code: GTA) (formula: $C_{21}H_{30}N_{10}O_{17}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
8	С	1	Total 77		Н 26				0	0

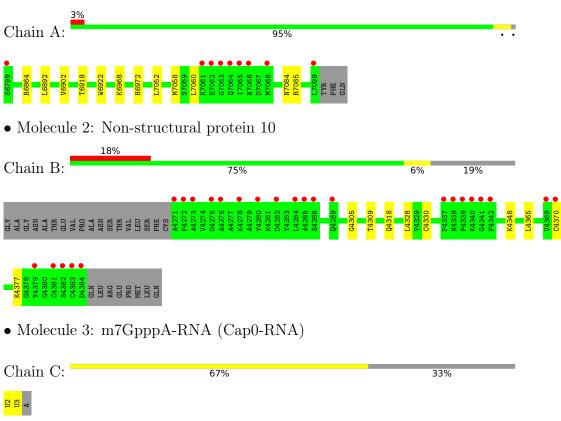
• Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	А	195	Total O 195 195	0	0
9	В	44	$\begin{array}{cc} \text{Total} & \text{O} \\ 44 & 44 \end{array}$	0	0
9	С	10	Total O 10 10	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: 2'-O-methyltransferase nsp16



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants	168.11Å 168.11Å 52.11Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.06 - 1.99	Depositor
Resolution (A)	49.06 - 1.99	EDS
% Data completeness	97.5 (49.06-1.99)	Depositor
(in resolution range)	97.5~(49.06-1.99)	EDS
R _{merge}	0.33	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.41 (at 2.00 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.21_5207	Depositor
D D.	0.189 , 0.223	Depositor
R, R_{free}	0.188 , 0.221	DCC
R_{free} test set	1047 reflections $(1.86%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	45.7	Xtriage
Anisotropy	0.172	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.37, 43.5	EDS
L-test for twinning ²	$< L > = 0.52, < L^2 > = 0.36$	Xtriage
Estimated twinning fraction	0.016 for -h,-k,l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6858	wwPDB-VP
Average B, all atoms $(Å^2)$	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.31% of the height of the origin peak. No significant pseudotranslation is detected.

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: TO1, ZN, GTA, MES, MG

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	Bo	nd angles
IVIOI	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.56	0/2459	0.73	1/3335~(0.0%)
2	В	0.51	0/871	0.63	0/1182
3	С	9.07	11/26~(42.3%)	4.12	6/38~(15.8%)
All	All	0.97	11/3356~(0.3%)	0.80	7/4555~(0.2%)

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\mathrm{Ideal}(\mathrm{\AA})$
3	С	2	U	C3'-C2'	-23.06	1.27	1.52
3	С	2	U	C2-N3	22.05	1.53	1.37
3	С	2	U	N1-C2	14.98	1.52	1.38
3	С	2	U	C5-C6	12.76	1.45	1.34
3	С	2	U	C2'-C1'	11.63	1.66	1.53

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

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
3	С	2	U	C5-C4-O4	-12.04	118.68	125.90
3	С	2	U	N3-C4-C5	11.46	121.48	114.60
3	С	2	U	C2-N3-C4	-7.73	122.36	127.00
3	С	2	U	C1'-O4'-C4'	-6.32	104.84	109.90
1	А	7052	LEU	CB-CG-CD1	5.73	120.74	111.00

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	2401	2381	2375	8	0
2	В	846	805	799	5	0
3	С	25	12	10	0	0
4	А	12	13	13	0	0
5	А	21	13	12	0	0
6	А	1	0	0	0	0
7	В	2	0	0	0	0
8	С	51	26	24	2	0
9	А	195	0	0	1	0
9	В	44	0	0	0	0
9	С	10	0	0	0	0
All	All	3608	3250	3233	13	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.

The worst 5 of 13 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)
8:C:1:GTA:O4A	8:C:1:GTA:C1A	1.63	1.23
2:B:4328:LEU:HD22	2:B:4365:LEU:HD21	1.66	0.76
1:A:6968:LYS:HZ1	8:C:1:GTA:H2B	1.74	0.53
1:A:6918:THR:HG21	1:A:6922:TRP:HE1	1.76	0.51
1:A:7058:MET:CE	1:A:7060:LEU:HD11	2.44	0.48

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.



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
1	А	304/304~(100%)	294~(97%)	10 (3%)	0	100	100
2	В	114/140~(81%)	110 (96%)	4 (4%)	0	100	100
All	All	418/444 (94%)	404 (97%)	14 (3%)	0	100	100

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

There are no Ramachandran outliers to report.

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	266/264~(101%)	265~(100%)	1 (0%)	91 93		
2	В	94/113~(83%)	94 (100%)	0	100 100		
All	All	360/377~(96%)	359 (100%)	1 (0%)	92 95		

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type	
1	А	7085	ARG	

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	С	0/3	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.



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 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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	Bond lengths			Bond angles		
	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	TO1	А	7202	-	21,23,23	5.24	10 (47%)	22,34,34	1.62	4 (18%)
8	GTA	С	1	3	46,56,56	4.32	19 (41%)	46,88,88	1.69	8 (17%)
4	MES	А	7201	-	12,12,12	1.57	1 (8%)	14,16,16	2.37	3 (21%)

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
5	TO1	А	7202	-	-	2/2/24/24	0/3/3/3
8	GTA	С	1	3	1/1/11/11	2/24/64/64	0/6/6/6
4	MES	А	7201	-	-	2/6/14/14	0/1/1/1

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
8	С	1	GTA	O4A-C1A	16.31	1.63	1.41
5	А	7202	TO1	O-C	15.85	1.63	1.41
5	А	7202	TO1	С9-С	-13.42	1.33	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	С	1	GTA	C2A-C1A	-11.99	1.35	1.53
8	С	1	GTA	C2B-C1B	9.26	1.67	1.53

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
4	А	7201	MES	O3S-S-C8	-6.52	95.23	105.77
8	С	1	GTA	O4B-C1B-C2B	-4.76	99.97	106.93
8	С	1	GTA	N3C-C2C-N1C	-4.74	121.27	128.68
4	А	7201	MES	O1S-S-C8	4.74	112.62	106.92
8	С	1	GTA	C2B-C3B-C4B	-3.95	94.96	102.64

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
8	С	1	GTA	C2B

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	С	1	GTA	C5A-O15-P1-O11
8	С	1	GTA	C5A-O15-P1-O13
4	А	7201	MES	C8-C7-N4-C5
4	А	7201	MES	C8-C7-N4-C3
5	А	7202	TO1	C10-C11-C12-O4

There are no ring outliers.

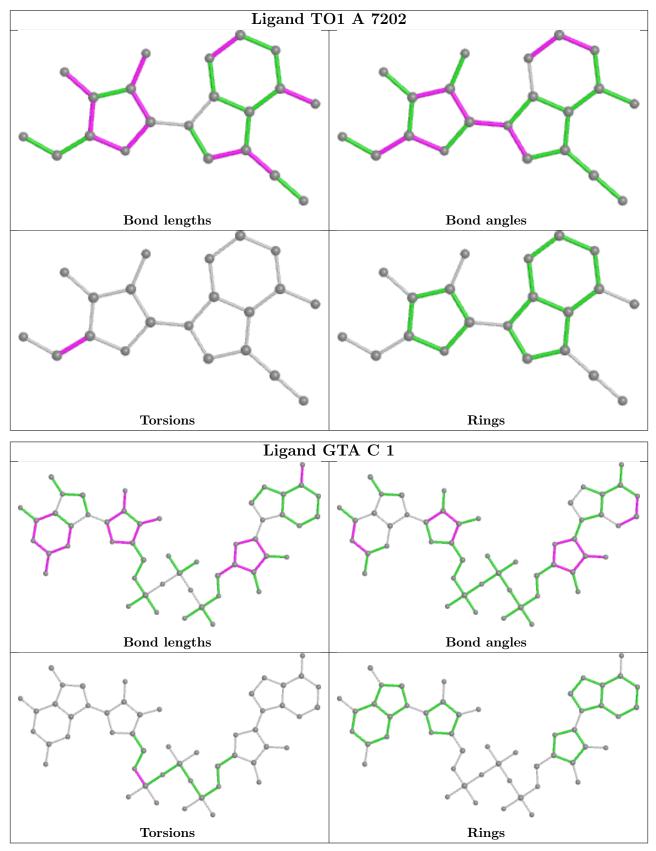
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	С	1	GTA	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 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	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q<0.9
1	А	301/304~(99%)	0.30	9 (2%) 50 49	36, 44, 70, 109	0
2	В	114/140 (81%)	1.01	25 (21%) 0 0	39, 56, 96, 114	0
3	С	2/3~(66%)	0.26	0 100 100	74, 74, 74, 89	0
All	All	417/447 (93%)	0.49	34 (8%) 11 11	36, 47, 85, 114	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	6799	SER	5.7
2	В	4383	CYS	5.1
1	А	7065	ILE	4.6
2	В	4339	PRO	4.1
2	В	4285	ALA	4.1

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.

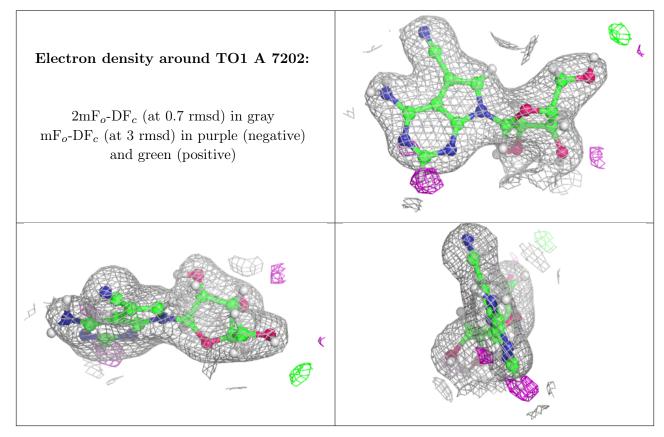
6.4 Ligands (i)

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.

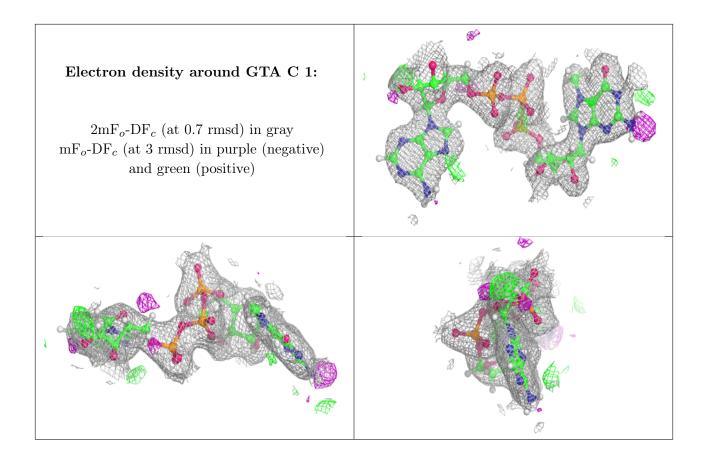


Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
4	MES	А	7201	12/12	0.93	0.15	48,63,89,92	0
5	TO1	А	7202	21/21	0.94	0.12	35,45,57,83	0
7	ZN	В	4402	1/1	0.95	0.04	82,82,82,82	0
6	MG	А	7203	1/1	0.96	0.06	54,54,54,54	0
8	GTA	С	1	51/51	0.97	0.13	37,50,74,76	0
7	ZN	В	4401	1/1	0.99	0.12	51,51,51,51	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.

