



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:24 AM UTC

PDB ID : 8S8W / pdb_00008s8w
Title : SARS-CoV-2 nsp10-16 methyltransferase in complex with Sangivamycin and m7GpppA-RNA (Cap0-RNA)
Authors : Kremling, V.; Sprenger, J.; Oberthuer, D.; Scheer, T.E.S.
Deposited on : 2024-03-07
Resolution : 2.10 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

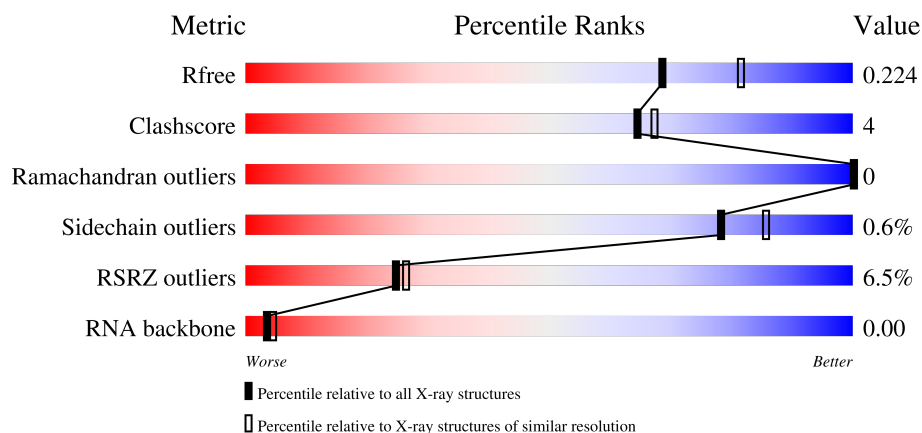
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)
RNA backbone	3983	1006 (2.42-1.78)

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 $\leq 5\%$. 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	304	4% 90% 8%
2	B	140	10% 76% 5% 19%
3	C	3	33% 33% 33%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 6899 atoms, of which 3308 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	Atoms						ZeroOcc	AltConf	Trace
1	A	299	Total	C	H	N	O	S	0	6	0
			4792	1531	2394	404	446	17			

There are 6 discrepancies between the modelled and reference sequences:

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

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	114	Total	C	H	N	O	S	0	1	0
			1637	522	798	141	161	15			

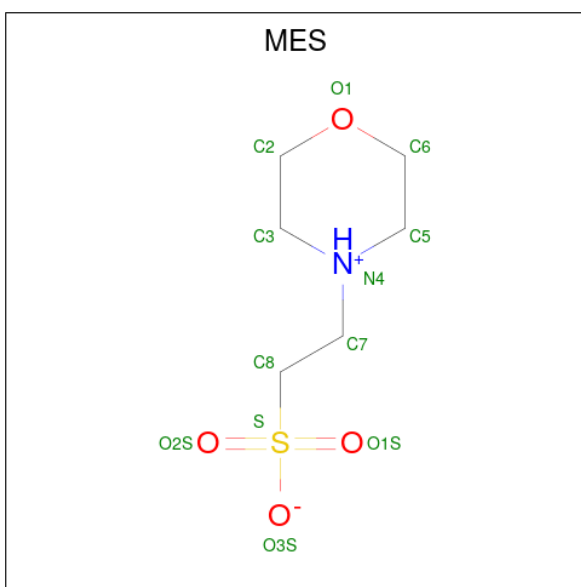
There is a discrepancy between the modelled and reference sequences:

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

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

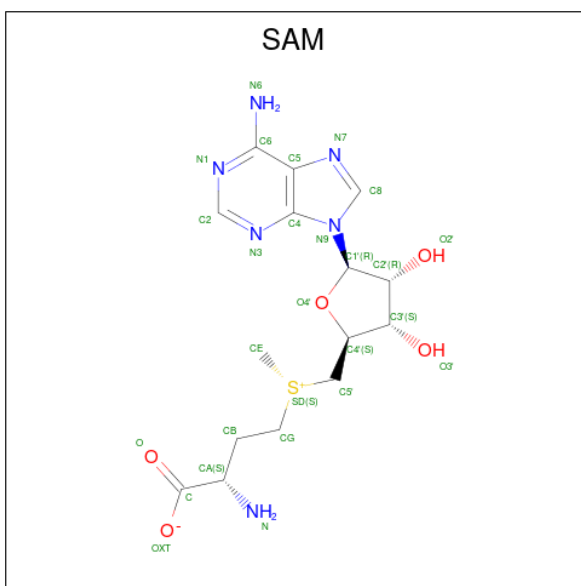
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	3	Total	C	H	N	O	P	0	0	0
			67	19	22	4	19	3			

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S).



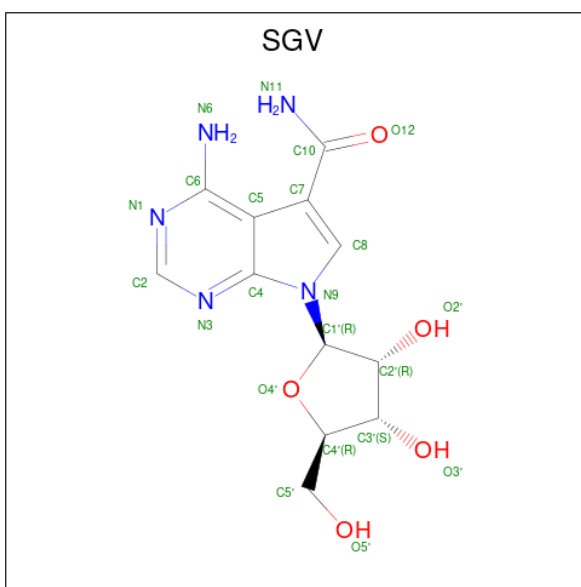
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	H	N	O	S	0	0
			25	6	13	1	4	1		

- Molecule 5 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



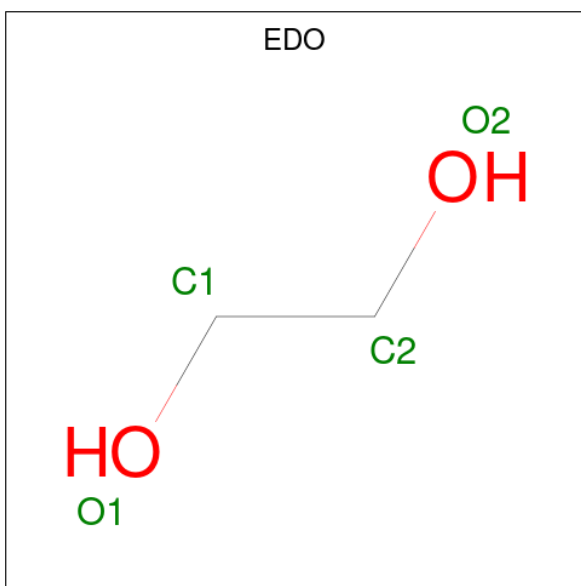
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	S	0	1
			49	15	22	6	5	1		

- Molecule 6 is SANGIVAMYCIN (CCD ID: SGV) (formula: $C_{12}H_{15}N_5O_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	H	N	O	0	1
			37	12	15	5	5		

- Molecule 7 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).

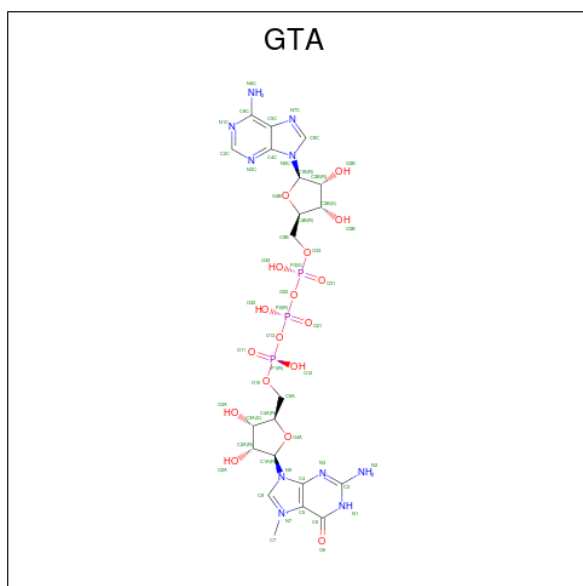


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	H	O	0	0
			10	2	6	2		
7	A	1	Total	C	H	O	0	0
			10	2	6	2		
7	A	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 8 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	2	Total	Zn	0	0
			2	2		

- Molecule 9 is P1-7-METHYLGUANOSINE-P3-ADENOSINE-5',5'-TRIPHOSPHATE (CCD ID: GTA) (formula: C₂₁H₃₀N₁₀O₁₇P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
9	C	1	Total	C	H	N	O	P	0	0
			77	21	26	10	17	3		

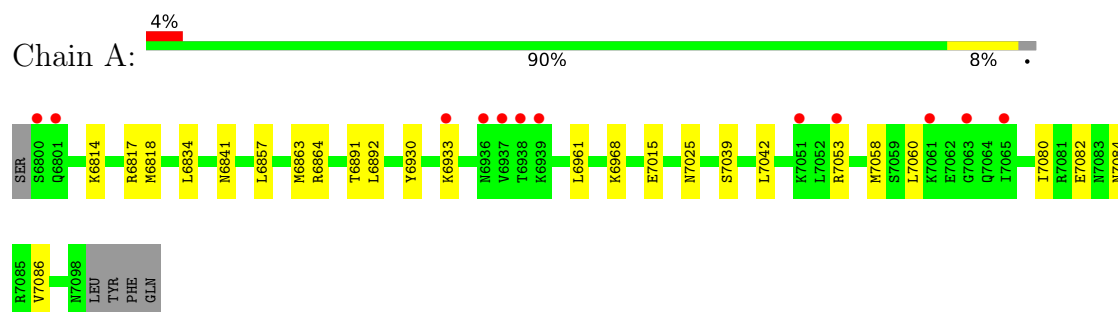
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	140	Total	O	0	0
			140	140		
10	B	36	Total	O	0	0
			36	36		
10	C	7	Total	O	0	0
			7	7		

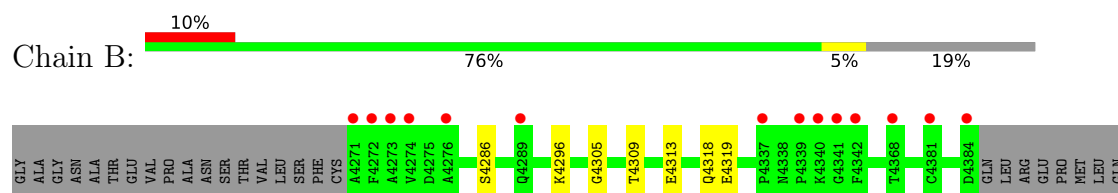
3 Residue-property plots

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.

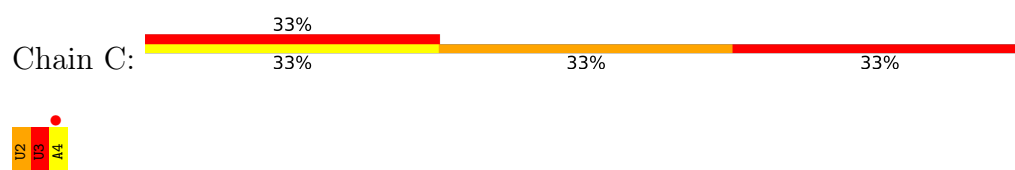
• Molecule 1: 2'-O-methyltransferase nsp16



• Molecule 2: Non-structural protein 10



• Molecule 3: m7GpppA-RNA (Cap0-RNA)



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	167.14Å 167.14Å 51.83Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.80 – 2.10 48.80 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.80-2.10) 99.8 (48.80-2.10)	Depositor EDS
R_{merge}	0.25	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.21_5207	Depositor
R, R_{free}	0.187 , 0.224 0.188 , 0.224	Depositor DCC
R_{free} test set	1080 reflections (1.01%)	wwPDB-VP
Wilson B-factor (Å ²)	45.5	Xtriage
Anisotropy	0.095	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 53.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.016 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6899	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.91% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

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: SGV, SAM, GTA, ZN, EDO, MES

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	0.51	0/2456	0.65	0/3328
2	B	0.45	0/864	0.62	0/1172
3	C	6.65	20/48 (41.7%)	2.00	1/72 (1.4%)
All	All	0.93	20/3368 (0.6%)	0.68	1/4572 (0.0%)

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	3	U	C3'-C2'	-17.89	1.25	1.52
3	C	3	U	P-O5'	14.97	1.82	1.59
3	C	2	U	C2'-C1'	-14.15	1.32	1.53
3	C	2	U	O4'-C1'	13.82	1.62	1.41
3	C	2	U	C4'-O4'	-11.39	1.28	1.45
3	C	3	U	C2'-C1'	10.27	1.68	1.53
3	C	2	U	C2-N3	9.31	1.56	1.37
3	C	3	U	O3'-P	9.03	1.74	1.61
3	C	2	U	N1-C2	8.64	1.55	1.38
3	C	3	U	C2-N3	8.27	1.54	1.37
3	C	3	U	N1-C2	7.23	1.53	1.38
3	C	3	U	C5'-C4'	-6.97	1.40	1.51
3	C	3	U	C3'-O3'	6.91	1.52	1.42
3	C	2	U	C2'-O2'	6.58	1.52	1.42
3	C	3	U	C5-C6	6.57	1.47	1.34
3	C	3	U	O5'-C5'	6.48	1.52	1.42
3	C	4	A	P-O5'	6.42	1.73	1.60
3	C	3	U	O4'-C1'	-6.26	1.32	1.41
3	C	3	U	C4'-O4'	6.03	1.54	1.45
3	C	3	U	C4'-C3'	5.68	1.61	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	2	U	C1'-O4'-C4'	-6.85	103.05	109.90

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	2398	2394	2382	20	0
2	B	839	798	793	3	0
3	C	45	22	20	2	0
4	A	12	13	13	0	0
5	A	27	22	21	3	0
6	A	22	15	14	1	0
7	A	12	18	18	4	0
8	B	2	0	0	0	0
9	C	51	26	25	3	0
10	A	140	0	0	0	0
10	B	36	0	0	0	0
10	C	7	0	0	0	0
All	All	3591	3308	3286	26	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 4.

All (26) 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)
6:A:7203[B]:SGV:O4'	6:A:7203[B]:SGV:C1'	1.69	1.21
5:A:7202[A]:SAM:HE3	9:C:101:GTA:O2B	1.97	0.64
1:A:6930:TYR:CD2	9:C:101:GTA:C4C	2.89	0.56
1:A:6841:ASN:ND2	5:A:7202[A]:SAM:OXT	2.38	0.55
5:A:7202[A]:SAM:HE2	3:C:2:U:O4'	2.07	0.55
1:A:7039:SER:HB2	1:A:7042:LEU:HD12	1.91	0.53
1:A:6864:ARG:NH2	1:A:7084:ASN:O	2.41	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6892:LEU:HD12	1:A:7086:VAL:HG21	1.92	0.52
1:A:7058:MET:CE	1:A:7060:LEU:HD21	2.42	0.49
1:A:6857:LEU:O	1:A:7053:ARG:NH1	2.43	0.49
1:A:7082:GLU:HB2	7:A:7205:EDO:H21	1.96	0.47
2:B:4305:GLY:HA2	2:B:4318:GLN:OE1	2.14	0.47
1:A:6933:LYS:N	1:A:6933:LYS:HD3	2.30	0.46
1:A:7058:MET:O	1:A:7080:ILE:HA	2.16	0.46
1:A:6961:LEU:HB2	1:A:7080:ILE:HB	1.98	0.45
1:A:7015:GLU:OE2	7:A:7206:EDO:O2	2.25	0.45
1:A:6834:LEU:HD12	3:C:3:U:C4	2.53	0.43
1:A:6863:MET:HB3	1:A:6891:THR:HG23	1.98	0.43
1:A:7058:MET:HE2	1:A:7060:LEU:HD11	2.00	0.43
1:A:6930:TYR:CE2	9:C:101:GTA:C8C	3.02	0.43
1:A:6818:MET:HG2	1:A:7025:ASN:OD1	2.19	0.42
1:A:6814:LYS:HB3	7:A:7206:EDO:H11	2.01	0.41
1:A:6817:ARG:HE	1:A:6817:ARG:HB3	1.75	0.41
2:B:4309:THR:HG21	2:B:4313:GLU:HG3	2.01	0.41
2:B:4296:LYS:HD2	2:B:4319:GLU:CD	2.46	0.41
1:A:7082:GLU:HB2	7:A:7205:EDO:C1	2.51	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	A	303/304 (100%)	293 (97%)	10 (3%)	0	100	100
2	B	113/140 (81%)	107 (95%)	6 (5%)	0	100	100
All	All	416/444 (94%)	400 (96%)	16 (4%)	0	100	100

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	A	265/264 (100%)	264 (100%)	1 (0%)	84	89
2	B	93/113 (82%)	92 (99%)	1 (1%)	65	74
All	All	358/377 (95%)	356 (99%)	2 (1%)	78	86

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6968	LYS
2	B	4286	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7008	ASN
1	A	7098	ASN
2	B	4306	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	C	1/3 (33%)	1 (100%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	C	3	U

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 2 are monoatomic - leaving 7 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
6	SGV	A	7203[B]	-	24,24,24	3.68	11 (45%)	34,36,36	2.23	7 (20%)
7	EDO	A	7205	-	3,3,3	0.27	0	2,2,2	0.76	0
7	EDO	A	7206	-	3,3,3	0.32	0	2,2,2	0.45	0
5	SAM	A	7202[A]	-	27,29,29	3.60	12 (44%)	34,42,42	2.08	12 (35%)
9	GTA	C	101	3	56,56,56	3.78	22 (39%)	83,88,88	1.78	16 (19%)
4	MES	A	7201	-	12,12,12	1.58	2 (16%)	15,16,16	1.54	4 (26%)
7	EDO	A	7204	-	3,3,3	0.31	0	2,2,2	0.07	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
6	SGV	A	7203[B]	-	-	6/10/26/26	0/3/3/3
7	EDO	A	7205	-	-	1/1/1/1	-
7	EDO	A	7206	-	-	0/1/1/1	-
5	SAM	A	7202[A]	-	-	2/17/33/33	0/3/3/3
9	GTA	C	101	3	-	4/32/64/64	0/6/6/6
4	MES	A	7201	-	-	2/6/14/14	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	EDO	A	7204	-	-	0/1/1/1	-

All (47) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	7203[B]	SGV	O4'-C1'	11.70	1.69	1.42
5	A	7202[A]	SAM	C2'-C3'	-9.33	1.28	1.53
9	C	101	GTA	O4A-C1A	9.19	1.63	1.42
9	C	101	GTA	O4B-C1B	9.15	1.63	1.42
9	C	101	GTA	P3-O23	8.51	1.68	1.59
5	A	7202[A]	SAM	O4'-C4'	-7.85	1.27	1.45
9	C	101	GTA	P2-O23	7.51	1.67	1.59
6	A	7203[B]	SGV	C2'-C1'	-7.47	1.30	1.53
9	C	101	GTA	O4B-C4B	-7.15	1.29	1.45
9	C	101	GTA	C2B-C1B	-7.03	1.31	1.53
9	C	101	GTA	C4-N3	6.80	1.49	1.34
9	C	101	GTA	C2-N3	6.76	1.49	1.33
9	C	101	GTA	P2-O13	6.55	1.66	1.59
5	A	7202[A]	SAM	O4'-C1'	6.48	1.57	1.42
5	A	7202[A]	SAM	C3'-C4'	6.46	1.69	1.53
6	A	7203[B]	SGV	O4'-C4'	-6.35	1.30	1.45
9	C	101	GTA	O4A-C4A	-6.34	1.30	1.45
5	A	7202[A]	SAM	C6-N6	5.76	1.48	1.34
9	C	101	GTA	P1-O13	5.41	1.65	1.59
9	C	101	GTA	C6C-N6C	4.99	1.47	1.34
9	C	101	GTA	C2A-C1A	-4.85	1.38	1.53
9	C	101	GTA	C2-N2	4.64	1.45	1.34
5	A	7202[A]	SAM	C1'-N9	-4.58	1.33	1.46
6	A	7203[B]	SGV	C6-N6	4.45	1.45	1.34
9	C	101	GTA	C5-C6	4.42	1.55	1.43
4	A	7201	MES	C8-S	4.13	1.83	1.77
6	A	7203[B]	SGV	C10-N11	4.11	1.45	1.33
9	C	101	GTA	O2B-C2B	3.85	1.52	1.43
6	A	7203[B]	SGV	O3'-C3'	-3.84	1.33	1.43
9	C	101	GTA	C6-N1	3.80	1.46	1.38
5	A	7202[A]	SAM	C8-N9	-3.33	1.31	1.37
5	A	7202[A]	SAM	C4-N3	3.28	1.40	1.34
5	A	7202[A]	SAM	O3'-C3'	3.23	1.51	1.43
9	C	101	GTA	O2A-C2A	3.19	1.50	1.43
9	C	101	GTA	C3A-C4A	3.07	1.60	1.53
9	C	101	GTA	C2-N1	2.99	1.44	1.37
6	A	7203[B]	SGV	C8-N9	-2.84	1.33	1.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	C	101	GTA	O3A-C3A	-2.73	1.36	1.43
6	A	7203[B]	SGV	O2'-C2'	2.53	1.49	1.43
5	A	7202[A]	SAM	O-C	2.44	1.29	1.22
5	A	7202[A]	SAM	O2'-C2'	2.40	1.48	1.43
9	C	101	GTA	C5-N7	-2.36	1.36	1.39
6	A	7203[B]	SGV	C3'-C2'	2.29	1.59	1.53
5	A	7202[A]	SAM	OXT-C	-2.25	1.23	1.30
6	A	7203[B]	SGV	O12-C10	-2.25	1.19	1.24
6	A	7203[B]	SGV	C3'-C4'	2.09	1.58	1.53
4	A	7201	MES	O1S-S	2.06	1.50	1.45

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	7203[B]	SGV	C5-C4-N3	-6.56	120.01	126.97
5	A	7202[A]	SAM	C5-C4-N3	-5.61	118.99	126.72
6	A	7203[B]	SGV	C7-C8-N9	-5.32	108.31	110.54
9	C	101	GTA	N3C-C2C-N1C	-5.07	120.91	128.58
9	C	101	GTA	C5-C4-N3	-5.00	118.71	128.15
9	C	101	GTA	C2-N3-C4	4.79	120.55	112.30
9	C	101	GTA	C5C-C4C-N3C	-4.66	120.30	126.72
6	A	7203[B]	SGV	N3-C2-N1	-4.53	121.72	128.58
6	A	7203[B]	SGV	C4-N9-C8	4.36	109.88	108.08
9	C	101	GTA	N3C-C4C-N9C	4.08	134.10	127.17
9	C	101	GTA	N9-C4-N3	3.93	133.81	125.95
5	A	7202[A]	SAM	N3-C4-N9	3.81	133.65	127.17
9	C	101	GTA	O6-C6-C5	-3.52	120.15	128.01
9	C	101	GTA	C5-C6-N1	3.48	119.03	111.84
5	A	7202[A]	SAM	N3-C2-N1	-3.48	123.32	128.58
5	A	7202[A]	SAM	C4-C5-N7	-3.47	106.61	110.58
6	A	7203[B]	SGV	C2-N3-C4	3.35	120.00	111.83
9	C	101	GTA	C2C-N3C-C4C	3.33	119.97	111.83
9	C	101	GTA	C2-N1-C6	-3.24	119.24	125.11
5	A	7202[A]	SAM	C2-N3-C4	3.16	119.54	111.83
5	A	7202[A]	SAM	C5-N7-C8	3.15	108.40	103.45
4	A	7201	MES	O3S-S-C8	-3.06	100.02	106.00
4	A	7201	MES	O1S-S-C8	3.04	111.32	106.73
9	C	101	GTA	C4C-N9C-C8C	3.03	108.92	105.74
9	C	101	GTA	N9C-C8C-N7C	-2.97	109.72	113.94
9	C	101	GTA	C3A-C2A-C1A	2.96	107.06	101.46
6	A	7203[B]	SGV	C6-C5-C4	2.90	117.92	115.74
5	A	7202[A]	SAM	C3'-C2'-C1'	2.77	106.70	101.46

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	7202[A]	SAM	N9-C8-N7	-2.68	110.14	113.94
5	A	7202[A]	SAM	O4'-C1'-N9	2.42	112.74	108.09
6	A	7203[B]	SGV	N3-C4-N9	2.39	131.23	127.17
4	A	7201	MES	C6-C5-N4	-2.32	106.60	110.12
5	A	7202[A]	SAM	C2'-C3'-C4'	2.31	107.08	102.61
4	A	7201	MES	O2S-S-C8	-2.31	103.24	106.73
9	C	101	GTA	O4A-C1A-N9	2.26	113.48	108.36
5	A	7202[A]	SAM	O4'-C1'-C2'	-2.19	101.93	106.62
9	C	101	GTA	C5C-N7C-C8C	2.13	106.80	103.45
5	A	7202[A]	SAM	C4'-O4'-C1'	-2.09	104.85	109.47
9	C	101	GTA	C5C-C6C-N6C	-2.05	118.21	123.29

There are no chirality outliers.

All (15) torsion outliers are listed below:

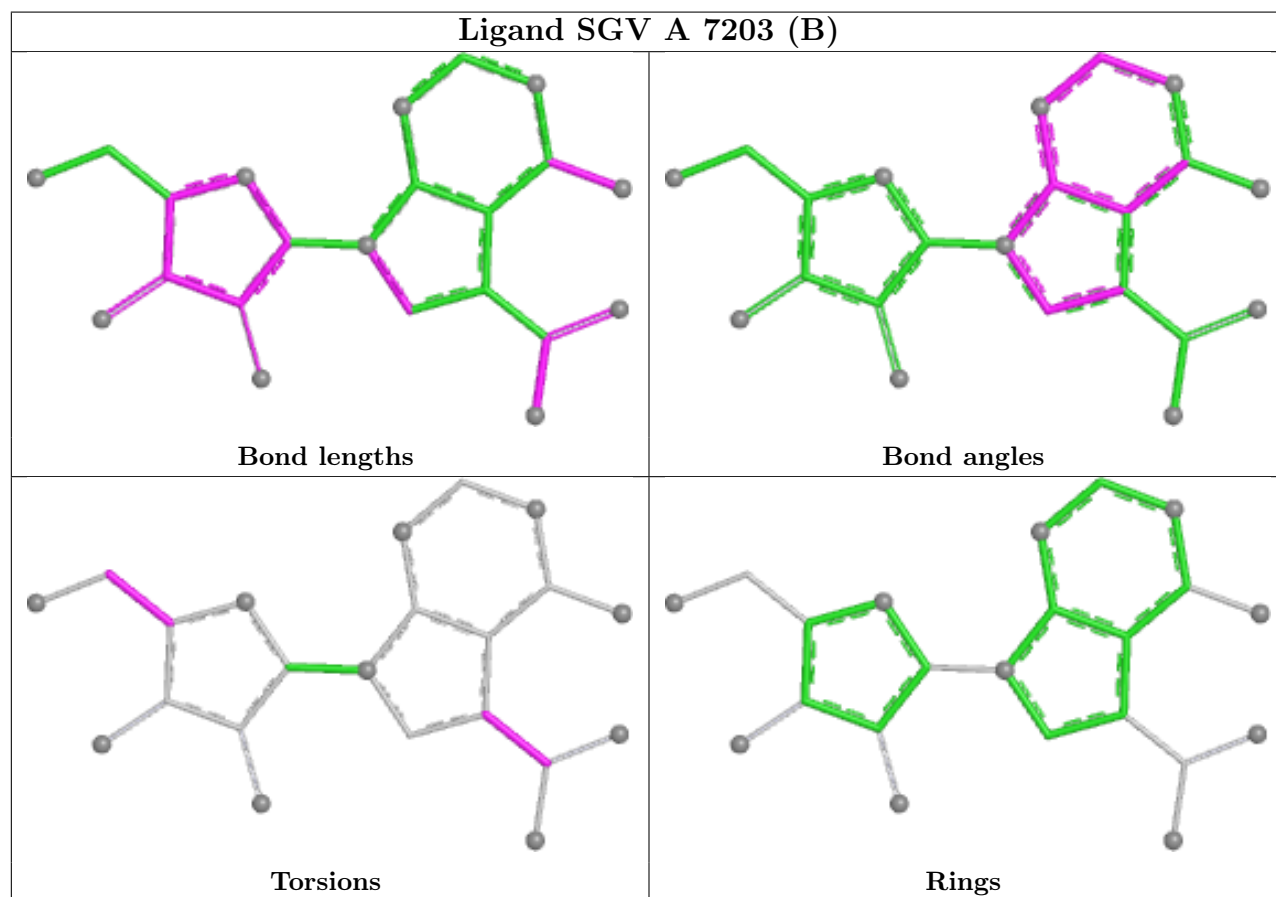
Mol	Chain	Res	Type	Atoms
6	A	7203[B]	SGV	N11-C10-C7-C5
6	A	7203[B]	SGV	N11-C10-C7-C8
9	C	101	GTA	C5A-O15-P1-O13
9	C	101	GTA	O4A-C4A-C5A-O15
4	A	7201	MES	C8-C7-N4-C5
9	C	101	GTA	C5A-O15-P1-O11
4	A	7201	MES	C8-C7-N4-C3
6	A	7203[B]	SGV	O12-C10-C7-C5
5	A	7202[A]	SAM	OXT-C-CA-CB
9	C	101	GTA	C3A-C4A-C5A-O15
5	A	7202[A]	SAM	O-C-CA-CB
7	A	7205	EDO	O1-C1-C2-O2
6	A	7203[B]	SGV	O4'-C4'-C5'-O5'
6	A	7203[B]	SGV	O12-C10-C7-C8
6	A	7203[B]	SGV	C3'-C4'-C5'-O5'

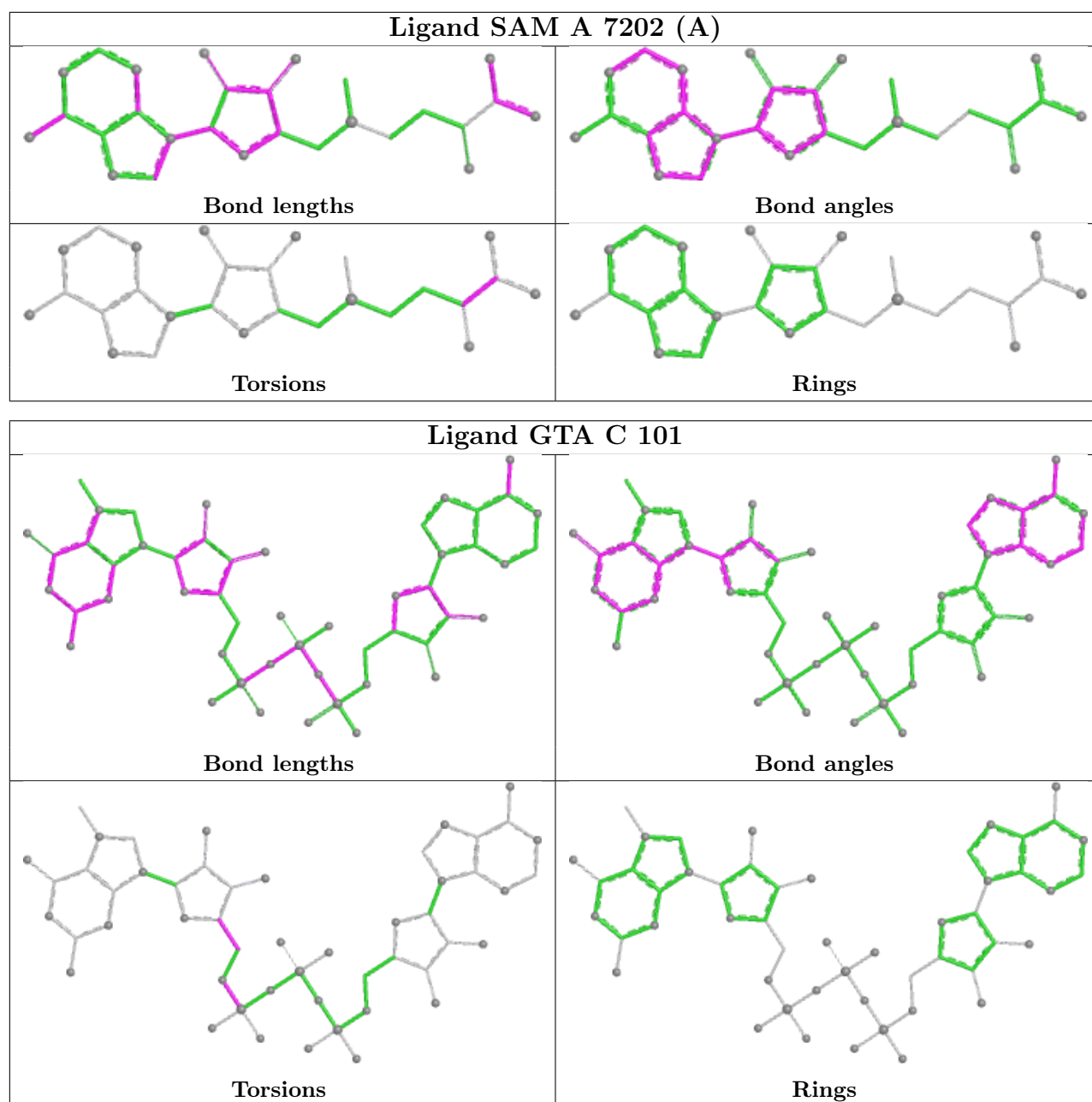
There are no ring outliers.

5 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	7203[B]	SGV	1	0
7	A	7205	EDO	2	0
7	A	7206	EDO	2	0
5	A	7202[A]	SAM	3	0
9	C	101	GTA	3	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 than 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

6.1 Protein, DNA and RNA chains

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, 95th 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 ²)	Q<0.9
1	A	299/304 (98%)	0.04	12 (4%)	42 44	24, 49, 80, 108	5 (1%)
2	B	114/140 (81%)	0.64	14 (12%)	8 8	42, 62, 103, 123	0
3	C	3/3 (100%)	2.11	1 (33%)	1 1	97, 97, 112, 144	0
All	All	416/447 (93%)	0.22	27 (6%)	25 26	24, 52, 93, 144	5 (1%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	4271	ALA	5.7
1	A	7051[A]	LYS	5.5
1	A	7061[A]	LYS	4.5
2	B	4342	PHE	4.5
1	A	6800	SER	3.9
1	A	6938	THR	3.6
2	B	4274	VAL	3.5
1	A	7063	GLY	3.4
1	A	6801[A]	GLN	3.4
3	C	4	A	3.2
2	B	4339	PRO	3.1
1	A	6937	VAL	2.9
2	B	4337	PRO	2.8
2	B	4340	LYS	2.6
1	A	7053	ARG	2.6
2	B	4273	ALA	2.6
2	B	4384	ASP	2.6
1	A	7065	ILE	2.5
2	B	4272	PHE	2.5
1	A	6936	ASN	2.4
1	A	6939	LYS	2.4
2	B	4276	ALA	2.3
2	B	4341	GLY	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	6933	LYS	2.3
2	B	4381	CYS	2.3
2	B	4289	GLN	2.2
2	B	4368	THR	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

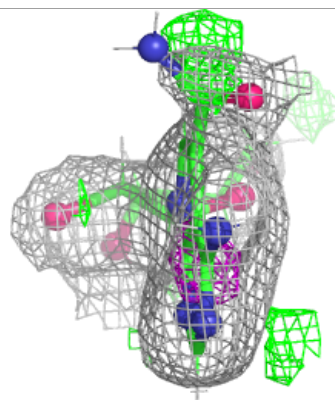
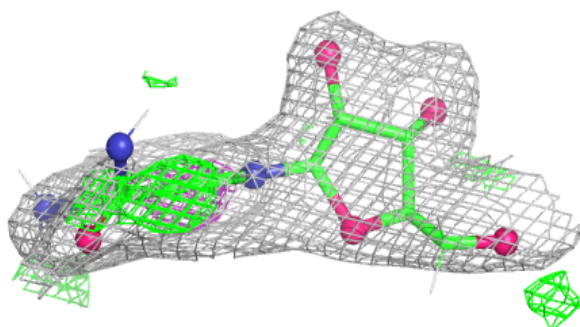
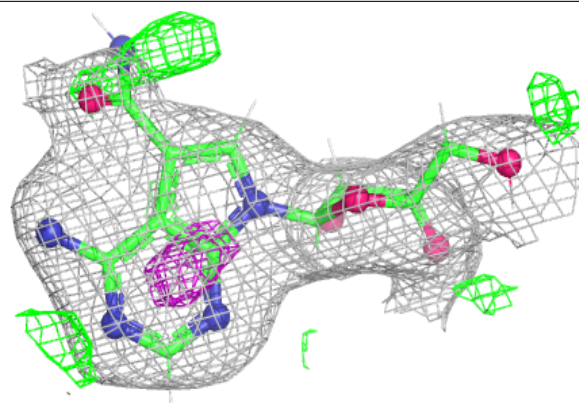
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	EDO	A	7205	4/4	0.87	0.17	57,75,92,92	0
6	SGV	A	7203[B]	22/22	0.88	0.19	44,53,66,70	37
7	EDO	A	7204	4/4	0.89	0.16	66,79,90,99	0
5	SAM	A	7202[A]	27/27	0.91	0.14	36,52,69,83	49
4	MES	A	7201	12/12	0.91	0.13	50,72,102,109	0
7	EDO	A	7206	4/4	0.94	0.13	57,79,95,95	0
9	GTA	C	101	51/51	0.94	0.11	47,68,94,97	0
8	ZN	B	4402	1/1	0.98	0.04	83,83,83,83	0
8	ZN	B	4401	1/1	1.00	0.02	51,51,51,51	0

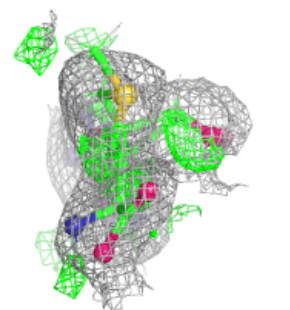
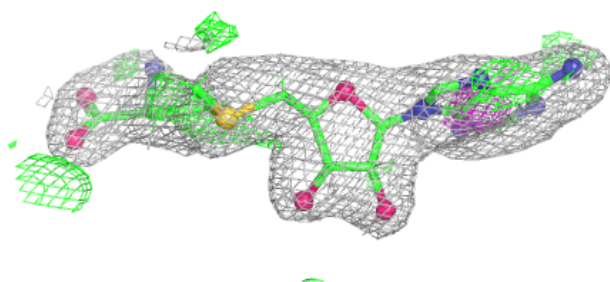
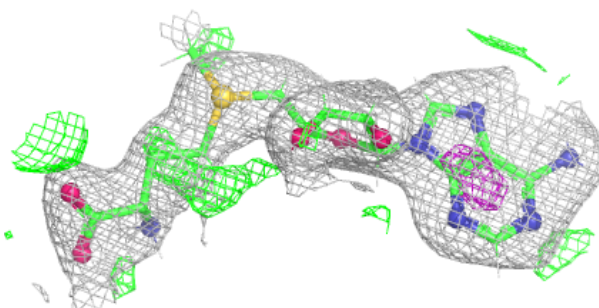
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

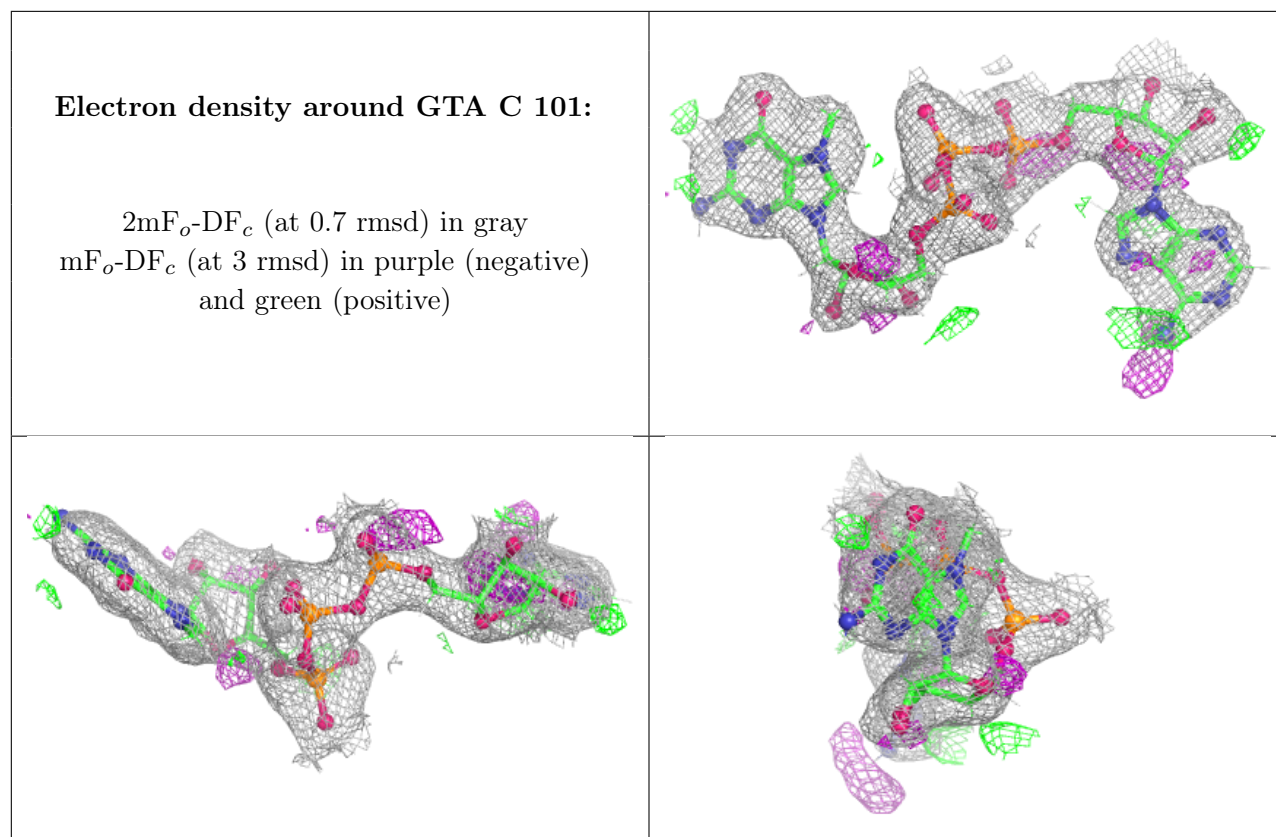
Electron density around SGV A 7203 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around SAM A 7202 (A):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.