WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 26, 2024 – 02:01 PM EST

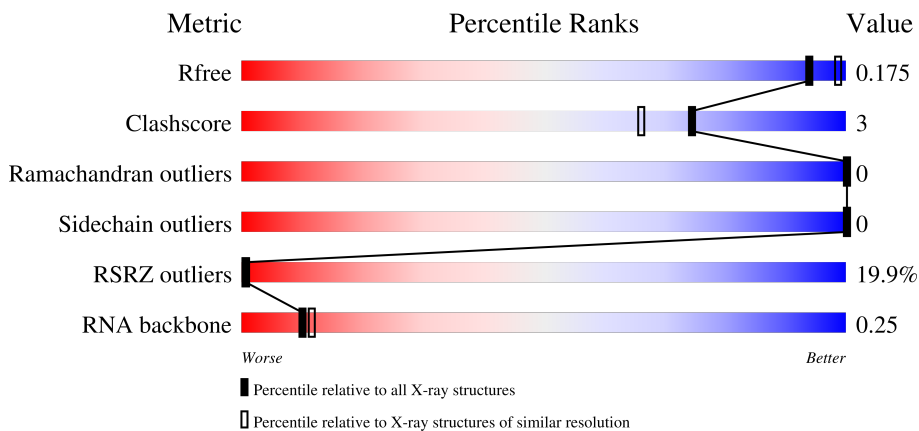|		
PDB ID	:	7L6R
Title	:	Crystal Structure of SARS-CoV-2 Nsp16/10 Heterodimer in Complex with (m7GpppA2m)pUpUpApApA (Cap-1), S-Adenosyl-L-homocysteine (SAH) and Manganese (Mn).
Authors	:	Minasov, G.; Shuvalova, L.; Rosas-Lemus, M.; Kiryukhina, O.; Brunzelle, J.S.; Satchell, K.J.F.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on	:	2020-12-23
Resolution	:	1.98 Å(reported)

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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 1.98 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	Percentile Ranks	Value
Rfree		0.175
Clashscore		3
Ramachandran outliers		0
Sidechain outliers		0
RSRZ outliers		19.9%
RNA backbone		0.25

Worse   *Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (2.00-1.96)
RNA backbone	3102	1105 (2.50-1.46)

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	300	15% / 95% / 5%
2	B	141	26% / 75% / · / 23%

Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

WORLDWIDE wwPDB PROTEIN DATA BANK

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Mol	Chain	Length	Quality of chain
3	C	7	29% / 29% / 29% / 29% / 14%

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	GLC	A	7107	-	-	-	X

2   Entry composition ⓘ

There are 11 unique types of molecules in this entry. The entry contains 3873 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 2'-O-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	300	Total 2482	C 1576	N 419	O 470	S 17	0	16	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6797	SER	-	expression tag	UNP P0DTD1
A	6798	ASN	-	expression tag	UNP P0DTD1

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	109	Total 820	C 510	N 137	O 157	S 16	0	2	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	4252	SER	-	expression tag	UNP P0DTD1
B	4253	ASN	-	expression tag	UNP P0DTD1

- Molecule 3 is a RNA chain called RNA (5'-D(*(M7G))-R(P*(A2M)P*UP*UP*AP*A)-3').

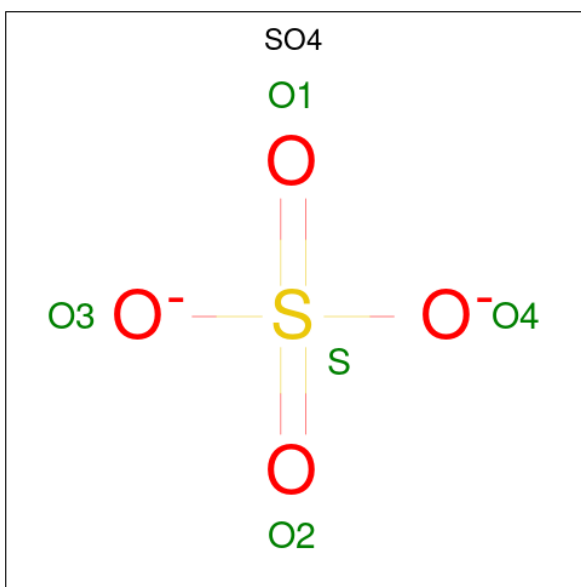| Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	6	Total 118	C 50	N 19	O 42	P 7	0	0	0

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Mn 1	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total 3	Cl 3	0	1

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O_4S).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total 5	O 4	S 1	0	0

- Molecule 7 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: $C_{14}H_{20}N_6O_5S$) (labeled as "Ligand of Interest" by depositor).
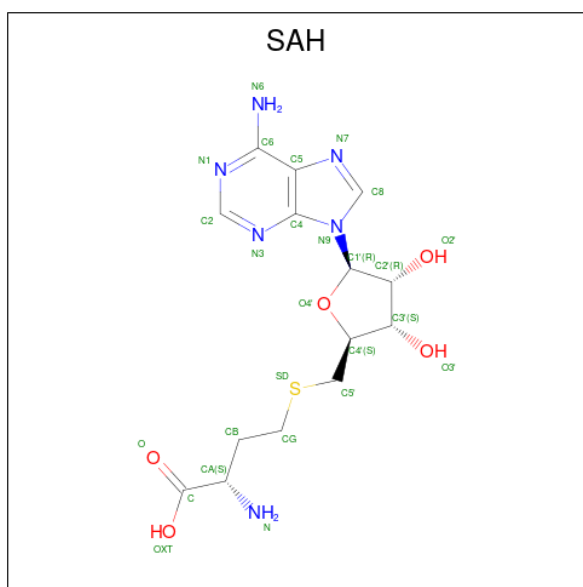
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
7	A	1	26	14	6	5	1	0	0

- Molecule 8 is alpha-D-glucopyranose (three-letter code: GLC) (formula: $C_6H_{12}O_6$).
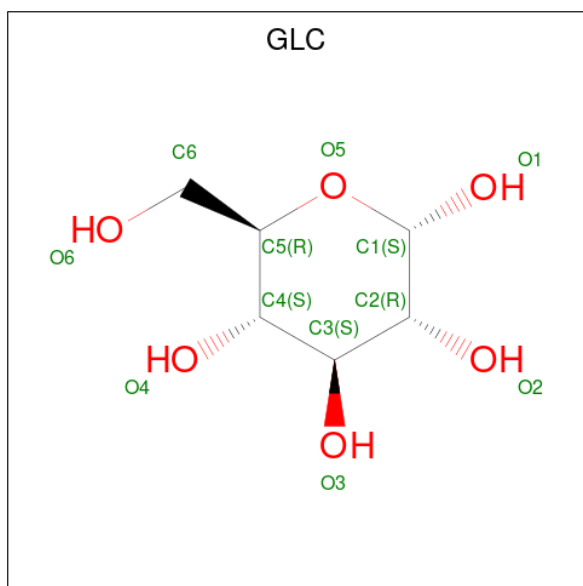
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
8	A	1	12	6	6	0	0
			Total	C	O		
8	A	1	12	6	6	0	0
			Total	C	O		
8	A	1	12	6	6	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total 12	C 6	O 6	0	0

- Molecule 9 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	1	Total 1	Zn 1	0	0

- Molecule 10 is beta-D-fructopyranose (three-letter code: BDF) (formula: $C_6H_{12}O_6$).

BDF
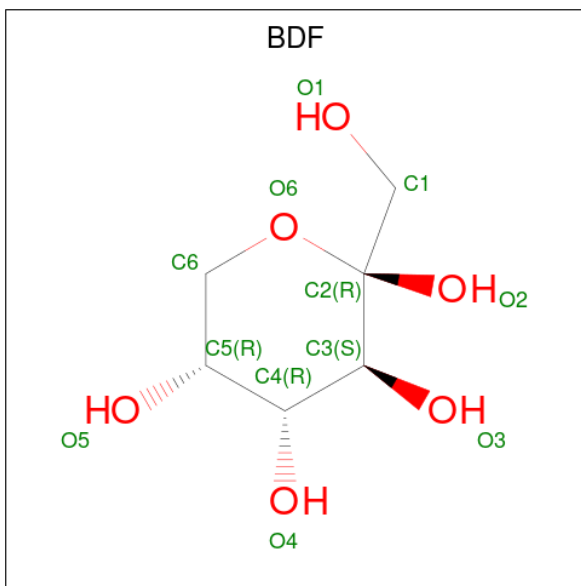
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	B	1	Total 12	C 6	O 6	0	0

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	269	Total 281	O 281	0	17
11	B	50	Total 53	O 53	0	3
11	C	22	Total 23	O 23	0	2

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.
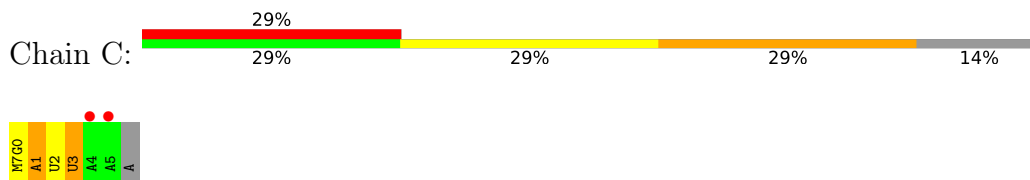
• Molecule 1: 2'-O-methyltransferase

Chain A:
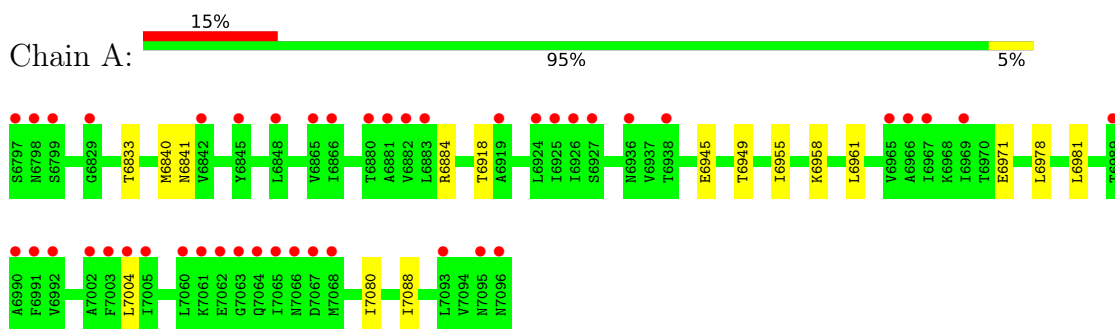
• Molecule 2: Non-structural protein 10

Chain B:
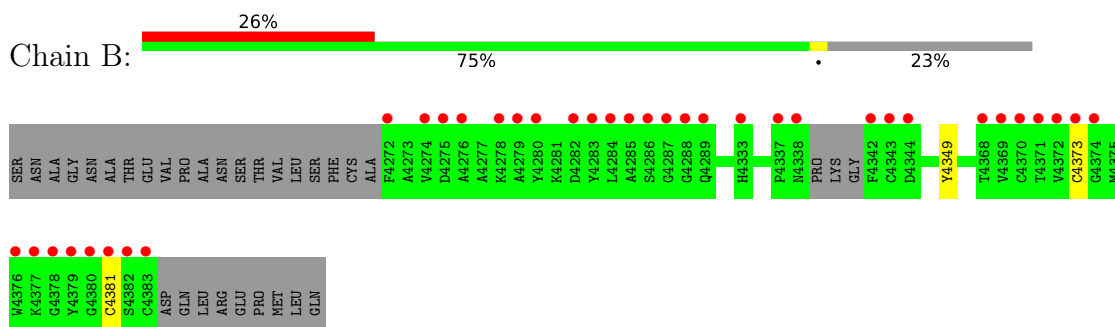
• Molecule 3: RNA (5'-D(*(M7G))-R(P*(A2M)P*UP*UP*AP*A)-3')

Chain C:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	168.76Å 168.76Å 52.27Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.95 – 1.98 29.95 – 1.98	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.95-1.98) 99.9 (29.95-1.98)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	2.66 (at 1.98Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.150 , 0.166 0.158 , 0.175	Depositor DCC
R_{free} test set	3093 reflections (5.20%)	wwPDB-VP
Wilson B-factor (Å^2)	33.0	Xtriage
Anisotropy	0.184	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 54.8	EDS
L-test for twinning[2]	$< \vert L \vert > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.029 for -h,-k,l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	3873	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< \vert L \vert >$, $< L^2 >$ 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: ZN, SAH, A2M, MN, M7G, SO4, CL, GLC, BDF

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	0.64	0/2534	0.72	0/3436
2	B	0.71	0/837	0.69	0/1133
3	C	0.26	0/73	0.71	0/114
All	All	0.65	0/3444	0.72	0/4683

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	A	2482	0	2447	15	0
2	B	820	0	780	6	0
3	C	118	0	60	6	0
4	A	1	0	0	0	0
5	A	3	0	0	0	0
6	A	5	0	0	1	0
7	A	26	0	19	2	0
8	A	48	0	48	4	0
9	B	1	0	0	0	0
10	B	12	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	A	281	0	0	0	0
11	B	53	0	0	0	0
11	C	23	0	0	0	0
All	All	3873	0	3366	22	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 3.

The worst 5 of 22 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:A:6833:THR:H	8:A:7107:GLC:H1	1.69	0.58
1:A:6840:MET:CE	3:C:3:U:C2	2.90	0.54
1:A:6918:THR:HG22	1:A:7088:ILE:HG22	1.89	0.54
1:A:6971:GLU:OE1	3:C:0:M7G:H82	2.07	0.54
1:A:6840:MET:HE2	3:C:3:U:N1	2.26	0.50

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	314/300 (105%)	309 (98%)	5 (2%)	0	100	100
2	B	107/141 (76%)	103 (96%)	4 (4%)	0	100	100
All	All	421/441 (96%)	412 (98%)	9 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	275/260 (106%)	275 (100%)	0	100	100
2	B	91/115 (79%)	91 (100%)	0	100	100
All	All	366/375 (98%)	366 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	C	3/7 (42%)	1 (33%)	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 ⓘ

1 non-standard protein/DNA/RNA residue is 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	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
3	A2M	C	1	3	18,25,26	1.08	1 (5%)	18,36,39	1.38	3 (16%)

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	A2M	C	1	3	-	0/5/27/28	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1	A2M	C5-C4	2.35	1.47	1.40

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	1	A2M	N3-C2-N1	-3.96	122.49	128.68
3	C	1	A2M	C4-C5-N7	-2.55	106.74	109.40
3	C	1	A2M	C2-N1-C6	2.15	122.44	118.75

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1	A2M	1	0

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 5 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	$\#|Z| > 2$
8	GLC	A	7106	-	12,12,12	0.44	0	17,17,17	1.11	1 (5%)
8	GLC	A	7108	-	12,12,12	0.53	0	17,17,17	0.69	0
8	GLC	A	7109	-	12,12,12	0.47	0	17,17,17	0.54	0
6	SO4	A	7104	-	4,4,4	0.38	0	6,6,6	0.06	0
7	SAH	A	7105	-	24,28,28	0.63	0	25,40,40	0.94	1 (4%)
8	GLC	A	7107	-	12,12,12	0.56	0	17,17,17	1.08	2 (11%)
10	BDF	B	4402	-	12,12,12	0.31	0	18,18,18	0.56	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
8	GLC	A	7106	-	-	0/2/22/22	0/1/1/1
8	GLC	A	7108	-	-	2/2/22/22	0/1/1/1
8	GLC	A	7109	-	-	2/2/22/22	0/1/1/1
7	SAH	A	7105	-	-	2/11/31/31	0/3/3/3
8	GLC	A	7107	-	-	0/2/22/22	0/1/1/1
10	BDF	B	4402	-	-	0/3/23/23	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	A	7107	GLC	O5-C1-C2	2.84	115.36	110.28
7	A	7105	SAH	C5-C6-N6	2.18	123.66	120.35
8	A	7106	GLC	O5-C5-C6	2.12	111.72	106.44
8	A	7107	GLC	C1-O5-C5	2.07	117.57	113.66

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	7109	GLC	O5-C5-C6-O6
8	A	7108	GLC	C4-C5-C6-O6
8	A	7109	GLC	C4-C5-C6-O6
8	A	7108	GLC	O5-C5-C6-O6
7	A	7105	SAH	O-C-CA-CB

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	7106	GLC	1	0
6	A	7104	SO4	1	0
7	A	7105	SAH	2	0
8	A	7107	GLC	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 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.

Ligand SAH A 7105

Bond lengths

Bond angles

Torsions

Rings
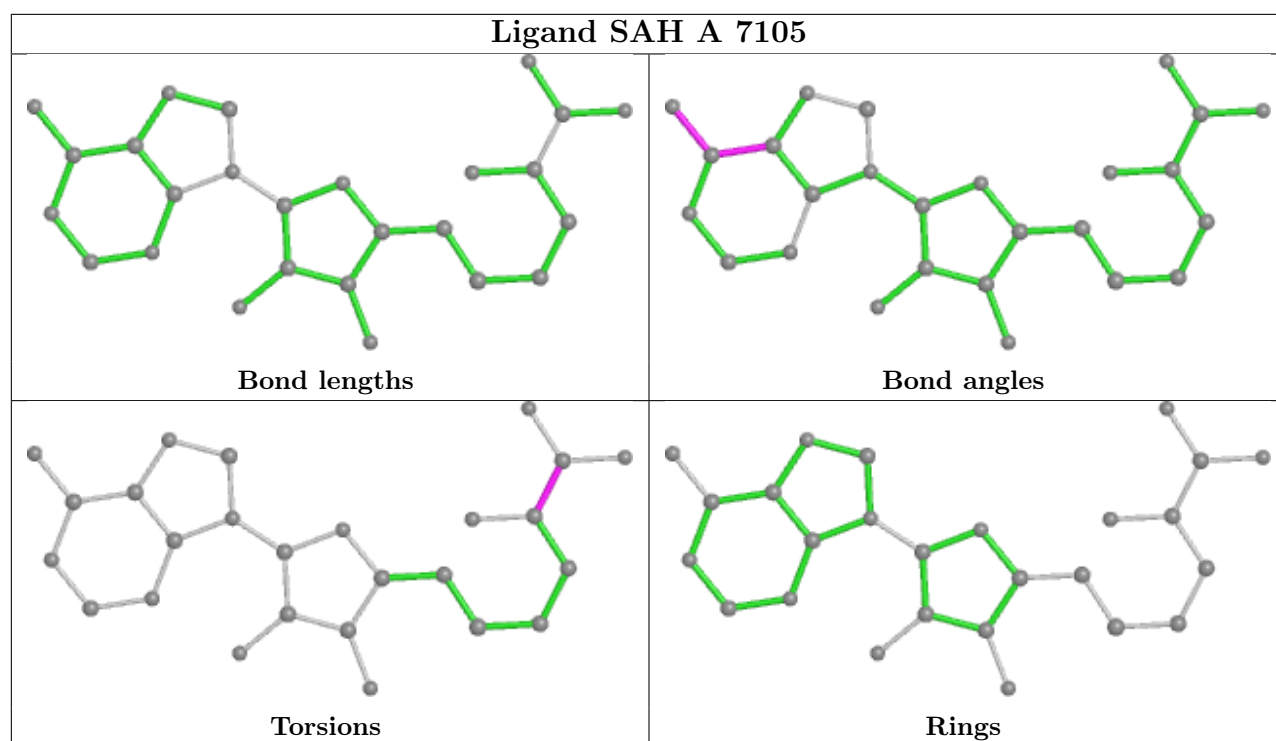
5.7 Other polymers (i)

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	300/300 (100%)	0.64	44 (14%)	2	2	23, 35, 67, 114	0
2	B	109/141 (77%)	1.61	36 (33%)	0	0	30, 58, 116, 146	0
3	C	4/7 (57%)	2.14	2 (50%)	0	0	49, 57, 117, 127	0
All	All	413/448 (92%)	0.91	82 (19%)	1	1	23, 39, 99, 146	0

The worst 5 of 82 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	4383	CYS	12.7
2	B	4342	PHE	8.8
2	B	4372	VAL	8.3
2	B	4371	THR	8.3
1	A	6797	SER	7.8

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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.

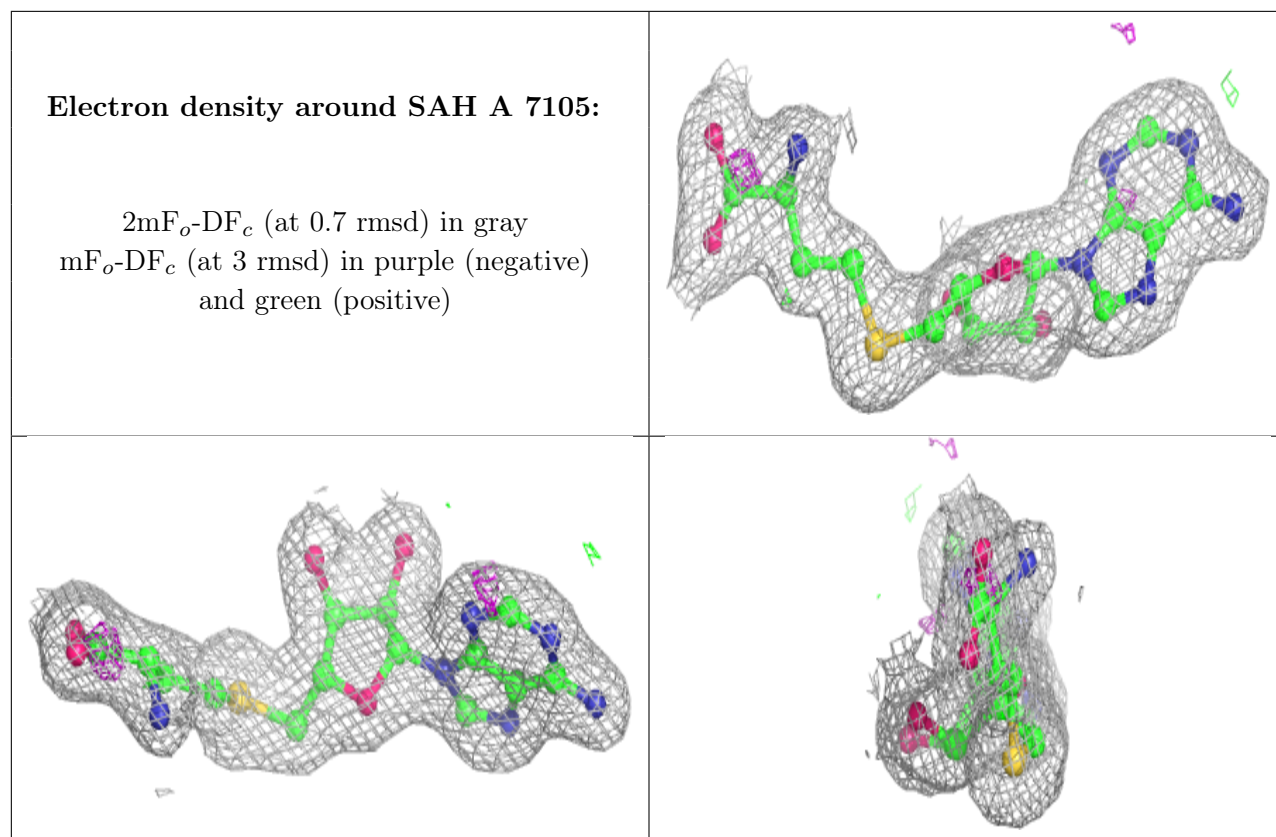| Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	A2M	C	1	23/24	0.95	0.10	34,39,50,50	0

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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.
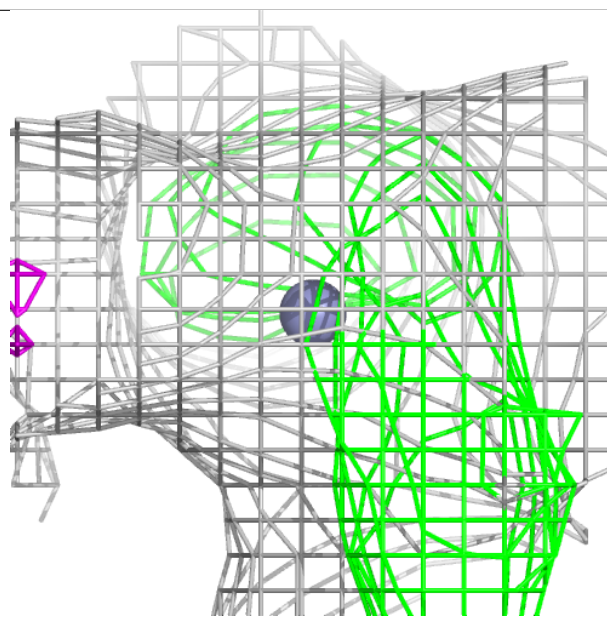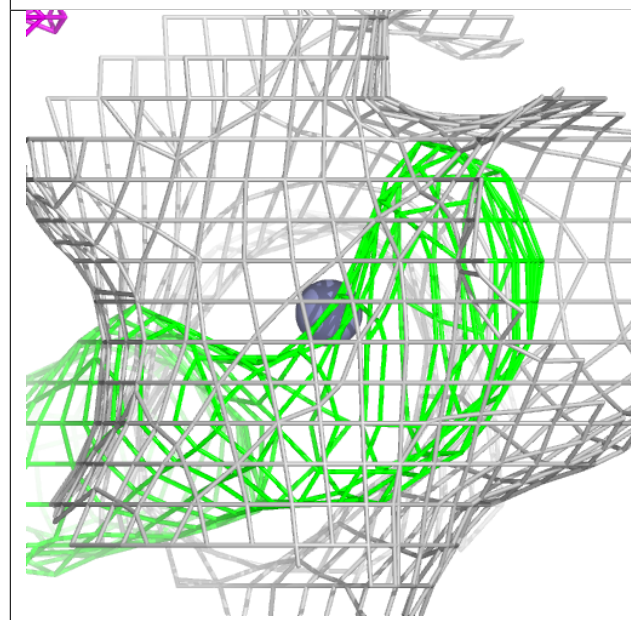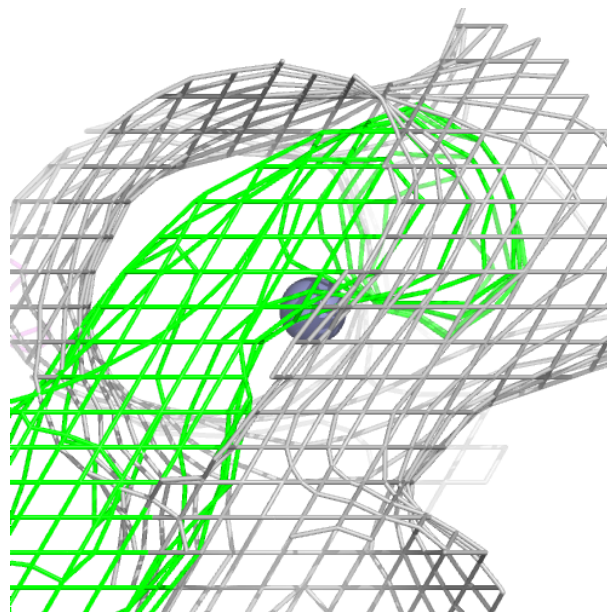
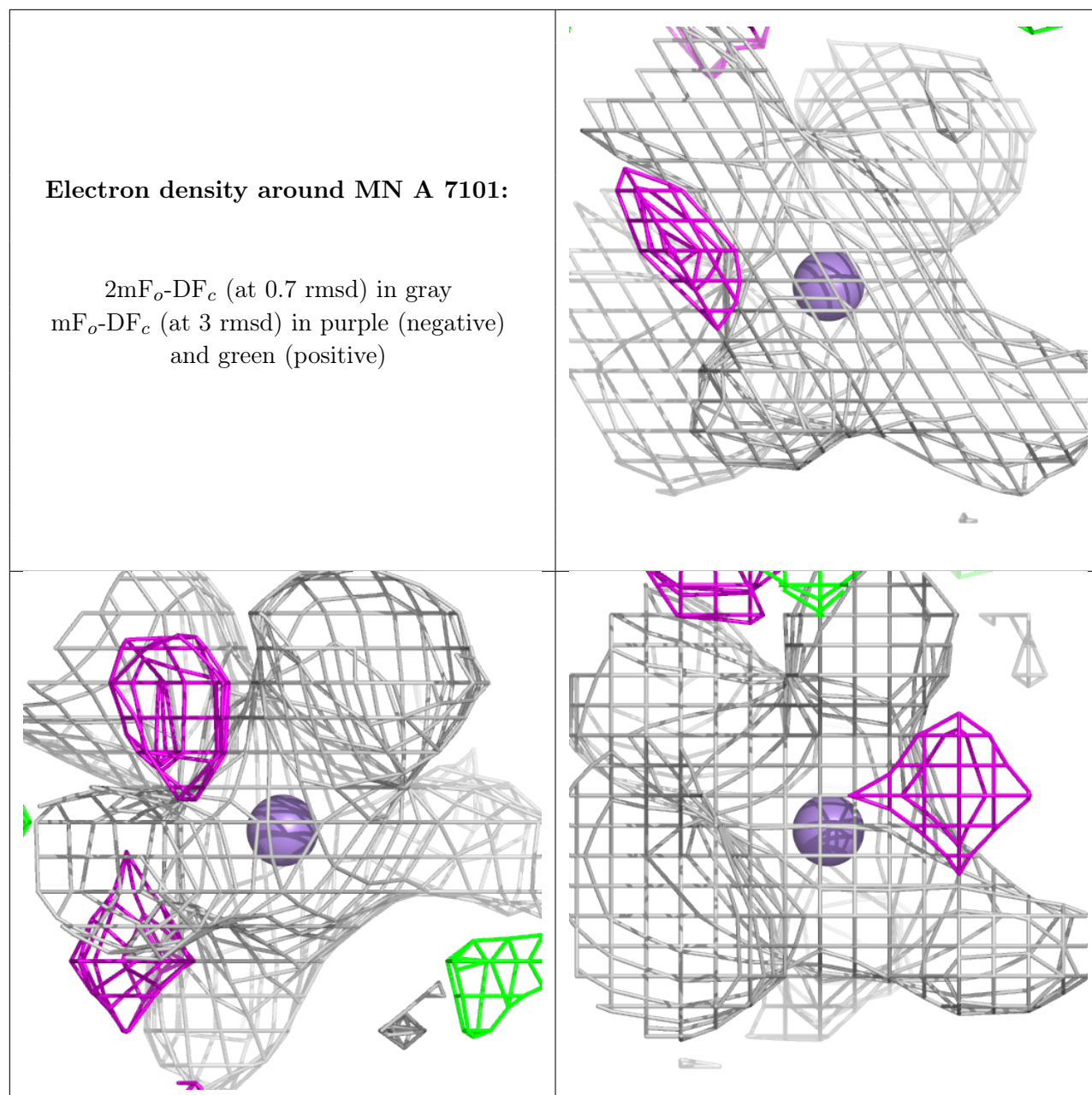| Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
8	GLC	A	7107	12/12	0.76	0.42	46,68,73,79	0
8	GLC	A	7109	12/12	0.76	0.37	101,105,112,113	0
8	GLC	A	7108	12/12	0.80	0.22	53,78,86,89	0
8	GLC	A	7106	12/12	0.81	0.44	41,56,63,67	12
6	SO4	A	7104	5/5	0.91	0.21	52,61,66,67	5
10	BDF	B	4402	12/12	0.91	0.20	51,60,65,67	0
5	CL	A	7102	1/1	0.92	0.23	65,65,65,65	1
5	CL	A	7103[A]	1/1	0.94	0.08	54,54,54,54	1
5	CL	A	7103[B]	1/1	0.94	0.08	57,57,57,57	1
7	SAH	A	7105	26/26	0.96	0.08	31,32,34,36	0
9	ZN	B	4401	1/1	0.96	0.09	39,39,39,39	1
4	MN	A	7101	1/1	0.96	0.09	41,41,41,41	1

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 SAH A 7105:

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

Electron density around ZN B 4401:

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

Electron density around MN A 7101:

$2mF_o$-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 ⓘ

There are no such residues in this entry.