



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 24, 2025 – 12:45 pm GMT

PDB ID : 9Q8H  
Title : SARS-CoV-2 methyltransferase nsp10-16 in complex with SAM and theophylline derivative BDH 34019023  
Authors : Kremling, V.; Sprenger, J.; Turk, D.; Oberthuer, D.; Kiene, A.  
Deposited on : 2025-02-24  
Resolution : 1.80 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.41.5

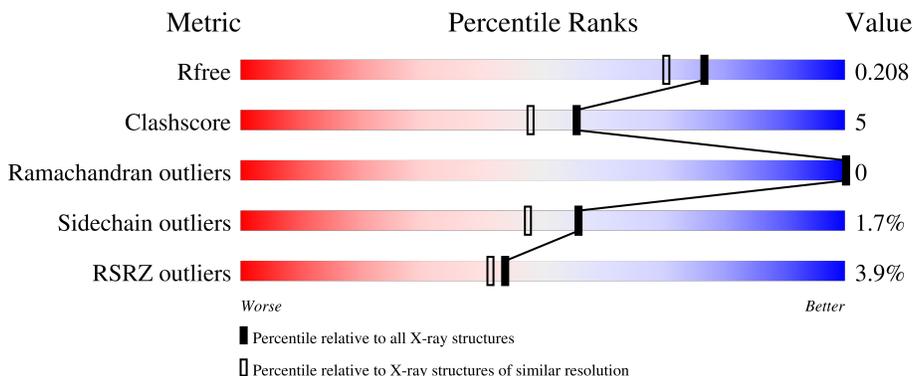
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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))
$R_{free}$	164625	7108 (1.80-1.80)
Clashscore	180529	8162 (1.80-1.80)
Ramachandran outliers	177936	8077 (1.80-1.80)
Sidechain outliers	177891	8076 (1.80-1.80)
RSRZ outliers	164620	7108 (1.80-1.80)

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  $\geq 3$ , 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	 3% 91% 7% ..
2	B	140	 5% 71% 10% • 18%

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
4	EDO	A	7215	-	-	X	-

## 2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 7019 atoms, of which 3331 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	
			Total	C	H	N	O				S
1	A	300	4730	1511	2361	400	441	17	0	1	0

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

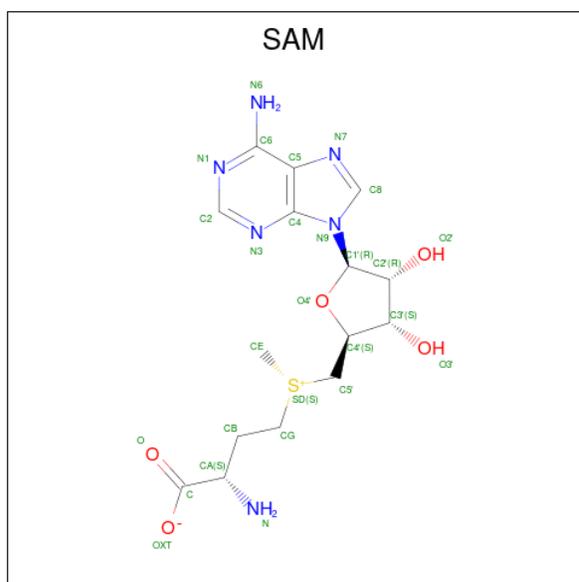
- Molecule 2 is a protein called Non-structural protein 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
2	B	115	1668	531	812	145	165	15	0	1	0

There is a discrepancy between the modelled and reference sequences:

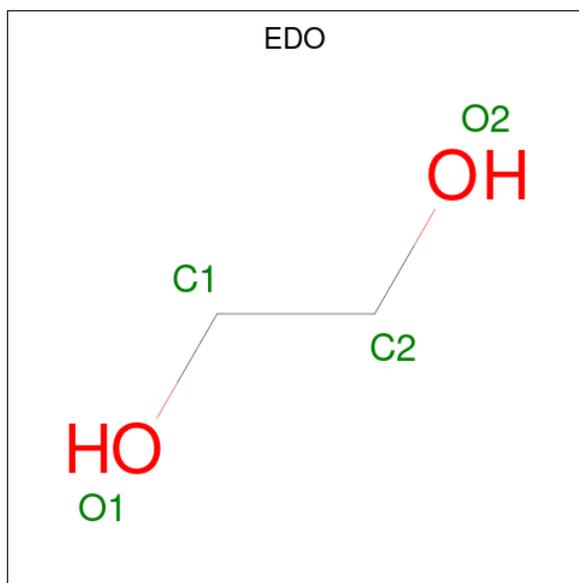
Chain	Residue	Modelled	Actual	Comment	Reference
B	4253	GLY	-	expression tag	UNP P0DTD1

- Molecule 3 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: C<sub>15</sub>H<sub>22</sub>N<sub>6</sub>O<sub>5</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			S
3	A	1	45	15	18	6	5	1	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



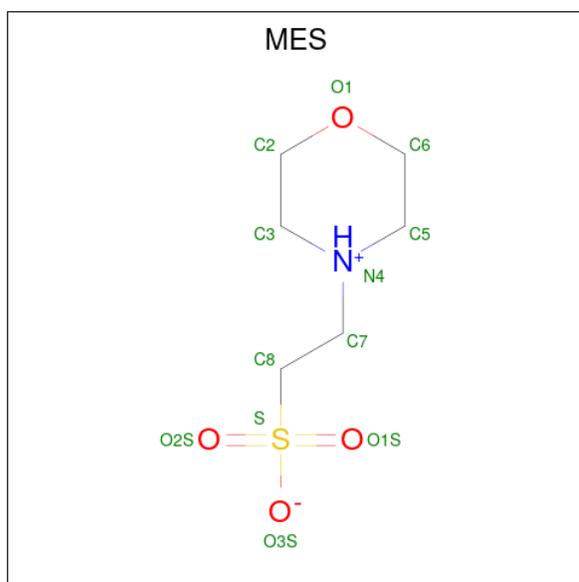
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	H			O
4	A	1	10	2	6	2	0	0
4	A	1	10	2	6	2	0	0
4	A	1	10	2	6	2	0	0

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

- Molecule 5 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>S).

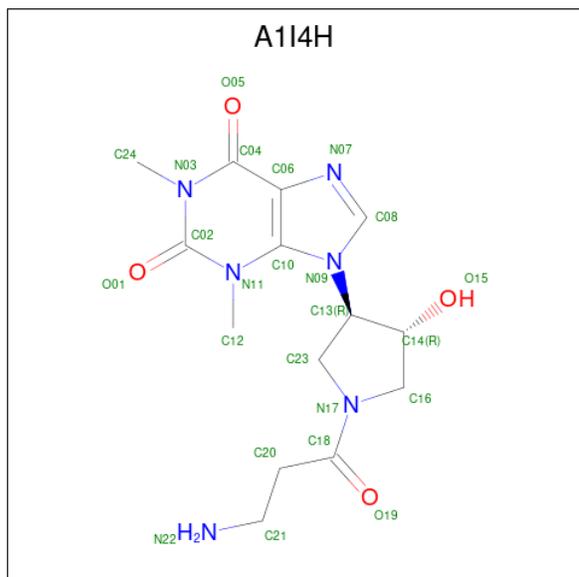


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			S
5	A	1	25	6	13	1	4	1	0	0

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
6	A	2	2	2	0	0

- Molecule 7 is 9-[(3 {R},4 {R})-1-(3-azanylpropanoyl)-4-oxidanyl-pyrrolidin-3-yl]-1,3-dimethyl-purine-2,6-dione (three-letter code: A114H) (formula: C<sub>14</sub>H<sub>20</sub>N<sub>6</sub>O<sub>4</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	H	N			O
7	A	1	44	14	20	6	4	0	0

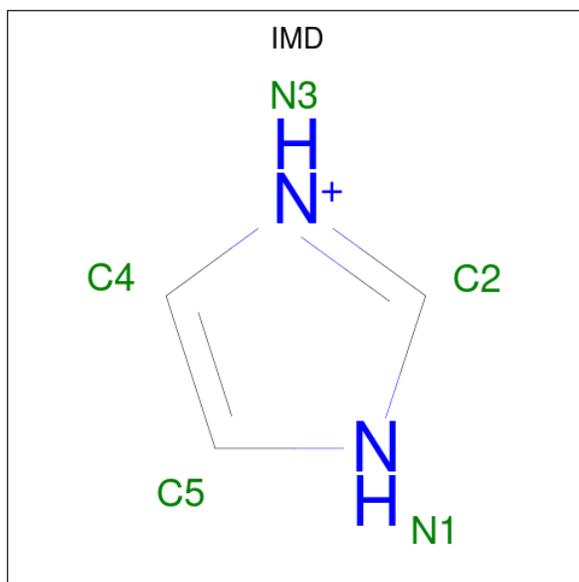
- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
8	A	1	1	1	0	0

- Molecule 9 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 10 is IMIDAZOLE (three-letter code: IMD) (formula: C<sub>3</sub>H<sub>5</sub>N<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	N		
10	B	1	10	3	5	2	0	0

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
11	A	240	240	240	0	0

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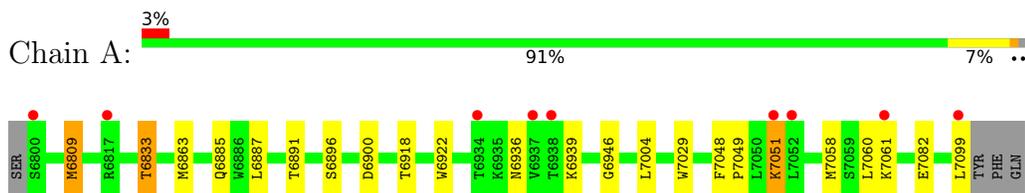
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
11	B	82	Total	O	0	0
			82	82		

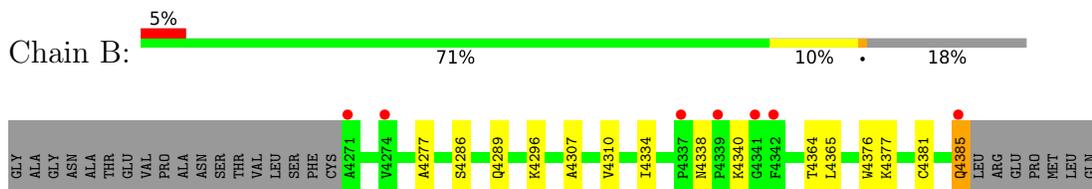
### 3 Residue-property plots [i](#)

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



- Molecule 2: Non-structural protein 10



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	168.20Å 168.20Å 52.01Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.56 – 1.80 48.56 – 1.80	Depositor EDS
% Data completeness (in resolution range)	90.9 (48.56-1.80) 90.9 (48.56-1.80)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.96 (at 1.57Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, $R_{free}$	0.193 , 0.219 0.189 , 0.208	Depositor DCC
$R_{free}$ test set	7777 reflections (1.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	44.2	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 48.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.017 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	7019	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<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.

## 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: A1I4H, EDO, MES, CL, IMD, SAM, NA, ZN

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	0.43	1/2420 (0.0%)	0.69	0/3282
2	B	0.40	0/875	0.65	0/1187
All	All	0.42	1/3295 (0.0%)	0.68	0/4469

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	6833	THR	C-N	-5.92	1.20	1.34

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	2369	2361	2358	19	0
2	B	856	812	810	11	0
3	A	27	18	22	0	0
4	A	48	72	72	6	0
4	B	20	30	30	3	0
5	A	12	13	12	0	0
6	A	2	0	0	0	0
7	A	24	20	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	A	1	0	0	0	0
9	B	2	0	0	0	0
10	B	5	5	5	0	0
11	A	240	0	0	3	0
11	B	82	0	0	2	0
All	All	3688	3331	3309	31	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 5.

The worst 5 of 31 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:7082:GLU:OE1	11:A:7301:HOH:O	1.96	0.83
1:A:7051:LYS:HE2	1:A:7051:LYS:H	1.48	0.78
2:B:4289:GLN:OE1	11:B:4501:HOH:O	2.03	0.76
2:B:4338:ASN:OD1	2:B:4340:LYS:N	2.24	0.70
2:B:4385:GLN:O	11:B:4502:HOH:O	2.09	0.69

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	299/304 (98%)	292 (98%)	7 (2%)	0	100	100
2	B	114/140 (81%)	110 (96%)	4 (4%)	0	100	100
All	All	413/444 (93%)	402 (97%)	11 (3%)	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	261/264 (99%)	257 (98%)	4 (2%)	60	53
2	B	94/113 (83%)	92 (98%)	2 (2%)	48	38
All	All	355/377 (94%)	349 (98%)	6 (2%)	56	47

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7099	LEU
2	B	4286	SER
2	B	4385	GLN
1	A	6900	ASP
1	A	6809	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7064	GLN

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 5 are monoatomic - leaving 21 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
4	EDO	A	7205	-	3,3,3	0.54	0	2,2,2	1.03	0
4	EDO	B	4401	-	3,3,3	0.51	0	2,2,2	0.42	0
10	IMD	B	4407	-	3,5,5	0.40	0	4,5,5	0.55	0
4	EDO	A	7203	-	3,3,3	0.48	0	2,2,2	0.62	0
3	SAM	A	7201	-	24,29,29	1.35	3 (12%)	23,42,42	1.75	4 (17%)
4	EDO	A	7212	-	3,3,3	0.53	0	2,2,2	0.21	0
7	A1I4H	A	7217	-	22,26,26	4.25	11 (50%)	25,39,39	2.53	10 (40%)
4	EDO	B	4405	-	3,3,3	0.54	0	2,2,2	0.22	0
4	EDO	A	7209	-	3,3,3	0.49	0	2,2,2	0.41	0
4	EDO	A	7211	-	3,3,3	0.50	0	2,2,2	0.08	0
4	EDO	A	7207	-	3,3,3	0.45	0	2,2,2	0.44	0
4	EDO	A	7208	-	3,3,3	0.58	0	2,2,2	0.38	0
4	EDO	A	7214	-	3,3,3	0.54	0	2,2,2	0.34	0
4	EDO	B	4404	-	3,3,3	0.54	0	2,2,2	0.34	0
5	MES	A	7204	-	12,12,12	2.18	1 (8%)	14,16,16	2.74	4 (28%)
4	EDO	A	7202	-	3,3,3	0.55	0	2,2,2	0.25	0
4	EDO	A	7215	-	3,3,3	0.48	0	2,2,2	0.71	0
4	EDO	B	4406	-	3,3,3	0.52	0	2,2,2	0.42	0
4	EDO	A	7206	-	3,3,3	0.55	0	2,2,2	0.48	0
4	EDO	B	4408	-	3,3,3	0.54	0	2,2,2	0.27	0
4	EDO	A	7213	-	3,3,3	0.56	0	2,2,2	0.10	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
4	EDO	A	7205	-	-	1/1/1/1	-
4	EDO	B	4401	-	-	0/1/1/1	-
10	IMD	B	4407	-	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	A	7203	-	-	1/1/1/1	-
3	SAM	A	7201	-	-	3/12/33/33	0/3/3/3
4	EDO	A	7212	-	-	0/1/1/1	-
7	A1I4H	A	7217	-	-	0/7/23/23	0/3/3/3
4	EDO	B	4405	-	-	1/1/1/1	-
4	EDO	A	7209	-	-	0/1/1/1	-
4	EDO	A	7211	-	-	0/1/1/1	-
4	EDO	A	7207	-	-	0/1/1/1	-
4	EDO	A	7208	-	-	0/1/1/1	-
4	EDO	A	7214	-	-	1/1/1/1	-
4	EDO	B	4404	-	-	0/1/1/1	-
5	MES	A	7204	-	-	0/6/14/14	0/1/1/1
4	EDO	A	7202	-	-	0/1/1/1	-
4	EDO	A	7215	-	-	1/1/1/1	-
4	EDO	B	4406	-	-	0/1/1/1	-
4	EDO	A	7206	-	-	0/1/1/1	-
4	EDO	B	4408	-	-	0/1/1/1	-
4	EDO	A	7213	-	-	1/1/1/1	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	7217	A1I4H	C16-C14	-12.11	1.33	1.52
5	A	7204	MES	C8-S	-7.23	1.67	1.77
7	A	7217	A1I4H	C02-N11	7.07	1.46	1.38
7	A	7217	A1I4H	C16-N17	6.77	1.60	1.46
7	A	7217	A1I4H	C18-N17	6.70	1.48	1.35

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	7204	MES	O2S-S-C8	8.27	116.88	106.92
7	A	7217	A1I4H	N03-C02-N11	5.97	121.27	116.97
7	A	7217	A1I4H	C04-N03-C02	-5.94	120.89	125.63
3	A	7201	SAM	N3-C2-N1	-5.04	120.80	128.68
7	A	7217	A1I4H	C12-N11-C10	4.38	124.48	116.71

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

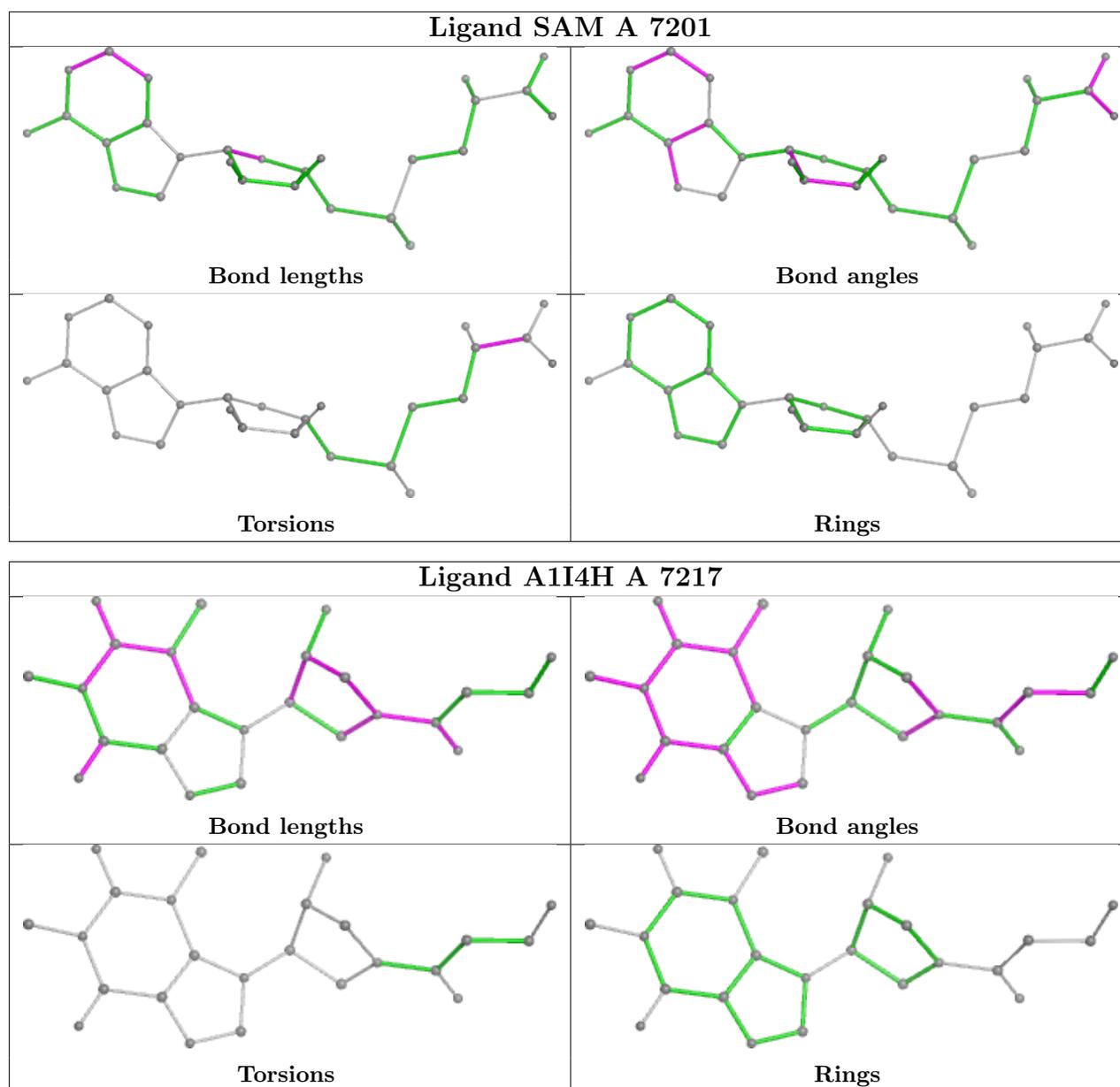
Mol	Chain	Res	Type	Atoms
3	A	7201	SAM	OXT-C-CA-CB
3	A	7201	SAM	O-C-CA-CB
4	A	7214	EDO	O1-C1-C2-O2
4	B	4405	EDO	O1-C1-C2-O2
4	A	7205	EDO	O1-C1-C2-O2

There are no ring outliers.

6 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	4401	EDO	2	0
4	A	7203	EDO	1	0
7	A	7217	A1I4H	1	0
4	A	7207	EDO	1	0
4	B	4404	EDO	1	0
4	A	7215	EDO	4	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	6833:THR	C	6834:LEU	N	1.20

## 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	300/304 (98%)	-0.22	9 (3%) 52 50	30, 48, 89, 124	1 (0%)
2	B	115/140 (82%)	0.25	7 (6%) 28 26	28, 58, 99, 124	1 (0%)
All	All	415/444 (93%)	-0.09	16 (3%) 44 41	28, 50, 93, 124	2 (0%)

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	7099	LEU	6.0
1	A	7052	LEU	5.0
1	A	6800	SER	3.9
2	B	4342	PHE	3.6
2	B	4339	PRO	3.4

### 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](#)

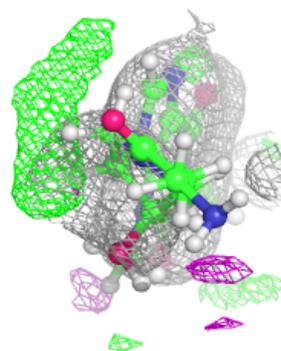
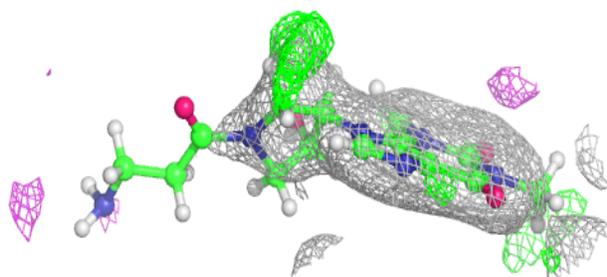
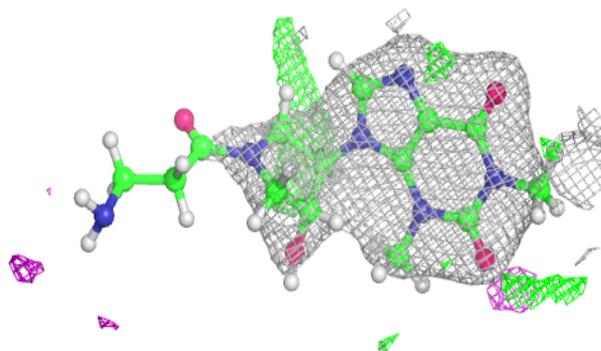
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 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
4	EDO	B	4405	4/4	0.81	0.25	71,97,131,131	0
4	EDO	A	7209	4/4	0.83	0.29	52,91,121,121	0
4	EDO	A	7202	4/4	0.83	0.24	63,81,103,103	0
4	EDO	A	7206	4/4	0.87	0.18	54,69,74,83	0
4	EDO	B	4408	4/4	0.87	0.17	64,93,120,120	0
4	EDO	A	7211	4/4	0.88	0.21	66,80,91,91	0
4	EDO	A	7208	4/4	0.90	0.19	47,73,96,96	0
4	EDO	B	4401	4/4	0.90	0.16	42,70,84,86	0
7	A1I4H	A	7217	24/24	0.90	0.14	58,106,149,155	0
4	EDO	A	7215	4/4	0.91	0.17	44,67,89,89	0
4	EDO	A	7203	4/4	0.91	0.14	48,63,80,96	0
4	EDO	A	7205	4/4	0.91	0.16	57,74,94,94	0
4	EDO	B	4406	4/4	0.91	0.15	56,83,90,100	0
3	SAM	A	7201	27/27	0.91	0.13	46,69,92,101	0
4	EDO	A	7214	4/4	0.91	0.15	58,70,84,97	0
4	EDO	A	7207	4/4	0.92	0.14	51,69,84,101	0
4	EDO	B	4404	4/4	0.92	0.13	58,71,110,110	0
4	EDO	A	7213	4/4	0.93	0.13	56,68,72,76	0
5	MES	A	7204	12/12	0.94	0.12	45,66,107,108	0
4	EDO	A	7212	4/4	0.94	0.13	65,86,92,103	0
10	IMD	B	4407	5/5	0.94	0.14	64,77,91,97	0
8	CL	A	7218	1/1	0.95	0.15	71,71,71,71	0
6	NA	A	7216	1/1	0.96	0.12	59,59,59,59	0
9	ZN	B	4403	1/1	0.98	0.05	69,69,69,69	0
6	NA	A	7210	1/1	0.99	0.07	51,51,51,51	0
9	ZN	B	4402	1/1	0.99	0.04	49,49,49,49	0

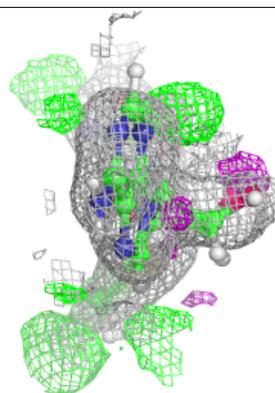
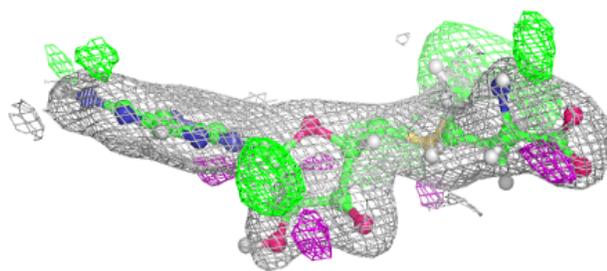
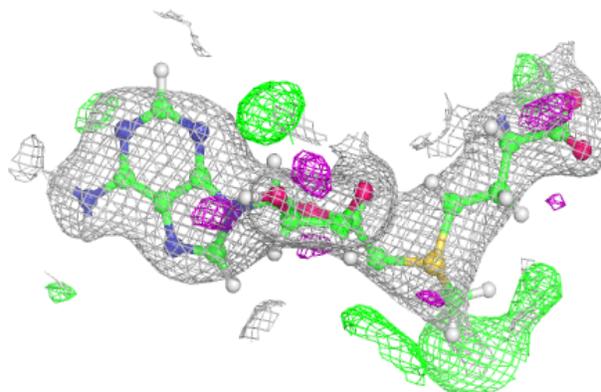
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around A1I4H A 7217:**

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

**Electron density around SAM A 7201:**

$2mF_o-DF_c$  (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.