



# wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 4, 2024 – 04:01 am GMT

PDB ID : 8RBD  
Title : Crystal structure of Mycobacterium tuberculosis MmaA1 with Sinefungin (SFG)  
Authors : Kobakhidze, G.; Wachelder, L.; Chaudhary, B.; Mazumdar, P.A.; Madhuran-takam, G.; Dong, G.  
Deposited on : 2023-12-04  
Resolution : 1.50 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) : 2.40

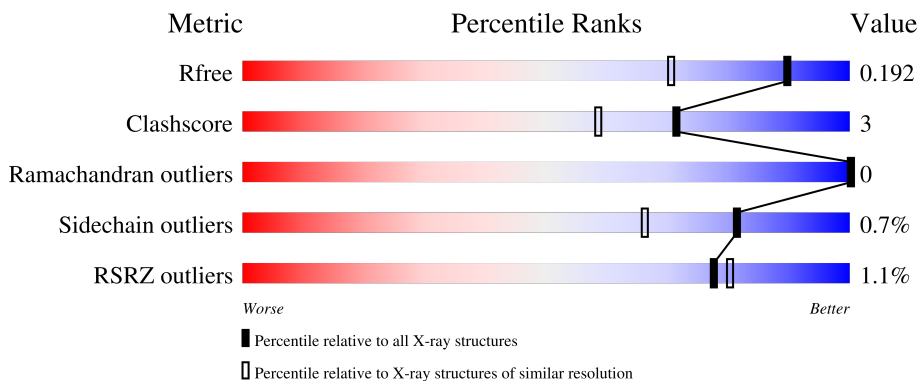
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.50 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	3717 (1.50-1.50)
Clashscore	180529	4048 (1.50-1.50)
Ramachandran outliers	177936	3970 (1.50-1.50)
Sidechain outliers	177891	3967 (1.50-1.50)
RSRZ outliers	164620	3718 (1.50-1.50)

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  $\geq 3$ , 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	287	
1	A0A0	287	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9661 atoms, of which 4403 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.

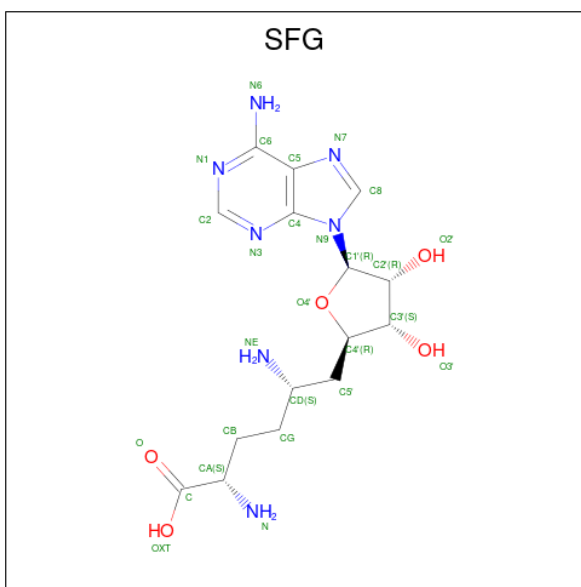
- Molecule 1 is a protein called Mycolic acid methyltransferase MmaA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	271	4348	1407	2135	382	415	9	0	0	0
1	A0A0	271	4369	1412	2148	385	415	9	0	1	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	HIS	-	expression tag	UNP P0A5Q1
A0A0	0	HIS	-	expression tag	UNP P0A5Q1

- Molecule 2 is SINEFUNGIN (three-letter code: SFG) (formula:  $C_{15}H_{23}N_7O_5$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
2	A	1	48	15	21	7	5	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	H	N			O
2	A0A0	1	48	15	21	7	5	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



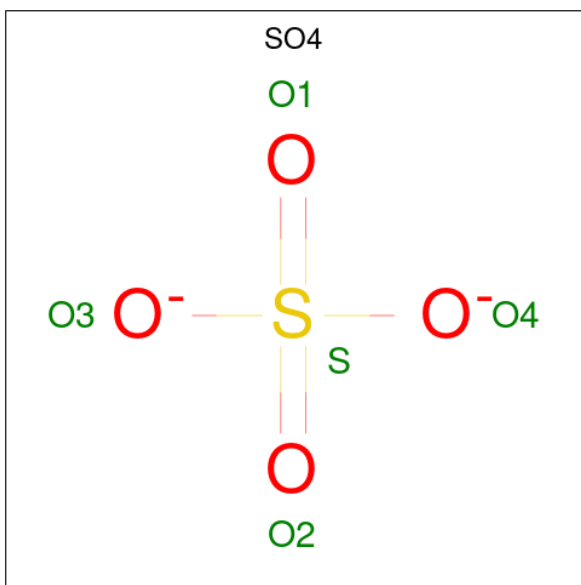
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
3	A	1	10	2	6	2	0	0
3	A	1	10	2	6	2	0	0
3	A	1	10	2	6	2	0	0
3	A	1	10	2	6	2	0	0
3	A	1	10	2	6	2	0	0
3	A	1	10	2	6	2	0	0
3	A	1	10	2	6	2	0	0
3	A0A0	1	10	2	6	2	0	0
3	A0A0	1	10	2	6	2	0	0
3	A0A0	1	10	2	6	2	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A0A0	1	Total	C	H	O	0	0
			10	2	6	2		
3	A0A0	1	Total	C	H	O	0	0
			10	2	6	2		
3	A0A0	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	371	Total	O	0	0
			371	371		
5	A0A0	337	Total	O	0	0
			337	337		

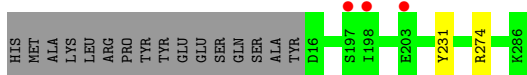
### 3 Residue-property plots [i](#)

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: Mycolic acid methyltransferase MmaA1



- Molecule 1: Mycolic acid methyltransferase MmaA1



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	41.23Å 74.14Å 96.77Å 90.00° 90.43° 90.00°	Depositor
Resolution (Å)	19.86 – 1.50 19.86 – 1.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.86-1.50) 99.8 (19.86-1.50)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.09 (at 1.50Å)	Xtrriage
Refinement program	PHENIX 1.20.1-4487-000	Depositor
R, $R_{free}$	0.165 , 0.192 0.167 , 0.192	Depositor DCC
$R_{free}$ test set	91153 reflections (2.17%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.9	Xtrriage
Anisotropy	0.232	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.42 , 45.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.021 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	9661	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.66% 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: SFG, CSO, SO4, EDO

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	0.47	0/2254	0.66	0/3046
1	A0A0	0.47	0/2265	0.67	0/3060
All	All	0.47	0/4519	0.66	0/6106

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	A0A0	0	2
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	174	ARG	Sidechain
1	A0A0	274[A]	ARG	Sidechain
1	A0A0	274[B]	ARG	Sidechain

### 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	2213	2135	2135	13	0
1	A0A0	2221	2148	0	0	0
2	A	27	21	22	0	0
2	A0A0	27	21	0	0	0
3	A	28	42	42	2	0
3	A0A0	24	36	0	0	0
4	A	10	0	0	0	0
5	A	371	0	0	10	2
5	A0A0	337	0	0	0	1
All	All	5258	4403	2199	14	2

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 14 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:100:GLU:OE1	5:A:401:HOH:O	1.90	0.90
1:A:268:CSO:SG	5:A:409:HOH:O	2.36	0.82
1:A:160:ASP:OD2	5:A:403:HOH:O	2.02	0.76
1:A:271:ARG:HG2	1:A:276:LEU:HD12	1.68	0.75
1:A:243:GLN:NE2	5:A:402:HOH:O	2.29	0.65

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:602:HOH:O	5:A0A0:644:HOH:O[1_455]	1.95	0.25
5:A:427:HOH:O	5:A:642:HOH:O[1_655]	1.96	0.24

## 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	268/287 (93%)	264 (98%)	4 (2%)	0	100	100
1	A0A0	269/287 (94%)	265 (98%)	4 (2%)	0	100	100
All	All	537/574 (94%)	529 (98%)	8 (2%)	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	228/242 (94%)	226 (99%)	2 (1%)	75	57
1	A0A0	229/242 (95%)	228 (100%)	1 (0%)	89	79
All	All	457/484 (94%)	454 (99%)	3 (1%)	81	66

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	116	GLU
1	A	231	TYR
1	A0A0	231	TYR

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

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

2 non-standard protein/DNA/RNA residues are 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
1	CSO	A0A0	268	1	3,6,7	0.58	0	0,6,8	-	-
1	CSO	A	268	1	3,6,7	0.69	0	0,6,8	-	-

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
1	CSO	A0A0	268	1	-	0/1/5/7	-
1	CSO	A	268	1	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

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
1	A	268	CSO	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

17 ligands are 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	EDO	A	307	-	3,3,3	0.47	0	2,2,2	0.36	0
3	EDO	A	303	-	3,3,3	0.39	0	2,2,2	0.44	0
3	EDO	A0A0	304	-	3,3,3	0.43	0	2,2,2	0.34	0
3	EDO	A	302	-	3,3,3	0.44	0	2,2,2	0.26	0
4	SO4	A	309	-	4,4,4	0.13	0	6,6,6	0.11	0
2	SFG	A	301	-	25,29,29	<b>3.73</b>	<b>9 (36%)</b>	23,42,42	<b>2.39</b>	<b>4 (17%)</b>
3	EDO	A	304	-	3,3,3	0.49	0	2,2,2	0.28	0
3	EDO	A	305	-	3,3,3	0.54	0	2,2,2	0.27	0
4	SO4	A	308	-	4,4,4	0.19	0	6,6,6	0.12	0
3	EDO	A	310	-	3,3,3	0.49	0	2,2,2	0.37	0
2	SFG	A0A0	301	-	25,29,29	<b>3.88</b>	<b>9 (36%)</b>	23,42,42	<b>2.38</b>	<b>5 (21%)</b>
3	EDO	A0A0	303	-	3,3,3	0.38	0	2,2,2	0.29	0
3	EDO	A0A0	307	-	3,3,3	0.41	0	2,2,2	0.31	0
3	EDO	A0A0	302	-	3,3,3	0.44	0	2,2,2	0.50	0
3	EDO	A	306	-	3,3,3	0.48	0	2,2,2	0.34	0
3	EDO	A0A0	306	-	3,3,3	0.42	0	2,2,2	0.41	0
3	EDO	A0A0	305	-	3,3,3	0.38	0	2,2,2	0.55	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
3	EDO	A	307	-	-	0/1/1/1	-
3	EDO	A	303	-	-	0/1/1/1	-
3	EDO	A0A0	304	-	-	1/1/1/1	-
3	EDO	A	302	-	-	0/1/1/1	-
2	SFG	A	301	-	-	<b>2/13/33/33</b>	0/3/3/3
3	EDO	A	304	-	-	1/1/1/1	-
3	EDO	A	305	-	-	0/1/1/1	-
3	EDO	A	310	-	-	1/1/1/1	-
2	SFG	A0A0	301	-	-	<b>3/13/33/33</b>	0/3/3/3
3	EDO	A0A0	303	-	-	1/1/1/1	-
3	EDO	A0A0	307	-	-	1/1/1/1	-
3	EDO	A0A0	302	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	A	306	-	-	0/1/1/1	-
3	EDO	A0A0	306	-	-	1/1/1/1	-
3	EDO	A0A0	305	-	-	0/1/1/1	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A0A0	301	SFG	O4'-C1'	12.71	1.58	1.41
2	A	301	SFG	O4'-C1'	11.88	1.57	1.41
2	A0A0	301	SFG	C2'-C1'	-11.86	1.35	1.53
2	A	301	SFG	C2'-C1'	-11.50	1.36	1.53
2	A	301	SFG	O4'-C4'	-4.62	1.34	1.45

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	SFG	C5-C6-N6	7.86	132.29	120.35
2	A0A0	301	SFG	C5-C6-N6	7.55	131.83	120.35
2	A	301	SFG	N3-C2-N1	-5.12	120.67	128.68
2	A	301	SFG	N6-C6-N1	-4.79	108.64	118.57
2	A0A0	301	SFG	N3-C2-N1	-4.77	121.22	128.68

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	SFG	N-CA-CB-CG
2	A	301	SFG	C-CA-CB-CG
2	A0A0	301	SFG	N-CA-CB-CG
3	A0A0	304	EDO	O1-C1-C2-O2
3	A0A0	306	EDO	O1-C1-C2-O2

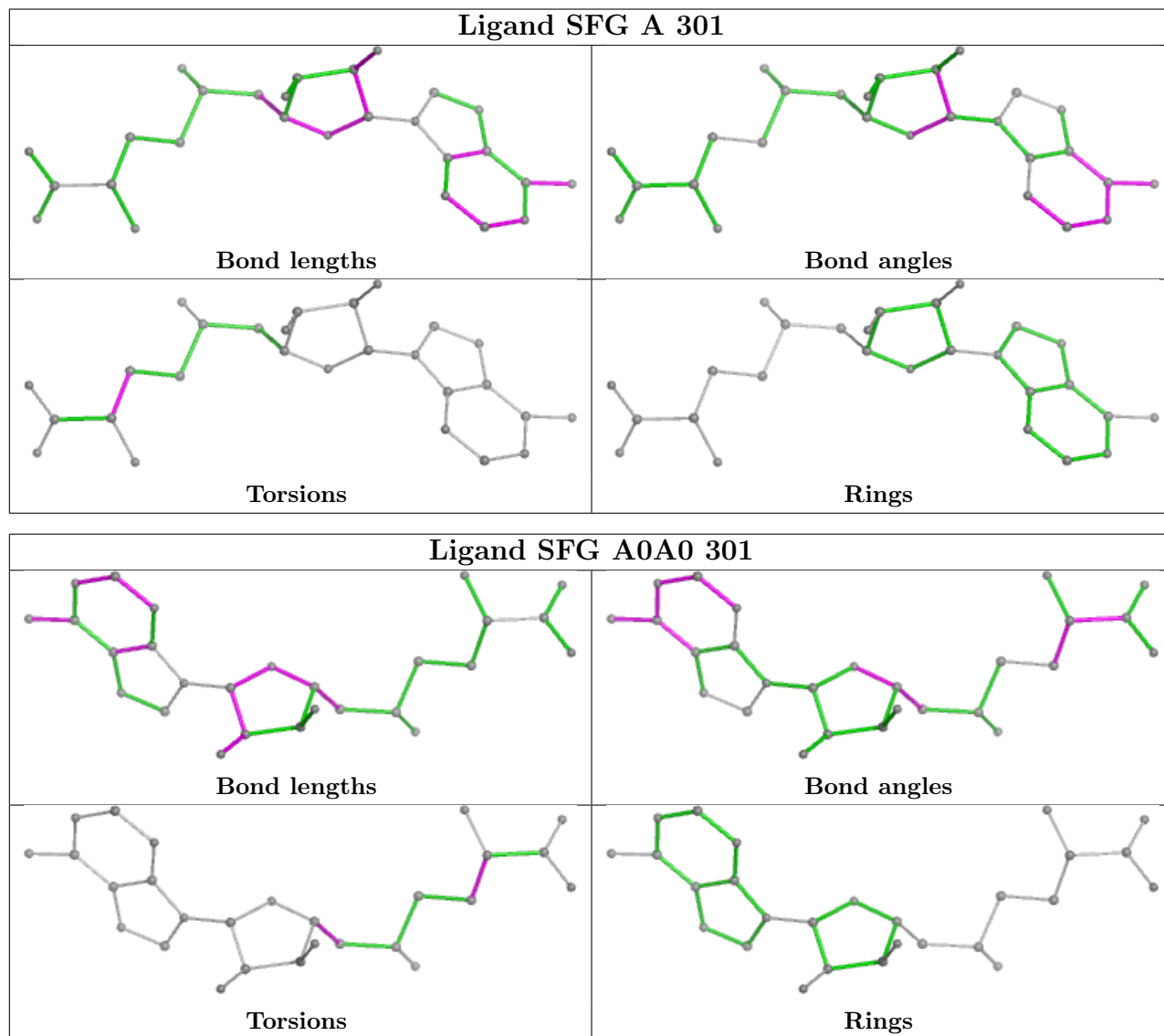
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	305	EDO	1	0
3	A	310	EDO	1	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

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<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	270/287 (94%)	-0.26	3 (1%) 77 80	22, 30, 51, 77	0
1	A0A0	270/287 (94%)	-0.26	3 (1%) 77 80	19, 32, 53, 79	1 (0%)
All	All	540/574 (94%)	-0.26	6 (1%) 77 80	19, 31, 52, 79	1 (0%)

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	198	ILE	2.9
1	A0A0	197	SER	2.8
1	A	175	TRP	2.6
1	A0A0	203	GLU	2.4
1	A	201	GLY	2.2

### 6.2 Non-standard residues in protein, DNA, RNA chains [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(Å <sup>2</sup> )	Q<0.9
1	CSO	A0A0	268	7/8	0.91	0.07	21,24,29,31	0
1	CSO	A	268	7/8	0.94	0.07	22,24,29,31	0

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.



## 6.4 Ligands

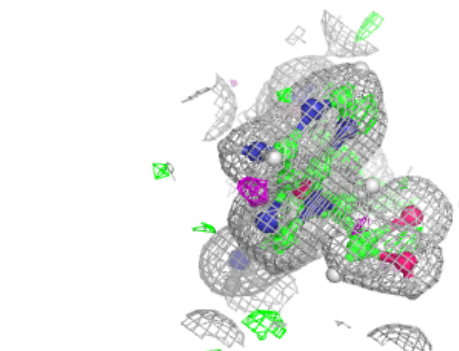
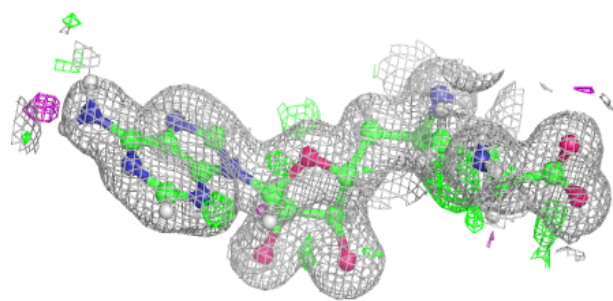
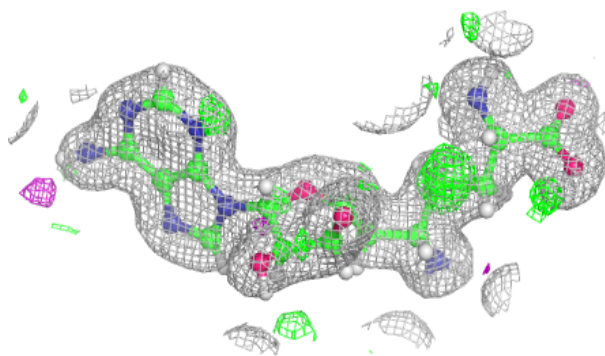
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	EDO	A	305	4/4	0.66	0.15	52,63,71,82	0
3	EDO	A	306	4/4	0.67	0.15	58,69,73,75	0
3	EDO	A	307	4/4	0.70	0.15	47,61,67,80	0
3	EDO	A0A0	303	4/4	0.74	0.14	48,57,61,63	0
3	EDO	A0A0	306	4/4	0.74	0.15	47,62,66,75	0
3	EDO	A0A0	302	4/4	0.75	0.13	53,64,74,77	0
3	EDO	A	310	4/4	0.76	0.13	39,47,58,70	0
3	EDO	A0A0	304	4/4	0.77	0.14	53,64,71,75	0
3	EDO	A	304	4/4	0.77	0.14	45,54,61,66	0
3	EDO	A	302	4/4	0.79	0.15	44,56,67,67	0
3	EDO	A0A0	305	4/4	0.83	0.15	53,63,69,69	0
3	EDO	A0A0	307	4/4	0.84	0.12	41,50,64,65	0
3	EDO	A	303	4/4	0.86	0.13	32,47,69,69	0
4	SO4	A	309	5/5	0.88	0.08	56,67,71,71	0
4	SO4	A	308	5/5	0.95	0.08	41,43,54,57	0
2	SFG	A0A0	301	27/27	0.95	0.07	20,28,34,36	0
2	SFG	A	301	27/27	0.96	0.06	21,26,33,35	0

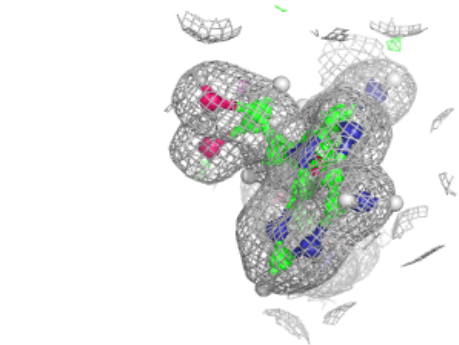
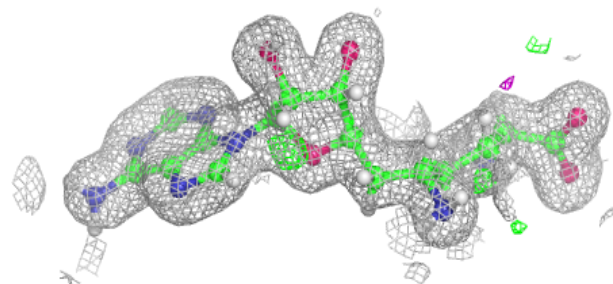
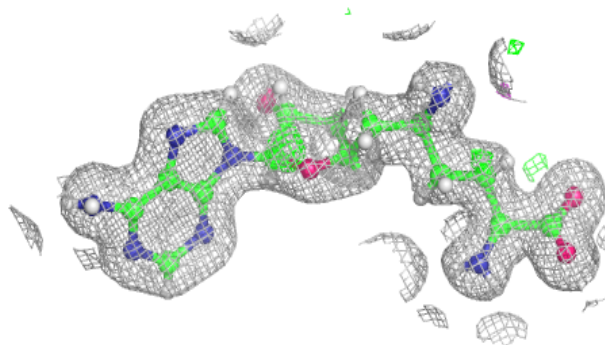
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around SFG A0A0 301:**

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

**Electron density around SFG A 301:**

$2mF_o-DF_c$  (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.