Full wwPDB X-ray Structure Validation Report (i)

Aug 22, 2023 – 08:12 PM EDT

PDB ID	:	3CBP
Title	:	Set7/9-ER-Sinefungin complex
Authors	:	Cheng, X.; Jia, D.
Deposited on	:	2008-02-22
Resolution	:	1.42 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

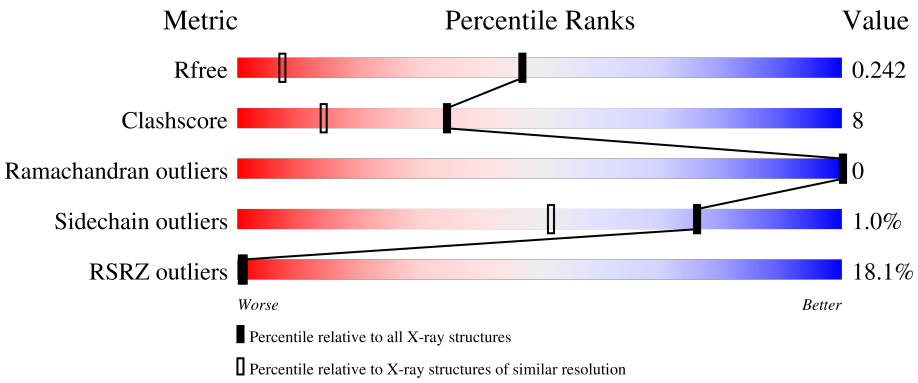
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.42 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}	130704	2579 (1.44-1.40)
Clashscore	141614	2696 (1.44-1.40)
Ramachandran outliers	138981	2632 (1.44-1.40)
Sidechain outliers	138945	2631 (1.44-1.40)
RSRZ outliers	127900	2528 (1.44-1.40)

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	256	16%, 82%, 11%, 7%
2	B	10	40%, 20%, 20%, 60%

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	BME	A	395	-	-	-	X
4	BME	A	397	-	-	X	-
5	GOL	A	1502	-	X	-	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 2108 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.

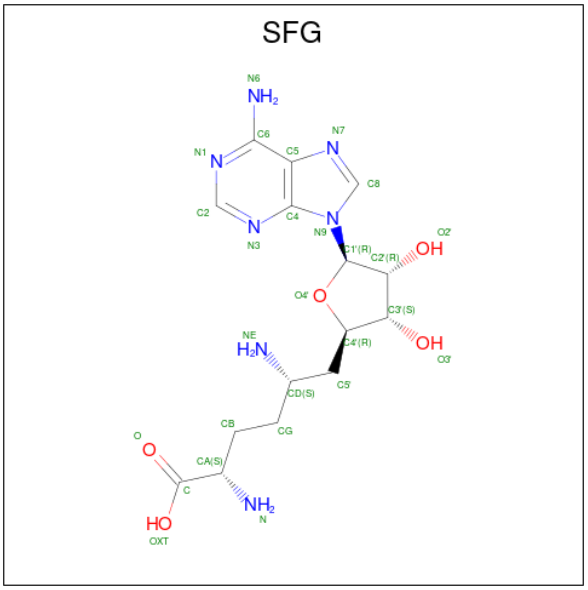
- Molecule 1 is a protein called Histone-lysine N-methyltransferase SETD7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	239	1915	1215	309	379	12	0	7	0

- Molecule 2 is a protein called Estrogen receptor.

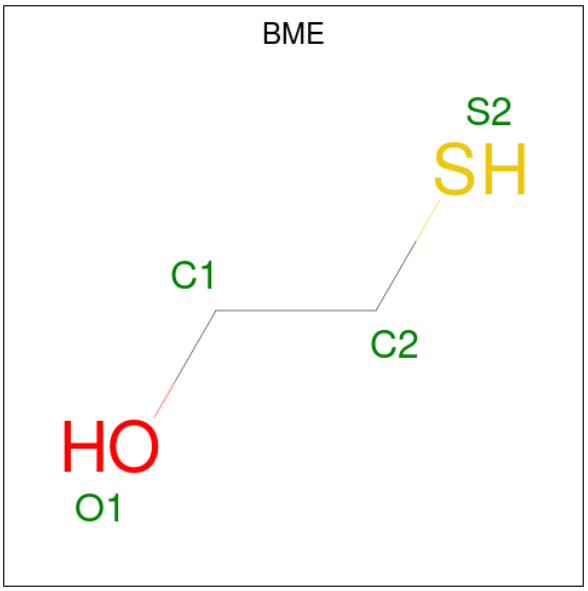
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	4	31	18	8	5	0	0	0

- Molecule 3 is SINEFUNGIN (three-letter code: SFG) (formula: $C_{15}H_{23}N_7O_5$).



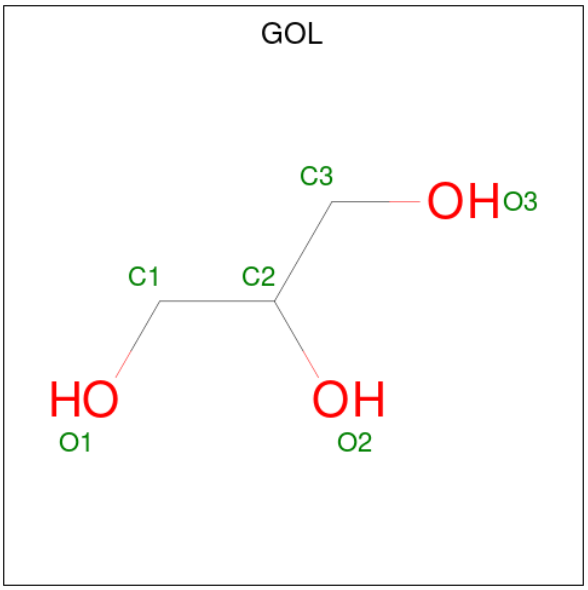
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	27	15	7	5	0	0

- Molecule 4 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	S		
4	A	1	4	2	1	1	0	0
			Total	C	O	S		
4	A	1	4	2	1	1	0	0
			Total	C	O	S		
4	A	1	4	2	1	1	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	6	3	3	0	0

- Molecule 6 is water.

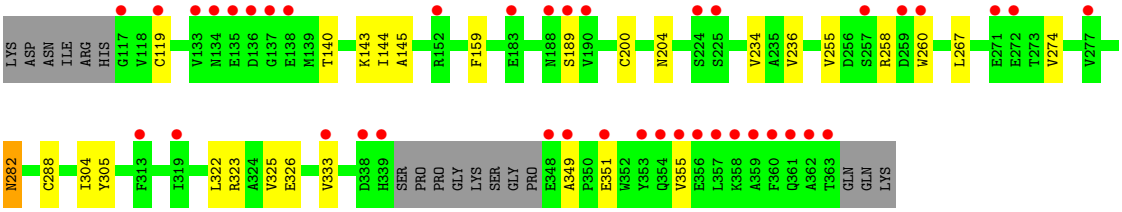
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	116	Total O 116 116	0	0
6	B	1	Total O 1 1	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

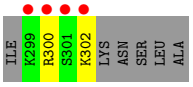
• Molecule 1: Histone-lysine N-methyltransferase SETD7

Chain A:



• Molecule 2: Estrogen receptor

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	102.04Å 38.79Å 66.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.82 – 1.42 23.82 – 1.42	Depositor EDS
% Data completeness (in resolution range)	95.9 (23.82-1.42) 95.9 (23.82-1.42)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.86 (at 1.42Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.239 , 0.243 0.231 , 0.242	Depositor DCC
R_{free} test set	2499 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	19.3	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.47 , 54.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	2108	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.45% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: GOL, BME, SFG

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	0.31	0/1964	0.59	0/2673
2	B	0.46	0/30	0.55	0/37
All	All	0.32	0/1994	0.59	0/2710

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	1915	0	1795	29	0
2	B	31	0	32	3	0
3	A	27	0	22	0	0
4	A	12	0	18	7	0
5	A	6	0	4	1	0
6	A	116	0	0	2	0
6	B	1	0	0	0	0
All	All	2108	0	1871	29	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 8.

All (29) 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:119[B]:CYS:SG	4:A:397:BME:S2	2.57	1.02
1:A:200:CYS:HG	4:A:396:BME:HS2	0.94	0.93
1:A:282:ASN:HD22	1:A:282:ASN:H	1.20	0.88
1:A:323:ARG:HD2	5:A:1502:GOL:O3	1.95	0.67
1:A:326:GLU:HG3	6:A:1575:HOH:O	1.96	0.64
1:A:288:CYS:HG	4:A:395:BME:HS2	1.45	0.63
1:A:282:ASN:HD22	1:A:282:ASN:N	1.91	0.61
1:A:144[B]:ILE:HD12	1:A:159:PHE:HB2	1.87	0.56
1:A:119[A]:CYS:CB	4:A:397:BME:S2	2.93	0.56
1:A:282:ASN:H	1:A:282:ASN:ND2	1.98	0.55
1:A:267:LEU:HD13	2:B:302:LYS:HB2	1.89	0.54
1:A:189:SER:HB2	6:A:1588:HOH:O	2.08	0.54
1:A:255:VAL:HG21	1:A:274:VAL:HG11	1.89	0.54
1:A:119[B]:CYS:CB	4:A:397:BME:S2	2.98	0.51
1:A:119[A]:CYS:HB3	4:A:397:BME:S2	2.51	0.51
1:A:305:TYR:CZ	1:A:333[A]:VAL:HG21	2.47	0.50
1:A:267:LEU:CD1	2:B:302:LYS:HB2	2.41	0.49
1:A:304:ILE:CG2	1:A:322:LEU:HD21	2.45	0.47
1:A:236:VAL:CG2	1:A:325[A]:VAL:HG22	2.47	0.44
1:A:234:VAL:HG23	1:A:236:VAL:HG13	2.00	0.42
1:A:258:ARG:O	2:B:300:ARG:NH1	2.52	0.42
1:A:200:CYS:CB	4:A:396:BME:HS2	2.30	0.42
1:A:260:TRP:CZ2	1:A:349:ALA:HA	2.54	0.42
1:A:144[B]:ILE:HG22	1:A:145:ALA:N	2.35	0.42
1:A:140:THR:C	1:A:144[B]:ILE:HD11	2.40	0.41
1:A:143:LYS:HB2	1:A:143:LYS:NZ	2.36	0.41
1:A:144[B]:ILE:CD1	1:A:159:PHE:HB2	2.50	0.41
1:A:304:ILE:HG23	1:A:322:LEU:HD21	2.03	0.41
1:A:351:GLU:O	1:A:355:VAL:HG23	2.21	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	242/256 (94%)	232 (96%)	10 (4%)	0	100	100
2	B	2/10 (20%)	1 (50%)	1 (50%)	0	100	100
All	All	244/266 (92%)	233 (96%)	11 (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	208/219 (95%)	206 (99%)	2 (1%)	76	52
2	B	3/9 (33%)	3 (100%)	0	100	100
All	All	211/228 (92%)	209 (99%)	2 (1%)	76	56

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

Mol	Chain	Res	Type
1	A	204	ASN
1	A	282	ASN

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	192	HIS
1	A	204	ASN
1	A	282	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

5 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	$\#\|Z\| > 2$
5	GOL	A	1502	-	5,5,5	5.16	5 (100%)	5,5,5	5.76	3 (60%)
3	SFG	A	1501	-	25,29,29	1.39	4 (16%)	23,42,42	1.74	3 (13%)
4	BME	A	397	1	3,3,3	0.38	0	1,2,2	0.34	0
4	BME	A	395	1	3,3,3	0.39	0	1,2,2	0.31	0
4	BME	A	396	1	3,3,3	0.30	0	1,2,2	0.42	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
5	GOL	A	1502	-	-	2/4/4/4	-
3	SFG	A	1501	-	-	2/13/33/33	0/3/3/3
4	BME	A	397	1	-	0/1/1/1	-
4	BME	A	395	1	-	0/1/1/1	-
4	BME	A	396	1	-	0/1/1/1	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1502	GOL	C3-C2	-7.60	1.20	1.51
5	A	1502	GOL	O2-C2	-6.00	1.25	1.43
5	A	1502	GOL	O1-C1	4.48	1.61	1.42
3	A	1501	SFG	C2-N3	3.47	1.37	1.32
5	A	1502	GOL	O3-C3	3.14	1.55	1.42
5	A	1502	GOL	C1-C2	-3.07	1.39	1.51
3	A	1501	SFG	C4-N3	2.49	1.39	1.35
3	A	1501	SFG	C5'-C4'	2.19	1.56	1.52
3	A	1501	SFG	C2-N1	2.15	1.37	1.33

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	1502	GOL	O3-C3-C2	10.46	160.34	110.20
5	A	1502	GOL	O2-C2-C3	6.81	139.13	109.12
3	A	1501	SFG	N3-C2-N1	-5.50	120.08	128.68
3	A	1501	SFG	O4'-C1'-C2'	-3.28	102.13	106.93
5	A	1502	GOL	O1-C1-C2	3.11	125.11	110.20
3	A	1501	SFG	C3'-C2'-C1'	2.47	104.70	100.98

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1502	GOL	O1-C1-C2-O2
5	A	1502	GOL	C1-C2-C3-O3
3	A	1501	SFG	C4'-C5'-CD-NE
3	A	1501	SFG	NE-CD-CG-CB

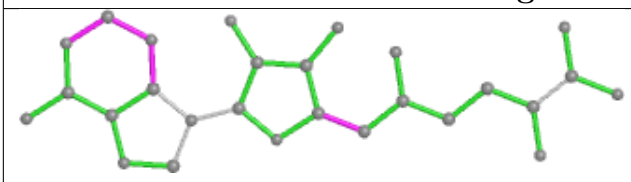
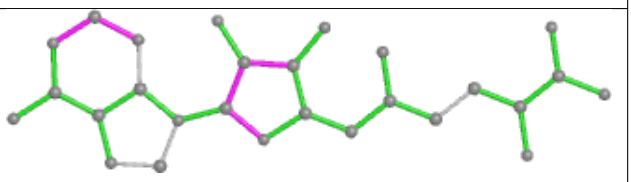
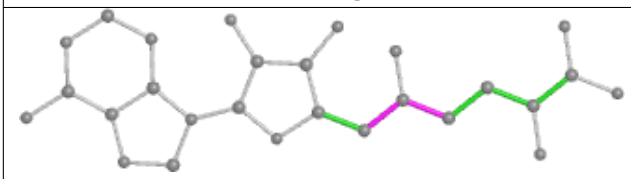
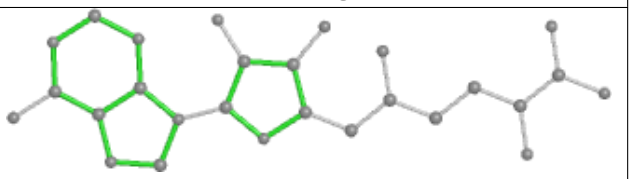
There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1502	GOL	1	0
4	A	397	BME	4	0
4	A	395	BME	1	0
4	A	396	BME	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is

within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand SFG A 1501	
 **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 (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, 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	239/256 (93%)	1.09	40 (16%)	1	1	12, 24, 43, 51	0
2	B	4/10 (40%)	5.19	4 (100%)	0	0	37, 42, 46, 46	0
All	All	243/266 (91%)	1.16	44 (18%)	1	1	12, 24, 44, 51	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	363	THR	13.8
1	A	362	ALA	8.8
1	A	348	GLU	7.2
1	A	339	HIS	7.0
1	A	360	PHE	6.8
2	B	299	LYS	6.8
1	A	135	GLU	6.0
1	A	136	ASP	6.0
2	B	300	ARG	5.7
1	A	338	ASP	5.6
1	A	119[A]	CYS	5.1
1	A	351	GLU	4.4
1	A	117	GLY	4.4
2	B	301	SER	4.3
1	A	319[A]	ILE	4.1
1	A	188	ASN	4.1
1	A	355	VAL	4.1
2	B	302	LYS	4.0
1	A	359	ALA	3.9
1	A	189	SER	3.9
1	A	349	ALA	3.8
1	A	190	VAL	3.5
1	A	137	GLY	3.4
1	A	260	TRP	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	354	GLN	3.4
1	A	134	ASN	3.3
1	A	361	GLN	3.3
1	A	259	ASP	3.1
1	A	138	GLU	3.1
1	A	333[A]	VAL	3.0
1	A	271	GLU	2.8
1	A	224	SER	2.8
1	A	257	SER	2.6
1	A	225	SER	2.6
1	A	272	GLU	2.6
1	A	356	GLU	2.6
1	A	277	VAL	2.5
1	A	313	PHE	2.4
1	A	152	ARG	2.3
1	A	183	GLU	2.2
1	A	133	VAL	2.2
1	A	358	LYS	2.2
1	A	353	TYR	2.1
1	A	357	LEU	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 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, 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
5	GOL	A	1502	6/6	0.48	0.38	47,47,48,48	0
4	BME	A	395	4/4	0.65	0.48	52,52,52,52	0
4	BME	A	397	4/4	0.72	0.37	51,51,51,52	0

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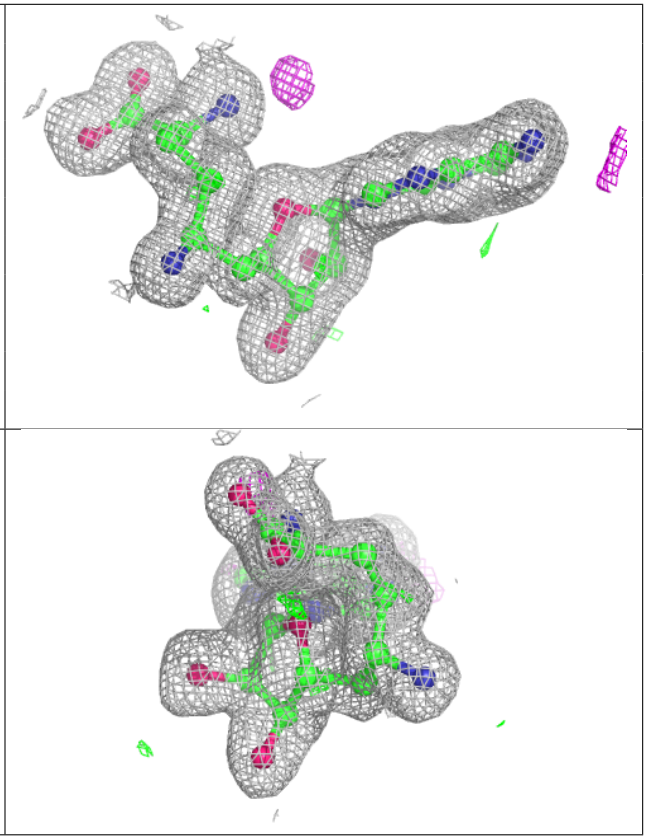
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	SFG	A	1501	27/27	0.87	0.10	17,21,23,23	0
4	BME	A	396	4/4	0.92	0.18	31,32,32,33	0

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 A 1501:

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.