Full wwPDB X-ray Structure Validation Report (i)

May 13, 2020 – 10:31 am BST

PDB ID	:	5YIB
Title	:	Crystal Structure of KNI-10743 bound Plasmepsin II (PMII) from Plasmodium falciparum
Authors	:	Rathore, I.; Mishra, V.; Bhaumik, P.
Deposited on	:	2017-10-03
Resolution	:	2.15 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 following versions of software and data (see references (i)) were used in the production of this report:

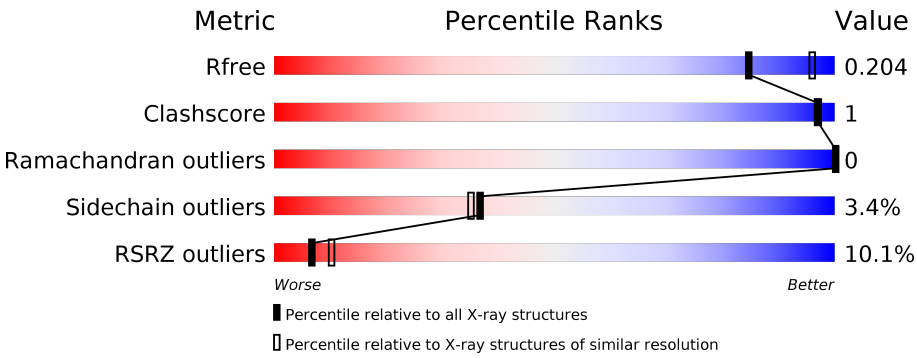
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

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

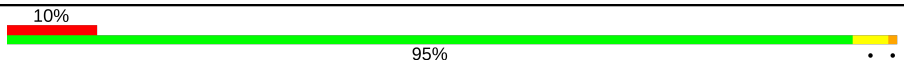
The reported resolution of this entry is 2.15 Å.

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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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 on 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	328	

2 Entry composition (i)

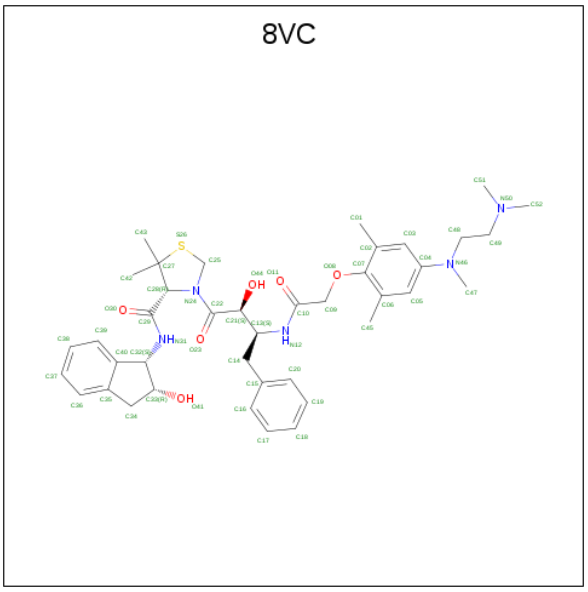
There are 6 unique types of molecules in this entry. The entry contains 2858 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Plasmepsin II.

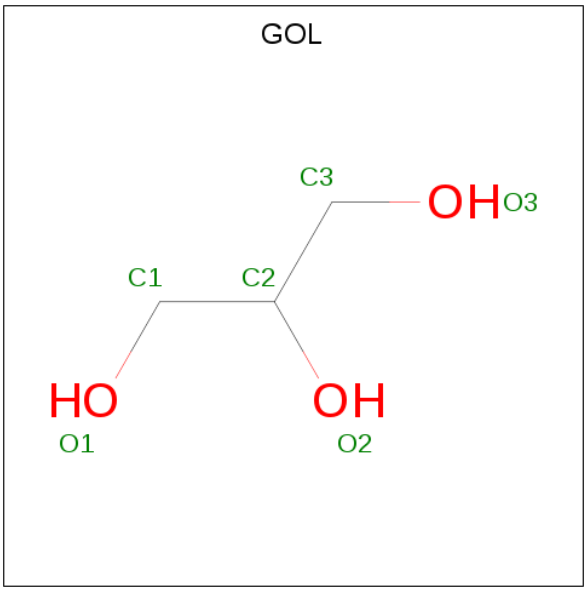
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	328	2623	1702	403	507	11	0	4	0

- Molecule 2 is (4R)-3-[(2S,3S)-3-[2-[4-[2-(dimethylamino)ethyl-methyl-amino]-2,6-dimethyl-phenoxy]ethanoylamino]-2-oxidanyl-4-phenyl-butanoyl]-5,5-dimethyl-N-[(1S,2R)-2-oxidanyl-2,3-dihydro-1H-inden-1-yl]-1,3-thiazolidine-4-carboxamide (three-letter code: 8VC) (formula: $C_{40}H_{53}N_5O_6S$) (labeled as "Ligand of Interest" by author).



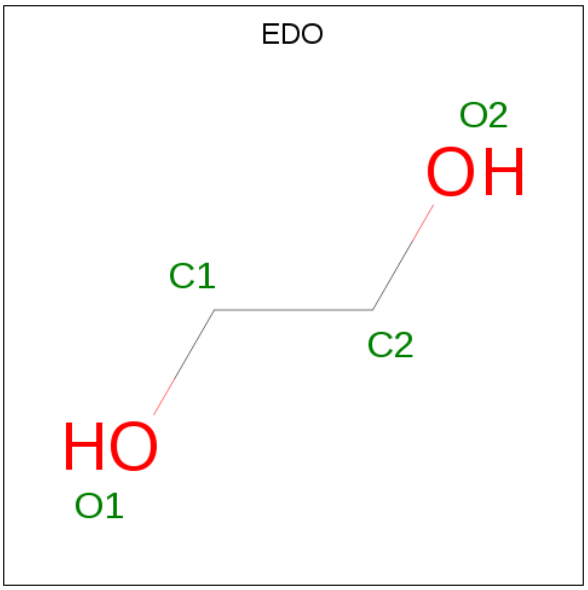
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	52	40	5	6	1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



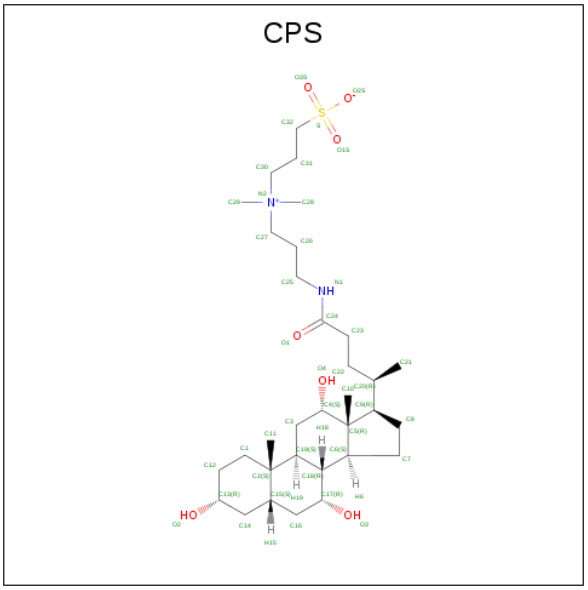
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	6	3	3	0	0
			Total	C	O		
3	A	1	6	3	3	0	0
			Total	C	O		
3	A	1	6	3	3	0	0
			Total	C	O		
3	A	1	6	3	3	0	0
			Total	C	O		
3	A	1	6	3	3	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 5 is 3-[(3-CHOLAMIDOPROPYL)DIMETHYLAMMONIO]-1-PROPANESULFONATE (three-letter code: CPS) (formula: $C_{32}H_{58}N_2O_7S$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	31	26	1	4	0	0

- Molecule 6 is water.

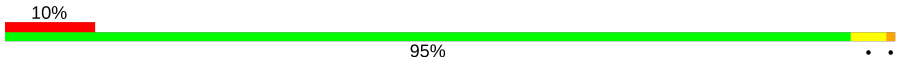
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	114	114	114	0	0

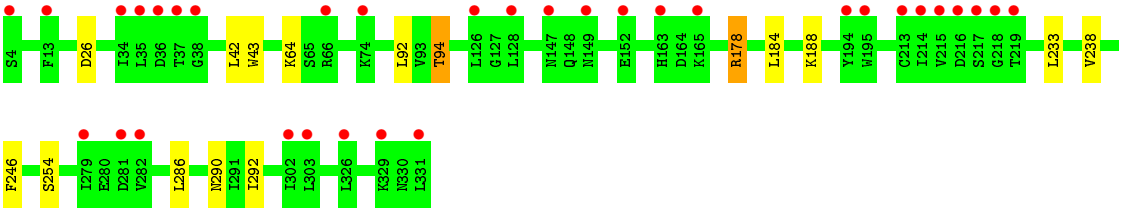
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: Plasmepsin II

Chain A:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α, β, γ	106.25Å 106.25Å 70.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.00 – 2.15 37.57 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.9 (39.00-2.15) 100.0 (37.57-2.15)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.48 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.178 , 0.196 0.192 , 0.204	Depositor DCC
R_{free} test set	1078 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	42.6	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 53.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.044 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	2858	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.03% 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, 8VC, CPS, 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	0.50	0/2702	0.72	1/3677 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	178	ARG	NE-CZ-NH1	5.55	123.08	120.30

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	2623	0	2555	4	0
2	A	52	0	0	1	0
3	A	30	0	40	0	0
4	A	8	0	12	0	0
5	A	31	0	42	0	0
6	A	114	0	0	1	0
All	All	2858	0	2649	5	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 1.

All (5) 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)
2:A:401:8VC:N24	2:A:401:8VC:C25	1.69	1.26
1:A:94:THR:HG23	6:A:537:HOH:O	2.13	0.48
1:A:233:LEU:HD22	1:A:238:VAL:HG21	1.97	0.47
1:A:246:PHE:CE1	1:A:292:ILE:HD11	2.49	0.47
1:A:42:LEU:HD23	1:A:43:TRP:N	2.33	0.43

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	330/328 (101%)	321 (97%)	9 (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	297/293 (101%)	286 (96%)	11 (4%)	34 32

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	ASP
1	A	64	LYS
1	A	92	LEU
1	A	94	THR
1	A	178	ARG
1	A	184	LEU
1	A	188	LYS
1	A	254[A]	SER
1	A	254[B]	SER
1	A	286	LEU
1	A	290	ASN

Some 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)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

9 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	CPS	A	409	-	34,34,45	0.51	0	52,53,70	1.23	6 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	GOL	A	404	-	5,5,5	0.30	0	5,5,5	0.41	0
3	GOL	A	403	-	5,5,5	0.32	0	5,5,5	0.22	0
2	8VC	A	401	-	56,56,56	3.32	20 (35%)	74,81,81	1.55	11 (14%)
4	EDO	A	408	-	3,3,3	0.51	0	2,2,2	0.23	0
3	GOL	A	406	-	5,5,5	0.32	0	5,5,5	0.28	0
4	EDO	A	407	-	3,3,3	0.35	0	2,2,2	0.31	0
3	GOL	A	405	-	5,5,5	0.36	0	5,5,5	0.66	0
3	GOL	A	402	-	5,5,5	0.35	0	5,5,5	0.20	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	CPS	A	409	-	-	2/12/77/90	1/4/4/4
3	GOL	A	404	-	-	4/4/4/4	-
3	GOL	A	403	-	-	3/4/4/4	-
2	8VC	A	401	-	-	8/42/70/70	0/5/5/5
4	EDO	A	408	-	-	1/1/1/1	-
3	GOL	A	406	-	-	0/4/4/4	-
4	EDO	A	407	-	-	1/1/1/1	-
3	GOL	A	405	-	-	2/4/4/4	-
3	GOL	A	402	-	-	2/4/4/4	-

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	8VC	C25-N24	13.13	1.69	1.46
2	A	401	8VC	C25-S26	-12.22	1.54	1.83
2	A	401	8VC	C29-N31	6.75	1.48	1.34
2	A	401	8VC	C10-N12	6.63	1.48	1.34
2	A	401	8VC	C22-N24	5.48	1.47	1.34
2	A	401	8VC	C27-S26	-5.35	1.74	1.85
2	A	401	8VC	C27-C28	4.09	1.65	1.56
2	A	401	8VC	C04-N46	3.66	1.49	1.39
2	A	401	8VC	C13-N12	3.48	1.52	1.46
2	A	401	8VC	C47-N46	2.83	1.50	1.46
2	A	401	8VC	C34-C35	2.82	1.55	1.50
2	A	401	8VC	O30-C29	-2.71	1.18	1.23
2	A	401	8VC	O11-C10	-2.47	1.18	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	8VC	C45-C06	2.31	1.55	1.51
2	A	401	8VC	O23-C22	-2.23	1.18	1.22
2	A	401	8VC	C21-C13	2.19	1.56	1.54
2	A	401	8VC	C09-C10	2.16	1.55	1.51
2	A	401	8VC	C40-C32	2.12	1.53	1.51
2	A	401	8VC	O08-C07	2.07	1.43	1.39
2	A	401	8VC	C39-C40	2.04	1.42	1.39

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	401	8VC	C40-C32-C33	5.21	106.28	102.58
2	A	401	8VC	C27-C28-N24	-4.48	99.75	106.48
2	A	401	8VC	O44-C21-C22	3.82	114.32	108.54
2	A	401	8VC	C25-N24-C28	-3.77	106.14	114.95
5	A	409	CPS	C23-C24-N1	3.50	122.32	116.42
2	A	401	8VC	C35-C40-C32	-3.33	107.44	110.22
2	A	401	8VC	C13-N12-C10	-2.91	118.58	123.48
2	A	401	8VC	C43-C27-C28	-2.82	105.30	111.57
2	A	401	8VC	C47-N46-C48	2.71	122.81	115.42
2	A	401	8VC	C42-C27-S26	2.61	113.59	109.22
5	A	409	CPS	C1-C2-C19	-2.33	107.69	111.35
5	A	409	CPS	O1-C24-C23	-2.30	117.81	122.02
5	A	409	CPS	C11-C2-C15	-2.16	106.69	110.36
5	A	409	CPS	C19-C3-C4	2.10	117.08	114.30
5	A	409	CPS	C3-C19-C18	2.08	113.91	110.88
2	A	401	8VC	O11-C10-N12	-2.07	119.46	122.95
2	A	401	8VC	C49-C48-N46	2.07	115.61	112.31

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	404	GOL	O1-C1-C2-C3
2	A	401	8VC	C03-C04-N46-C47
2	A	401	8VC	C05-C04-N46-C47
2	A	401	8VC	C49-C48-N46-C47
3	A	405	GOL	C1-C2-C3-O3
5	A	409	CPS	C23-C24-N1-C25
5	A	409	CPS	O1-C24-N1-C25
3	A	404	GOL	C1-C2-C3-O3
3	A	403	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
3	A	404	GOL	O1-C1-C2-O2
3	A	403	GOL	O2-C2-C3-O3
3	A	405	GOL	O2-C2-C3-O3
3	A	404	GOL	O2-C2-C3-O3
4	A	408	EDO	O1-C1-C2-O2
2	A	401	8VC	C05-C04-N46-C48
3	A	402	GOL	O2-C2-C3-O3
4	A	407	EDO	O1-C1-C2-O2
2	A	401	8VC	C03-C04-N46-C48
3	A	403	GOL	O1-C1-C2-C3
2	A	401	8VC	N12-C13-C21-C22
2	A	401	8VC	C48-C49-N50-C52
3	A	402	GOL	C1-C2-C3-O3
2	A	401	8VC	N46-C48-C49-N50

All (1) ring outliers are listed below:

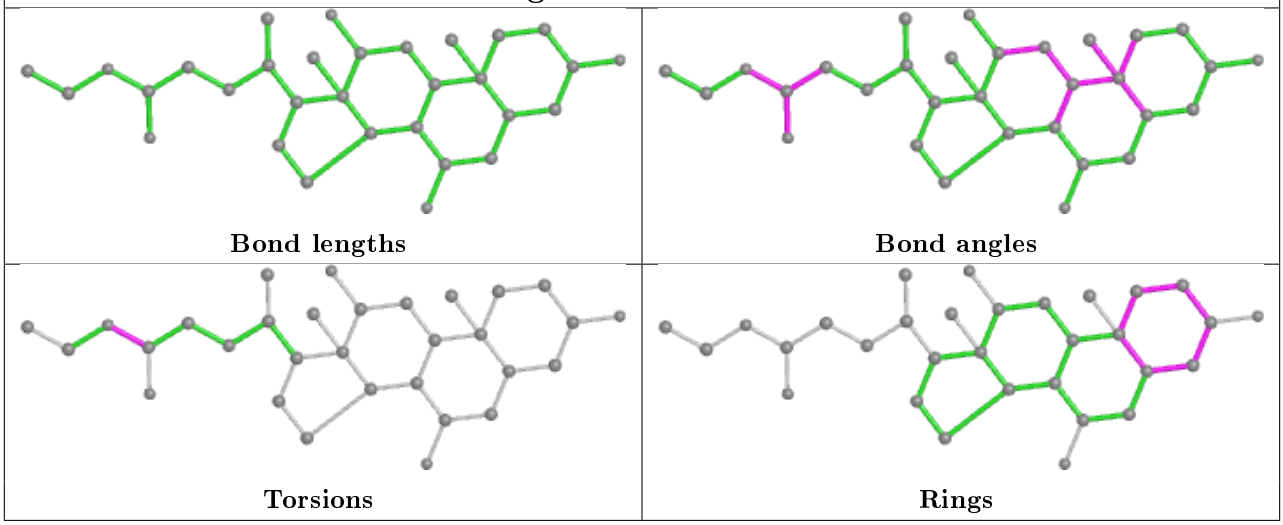
Mol	Chain	Res	Type	Atoms
5	A	409	CPS	C1-C12-C13-C14-C15-C2

1 monomer is involved in 1 short contact:

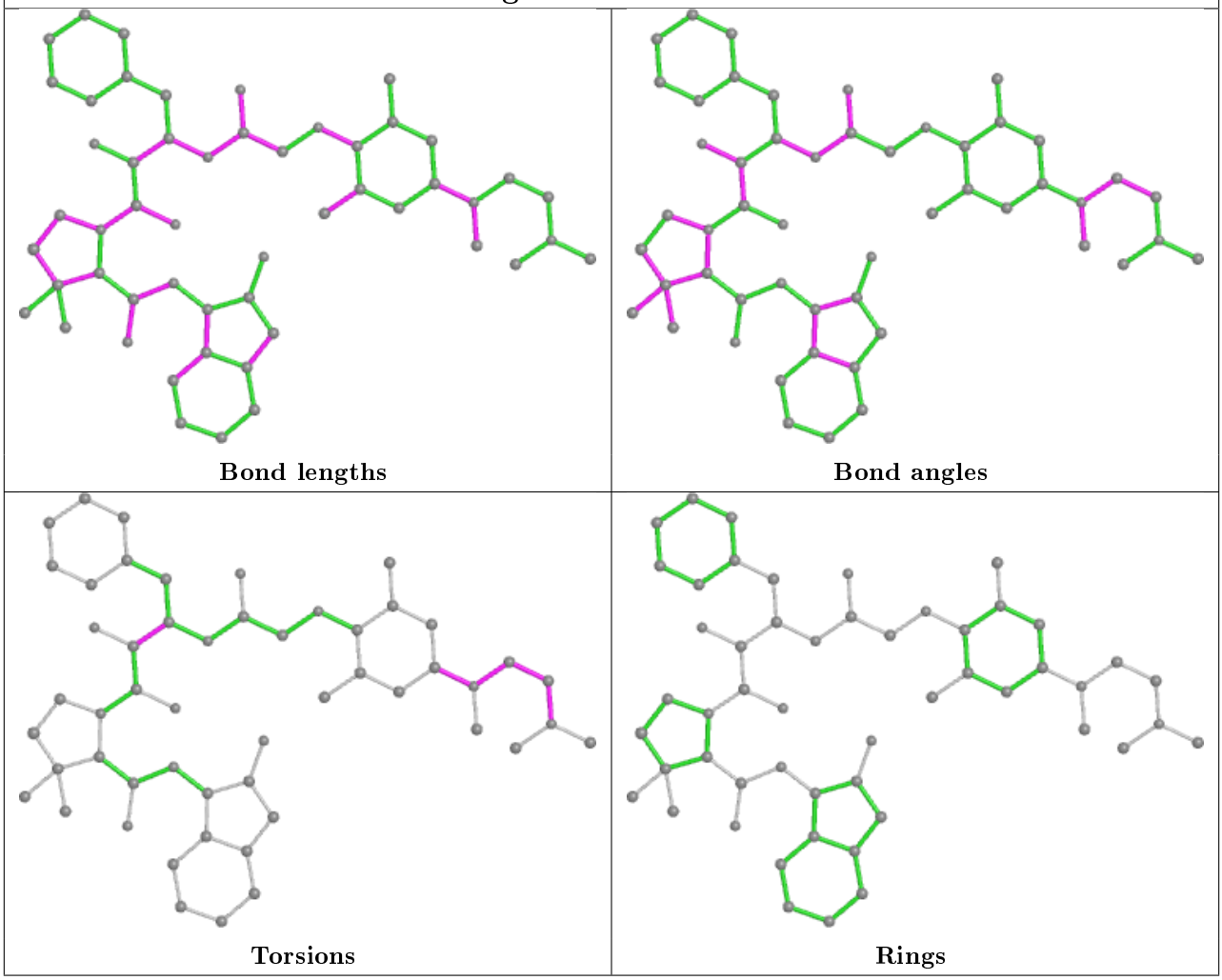
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	8VC	1	0

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 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 CPS A 409



Ligand 8VC A 401



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	328/328 (100%)	0.54	33 (10%) 7 10	37, 48, 73, 109	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	282	VAL	7.4
1	A	4	SER	4.9
1	A	214	ILE	4.7
1	A	66	ARG	4.3
1	A	331	LEU	4.0
1	A	37	THR	3.9
1	A	163	HIS	3.5
1	A	281	ASP	3.5
1	A	165	LYS	3.4
1	A	217	SER	3.4
1	A	215	VAL	3.4
1	A	219	THR	3.3
1	A	303	LEU	3.2
1	A	149	ASN	3.2
1	A	126	LEU	3.2
1	A	326	LEU	3.1
1	A	218	GLY	2.9
1	A	38	GLY	2.8
1	A	74	LYS	2.8
1	A	13	PHE	2.8
1	A	216	ASP	2.7
1	A	36	ASP	2.7
1	A	213	CYS	2.7
1	A	35	LEU	2.6
1	A	128	LEU	2.6
1	A	195	TRP	2.6
1	A	329	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	147	ASN	2.6
1	A	194	TYR	2.5
1	A	302	ILE	2.5
1	A	34	ILE	2.3
1	A	279	ILE	2.2
1	A	152	GLU	2.1

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 carbohydrates in this entry.

6.4 Ligands (i)

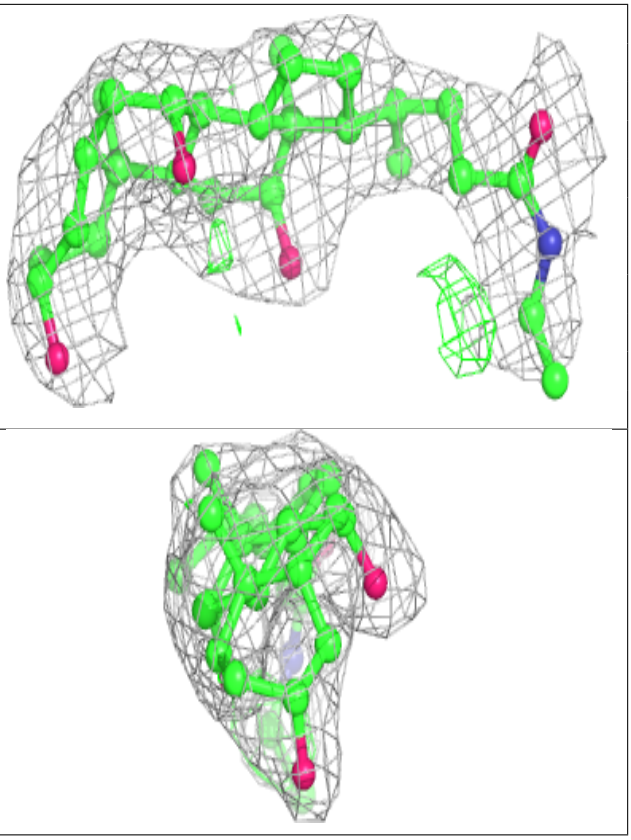
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	GOL	A	403	6/6	0.79	0.18	73,75,77,78	0
3	GOL	A	406	6/6	0.79	0.20	80,81,83,83	0
4	EDO	A	408	4/4	0.82	0.38	70,71,72,75	0
3	GOL	A	402	6/6	0.83	0.28	69,71,71,72	0
3	GOL	A	405	6/6	0.85	0.29	51,55,56,62	0
3	GOL	A	404	6/6	0.86	0.16	61,68,71,74	0
4	EDO	A	407	4/4	0.88	0.37	46,52,54,56	0
5	CPS	A	409	31/42	0.89	0.13	48,55,63,70	0
2	8VC	A	401	52/52	0.94	0.19	32,36,87,90	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.

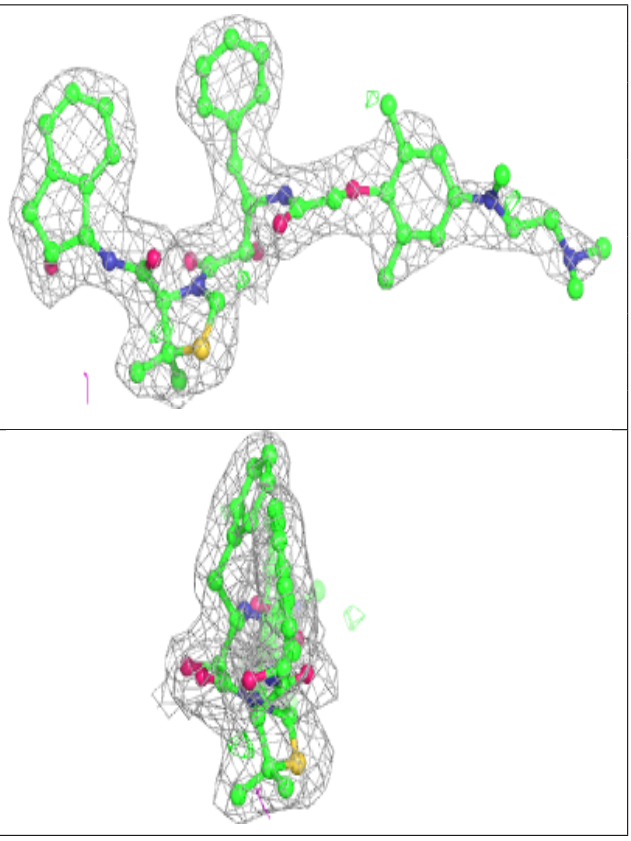
Electron density around CPS A 409:

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



Electron density around 8VC A 401:

$2mF_o$-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.