



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 06:54 PM EDT

PDB ID : 5YIE  
Title : Crystal Structure of KNI-10742 bound Plasmepsin II (PMII) from Plasmodium falciparum  
Authors : Mishra, V.; Rathore, I.; Bhaumik, P.  
Deposited on : 2017-10-04  
Resolution : 2.10 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](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	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
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)	:	2.37.1

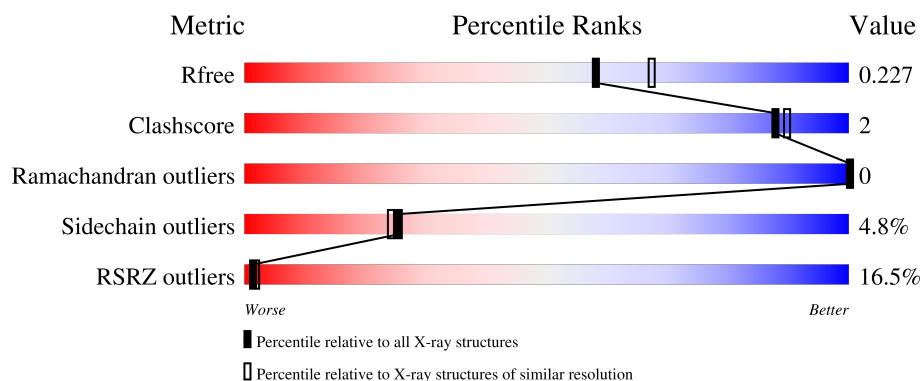
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	327	<div> <div>17%</div> <div>92%</div> <div>7%</div> </div>

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	NA	A	404	-	-	X	-

## 2 Entry composition [i](#)

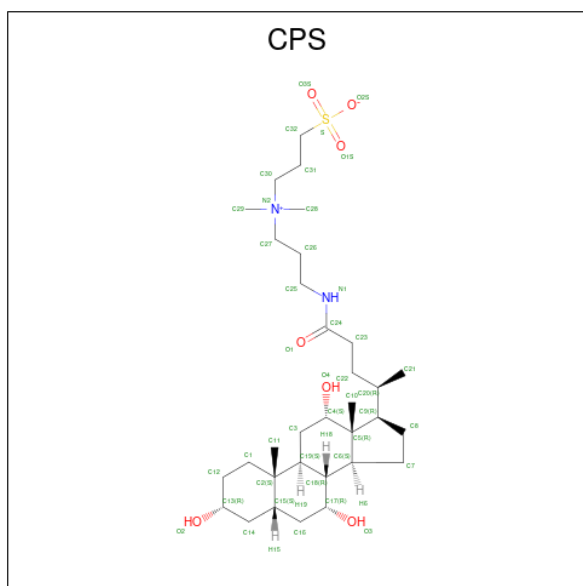
There are 5 unique types of molecules in this entry. The entry contains 2883 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

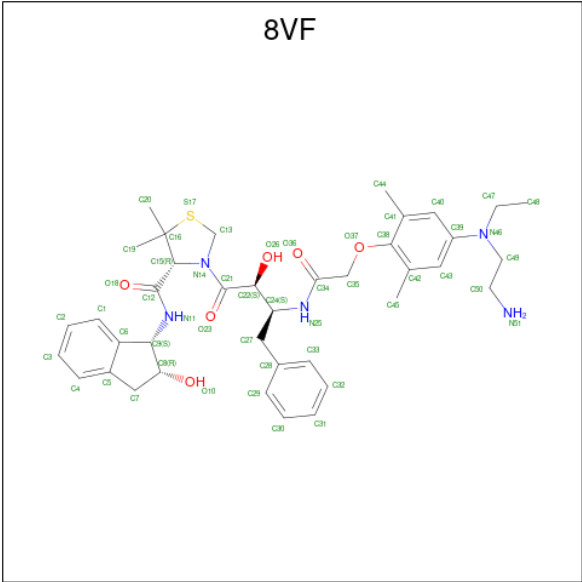
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	S	0	5	0
			2623	1700	404	508	11			

- Molecule 2 is 3-[(3-CHOLAMIDOPROPYL)DIMETHYLAMMONIO]-1-PROPANESULFONATE (three-letter code: CPS) (formula: C<sub>32</sub>H<sub>58</sub>N<sub>2</sub>O<sub>7</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			42	32	2	7	1		
2	A	1	Total	C	O			0	0
			24	21	3				

- Molecule 3 is (4R)-3-[(2S,3S)-3-[2-[4-[2-azanylethyl(ethyl)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: 8VF) (formula: C<sub>39</sub>H<sub>51</sub>N<sub>5</sub>O<sub>6</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			51	39	5	6	1		

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

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

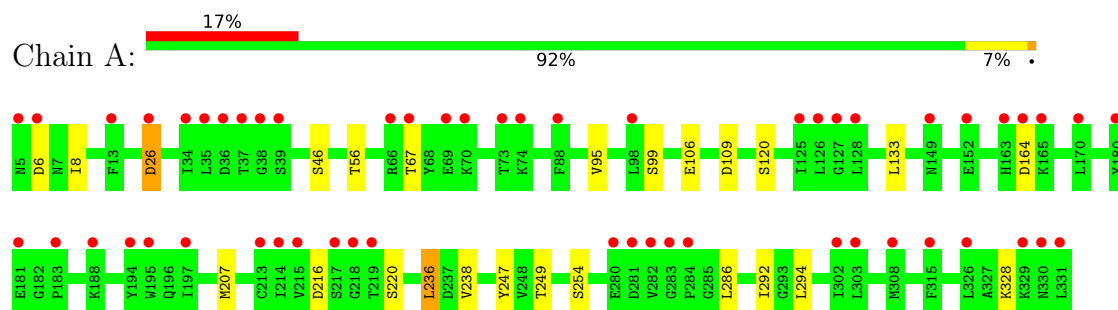
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	142	Total	O	0	0
			142	142		

### 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: Plasmepsin II



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	106.60Å 106.60Å 72.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.00 – 2.10 37.69 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (38.00-2.10) 100.0 (37.69-2.10)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.58 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, $R_{free}$	0.173 , 0.219 0.178 , 0.227	Depositor DCC
$R_{free}$ test set	1185 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	48.9	Xtriage
Anisotropy	0.149	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 67.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.042 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	2883	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.01% 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: 8VF, NA, CPS

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	0.63	0/2698	0.79	2/3672 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	109	ASP	CB-CG-OD1	6.04	123.74	118.30
1	A	236	LEU	CA-CB-CG	5.09	127.00	115.30

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	2553	11	0
2	A	66	0	92	0	0
3	A	51	0	0	0	0
4	A	1	0	0	3	0
5	A	142	0	0	0	0
All	All	2883	0	2645	11	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 2.

All (11) 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:8:ILE:HD11	1:A:95:VAL:HG13	1.71	0.72
1:A:216[A]:ASP:OD1	4:A:404:NA:NA	1.65	0.67
1:A:216[A]:ASP:CG	4:A:404:NA:NA	1.85	0.67
1:A:8:ILE:CD1	1:A:95:VAL:HG13	2.30	0.62
1:A:216[A]:ASP:OD2	4:A:404:NA:NA	1.74	0.61
1:A:238:VAL:HG22	1:A:249:THR:HB	1.87	0.56
1:A:238:VAL:HG13	1:A:247:TYR:HB3	1.94	0.49
1:A:220[A]:SER:O	1:A:220[A]:SER:OG	2.31	0.46
1:A:26:ASP:OD1	1:A:26:ASP:C	2.56	0.43
1:A:26:ASP:HB3	1:A:67:THR:OG1	2.19	0.42
1:A:46:SER:HB2	1:A:106:GLU:HG2	2.02	0.41

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	330/327 (101%)	320 (97%)	10 (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	297/292 (102%)	282 (95%)	15 (5%)	24	22

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ASP
1	A	26	ASP
1	A	56	THR
1	A	99	SER
1	A	120	SER
1	A	133	LEU
1	A	164	ASP
1	A	207	MET
1	A	236	LEU
1	A	254	SER
1	A	286	LEU
1	A	292[A]	ILE
1	A	292[B]	ILE
1	A	294	LEU
1	A	328	LYS

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](#)

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](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	$\# Z  > 2$
3	8VF	A	403	4	55,55,55	2.57	16 (29%)	72,79,79	1.64	10 (13%)
2	CPS	A	402	-	26,27,45	0.58	0	41,44,70	1.13	5 (12%)
2	CPS	A	401	-	45,45,45	1.25	1 (2%)	69,70,70	1.18	2 (2%)

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	8VF	A	403	4	-	8/42/70/70	0/5/5/5
2	CPS	A	402	-	-	0/2/67/90	0/4/4/4
2	CPS	A	401	-	-	6/25/90/90	0/4/4/4

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	403	8VF	C1-C6	7.34	1.49	1.39
2	A	401	CPS	C32-S	-7.14	1.67	1.77
3	A	403	8VF	C13-S17	-6.16	1.68	1.83
3	A	403	8VF	C4-C5	5.75	1.49	1.39
3	A	403	8VF	C8-C9	-5.66	1.49	1.55
3	A	403	8VF	C12-N11	5.50	1.46	1.34
3	A	403	8VF	C15-N14	-5.43	1.42	1.46
3	A	403	8VF	C16-S17	-4.60	1.75	1.85
3	A	403	8VF	C21-N14	4.27	1.44	1.34
3	A	403	8VF	C39-N46	3.43	1.48	1.38
3	A	403	8VF	C34-N25	3.27	1.41	1.34
3	A	403	8VF	C5-C6	-2.86	1.34	1.39
3	A	403	8VF	O37-C38	2.80	1.44	1.39
3	A	403	8VF	C38-C41	2.47	1.44	1.40
3	A	403	8VF	C15-C12	-2.41	1.49	1.53
3	A	403	8VF	C43-C39	2.17	1.43	1.39
3	A	403	8VF	C35-C34	2.09	1.55	1.51

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	403	8VF	C5-C7-C8	-6.59	97.16	103.50
3	A	403	8VF	C7-C8-C9	6.39	109.24	103.78
2	A	401	CPS	O1S-S-C32	4.44	112.27	106.92
3	A	403	8VF	C16-C15-N14	-3.65	101.00	106.48
3	A	403	8VF	C6-C9-C8	-3.18	100.32	102.58
3	A	403	8VF	O26-C22-C21	-3.12	103.82	108.54
2	A	401	CPS	O2S-S-C32	2.71	110.15	105.77
3	A	403	8VF	C35-O37-C38	-2.30	108.13	114.73
2	A	402	CPS	C3-C19-C2	2.30	116.10	113.73
2	A	402	CPS	C9-C5-C4	2.23	119.70	117.67
2	A	402	CPS	C11-C2-C1	-2.10	104.88	108.26
2	A	402	CPS	C7-C6-C5	2.08	105.59	103.55
2	A	402	CPS	C16-C15-C14	-2.07	108.80	111.19
3	A	403	8VF	O37-C35-C34	-2.06	105.08	110.78
3	A	403	8VF	S17-C13-N14	2.05	108.20	105.37
3	A	403	8VF	C24-N25-C34	-2.01	120.09	123.48
3	A	403	8VF	C2-C1-C6	-2.01	118.46	121.01

There are no chirality outliers.

All (14) torsion outliers are listed below:

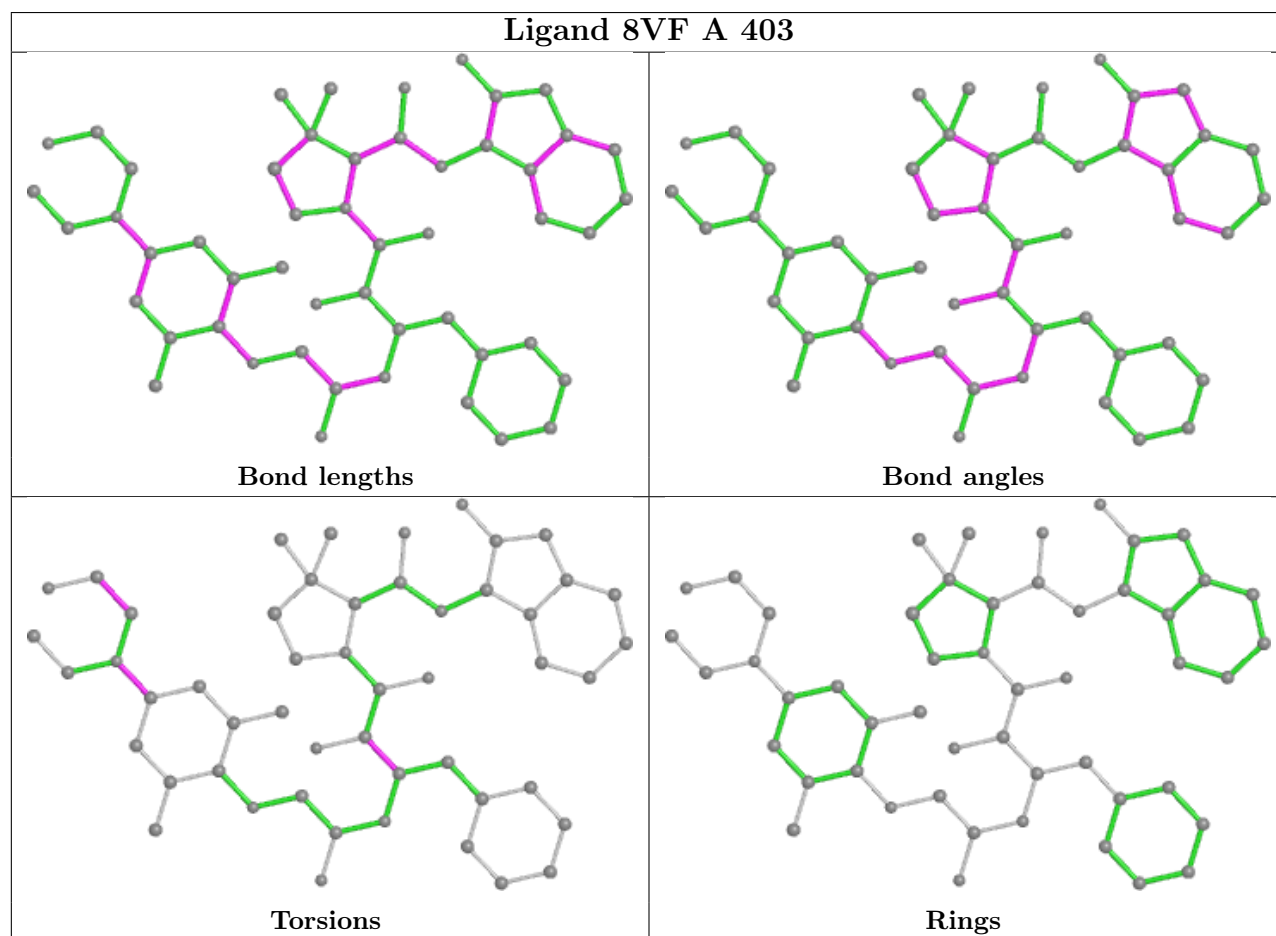
Mol	Chain	Res	Type	Atoms
2	A	401	CPS	N2-C30-C31-C32
2	A	401	CPS	C31-C30-N2-C27
2	A	401	CPS	C31-C30-N2-C28
2	A	401	CPS	N1-C25-C26-C27
2	A	401	CPS	C31-C30-N2-C29
2	A	401	CPS	C25-C26-C27-N2
3	A	403	8VF	N46-C49-C50-N51
3	A	403	8VF	C21-C22-C24-N25
3	A	403	8VF	C40-C39-N46-C47
3	A	403	8VF	C40-C39-N46-C49
3	A	403	8VF	O26-C22-C24-N25
3	A	403	8VF	C43-C39-N46-C49
3	A	403	8VF	C43-C39-N46-C47
3	A	403	8VF	O26-C22-C24-C27

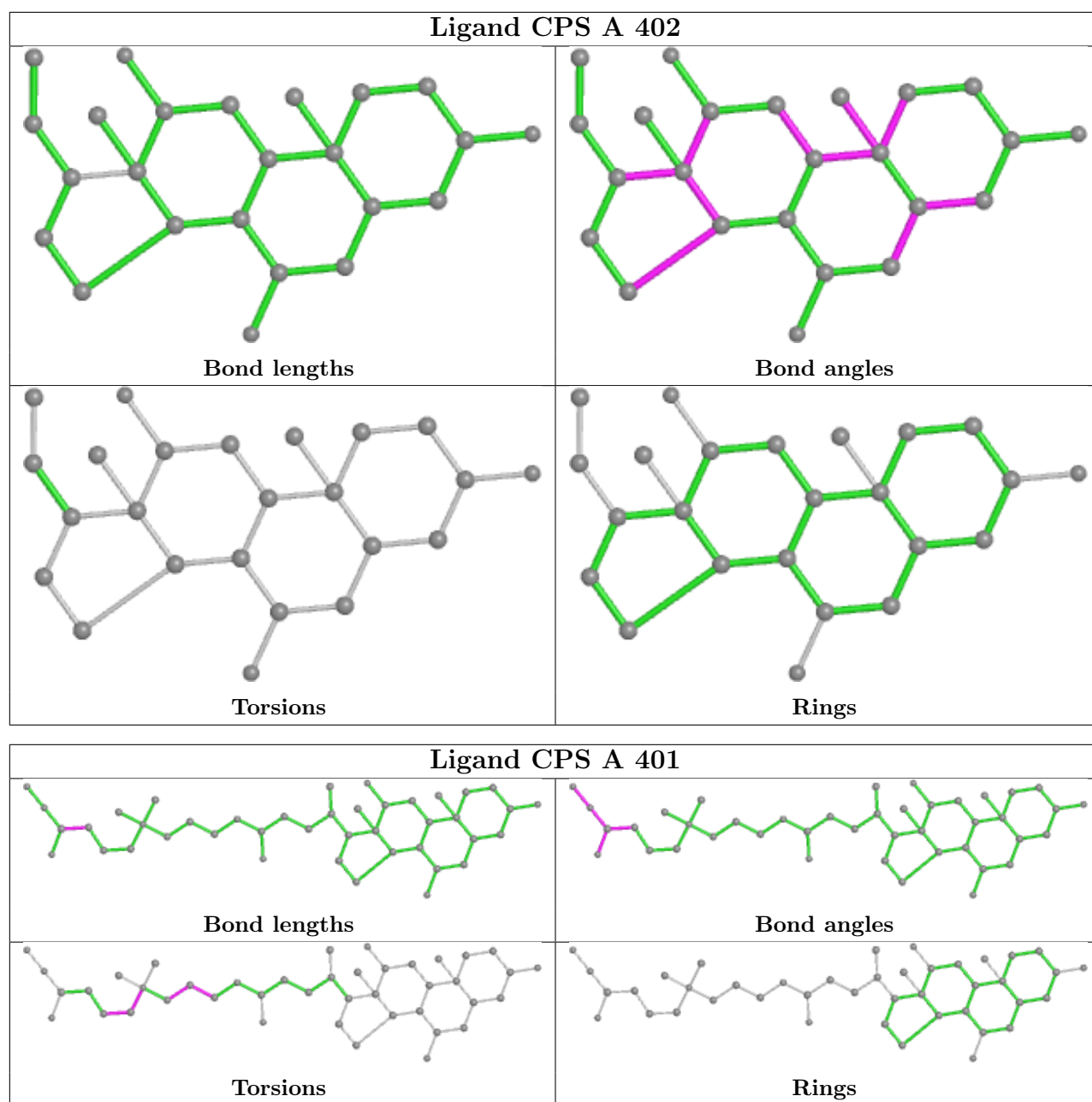
There are no ring outliers.

No monomer is involved in short contacts.

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](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	327/327 (100%)	0.74	54 (16%) <b>1</b> <b>2</b>	36, 60, 91, 108	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	282	VAL	7.6
1	A	331	LEU	5.5
1	A	281	ASP	5.2
1	A	128	LEU	4.5
1	A	303	LEU	4.2
1	A	195	TRP	4.2
1	A	152	GLU	4.0
1	A	215	VAL	4.0
1	A	37	THR	3.9
1	A	194	TYR	3.8
1	A	35	LEU	3.7
1	A	326	LEU	3.6
1	A	34	ILE	3.4
1	A	217	SER	3.2
1	A	164	ASP	3.2
1	A	66	ARG	3.2
1	A	165	LYS	3.0
1	A	126	LEU	3.0
1	A	214	ILE	2.9
1	A	38	GLY	2.9
1	A	98	LEU	2.9
1	A	218	GLY	2.8
1	A	5	ASN	2.8
1	A	213	CYS	2.8
1	A	163	HIS	2.7
1	A	181	GLU	2.7
1	A	67	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	149	ASN	2.7
1	A	170	LEU	2.6
1	A	127	GLY	2.6
1	A	283	GLY	2.6
1	A	26	ASP	2.5
1	A	302	ILE	2.5
1	A	88	PHE	2.5
1	A	280	GLU	2.5
1	A	74	LYS	2.5
1	A	6	ASP	2.5
1	A	13	PHE	2.4
1	A	315	PHE	2.4
1	A	70	LYS	2.4
1	A	330	ASN	2.4
1	A	183	PRO	2.4
1	A	69	GLU	2.3
1	A	197	ILE	2.2
1	A	284	PRO	2.2
1	A	39	SER	2.2
1	A	188	LYS	2.2
1	A	36	ASP	2.1
1	A	329	LYS	2.1
1	A	180	TYR	2.1
1	A	125	ILE	2.0
1	A	308	MET	2.0
1	A	73	THR	2.0
1	A	219	THR	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.

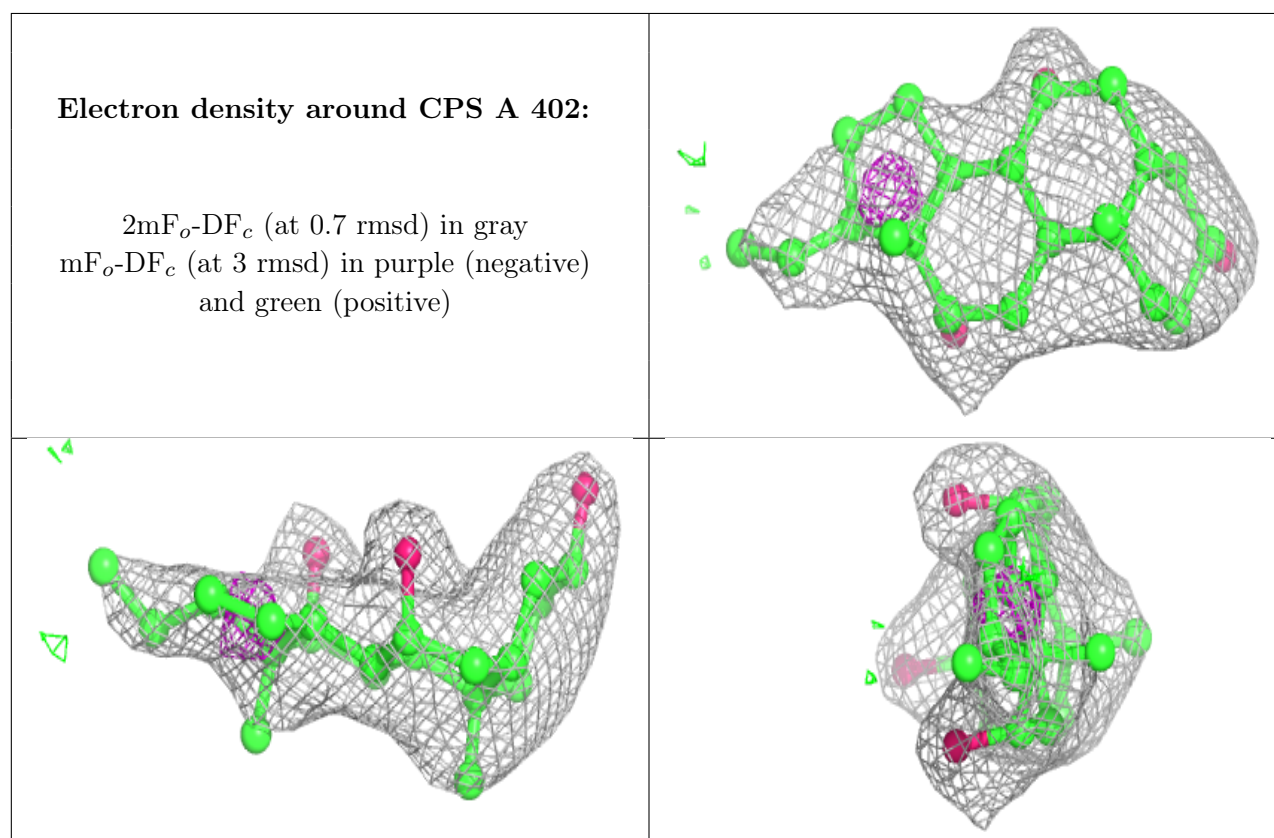
## 6.4 Ligands [i](#)

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, 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
2	CPS	A	402	24/42	0.88	0.17	67,70,73,78	0
2	CPS	A	401	42/42	0.89	0.21	46,55,169,172	0
3	8VF	A	403	51/51	0.96	0.21	35,41,85,101	0
4	NA	A	404	1/1	0.96	0.21	46,46,46,46	1

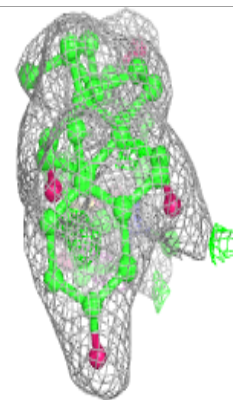
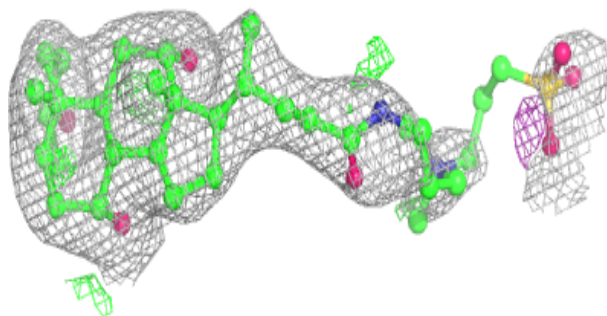
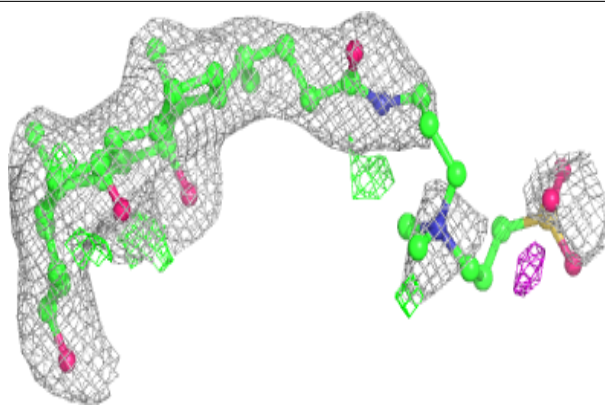
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



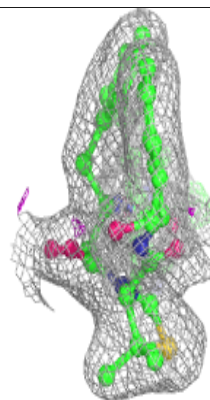
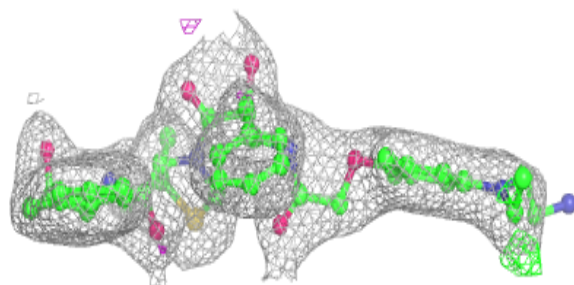
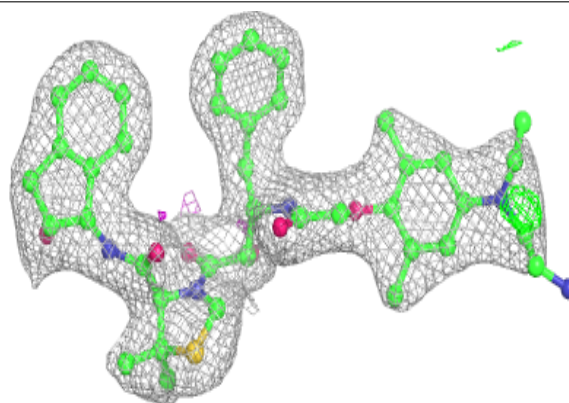


**Electron density around CPS A 401:**

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

**Electron density around 8VF A 403:**

$2mF_o-DF_c$  (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.