



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 6, 2022 – 12:18 AM JST

PDB ID : 7X17  
Title : Structure of Pseudomonas NRPS protein, AmbB-TC bound to Ppant-L-Ala  
Authors : ChuYuanKee, M.; Bharath, S.R.; Song, H.  
Deposited on : 2022-02-23  
Resolution : 2.50 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>.

---

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

MolProbity : 4.02b-467  
Mogul : ?? (??), CSD ??CSD?? (????)  
Xtriage (Phenix) : 1.13  
EDS : 2.29  
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) : 2.29

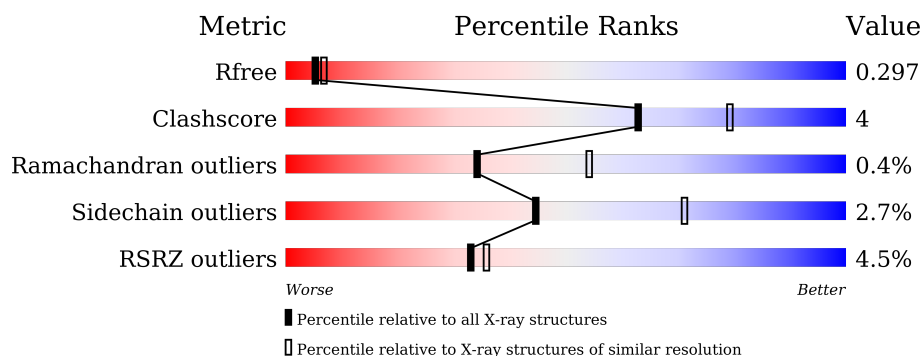
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
$R_{free}$	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	523	 4% 70% 7% 22%
1	B	523	 3% 70% 10% 20%
1	C	523	 2% 77% 10% 13%
1	D	523	 6% 73% 12% 15%

## 2 Entry composition [i](#)

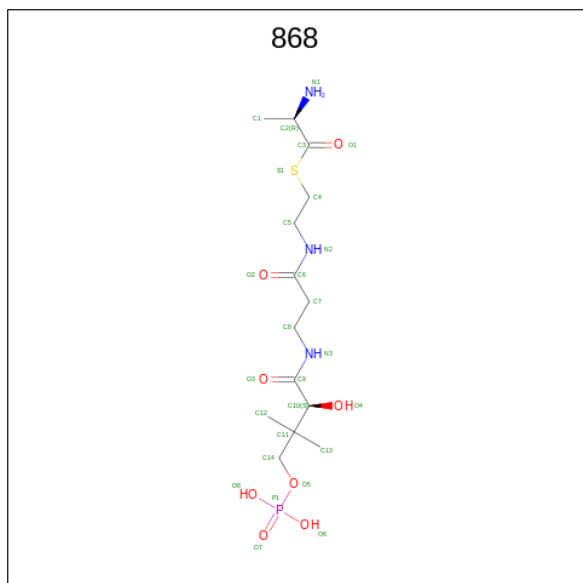
There are 3 unique types of molecules in this entry. The entry contains 13793 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 AMB antimetabolite synthase AmbB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	410	Total	C	N	O	S	0	0	0
			3161	1990	606	560	5			
1	B	421	Total	C	N	O	S	0	0	0
			3225	2031	618	571	5			
1	C	455	Total	C	N	O	S	0	0	0
			3488	2196	666	621	5			
1	D	443	Total	C	N	O	S	0	0	0
			3399	2144	650	600	5			

- Molecule 2 is S-[2-[3-[(2S)-3,3-dimethyl-2-oxidanyl-4-phosphonooxy-butanoyl]amino]propanoylamino]ethyl] (2R)-2-azanylpropanethioate (three-letter code: 868) (formula: C<sub>14</sub>H<sub>28</sub>N<sub>3</sub>O<sub>8</sub>PS) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P S	0	0
			26	14	3	7	1 1		

*Continued on next page...*

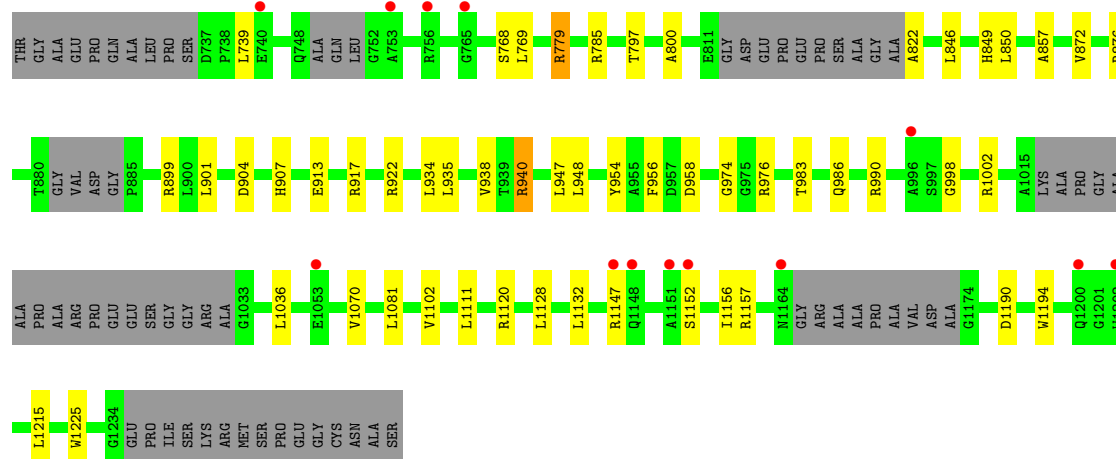
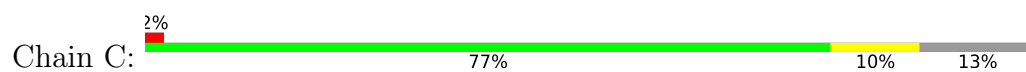
*Continued from previous page...*

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	S	0	0
			26	14	3	7	1	1		
2	C	1	Total	C	N	O	P	S	0	0
			26	14	3	7	1	1		
2	D	1	Total	C	N	O	P	S	0	0
			26	14	3	7	1	1		

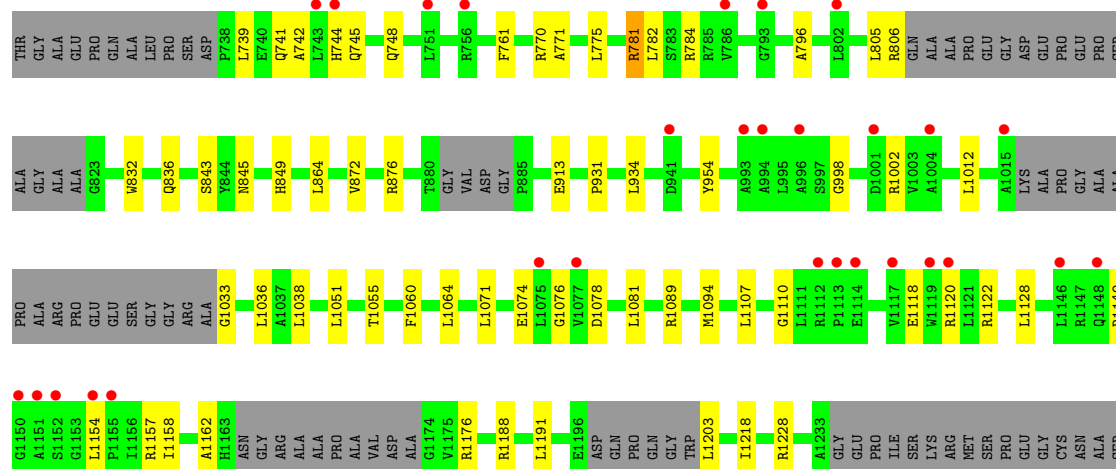
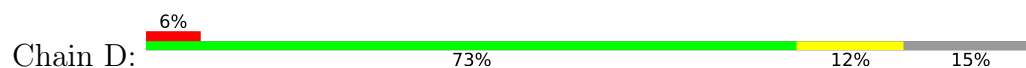
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	90	Total	O	0	0
			90	90		
3	B	122	Total	O	0	0
			122	122		
3	C	113	Total	O	0	0
			113	113		
3	D	91	Total	O	0	0
			91	91		





● Molecule 1: AMB antimetabolite synthase AmbB



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	198.50Å 71.61Å 173.76Å 90.00° 110.14° 90.00°	Depositor
Resolution (Å)	46.59 – 2.50 48.83 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.9 (46.59-2.50) 99.0 (48.83-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.94 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.20_4459, PHENIX 1.20_4459	Depositor
R, $R_{free}$	0.246 , 0.299 0.245 , 0.297	Depositor DCC
$R_{free}$ test set	3952 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.5	Xtriage
Anisotropy	0.164	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 50.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	13793	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.57% 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: 868

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	0.24	0/3211	0.52	0/4361
1	B	0.24	0/3274	0.52	0/4443
1	C	0.24	0/3550	0.51	0/4825
1	D	0.24	0/3457	0.52	0/4695
All	All	0.24	0/13492	0.52	0/18324

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	3161	0	3231	23	0
1	B	3225	0	3310	33	0
1	C	3488	0	3540	32	0
1	D	3399	0	3476	34	0
2	A	26	0	0	0	0
2	B	26	0	0	0	0
2	C	26	0	0	3	0
2	D	26	0	0	1	0
3	A	90	0	0	0	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	122	0	0	3	0
3	C	113	0	0	3	0
3	D	91	0	0	2	0
All	All	13793	0	13557	117	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 4.

The worst 5 of 117 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:B:1213:PHE:HB3	1:B:1218:ILE:HD11	1.58	0.85
1:D:1071:LEU:HD11	1:D:1191:LEU:HD23	1.70	0.74
1:C:1081:LEU:HD11	1:C:1156:ILE:HG12	1.69	0.72
1:A:787:PRO:O	1:A:789:GLN:N	2.25	0.69
1:D:781:ARG:HG3	1:D:782:LEU:HD12	1.77	0.66

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	398/523 (76%)	387 (97%)	5 (1%)	6 (2%)	10	18
1	B	407/523 (78%)	401 (98%)	6 (2%)	0	100	100
1	C	443/523 (85%)	434 (98%)	9 (2%)	0	100	100
1	D	431/523 (82%)	424 (98%)	7 (2%)	0	100	100
All	All	1679/2092 (80%)	1646 (98%)	27 (2%)	6 (0%)	34	54

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	788	LEU
1	A	791	PHE
1	A	786	VAL
1	A	784	ARG
1	A	787	PRO

### 5.3.2 Protein sidechains ⓘ

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	318/390 (82%)	310 (98%)	8 (2%)	47	73
1	B	323/390 (83%)	313 (97%)	10 (3%)	40	67
1	C	347/390 (89%)	339 (98%)	8 (2%)	50	76
1	D	339/390 (87%)	329 (97%)	10 (3%)	42	69
All	All	1327/1560 (85%)	1291 (97%)	36 (3%)	44	71

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	805	LEU
1	D	1228	ARG
1	D	806	ARG
1	D	1078	ASP
1	B	1056	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	744	HIS
1	D	745	GLN
1	D	862	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

### 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

4 ligands are modelled in this entry.

There are no bond length outliers.

There are no bond angle outliers.

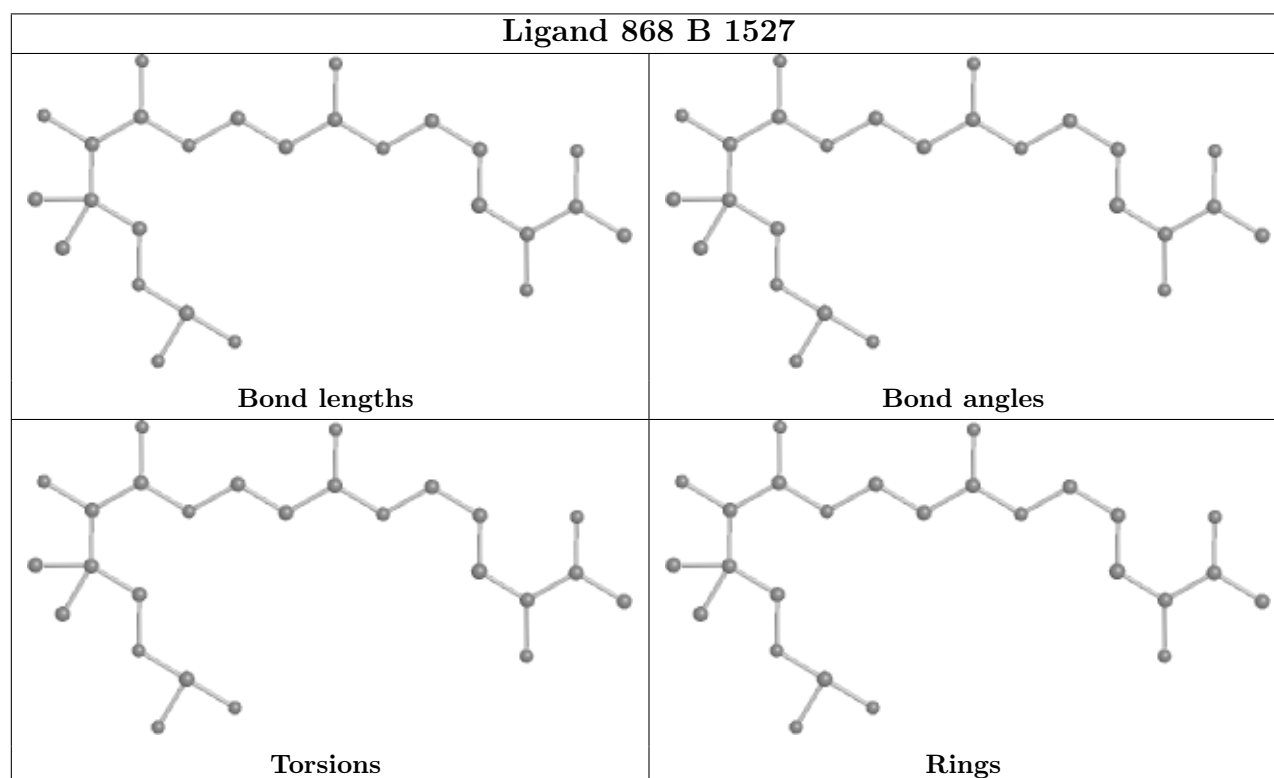
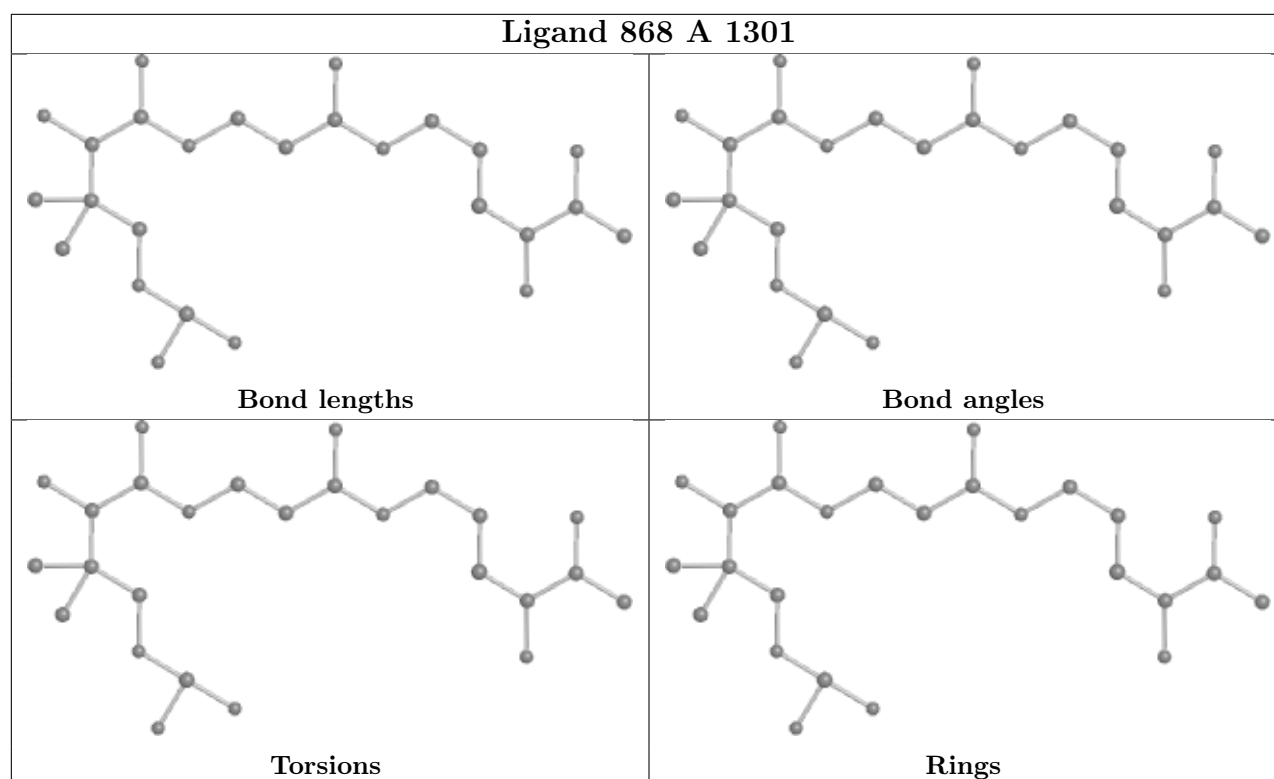
There are no chirality outliers.

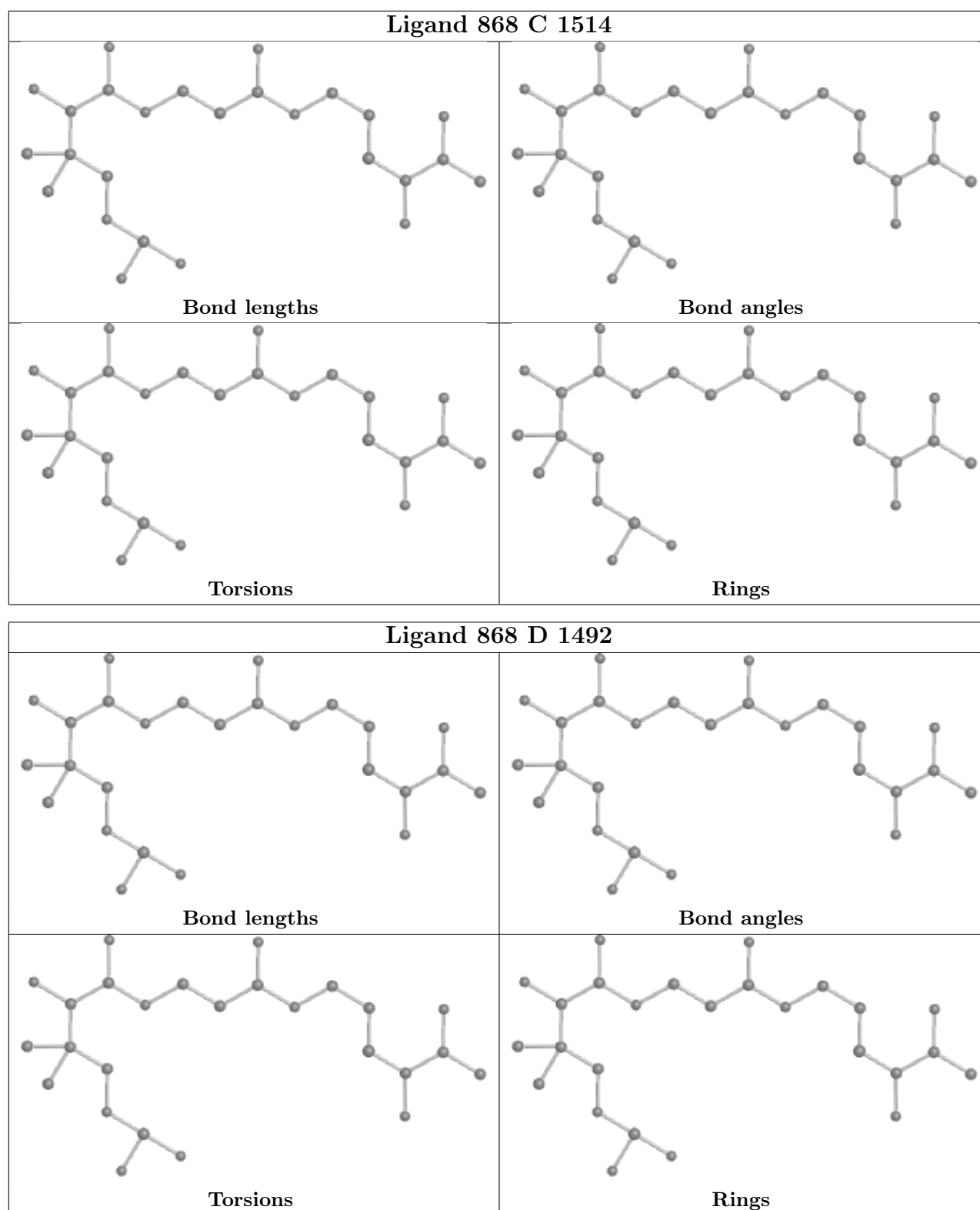
There are no torsion outliers.

There are no ring outliers.

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 ⓘ

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	410/523 (78%)	0.30	21 (5%) 28 29	9, 25, 56, 68	0
1	B	421/523 (80%)	0.26	15 (3%) 42 46	11, 26, 46, 60	0
1	C	455/523 (86%)	0.27	13 (2%) 51 55	13, 28, 52, 70	0
1	D	443/523 (84%)	0.42	29 (6%) 18 19	12, 33, 53, 74	0
All	All	1729/2092 (82%)	0.31	78 (4%) 33 36	9, 27, 52, 74	0

The worst 5 of 78 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	747	TRP	4.7
1	A	748	GLN	4.6
1	A	786	VAL	4.3
1	A	790	ALA	4.2
1	A	792	ALA	3.9

### 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](#)

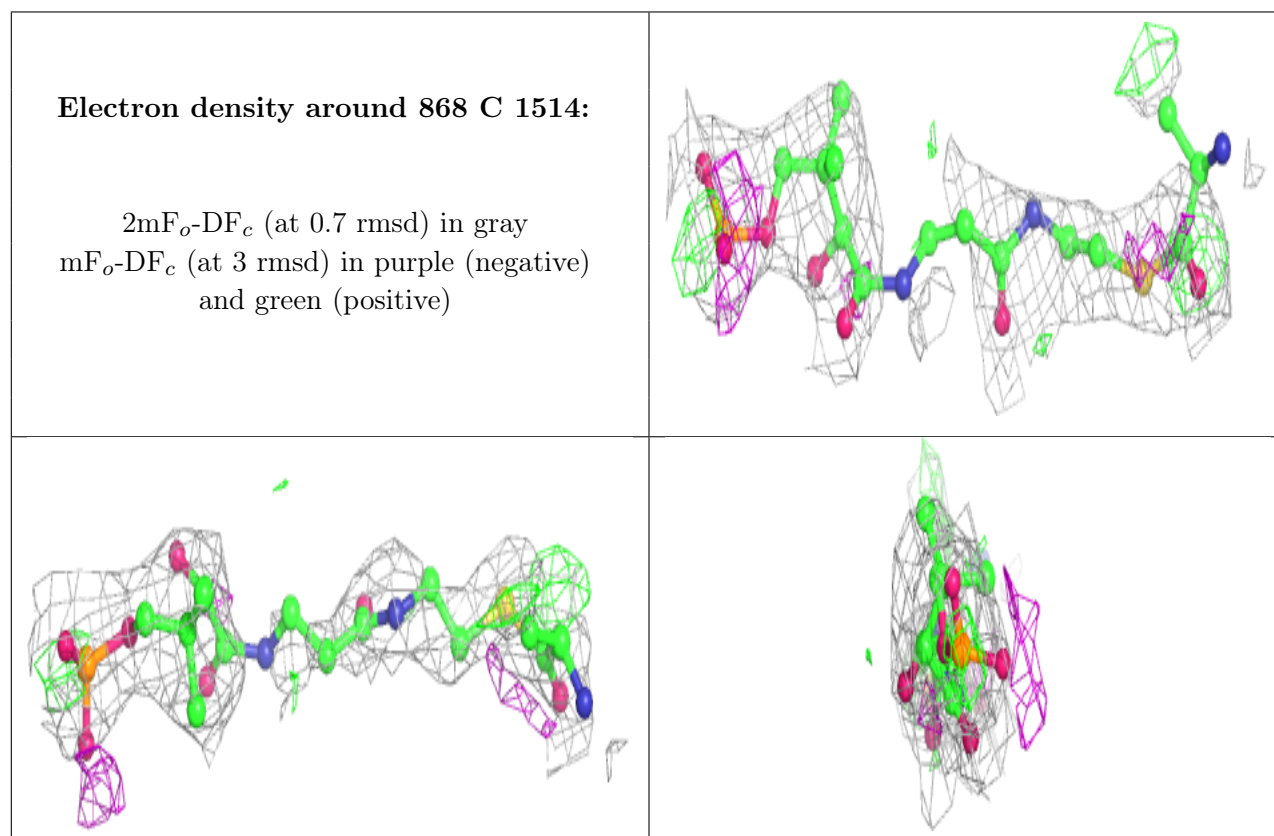
There are no monosaccharides in this entry.

### 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
2	868	C	1514	26/27	0.81	0.31	33,47,60,65	0
2	868	A	1301	26/27	0.82	0.29	23,45,60,89	0
2	868	D	1492	26/27	0.83	0.24	34,44,60,67	0
2	868	B	1527	26/27	0.88	0.24	13,38,46,97	0

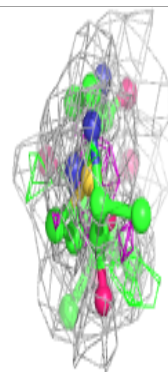
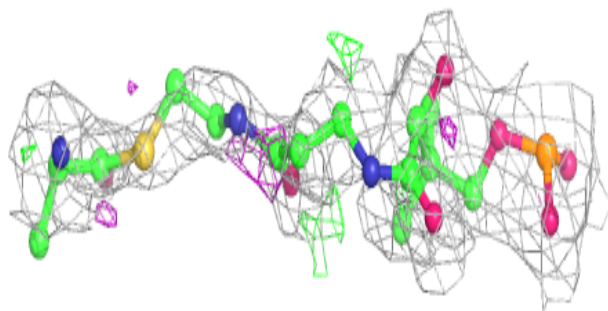
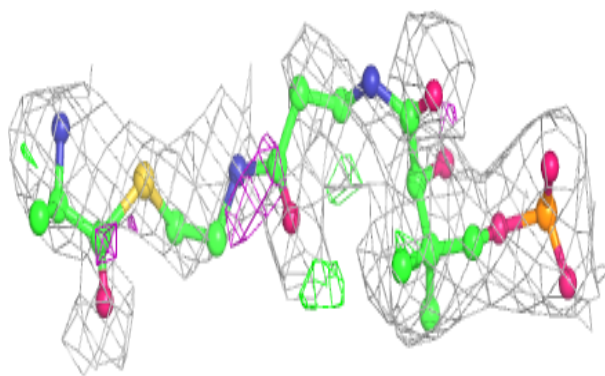
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



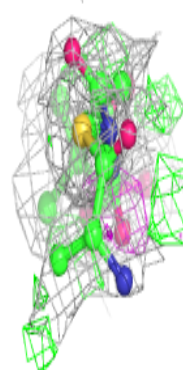
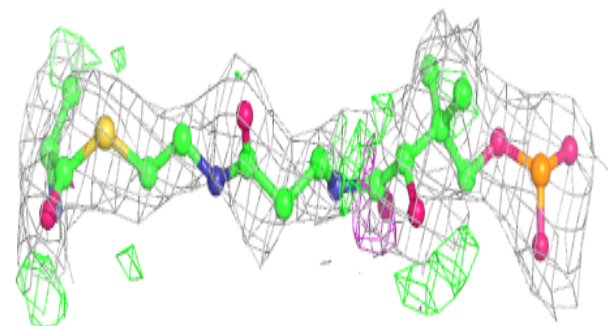
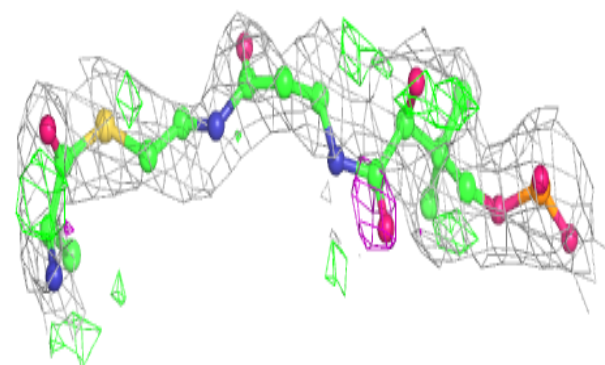


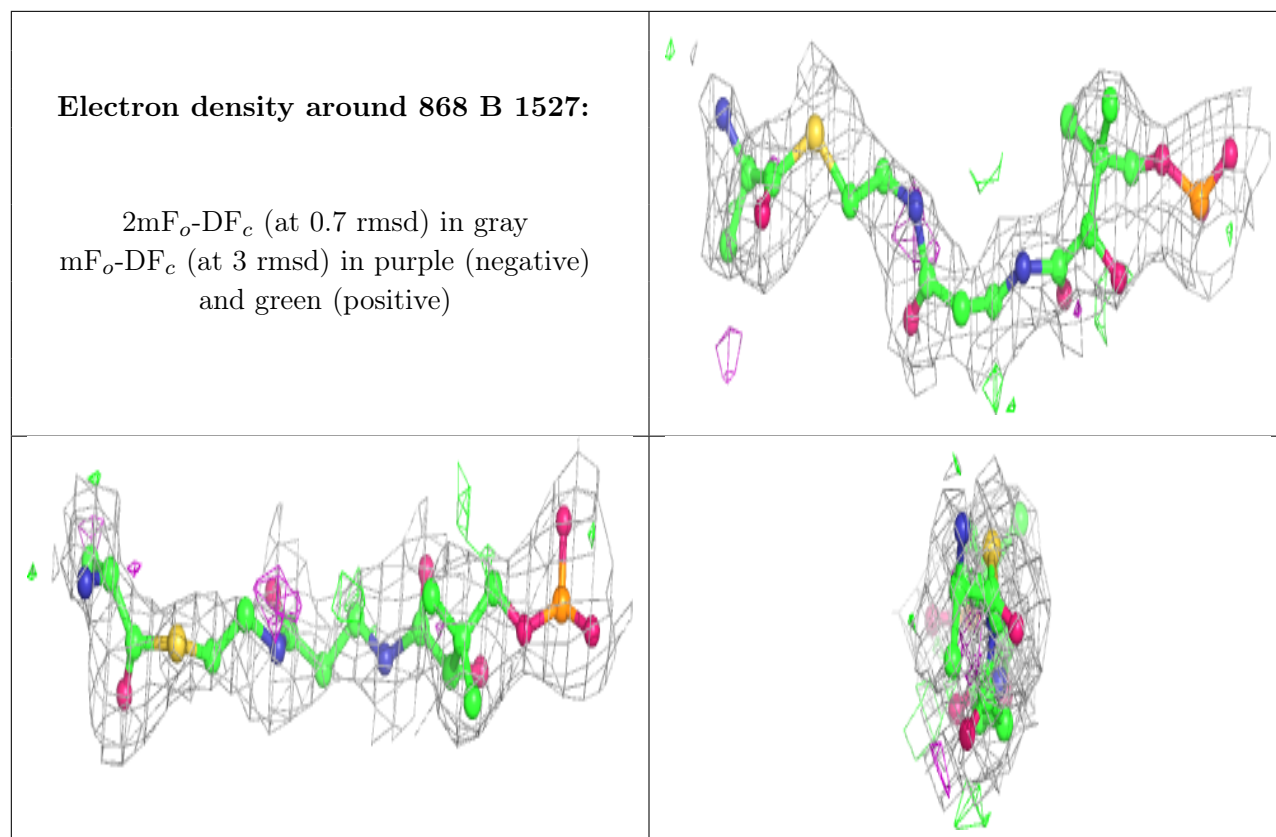
**Electron density around 868 A 1301:**

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

**Electron density around 868 D 1492:**

$2mF_o-DF_c$  (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.