



# Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 08:01 pm BST

PDB ID : 2CLH  
Title : Tryptophan Synthase in complex with (naphthalene-2'-sulfonyl)-2-amino-1-ethylphosphate (F19)  
Authors : Ngo, H.; Harris, R.; Kimmich, N.; Casino, P.; Niks, D.; Blumenstein, L.; Barends, T.R.; Kulik, V.; Weyand, M.; Schlichting, I.; Dunn, M.F.  
Deposited on : 2006-04-27  
Resolution : 1.70 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.

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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 : 2.11  
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

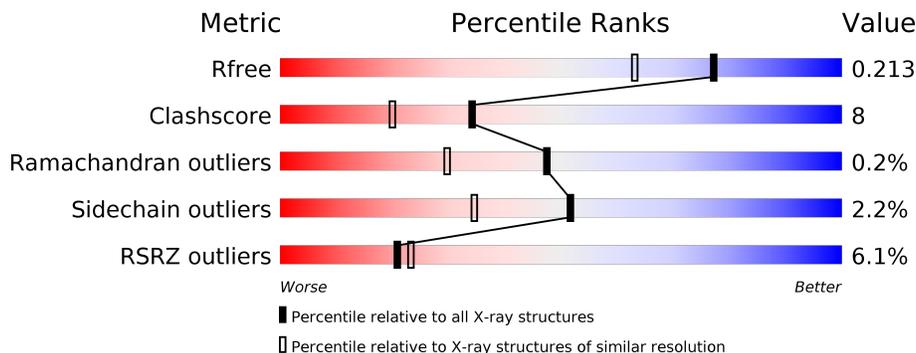
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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  $\geq 3$ , 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	268	
2	B	396	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5522 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 Tryptophan synthase alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	259	1949	1238	339	364	8	0	0	1

- Molecule 2 is a protein called Tryptophan synthase beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	395	2983	1873	527	564	19	0	0	1

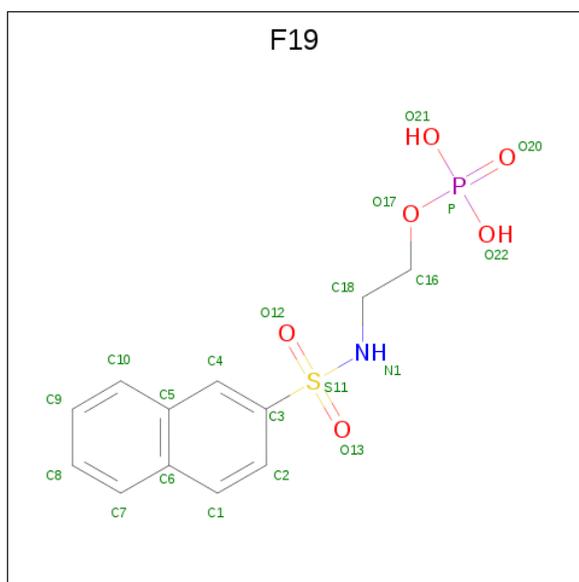
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	34	ARG	SER	conflict	UNP P0A2K1

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

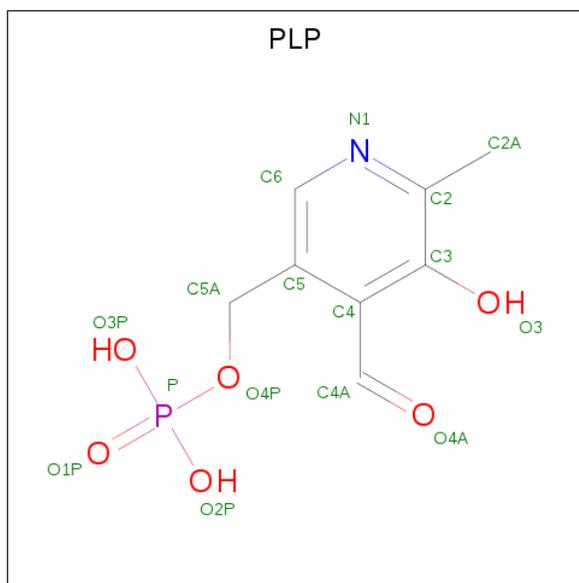
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		

- Molecule 4 is 2-[(2-NAPHTHYLSULFONYL)AMINO]ETHYL DIHYDROGEN PHOSPHATE (three-letter code: F19) (formula: C<sub>12</sub>H<sub>14</sub>NO<sub>6</sub>PS).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			S
4	A	1	21	12	1	6	1	1	0	0

- Molecule 5 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula:  $C_8H_{10}NO_6P$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
5	B	1	15	8	1	5	1	0	0

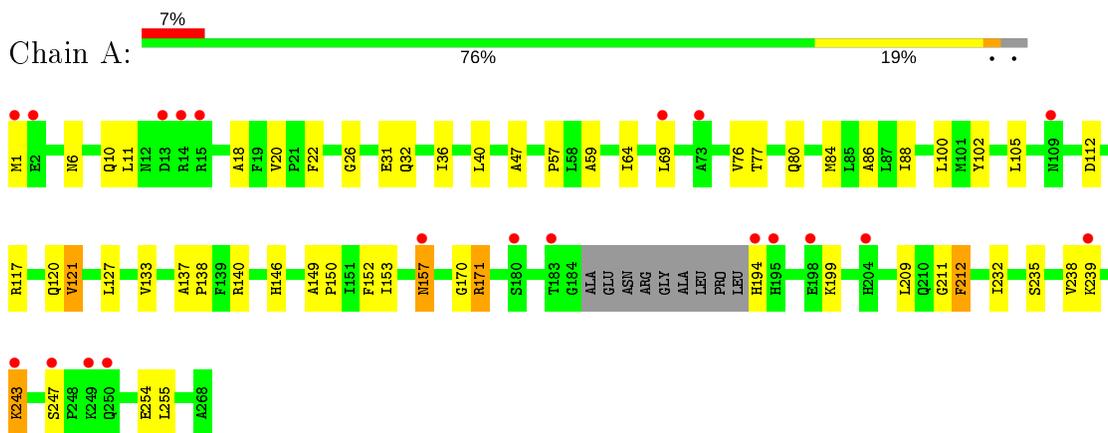
- Molecule 6 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
6	A	188	Total 188	O 188	0	0
6	B	365	Total 365	O 365	0	0

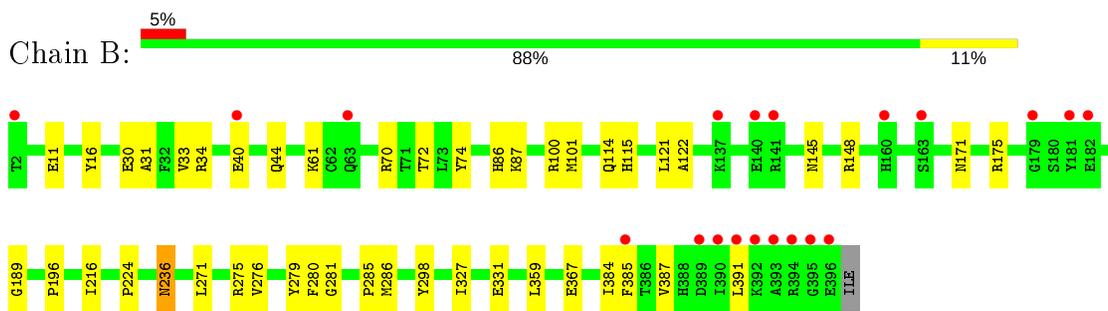
### 3 Residue-property plots [i](#)

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: Tryptophan synthase alpha chain



- Molecule 2: Tryptophan synthase beta chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	181.62Å 59.01Å 67.08Å 90.00° 94.63° 90.00°	Depositor
Resolution (Å)	19.56 – 1.70 19.55 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.0 (19.56-1.70) 98.2 (19.55-1.70)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.78 (at 1.70Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.196 , 0.220 0.189 , 0.213	Depositor DCC
$R_{free}$ test set	3830 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.2	Xtrriage
Anisotropy	0.605	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 51.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5522	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.50% 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: NA, F19, PLP

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	0/1987	0.56	0/2698
2	B	0.31	0/3041	0.61	0/4109
All	All	0.31	0/5028	0.59	0/6807

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
2	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	298	TYR	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	1949	0	1955	47	0
2	B	2983	0	2954	35	0
3	A	1	0	0	0	0
4	A	21	0	12	3	0
5	B	15	0	7	0	0
6	A	188	0	0	5	0
6	B	365	0	0	9	0
All	All	5522	0	4928	83	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 (83) 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:B:34:ARG:HB2	6:B:2136:HOH:O	1.62	1.00
1:A:64:ILE:HD11	1:A:238:VAL:HG21	1.57	0.85
1:A:211:GLY:O	1:A:212:PHE:HB2	1.82	0.79
1:A:64:ILE:CD1	1:A:238:VAL:HG21	2.13	0.78
2:B:30:GLU:HG2	6:B:2061:HOH:O	1.82	0.78
2:B:34:ARG:HG3	2:B:100:ARG:HE	1.50	0.77
2:B:87:LYS:HD2	2:B:114:GLN:HG3	1.65	0.76
1:A:137:ALA:HB3	1:A:138:PRO:HD3	1.69	0.75
1:A:153:ILE:HG12	4:A:1268:F19:H9	1.69	0.73
1:A:170:GLY:O	1:A:171:ARG:HD3	1.94	0.68
2:B:145:ASN:ND2	2:B:148:ARG:HH21	1.93	0.67
1:A:133:VAL:HG12	1:A:152:PHE:HD1	1.61	0.66
2:B:101:MET:HG2	6:B:2060:HOH:O	1.96	0.65
1:A:1:MET:HG2	1:A:149:ALA:HB2	1.79	0.65
1:A:157:ASN:HD22	1:A:157:ASN:H	1.44	0.64
1:A:153:ILE:HD12	1:A:153:ILE:N	2.14	0.63
2:B:279:TYR:HB3	2:B:286:MET:HE1	1.80	0.63
1:A:157:ASN:ND2	1:A:157:ASN:H	1.97	0.63
2:B:34:ARG:HD3	6:B:2061:HOH:O	1.99	0.62
1:A:133:VAL:HG12	1:A:152:PHE:CD1	2.37	0.59
2:B:70:ARG:HD3	2:B:367:GLU:O	2.03	0.58
1:A:59:ALA:HB1	4:A:1268:F19:H7	1.85	0.57
1:A:157:ASN:HD22	1:A:157:ASN:N	2.01	0.57
2:B:31:ALA:O	2:B:34:ARG:HG2	2.05	0.57
2:B:61:LYS:HZ2	2:B:72:THR:HG23	1.70	0.56
1:A:239:LYS:O	1:A:243:LYS:HG2	2.06	0.55
1:A:36:ILE:HG23	1:A:255:LEU:HD13	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:ALA:HB2	1:A:121:VAL:HG22	1.86	0.55
1:A:235:SER:O	1:A:239:LYS:HG3	2.07	0.55
2:B:61:LYS:NZ	2:B:72:THR:HG23	2.23	0.53
1:A:22:PHE:HE1	1:A:64:ILE:HD12	1.73	0.53
2:B:34:ARG:HG3	2:B:100:ARG:NE	2.21	0.52
1:A:11:LEU:CD1	1:A:18:ALA:HB2	2.40	0.52
1:A:140:ARG:HD3	1:A:152:PHE:HZ	1.75	0.51
2:B:16:TYR:O	2:B:281:GLY:HA2	2.10	0.50
1:A:194:HIS:HB2	6:A:2146:HOH:O	2.11	0.50
2:B:216:ILE:HG21	2:B:224:PRO:HD3	1.92	0.50
2:B:271:LEU:O	2:B:271:LEU:HD23	2.11	0.50
1:A:26:GLY:HA3	1:A:76:VAL:HG21	1.93	0.50
2:B:34:ARG:NH1	6:B:2061:HOH:O	2.45	0.49
1:A:100:LEU:C	1:A:100:LEU:HD13	2.34	0.48
1:A:127:LEU:HD23	1:A:127:LEU:C	2.35	0.47
1:A:243:LYS:HE3	1:A:254:GLU:OE2	2.14	0.47
2:B:145:ASN:HD22	2:B:148:ARG:HE	1.62	0.47
1:A:247:SER:HB2	6:A:2174:HOH:O	2.13	0.47
1:A:84:MET:O	1:A:88:ILE:HG13	2.15	0.47
2:B:276:VAL:HA	2:B:285:PRO:HA	1.96	0.47
1:A:32:GLN:O	1:A:36:ILE:HG13	2.15	0.47
1:A:1:MET:SD	1:A:171:ARG:HG2	2.54	0.47
1:A:22:PHE:CD1	1:A:22:PHE:C	2.88	0.47
1:A:57:PRO:HA	1:A:102:TYR:CZ	2.50	0.46
2:B:33:VAL:HB	6:B:2053:HOH:O	2.15	0.46
1:A:20:VAL:HB	1:A:232:ILE:HG12	1.97	0.46
2:B:40:GLU:O	2:B:44:GLN:HG3	2.16	0.46
2:B:327:ILE:HG23	2:B:331:GLU:HB2	1.97	0.45
2:B:61:LYS:HB2	2:B:74:TYR:CE1	2.52	0.45
1:A:211:GLY:O	1:A:212:PHE:CB	2.61	0.45
2:B:271:LEU:C	2:B:271:LEU:HD23	2.37	0.45
2:B:115:HIS:CE1	2:B:189:GLY:HA2	2.52	0.45
2:B:171:ASN:O	2:B:175:ARG:HG3	2.17	0.44
2:B:100:ARG:NH2	6:B:2136:HOH:O	2.38	0.44
1:A:254:GLU:HG3	6:A:2176:HOH:O	2.17	0.44
1:A:20:VAL:O	1:A:232:ILE:HA	2.18	0.44
2:B:275:ARG:HD2	6:B:2266:HOH:O	2.18	0.43
1:A:153:ILE:CD1	1:A:153:ILE:N	2.81	0.43
2:B:384:ILE:HG13	2:B:385:PHE:N	2.34	0.43
2:B:34:ARG:CG	2:B:100:ARG:HE	2.26	0.43
1:A:150:PRO:HD2	1:A:171:ARG:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194:HIS:N	6:A:2146:HOH:O	2.52	0.43
1:A:117:ARG:NH1	1:A:120:GLN:OE1	2.52	0.42
1:A:77:THR:OG1	1:A:80:GLN:HG3	2.19	0.42
2:B:121:LEU:HD12	2:B:122:ALA:N	2.35	0.42
1:A:6:ASN:O	1:A:10:GLN:HG3	2.20	0.42
2:B:86:HIS:CD2	2:B:236:ASN:HB3	2.55	0.42
2:B:11:GLU:HG2	6:B:2024:HOH:O	2.20	0.41
1:A:20:VAL:HG22	1:A:47:ALA:HB3	2.01	0.41
2:B:387:VAL:O	2:B:391:LEU:HG	2.20	0.41
1:A:112:ASP:OD1	1:A:146:HIS:HE1	2.03	0.41
4:A:1268:F19:H2	6:A:2052:HOH:O	2.20	0.41
1:A:36:ILE:O	1:A:40:LEU:HD13	2.21	0.41
2:B:279:TYR:CG	2:B:280:PHE:N	2.88	0.41
1:A:69:LEU:HD12	1:A:69:LEU:HA	1.92	0.40
1:A:243:LYS:NZ	1:A:243:LYS:HB2	2.37	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	255/268 (95%)	246 (96%)	8 (3%)	1 (0%)	34	18
2	B	393/396 (99%)	383 (98%)	10 (2%)	0	100	100
All	All	648/664 (98%)	629 (97%)	18 (3%)	1 (0%)	47	30

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	212	PHE

### 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	202/208 (97%)	194 (96%)	8 (4%)	31	13
2	B	307/310 (99%)	304 (99%)	3 (1%)	76	67
All	All	509/518 (98%)	498 (98%)	11 (2%)	52	34

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

Mol	Chain	Res	Type
1	A	31	GLU
1	A	105	LEU
1	A	121	VAL
1	A	157	ASN
1	A	171	ARG
1	A	199	LYS
1	A	209	LEU
1	A	243	LYS
2	B	196	PRO
2	B	236	ASN
2	B	359	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	157	ASN
1	A	250	GLN
2	B	26	ASN
2	B	44	GLN
2	B	64	ASN
2	B	114	GLN
2	B	142	GLN
2	B	145	ASN
2	B	236	ASN
2	B	375	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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
5	PLP	B	1396	2	15,15,16	1.74	4 (26%)	20,22,23	1.81	2 (10%)
4	F19	A	1268	-	22,22,22	3.13	10 (45%)	31,32,32	2.24	9 (29%)

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	PLP	B	1396	2	-	0/6/6/8	0/1/1/1
4	F19	A	1268	-	-	7/15/15/15	0/2/2/2

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1268	F19	C8-C7	9.25	1.57	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1268	F19	S11-N1	5.75	1.70	1.61
4	A	1268	F19	C9-C10	4.38	1.46	1.36
4	A	1268	F19	C2-C3	4.25	1.45	1.38
5	B	1396	PLP	C3-C2	-3.04	1.37	1.40
4	A	1268	F19	O12-S11	2.98	1.46	1.43
4	A	1268	F19	C4-C3	2.85	1.41	1.36
4	A	1268	F19	C3-S11	2.77	1.80	1.76
4	A	1268	F19	P-O20	-2.69	1.41	1.50
5	B	1396	PLP	C4A-C4	2.66	1.57	1.51
5	B	1396	PLP	C2A-C2	2.54	1.54	1.50
5	B	1396	PLP	C5A-C5	2.27	1.57	1.50
4	A	1268	F19	C9-C8	2.25	1.44	1.38
4	A	1268	F19	P-O22	-2.21	1.46	1.54

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1396	PLP	O4P-C5A-C5	6.32	121.40	109.35
4	A	1268	F19	C8-C9-C10	-5.47	112.77	120.44
4	A	1268	F19	O17-P-O20	5.45	121.76	106.47
4	A	1268	F19	O13-S11-O12	-5.26	113.08	119.55
4	A	1268	F19	C8-C7-C6	-3.22	115.41	120.44
4	A	1268	F19	O12-S11-N1	3.18	112.00	107.04
4	A	1268	F19	C2-C3-C4	-2.98	117.40	121.05
4	A	1268	F19	C3-S11-N1	2.97	111.67	107.55
5	B	1396	PLP	O4P-P-O1P	-2.88	98.38	106.47
4	A	1268	F19	C9-C8-C7	2.80	124.37	120.44
4	A	1268	F19	C4-C3-S11	2.55	122.18	120.03

There are no chirality outliers.

All (7) torsion outliers are listed below:

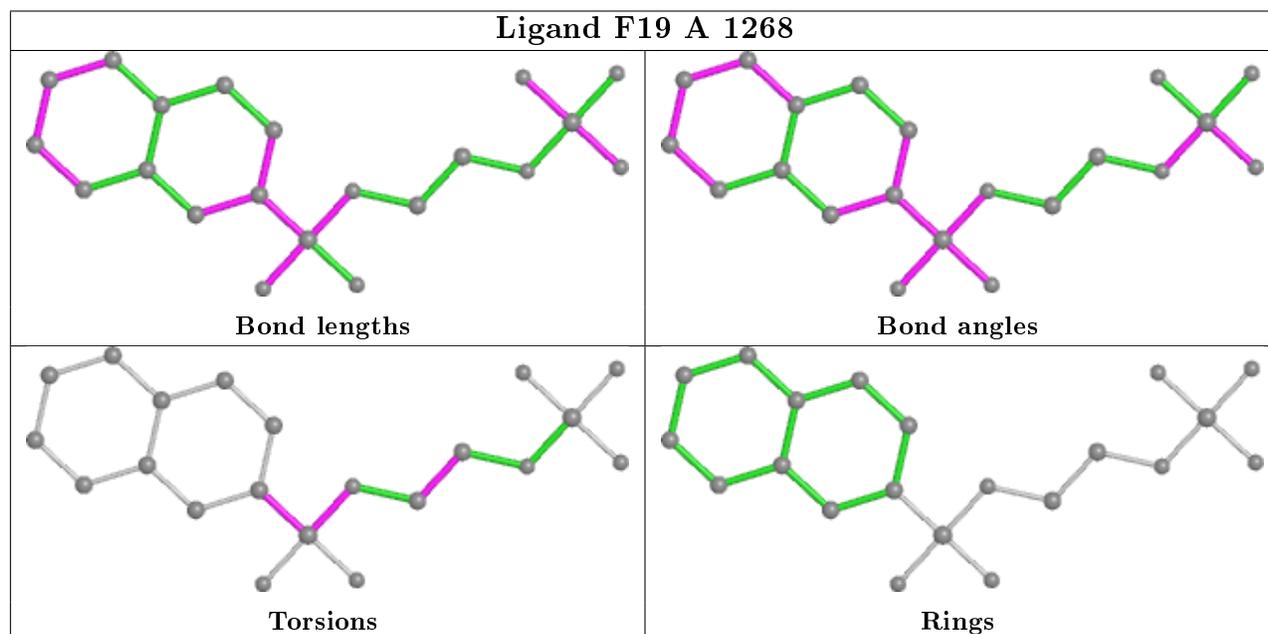
Mol	Chain	Res	Type	Atoms
4	A	1268	F19	C18-N1-S11-O12
4	A	1268	F19	C2-C3-S11-O13
4	A	1268	F19	C4-C3-S11-O13
4	A	1268	F19	C2-C3-S11-N1
4	A	1268	F19	C4-C3-S11-N1
4	A	1268	F19	O17-C16-C18-N1
4	A	1268	F19	C18-N1-S11-C3

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1268	F19	3	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 [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	259/268 (96%)	0.46	20 (7%) 13 15	13, 22, 35, 42	0
2	B	395/396 (99%)	0.31	20 (5%) 28 31	9, 15, 32, 53	0
All	All	654/664 (98%)	0.37	40 (6%) 21 23	9, 19, 34, 53	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	396	GLU	13.8
2	B	395	GLY	8.9
2	B	393	ALA	7.6
2	B	2	THR	5.5
1	A	195	HIS	5.0
2	B	141	ARG	4.6
2	B	394	ARG	4.3
1	A	15	ARG	4.3
1	A	194	HIS	4.1
1	A	249	LYS	4.1
2	B	63	GLN	3.9
2	B	140	GLU	3.6
2	B	385	PHE	3.5
1	A	13	ASP	3.2
2	B	182	GLU	3.2
1	A	243	LYS	3.2
1	A	157	ASN	3.1
2	B	160	HIS	3.1
1	A	204	HIS	3.0
1	A	2	GLU	2.9
1	A	14	ARG	2.7
2	B	181	TYR	2.6
1	A	73	ALA	2.6
1	A	247	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	180	SER	2.6
2	B	392	LYS	2.6
1	A	109	ASN	2.4
2	B	163	SER	2.4
2	B	390	ILE	2.4
1	A	239	LYS	2.3
2	B	137	LYS	2.3
2	B	391	LEU	2.3
1	A	198	GLU	2.3
1	A	1	MET	2.3
2	B	389	ASP	2.2
1	A	250	GLN	2.2
2	B	179	GLY	2.1
2	B	40	GLU	2.0
1	A	69	LEU	2.0
1	A	183	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](#)

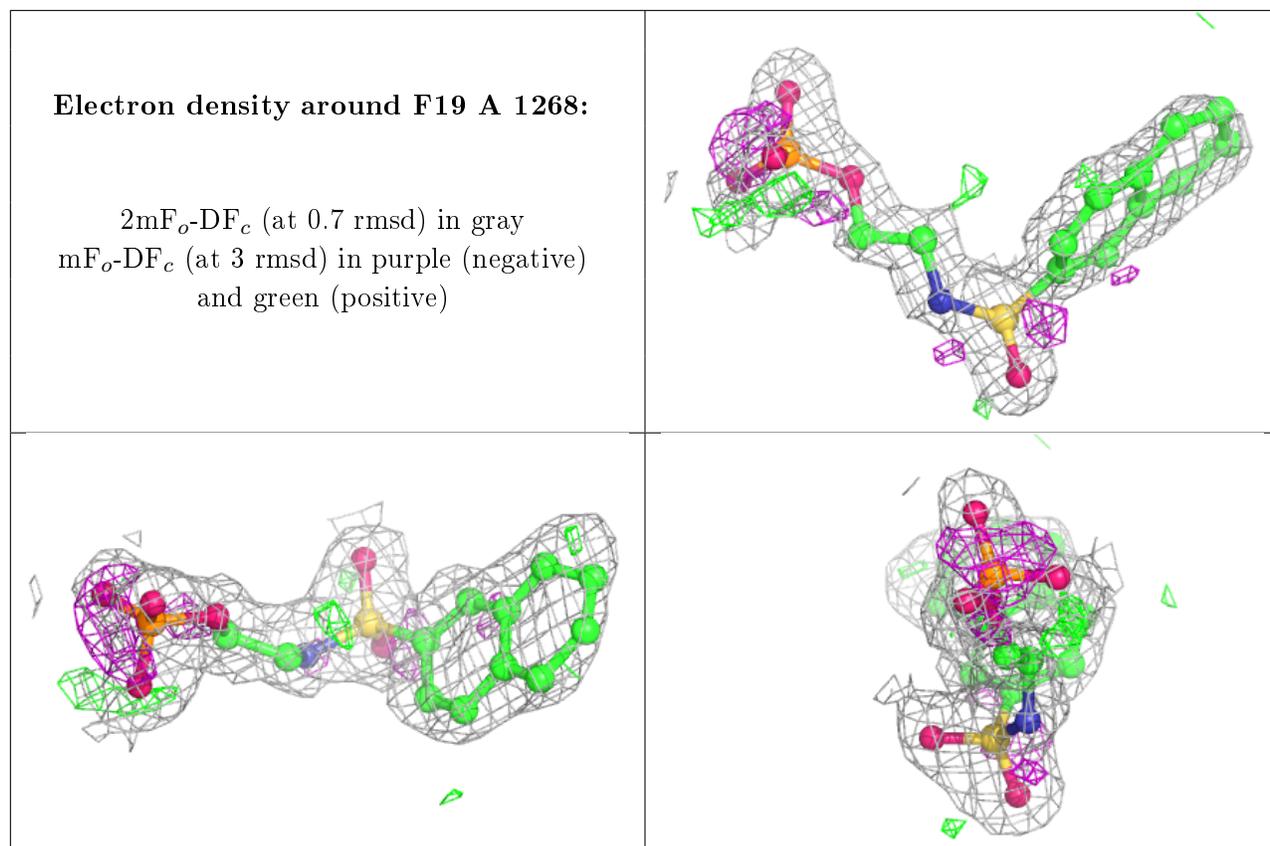
There are no carbohydrates in this entry.

## 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, 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
4	F19	A	1268	21/21	0.92	0.13	28,32,35,36	0
3	NA	A	1267	1/1	0.95	0.08	15,15,15,15	0
5	PLP	B	1396	15/16	0.97	0.08	11,12,19,20	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.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.