



# Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 12:47 pm BST

PDB ID : 6EWQ  
Title : Putative sugar aminotransferase Spr1654 from *Streptococcus pneumoniae*, PLP-form  
Authors : Achour, A.; Sun, R.; Sandalova, T.; Han, X.  
Deposited on : 2017-11-06  
Resolution : 2.20 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

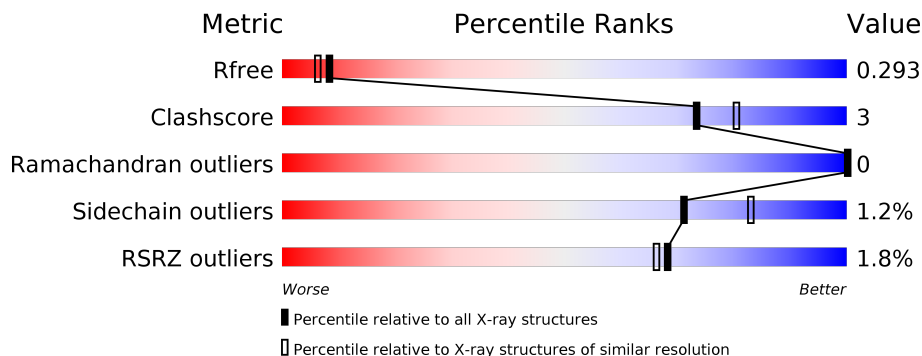
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	427	 % 87% 6% • 6%
1	B	427	 % 84% 7% • 8%
1	C	427	 2% 86% 7% • 6%
1	D	427	 2% 86% 5% • 8%

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 13383 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 Putative capsular polysaccharide biosynthesis protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	401	Total 3155	C 2015	N 516	O 612	S 12	0	0	0
1	B	392	Total 3086	C 1971	N 504	O 600	S 11	0	0	0
1	C	402	Total 3163	C 2021	N 517	O 613	S 12	0	0	0
1	D	394	Total 3102	C 1981	N 507	O 603	S 11	0	0	0

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	initiating methionine	UNP A0A0H2URM1
A	-4	ALA	-	expression tag	UNP A0A0H2URM1
A	-3	SER	-	expression tag	UNP A0A0H2URM1
A	-2	MET	-	expression tag	UNP A0A0H2URM1
A	-1	THR	-	expression tag	UNP A0A0H2URM1
A	0	GLY	-	expression tag	UNP A0A0H2URM1
A	178	THR	ILE	conflict	UNP A0A0H2URM1
A	409	LYS	-	expression tag	UNP A0A0H2URM1
A	410	LEU	-	expression tag	UNP A0A0H2URM1
A	411	ALA	-	expression tag	UNP A0A0H2URM1
A	412	ALA	-	expression tag	UNP A0A0H2URM1
A	413	ALA	-	expression tag	UNP A0A0H2URM1
A	414	LEU	-	expression tag	UNP A0A0H2URM1
A	415	GLU	-	expression tag	UNP A0A0H2URM1
A	416	HIS	-	expression tag	UNP A0A0H2URM1
A	417	HIS	-	expression tag	UNP A0A0H2URM1
A	418	HIS	-	expression tag	UNP A0A0H2URM1
A	419	HIS	-	expression tag	UNP A0A0H2URM1
A	420	HIS	-	expression tag	UNP A0A0H2URM1
A	421	HIS	-	expression tag	UNP A0A0H2URM1
B	-5	MET	-	initiating methionine	UNP A0A0H2URM1

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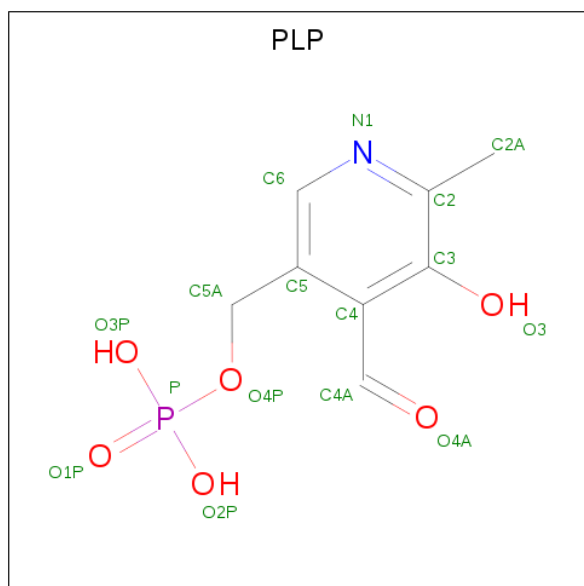
Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	ALA	-	expression tag	UNP A0A0H2URM1
B	-3	SER	-	expression tag	UNP A0A0H2URM1
B	-2	MET	-	expression tag	UNP A0A0H2URM1
B	-1	THR	-	expression tag	UNP A0A0H2URM1
B	0	GLY	-	expression tag	UNP A0A0H2URM1
B	178	THR	ILE	conflict	UNP A0A0H2URM1
B	409	LYS	-	expression tag	UNP A0A0H2URM1
B	410	LEU	-	expression tag	UNP A0A0H2URM1
B	411	ALA	-	expression tag	UNP A0A0H2URM1
B	412	ALA	-	expression tag	UNP A0A0H2URM1
B	413	ALA	-	expression tag	UNP A0A0H2URM1
B	414	LEU	-	expression tag	UNP A0A0H2URM1
B	415	GLU	-	expression tag	UNP A0A0H2URM1
B	416	HIS	-	expression tag	UNP A0A0H2URM1
B	417	HIS	-	expression tag	UNP A0A0H2URM1
B	418	HIS	-	expression tag	UNP A0A0H2URM1
B	419	HIS	-	expression tag	UNP A0A0H2URM1
B	420	HIS	-	expression tag	UNP A0A0H2URM1
B	421	HIS	-	expression tag	UNP A0A0H2URM1
C	-5	MET	-	initiating methionine	UNP A0A0H2URM1
C	-4	ALA	-	expression tag	UNP A0A0H2URM1
C	-3	SER	-	expression tag	UNP A0A0H2URM1
C	-2	MET	-	expression tag	UNP A0A0H2URM1
C	-1	THR	-	expression tag	UNP A0A0H2URM1
C	0	GLY	-	expression tag	UNP A0A0H2URM1
C	178	THR	ILE	conflict	UNP A0A0H2URM1
C	409	LYS	-	expression tag	UNP A0A0H2URM1
C	410	LEU	-	expression tag	UNP A0A0H2URM1
C	411	ALA	-	expression tag	UNP A0A0H2URM1
C	412	ALA	-	expression tag	UNP A0A0H2URM1
C	413	ALA	-	expression tag	UNP A0A0H2URM1
C	414	LEU	-	expression tag	UNP A0A0H2URM1
C	415	GLU	-	expression tag	UNP A0A0H2URM1
C	416	HIS	-	expression tag	UNP A0A0H2URM1
C	417	HIS	-	expression tag	UNP A0A0H2URM1
C	418	HIS	-	expression tag	UNP A0A0H2URM1
C	419	HIS	-	expression tag	UNP A0A0H2URM1
C	420	HIS	-	expression tag	UNP A0A0H2URM1
C	421	HIS	-	expression tag	UNP A0A0H2URM1
D	-5	MET	-	initiating methionine	UNP A0A0H2URM1
D	-4	ALA	-	expression tag	UNP A0A0H2URM1
D	-3	SER	-	expression tag	UNP A0A0H2URM1

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	MET	-	expression tag	UNP A0A0H2URM1
D	-1	THR	-	expression tag	UNP A0A0H2URM1
D	0	GLY	-	expression tag	UNP A0A0H2URM1
D	178	THR	ILE	conflict	UNP A0A0H2URM1
D	409	LYS	-	expression tag	UNP A0A0H2URM1
D	410	LEU	-	expression tag	UNP A0A0H2URM1
D	411	ALA	-	expression tag	UNP A0A0H2URM1
D	412	ALA	-	expression tag	UNP A0A0H2URM1
D	413	ALA	-	expression tag	UNP A0A0H2URM1
D	414	LEU	-	expression tag	UNP A0A0H2URM1
D	415	GLU	-	expression tag	UNP A0A0H2URM1
D	416	HIS	-	expression tag	UNP A0A0H2URM1
D	417	HIS	-	expression tag	UNP A0A0H2URM1
D	418	HIS	-	expression tag	UNP A0A0H2URM1
D	419	HIS	-	expression tag	UNP A0A0H2URM1
D	420	HIS	-	expression tag	UNP A0A0H2URM1
D	421	HIS	-	expression tag	UNP A0A0H2URM1

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C<sub>8</sub>H<sub>10</sub>NO<sub>6</sub>P) (labeled as "Ligand of Interest" by author).



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

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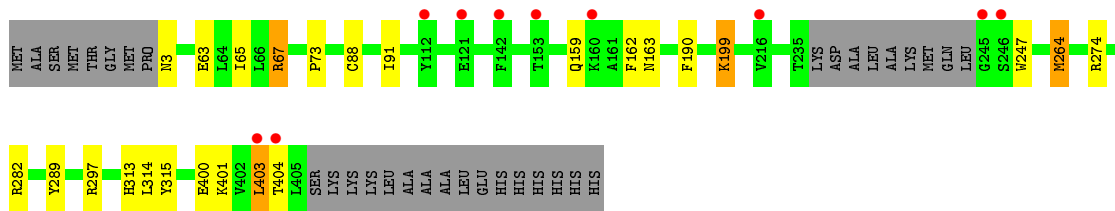
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	198	Total	O	0	0
			198	198		
3	B	216	Total	O	0	0
			216	216		
3	C	227	Total	O	0	0
			227	227		
3	D	176	Total	O	0	0
			176	176		







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	79.01Å 99.32Å 107.61Å 90.00° 97.74° 90.00°	Depositor
Resolution (Å)	29.70 – 2.20 55.88 – 2.17	Depositor EDS
% Data completeness (in resolution range)	95.0 (29.70-2.20) 93.9 (55.88-2.17)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.47 (at 2.16Å)	Xtrriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.238 , 0.288 0.242 , 0.293	Depositor DCC
$R_{free}$ test set	4032 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.6	Xtrriage
Anisotropy	0.840	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 39.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.24$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	13383	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.01% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.67	0/3221	0.79	4/4376 (0.1%)
1	B	0.74	1/3152 (0.0%)	0.82	5/4285 (0.1%)
1	C	0.76	3/3229 (0.1%)	0.82	6/4387 (0.1%)
1	D	0.76	0/3167	0.84	7/4304 (0.2%)
All	All	0.73	4/12769 (0.0%)	0.82	22/17352 (0.1%)

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
1	D	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	57	SER	CB-OG	-5.88	1.34	1.42
1	C	7	PRO	N-CD	5.49	1.55	1.47
1	B	7	PRO	N-CD	5.29	1.55	1.47
1	C	26	ARG	CZ-NH2	-5.12	1.26	1.33

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	67	ARG	NE-CZ-NH2	-9.69	115.46	120.30
1	B	67	ARG	NE-CZ-NH2	-9.01	115.79	120.30
1	C	67	ARG	NE-CZ-NH1	9.00	124.80	120.30
1	A	282	ARG	NE-CZ-NH2	-8.58	116.01	120.30
1	B	282	ARG	NE-CZ-NH2	-8.18	116.21	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	282	ARG	NE-CZ-NH2	-8.14	116.23	120.30
1	C	67	ARG	NE-CZ-NH2	-7.89	116.35	120.30
1	D	282	ARG	NE-CZ-NH2	-7.55	116.53	120.30
1	A	282	ARG	NE-CZ-NH1	7.51	124.06	120.30
1	C	282	ARG	NE-CZ-NH1	7.23	123.92	120.30
1	B	282	ARG	NE-CZ-NH1	6.96	123.78	120.30
1	D	282	ARG	NE-CZ-NH1	6.92	123.76	120.30
1	C	26	ARG	NE-CZ-NH1	6.47	123.54	120.30
1	D	274	ARG	NE-CZ-NH1	6.26	123.43	120.30
1	D	264	MET	CG-SD-CE	5.89	109.63	100.20
1	A	67	ARG	NE-CZ-NH2	-5.77	117.42	120.30
1	D	67	ARG	NE-CZ-NH1	5.45	123.02	120.30
1	B	274	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	B	6	ILE	C-N-CD	5.33	139.59	128.40
1	A	67	ARG	NE-CZ-NH1	5.31	122.95	120.30
1	C	6	ILE	C-N-CD	5.15	139.22	128.40
1	D	264	MET	CB-CG-SD	5.13	127.78	112.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	403	LEU	Peptide

## 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	3155	0	3134	21	0
1	B	3086	0	3055	27	0
1	C	3163	0	3145	20	0
1	D	3102	0	3071	15	0
2	A	15	0	6	1	0
2	B	15	0	6	0	0
2	C	15	0	6	1	0
2	D	15	0	6	0	0
3	A	198	0	0	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	216	0	0	17	0
3	C	227	0	0	6	0
3	D	176	0	0	3	0
All	All	13383	0	12429	82	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 3.

All (82) 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:160:LYS:HB3	3:B:645:HOH:O	1.71	0.88
1:B:252:VAL:HG22	3:B:650:HOH:O	1.77	0.83
1:B:235:THR:HG23	3:B:650:HOH:O	1.77	0.82
1:C:63:GLU:OE2	1:C:67:ARG:NH1	2.20	0.75
1:C:68:VAL:HG13	3:C:607:HOH:O	1.95	0.65
1:D:400:GLU:HG2	3:D:601:HOH:O	1.97	0.64
1:D:3:ASN:N	1:D:3:ASN:OD1	2.30	0.64
1:C:224:LYS:HB2	3:C:680:HOH:O	1.99	0.63
1:B:49:THR:CG2	3:B:602:HOH:O	2.48	0.62
1:D:401:LYS:O	1:D:403:LEU:HG	2.00	0.61
1:A:12:ASP:HB3	3:A:734:HOH:O	2.00	0.60
1:A:53:VAL:HG13	3:A:702:HOH:O	2.04	0.58
1:D:403:LEU:C	1:D:404:THR:HG23	2.25	0.57
1:A:336:LYS:NZ	3:A:602:HOH:O	2.36	0.56
1:B:252:VAL:CG2	3:B:650:HOH:O	2.45	0.56
1:B:124:LYS:HE2	3:B:732:HOH:O	2.05	0.55
1:A:227:GLN:HG2	3:A:702:HOH:O	2.07	0.55
1:C:159:GLN:O	1:C:162:PHE:O	2.25	0.55
1:A:159:GLN:O	1:A:162:PHE:O	2.25	0.55
1:B:26:ARG:HD3	1:C:26:ARG:NH1	2.22	0.55
1:A:400:GLU:HG2	3:A:737:HOH:O	2.07	0.54
1:A:4:TYR:N	1:A:4:TYR:CD1	2.73	0.54
1:B:159:GLN:O	1:B:162:PHE:O	2.25	0.54
1:D:159:GLN:O	1:D:162:PHE:O	2.25	0.54
1:D:63:GLU:OE2	1:D:67:ARG:NH1	2.42	0.53
1:B:49:THR:HG21	3:B:602:HOH:O	2.09	0.53
1:A:53:VAL:CG1	3:A:702:HOH:O	2.59	0.50
1:B:231:LEU:HD23	3:B:668:HOH:O	2.12	0.50
1:D:297:ARG:NE	3:D:601:HOH:O	2.36	0.50
1:A:288:ARG:NH1	3:A:608:HOH:O	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:399:SER:HB2	3:A:737:HOH:O	2.12	0.50
1:C:296:SER:HB3	3:C:606:HOH:O	2.12	0.49
1:B:313:HIS:CD2	1:B:314:LEU:HG	2.48	0.48
1:C:65:ILE:HD13	1:C:190:PHE:HB3	1.96	0.48
1:A:63:GLU:OE2	1:A:67:ARG:NH1	2.47	0.47
1:B:257:LYS:HD2	3:B:668:HOH:O	2.14	0.47
1:B:49:THR:HG23	3:B:602:HOH:O	2.13	0.46
1:C:56:ASN:HD22	1:C:56:ASN:C	2.19	0.46
1:A:160:LYS:HD3	3:A:636:HOH:O	2.14	0.45
1:B:57:SER:HB3	3:B:615:HOH:O	2.17	0.45
1:C:56:ASN:OD1	1:C:258:CYS:HA	2.16	0.45
1:B:283:LYS:HD3	3:B:767:HOH:O	2.17	0.45
1:D:199:LYS:HA	1:D:313:HIS:CE1	2.52	0.45
1:A:313:HIS:CD2	1:A:314:LEU:HG	2.53	0.44
1:B:185:GLY:HA3	3:B:602:HOH:O	2.18	0.44
1:A:194:SER:OG	2:A:500:PLP:O3P	2.24	0.44
1:C:400:GLU:O	1:C:403:LEU:N	2.51	0.44
3:C:604:HOH:O	1:D:247:TRP:HB2	2.17	0.44
1:B:199:LYS:HA	1:B:313:HIS:CE1	2.53	0.44
1:B:47:THR:HB	3:B:602:HOH:O	2.18	0.44
1:B:63:GLU:OE2	1:B:67:ARG:NH1	2.51	0.43
1:B:400:GLU:O	1:B:403:LEU:HD23	2.18	0.43
1:C:313:HIS:CD2	1:C:314:LEU:HG	2.53	0.43
1:C:382:LYS:HG2	3:C:650:HOH:O	2.18	0.43
1:D:65:ILE:HD13	1:D:190:PHE:HB3	2.01	0.43
1:C:58:ALA:HB2	1:C:194:SER:HB2	2.00	0.43
1:D:313:HIS:CD2	1:D:314:LEU:HG	2.53	0.43
1:B:234:GLN:HA	1:B:251:ILE:HD13	2.00	0.43
1:C:173:HIS:NE2	2:C:500:PLP:O3	2.47	0.43
1:C:289:TYR:HB3	1:C:315:TYR:CZ	2.54	0.42
1:A:234:GLN:HA	1:A:251:ILE:HD13	2.02	0.42
1:C:201:PHE:HB3	3:C:710:HOH:O	2.20	0.42
1:B:235:THR:CG2	3:B:650:HOH:O	2.52	0.42
1:C:88:CYS:HA	1:C:91:ILE:HD12	2.02	0.42
1:B:210:THR:HG21	3:B:602:HOH:O	2.19	0.42
1:B:196:HIS:HD2	1:B:198:VAL:HG22	1.84	0.42
1:A:53:VAL:HG22	3:A:702:HOH:O	2.19	0.42
1:C:199:LYS:HA	1:C:313:HIS:CE1	2.55	0.42
1:A:12:ASP:CG	3:A:734:HOH:O	2.58	0.41
1:B:88:CYS:HA	1:B:91:ILE:HD12	2.03	0.41
1:A:199:LYS:HA	1:A:313:HIS:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:ASN:ND2	1:A:258:CYS:HA	2.36	0.41
1:D:400:GLU:O	1:D:403:LEU:HD23	2.21	0.41
1:A:88:CYS:HA	1:A:91:ILE:HD12	2.03	0.41
1:C:234:GLN:HA	1:C:251:ILE:HD13	2.03	0.41
1:D:88:CYS:HA	1:D:91:ILE:HD12	2.03	0.41
1:B:47:THR:CB	3:B:602:HOH:O	2.68	0.40
1:D:73:PRO:HG3	3:D:760:HOH:O	2.21	0.40
1:A:289:TYR:HB3	1:A:315:TYR:CZ	2.57	0.40
1:D:289:TYR:HB3	1:D:315:TYR:CZ	2.56	0.40
1:B:7:PRO:HG2	1:B:10:PRO:HD3	2.03	0.40
1:C:56:ASN:HD22	1:C:57:SER:N	2.19	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	397/427 (93%)	380 (96%)	17 (4%)	0	100	100
1	B	388/427 (91%)	372 (96%)	16 (4%)	0	100	100
1	C	398/427 (93%)	381 (96%)	17 (4%)	0	100	100
1	D	389/427 (91%)	371 (95%)	18 (5%)	0	100	100
All	All	1572/1708 (92%)	1504 (96%)	68 (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	348/371 (94%)	343 (99%)	5 (1%)	67	80
1	B	341/371 (92%)	338 (99%)	3 (1%)	78	88
1	C	349/371 (94%)	344 (99%)	5 (1%)	67	80
1	D	343/371 (92%)	340 (99%)	3 (1%)	78	88
All	All	1381/1484 (93%)	1365 (99%)	16 (1%)	71	83

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	TYR
1	A	5	ASN
1	A	163	ASN
1	A	199	LYS
1	A	264	MET
1	B	163	ASN
1	B	199	LYS
1	B	264	MET
1	C	56	ASN
1	C	163	ASN
1	C	199	LYS
1	C	264	MET
1	C	403	LEU
1	D	163	ASN
1	D	199	LYS
1	D	264	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	B	232	HIS
1	C	56	ASN
1	D	3	ASN
1	D	227	GLN
1	D	234	GLN
1	D	280	GLN

### 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](#)

4 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
2	PLP	B	500	1	15,15,16	3.62	3 (20%)	20,22,23	2.25	6 (30%)
2	PLP	C	500	1	15,15,16	3.60	5 (33%)	20,22,23	2.43	4 (20%)
2	PLP	A	500	1	15,15,16	3.81	4 (26%)	20,22,23	2.54	7 (35%)
2	PLP	D	500	1	15,15,16	3.79	4 (26%)	20,22,23	2.13	7 (35%)

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
2	PLP	B	500	1	-	5/6/6/8	0/1/1/1
2	PLP	C	500	1	-	2/6/6/8	0/1/1/1
2	PLP	A	500	1	-	5/6/6/8	0/1/1/1
2	PLP	D	500	1	-	2/6/6/8	0/1/1/1



All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	PLP	C5-C4	11.33	1.53	1.40
2	D	500	PLP	C5-C4	11.12	1.52	1.40
2	A	500	PLP	C5-C4	10.96	1.52	1.40
2	C	500	PLP	C5-C4	9.18	1.50	1.40
2	C	500	PLP	C3-C2	8.69	1.49	1.40
2	A	500	PLP	C3-C2	8.53	1.49	1.40
2	D	500	PLP	C3-C2	7.50	1.48	1.40
2	B	500	PLP	C3-C2	5.82	1.46	1.40
2	B	500	PLP	C3-C4	4.78	1.50	1.40
2	D	500	PLP	C3-C4	4.58	1.49	1.40
2	C	500	PLP	C3-C4	3.99	1.48	1.40
2	A	500	PLP	C4A-C4	2.73	1.57	1.51
2	A	500	PLP	C3-C4	2.52	1.45	1.40
2	D	500	PLP	C6-C5	2.37	1.42	1.37
2	C	500	PLP	P-O3P	-2.28	1.46	1.54
2	C	500	PLP	C4A-C4	2.17	1.56	1.51

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	PLP	C4A-C4-C5	6.59	127.72	120.94
2	C	500	PLP	C4A-C4-C5	5.65	126.76	120.94
2	C	500	PLP	C3-C4-C5	-5.60	112.69	118.74
2	C	500	PLP	C6-C5-C4	5.59	122.56	118.16
2	A	500	PLP	C3-C4-C5	-5.54	112.76	118.74
2	B	500	PLP	C4A-C4-C5	4.94	126.02	120.94
2	B	500	PLP	C6-C5-C4	4.38	121.61	118.16
2	D	500	PLP	C4A-C4-C5	4.29	125.36	120.94
2	B	500	PLP	C3-C4-C5	-4.26	114.14	118.74
2	A	500	PLP	C6-C5-C4	3.95	121.27	118.16
2	D	500	PLP	C3-C4-C5	-3.40	115.07	118.74
2	D	500	PLP	O2P-P-O4P	-3.37	97.78	106.73
2	D	500	PLP	C6-C5-C4	3.31	120.76	118.16
2	B	500	PLP	C6-N1-C2	3.22	125.14	119.17
2	C	500	PLP	C5A-C5-C6	-2.98	114.47	119.37
2	A	500	PLP	O3-C3-C2	2.93	123.88	117.49
2	A	500	PLP	O3P-P-O4P	-2.75	99.41	106.73
2	D	500	PLP	C6-N1-C2	2.68	124.14	119.17
2	D	500	PLP	O3-C3-C2	2.61	123.17	117.49
2	A	500	PLP	O3P-P-O1P	2.41	120.14	110.68
2	D	500	PLP	O2P-P-O1P	2.40	120.07	110.68
2	A	500	PLP	O3P-P-O2P	2.34	116.58	107.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	500	PLP	C5-C6-N1	-2.14	120.25	123.82
2	B	500	PLP	O3P-P-O2P	2.04	115.42	107.64

There are no chirality outliers.

All (14) torsion outliers are listed below:

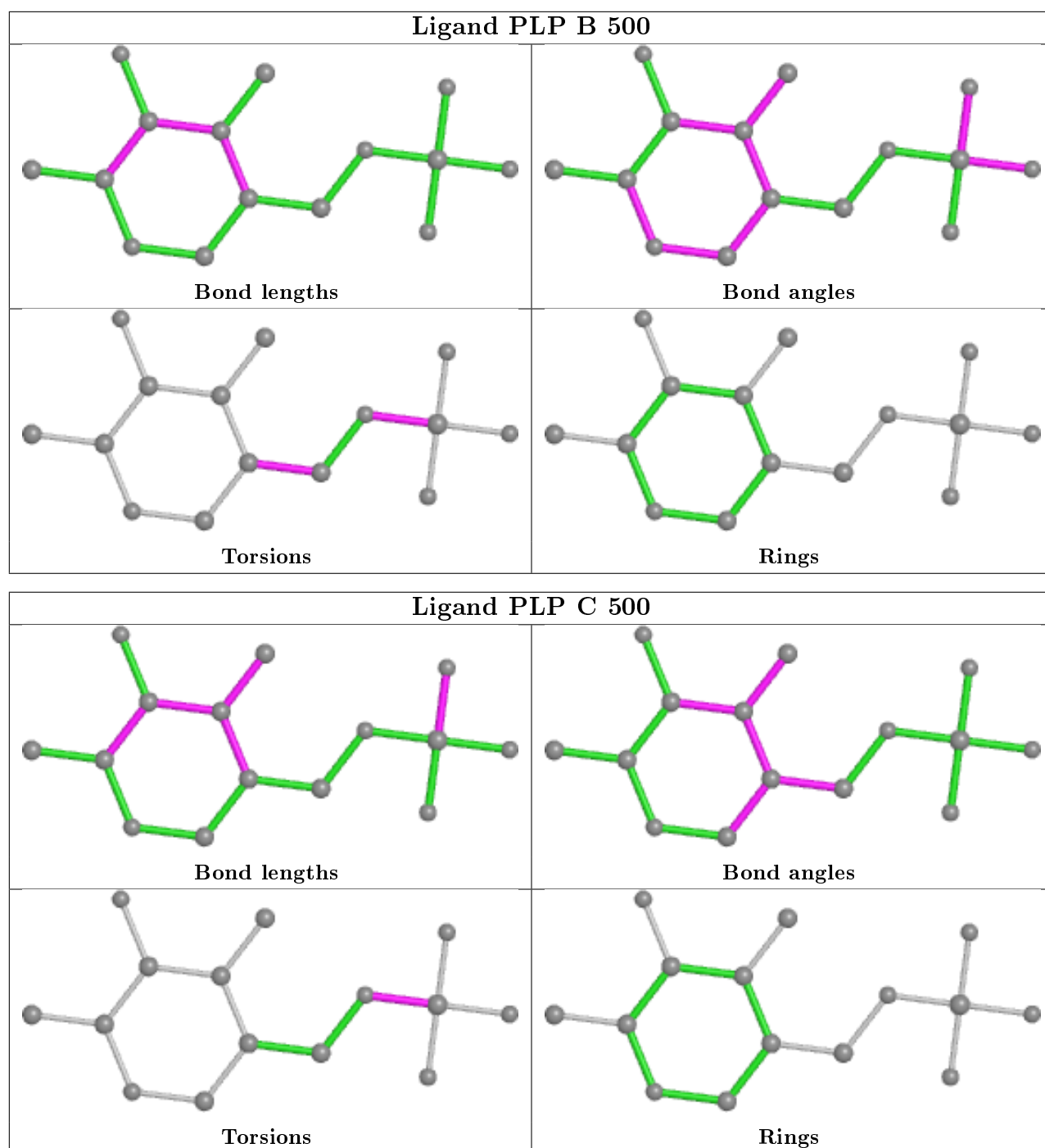
Mol	Chain	Res	Type	Atoms
2	B	500	PLP	C4-C5-C5A-O4P
2	B	500	PLP	C6-C5-C5A-O4P
2	B	500	PLP	C5A-O4P-P-O2P
2	B	500	PLP	C5A-O4P-P-O3P
2	C	500	PLP	C5A-O4P-P-O2P
2	C	500	PLP	C5A-O4P-P-O3P
2	A	500	PLP	C4-C5-C5A-O4P
2	A	500	PLP	C6-C5-C5A-O4P
2	A	500	PLP	C5A-O4P-P-O2P
2	A	500	PLP	C5A-O4P-P-O3P
2	D	500	PLP	C5A-O4P-P-O2P
2	D	500	PLP	C5A-O4P-P-O3P
2	A	500	PLP	C5A-O4P-P-O1P
2	B	500	PLP	C5A-O4P-P-O1P

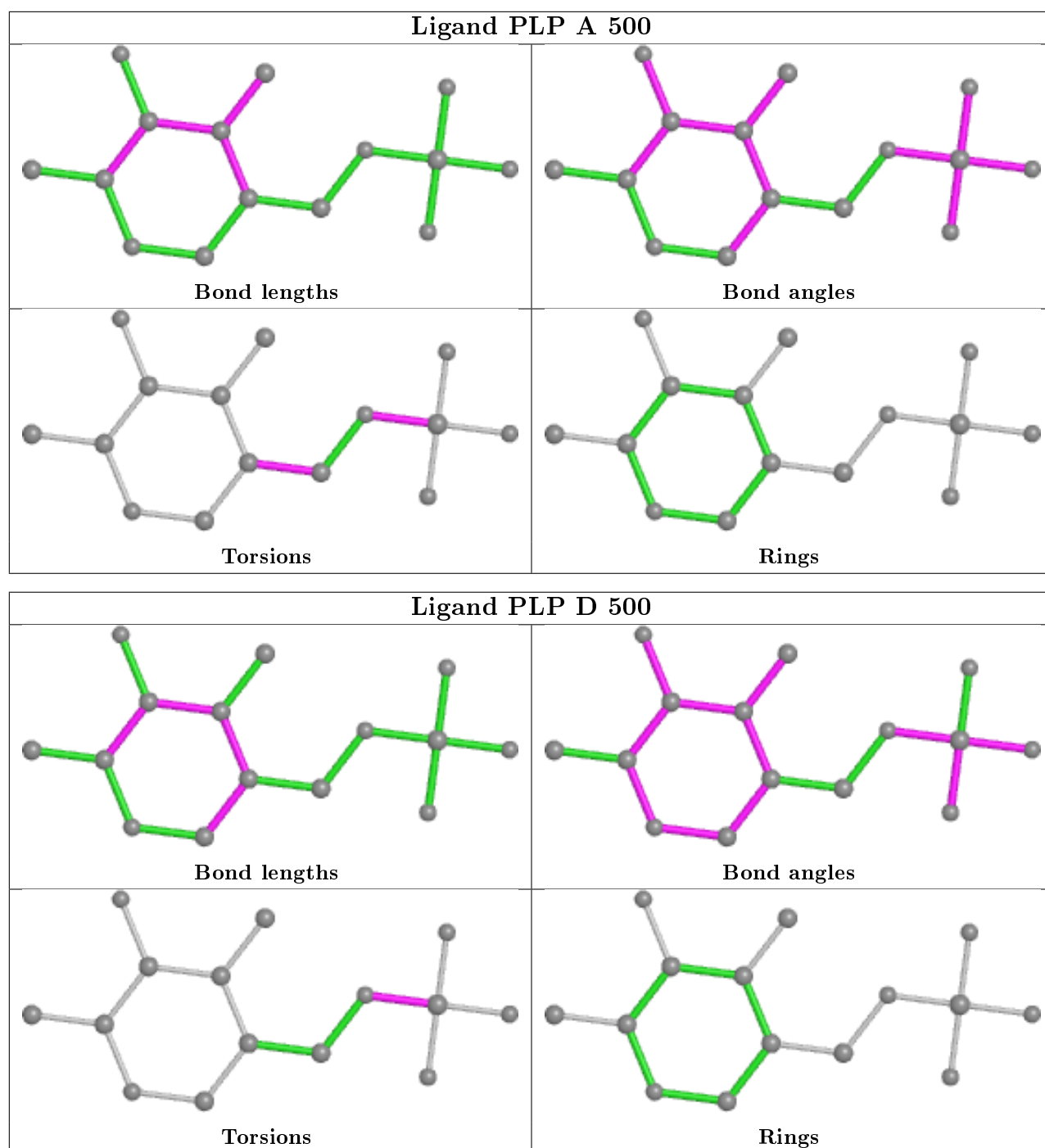
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	500	PLP	1	0
2	A	500	PLP	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 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1
1	D	1
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	404:THR	C	405:LEU	N	3.28
1	C	402:VAL	C	403:LEU	N	3.14
1	A	402:VAL	C	403:LEU	N	3.09

## 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	401/427 (93%)	0.11	6 (1%) 73 72	11, 22, 42, 67	0
1	B	392/427 (91%)	0.08	6 (1%) 73 72	11, 22, 40, 59	0
1	C	402/427 (94%)	0.00	7 (1%) 70 68	9, 22, 41, 71	0
1	D	394/427 (92%)	0.07	10 (2%) 57 55	10, 21, 41, 67	0
All	All	1589/1708 (93%)	0.06	29 (1%) 68 66	9, 22, 42, 71	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	246	SER	4.7
1	D	160	LYS	3.9
1	A	4	TYR	3.8
1	A	150	ASP	3.7
1	B	404	THR	3.5
1	B	246	SER	3.4
1	C	4	TYR	3.3
1	B	153	THR	3.2
1	D	245	GLY	3.2
1	B	403	LEU	3.1
1	C	5	ASN	2.9
1	D	404	THR	2.9
1	D	153	THR	2.8
1	B	141	LEU	2.8
1	D	216	VAL	2.7
1	A	142	PHE	2.7
1	D	403	LEU	2.7
1	B	216	VAL	2.6
1	D	112	TYR	2.4
1	C	144	VAL	2.4
1	C	329	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	150	ASP	2.2
1	A	160	LYS	2.1
1	C	405	LEU	2.1
1	A	215	PRO	2.1
1	D	121	GLU	2.0
1	A	151	PHE	2.0
1	D	142	PHE	2.0
1	C	163	ASN	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](#)

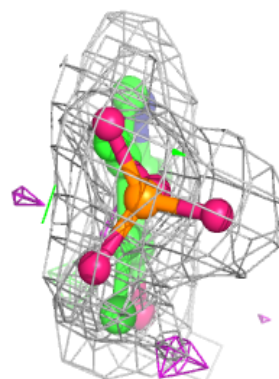
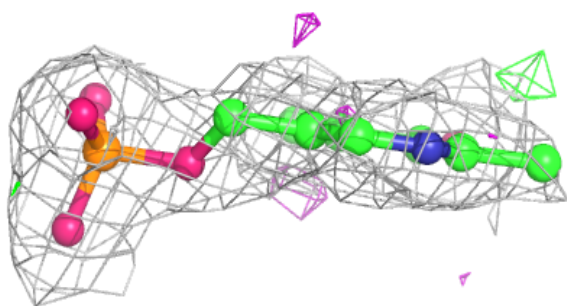
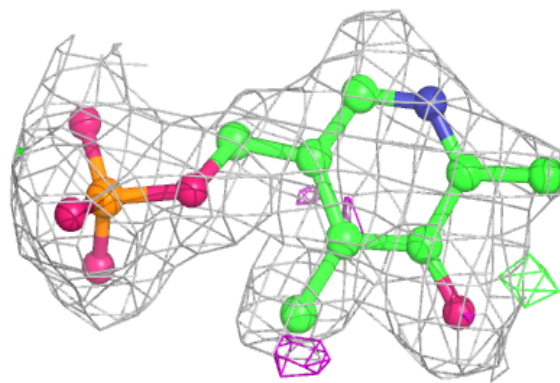
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	PLP	B	500	15/16	0.95	0.14	15,23,25,26	0
2	PLP	D	500	15/16	0.95	0.16	13,20,24,24	0
2	PLP	A	500	15/16	0.96	0.12	14,16,17,23	0
2	PLP	C	500	15/16	0.96	0.12	16,20,29,31	0

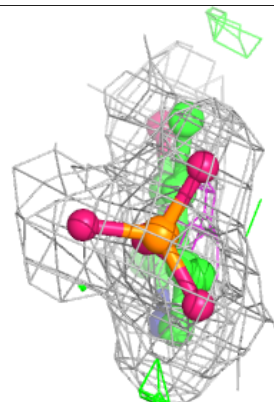
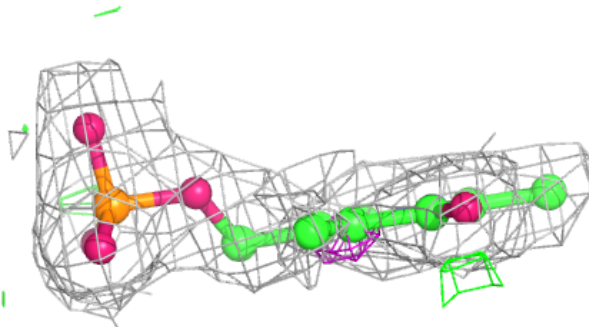
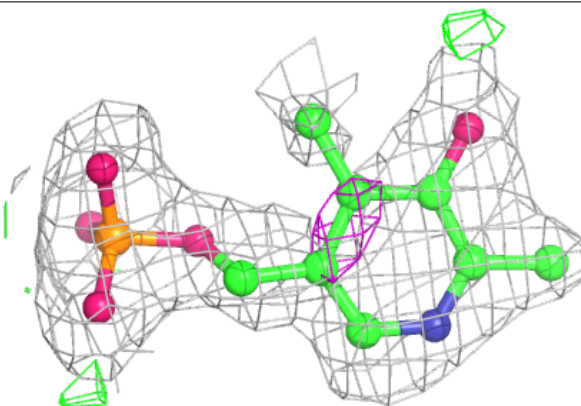
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around PLP B 500:**

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

**Electron density around PLP D 500:**

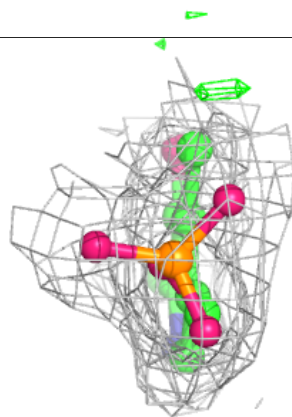
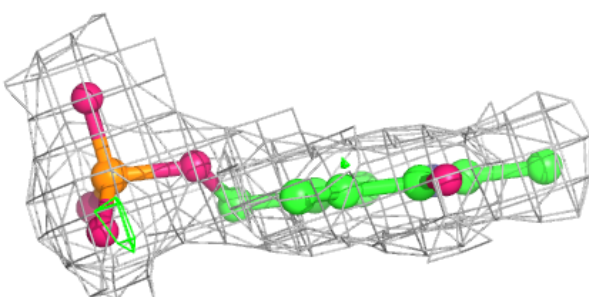
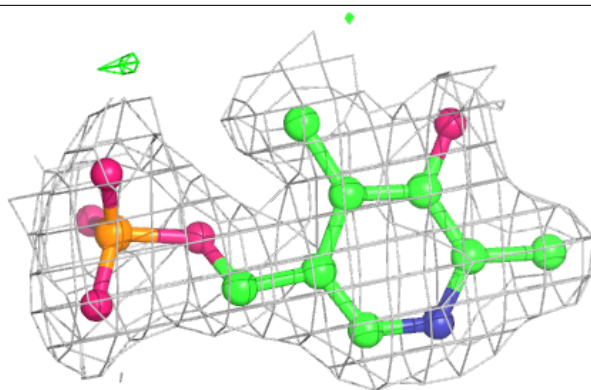
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



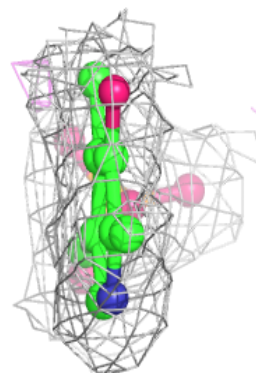
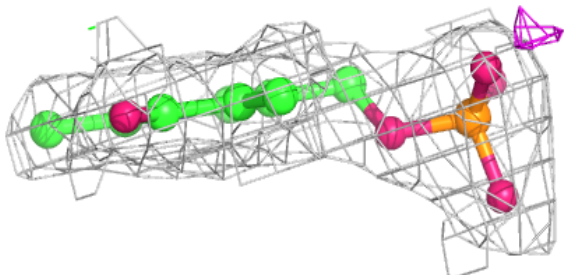
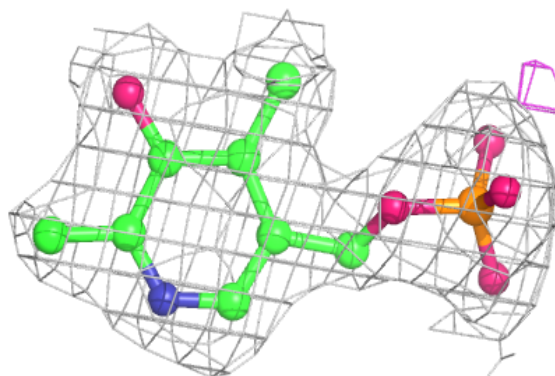


**Electron density around PLP A 500:**

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

**Electron density around PLP C 500:**

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



## 6.5 Other polymers

There are no such residues in this entry.