



# Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 03:41 am BST

PDB ID : 2BMB  
Title : X-ray structure of the bifunctional 6-hydroxymethyl-7,8- dihydroxypterin pyrophosphokinase dihydropteroate synthase from *Saccharomyces cerevisiae*  
Authors : Lawrence, M.C.; Iliades, P.; Fernley, R.T.; Berglez, J.; Pilling, P.A.; Macreadie, I.G.  
Deposited on : 2005-03-11  
Resolution : 2.30 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

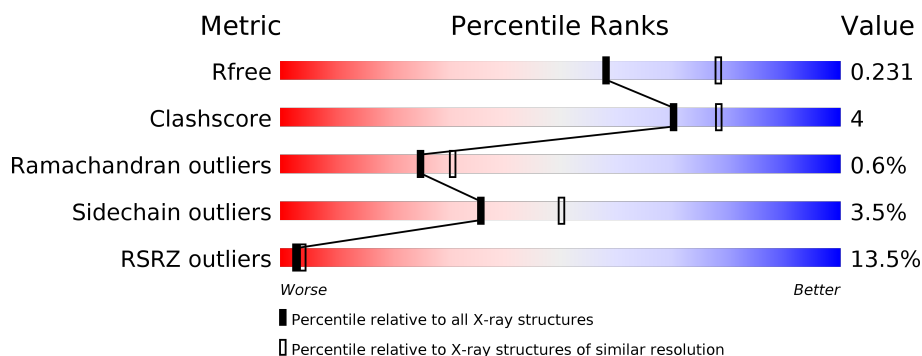
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	545	

## 2 Entry composition [i](#)

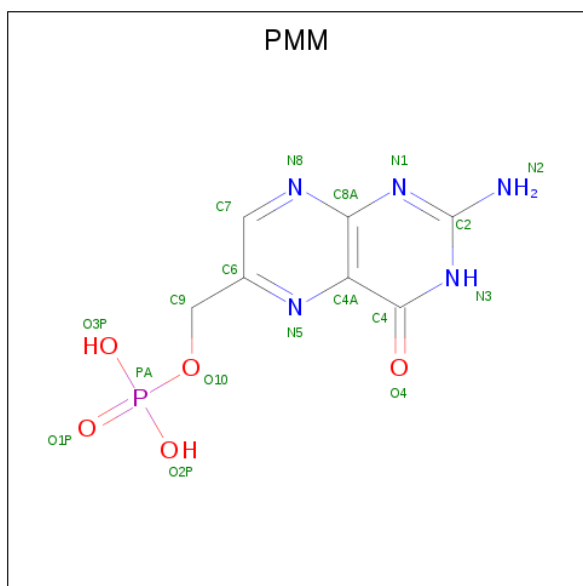
There are 3 unique types of molecules in this entry. The entry contains 4282 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 FOLIC ACID SYNTHESIS PROTEIN FOL1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	513	Total	C	N	O	S	0	8	0
			4122	2617	706	778	21			

- Molecule 2 is PTERIN-6-YL-METHYL-MONOPHOSPHATE (three-letter code: PMM) (formula:  $C_7H_8N_5O_5P$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			18	7	5	5	1		
2	A	1	Total	C	N	O	P	0	0
			18	7	5	5	1		

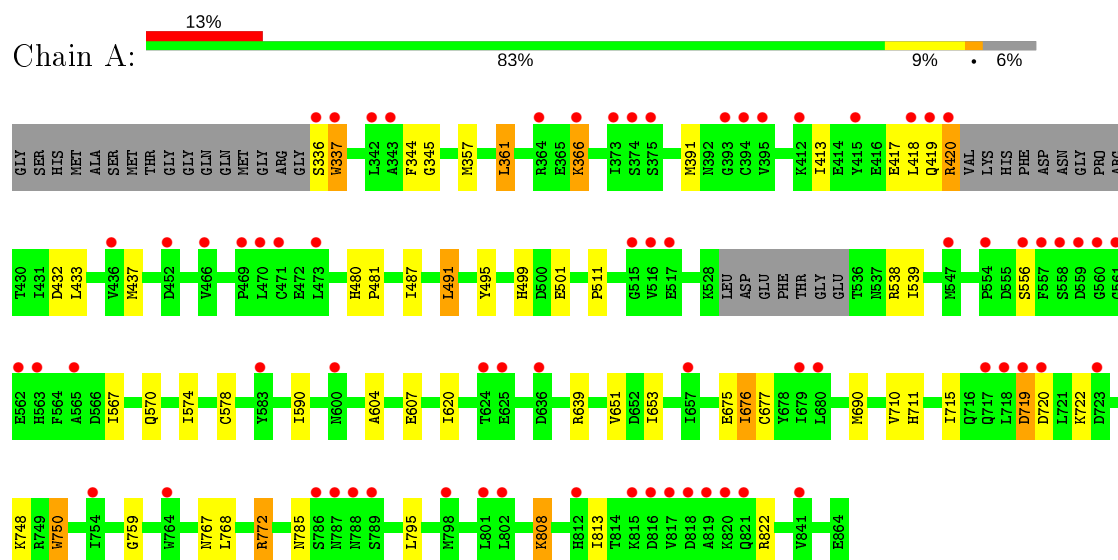
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	124	Total	O	0	0
			124	124		

### 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: FOLIC ACID SYNTHESIS PROTEIN FOL1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	92.57Å 92.57Å 192.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.30 29.59 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.1 (40.00-2.30) 99.2 (29.59-2.30)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.14 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.178 , 0.216 0.210 , 0.231	Depositor DCC
$R_{free}$ test set	1877 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	46.7	Xtriage
Anisotropy	0.046	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 44.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4282	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.51% 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: PMM

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	0.46	0/4241	0.57	2/5733 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	772	ARG	NE-CZ-NH1	5.34	122.97	120.30
1	A	772	ARG	NE-CZ-NH2	-5.24	117.68	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4122	0	4149	30	0
2	A	36	0	12	0	0
3	A	124	0	0	5	0
All	All	4282	0	4161	30	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.

All (30) 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:690:MET:CE	3:A:2075:HOH:O	2.22	0.86
1:A:604:ALA:O	1:A:639:ARG:NH2	2.14	0.81
1:A:690:MET:HE2	3:A:2075:HOH:O	1.81	0.80
1:A:808:LYS:HE2	1:A:822:ARG:HH12	1.52	0.72
1:A:366:LYS:HD2	1:A:366:LYS:H	1.58	0.67
1:A:759:GLY:H	1:A:767:ASN:HD21	1.46	0.62
1:A:690:MET:HE1	3:A:2075:HOH:O	1.92	0.59
1:A:715:ILE:HD12	1:A:722:LYS:HG3	1.87	0.55
1:A:578:CYS:SG	1:A:590:ILE:HD11	2.48	0.54
1:A:511:PRO:HG3	1:A:676:ILE:HD12	1.90	0.53
1:A:748:LYS:HD3	1:A:750:TRP:CZ2	2.45	0.52
1:A:538:ARG:HB3	3:A:2050:HOH:O	2.10	0.51
1:A:437:MET:HE3	1:A:487:ILE:HD11	1.92	0.50
1:A:419:GLN:HB2	1:A:420:ARG:HH21	1.77	0.50
1:A:336:SER:OG	1:A:337:TRP:N	2.45	0.50
1:A:491:LEU:HD22	1:A:495:TYR:CE2	2.46	0.50
1:A:567:ILE:HA	1:A:570:GLN:HE21	1.80	0.46
1:A:344:PHE:HA	1:A:432:ASP:O	2.16	0.45
1:A:357[B]:MET:SD	1:A:417:GLU:HG2	2.57	0.45
1:A:710:VAL:HG12	1:A:711[B]:HIS:CD2	2.52	0.44
1:A:574:ILE:HD13	1:A:620:ILE:HD11	2.01	0.43
1:A:361:LEU:HB3	1:A:413:ILE:HG12	2.01	0.43
1:A:759:GLY:H	1:A:767:ASN:ND2	2.16	0.42
1:A:499:HIS:HB3	1:A:501:GLU:OE1	2.21	0.41
1:A:768:LEU:HD11	1:A:813:ILE:HD11	2.03	0.41
1:A:772:ARG:NH2	3:A:2102:HOH:O	2.43	0.41
1:A:653:ILE:HG12	1:A:677:CYS:HB3	2.03	0.41
1:A:345:GLY:HA2	1:A:391:MET:O	2.21	0.40
1:A:480:HIS:HA	1:A:481:PRO:HD3	1.95	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	515/545 (94%)	503 (98%)	9 (2%)	3 (1%)	25	31

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	556	SER
1	A	337	TRP
1	A	719	ASP

### 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	470/486 (97%)	454 (97%)	16 (3%)	37	51

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

Mol	Chain	Res	Type
1	A	361	LEU
1	A	366	LYS
1	A	418	LEU
1	A	420	ARG
1	A	433	LEU
1	A	491	LEU
1	A	539	ILE
1	A	651	VAL
1	A	675	GLU
1	A	676	ILE
1	A	719	ASP
1	A	720	ASP
1	A	750	TRP
1	A	785	ASN
1	A	795	LEU
1	A	808	LYS



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

Mol	Chain	Res	Type
1	A	570	GLN
1	A	767	ASN
1	A	785	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](#)

2 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	PMM	A	1865	-	19,19,19	3.58	6 (31%)	23,28,28	3.45	11 (47%)
2	PMM	A	1866	-	19,19,19	3.74	6 (31%)	23,28,28	2.91	11 (47%)

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	PMM	A	1865	-	-	4/6/6/6	0/2/2/2
2	PMM	A	1866	-	-	2/6/6/6	0/2/2/2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1866	PMM	C7-N8	9.53	1.47	1.31
2	A	1865	PMM	C4A-N5	8.83	1.45	1.33
2	A	1865	PMM	C7-N8	8.69	1.45	1.31
2	A	1866	PMM	C4A-N5	8.35	1.45	1.33
2	A	1866	PMM	C7-C6	8.06	1.53	1.39
2	A	1865	PMM	C7-C6	7.03	1.51	1.39
2	A	1865	PMM	C4-C4A	4.08	1.48	1.41
2	A	1866	PMM	C4A-C8A	3.69	1.47	1.40
2	A	1865	PMM	C4A-C8A	3.47	1.47	1.40
2	A	1866	PMM	C4-C4A	3.31	1.47	1.41
2	A	1866	PMM	C6-N5	-2.88	1.26	1.32
2	A	1865	PMM	C6-N5	-2.24	1.28	1.32

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1865	PMM	C6-C7-N8	-7.27	116.00	123.13
2	A	1866	PMM	N8-C8A-N1	6.57	123.32	115.82
2	A	1866	PMM	C6-C7-N8	-5.81	117.44	123.13
2	A	1865	PMM	C7-N8-C8A	5.76	122.48	116.69
2	A	1865	PMM	C2-N1-C8A	5.33	121.45	115.36
2	A	1865	PMM	N8-C8A-N1	5.28	121.85	115.82
2	A	1865	PMM	C4-C4A-N5	5.17	124.51	118.60
2	A	1865	PMM	C4-C4A-C8A	-5.00	116.64	119.95
2	A	1866	PMM	C2-N1-C8A	4.75	120.79	115.36
2	A	1866	PMM	C4A-C4-N3	-4.13	117.78	123.43
2	A	1866	PMM	C4-N3-C2	4.11	122.46	115.93
2	A	1866	PMM	C7-N8-C8A	4.09	120.80	116.69
2	A	1865	PMM	C4-N3-C2	4.06	122.37	115.93
2	A	1865	PMM	N1-C2-N3	-3.96	121.94	127.22
2	A	1865	PMM	C4A-C4-N3	-3.65	118.45	123.43
2	A	1866	PMM	N1-C2-N3	-3.23	122.91	127.22
2	A	1865	PMM	C6-N5-C4A	3.19	122.22	118.45
2	A	1866	PMM	C4-C4A-C8A	-3.13	117.88	119.95
2	A	1865	PMM	C8A-C4A-N5	-3.07	118.85	122.33
2	A	1866	PMM	C6-N5-C4A	2.45	121.34	118.45
2	A	1866	PMM	C4A-C8A-N1	-2.16	118.18	121.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1866	PMM	C4-C4A-N5	2.11	121.01	118.60

There are no chirality outliers.

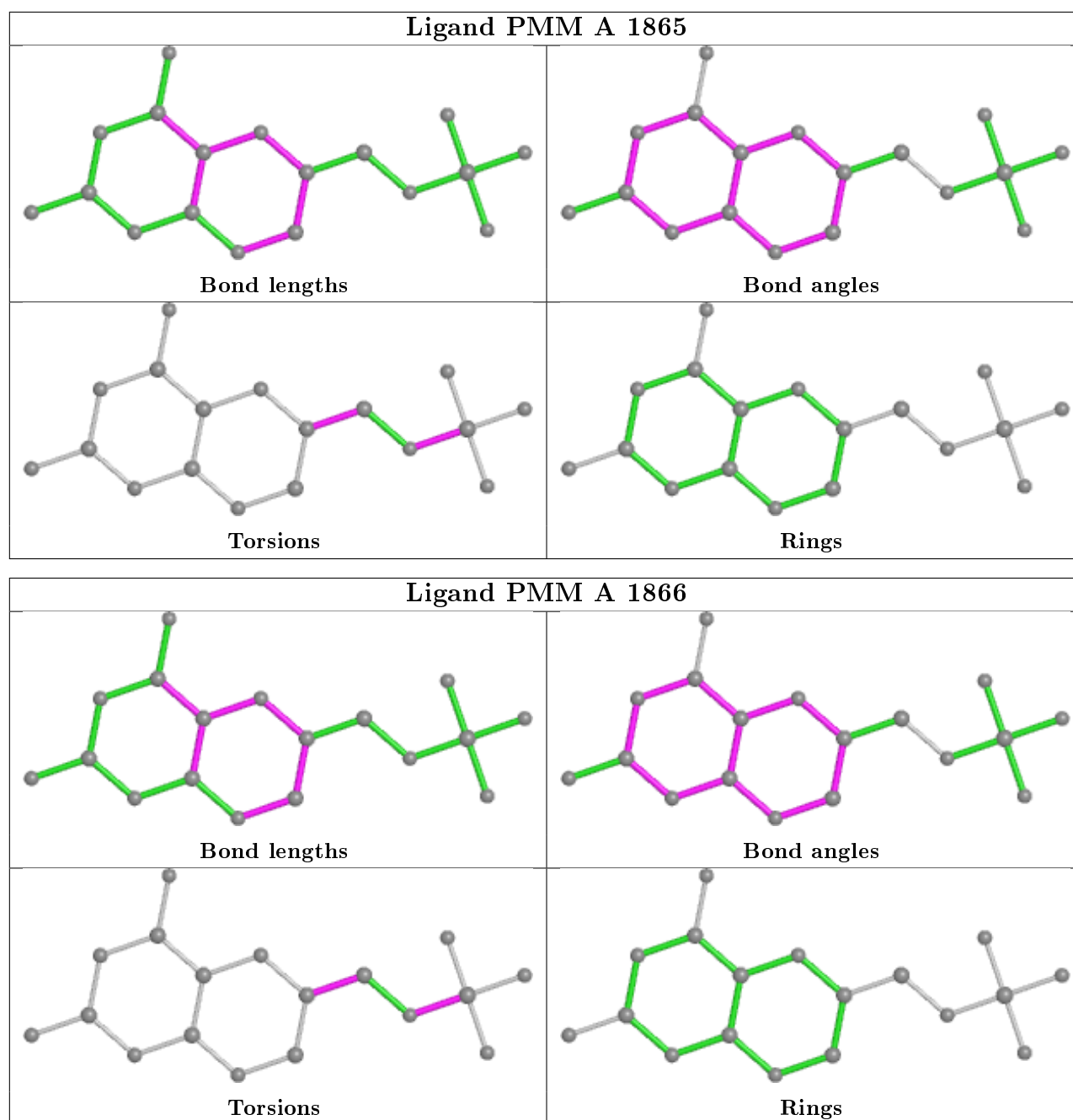
All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1865	PMM	C9-O10-PA-O3P
2	A	1865	PMM	C9-O10-PA-O2P
2	A	1865	PMM	N5-C6-C9-O10
2	A	1865	PMM	C7-C6-C9-O10
2	A	1866	PMM	C9-O10-PA-O1P
2	A	1866	PMM	C7-C6-C9-O10

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	513/545 (94%)	0.58	69 (13%) 3 4	14, 28, 60, 91	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	788	ASN	7.6
1	A	817	VAL	6.8
1	A	557	PHE	6.6
1	A	558	SER	5.6
1	A	515	GLY	5.4
1	A	818	ASP	5.1
1	A	560	GLY	5.0
1	A	394[A]	CYS	4.9
1	A	419	GLN	4.9
1	A	415	TYR	4.5
1	A	821	GLN	4.4
1	A	336	SER	4.4
1	A	787	ASN	4.3
1	A	561	GLY	4.2
1	A	718	LEU	4.1
1	A	819	ALA	4.0
1	A	719	ASP	4.0
1	A	717	GLN	4.0
1	A	720	ASP	3.8
1	A	559	ASP	3.7
1	A	816	ASP	3.7
1	A	366	LYS	3.7
1	A	516	VAL	3.6
1	A	679	ILE	3.5
1	A	562	GLU	3.5
1	A	420	ARG	3.5
1	A	393	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	556	SER	3.4
1	A	789	SER	3.3
1	A	469	PRO	3.2
1	A	820	LYS	3.1
1	A	342	LEU	2.9
1	A	418	LEU	2.9
1	A	625	GLU	2.8
1	A	517	GLU	2.8
1	A	815	LYS	2.8
1	A	802	LEU	2.8
1	A	436	VAL	2.8
1	A	547	MET	2.8
1	A	364	ARG	2.8
1	A	723	ASP	2.7
1	A	395	VAL	2.6
1	A	801	LEU	2.6
1	A	343	ALA	2.6
1	A	812	HIS	2.6
1	A	754	ILE	2.6
1	A	583	TYR	2.6
1	A	786	SER	2.5
1	A	764	TRP	2.5
1	A	375	SER	2.5
1	A	337	TRP	2.5
1	A	624	THR	2.4
1	A	412	LYS	2.4
1	A	473	LEU	2.3
1	A	554	PRO	2.3
1	A	680	LEU	2.3
1	A	841	VAL	2.3
1	A	470	LEU	2.3
1	A	471	CYS	2.3
1	A	452	ASP	2.2
1	A	636	ASP	2.2
1	A	374	SER	2.2
1	A	798	MET	2.1
1	A	373	ILE	2.1
1	A	600	ASN	2.1
1	A	657	ILE	2.1
1	A	563	HIS	2.1
1	A	565	ALA	2.0
1	A	466	VAL	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](#)

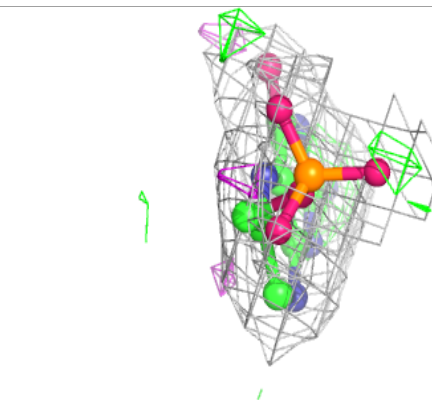
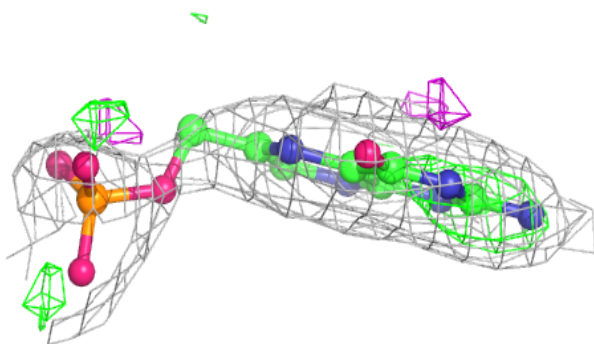
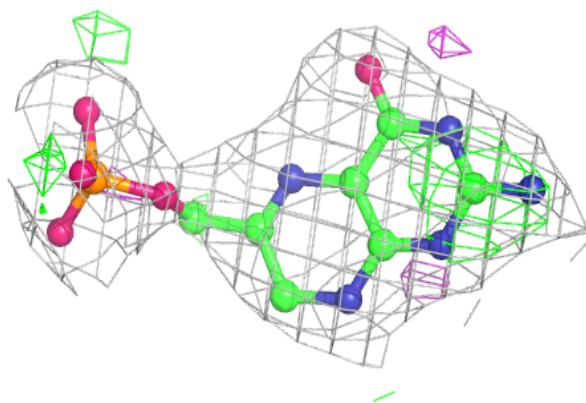
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
2	PMM	A	1866	18/18	0.85	0.28	43,48,88,89	0
2	PMM	A	1865	18/18	0.91	0.32	46,49,81,81	0

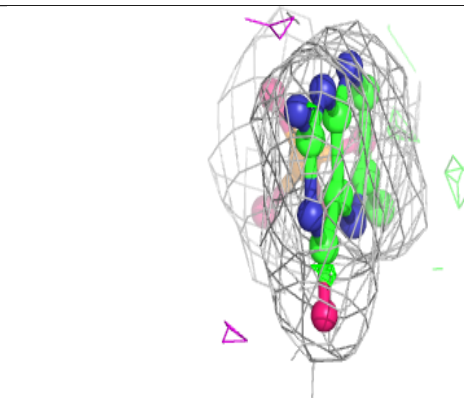
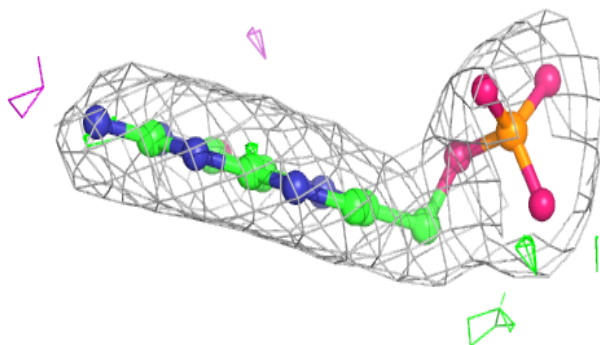
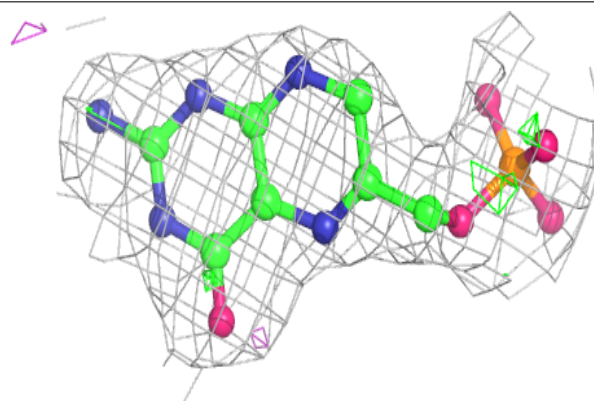
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around PMM A 1866:**

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

**Electron density around PMM A 1865:**

$2mF_o-DF_c$  (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.