



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 24, 2023 – 01:48 PM EST

PDB ID : 3IF2  
Title : Crystal structure of Putative amino-acid aminotransferase (YP\_265399.1) from *Psychrobacter arcticum* 273-4 at 2.50 Å resolution  
Authors : Joint Center for Structural Genomics (JCSG)  
Deposited on : 2009-07-23  
Resolution : 2.50 Å (reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

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 : 2.31.2  
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) : 2.31.2

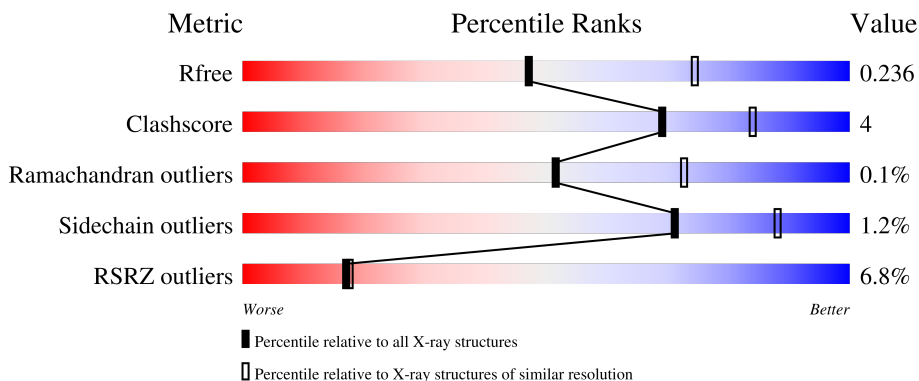
# 1 Overall quality at a glance

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	444	 6% 90% 8% .
1	B	444	 7% 88% 10% .

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7113 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.

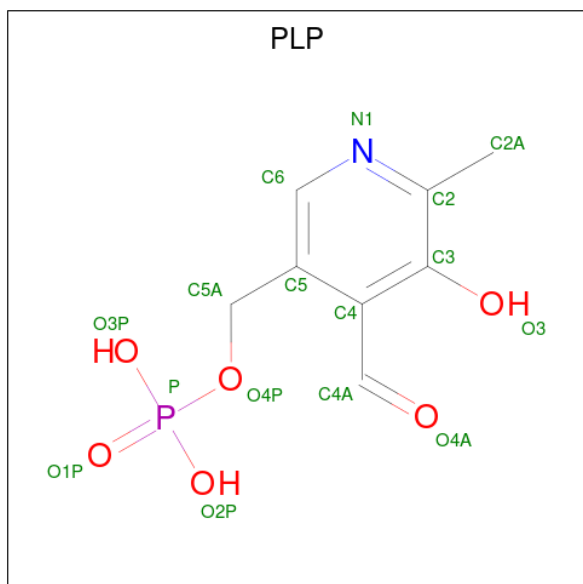
- Molecule 1 is a protein called Aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	S				Se
1	A	437	Total 3436	C 2205	N 566	O 651	S 4	Se 10	0	9	0
1	B	437	Total 3426	C 2196	N 561	O 655	S 4	Se 10	0	7	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q4FPU3
B	0	GLY	-	expression tag	UNP Q4FPU3

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C<sub>8</sub>H<sub>10</sub>NO<sub>6</sub>P).



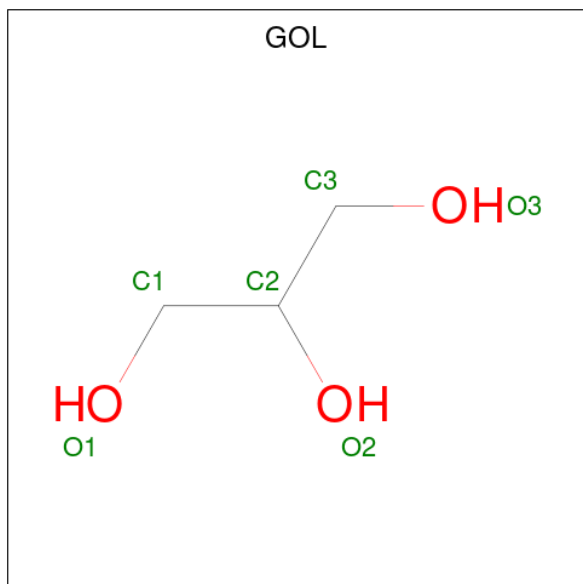
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total 16	C 8	N 1	O 6	P 1	0	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	B	1	16	8	1	6	1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	6	3	3	0	0
3	B	1	6	3	3	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 4 2 2	0	0

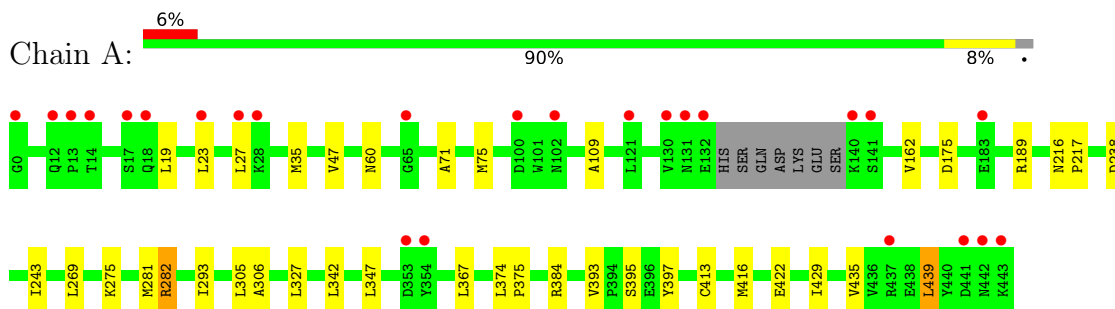
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	105	Total O 105 105	0	0
5	B	98	Total O 98 98	0	0

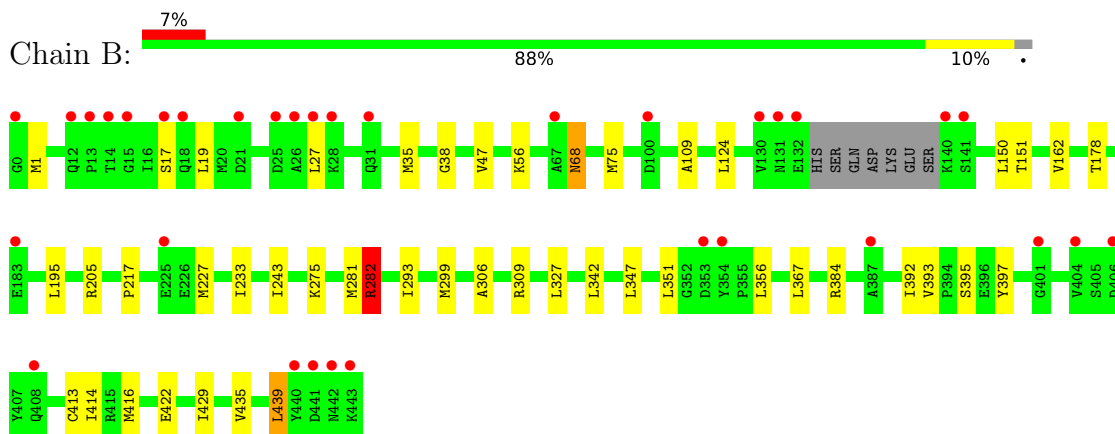
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Aminotransferase



- Molecule 1: Aminotransferase



## 4 Data and refinement statistics i

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	152.81Å 152.81Å 100.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.98 – 2.50 29.97 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.8 (29.98-2.50) 98.9 (29.97-2.50)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.64 (at 2.51Å)	Xtrriage
Refinement program	REFMAC 5.5.0053, PHENIX	Depositor
R, $R_{free}$	0.178 , 0.221 0.190 , 0.236	Depositor DCC
$R_{free}$ test set	1986 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.6	Xtrriage
Anisotropy	0.081	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 43.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.023 for -k,-h,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7113	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% 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: ACT, GOL, 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	0.71	0/3532	0.87	4/4781 (0.1%)
1	B	0.73	0/3513	0.89	6/4756 (0.1%)
All	All	0.72	0/7045	0.88	10/9537 (0.1%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	282	ARG	NE-CZ-NH2	-11.28	114.66	120.30
1	A	282	ARG	NE-CZ-NH1	10.03	125.32	120.30
1	B	282	ARG	NE-CZ-NH1	8.77	124.69	120.30
1	B	282	ARG	NE-CZ-NH2	-8.54	116.03	120.30
1	B	205	ARG	NE-CZ-NH1	6.03	123.32	120.30
1	B	309	ARG	NE-CZ-NH2	-5.49	117.55	120.30
1	B	384	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	A	216	ASN	N-CA-C	-5.16	97.07	111.00
1	B	68	ASN	N-CA-C	5.12	124.84	111.00
1	A	384	ARG	NE-CZ-NH2	-5.09	117.76	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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	3436	0	3376	29	0
1	B	3426	0	3349	32	0
2	A	16	0	8	2	0
2	B	16	0	8	2	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0
4	B	4	0	3	0	0
5	A	105	0	0	0	0
5	B	98	0	0	0	0
All	All	7113	0	6760	50	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 (50) 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:162:VAL:HG11	1:B:162:VAL:HG11	1.20	1.11
1:B:27:LEU:HD11	1:B:35:MSE:HE2	1.67	0.75
1:A:109:ALA:HB2	1:A:293:ILE:HG23	1.75	0.69
1:A:281:MSE:HE2	1:B:75:MSE:CG	2.23	0.68
1:A:75:MSE:CG	1:B:281:MSE:HE2	2.24	0.67
1:A:75:MSE:HG2	1:B:281:MSE:HE2	1.79	0.64
1:A:19:LEU:HD21	1:A:393:VAL:HG13	1.85	0.58
1:A:60:ASN:OD1	1:B:56:LYS:NZ	2.37	0.58
1:A:162:VAL:CG1	1:B:162:VAL:HG11	2.14	0.57
1:B:342:LEU:HD21	1:B:422:GLU:HG3	1.86	0.57
1:B:195:LEU:HD22	1:B:233:ILE:HD13	1.87	0.56
1:A:275:LYS:HZ1	2:A:500:PLP:C4A	2.20	0.55
1:A:281:MSE:HE2	1:B:75:MSE:HG2	1.88	0.55
1:B:275:LYS:HZ1	2:B:500:PLP:C4A	2.22	0.53
1:A:282:ARG:NH2	2:A:500:PLP:O3P	2.35	0.53
1:A:342:LEU:HD21	1:A:422:GLU:HG3	1.91	0.52
1:B:19:LEU:HD21	1:B:393:VAL:HG13	1.91	0.52
1:B:351:LEU:HD12	1:B:356:LEU:HD22	1.91	0.51
1:A:19:LEU:HD22	1:A:397:TYR:CD2	2.45	0.51
1:B:109:ALA:HB2	1:B:293:ILE:HG23	1.91	0.50
1:B:275:LYS:NZ	2:B:500:PLP:C4A	2.75	0.50
1:A:27:LEU:HD11	1:A:35:MSE:HE2	1.93	0.49
1:A:162:VAL:HG11	1:B:162:VAL:CG1	2.14	0.49
1:B:47:VAL:HA	1:B:327:LEU:HD11	1.94	0.48
1:A:435:VAL:O	1:A:439:LEU:HD13	2.14	0.48

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:306:ALA:O	1:B:282:ARG:HD3	2.15	0.47
1:B:367:LEU:HD12	1:B:416:MSE:CE	2.45	0.47
1:A:281:MSE:HE2	1:B:75:MSE:HG3	1.96	0.46
1:B:124:LEU:HB2	1:B:299:MSE:HE1	1.98	0.46
1:A:175[B]:ASP:OD2	1:A:189[B]:ARG:HD2	2.17	0.45
1:B:19:LEU:HD22	1:B:397:TYR:CD2	2.52	0.45
1:B:392:ILE:HD13	1:B:414:ILE:HB	1.98	0.44
1:A:367:LEU:HB2	1:A:416:MSE:HE2	1.99	0.44
1:B:47:VAL:HG22	1:B:327:LEU:HD11	2.00	0.44
1:A:71:ALA:O	1:A:75:MSE:HE3	2.18	0.44
1:A:395:SER:HB3	1:A:413:CYS:HB2	2.01	0.42
1:A:282:ARG:HD3	1:B:306:ALA:O	2.18	0.42
1:B:347:LEU:HD23	1:B:429:ILE:HG23	2.02	0.42
1:B:367:LEU:HB2	1:B:416:MSE:HE2	2.01	0.42
1:A:47:VAL:HA	1:A:327:LEU:HD11	2.02	0.42
1:A:243:ILE:HB	1:A:269:LEU:HD23	2.02	0.41
1:A:347:LEU:HD23	1:A:429:ILE:HG23	2.01	0.41
1:A:374:LEU:HD12	1:A:375:PRO:HD2	2.02	0.41
1:B:227:MSE:HE2	1:B:243:ILE:HD13	2.03	0.41
1:B:395:SER:HB3	1:B:413:CYS:HB2	2.02	0.41
1:B:150:LEU:HD23	1:B:151:THR:N	2.36	0.41
1:B:35:MSE:HE3	1:B:38:GLY:HA3	2.03	0.41
1:B:435:VAL:O	1:B:439:LEU:HD13	2.21	0.41
1:A:305:LEU:HD12	1:A:305:LEU:HA	1.98	0.40
1:A:23:LEU:O	1:A:27:LEU:HD13	2.21	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	442/444 (100%)	426 (96%)	16 (4%)	0	<b>100</b> <b>100</b>

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	440/444 (99%)	425 (97%)	14 (3%)	1 (0%)	47	68
All	All	882/888 (99%)	851 (96%)	30 (3%)	1 (0%)	51	73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	68	ASN

### 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	369/362 (102%)	366 (99%)	3 (1%)	81	93
1	B	368/362 (102%)	362 (98%)	6 (2%)	62	84
All	All	737/724 (102%)	728 (99%)	9 (1%)	71	88

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	217	PRO
1	A	238	ASP
1	A	439	LEU
1	B	1	MSE
1	B	17	SER
1	B	178	THR
1	B	217	PRO
1	B	282	ARG
1	B	439	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

5 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
3	GOL	A	444	-	5,5,5	0.51	0	5,5,5	0.74	0
4	ACT	B	444	-	3,3,3	0.75	0	3,3,3	1.95	2 (66%)
2	PLP	A	500	-	16,16,16	1.37	2 (12%)	20,23,23	1.67	3 (15%)
3	GOL	B	445	-	5,5,5	0.31	0	5,5,5	0.47	0
2	PLP	B	500	-	16,16,16	1.36	2 (12%)	20,23,23	1.26	2 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	B	445	-	-	2/4/4/4	-
3	GOL	A	444	-	-	1/4/4/4	-
2	PLP	B	500	-	-	5/8/8/8	0/1/1/1
2	PLP	A	500	-	-	6/8/8/8	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	PLP	C4-C4A	2.88	1.53	1.46
2	A	500	PLP	C4-C4A	2.80	1.52	1.46
2	B	500	PLP	C2-N1	2.44	1.38	1.33
2	A	500	PLP	C2-N1	2.36	1.38	1.33

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	PLP	O4P-P-O1P	4.85	120.09	106.47
2	B	500	PLP	O4P-P-O1P	2.60	113.77	106.47
4	B	444	ACT	OXT-C-O	-2.57	112.60	122.05
2	A	500	PLP	O4P-C5A-C5	2.38	113.88	109.35
2	B	500	PLP	C2A-C2-C3	2.34	123.78	120.89
4	B	444	ACT	OXT-C-CH3	2.19	124.22	115.18
2	A	500	PLP	O2P-P-O4P	-2.09	101.18	106.73

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500	PLP	C3-C4-C4A-O4A
2	A	500	PLP	C5A-O4P-P-O1P
2	A	500	PLP	C5A-O4P-P-O2P
2	A	500	PLP	C5A-O4P-P-O3P
2	B	500	PLP	C5A-O4P-P-O1P
2	B	500	PLP	C5A-O4P-P-O2P
2	B	500	PLP	C5A-O4P-P-O3P
3	B	445	GOL	C1-C2-C3-O3
2	B	500	PLP	C3-C4-C4A-O4A
2	A	500	PLP	C5-C4-C4A-O4A
3	B	445	GOL	O2-C2-C3-O3
2	A	500	PLP	C4-C5-C5A-O4P
3	A	444	GOL	C1-C2-C3-O3
2	B	500	PLP	C5-C4-C4A-O4A

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	PLP	2	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	500	PLP	2	0

## 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	427/444 (96%)	0.22	25 (5%) 22 23	28, 37, 51, 66	0
1	B	427/444 (96%)	0.25	33 (7%) 13 13	28, 37, 52, 64	0
All	All	854/888 (96%)	0.24	58 (6%) 17 17	28, 37, 52, 66	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	132	GLU	4.7
1	B	13	PRO	4.4
1	A	12	GLN	4.1
1	A	132	GLU	3.8
1	B	353	ASP	3.8
1	A	27	LEU	3.7
1	A	131	ASN	3.7
1	B	18	GLN	3.7
1	A	141	SER	3.6
1	B	406	ASP	3.5
1	B	12	GLN	3.4
1	B	441	ASP	3.4
1	B	28	LYS	3.4
1	B	443	LYS	3.3
1	B	27	LEU	3.2
1	B	140	LYS	3.2
1	A	13	PRO	3.2
1	A	443	LYS	3.2
1	B	130	VAL	3.1
1	A	442	ASN	3.1
1	B	442	ASN	3.0
1	A	18	GLN	3.0
1	A	353	ASP	2.9
1	A	130	VAL	2.9

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	25	ASP	2.8
1	A	441	ASP	2.8
1	B	21	ASP	2.8
1	A	100	ASP	2.8
1	B	225[A]	GLU	2.7
1	B	131	ASN	2.7
1	A	140	LYS	2.7
1	B	17	SER	2.7
1	A	183	GLU	2.6
1	B	354	TYR	2.6
1	A	437	ARG	2.6
1	B	387	ALA	2.6
1	B	0	GLY	2.6
1	B	67	ALA	2.5
1	B	31	GLN	2.4
1	A	121	LEU	2.4
1	A	14	THR	2.4
1	A	0	GLY	2.4
1	B	404	VAL	2.4
1	B	14	THR	2.4
1	A	65	GLY	2.3
1	A	23	LEU	2.3
1	A	17	SER	2.3
1	A	102[A]	ASN	2.3
1	B	100	ASP	2.2
1	B	183	GLU	2.2
1	B	440	TYR	2.2
1	B	408	GLN	2.1
1	B	26	ALA	2.1
1	B	401	GLY	2.1
1	B	15	GLY	2.1
1	A	354	TYR	2.0
1	A	28	LYS	2.0
1	B	141	SER	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [\(i\)](#)

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



### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	GOL	B	445	6/6	0.82	0.28	59,59,60,60	0
3	GOL	A	444	6/6	0.86	0.20	56,57,57,57	0
4	ACT	B	444	4/4	0.90	0.26	60,60,61,62	0
2	PLP	A	500	16/16	0.94	0.20	38,49,53,54	0
2	PLP	B	500	16/16	0.96	0.19	37,47,50,53	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.