



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 13, 2024 – 12:11 AM JST

PDB ID : 9JWC
Title : Three-dimensional structure of homo-dimer of cystathione beta lyase/PLP/+L-alliin complex from lactobacillus delbrueckii(LdPatB)
Authors : Liu, Y.; Yang, C.
Deposited on : 2024-10-10
Resolution : 2.08 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

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 : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

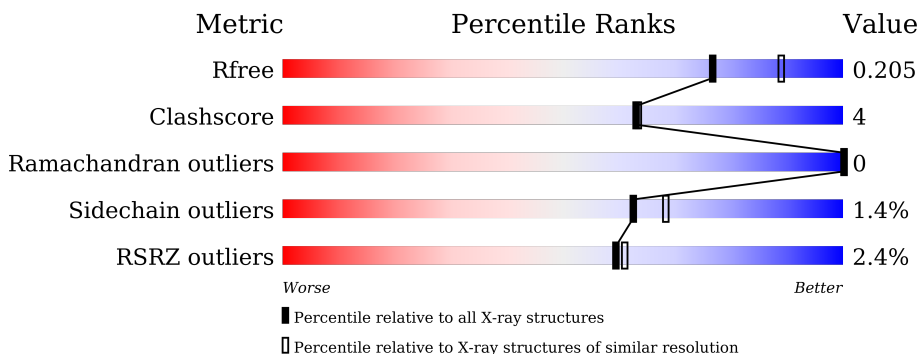
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

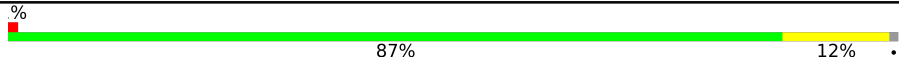
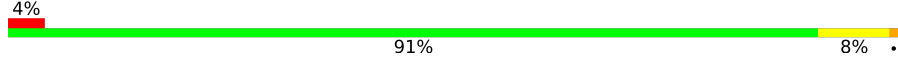
The reported resolution of this entry is 2.08 Å.

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}	164625	7574 (2.10-2.06)
Clashscore	180529	8325 (2.10-2.06)
Ramachandran outliers	177936	8271 (2.10-2.06)
Sidechain outliers	177891	8272 (2.10-2.06)
RSRZ outliers	164620	7574 (2.10-2.06)

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 ≥ 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	390	 87% 12% .
1	B	390	 4% 91% 8% .

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6701 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.

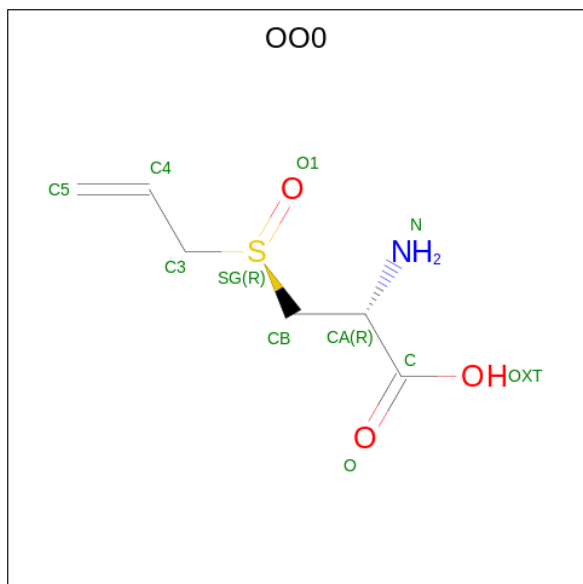
- Molecule 1 is a protein called cysteine-S-conjugate beta-lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	386	Total 3069	C 1964	N 517	O 572	S 16	0	0	0
1	B	390	Total 3100	C 1983	N 522	O 578	S 17	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

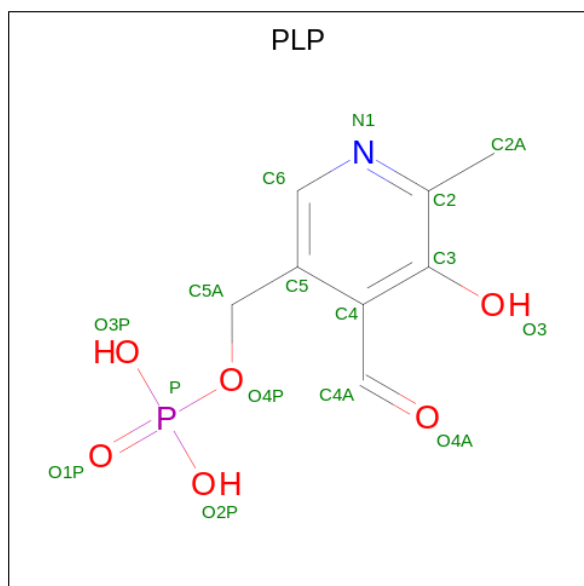
Chain	Residue	Modelled	Actual	Comment	Reference
A	311	GLU	VAL	engineered mutation	UNP A0AAC9VP02
A	326	ASP	ASN	engineered mutation	UNP A0AAC9VP02
B	311	GLU	VAL	engineered mutation	UNP A0AAC9VP02
B	326	ASP	ASN	engineered mutation	UNP A0AAC9VP02

- Molecule 2 is ALLIIN (three-letter code: OOO) (formula: C₆H₁₁NO₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	11	6	1	3	1	0	0

- Molecule 3 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P).



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

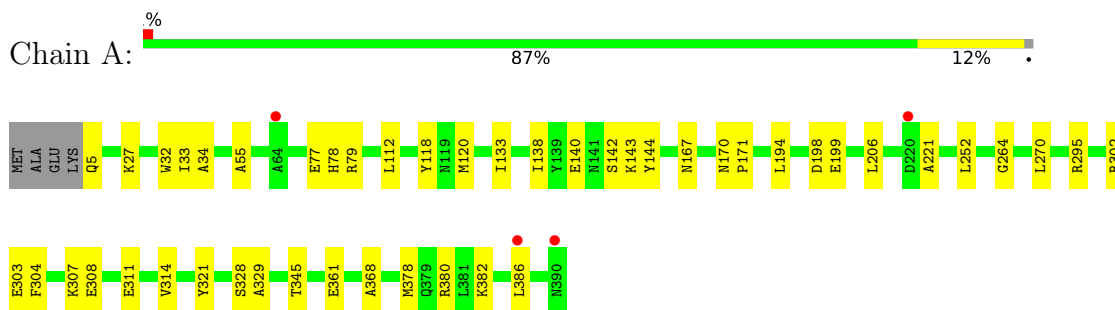
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	247	247	247	0	0
4	B	242	242	242	0	0

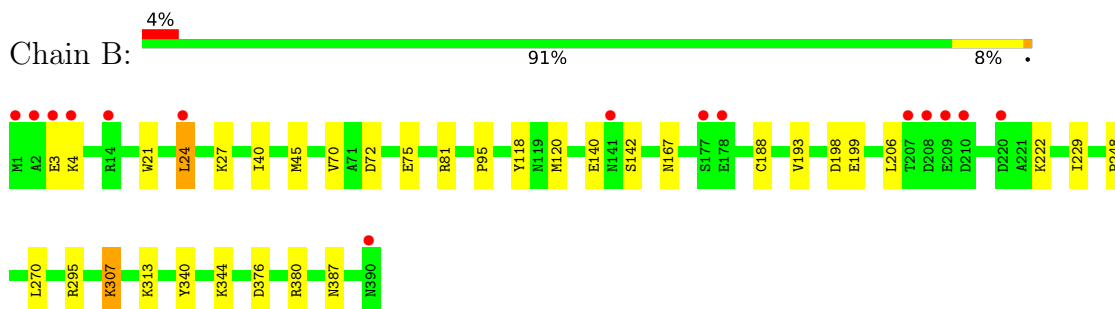
3 Residue-property plots [i](#)

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: cysteine-S-conjugate beta-lyase



- Molecule 1: cysteine-S-conjugate beta-lyase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	115.10Å 92.00Å 81.59Å 90.00° 126.05° 90.00°	Depositor
Resolution (Å)	65.42 – 2.08 65.42 – 2.08	Depositor EDS
% Data completeness (in resolution range)	99.6 (65.42-2.08) 99.5 (65.42-2.08)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 1.75Å)	Xtrriage
Refinement program	PHENIX 1.16	Depositor
R, R_{free}	0.187 , 0.218 0.178 , 0.205	Depositor DCC
R_{free} test set	39985 reflections (3.32%)	wwPDB-VP
Wilson B-factor (Å ²)	16.7	Xtrriage
Anisotropy	0.140	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 49.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6701	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.13% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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, OOO

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	0.40	0/3144	0.59	0/4268
1	B	0.42	0/3175	0.60	0/4308
All	All	0.41	0/6319	0.60	0/8576

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	3069	0	3012	28	0
1	B	3100	0	3045	20	0
2	A	11	0	0	4	0
3	A	16	0	7	3	0
3	B	16	0	7	1	0
4	A	247	0	0	1	0
4	B	242	0	0	0	0
All	All	6701	0	6071	48	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 (48) 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:A:401:OO0:N	3:A:402:PLP:H4A	1.91	0.86
1:A:194:LEU:HD21	1:A:252:LEU:HD11	1.78	0.63
1:B:40:ILE:HD11	1:B:45:MET:HE2	1.82	0.62
2:A:401:OO0:N	3:A:402:PLP:C4A	2.64	0.59
1:B:70:VAL:HG13	1:B:229:ILE:HD11	1.88	0.55
1:A:308:GLU:HB3	1:A:382:LYS:HD2	1.89	0.53
1:B:72:ASP:OD1	1:B:81:ARG:NH1	2.36	0.53
1:A:303:GLU:O	1:A:307:LYS:HG3	2.09	0.53
1:A:118:TYR:CE2	1:A:120:MET:HB2	2.45	0.51
1:A:206:LEU:O	1:A:295:ARG:NH1	2.41	0.51
1:A:138:ILE:HG22	1:A:140:GLU:HG3	1.91	0.51
1:A:167:ASN:O	1:A:199:GLU:HA	2.11	0.50
1:A:142:SER:O	1:A:142:SER:OG	2.30	0.50
1:B:340:TYR:CE1	1:B:344:LYS:HG3	2.49	0.47
1:A:221:ALA:N	4:A:512:HOH:O	2.46	0.47
1:B:307:LYS:HB2	1:B:307:LYS:HE3	1.74	0.46
1:B:24:LEU:HD12	1:B:24:LEU:HA	1.73	0.46
1:B:188:CYS:HB3	1:B:193:VAL:O	2.16	0.46
1:A:118:TYR:HE1	2:A:401:OO0:CB	2.29	0.46
1:B:27:LYS:HG2	1:B:27:LYS:O	2.16	0.46
1:A:27:LYS:HA	1:A:27:LYS:HD2	1.80	0.45
1:A:138:ILE:O	1:A:144:TYR:HA	2.17	0.45
1:A:328:SER:HB3	1:A:361:GLU:HB3	1.99	0.45
1:B:206:LEU:O	1:B:295:ARG:HD3	2.17	0.45
1:A:321:TYR:CG	1:A:368:ALA:HB2	2.52	0.45
1:A:382:LYS:HE2	1:A:386:LEU:HD11	1.99	0.45
1:B:167:ASN:O	1:B:199:GLU:HA	2.17	0.45
1:B:198:ASP:OD2	3:B:401:PLP:N1	2.50	0.44
1:B:222:LYS:HG2	1:B:248:PRO:HG2	1.99	0.44
1:B:118:TYR:CE2	1:B:120:MET:HB2	2.53	0.44
1:B:21:TRP:HA	1:B:24:LEU:HD22	2.00	0.44
1:B:340:TYR:OH	1:B:387:ASN:HB3	2.17	0.44
1:A:170:ASN:OD1	1:A:171:PRO:HA	2.18	0.43
1:B:376:ASP:O	1:B:380:ARG:HG3	2.18	0.43
1:A:302:ARG:HG2	1:A:314:VAL:HB	2.00	0.43
1:A:345:THR:O	1:A:380:ARG:HD3	2.19	0.43
1:B:142:SER:HB3	1:B:313:LYS:HD3	2.01	0.43
1:A:77:GLU:HG3	1:A:78:HIS:CE1	2.55	0.42
1:A:311:GLU:O	1:A:329:ALA:HB3	2.18	0.42
1:A:112:LEU:HA	1:A:133:ILE:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:304:PHE:CD1	1:A:378:MET:HB3	2.54	0.42
1:B:75:GLU:HB2	1:B:81:ARG:HB2	2.02	0.42
1:A:55:ALA:HA	1:B:45:MET:HE1	2.02	0.41
1:A:264:GLY:HA3	1:B:95:PRO:HB3	2.03	0.41
1:A:32:TRP:CG	1:A:33:ILE:N	2.89	0.41
1:A:143:LYS:HB3	1:A:143:LYS:HE3	1.75	0.41
1:A:34:ALA:N	2:A:401:OO0:O1	2.46	0.40
1:A:198:ASP:OD2	3:A:402:PLP:N1	2.54	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	384/390 (98%)	371 (97%)	13 (3%)	0	100	100
1	B	388/390 (100%)	379 (98%)	9 (2%)	0	100	100
All	All	772/780 (99%)	750 (97%)	22 (3%)	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	325/328 (99%)	322 (99%)	3 (1%)	75	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	328/328 (100%)	322 (98%)	6 (2%)	54	59
All	All	653/656 (100%)	644 (99%)	9 (1%)	62	68

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

Mol	Chain	Res	Type
1	A	5	GLN
1	A	79	ARG
1	A	270	LEU
1	B	3	GLU
1	B	4	LYS
1	B	24	LEU
1	B	140	GLU
1	B	270	LEU
1	B	307	LYS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 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	OO0	A	401	-	8,10,10	1.83	2 (25%)	7,12,12	3.08	3 (42%)
3	PLP	A	402	-	16,16,16	0.63	0	20,23,23	0.86	1 (5%)
3	PLP	B	401	-	16,16,16	0.57	0	20,23,23	0.83	1 (5%)

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	OO0	A	401	-	-	7/11/11/11	-
3	PLP	A	402	-	-	5/8/8/8	0/1/1/1
3	PLP	B	401	-	-	5/8/8/8	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	OO0	O1-SG	-3.51	1.37	1.50
2	A	401	OO0	OXT-C	-2.67	1.21	1.30

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	OO0	O1-SG-C3	4.78	123.43	106.64
2	A	401	OO0	O1-SG-CB	4.35	112.22	106.09
2	A	401	OO0	OXT-C-O	-4.19	114.57	124.09
3	B	401	PLP	O4P-C5A-C5	2.47	114.07	109.35
3	A	402	PLP	O4P-C5A-C5	2.31	113.76	109.35

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	OO0	N-CA-CB-SG
2	A	401	OO0	OXT-C-CA-CB
2	A	401	OO0	O-C-CA-CB

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Mol	Chain	Res	Type	Atoms
2	A	401	OOO	CA-CB-SG-O1
2	A	401	OOO	C4-C3-SG-CB
2	A	401	OOO	SG-C3-C4-C5
3	A	402	PLP	C3-C4-C4A-O4A
3	A	402	PLP	C5-C4-C4A-O4A
3	A	402	PLP	C5A-O4P-P-O1P
3	A	402	PLP	C5A-O4P-P-O2P
3	A	402	PLP	C5A-O4P-P-O3P
3	B	401	PLP	C5-C4-C4A-O4A
3	B	401	PLP	C5A-O4P-P-O1P
3	B	401	PLP	C5A-O4P-P-O2P
3	B	401	PLP	C5A-O4P-P-O3P
3	B	401	PLP	C3-C4-C4A-O4A
2	A	401	OOO	C-CA-CB-SG

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	OOO	4	0
3	A	402	PLP	3	0
3	B	401	PLP	1	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 [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, 95th 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 ²)	Q<0.9
1	A	386/390 (98%)	-0.30	4 (1%) 79 80	11, 16, 30, 49	1 (0%)
1	B	390/390 (100%)	-0.21	15 (3%) 44 46	11, 16, 33, 56	0
All	All	776/780 (99%)	-0.25	19 (2%) 59 61	11, 16, 32, 56	1 (0%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	208	ASP	8.0
1	B	2	ALA	7.2
1	B	1	MET	5.7
1	A	220	ASP	4.2
1	B	177	SER	3.8
1	A	64	ALA	3.7
1	B	220	ASP	3.5
1	A	390	ASN	3.3
1	B	390	ASN	3.3
1	B	3	GLU	3.2
1	B	4	LYS	3.1
1	B	207	THR	3.1
1	B	14	ARG	2.8
1	A	386	LEU	2.6
1	B	178	GLU	2.4
1	B	209	GLU	2.4
1	B	24	LEU	2.3
1	B	141	ASN	2.3
1	B	210	ASP	2.1

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, 95th 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 ²)	Q<0.9
3	PLP	B	401	16/16	0.49	0.27	0,0,0,0	2
3	PLP	A	402	16/16	0.63	0.23	0,0,0,0	2
2	OO0	A	401	11/11	0.70	0.18	17,28,36,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.