



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 05:21 AM UTC

PDB ID : 3VBE / pdb\_00003vbe  
Title : Crystal structure of beta-cyanoalanine synthase in soybean  
Authors : Yi, H.; Jez, J.M.  
Deposited on : 2012-01-02  
Resolution : 2.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

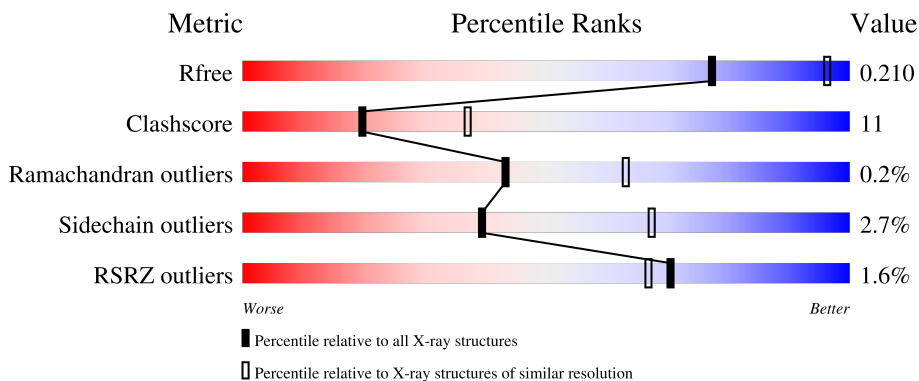
# 1 Overall quality at a glance

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))
$R_{free}$	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (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	344	 79% 11% • 8%
1	B	344	 74% 18% • 7%
1	C	344	 74% 19% • •
1	D	344	 71% 19% •• 8%

## 2 Entry composition [i](#)

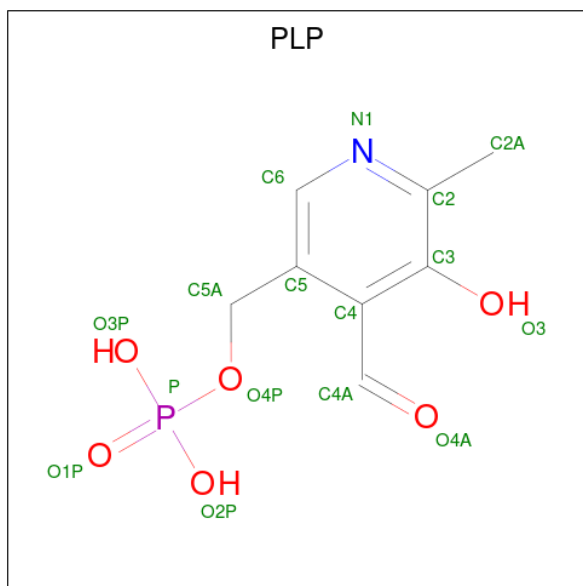
There are 3 unique types of molecules in this entry. The entry contains 9973 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 beta-cyanoalnine synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	317	Total 2394	C 1507	N 407	O 462	S 18	0	0	0
1	B	321	Total 2423	C 1527	N 412	O 466	S 18	0	0	0
1	C	329	Total 2488	C 1570	N 423	O 477	S 18	0	0	0
1	D	317	Total 2394	C 1507	N 407	O 462	S 18	0	0	0

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: 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 15	C 8	N 1	O 5	P 1	0	0
2	B	1	Total 15	C 8	N 1	O 5	P 1	0	0

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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		

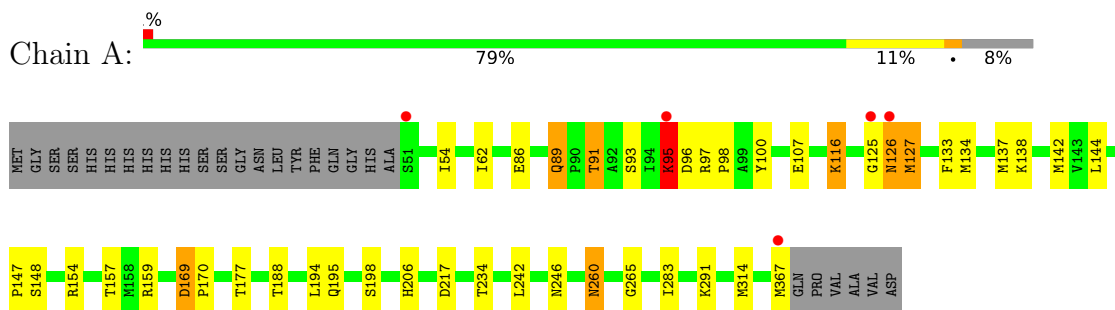
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	51	Total	O	0	0
			51	51		
3	B	54	Total	O	0	0
			54	54		
3	C	50	Total	O	0	0
			50	50		
3	D	59	Total	O	0	0
			59	59		

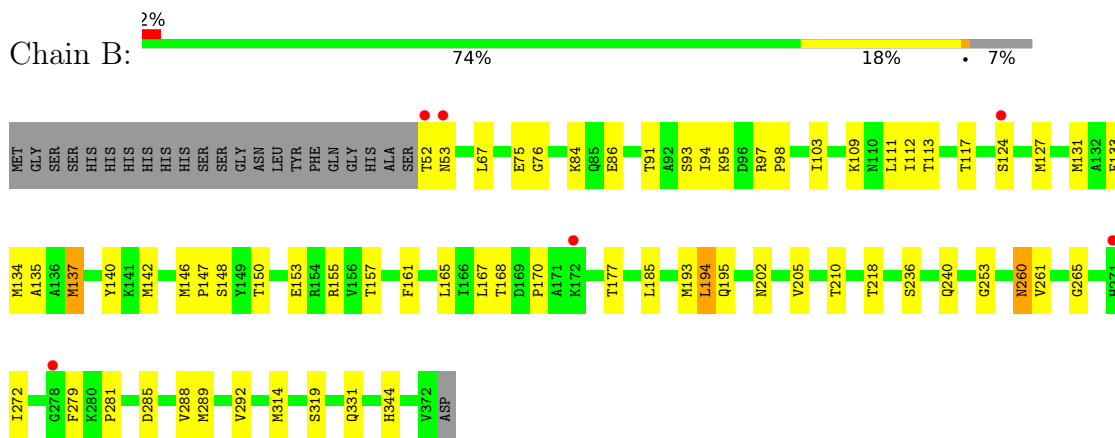
### 3 Residue-property plots [i](#)

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.

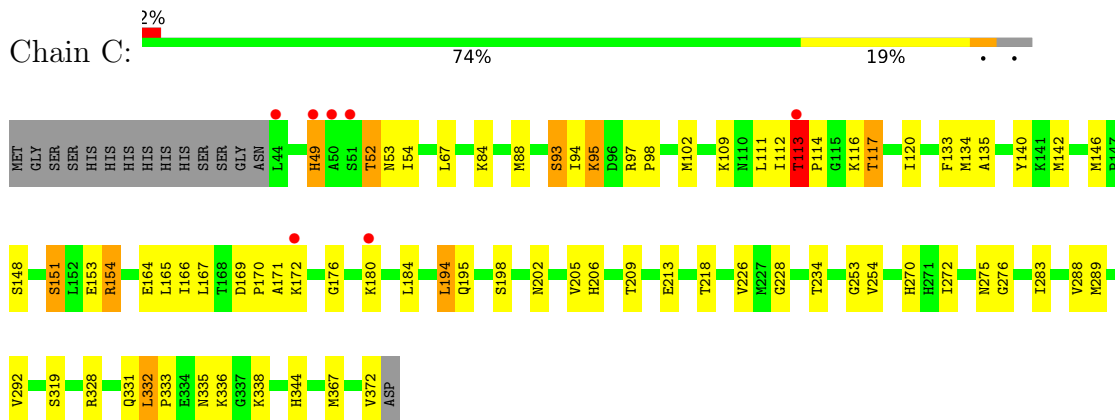
- Molecule 1: beta-cyanoalnine synthase



- Molecule 1: beta-cyanoalnine synthase

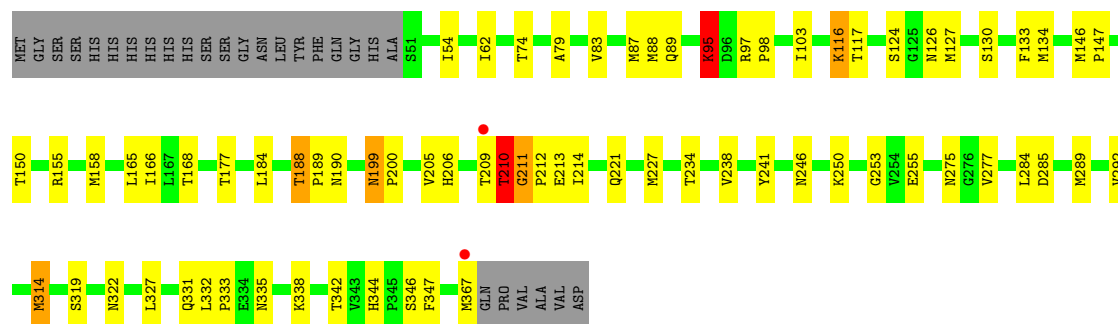


- Molecule 1: beta-cyanoalnine synthase



- Molecule 1: beta-cyanoalnine synthase

Chain D:  %



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	190.32Å 154.58Å 70.80Å 90.00° 101.89° 90.00°	Depositor
Resolution (Å)	49.16 – 2.50 49.16 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.2 (49.16-2.50) 99.2 (49.16-2.50)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.95 (at 2.51Å)	Xtrriage
Refinement program	PHENIX 1.7.1_743	Depositor
R, $R_{free}$	0.167 , 0.210 0.172 , 0.210	Depositor DCC
$R_{free}$ test set	3463 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	45.2	Xtrriage
Anisotropy	0.012	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 51.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	9973	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% 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: 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	0.78	3/2435 (0.1%)	0.98	10/3293 (0.3%)
1	B	0.67	0/2465	0.88	6/3336 (0.2%)
1	C	0.57	0/2533	0.89	6/3428 (0.2%)
1	D	0.63	1/2435 (0.0%)	0.93	10/3293 (0.3%)
All	All	0.67	4/9868 (0.0%)	0.92	32/13350 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	89	GLN	C-O	-6.83	1.18	1.24
1	D	89	GLN	C-O	-5.54	1.19	1.24
1	A	169	ASP	C-O	-5.18	1.18	1.24
1	A	126	ASN	CA-C	-5.01	1.46	1.52

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	127	MET	N-CA-C	-13.10	96.93	113.43
1	A	126	ASN	CB-CA-C	-11.60	89.14	111.06
1	D	116	LYS	CA-C-N	9.10	133.66	120.82
1	D	116	LYS	C-N-CA	9.10	133.66	120.82
1	D	95	LYS	CG-CD-CE	7.97	129.63	111.30

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	2394	0	2423	44	0
1	B	2423	0	2457	55	0
1	C	2488	0	2513	65	0
1	D	2394	0	2423	71	0
2	A	15	0	7	0	0
2	B	15	0	7	0	0
2	C	15	0	7	1	0
2	D	15	0	6	3	0
3	A	51	0	0	1	0
3	B	54	0	0	2	0
3	C	50	0	0	2	0
3	D	59	0	0	1	0
All	All	9973	0	9843	225	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 11.

The worst 5 of 225 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:D:146:MET:HE2	1:D:150:THR:HG21	1.26	1.12
1:B:289:MET:HE1	1:B:292:VAL:HG22	1.36	1.07
1:D:289:MET:HE1	1:D:292:VAL:HG22	1.39	1.04
1:C:289:MET:HE1	1:C:292:VAL:HG22	1.44	1.00
1:D:124:SER:HB3	1:D:146:MET:HE3	1.44	1.00

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	315/344 (92%)	307 (98%)	8 (2%)	0	100	100
1	B	319/344 (93%)	310 (97%)	9 (3%)	0	100	100
1	C	327/344 (95%)	321 (98%)	6 (2%)	0	100	100
1	D	315/344 (92%)	301 (96%)	12 (4%)	2 (1%)	21	38
All	All	1276/1376 (93%)	1239 (97%)	35 (3%)	2 (0%)	43	63

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	211	GLY
1	D	210	THR

### 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	263/285 (92%)	258 (98%)	5 (2%)	50	76
1	B	266/285 (93%)	261 (98%)	5 (2%)	50	76
1	C	272/285 (95%)	259 (95%)	13 (5%)	23	46
1	D	263/285 (92%)	257 (98%)	6 (2%)	44	72
All	All	1064/1140 (93%)	1035 (97%)	29 (3%)	39	67

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	113	THR
1	D	314	MET
1	C	154	ARG
1	D	165	LEU
1	C	151	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	85	GLN
1	D	126	ASN
1	D	219	ASN
1	B	248	ASN
1	B	192	HIS

### 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](#)

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	A	500	1	15,15,16	1.28	2 (13%)	21,22,23	1.54	4 (19%)
2	PLP	D	401	1	15,15,16	1.04	1 (6%)	21,22,23	7.73	3 (14%)
2	PLP	C	401	1	15,15,16	2.85	2 (13%)	21,22,23	5.40	3 (14%)
2	PLP	B	501	1	15,15,16	0.96	1 (6%)	21,22,23	5.99	5 (23%)

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	A	500	1	-	0/6/6/8	0/1/1/1
2	PLP	D	401	1	-	2/6/6/8	0/1/1/1
2	PLP	C	401	1	-	0/6/6/8	0/1/1/1
2	PLP	B	501	1	-	3/6/6/8	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	401	PLP	C4A-C4	-10.33	1.31	1.51
2	A	500	PLP	C3-C2	-2.68	1.38	1.41
2	A	500	PLP	C2-N1	2.63	1.38	1.33
2	C	401	PLP	C2-N1	2.41	1.38	1.33
2	D	401	PLP	C2-N1	2.29	1.37	1.33

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	401	PLP	C4A-C4-C5	29.94	151.80	120.94
2	B	501	PLP	C4A-C4-C5	23.06	144.70	120.94
2	C	401	PLP	C4A-C4-C5	20.39	141.96	120.94
2	D	401	PLP	C4A-C4-C3	-18.46	89.73	120.52
2	B	501	PLP	C4A-C4-C3	-13.93	97.30	120.52

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	501	PLP	C4-C5-C5A-O4P
2	B	501	PLP	C6-C5-C5A-O4P
2	D	401	PLP	C4-C5-C5A-O4P
2	D	401	PLP	C6-C5-C5A-O4P
2	B	501	PLP	C5A-O4P-P-O3P

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	401	PLP	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	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, 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	317/344 (92%)	-0.21	5 (1%) 70 67	30, 47, 78, 109	0
1	B	321/344 (93%)	-0.13	6 (1%) 66 62	28, 50, 79, 115	0
1	C	329/344 (95%)	-0.05	7 (2%) 63 59	27, 52, 92, 128	0
1	D	317/344 (92%)	-0.14	2 (0%) 85 83	29, 50, 84, 109	0
All	All	1284/1376 (93%)	-0.13	20 (1%) 70 67	27, 50, 84, 128	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	50	ALA	6.7
1	B	52	THR	4.6
1	D	209	THR	3.8
1	A	51	SER	3.1
1	B	278	GLY	3.1

### 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 oligosaccharides 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	PLP	B	501	15/16	0.97	0.06	31,44,48,51	0
2	PLP	C	401	15/16	0.97	0.07	38,46,53,55	0
2	PLP	D	401	15/16	0.97	0.07	35,41,51,53	0
2	PLP	A	500	15/16	0.98	0.05	26,36,46,49	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.