



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 10:51 pm GMT

PDB ID : 2BYL  
Title : Structure of ornithine aminotransferase triple mutant Y85I Y55A G320F  
Authors : Markova, M.; Peneff, C.; Hewlins, M.J.E.; Schirmer, T.; John, R.A.  
Deposited on : 2005-08-03  
Resolution : 2.15 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

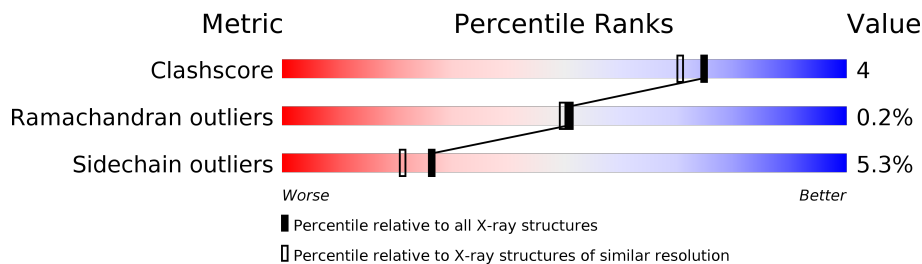
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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))
Clashscore	112137	1278 (2.16-2.16)
Ramachandran outliers	110173	1256 (2.16-2.16)
Sidechain outliers	110143	1255 (2.16-2.16)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	439	
1	B	439	
1	C	439	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10096 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.

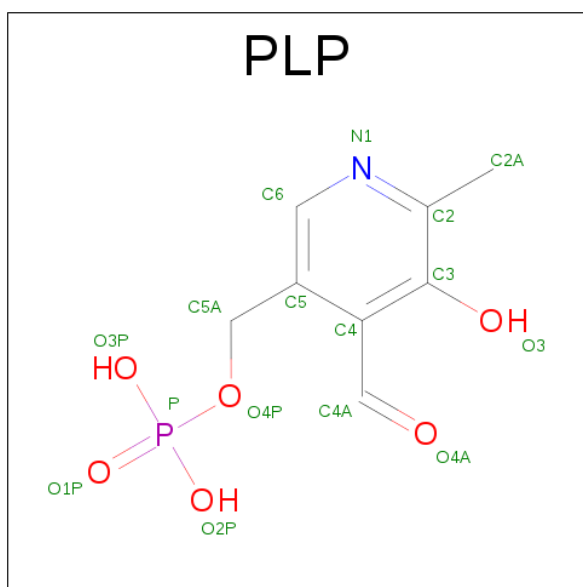
- Molecule 1 is a protein called ORNITHINE AMINOTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	404	Total	C	N	O	S	0	0	0
			3157	2028	533	584	12			
1	B	404	Total	C	N	O	S	0	0	0
			3157	2028	533	584	12			
1	C	404	Total	C	N	O	S	0	0	0
			3157	2028	533	584	12			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	55	ALA	TYR	ENGINEERED MUTATION	UNP P04181
A	85	ILE	TYR	ENGINEERED MUTATION	UNP P04181
A	320	PHE	GLY	ENGINEERED MUTATION	UNP P04181
B	55	ALA	TYR	ENGINEERED MUTATION	UNP P04181
B	85	ILE	TYR	ENGINEERED MUTATION	UNP P04181
B	320	PHE	GLY	ENGINEERED MUTATION	UNP P04181
C	55	ALA	TYR	ENGINEERED MUTATION	UNP P04181
C	85	ILE	TYR	ENGINEERED MUTATION	UNP P04181
C	320	PHE	GLY	ENGINEERED MUTATION	UNP P04181

- 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
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		
2	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 3 is water.

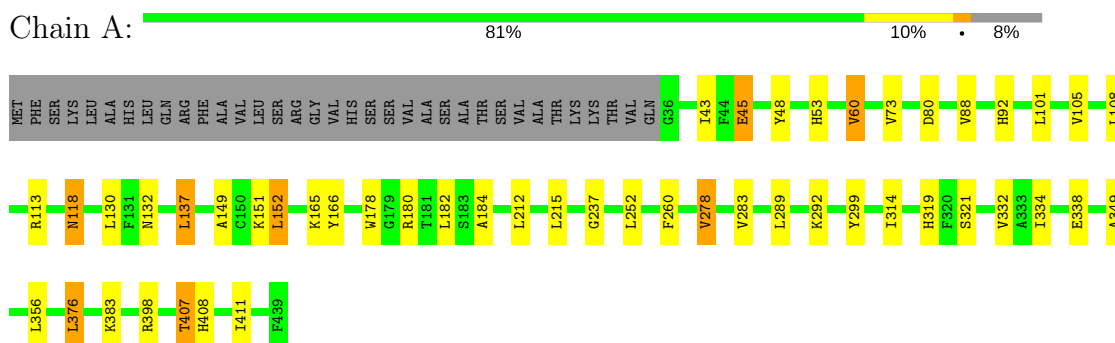
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	167	Total	O	0	0
			167	167		
3	B	237	Total	O	0	0
			237	237		
3	C	176	Total	O	0	0
			176	176		

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

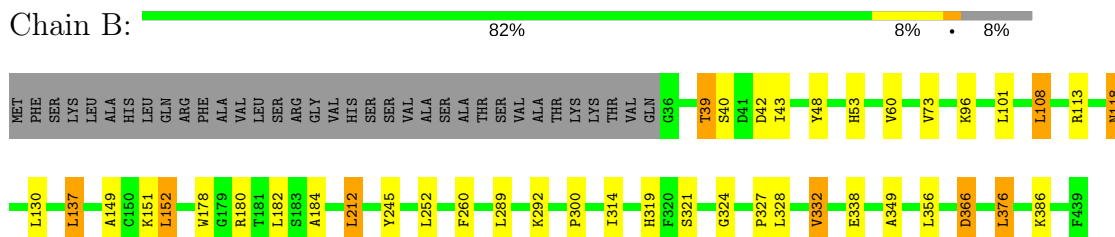
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

Note EDS was not executed.

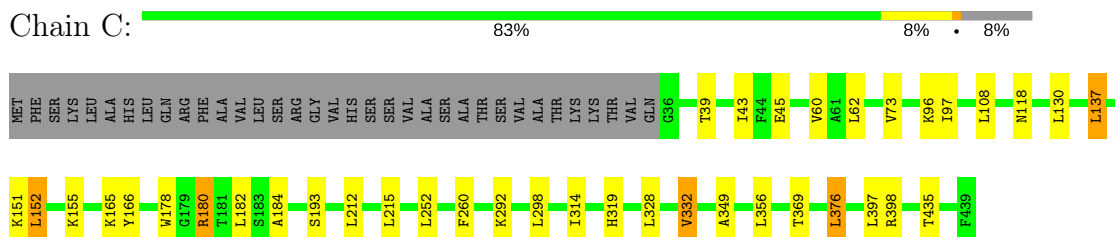
#### • Molecule 1: ORNITHINE AMINOTRANSFERASE



#### • Molecule 1: ORNITHINE AMINOTRANSFERASE



#### • Molecule 1: ORNITHINE AMINOTRANSFERASE



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	115.95Å 115.95Å 188.34Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.15	Depositor
% Data completeness (in resolution range)	97.9 (30.00-2.15)	Depositor
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.159 , 0.191	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10096	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

## 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	0.51	0/3230	0.64	3/4386 (0.1%)
1	B	0.55	0/3230	0.66	1/4386 (0.0%)
1	C	0.50	0/3230	0.62	1/4386 (0.0%)
All	All	0.52	0/9690	0.64	5/13158 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	137	LEU	CA-CB-CG	6.62	130.54	115.30
1	B	137	LEU	CA-CB-CG	5.57	128.11	115.30
1	A	180	ARG	NE-CZ-NH1	5.37	122.98	120.30
1	C	137	LEU	CA-CB-CG	5.31	127.51	115.30
1	A	137	LEU	CB-CG-CD1	5.23	119.90	111.00

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	3157	0	3167	30	0
1	B	3157	0	3167	28	0
1	C	3157	0	3167	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	15	0	7	0	0
2	B	15	0	6	0	0
2	C	15	0	6	1	0
3	A	167	0	0	4	0
3	B	237	0	0	2	0
3	C	176	0	0	0	0
All	All	10096	0	9520	71	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 (71) 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:151:LYS:NZ	1:B:319:HIS:HD2	1.80	0.79
1:A:237:GLY:HA2	1:A:407:THR:HG21	1.67	0.75
1:A:407:THR:HG23	1:A:408:HIS:ND1	2.01	0.74
1:C:151:LYS:NZ	1:C:319:HIS:HD2	1.87	0.73
1:A:151:LYS:HZ3	1:A:319:HIS:HD2	1.37	0.72
1:B:151:LYS:HZ3	1:B:319:HIS:HD2	1.34	0.72
1:A:45:GLU:HG3	3:A:2001:HOH:O	1.91	0.71
1:C:152:LEU:HD13	1:C:314:ILE:HD12	1.74	0.70
1:C:152:LEU:HD13	1:C:314:ILE:CD1	2.21	0.70
1:C:349:ALA:HA	1:C:376:LEU:HD22	1.74	0.69
1:A:151:LYS:NZ	1:A:319:HIS:HD2	1.93	0.67
1:B:152:LEU:HD13	1:B:314:ILE:HD12	1.81	0.63
1:A:407:THR:HG22	1:A:411:ILE:HB	1.81	0.62
1:A:349:ALA:HA	1:A:376:LEU:HD22	1.80	0.62
1:B:152:LEU:HD13	1:B:314:ILE:CD1	2.29	0.62
1:A:113:ARG:HG2	3:A:2148:HOH:O	2.00	0.61
1:A:88:VAL:HG23	1:A:88:VAL:O	2.02	0.60
1:A:118:ASN:HD22	1:A:118:ASN:H	1.52	0.57
1:B:366:ASP:N	1:B:366:ASP:OD1	2.35	0.57
1:C:151:LYS:HZ3	1:C:319:HIS:HD2	1.51	0.56
1:A:152:LEU:HD13	1:A:314:ILE:CD1	2.36	0.56
1:B:151:LYS:HZ3	1:B:319:HIS:CD2	2.20	0.56
1:B:101:LEU:HD12	1:B:328:LEU:HD11	1.88	0.55
1:B:349:ALA:HA	1:B:376:LEU:HD22	1.88	0.55
1:B:39:THR:HG23	1:B:42:ASP:H	1.73	0.54
1:A:80:ASP:OD2	1:A:92:HIS:HE1	1.91	0.54
1:A:152:LEU:HD13	1:A:314:ILE:HD12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:ARG:CG	3:A:2148:HOH:O	2.56	0.53
1:C:180:ARG:NH1	1:C:193:SER:OG	2.42	0.52
1:B:43:ILE:CD1	1:B:73:VAL:HG11	2.40	0.52
1:A:278:VAL:HG13	1:A:283:VAL:O	2.10	0.52
1:B:39:THR:OG1	1:B:40:SER:N	2.44	0.51
1:C:43:ILE:HD11	1:C:73:VAL:HG11	1.92	0.51
1:A:105:VAL:HG21	1:B:101:LEU:HD23	1.92	0.51
1:B:149:ALA:HB2	1:B:289:LEU:HD21	1.93	0.51
1:C:43:ILE:CD1	1:C:73:VAL:HG11	2.41	0.51
1:A:151:LYS:HZ3	1:A:319:HIS:CD2	2.25	0.50
1:B:113:ARG:HD3	1:B:324:GLY:O	2.11	0.49
1:B:101:LEU:HD13	1:B:332:VAL:HG11	1.95	0.48
1:A:60:VAL:HG13	1:A:398:ARG:HD2	1.96	0.47
1:B:118:ASN:H	1:B:118:ASN:HD22	1.62	0.47
1:A:48:TYR:O	1:A:53:HIS:HE1	1.97	0.46
1:B:328:LEU:O	1:B:332:VAL:HG13	2.16	0.46
1:A:299:TYR:CZ	1:B:300:PRO:HD3	2.50	0.46
1:A:334:ILE:O	1:A:338:GLU:HG3	2.16	0.46
1:C:97:ILE:HG22	1:C:298:LEU:HD22	1.97	0.46
1:A:321:SER:HB2	3:A:2059:HOH:O	2.15	0.45
1:A:43:ILE:CD1	1:A:73:VAL:HG11	2.47	0.44
1:B:108:LEU:HD13	1:B:327:PRO:HG3	1.98	0.44
1:C:151:LYS:HZ2	1:C:319:HIS:HD2	1.62	0.44
1:B:212:LEU:HD13	1:B:245:TYR:CD1	2.53	0.44
1:B:48:TYR:O	1:B:53:HIS:HE1	2.00	0.44
1:C:165:LYS:HA	1:C:166:TYR:HA	1.86	0.44
1:C:60:VAL:HG12	1:C:398:ARG:HD2	2.00	0.44
1:B:151:LYS:NZ	1:B:319:HIS:CD2	2.72	0.43
1:C:328:LEU:O	1:C:332:VAL:HG13	2.18	0.43
1:A:149:ALA:HB2	1:A:289:LEU:HD21	2.00	0.43
1:C:178:TRP:HA	2:C:500:PLP:C6	2.50	0.42
1:B:321:SER:HB2	3:B:2072:HOH:O	2.18	0.42
1:A:319:HIS:HA	1:B:180:ARG:HH11	1.84	0.42
1:B:96:LYS:HE2	1:B:338:GLU:HB2	2.01	0.42
1:A:101:LEU:HD13	1:A:332:VAL:HG11	2.01	0.42
1:A:178:TRP:CZ2	1:A:184:ALA:HA	2.55	0.41
1:A:92:HIS:HD2	3:B:2045:HOH:O	2.03	0.41
1:A:165:LYS:HA	1:A:166:TYR:HA	1.84	0.41
1:B:39:THR:HG22	1:B:42:ASP:OD2	2.21	0.41
1:B:178:TRP:CZ2	1:B:184:ALA:HA	2.56	0.41
1:C:397:LEU:HD13	1:C:435:THR:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:237:GLY:CA	1:A:407:THR:HG21	2.42	0.40
1:C:178:TRP:CZ2	1:C:184:ALA:HA	2.57	0.40
1:B:101:LEU:HD12	1:B:328:LEU:CD1	2.49	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	402/439 (92%)	387 (96%)	14 (4%)	1 (0%)	51	50
1	B	402/439 (92%)	385 (96%)	16 (4%)	1 (0%)	51	50
1	C	402/439 (92%)	388 (96%)	13 (3%)	1 (0%)	51	50
All	All	1206/1317 (92%)	1160 (96%)	43 (4%)	3 (0%)	51	50

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	292	LYS
1	C	292	LYS
1	A	292	LYS

### 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	337/366 (92%)	319 (95%)	18 (5%)	26	21
1	B	337/366 (92%)	321 (95%)	16 (5%)	30	26
1	C	337/366 (92%)	317 (94%)	20 (6%)	23	17
All	All	1011/1098 (92%)	957 (95%)	54 (5%)	26	21

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	GLU
1	A	60	VAL
1	A	108	LEU
1	A	118	ASN
1	A	130	LEU
1	A	132	ASN
1	A	137	LEU
1	A	152	LEU
1	A	182	LEU
1	A	212	LEU
1	A	215	LEU
1	A	252	LEU
1	A	260	PHE
1	A	278	VAL
1	A	356	LEU
1	A	376	LEU
1	A	383	LYS
1	A	407	THR
1	B	39	THR
1	B	60	VAL
1	B	108	LEU
1	B	118	ASN
1	B	130	LEU
1	B	137	LEU
1	B	152	LEU
1	B	182	LEU
1	B	212	LEU
1	B	252	LEU
1	B	260	PHE
1	B	332	VAL
1	B	356	LEU
1	B	366	ASP
1	B	376	LEU
1	B	386	LYS

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Mol	Chain	Res	Type
1	C	39	THR
1	C	45	GLU
1	C	62	LEU
1	C	96	LYS
1	C	108	LEU
1	C	118	ASN
1	C	130	LEU
1	C	137	LEU
1	C	152	LEU
1	C	155	LYS
1	C	180	ARG
1	C	182	LEU
1	C	212	LEU
1	C	215	LEU
1	C	252	LEU
1	C	260	PHE
1	C	332	VAL
1	C	356	LEU
1	C	369	THR
1	C	376	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	HIS
1	A	92	HIS
1	A	118	ASN
1	A	282	ASN
1	A	319	HIS
1	A	400	ASN
1	B	53	HIS
1	B	118	ASN
1	B	132	ASN
1	B	164	GLN
1	B	319	HIS
1	B	400	ASN
1	C	118	ASN
1	C	132	ASN
1	C	319	HIS
1	C	400	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

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	PLP	A	500	1	15,15,16	1.03	1 (6%)	20,22,23	1.59	3 (15%)
2	PLP	B	500	1	15,15,16	1.00	0	20,22,23	1.42	2 (10%)
2	PLP	C	500	1	15,15,16	1.06	2 (13%)	20,22,23	1.43	3 (15%)

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	B	500	1	-	0/6/6/8	0/1/1/1
2	PLP	C	500	1	-	0/6/6/8	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	500	PLP	C2-N1	2.17	1.38	1.33
2	A	500	PLP	C6-N1	2.20	1.39	1.34
2	C	500	PLP	C6-N1	2.39	1.39	1.34

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	PLP	C4A-C4-C3	-2.45	116.31	120.54
2	C	500	PLP	C4A-C4-C3	-2.41	116.38	120.54
2	A	500	PLP	C4A-C4-C5	2.34	123.22	120.86
2	B	500	PLP	C4A-C4-C5	2.38	123.26	120.86
2	C	500	PLP	C4A-C4-C5	3.33	124.22	120.86
2	C	500	PLP	O4P-C5A-C5	3.63	116.63	109.32
2	B	500	PLP	O4P-C5A-C5	3.78	116.92	109.32
2	A	500	PLP	O4P-C5A-C5	4.40	118.17	109.32

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	500	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

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.