



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2023 – 02:35 PM EDT

PDB ID : 2000  
Title : A structural insight into the inhibition of human and *Leishmania donovani* ornithine decarboxylases by 3-aminooxy-1-aminopropane  
Authors : Dufe, V.T.; Ingner, D.; Khomutov, A.R.; Heby, O.; Persson, L.; Al-Karadaghi, S.  
Deposited on : 2007-01-25  
Resolution : 1.90 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>.

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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 : 2.35  
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) : 2.35

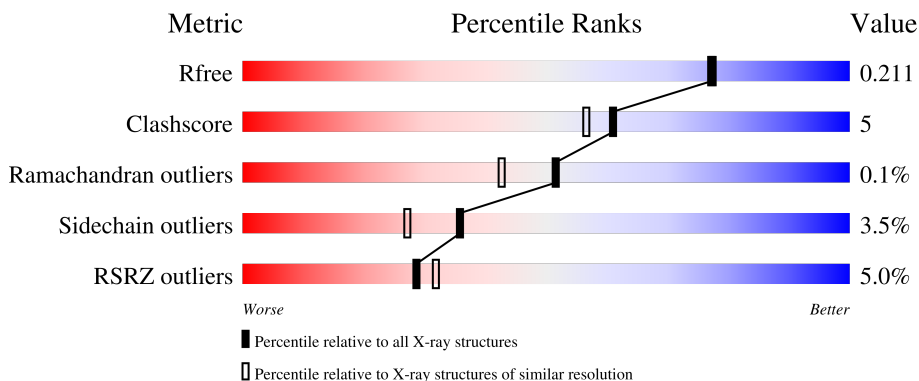
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	471	
1	B	471	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	XAP	B	601	-	-	X	-

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7196 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 decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	419	3307	2115	547	622	23	0	4	0
1	B	418	3296	2110	545	618	23	0	3	0

There are 20 discrepancies between the modelled and reference sequences:

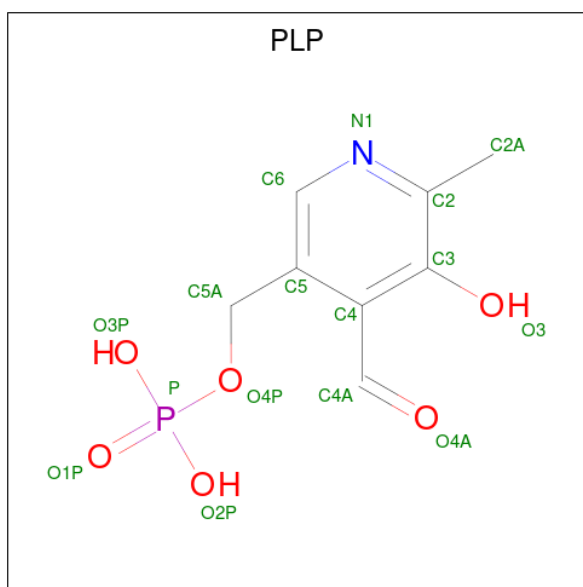
Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	ALA	-	cloning artifact	UNP P11926
A	-8	GLY	-	cloning artifact	UNP P11926
A	-7	GLU	-	cloning artifact	UNP P11926
A	-6	ASN	-	cloning artifact	UNP P11926
A	-5	LEU	-	cloning artifact	UNP P11926
A	-4	TYR	-	cloning artifact	UNP P11926
A	-3	PHE	-	cloning artifact	UNP P11926
A	-2	GLN	-	cloning artifact	UNP P11926
A	-1	SER	-	cloning artifact	UNP P11926
A	0	LEU	-	cloning artifact	UNP P11926
B	-9	ALA	-	cloning artifact	UNP P11926
B	-8	GLY	-	cloning artifact	UNP P11926
B	-7	GLU	-	cloning artifact	UNP P11926
B	-6	ASN	-	cloning artifact	UNP P11926
B	-5	LEU	-	cloning artifact	UNP P11926
B	-4	TYR	-	cloning artifact	UNP P11926
B	-3	PHE	-	cloning artifact	UNP P11926
B	-2	GLN	-	cloning artifact	UNP P11926
B	-1	SER	-	cloning artifact	UNP P11926
B	0	LEU	-	cloning artifact	UNP P11926

- Molecule 2 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
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C<sub>8</sub>H<sub>10</sub>NO<sub>6</sub>P).



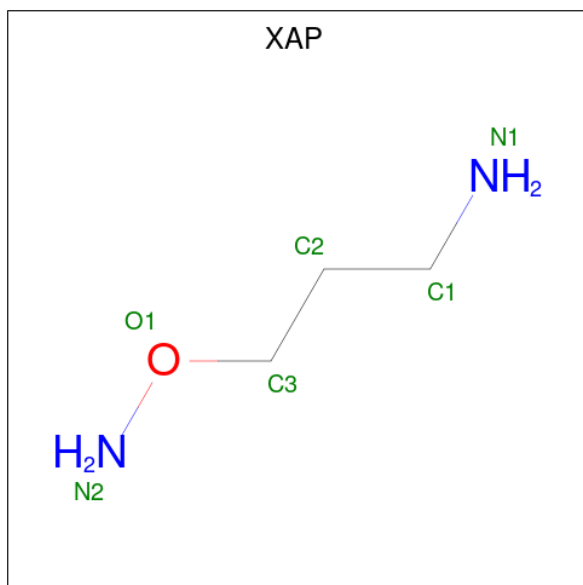
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			16	8	1	6	1		

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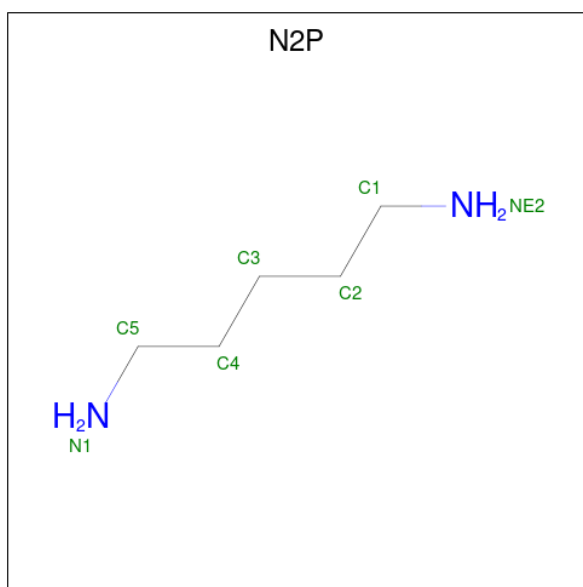
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	B	1	16	8	1	6	1	0	0

- Molecule 4 is 3-AMINOXY-1-AMINOPROPANE (three-letter code: XAP) (formula:  $C_3H_{10}N_2O$ ).



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

- Molecule 5 is PENTANE-1,5-DIAMINE (three-letter code: N2P) (formula:  $C_5H_{14}N_2$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N 7 5 2	0	0
5	B	1	Total C N 7 5 2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	250	Total O 250 250	0	0
6	B	273	Total O 273 273	0	0





## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	108.02Å 87.11Å 130.08Å 90.00° 91.02° 90.00°	Depositor
Resolution (Å)	29.45 – 1.90 29.45 – 1.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.45-1.90) 99.7 (29.45-1.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.43 (at 1.91Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.184 , 0.213 0.183 , 0.211	Depositor DCC
$R_{free}$ test set	9468 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.2	Xtrriage
Anisotropy	0.045	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 48.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.021 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7196	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.75% 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: N2P, XAP, ACT, 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	0.49	0/3383	0.58	0/4579
1	B	0.50	0/3372	0.60	1/4564 (0.0%)
All	All	0.50	0/6755	0.59	1/9143 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	363	LEU	CA-CB-CG	5.18	127.21	115.30

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	3307	0	3261	26	0
1	B	3296	0	3257	33	0
2	A	8	0	6	1	0
2	B	4	0	3	0	0
3	A	16	0	8	1	0
3	B	16	0	8	1	0
4	A	6	0	10	3	0
4	B	6	0	10	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	7	0	14	4	0
5	B	7	0	14	2	0
6	A	250	0	0	0	0
6	B	273	0	0	3	0
All	All	7196	0	6591	60	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 5.

All (60) 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:421:GLN:O	1:B:422:ASN:ND2	1.70	1.24
1:B:421:GLN:C	1:B:422:ASN:HD22	1.46	1.18
1:A:166:LEU:HD21	4:A:601:XAP:HN22	1.33	0.92
1:B:332:ASP:OD2	4:B:601:XAP:H11	1.71	0.90
1:B:132:THR:HG21	6:B:821:HOH:O	1.74	0.87
1:B:166:LEU:HD21	4:B:601:XAP:HN22	1.42	0.83
1:B:421:GLN:C	1:B:422:ASN:ND2	2.22	0.83
1:A:239:PRO:HA	5:A:700:N2P:H2C1	1.62	0.82
1:A:136:GLU:H	2:A:801:ACT:H2	1.44	0.81
1:A:244:VAL:HG11	5:A:700:N2P:H2C2	1.67	0.76
1:B:322[B]:VAL:CG1	1:B:330:LEU:HD13	2.18	0.72
1:B:246:LEU:H	5:B:700:N2P:H4C1	1.56	0.70
1:A:332:ASP:OD2	4:A:601:XAP:H11	1.96	0.65
1:A:263:PHE:HB3	1:A:269:VAL:HG11	1.80	0.63
1:B:282:SER:HA	1:B:385:ASN:HD22	1.67	0.59
1:B:341:GLN:HE22	1:B:342:LYS:HZ1	1.51	0.58
1:B:263:PHE:HB3	1:B:269:VAL:HG11	1.85	0.58
1:A:239:PRO:CA	5:A:700:N2P:H2C1	2.34	0.57
1:A:48:ILE:CD1	1:A:76:ILE:HD12	2.36	0.56
1:A:240:GLY:H	5:A:700:N2P:H3C2	1.70	0.55
1:A:282:SER:HA	1:A:385:ASN:HD22	1.73	0.53
1:A:34:SER:O	1:A:37:LYS:HE3	2.08	0.53
1:B:322[B]:VAL:HG11	1:B:330:LEU:CD1	2.39	0.53
1:A:421:GLN:O	1:A:422:ASN:HB3	2.09	0.52
1:B:-4:TYR:CZ	1:B:0:LEU:HD11	2.45	0.52
1:B:341:GLN:HG2	1:B:380:TRP:HB2	1.92	0.51
1:B:274:GLU:O	3:B:600:PLP:H6	2.10	0.51
1:B:322[B]:VAL:HG13	1:B:330:LEU:HD13	1.93	0.51
1:B:111:ALA:HA	1:B:132:THR:HB	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:GLU:O	3:A:600:PLP:H6	2.11	0.50
1:B:27:LYS:HE3	1:B:406:TYR:CG	2.47	0.49
1:B:246:LEU:HB3	5:B:700:N2P:H4C2	1.94	0.49
1:B:322[B]:VAL:HG11	1:B:330:LEU:HD13	1.94	0.49
4:B:601:XAP:N1	6:B:886:HOH:O	2.34	0.49
1:B:332:ASP:OD2	4:B:601:XAP:C1	2.53	0.49
1:B:345:LYS:HB2	1:B:348:GLU:HB3	1.93	0.49
1:B:341:GLN:HE22	1:B:342:LYS:NZ	2.12	0.48
1:B:52:HIS:CD2	1:B:83:THR:CG2	2.97	0.47
1:A:99:GLN:HE22	1:A:126:ASN:HB3	1.79	0.47
1:B:322[B]:VAL:CG1	1:B:330:LEU:CD1	2.91	0.46
1:B:404[A]:THR:HG23	6:B:813:HOH:O	2.16	0.45
1:A:73:SER:HB2	1:A:76:ILE:HG12	1.97	0.45
1:A:345:LYS:HB2	1:A:348:GLU:HB3	1.99	0.44
1:B:295:ILE:HG12	1:B:314:PHE:CE1	2.52	0.44
1:A:88:ASP:OD1	1:A:111:ALA:HB3	2.17	0.44
1:A:48:ILE:HD11	1:A:76:ILE:HD12	1.98	0.44
1:A:322[B]:VAL:CG1	1:A:330:LEU:HD13	2.48	0.43
4:A:601:XAP:HN21	4:A:601:XAP:H21	1.25	0.43
1:B:422:ASN:ND2	1:B:422:ASN:N	2.59	0.42
1:B:16:GLU:H	1:B:16:GLU:HG3	1.62	0.41
1:A:414:TRP:O	1:A:418:GLN:HG2	2.21	0.41
1:B:76:ILE:HD11	1:B:284:PHE:CE1	2.56	0.41
1:B:341:GLN:NE2	1:B:342:LYS:NZ	2.68	0.41
1:A:27:LYS:HE3	1:A:406:TYR:CG	2.56	0.40
1:A:421:GLN:O	1:A:422:ASN:CB	2.69	0.40
1:B:110:TYR:HB3	1:B:131:MET:HG2	2.03	0.40
1:A:322[B]:VAL:HG11	1:A:330:LEU:HD13	2.02	0.40
1:A:93:THR:HA	1:A:96:GLN:HE21	1.87	0.40
1:A:356:TRP:HB3	1:B:169:LYS:HE3	2.03	0.40
1:A:143:ALA:HB2	1:A:189:ILE:HD11	2.03	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	419/471 (89%)	410 (98%)	9 (2%)	0	100	100
1	B	417/471 (88%)	407 (98%)	9 (2%)	1 (0%)	47	38
All	All	836/942 (89%)	817 (98%)	18 (2%)	1 (0%)	51	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	16	GLU

### 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	359/399 (90%)	348 (97%)	11 (3%)	40	32
1	B	358/399 (90%)	343 (96%)	15 (4%)	30	20
All	All	717/798 (90%)	691 (96%)	26 (4%)	36	26

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	110	TYR
1	A	188	ASN
1	A	231	LEU
1	A	254	VAL
1	A	297	LEU
1	A	311	GLU
1	A	339	LEU
1	A	340	LEU
1	A	341	GLN
1	A	345	LYS
1	A	369	ARG
1	B	7	GLU

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Mol	Chain	Res	Type
1	B	16	GLU
1	B	49	LEU
1	B	53	LEU
1	B	110	TYR
1	B	132	THR
1	B	186	GLU
1	B	254	VAL
1	B	340	LEU
1	B	369	ARG
1	B	398	ASN
1	B	402	ARG
1	B	404[A]	THR
1	B	404[B]	THR
1	B	422	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	ASN
1	A	96	GLN
1	A	125	ASN
1	A	341	GLN
1	A	385	ASN
1	A	421	GLN
1	B	96	GLN
1	B	99	GLN
1	B	125	ASN
1	B	210	GLN
1	B	312	GLN
1	B	341	GLN
1	B	385	ASN
1	B	422	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

9 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	ACT	B	803	-	3,3,3	0.76	0	3,3,3	1.29	0
2	ACT	A	802	-	3,3,3	0.75	0	3,3,3	1.28	0
3	PLP	A	600	-	16,16,16	1.14	1 (6%)	20,23,23	1.00	2 (10%)
2	ACT	A	801	-	3,3,3	0.66	0	3,3,3	1.51	0
4	XAP	A	601	-	3,5,5	0.29	0	3,4,4	0.52	0
5	N2P	B	700	-	6,6,6	0.25	0	5,5,5	0.30	0
4	XAP	B	601	-	3,5,5	0.33	0	3,4,4	0.70	0
5	N2P	A	700	-	6,6,6	0.20	0	5,5,5	0.69	0
3	PLP	B	600	-	16,16,16	1.11	2 (12%)	20,23,23	1.42	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
3	PLP	A	600	-	-	2/8/8/8	0/1/1/1
4	XAP	A	601	-	-	1/2/3/3	-
5	N2P	B	700	-	-	0/4/4/4	-
4	XAP	B	601	-	-	1/2/3/3	-
5	N2P	A	700	-	-	1/4/4/4	-
3	PLP	B	600	-	-	1/8/8/8	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	600	PLP	C2-N1	2.74	1.39	1.33
3	B	600	PLP	C2-N1	2.34	1.38	1.33
3	B	600	PLP	C6-N1	2.27	1.39	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	600	PLP	O4A-C4A-C4	-3.42	117.46	124.91
3	B	600	PLP	C5-C6-N1	-2.72	119.29	123.82
3	A	600	PLP	O4A-C4A-C4	-2.32	119.85	124.91
3	A	600	PLP	C5-C6-N1	-2.26	120.06	123.82
3	B	600	PLP	O2P-P-O4P	2.03	112.12	106.73

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	601	XAP	C1-C2-C3-O1
4	B	601	XAP	C1-C2-C3-O1
3	A	600	PLP	C3-C4-C4A-O4A
3	B	600	PLP	C3-C4-C4A-O4A
5	A	700	N2P	C1-C2-C3-C4
3	A	600	PLP	C5-C4-C4A-O4A

There are no ring outliers.

7 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	600	PLP	1	0
2	A	801	ACT	1	0
4	A	601	XAP	3	0
5	B	700	N2P	2	0
4	B	601	XAP	4	0
5	A	700	N2P	4	0
3	B	600	PLP	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.



## 5.8 Polymer linkage issues

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	419/471 (88%)	0.23	19 (4%) 33 36	15, 23, 38, 55	0
1	B	418/471 (88%)	0.24	23 (5%) 25 28	13, 22, 37, 53	0
All	All	837/942 (88%)	0.24	42 (5%) 28 32	13, 22, 38, 55	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	-5	LEU	6.9
1	A	422	ASN	6.3
1	B	16	GLU	5.4
1	A	311	GLU	5.2
1	B	311	GLU	5.0
1	B	422	ASN	5.0
1	A	18	PHE	4.9
1	B	297	LEU	4.7
1	A	297	LEU	4.6
1	B	7	GLU	4.3
1	A	36	ASP	4.3
1	B	33	SER	4.2
1	B	347	ASP	4.1
1	A	33	SER	4.0
1	B	-6	ASN	3.8
1	B	-8	GLY	3.8
1	A	16	GLU	3.6
1	A	15	ASP	3.4
1	A	17	GLY	3.3
1	B	-7	GLU	2.7
1	B	34	SER	2.7
1	A	-9	ALA	2.7
1	B	346	PRO	2.7
1	B	345	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	420	PHE	2.6
1	B	312	GLN	2.6
1	A	105	PRO	2.6
1	B	228	SER	2.6
1	A	349	LYS	2.5
1	B	18	PHE	2.4
1	A	280	VAL	2.4
1	A	7	GLU	2.4
1	A	419	GLN	2.4
1	B	36	ASP	2.3
1	B	32	SER	2.3
1	B	349	LYS	2.3
1	A	312	GLN	2.2
1	A	347	ASP	2.1
1	B	335	HIS	2.1
1	B	421	GLN	2.1
1	A	284	PHE	2.0
1	B	266	ASP	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
5	N2P	A	700	7/7	0.73	0.28	38,39,40,40	0
5	N2P	B	700	7/7	0.73	0.29	35,38,40,41	0
4	XAP	B	601	6/6	0.82	0.23	30,32,36,38	0
2	ACT	B	803	4/4	0.88	0.12	53,53,53,53	0
2	ACT	A	802	4/4	0.88	0.20	24,24,24,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	XAP	A	601	6/6	0.89	0.19	26,31,36,37	0
2	ACT	A	801	4/4	0.92	0.17	22,22,23,23	0
3	PLP	B	600	16/16	0.98	0.14	16,18,21,24	0
3	PLP	A	600	16/16	0.99	0.12	16,17,21,26	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.