



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 01:56 PM UTC

PDB ID : 4B7U / pdb_00004b7u
Title : PLASMODIUM FALCIPARUM L-LACTATE DEHYDROGENASE COM-
PLEXED WITH BICINE
Authors : Birkinshaw, R.W.; Brady, R.L.
Deposited on : 2012-08-22
Resolution : 1.88 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

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	:	4-5-2 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

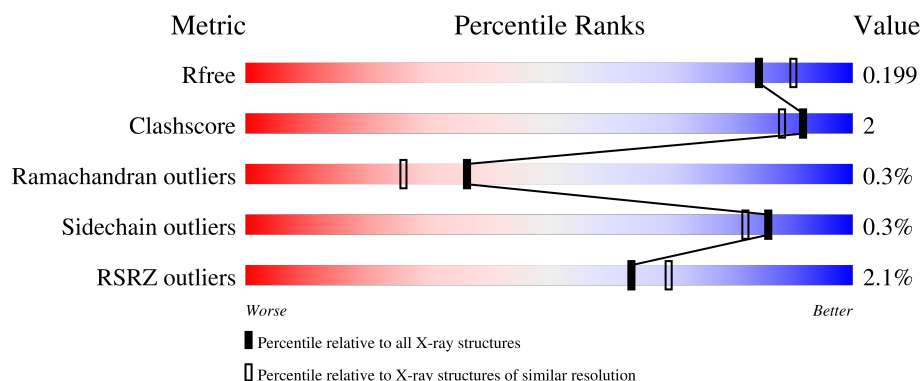
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.88 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	1220 (1.88-1.88)
Clashscore	190562	1234 (1.88-1.88)
Ramachandran outliers	187476	1222 (1.88-1.88)
Sidechain outliers	187428	1222 (1.88-1.88)
RSRZ outliers	180081	1220 (1.88-1.88)

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	322	2% 92% 6%
1	B	322	2% 89% 5% 5%
1	C	322	2% 89% 5% 5%
1	D	322	2% 89% 6% 5%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10481 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 L-LACTATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	316	Total	C	N	O	S	17	6	0
			2445	1557	418	457	13			
1	B	305	Total	C	N	O	S	9	4	0
			2340	1490	399	437	14			
1	C	305	Total	C	N	O	S	10	7	0
			2361	1505	404	439	13			
1	D	306	Total	C	N	O	S	10	8	0
			2379	1514	407	444	14			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	330	HIS	-	expression tag	UNP Q71T02
A	331	HIS	-	expression tag	UNP Q71T02
A	332	HIS	-	expression tag	UNP Q71T02
A	333	HIS	-	expression tag	UNP Q71T02
A	334	HIS	-	expression tag	UNP Q71T02
A	335	HIS	-	expression tag	UNP Q71T02
B	330	HIS	-	expression tag	UNP Q71T02
B	331	HIS	-	expression tag	UNP Q71T02
B	332	HIS	-	expression tag	UNP Q71T02
B	333	HIS	-	expression tag	UNP Q71T02
B	334	HIS	-	expression tag	UNP Q71T02
B	335	HIS	-	expression tag	UNP Q71T02
C	330	HIS	-	expression tag	UNP Q71T02
C	331	HIS	-	expression tag	UNP Q71T02
C	332	HIS	-	expression tag	UNP Q71T02
C	333	HIS	-	expression tag	UNP Q71T02
C	334	HIS	-	expression tag	UNP Q71T02
C	335	HIS	-	expression tag	UNP Q71T02
D	330	HIS	-	expression tag	UNP Q71T02
D	331	HIS	-	expression tag	UNP Q71T02
D	332	HIS	-	expression tag	UNP Q71T02

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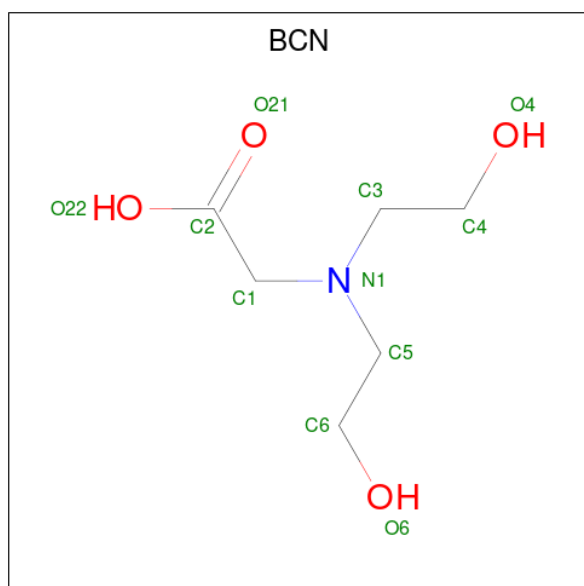
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Chain	Residue	Modelled	Actual	Comment	Reference
D	333	HIS	-	expression tag	UNP Q71T02
D	334	HIS	-	expression tag	UNP Q71T02
D	335	HIS	-	expression tag	UNP Q71T02

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0
2	B	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0
2	D	1	Total Ca 1 1	0	0

- Molecule 3 is BICINE (CCD ID: BCN) (formula: C₆H₁₃NO₄).



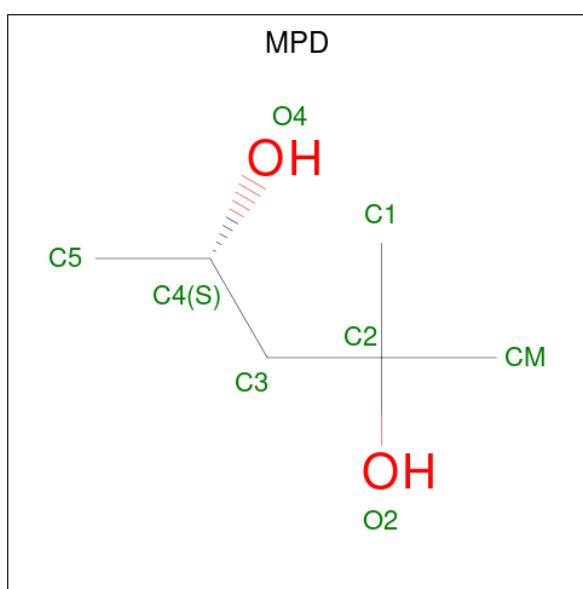
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 11 6 1 4	0	0
3	B	1	Total C N O 11 6 1 4	0	0
3	B	1	Total C N O 11 6 1 4	0	0
3	B	1	Total C N O 11 6 1 4	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total	C	N	O	0	0
			11	6	1	4		
3	D	1	Total	C	N	O	0	0
			11	6	1	4		
3	D	1	Total	C	N	O	0	0
			11	6	1	4		
3	D	1	Total	C	N	O	0	0
			11	6	1	4		

- Molecule 4 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			8	6	2		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	266	Total	O	0	0
			266	266		
6	B	211	Total	O	0	0
			211	211		
6	C	196	Total	O	0	0
			196	196		
6	D	171	Total	O	0	0
			171	171		

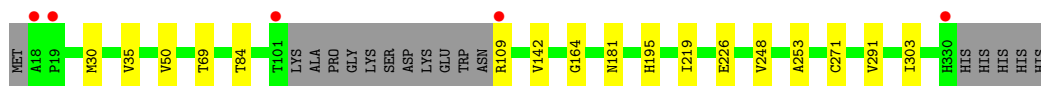
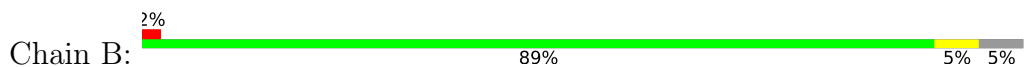
3 Residue-property plots [i](#)

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.

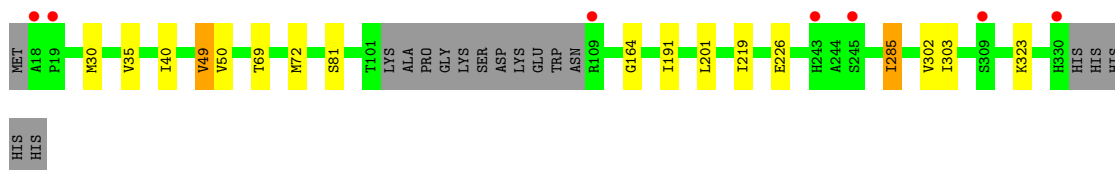
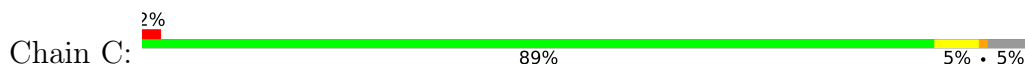
- Molecule 1: L-LACTATE DEHYDROGENASE



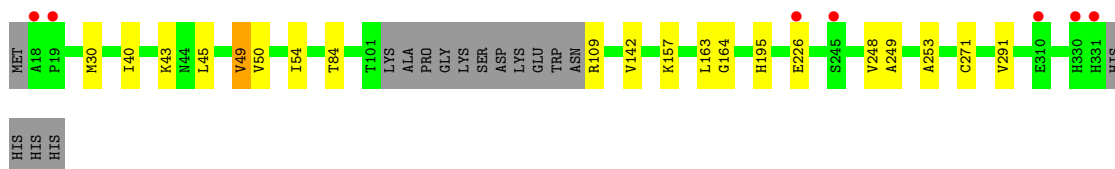
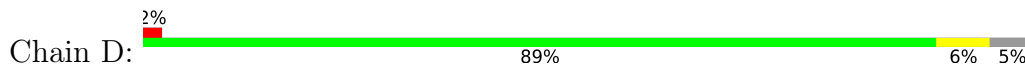
- Molecule 1: L-LACTATE DEHYDROGENASE



- Molecule 1: L-LACTATE DEHYDROGENASE



- Molecule 1: L-LACTATE DEHYDROGENASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	155.29Å 154.78Å 58.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.96 – 1.88 48.96 – 1.88	Depositor EDS
% Data completeness (in resolution range)	99.4 (48.96-1.88) 99.4 (48.96-1.88)	Depositor EDS
R_{merge}	0.01	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.17 (at 1.88Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.176 , 0.201 0.174 , 0.199	Depositor DCC
R_{free} test set	5793 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	20.5	Xtriage
Anisotropy	0.021	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for k,h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10481	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.40% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BCN, MPD, CA, EDO

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	0.77	8/2483 (0.3%)	0.75	3/3364 (0.1%)
1	B	0.74	7/2375 (0.3%)	0.70	0/3217
1	C	0.75	9/2398 (0.4%)	0.71	0/3250
1	D	0.74	6/2415 (0.2%)	0.74	2/3272 (0.1%)
All	All	0.75	30/9671 (0.3%)	0.72	5/13103 (0.0%)

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	109	ARG	CG-CD	-8.74	1.26	1.52
1	B	50	VAL	C-O	-7.57	1.16	1.24
1	A	303	ILE	C-O	-7.34	1.16	1.24
1	C	35	VAL	C-O	-7.16	1.15	1.24
1	C	49	VAL	C-O	-6.88	1.17	1.24

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	109	ARG	CB-CG-CD	8.88	131.74	111.30
1	D	109	ARG	CG-CD-NE	-8.45	93.41	112.00
1	A	310	GLU	CG-CD-OE1	-7.56	101.01	118.40
1	A	310	GLU	CG-CD-OE2	7.21	134.98	118.40
1	A	314	LYS	CG-CD-CE	6.83	127.01	111.30

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	2445	0	2516	15	0
1	B	2340	0	2411	7	0
1	C	2361	0	2436	10	0
1	D	2379	0	2445	12	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	11	0	11	0	0
3	B	33	0	35	0	0
3	C	11	0	11	0	0
3	D	33	0	35	0	0
4	A	8	0	14	5	0
5	A	8	0	12	0	0
5	D	4	0	6	0	0
6	A	266	0	0	1	0
6	B	211	0	0	0	0
6	C	196	0	0	0	0
6	D	171	0	0	0	0
All	All	10481	0	9932	32	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 2.

The worst 5 of 32 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:103(E):SER:C	1:A:105(A):ASP:N	2.01	1.19
1:A:30:MET:HE1	1:B:30:MET:HE1	1.35	1.08
1:C:30:MET:HE1	1:D:30:MET:CE	2.04	0.88
1:C:30:MET:HE1	1:D:30:MET:HE1	1.54	0.88
1:C:30:MET:CE	1:D:30:MET:HE1	2.27	0.64

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	318/322 (99%)	310 (98%)	7 (2%)	1 (0%)	36	26
1	B	305/322 (95%)	298 (98%)	6 (2%)	1 (0%)	36	26
1	C	308/322 (96%)	299 (97%)	8 (3%)	1 (0%)	36	26
1	D	310/322 (96%)	305 (98%)	4 (1%)	1 (0%)	36	26
All	All	1241/1288 (96%)	1212 (98%)	25 (2%)	4 (0%)	36	26

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	164	GLY
1	D	164	GLY
1	A	164	GLY
1	C	164	GLY

5.3.2 Protein sidechains

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	269/269 (100%)	268 (100%)	1 (0%)	84	79
1	B	258/269 (96%)	257 (100%)	1 (0%)	84	79
1	C	260/269 (97%)	260 (100%)	0	100	100
1	D	263/269 (98%)	262 (100%)	1 (0%)	84	79
All	All	1050/1076 (98%)	1047 (100%)	3 (0%)	86	82

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	245	SER
1	B	181	ASN
1	D	54	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	140	ASN
1	C	152	HIS
1	D	83	ASN
1	C	330	HIS
1	B	181	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 4 are monoatomic - leaving 12 for Mogul analysis.

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	BCN	B	1332	-	10,10,10	0.77	0	11,11,11	0.77	0
5	EDO	A	1334	-	3,3,3	0.40	0	2,2,2	0.35	0
5	EDO	A	1333	-	3,3,3	0.45	0	2,2,2	0.33	0
3	BCN	B	1333	-	10,10,10	0.71	0	11,11,11	0.85	0
3	BCN	D	1334	-	10,10,10	0.70	0	11,11,11	0.85	0
4	MPD	A	1332	-	7,7,7	0.30	0	9,10,10	0.43	0
3	BCN	C	1331	2	10,10,10	0.68	0	11,11,11	0.96	0
3	BCN	B	1331	2	10,10,10	0.73	0	11,11,11	0.95	1 (9%)
3	BCN	D	1333	-	10,10,10	0.81	0	11,11,11	0.85	0
3	BCN	A	1331	2	10,10,10	0.75	0	11,11,11	0.84	0
5	EDO	D	1335	-	3,3,3	0.41	0	2,2,2	0.25	0
3	BCN	D	1332	2	10,10,10	0.81	0	11,11,11	0.70	0

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	BCN	B	1332	-	-	2/10/10/10	-
5	EDO	A	1334	-	-	1/1/1/1	-
5	EDO	A	1333	-	-	1/1/1/1	-
3	BCN	B	1333	-	-	3/10/10/10	-
3	BCN	D	1334	-	-	1/10/10/10	-
4	MPD	A	1332	-	-	5/5/5/5	-
3	BCN	C	1331	2	-	2/10/10/10	-
3	BCN	B	1331	2	-	2/10/10/10	-
3	BCN	D	1333	-	-	5/10/10/10	-
3	BCN	A	1331	2	-	2/10/10/10	-
5	EDO	D	1335	-	-	1/1/1/1	-
3	BCN	D	1332	2	-	0/10/10/10	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1331	BCN	O22-C2-C1	2.04	121.42	113.38

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	1333	BCN	C4-C3-N1-C1
4	A	1332	MPD	C2-C3-C4-O4
4	A	1332	MPD	C2-C3-C4-C5
3	B	1333	BCN	N1-C3-C4-O4
3	D	1333	BCN	N1-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1332	MPD	5	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	103(E):SER	C	105(A):ASP	N	2.01

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	316/322 (98%)	-0.15	7 (2%) 62 68	8, 18, 27, 44	13 (4%)
1	B	305/322 (94%)	-0.12	5 (1%) 70 75	8, 19, 29, 38	7 (2%)
1	C	305/322 (94%)	-0.06	7 (2%) 61 67	8, 19, 28, 40	10 (3%)
1	D	306/322 (95%)	-0.12	7 (2%) 61 67	8, 19, 28, 38	12 (3%)
All	All	1232/1288 (95%)	-0.11	26 (2%) 63 70	8, 19, 28, 44	42 (3%)

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	330	HIS	8.8
1	B	330	HIS	8.8
1	A	330	HIS	8.1
1	D	330	HIS	7.5
1	C	18	ALA	7.3

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, 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($\text{\AA}^2$)	Q<0.9
4	MPD	A	1332	8/8	0.64	0.26	50,52,53,53	0
3	BCN	D	1333	11/11	0.68	0.25	62,64,65,65	0
3	BCN	B	1333	11/11	0.76	0.17	41,48,50,50	0
5	EDO	A	1333	4/4	0.78	0.24	54,54,54,54	0
2	CA	D	401	1/1	0.82	0.32	78,78,78,78	0
3	BCN	D	1334	11/11	0.82	0.13	36,42,46,46	0
3	BCN	D	1332	11/11	0.83	0.14	32,36,37,39	0
3	BCN	C	1331	11/11	0.86	0.13	38,39,40,41	0
3	BCN	B	1332	11/11	0.87	0.13	31,35,38,40	0
5	EDO	D	1335	4/4	0.88	0.14	43,43,43,43	0
5	EDO	A	1334	4/4	0.89	0.15	49,50,50,50	0
2	CA	B	401	1/1	0.89	0.29	66,66,66,66	0
3	BCN	B	1331	11/11	0.90	0.11	33,35,36,38	0
3	BCN	A	1331	11/11	0.91	0.10	23,25,26,27	0
2	CA	C	401	1/1	0.93	0.24	61,61,61,61	0
2	CA	A	401	1/1	0.97	0.20	48,48,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.