



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 11:55 PM GMT

PDB ID : 5LDH  
Title : STRUCTURE OF THE ACTIVE TERNARY COMPLEX OF PIG HEART  
LACTATE DEHYDROGENASE WITH S-LAC-NAD AT 2.7 ANGSTROMS  
RESOLUTION  
Authors : Grau, U.M.; Rossmann, M.G.  
Deposited on : 1980-10-29  
Resolution : 2.70 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  
<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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

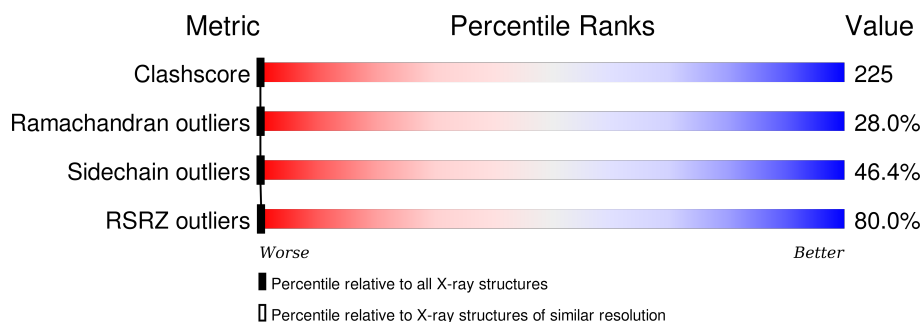
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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.

Mol	Chain	Length	Quality of chain
1	A	334	
1	B	334	

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
2	LNC	A	332	-	-	X	-
2	LNC	B	332	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CIT	A	333	-	-	X	-
3	CIT	B	333	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5248 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.

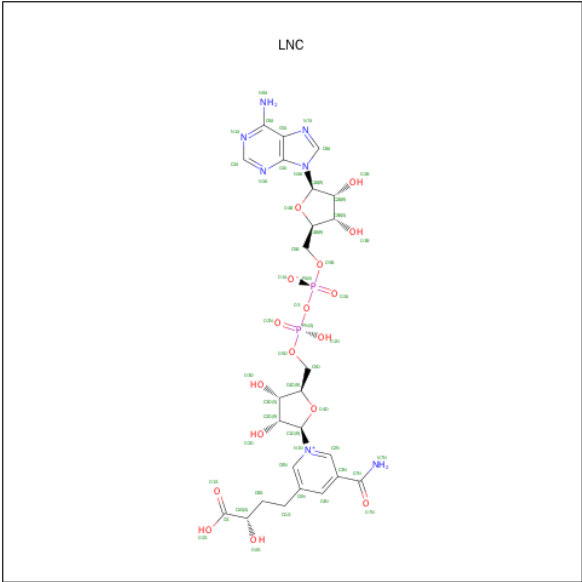
- Molecule 1 is a protein called LACTATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	334	Total	C	N	O	S	0	0	0
			2560	1626	435	485	14			
1	B	334	Total	C	N	O	S	0	0	0
			2560	1626	435	485	14			

There are 18 discrepancies between the modelled and reference sequences:

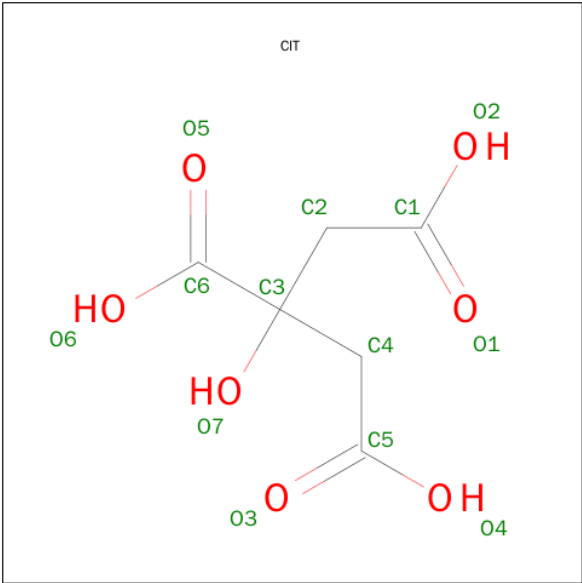
Chain	Residue	Modelled	Actual	Comment	Reference
A	13	GLN	GLU	CONFLICT	UNP P00336
A	14	GLN	GLU	CONFLICT	UNP P00336
A	20	ASP	ASN	CONFLICT	UNP P00336
A	81	ASN	ASP	CONFLICT	UNP P00336
A	132B	ASN	ASP	CONFLICT	UNP P00336
A	149	ALA	THR	CONFLICT	UNP P00336
A	177	GLY	ALA	CONFLICT	UNP P00336
A	209C	VAL	SER	CONFLICT	UNP P00336
A	211	GLN	GLU	CONFLICT	UNP P00336
B	13	GLN	GLU	CONFLICT	UNP P00336
B	14	GLN	GLU	CONFLICT	UNP P00336
B	20	ASP	ASN	CONFLICT	UNP P00336
B	81	ASN	ASP	CONFLICT	UNP P00336
B	132B	ASN	ASP	CONFLICT	UNP P00336
B	149	ALA	THR	CONFLICT	UNP P00336
B	177	GLY	ALA	CONFLICT	UNP P00336
B	209C	VAL	SER	CONFLICT	UNP P00336
B	211	GLN	GLU	CONFLICT	UNP P00336

- Molecule 2 is (3S)-5-(3-CARBOXY-3-HYDROXYPROPYL) NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: LNC) (formula: C<sub>25</sub>H<sub>33</sub>N<sub>7</sub>O<sub>17</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0
			51	25	7	17	2	
2	B	1	Total	C	N	O	P	0
			51	25	7	17	2	

- Molecule 3 is CITRIC ACID (three-letter code: CIT) (formula: C<sub>6</sub>H<sub>8</sub>O<sub>7</sub>).

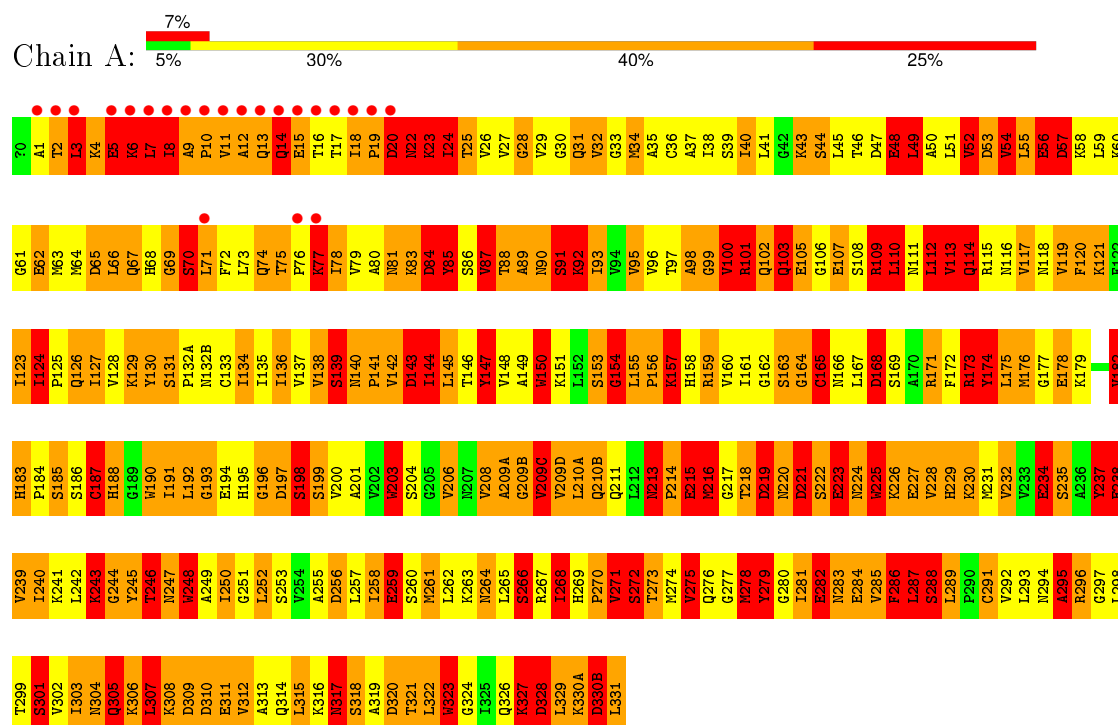


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		
3	B	1	Total	C	O	0	0
			13	6	7		

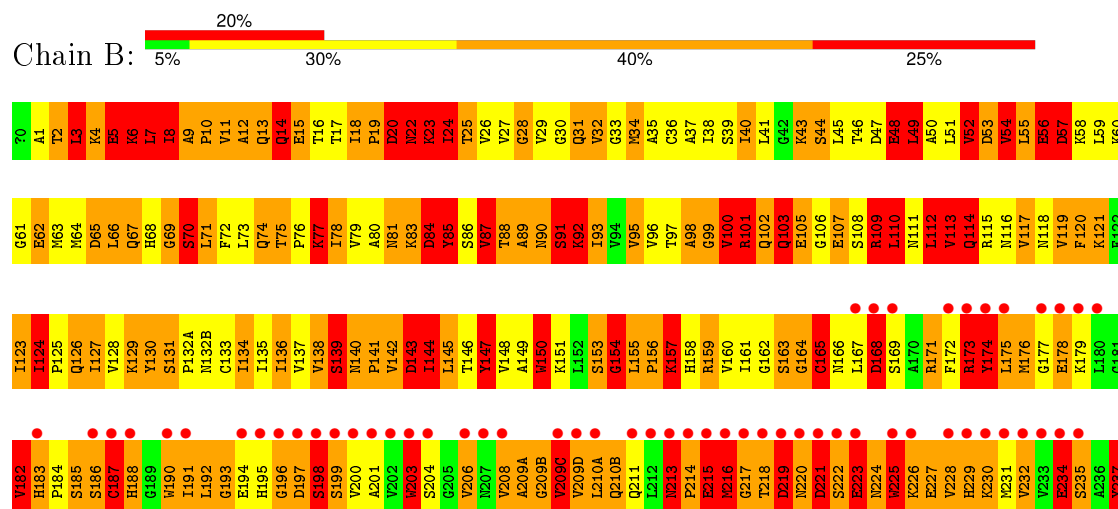
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: LACTATE DEHYDROGENASE



#### • Molecule 1: LACTATE DEHYDROGENASE



L298	E238
L299	V239
S301	I240
V302	I241
I303	I242
N304	K243
Q305	Q244
K306	Y245
L307	T246
K308	I247
D309	K248
D310	A249
E311	I250
V312	G251
A313	L252
Q314	S253
L315	V254
K316	A255
N317	D256
S318	L257
A319	I258
D320	E259
T321	S260
L322	I261
N323	L262
G324	K263
I325	I264
Q326	L265
K327	S266
D328	R267
L329	T268
K330A	H269
D330B	F270
L331	V271
	S272
	T273
	I274
	V275
	Q276
	G277
	V278
	V279
	G280
	I281
	E282
	I283
	E284
	Y285
	F286
	L287
	S288
	L289
	P290
	G291
	V292
	L293
	I294
	A295
	R296
	G297

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	133.60Å 133.60Å 113.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 2.70 43.73 – 2.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-2.70) 69.4 (43.73-2.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	unknown	Depositor
R, $R_{free}$	0.196 , (Not available) 0.498 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	44.7	Xtriage
Anisotropy	0.037	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , -40.6	EDS
Estimated twinning fraction	0.077 for -h,-k,l	Xtriage
L-test for twinning <sup>1</sup>	$\langle  L  \rangle = 0.38$ , $\langle L^2 \rangle = 0.20$	Xtriage
Outliers	0 of 22588 reflections	Xtriage
$F_o, F_c$ correlation	0.41	EDS
Total number of atoms	5248	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	0.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: ACE, LNC, CIT

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	1.11	24/2599 (0.9%)	1.88	150/3525 (4.3%)
1	B	1.11	24/2599 (0.9%)	1.88	150/3525 (4.3%)
All	All	1.11	48/5198 (0.9%)	1.88	300/7050 (4.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	3
All	All	0	6

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	150	TRP	NE1-CE2	-7.38	1.27	1.37
1	B	150	TRP	NE1-CE2	-7.38	1.27	1.37
1	A	203	TRP	NE1-CE2	-7.37	1.27	1.37
1	B	203	TRP	NE1-CE2	-7.37	1.27	1.37
1	A	190	TRP	NE1-CE2	-7.35	1.27	1.37

The worst 5 of 300 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	20	ASP	N-CA-C	-10.06	83.85	111.00
1	B	20	ASP	N-CA-C	-10.06	83.85	111.00
1	A	304	ASN	N-CA-C	9.96	137.88	111.00
1	B	304	ASN	N-CA-C	9.96	137.88	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	209(C)	VAL	N-CA-C	-9.69	84.83	111.00

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	109	ARG	Sidechain
1	A	171	ARG	Sidechain
1	A	173	ARG	Sidechain
1	B	109	ARG	Sidechain
1	B	171	ARG	Sidechain

## 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	2560	0	2628	1248	1
1	B	2560	0	2628	1225	2
2	A	51	0	31	50	0
2	B	51	0	31	48	0
3	A	13	0	4	15	0
3	B	13	0	4	15	0
All	All	5248	0	5326	2375	3

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 225.

The worst 5 of 2375 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:150:TRP:CB	1:B:160:VAL:HG21	1.22	1.65
3:B:333:CIT:C4	3:B:333:CIT:C3	1.75	1.62
1:A:150:TRP:CB	1:A:160:VAL:HG21	1.22	1.62
1:A:150:TRP:HB2	1:A:160:VAL:CG2	1.21	1.62
1:B:150:TRP:HB2	1:B:160:VAL:CG2	1.21	1.62

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:8:ILE:CD1	1:B:107:GLU:OE2[3_565]	2.02	0.18
1:B:183:HIS:CB	1:B:266:SER:O[6_555]	2.14	0.06
1:A:183:HIS:CB	1:A:266:SER:O[6_555]	2.14	0.06

## 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	332/334 (99%)	167 (50%)	72 (22%)	93 (28%)	0	0
1	B	332/334 (99%)	167 (50%)	72 (22%)	93 (28%)	0	0
All	All	664/668 (99%)	334 (50%)	144 (22%)	186 (28%)	0	0

5 of 186 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	3	LEU
1	A	4	LYS
1	A	6	LYS
1	A	9	ALA

### 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	289/289 (100%)	155 (54%)	134 (46%)	0	0
1	B	289/289 (100%)	155 (54%)	134 (46%)	0	0
All	All	578/578 (100%)	310 (54%)	268 (46%)	0	0

5 of 268 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	312	VAL
1	B	56	GLU
1	B	288	SER
1	A	318	SER
1	B	7	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	229	HIS
1	A	317	ASN
1	B	220	ASN
1	A	224	ASN
1	B	114	GLN

### 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 ⓘ

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	LNC	A	332	-	41,55,55	0.88	2 (4%)	54,83,83	2.24	8 (14%)
3	CIT	A	333	1	3,12,12	10.72	2 (66%)	3,17,17	5.01	2 (66%)
2	LNC	B	332	-	41,55,55	0.88	2 (4%)	54,83,83	2.24	8 (14%)
3	CIT	B	333	1	3,12,12	10.72	2 (66%)	3,17,17	5.01	2 (66%)

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	LNC	A	332	-	-	0/27/71/71	0/5/5/5
3	CIT	A	333	1	-	0/6/16/16	0/0/0/0
2	LNC	B	332	-	-	0/27/71/71	0/5/5/5
3	CIT	B	333	1	-	0/6/16/16	0/0/0/0

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	333	CIT	O7-C3	-12.74	1.22	1.43
3	A	333	CIT	O7-C3	-12.74	1.22	1.43
2	A	332	LNC	C4N-C3N	-3.29	1.34	1.39
2	B	332	LNC	C4N-C3N	-3.29	1.34	1.39
2	A	332	LNC	C8A-N7A	-2.34	1.30	1.34

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	332	LNC	PA-O3-PN	-11.17	101.37	132.73
2	B	332	LNC	PA-O3-PN	-11.17	101.37	132.73
3	B	333	CIT	C3-C2-C1	-7.00	103.77	114.96
3	A	333	CIT	C3-C2-C1	-7.00	103.77	114.96
3	B	333	CIT	C3-C4-C5	-4.78	107.31	114.96

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 128 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	332	LNC	50	0
3	A	333	CIT	15	0
2	B	332	LNC	48	0
3	B	333	CIT	15	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	23/334 (6%)	4.73	22 (95%) 0 0	0, 0, 0, 0	0
1	B	87/334 (26%)	4.63	66 (75%) 0 0	0, 0, 0, 0	0
All	All	110/668 (16%)	4.65	88 (80%) 0 0	0, 0, 0, 0	0

The worst 5 of 88 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	167	LEU	53.6
1	B	195	HIS	23.7
1	B	325	ILE	18.5
1	A	77	LYS	12.2
1	B	218	THR	11.5

### 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	CIT	B	333	13/13	-	-	-	0,0,0,0	0
2	LNC	A	332	51/51	-	-	-	0,0,0,0	0
2	LNC	B	332	51/51	-	-	-	0,0,0,0	0
3	CIT	A	333	13/13	-	-	-	0,0,0,0	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.