



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 10:55 AM UTC

PDB ID : 5LDH / pdb_00005ldh
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

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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

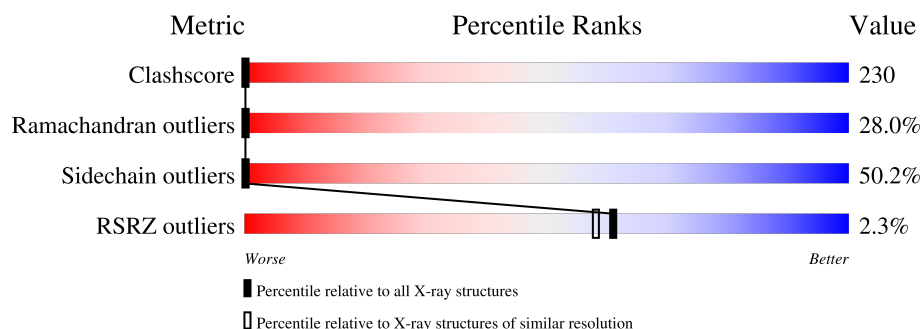
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (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 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	334	3% 26% 38% 33%
1	B	334	% 26% 38% 33%

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	-
3	CIT	A	333	-	X	X	-
3	CIT	B	333	-	X	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.

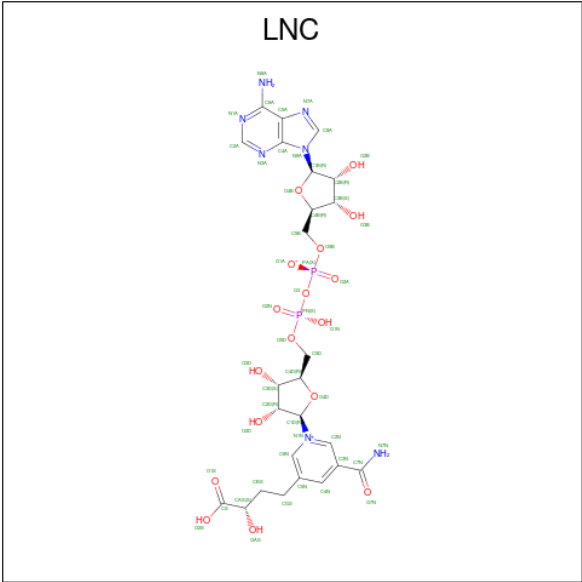
- Molecule 1 is a protein called LACTATE DEHYDROGENASE.

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:

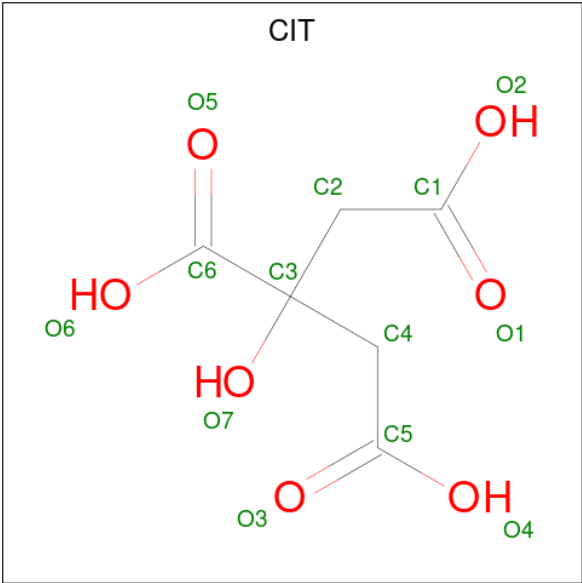
Chain	Residue	Modelled	Actual	Comment	Reference
A	13	GLN	GLU	conflict	UNP P00336
A	14	GLN	GLU	conflict	UNP P00336
A	20	ASP	ASN	conflict	UNP P00336
A	81	ASN	ASP	conflict	UNP P00336
A	132B	ASN	ASP	conflict	UNP P00336
A	149	ALA	THR	conflict	UNP P00336
A	177	GLY	ALA	conflict	UNP P00336
A	209C	VAL	SER	conflict	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 (CCD ID: LNC) (formula: C₂₅H₃₃N₇O₁₇P₂).



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

- Molecule 3 is CITRIC ACID (CCD ID: CIT) (formula: C₆H₈O₇).

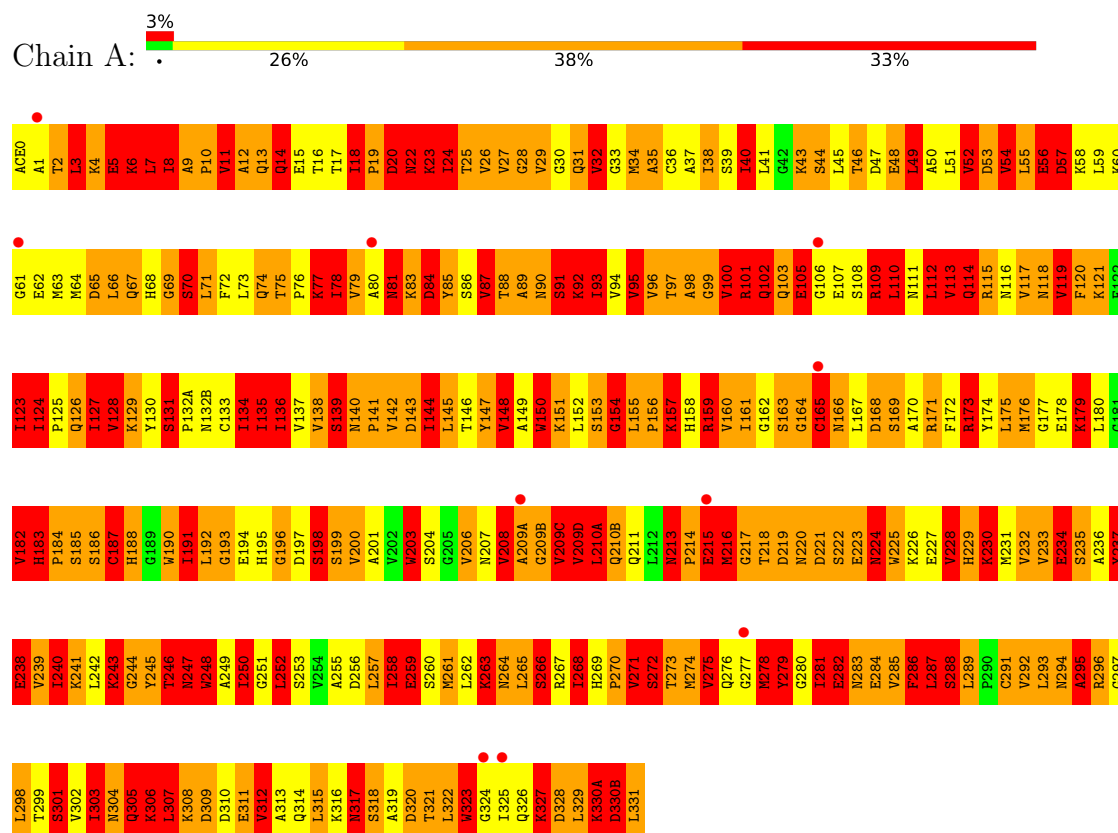


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		
3	B	1	Total	C	O	0	0
			13	6	7		

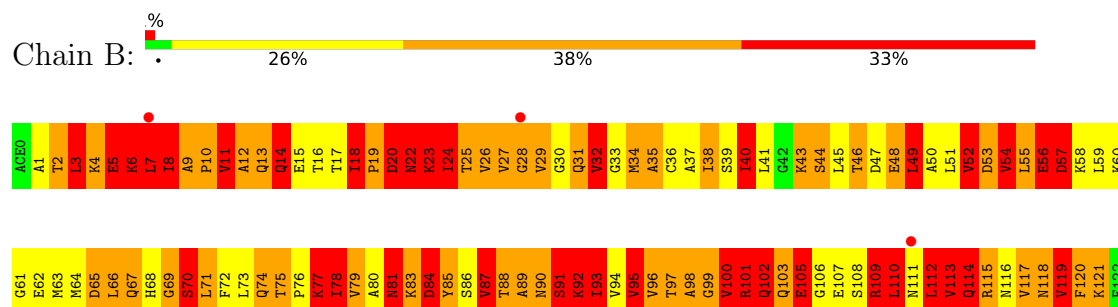
3 Residue-property plots

These plots are drawn for all protein, RNA, 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: LACTATE DEHYDROGENASE



• Molecule 1: LACTATE DEHYDROGENASE



L298	E288	V182	I123
T299	V239	H183	I124
SS01	I240	P184	P125
V302	K241	S185	Q126
I303	L242	S186	I127
N304	K243	G187	V128
Q305	G244	H188	K129
K306	Y245	G189	Y130
L307	T246	W190	S131
K308	N247	I191	P132A
D309	V248	L192	N132B
D310	A249	G193	C133
E311	I250	E194	I134
V312	G251	H195	I135
A313	L252	G196	I136
Q314	S253	D197	V137
L315	V254	S198	V138
K316	A255	S199	S139
N317	D256	V200	N140
S318	L257	A201	P141
A319	I258	V202	V142
D320	E259	W203	D143
T321	S260	S204	I144
L322	M261	G205	L145
V323	L262	V206	T146
G324	K263	N207	Y147
I325	N264	V208	V148
Q326	L265	A209A	A149
K327	S266	G209B	W150
D328	R267	V209C	K151
L329	I268	V209D	L152
K330A	H269	L210A	S153
D330B	P270	Q210B	G154
L331	V271	Q211	L155
	S272	L212	P156
	T273	N213	K157
	M274	P214	H158
	V275	E215	R159
	Q276	N216	V160
	G277	G217	I161
	M278	T218	G162
	Y279	D219	S163
	G280	N220	G164
	L281	D221	G165
	E282	S222	N166
	N283	E223	L167
	E284	N224	D168
	V285	W225	S169
	F286	K226	A170
	L287	E227	R171
	S288	V228	F172
	L289	H229	R173
	F290	K230	Y174
	G291	N231	L175
	V292	V232	M176
	L293	V233	G177
	N294	E234	E178
	A295	S235	K179
	R296	A236	L180
	G297	Y237	G181

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	133.60Å 133.60Å 113.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 2.70 115.70 – 2.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-2.70) 69.4 (115.70-2.70)	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) (Not available) , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	44.7	Xtriage
Anisotropy	0.037	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 60.5	EDS
L-test for twinning ¹	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	0.077 for -h,-k,l	Xtriage
F_o, F_c correlation	0.67	EDS
Total number of atoms	5248	wwPDB-VP
Average B, all atoms (Å ²)	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.*

¹Theoretical 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: LNC, ACE, 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	1.07	6/2599 (0.2%)	2.42	191/3525 (5.4%)
1	B	1.07	6/2599 (0.2%)	2.42	191/3525 (5.4%)
All	All	1.07	12/5198 (0.2%)	2.42	382/7050 (5.4%)

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 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	150	TRP	NE1-CE2	-8.70	1.27	1.37
1	B	225	TRP	NE1-CE2	-8.64	1.27	1.37
1	B	323	TRP	NE1-CE2	-8.61	1.27	1.37
1	A	150	TRP	NE1-CE2	-8.60	1.27	1.37
1	B	203	TRP	NE1-CE2	-8.59	1.27	1.37

The worst 5 of 382 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	246	THR	N-CA-C	-23.64	85.61	111.14
1	B	246	THR	N-CA-C	-23.59	85.66	111.14
1	B	185	SER	N-CA-C	23.00	136.35	111.28
1	A	185	SER	N-CA-C	22.96	136.31	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	47	ASP	N-CA-C	-20.60	88.54	113.88

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	1258	32
1	B	2560	0	2628	1275	32
2	A	51	0	31	50	0
2	B	51	0	31	51	0
3	A	13	0	4	16	0
3	B	13	0	4	17	0
All	All	5248	0	5326	2431	33

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 230.

The worst 5 of 2431 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance ($\text{\AA}$)	Clash overlap ($\text{\AA}$)
3:B:333:CIT:C3	3:B:333:CIT:C4	1.75	1.64
1:A:150:TRP:HB2	1:A:160:VAL:CG2	1.21	1.60
3:A:333:CIT:C4	3:A:333:CIT:C3	1.75	1.59
1:B:150:TRP:HB2	1:B:160:VAL:CG2	1.21	1.57
1:A:150:TRP:CB	1:A:160:VAL:HG21	1.22	1.55

The worst 5 of 33 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:A:0:ACE:CH3	1:B:84:ASP:CG[5_545]	0.98	1.22
1:A:0:ACE:CH3	1:B:84:ASP:OD1[5_545]	1.05	1.15
1:A:0:ACE:C	1:B:84:ASP:OD1[5_545]	1.11	1.09
1:A:308:LYS:CD	1:B:56:GLU:CD[2_454]	1.13	1.07
1:A:308:LYS:CD	1:B:56:GLU:OE1[2_454]	1.25	0.95

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	332/334 (99%)	167 (50%)	72 (22%)	93 (28%)	0	0
1	B	332/334 (99%)	168 (51%)	71 (21%)	93 (28%)	0	0
All	All	664/668 (99%)	335 (50%)	143 (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 [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	289/289 (100%)	144 (50%)	145 (50%)	0	0
1	B	289/289 (100%)	144 (50%)	145 (50%)	0	0
All	All	578/578 (100%)	288 (50%)	290 (50%)	0	0

5 of 290 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	215	GLU
1	B	329	LEU
1	B	230	LYS
1	B	273	THR
1	A	235	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	111	ASN
1	B	220	ASN
1	B	294	ASN
1	B	224	ASN
1	B	211	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 oligosaccharides 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	$\# Z > 2$
3	CIT	A	333	-	12,12,12	6.52	10 (83%)	17,17,17	2.46	7 (41%)
2	LNC	B	332	-	53,55,55	2.03	3 (5%)	72,83,83	1.28	8 (11%)
2	LNC	A	332	-	53,55,55	2.03	3 (5%)	72,83,83	1.29	8 (11%)
3	CIT	B	333	-	12,12,12	6.52	10 (83%)	17,17,17	2.46	7 (41%)

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	CIT	A	333	-	-	9/16/16/16	-
2	LNC	B	332	-	-	17/39/71/71	0/5/5/5
2	LNC	A	332	-	-	17/39/71/71	0/5/5/5
3	CIT	B	333	-	-	9/16/16/16	-

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	333	CIT	C4-C3	17.18	1.75	1.54
3	B	333	CIT	C4-C3	17.13	1.75	1.54
2	B	332	LNC	C2N-N1N	-13.53	1.20	1.35
2	A	332	LNC	C2N-N1N	-13.51	1.20	1.35
3	B	333	CIT	O7-C3	-11.02	1.22	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	333	CIT	O7-C3-C4	4.38	119.38	109.38
3	B	333	CIT	O7-C3-C4	4.38	119.36	109.38
3	A	333	CIT	O6-C6-C3	4.28	121.36	113.14
3	B	333	CIT	O6-C6-C3	4.28	121.35	113.14
2	A	332	LNC	C6N-N1N-C2N	-4.24	118.27	121.88

There are no chirality outliers.

5 of 52 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	332	LNC	CAS-CBS-CGS-C5N
2	A	332	LNC	OAS-CAS-CBS-CGS
2	A	332	LNC	CS-CAS-CBS-CGS
2	A	332	LNC	O4D-C1D-N1N-C6N
2	A	332	LNC	C2D-C1D-N1N-C6N

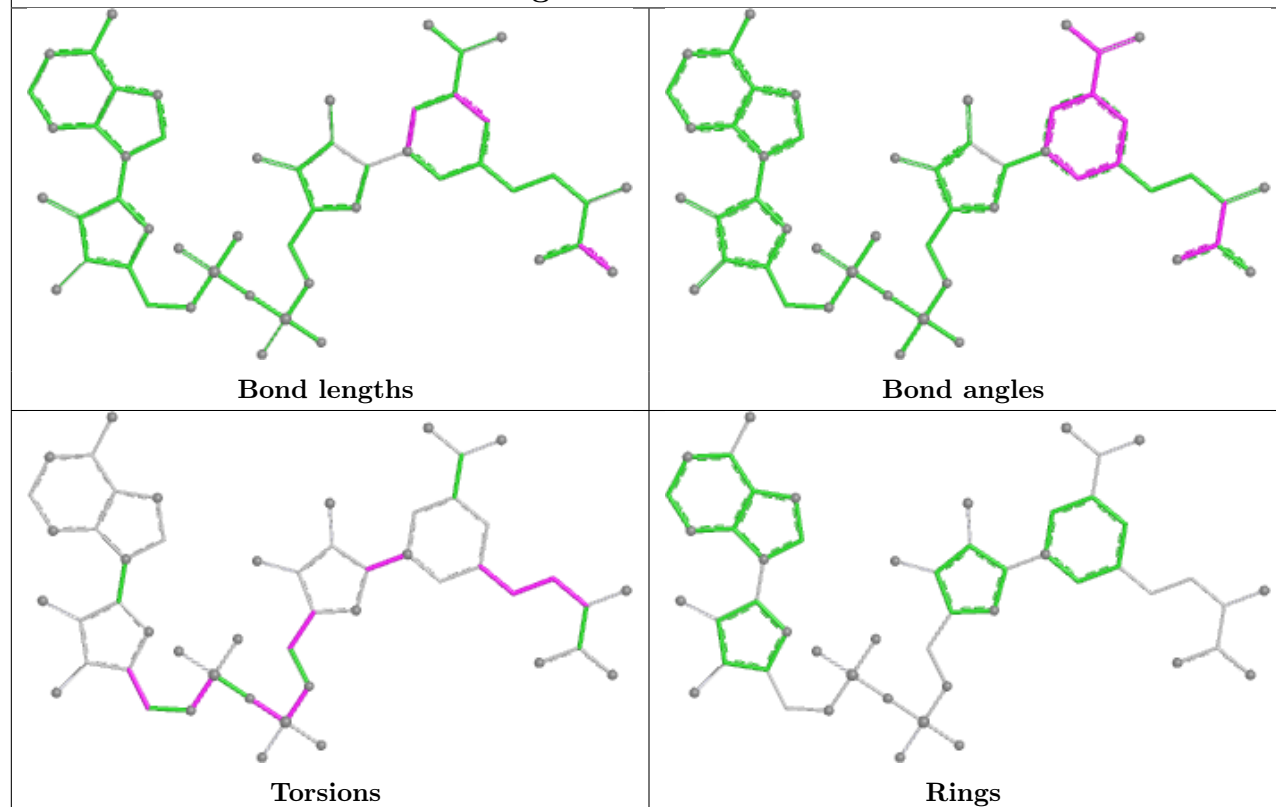
There are no ring outliers.

4 monomers are involved in 134 short contacts:

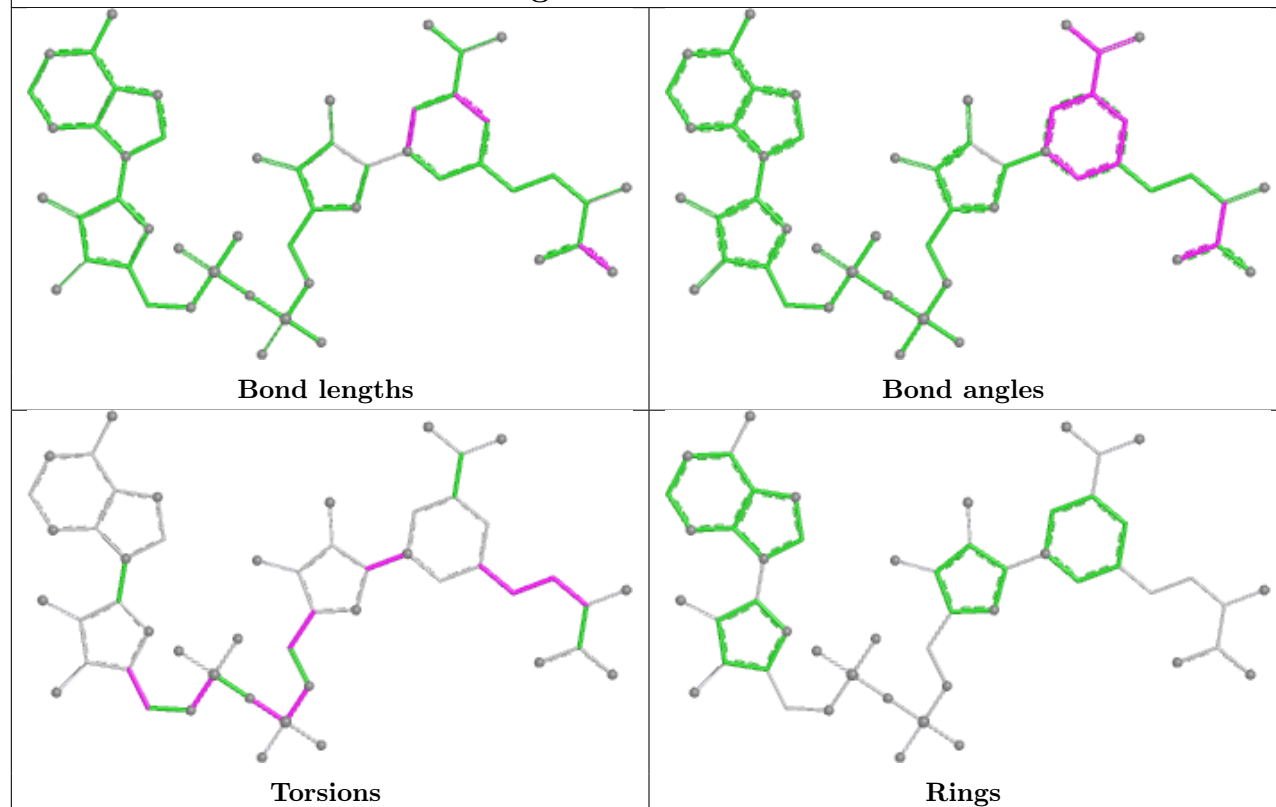
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	333	CIT	16	0
2	B	332	LNC	51	0
2	A	332	LNC	50	0
3	B	333	CIT	17	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand LNC B 332



Ligand LNC A 332



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, 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	333/334 (99%)	-0.10	10 (3%) 52 49	0, 0, 0, 0	0
1	B	333/334 (99%)	-0.11	5 (1%) 72 70	0, 0, 0, 0	0
All	All	666/668 (99%)	-0.11	15 (2%) 61 58	0, 0, 0, 0	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	165	CYS	4.0
1	A	325	ILE	3.6
1	B	111	ASN	3.5
1	A	165	CYS	3.4
1	A	215	GLU	3.3

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](#)

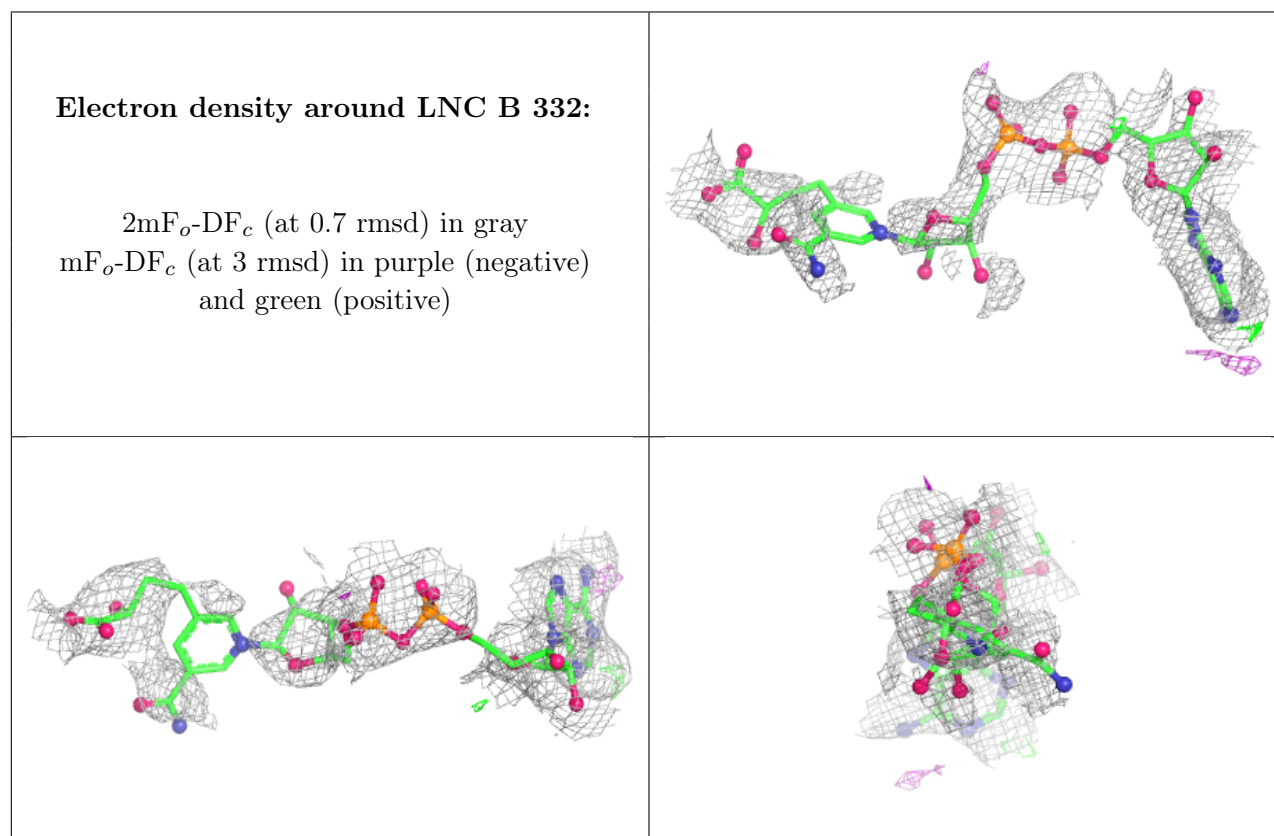
There are no oligosaccharides in this entry.

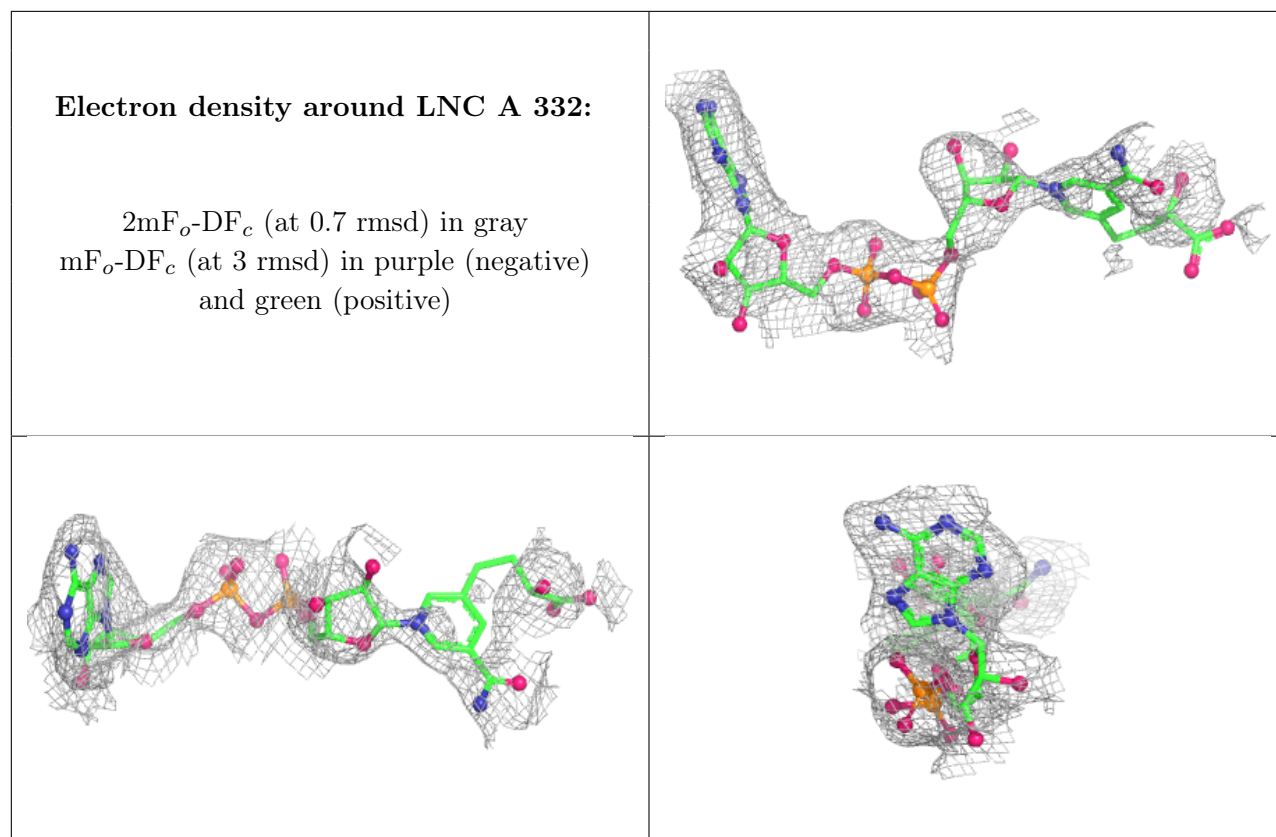
6.4 Ligands [i](#)

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
3	CIT	A	333	13/13	0.96	0.13	0,0,0,0	0
2	LNC	B	332	51/51	0.98	0.09	0,0,0,0	0
2	LNC	A	332	51/51	0.98	0.07	0,0,0,0	0
3	CIT	B	333	13/13	0.99	0.06	0,0,0,0	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers [i](#)

There are no such residues in this entry.