



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 03:15 am GMT

PDB ID : 1I32
Title : LEISHMANIA MEXICANA GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE IN COMPLEX WITH INHIBITORS
Authors : Suresh, S.; Bressi, J.C.; Kennedy, K.J.; Verlinde, C.L.M.J.; Gelb, M.H.; Hol, W.G.J.
Deposited on : 2001-02-12
Resolution : 2.60 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

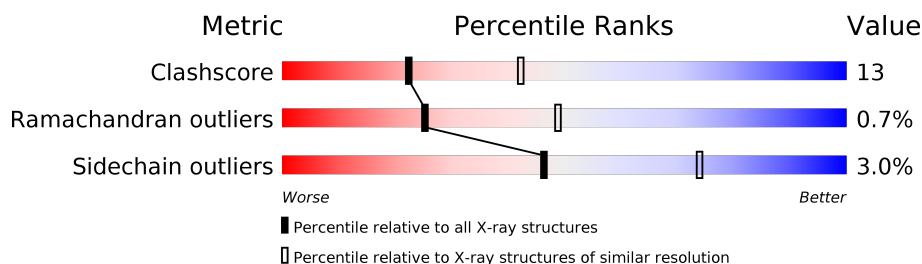
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)

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 ≥ 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	360	
1	B	360	
1	C	360	
1	D	360	
1	E	360	
1	F	360	

2 Entry composition [i](#)

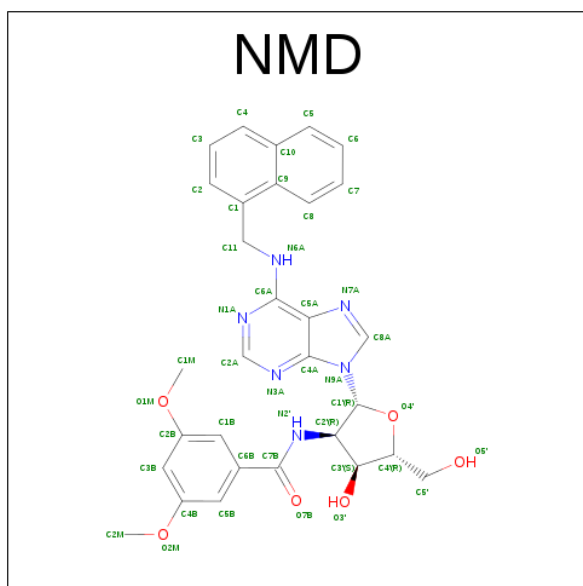
There are 3 unique types of molecules in this entry. The entry contains 17199 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	358	Total	C	N	O	S	0	0	0
			2715	1712	474	516	13			
1	B	358	Total	C	N	O	S	0	0	0
			2715	1712	474	516	13			
1	C	358	Total	C	N	O	S	0	0	0
			2715	1712	474	516	13			
1	D	358	Total	C	N	O	S	0	0	0
			2715	1712	474	516	13			
1	E	358	Total	C	N	O	S	0	0	0
			2715	1712	474	516	13			
1	F	358	Total	C	N	O	S	0	0	0
			2715	1712	474	516	13			

- Molecule 2 is N-NAPHTHALEN-1-YLMETHYL-2'-[3,5-DIMETHOXYBENZAMIDO]-2'-DEOXY-ADENOSINE (three-letter code: NMD) (formula: C₃₀H₃₀N₆O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			42	30	6	6		
2	B	1	Total	C	N	O	0	0
			42	30	6	6		
2	C	1	Total	C	N	O	0	0
			42	30	6	6		
2	D	1	Total	C	N	O	0	0
			42	30	6	6		
2	E	1	Total	C	N	O	0	0
			42	30	6	6		
2	F	1	Total	C	N	O	0	0
			42	30	6	6		

- Molecule 3 is water.

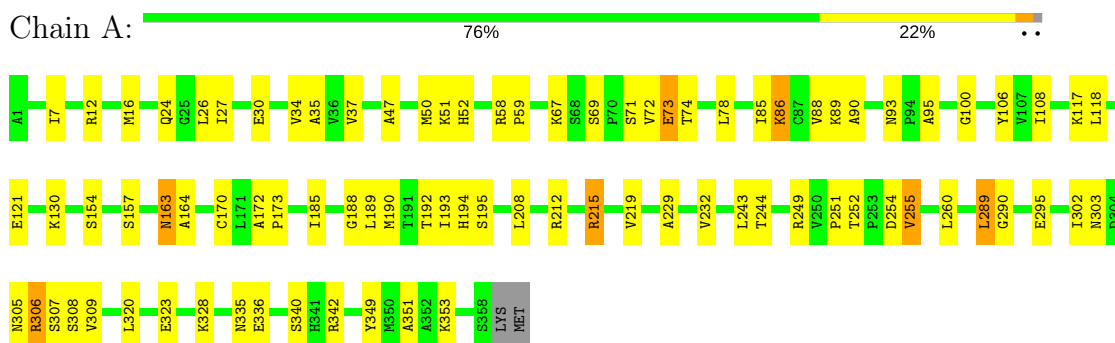
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	86	Total	O	0	0
			86	86		
3	B	122	Total	O	0	0
			122	122		
3	C	157	Total	O	0	0
			157	157		
3	D	102	Total	O	0	0
			102	102		
3	E	125	Total	O	0	0
			125	125		
3	F	65	Total	O	0	0
			65	65		

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 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.

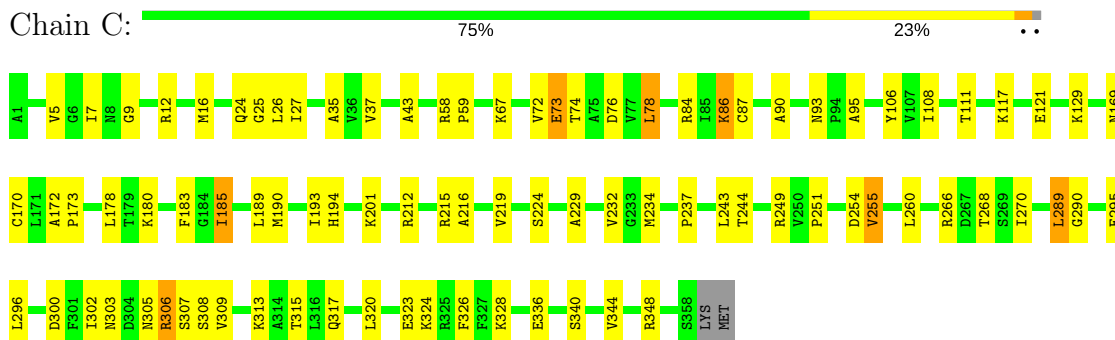
• Molecule 1: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE



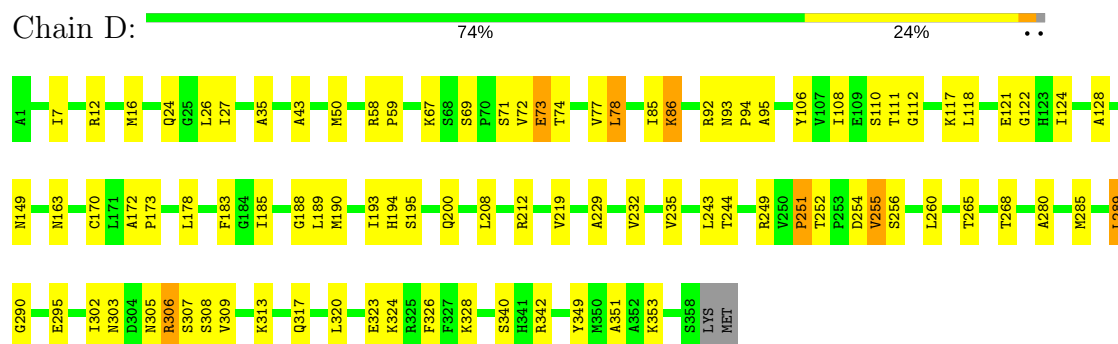
• Molecule 1: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE



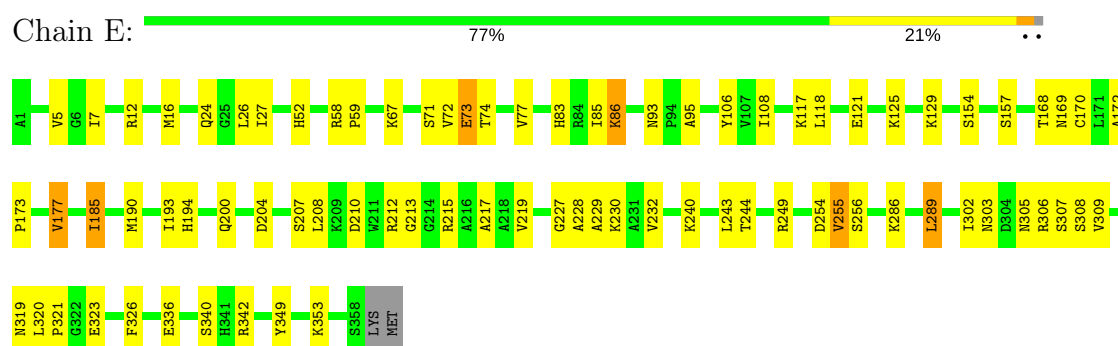
• Molecule 1: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE



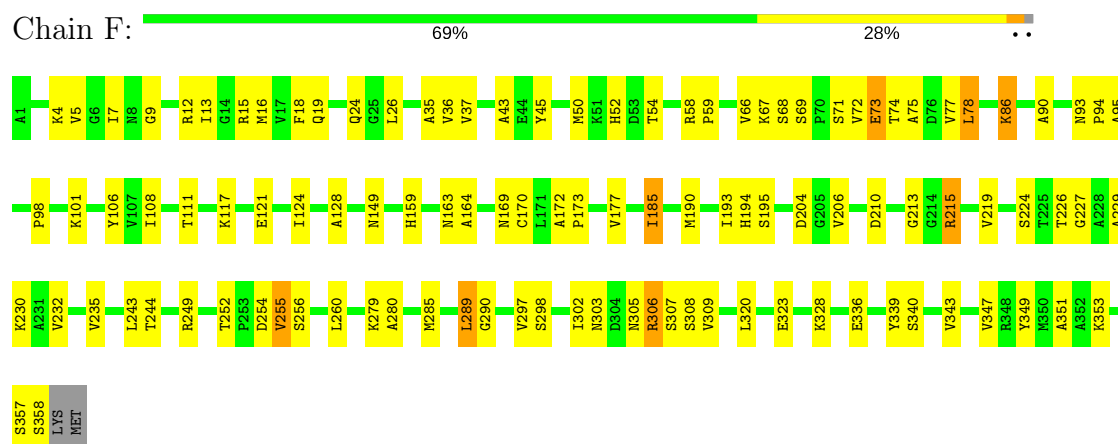
• Molecule 1: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE



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4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	80.39Å 394.11Å 70.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.60	Depositor
% Data completeness (in resolution range)	(Not available) (15.00-2.60)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.205 , 0.256	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	17199	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

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: NMD

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	0.35	0/2767	0.56	0/3752
1	B	0.39	0/2767	0.57	0/3752
1	C	0.40	0/2767	0.57	0/3752
1	D	0.36	0/2767	0.57	0/3752
1	E	0.38	0/2767	0.58	0/3752
1	F	0.36	0/2767	0.55	0/3752
All	All	0.37	0/16602	0.57	0/22512

There are no bond length outliers.

There are no bond angle outliers.

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	2715	0	2736	69	0
1	B	2715	0	2736	89	0
1	C	2715	0	2736	67	0
1	D	2715	0	2736	74	0
1	E	2715	0	2736	70	0
1	F	2715	0	2736	90	0
2	A	42	0	30	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	42	0	30	0	0
2	C	42	0	30	2	0
2	D	42	0	30	4	0
2	E	42	0	30	0	0
2	F	42	0	30	0	0
3	A	86	0	0	5	0
3	B	122	0	0	20	0
3	C	157	0	0	12	0
3	D	102	0	0	10	0
3	E	125	0	0	11	0
3	F	65	0	0	14	0
All	All	17199	0	16596	433	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 13.

The worst 5 of 433 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:F:73:GLU:HG2	1:F:74:THR:HG23	1.47	0.97
1:B:73:GLU:HG2	1:B:74:THR:HG23	1.52	0.91
1:A:328:LYS:HB2	1:D:189:LEU:HD23	1.54	0.89
1:D:229:ALA:O	1:D:232:VAL:HG12	1.73	0.88
1:C:229:ALA:O	1:C:232:VAL:HG12	1.72	0.88

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	356/360 (99%)	323 (91%)	31 (9%)	2 (1%)	28 53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	356/360 (99%)	325 (91%)	27 (8%)	4 (1%)	17	35
1	C	356/360 (99%)	329 (92%)	25 (7%)	2 (1%)	28	53
1	D	356/360 (99%)	326 (92%)	28 (8%)	2 (1%)	28	53
1	E	356/360 (99%)	325 (91%)	29 (8%)	2 (1%)	28	53
1	F	356/360 (99%)	323 (91%)	31 (9%)	2 (1%)	28	53
All	All	2136/2160 (99%)	1951 (91%)	171 (8%)	14 (1%)	25	49

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	255	VAL
1	B	255	VAL
1	D	255	VAL
1	E	185	ILE
1	F	255	VAL

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	294/296 (99%)	284 (97%)	10 (3%)	42	69
1	B	294/296 (99%)	286 (97%)	8 (3%)	50	77
1	C	294/296 (99%)	285 (97%)	9 (3%)	45	73
1	D	294/296 (99%)	286 (97%)	8 (3%)	50	77
1	E	294/296 (99%)	285 (97%)	9 (3%)	45	73
1	F	294/296 (99%)	285 (97%)	9 (3%)	45	73
All	All	1764/1776 (99%)	1711 (97%)	53 (3%)	46	74

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	289	LEU

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Mol	Chain	Res	Type
1	D	86	LYS
1	F	215	ARG
1	C	305	ASN
1	C	309	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	305	ASN
1	D	163	ASN
1	F	282	GLN
1	C	341	HIS
1	D	49	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

6 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	NMD	A	361	-	42,47,47	1.51	11 (26%)	50,67,67	1.29	4 (8%)
2	NMD	B	362	-	42,47,47	1.49	11 (26%)	50,67,67	1.31	4 (8%)
2	NMD	C	363	-	42,47,47	1.49	10 (23%)	50,67,67	1.33	5 (10%)
2	NMD	D	364	-	42,47,47	1.49	10 (23%)	50,67,67	1.23	4 (8%)
2	NMD	E	365	-	42,47,47	1.51	11 (26%)	50,67,67	1.27	4 (8%)
2	NMD	F	366	-	42,47,47	1.51	11 (26%)	50,67,67	1.25	4 (8%)

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	NMD	A	361	-	-	0/19/39/39	0/6/6/6
2	NMD	B	362	-	-	0/19/39/39	0/6/6/6
2	NMD	C	363	-	-	0/19/39/39	0/6/6/6
2	NMD	D	364	-	-	0/19/39/39	0/6/6/6
2	NMD	E	365	-	-	0/19/39/39	0/6/6/6
2	NMD	F	366	-	-	0/19/39/39	0/6/6/6

The worst 5 of 64 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	365	NMD	C6A-N1A	2.02	1.36	1.34
2	D	364	NMD	C6A-N1A	2.02	1.36	1.34
2	A	361	NMD	C5B-C4B	2.07	1.42	1.38
2	A	361	NMD	C6A-N1A	2.08	1.37	1.34
2	F	366	NMD	C6A-N1A	2.13	1.37	1.34

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	362	NMD	N6A-C6A-N1A	-2.08	115.98	118.97
2	C	363	NMD	C2B-C3B-C4B	2.05	121.68	118.56
2	D	364	NMD	C2'-N2'-C7B	2.29	125.86	122.11
2	F	366	NMD	C2'-N2'-C7B	2.33	125.94	122.11
2	F	366	NMD	C11-N6A-C6A	2.55	126.62	123.24

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	363	NMD	2	0
2	D	364	NMD	4	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.