



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 10:05 am GMT

PDB ID : 1N47
Title : Isolectin B4 from Vicia villosa in complex with the Tn antigen
Authors : Babino, A.; Tello, D.; Rojas, A.; Bay, S.; Osinaga, E.; Alzari, P.M.
Deposited on : 2002-10-30
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

<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

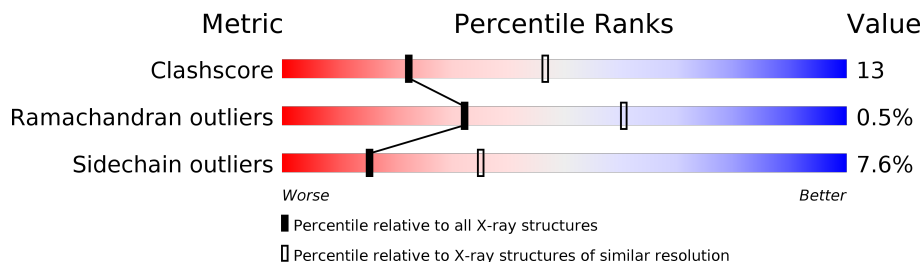
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (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 ≥ 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	233	
1	B	233	
1	C	233	
1	D	233	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7293 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 Isolectin B4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	233	Total	C	N	O	S	0	0	0
			1748	1113	286	347	2			
1	B	233	Total	C	N	O	S	0	0	0
			1748	1113	286	347	2			
1	C	233	Total	C	N	O	S	0	0	0
			1748	1113	286	347	2			
1	D	233	Total	C	N	O	S	0	0	0
			1748	1113	286	347	2			

- Molecule 2 is a polymer of unknown type called SUGAR (FUC-NAG-NAG).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	3	Total	C	N	O	0	0
			38	22	2	14		
2	B	3	Total	C	N	O	0	0
			38	22	2	14		
2	C	3	Total	C	N	O	0	0
			38	22	2	14		
2	D	3	Total	C	N	O	0	0
			38	22	2	14		

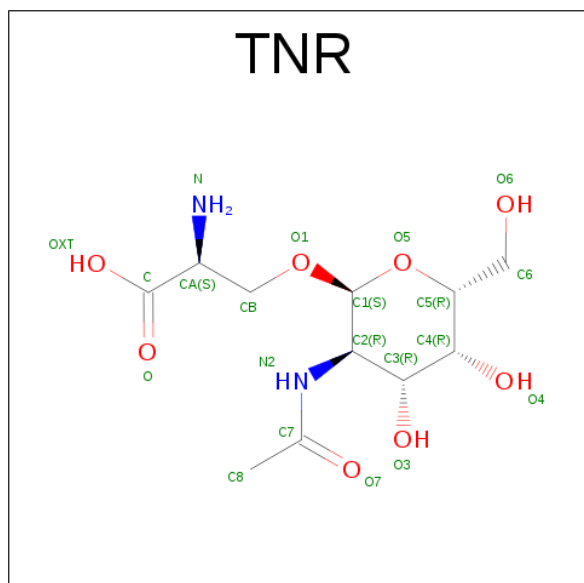
- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mn	0	0
			1	1		
4	A	1	Total	Mn	0	0
			1	1		
4	D	1	Total	Mn	0	0
			1	1		
4	C	1	Total	Mn	0	0
			1	1		

- Molecule 5 is O-(2-ACETAMIDO-2-DEOXY-ALPHA-D-GALACTOPYRANOSYL)-L-SERINE (three-letter code: TNR) (formula: C₁₁H₂₀N₂O₈).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			21	11	2	8		
5	B	1	Total	C	N	O	0	0
			21	11	2	8		
5	C	1	Total	C	N	O	0	0
			21	11	2	8		
5	D	1	Total	C	N	O	0	0
			21	11	2	8		

- Molecule 6 is water.

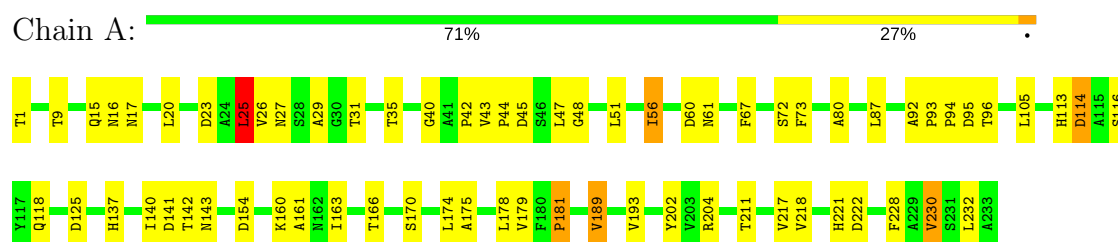
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	9	Total 9	O 9	0	0
6	B	15	Total 15	O 15	0	0
6	C	17	Total 17	O 17	0	0
6	D	16	Total 16	O 16	0	0

3 Residue-property plots

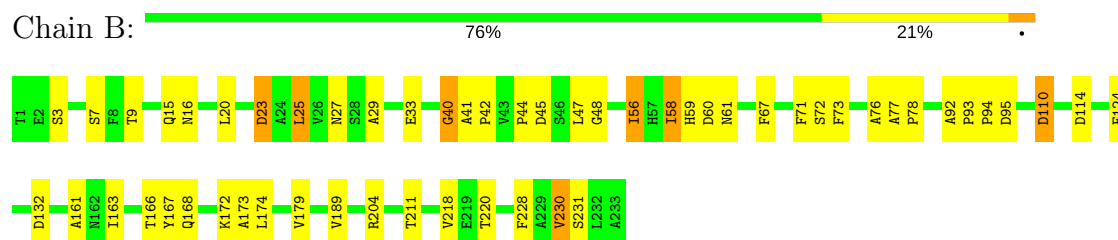
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

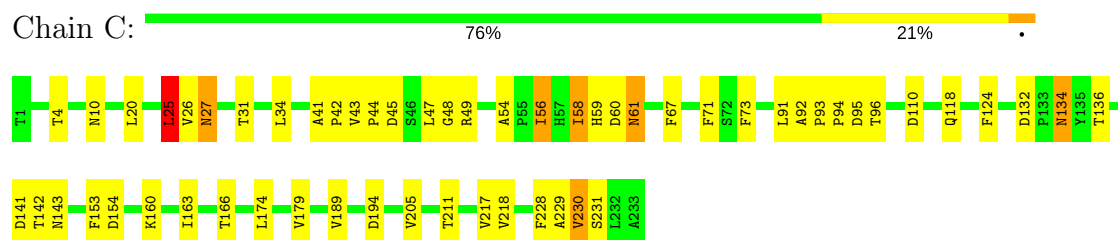
• Molecule 1: Isolectin B4



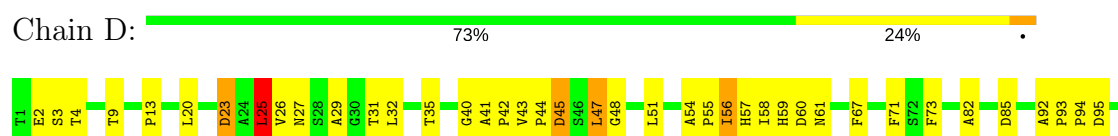
• Molecule 1: Isolectin B4



• Molecule 1: Isolectin B4



• Molecule 1: Isolectin B4



R101	D114	Q118	F124	Y135	T136	D154	T163	T166	K172	A173	L174	V179	V189	R192	L199	Y202	T211	V217	V218	H221	D222	I223	F228	A229	V230	A233
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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 43	Depositor
Cell constants a, b, c, α , β , γ	85.51Å 85.51Å 153.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70	Depositor
% Data completeness (in resolution range)	99.9 (20.00-2.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
Refinement program	REFMAC 5	Depositor
R, R_{free}	0.188 , 0.238	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7293	wwPDB-VP
Average B, all atoms (Å ²)	33.0	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: FUC, CA, MN, NAG, TNR

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	0.62	0/1791	0.93	8/2455 (0.3%)
1	B	0.65	0/1791	0.93	6/2455 (0.2%)
1	C	0.67	0/1791	0.94	9/2455 (0.4%)
1	D	0.66	0/1791	0.94	7/2455 (0.3%)
All	All	0.65	0/7164	0.93	30/9820 (0.3%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	114	ASP	CB-CG-OD2	7.78	125.30	118.30
1	C	110	ASP	CB-CG-OD2	7.74	125.27	118.30
1	D	85	ASP	CB-CG-OD2	7.26	124.83	118.30
1	B	95	ASP	CB-CG-OD2	6.51	124.16	118.30
1	C	25	LEU	CA-CB-CG	6.50	130.26	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	1748	0	1679	47	0
1	B	1748	0	1679	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1748	0	1679	47	0
1	D	1748	0	1679	52	0
2	A	38	0	34	0	0
2	B	38	0	34	0	0
2	C	38	0	34	0	0
2	D	38	0	34	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	21	0	19	0	0
5	B	21	0	19	0	0
5	C	21	0	19	0	0
5	D	21	0	19	0	0
6	A	9	0	0	0	0
6	B	15	0	0	0	0
6	C	17	0	0	0	0
6	D	16	0	0	1	0
All	All	7293	0	6928	185	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 185 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:D:73:PHE:HE2	1:D:163:ILE:HD11	1.07	1.17
1:C:73:PHE:HE2	1:C:163:ILE:HD11	1.11	1.13
1:A:179:VAL:HG12	1:A:181:PRO:HD3	1.37	1.05
1:D:73:PHE:CE2	1:D:163:ILE:HD11	1.92	1.03
1:D:67:PHE:HB3	1:D:230:VAL:HG12	1.36	1.03

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	231/233 (99%)	208 (90%)	22 (10%)	1 (0%)	38	66
1	B	231/233 (99%)	214 (93%)	15 (6%)	2 (1%)	20	46
1	C	231/233 (99%)	215 (93%)	15 (6%)	1 (0%)	38	66
1	D	231/233 (99%)	217 (94%)	13 (6%)	1 (0%)	38	66
All	All	924/932 (99%)	854 (92%)	65 (7%)	5 (0%)	32	60

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	80	ALA
1	C	61	ASN
1	B	15	GLN
1	B	40	GLY
1	D	40	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	184/184 (100%)	169 (92%)	15 (8%)	13	30
1	B	184/184 (100%)	171 (93%)	13 (7%)	17	39
1	C	184/184 (100%)	170 (92%)	14 (8%)	15	35
1	D	184/184 (100%)	170 (92%)	14 (8%)	15	35
All	All	736/736 (100%)	680 (92%)	56 (8%)	15	35

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	189	VAL
1	C	47	LEU
1	D	174	LEU
1	B	230	VAL
1	C	10	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	221	HIS
1	C	16	ASN
1	D	16	ASN
1	B	59	HIS
1	D	10	ASN

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 ⓘ

12 carbohydrates 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	NAG	A	301	1,2	14,14,15	0.69	0	15,19,21	1.19	2 (13%)
2	FUC	A	302	2	9,10,11	0.64	0	13,14,16	1.74	3 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	A	303	2	14,14,15	0.42	0	15,19,21	1.08	1 (6%)
2	NAG	B	301	1,2	14,14,15	0.66	0	15,19,21	1.54	2 (13%)
2	FUC	B	302	2	9,10,11	0.85	0	13,14,16	1.15	1 (7%)
2	NAG	B	303	2	14,14,15	0.56	0	15,19,21	1.22	1 (6%)
2	NAG	C	301	1,2	14,14,15	0.67	0	15,19,21	1.84	2 (13%)
2	FUC	C	302	2	9,10,11	0.65	0	13,14,16	1.29	3 (23%)
2	NAG	C	303	2	14,14,15	0.63	0	15,19,21	1.55	3 (20%)
2	NAG	D	301	1,2	14,14,15	0.73	0	15,19,21	1.55	3 (20%)
2	FUC	D	302	2	9,10,11	0.68	0	13,14,16	1.83	5 (38%)
2	NAG	D	303	2	14,14,15	0.50	0	15,19,21	1.49	3 (20%)

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	NAG	A	301	1,2	-	0/6/23/26	0/1/1/1
2	FUC	A	302	2	-	0/0/17/20	0/1/1/1
2	NAG	A	303	2	-	0/6/23/26	0/1/1/1
2	NAG	B	301	1,2	-	0/6/23/26	0/1/1/1
2	FUC	B	302	2	-	0/0/17/20	0/1/1/1
2	NAG	B	303	2	-	0/6/23/26	0/1/1/1
2	NAG	C	301	1,2	-	0/6/23/26	0/1/1/1
2	FUC	C	302	2	-	0/0/17/20	0/1/1/1
2	NAG	C	303	2	-	0/6/23/26	0/1/1/1
2	NAG	D	301	1,2	-	0/6/23/26	0/1/1/1
2	FUC	D	302	2	-	0/0/17/20	0/1/1/1
2	NAG	D	303	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	NAG	O5-C1-C2	-4.46	105.27	111.47
2	C	303	NAG	C2-N2-C7	-4.38	116.55	122.94
2	A	302	FUC	C6-C5-C4	-3.75	106.39	113.07
2	A	301	NAG	C2-N2-C7	-3.52	117.81	122.94
2	C	301	NAG	C2-N2-C7	-3.46	117.89	122.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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$
5	TNR	A	1401	-	17,21,21	0.67	0	21,29,29	1.25	2 (9%)
5	TNR	B	2401	-	17,21,21	0.58	0	21,29,29	1.81	4 (19%)
5	TNR	C	3401	-	17,21,21	0.65	1 (5%)	21,29,29	1.20	3 (14%)
5	TNR	D	4401	-	17,21,21	0.68	1 (5%)	21,29,29	1.22	2 (9%)

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
5	TNR	A	1401	-	-	0/11/35/35	0/1/1/1
5	TNR	B	2401	-	-	0/11/35/35	0/1/1/1
5	TNR	C	3401	-	-	0/11/35/35	0/1/1/1
5	TNR	D	4401	-	-	0/11/35/35	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	4401	TNR	O1-C1	2.12	1.43	1.40
5	C	3401	TNR	O1-C1	2.16	1.43	1.40

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	2401	TNR	C1-C2-N2	-4.87	102.78	111.03
5	D	4401	TNR	C1-C2-N2	-3.26	105.51	111.03
5	A	1401	TNR	C1-C2-N2	-2.71	106.44	111.03
5	C	3401	TNR	C6-C5-C4	-2.17	107.92	113.00
5	B	2401	TNR	C6-C5-C4	-2.10	108.08	113.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.