



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 06:35 am GMT

PDB ID : 2DT5
Title : Crystal Structure of TTHA1657 (AT-rich DNA-binding protein) from *Thermus thermophilus* HB8
Authors : Nakamura, A.; Sosa, A.; Komori, H.; Kita, A.; Miki, K.
Deposited on : 2006-07-11
Resolution : 2.16 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

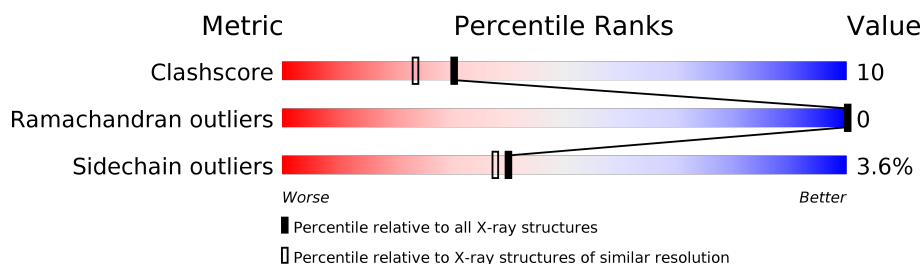
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.16 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	1278 (2.16-2.16)
Ramachandran outliers	110173	1256 (2.16-2.16)
Sidechain outliers	110143	1255 (2.16-2.16)

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	211	
1	B	211	

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	SO4	A	406	-	-	X	-
5	GOL	A	601	-	X	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 3667 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 AT-rich DNA-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	210	Total	C	N	O	S	0	0	0
			1621	1041	287	289	4			
1	B	211	Total	C	N	O	S	0	0	0
			1629	1046	288	290	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	36	GLY	GLU	ENGINEERED	UNP Q5SHS3
B	36	GLY	GLU	ENGINEERED	UNP Q5SHS3

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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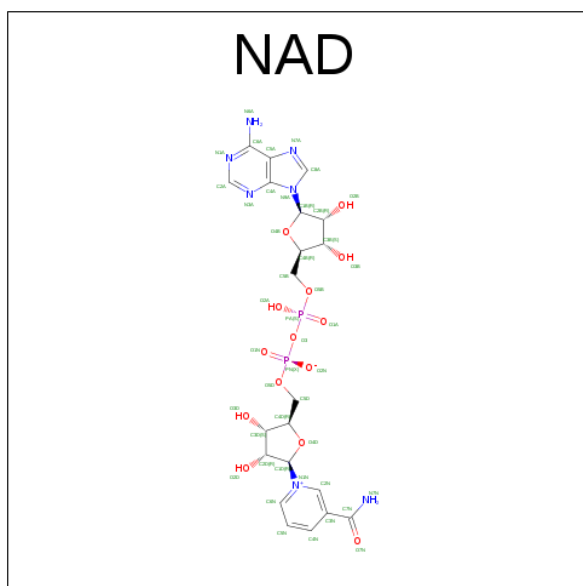
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 44	C 21	N 7	O 14	P 2	0	0
4	B	1	Total 44	C 21	N 7	O 14	P 2	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is water.

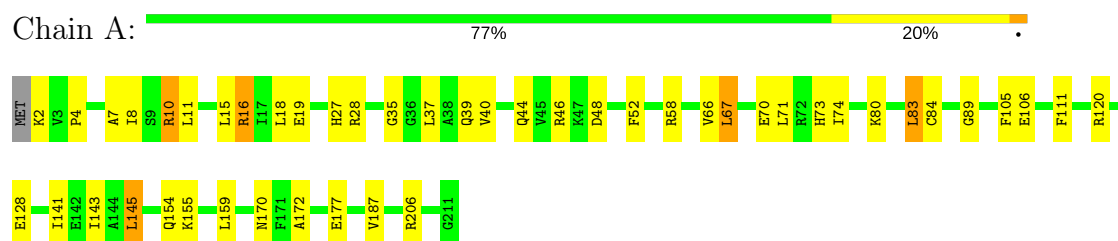
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	181	Total	O	0	0
			181	181		
6	B	111	Total	O	0	0
			111	111		

3 Residue-property plots [i](#)

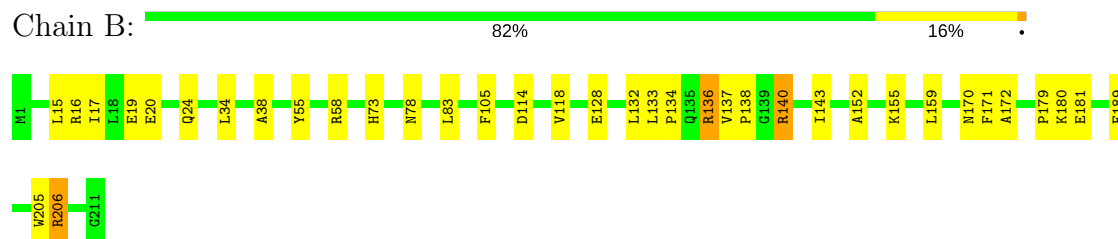
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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



- Molecule 1: AT-rich DNA-binding protein



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	135.59Å 135.59Å 68.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.63 – 2.16	Depositor
% Data completeness (in resolution range)	95.6 (19.63-2.16)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.195 , 0.238	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3667	wwPDB-VP
Average B, all atoms (Å ²)	38.0	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: GOL, SO4, NAD, CL

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	0.47	0/1652	0.71	1/2235 (0.0%)
1	B	0.41	0/1660	0.64	0/2245
All	All	0.44	0/3312	0.67	1/4480 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	10	ARG	NE-CZ-NH2	-5.12	117.74	120.30

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	1621	0	1668	42	0
1	B	1629	0	1680	27	0
2	A	20	0	0	3	0
2	B	10	0	0	0	0
3	A	1	0	0	0	0
4	A	44	0	26	1	0
4	B	44	0	26	2	0
5	A	6	0	5	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	181	0	0	5	0
6	B	111	0	0	2	0
All	All	3667	0	3405	71	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 10.

All (71) 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)
5:A:601:GOL:C1	5:A:601:GOL:O1	1.65	1.44
1:A:154:GLN:HE22	1:A:177:GLU:H	1.12	0.95
1:A:27:HIS:H	5:A:601:GOL:H11	1.40	0.85
1:B:73:HIS:HD2	1:B:78:ASN:HD21	1.25	0.80
1:A:70:GLU:O	1:A:74:ILE:HG23	1.85	0.77
1:A:159:LEU:HD21	2:A:406:SO4:O2	1.84	0.76
1:A:10:ARG:HD2	1:A:48:ASP:OD2	1.87	0.74
1:A:11:LEU:HD22	1:A:71:LEU:HD22	1.76	0.68
1:B:206:ARG:HH11	1:B:206:ARG:HG3	1.58	0.68
1:B:155:LYS:HE3	1:B:159:LEU:HG	1.74	0.67
1:A:18:LEU:HD11	1:A:67:LEU:HD13	1.78	0.66
1:B:83:LEU:HD22	1:B:143:ILE:HB	1.78	0.65
1:B:205:TRP:CE2	1:B:206:ARG:HD3	2.31	0.65
1:B:15:LEU:O	1:B:19:GLU:HG3	1.97	0.65
1:A:155:LYS:NZ	2:A:406:SO4:O4	2.25	0.62
1:A:27:HIS:N	5:A:601:GOL:H11	2.14	0.62
1:B:189:PHE:HB2	4:B:302:NAD:O7N	2.01	0.60
5:A:601:GOL:HO1	5:A:601:GOL:C1	2.09	0.60
1:A:11:LEU:HD13	1:A:74:ILE:HD11	1.85	0.58
1:B:137:VAL:HB	1:B:138:PRO:HD3	1.85	0.58
1:A:46:ARG:HD3	1:A:58:ARG:NH1	2.20	0.57
1:A:11:LEU:CD1	1:A:74:ILE:HD11	2.35	0.56
1:A:40:VAL:CG1	1:A:44:GLN:HB3	2.37	0.55
1:B:179:PRO:HB2	1:B:181:GLU:OE1	2.05	0.55
1:A:27:HIS:H	5:A:601:GOL:C1	2.16	0.55
1:A:154:GLN:HE22	1:A:177:GLU:N	1.94	0.54
1:B:73:HIS:CD2	1:B:78:ASN:HD21	2.16	0.54
1:A:11:LEU:HD22	1:A:71:LEU:CD2	2.38	0.54
1:A:73:HIS:HB2	6:A:727:HOH:O	2.08	0.53
1:B:16:ARG:NH2	6:B:510:HOH:O	2.31	0.52
1:A:16:ARG:HD3	6:A:772:HOH:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:LEU:HD22	1:A:143:ILE:HB	1.92	0.51
1:A:120:ARG:HD3	6:A:696:HOH:O	2.10	0.51
1:B:114:ASP:O	1:B:118:VAL:HG23	2.12	0.49
1:B:128:GLU:HB3	1:B:132:LEU:HD12	1.95	0.48
1:A:206:ARG:NH1	1:A:206:ARG:HB2	2.28	0.47
1:B:206:ARG:CG	1:B:206:ARG:HH11	2.26	0.47
1:A:66:VAL:O	1:A:70:GLU:HG3	2.14	0.47
1:B:16:ARG:O	1:B:20:GLU:HG2	2.14	0.47
1:A:80:LYS:HE3	1:A:106:GLU:HB2	1.96	0.47
1:B:133:LEU:N	1:B:134:PRO:HD2	2.30	0.47
1:B:171:PHE:O	4:B:302:NAD:H2N	2.15	0.47
1:A:44:GLN:HE21	1:A:48:ASP:CG	2.18	0.47
1:B:152:ALA:HB1	6:B:449:HOH:O	2.14	0.47
1:A:89:GLY:HA3	4:A:301:NAD:O5B	2.15	0.46
1:A:83:LEU:HD11	1:A:105:PHE:HB3	1.97	0.46
1:A:11:LEU:HD11	1:A:52:PHE:CD1	2.50	0.45
1:B:155:LYS:HA	1:B:155:LYS:HD2	1.75	0.45
1:A:159:LEU:CD2	2:A:406:SO4:O2	2.59	0.45
1:A:111:PHE:HA	1:A:128:GLU:O	2.16	0.45
1:A:145:LEU:N	1:A:145:LEU:HD23	2.32	0.45
1:A:4:PRO:HB2	1:A:7:ALA:HB3	1.97	0.45
1:B:180:LYS:HG3	1:B:181:GLU:OE2	2.16	0.45
1:B:170:ASN:HD21	1:B:172:ALA:HB3	1.81	0.45
1:B:20:GLU:O	1:B:24:GLN:HG3	2.17	0.44
1:A:84:CYS:HB3	1:A:141:ILE:HD13	1.99	0.44
1:A:2:LYS:N	6:A:763:HOH:O	2.50	0.44
1:B:83:LEU:HD11	1:B:105:PHE:HB3	1.99	0.43
1:A:4:PRO:O	1:A:8:ILE:HG12	2.18	0.43
1:A:10:ARG:CD	1:A:48:ASP:OD2	2.63	0.43
1:A:35:GLY:O	1:A:39:GLN:N	2.52	0.43
1:B:55:TYR:OH	1:B:58:ARG:HA	2.19	0.42
1:B:17:ILE:CD1	1:B:38:ALA:HB2	2.49	0.42
1:B:16:ARG:HA	1:B:19:GLU:OE1	2.19	0.42
1:A:28:ARG:NH2	6:A:699:HOH:O	2.53	0.41
1:A:206:ARG:HB2	1:A:206:ARG:HH11	1.86	0.41
1:A:40:VAL:HG12	1:A:44:GLN:HB3	2.03	0.41
1:A:11:LEU:HD11	1:A:52:PHE:CG	2.56	0.41
1:B:136:ARG:HD3	1:B:140:ARG:NH2	2.36	0.41
1:A:58:ARG:HD2	1:A:58:ARG:HA	1.95	0.40
1:A:170:ASN:HD21	1:A:172:ALA:HB3	1.87	0.40

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	208/211 (99%)	202 (97%)	6 (3%)	0	100	100
1	B	209/211 (99%)	202 (97%)	7 (3%)	0	100	100
All	All	417/422 (99%)	404 (97%)	13 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	168/170 (99%)	160 (95%)	8 (5%)	30	25
1	B	169/170 (99%)	165 (98%)	4 (2%)	54	57
All	All	337/340 (99%)	325 (96%)	12 (4%)	40	38

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	LEU
1	A	16	ARG
1	A	19	GLU
1	A	37	LEU
1	A	67	LEU
1	A	83	LEU
1	A	145	LEU
1	A	187	VAL

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Mol	Chain	Res	Type
1	B	34	LEU
1	B	136	ARG
1	B	140	ARG
1	B	206	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	HIS
1	A	44	GLN
1	A	154	GLN
1	A	170	ASN
1	B	33	GLN
1	B	39	GLN
1	B	73	HIS
1	B	135	GLN
1	B	170	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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	$\# Z > 2$
4	NAD	A	301	-	41,48,48	2.37	10 (24%)	43,73,73	2.36	8 (18%)
2	SO4	A	401	-	4,4,4	0.32	0	6,6,6	0.15	0
2	SO4	A	403	-	4,4,4	0.38	0	6,6,6	0.11	0
2	SO4	A	405	-	4,4,4	0.39	0	6,6,6	0.13	0
2	SO4	A	406	-	4,4,4	0.39	0	6,6,6	1.51	1 (16%)
5	GOL	A	601	-	5,5,5	5.17	4 (80%)	5,5,5	5.53	3 (60%)
4	NAD	B	302	-	41,48,48	2.44	11 (26%)	43,73,73	2.43	8 (18%)
2	SO4	B	402	-	4,4,4	0.31	0	6,6,6	0.20	0
2	SO4	B	404	-	4,4,4	0.34	0	6,6,6	0.06	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
4	NAD	A	301	-	-	0/22/62/62	0/5/5/5
2	SO4	A	401	-	-	0/0/0/0	0/0/0/0
2	SO4	A	403	-	-	0/0/0/0	0/0/0/0
2	SO4	A	405	-	-	0/0/0/0	0/0/0/0
2	SO4	A	406	-	-	0/0/0/0	0/0/0/0
5	GOL	A	601	-	-	0/4/4/4	0/0/0/0
4	NAD	B	302	-	-	0/22/62/62	0/5/5/5
2	SO4	B	402	-	-	0/0/0/0	0/0/0/0
2	SO4	B	404	-	-	0/0/0/0	0/0/0/0

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	601	GOL	C3-C2	-8.56	1.20	1.52
4	A	301	NAD	C2N-C3N	-4.56	1.32	1.39
4	B	302	NAD	C2N-C3N	-3.99	1.32	1.39
5	A	601	GOL	C1-C2	-3.92	1.37	1.52
4	B	302	NAD	O2B-C2B	-2.09	1.38	1.43
4	B	302	NAD	C3B-C4B	2.04	1.58	1.53
4	A	301	NAD	C6N-C5N	2.07	1.43	1.38
4	A	301	NAD	O4D-C4D	2.10	1.49	1.45
4	B	302	NAD	C3D-C4D	2.34	1.59	1.53
4	A	301	NAD	C2D-C1D	2.43	1.57	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	302	NAD	C2D-C1D	2.44	1.57	1.53
4	A	301	NAD	C3D-C4D	2.51	1.59	1.53
4	B	302	NAD	O4D-C4D	2.70	1.51	1.45
4	A	301	NAD	C4A-N3A	3.22	1.40	1.35
5	A	601	GOL	O3-C3	3.32	1.56	1.42
4	B	302	NAD	C4A-N3A	3.62	1.40	1.35
4	A	301	NAD	C6N-N1N	4.27	1.46	1.35
4	A	301	NAD	C2A-N3A	4.65	1.39	1.32
4	B	302	NAD	C6N-N1N	4.83	1.47	1.35
4	B	302	NAD	C2A-N3A	5.10	1.40	1.32
5	A	601	GOL	O1-C1	5.48	1.65	1.42
4	A	301	NAD	C5N-C4N	6.58	1.51	1.38
4	B	302	NAD	C5N-C4N	6.95	1.52	1.38
4	A	301	NAD	C4N-C3N	8.22	1.52	1.39
4	B	302	NAD	C4N-C3N	8.33	1.53	1.39

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	302	NAD	C5N-C4N-C3N	-10.04	108.54	120.35
4	A	301	NAD	C5N-C4N-C3N	-9.09	109.66	120.35
4	B	302	NAD	N3A-C2A-N1A	-8.34	121.60	128.86
4	A	301	NAD	N3A-C2A-N1A	-8.15	121.76	128.86
4	B	302	NAD	C4B-O4B-C1B	-3.42	106.12	109.77
4	A	301	NAD	C4B-O4B-C1B	-3.11	106.46	109.77
4	B	302	NAD	C6N-C5N-C4N	-2.79	115.22	119.44
2	A	406	SO4	O4-S-O2	-2.40	96.02	109.26
4	B	302	NAD	C1B-N9A-C4A	-2.11	122.98	126.64
4	A	301	NAD	N6A-C6A-N1A	2.05	122.82	118.77
4	A	301	NAD	C2B-C3B-C4B	2.05	106.62	102.62
4	B	302	NAD	C2N-C3N-C4N	2.48	121.09	118.26
4	B	302	NAD	C3N-C2N-N1N	2.51	122.96	120.43
4	A	301	NAD	C2N-C3N-C4N	2.90	121.56	118.26
5	A	601	GOL	O1-C1-C2	3.55	127.93	110.07
4	A	301	NAD	C3N-C2N-N1N	3.55	124.00	120.43
4	B	302	NAD	C2A-N1A-C6A	3.91	125.61	118.77
4	A	301	NAD	C2A-N1A-C6A	4.11	125.96	118.77
5	A	601	GOL	O2-C2-C3	6.37	138.90	108.84
5	A	601	GOL	O3-C3-C2	9.94	160.12	110.07

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	301	NAD	1	0
2	A	406	SO4	3	0
5	A	601	GOL	5	0
4	B	302	NAD	2	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.