



wwPDB X-ray Structure Validation Summary Report i

Feb 27, 2014 – 03:49 PM GMT

PDB ID : 1TOX
Title : DIPHTHERIA TOXIN DIMER COMPLEXED WITH NAD
Authors : Bell, C.E.; Eisenberg, D.
Deposited on : 1995-10-06
Resolution : 2.30 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

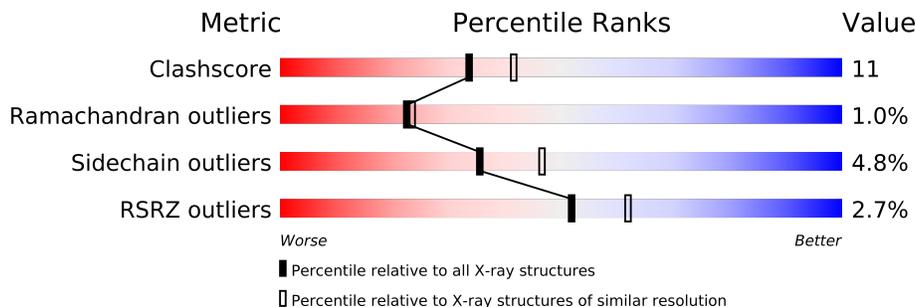
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.30 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	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (2.30-2.30)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	535	
1	B	535	

2 Entry composition (i)

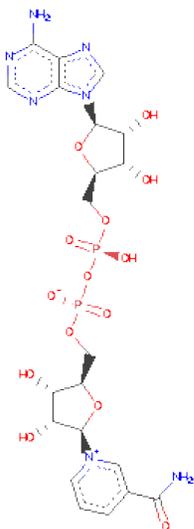
There are 3 unique types of molecules in this entry. The entry contains 8295 atoms, of which 0 are hydrogen and 0 are deuterium.

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 DIPHTHERIA TOXIN (DIMERIC).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	515	Total 3960	C 2496	N 672	O 780	S 12	0	0	0
1	B	513	Total 3945	C 2487	N 670	O 776	S 12	0	0	0

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



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

- Molecule 3 is water.

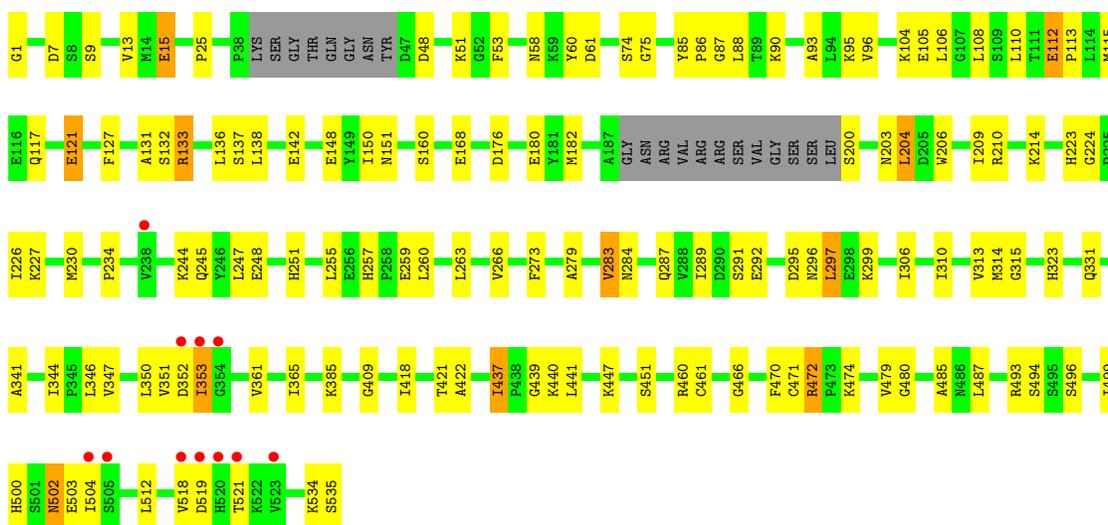
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	150	Total 150	O 150	0	0
3	B	152	Total 152	O 152	0	0

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 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.

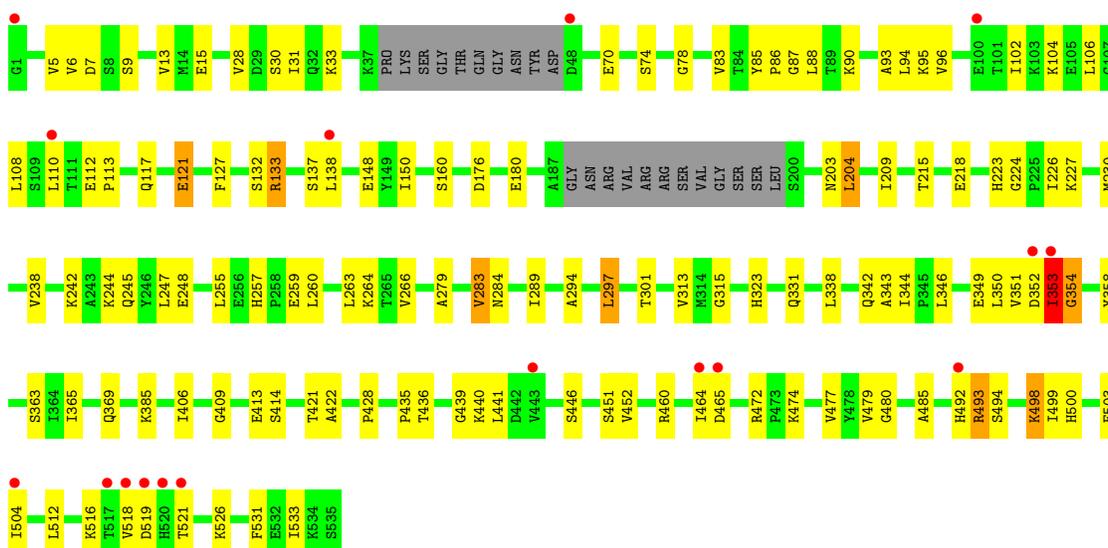
- Molecule 1: DIPHTHERIA TOXIN (DIMERIC)

Chain A:



- Molecule 1: DIPHTHERIA TOXIN (DIMERIC)

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	105.00Å 89.50Å 130.10Å 90.00° 94.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.30 68.04 – 2.31	Depositor EDS
% Data completeness (in resolution range)	92.6 (10.00-2.30) 93.2 (68.04-2.31)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.32Å)	Xtrriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.227 , 0.307 0.213 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	27.6	Xtrriage
Anisotropy	0.127	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.4	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.37$	Xtrriage
Outliers	4 of 48977 reflections (0.008%)	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8295	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 49.44 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 7.4607e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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:
NAD

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	0.60	0/4039	0.76	4/5471 (0.1%)
1	B	0.59	0/4023	0.76	2/5448 (0.0%)
All	All	0.60	0/8062	0.76	6/10919 (0.1%)

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	B	0	1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	472	ARG	NE-CZ-NH2	-5.79	117.40	120.30
1	A	437	ILE	N-CA-C	-5.60	95.87	111.00
1	A	472	ARG	NE-CZ-NH1	5.51	123.06	120.30
1	A	466	GLY	N-CA-C	5.44	126.69	113.10
1	B	472	ARG	NE-CZ-NH2	-5.43	117.58	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	358	TYR	Sidechain

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3960	0	3896	89	0
1	B	3945	0	3885	85	0
2	A	44	0	26	1	0
2	B	44	0	26	1	0
3	A	150	0	0	2	0
3	B	152	0	0	3	0
All	All	8295	0	7833	174	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 11.

The worst 5 of 174 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:460:ARG:HG3	1:B:474:LYS:HE2	1.38	1.02
1:A:500:HIS:H	1:A:503:GLU:HG3	1.32	0.93
1:A:214:LYS:HE2	3:A:685:HOH:O	1.73	0.87
1:B:409:GLY:HA2	1:B:498:LYS:HE2	1.59	0.85
1:A:74:SER:HB2	1:A:297:LEU:HD13	1.60	0.84

There are no symmetry-related clashes.

5.3 Torsion angles

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	509/535 (95%)	482 (95%)	23 (4%)	4 (1%)	27	30
1	B	507/535 (95%)	486 (96%)	15 (3%)	6 (1%)	19	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1016/1070 (95%)	968 (95%)	38 (4%)	10 (1%)	22	23

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	353	ILE
1	A	502	ASN
1	A	224	GLY
1	B	350	LEU
1	B	224	GLY

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	436/452 (96%)	412 (94%)	24 (6%)	30	39
1	B	434/452 (96%)	416 (96%)	18 (4%)	41	55
All	All	870/904 (96%)	828 (95%)	42 (5%)	35	46

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	313	VAL
1	A	512	LEU
1	B	446	SER
1	A	385	LYS
1	A	493	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	36	GLN
1	B	203	ASN
1	B	331	GLN
1	A	524	ASN
1	B	369	GLN

5.3.3 RNA i

There are no RNA chains 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

2 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	NAD	A	536	-	48,48,48	1.28	6 (12%)	73,73,73	2.67	25 (34%)
2	NAD	B	536	-	48,48,48	1.14	5 (10%)	73,73,73	2.53	20 (27%)

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	NAD	A	536	-	-	0/30/62/62	0/3/5/5
2	NAD	B	536	-	-	0/30/62/62	0/3/5/5

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	536	NAD	C2N-N1N	4.48	1.41	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	536	NAD	C2N-N1N	4.07	1.40	1.35
2	A	536	NAD	C6N-N1N	2.86	1.43	1.35
2	A	536	NAD	C2D-C1D	-2.64	1.49	1.53
2	B	536	NAD	PA-O3	2.52	1.64	1.59

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	536	NAD	O4B-C1B-N9A	11.89	119.50	108.44
2	B	536	NAD	O4B-C1B-N9A	10.50	118.20	108.44
2	B	536	NAD	N3A-C2A-N1A	-8.55	121.56	128.71
2	A	536	NAD	N3A-C4A-N9A	8.05	139.97	125.43
2	A	536	NAD	N3A-C2A-N1A	-7.73	122.25	128.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	515/535 (96%)	-0.07	11 (2%) 60 70	10, 21, 56, 90	0
1	B	513/535 (95%)	0.02	17 (3%) 44 54	10, 24, 56, 96	0
All	All	1028/1070 (96%)	-0.03	28 (2%) 52 62	10, 22, 56, 96	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	518	VAL	8.9
1	B	518	VAL	7.8
1	B	464	ILE	6.9
1	B	353	ILE	6.2
1	A	519	ASP	5.8

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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, 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	NAD	A	536	44/44	0.10	-0.18	12,24,40,44	0
2	NAD	B	536	44/44	0.12	-0.23	14,32,47,52	0

6.5 Other polymers

There are no such residues in this entry.