



Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 11:42 PM GMT

PDB ID : 1M6F
Title : Strong Binding in the DNA Minor Groove by an Aromatic Diamidine With a Shape That Does Not Match the Curvature of the Groove
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Deposited on : 2002-07-16
Resolution : 1.78 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

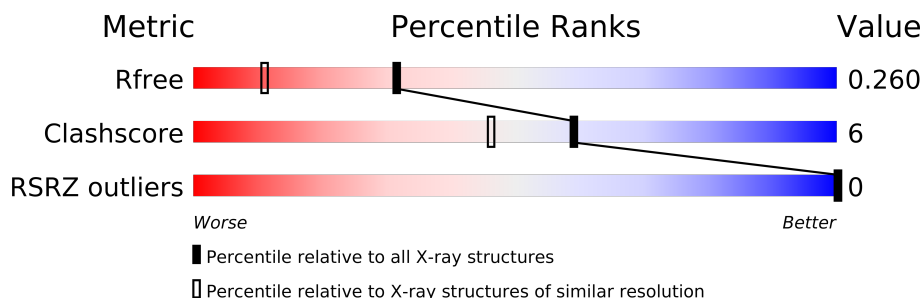
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.78 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))
R_{free}	66092	4987 (1.80-1.76)
Clashscore	79885	6152 (1.80-1.76)
RSRZ outliers	66119	4990 (1.80-1.76)

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	12	
1	B	12	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	CGQ	B	3025[A]	-	X
2	CGQ	B	3025[B]	-	X

2 Entry composition i

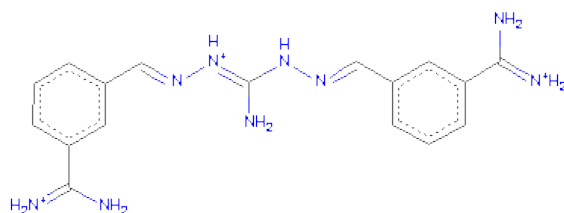
There are 4 unique types of molecules in this entry. The entry contains 639 atoms, of which 0 are hydrogen and 0 are deuterium.

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 DNA chain called DNA (5'-D(*CP*GP*CP*GP*AP*AP*TP*TP*CP*GP*CP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	12	Total	C	N	O	P	0	0	0
			243	116	46	70	11			
1	B	12	Total	C	N	O	P	0	0	0
			243	116	46	70	11			

- Molecule 2 is 3-[C-[N'-(3-CARBAMIMIDOYL-BENZYLIDENIUM)-HYDRAZINO]-[[AMINOMETHYLIDENE]AMINIUM]-IMINOMETHYL]-BENZAMIDINIUM (three-letter code: CGQ) (formula: C₁₇H₂₂N₉).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	N	0	1
			35	24	11		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	62	Total 62	O 62	0	0
4	B	55	Total 55	O 55	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: DNA (5'-D(*CP*GP*CP*GP*AP*AP*TP*TP*CP*GP*CP*G)-3')

Chain A: 

G1001	G1002	G1003	G1004	A1005	A1006	T1007	T1008	C1009	G1010	C1011	G1012
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- Molecule 1: DNA (5'-D(*CP*GP*CP*GP*AP*AP*TP*TP*CP*GP*CP*G)-3')

Chain B: 

C2013	G2014	C2015	G2016	A2017	A2018	T2019	T2020	C2021	G2024
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	24.10Å 39.82Å 65.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.78 16.20 – 1.78	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-1.78) 92.5 (16.20-1.78)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	10.46 (at 1.77Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.202 , 0.277 0.204 , 0.260	Depositor DCC
R_{free} test set	300 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	24.4	Xtriage
Anisotropy	0.188	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 75.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 6024 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	639	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.38% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CGQ, MG

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	0.84	0/272	2.34	14/418 (3.3%)
1	B	0.83	0/272	2.59	16/418 (3.8%)
All	All	0.84	0/544	2.46	30/836 (3.6%)

There are no bond length outliers.

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2018	DA	O4'-C1'-N9	-17.25	95.92	108.00
1	B	2021	DC	O4'-C1'-N1	-16.22	96.65	108.00
1	B	2017	DA	O4'-C1'-N9	-16.01	96.79	108.00
1	B	2020	DT	O4'-C1'-N1	-13.77	98.36	108.00
1	A	1007	DT	O4'-C1'-N1	-13.24	98.73	108.00
1	A	1011	DC	O4'-C1'-N1	-12.84	99.01	108.00
1	A	1006	DA	O4'-C1'-N9	-12.12	99.52	108.00
1	A	1008	DT	O4'-C1'-N1	-11.49	99.96	108.00
1	A	1005	DA	O4'-C1'-N9	-11.34	100.06	108.00
1	B	2015	DC	O4'-C1'-N1	-10.26	100.82	108.00
1	A	1001	DC	O4'-C1'-N1	-9.80	101.14	108.00
1	A	1009	DC	O4'-C1'-N1	-8.61	101.97	108.00
1	A	1003	DC	O4'-C1'-N1	-7.71	102.61	108.00
1	B	2019	DT	O4'-C1'-N1	-6.82	103.23	108.00
1	B	2020	DT	N3-C4-O4	6.69	123.91	119.90
1	B	2016	DG	O4'-C1'-N9	-6.63	103.36	108.00
1	B	2024	DG	O4'-C1'-N9	-6.14	103.70	108.00
1	A	1002	DG	P-O3'-C3'	6.05	126.96	119.70
1	A	1007	DT	N1-C1'-C2'	5.98	123.96	112.60
1	B	2020	DT	N1-C1'-C2'	5.93	123.88	112.60
1	A	1006	DA	P-O3'-C3'	5.84	126.71	119.70
1	B	2018	DA	N9-C1'-C2'	5.82	123.65	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2014	DG	O4'-C1'-N9	-5.70	104.01	108.00
1	A	1008	DT	N1-C1'-C2'	5.55	123.15	112.60
1	A	1006	DA	N1-C6-N6	5.45	121.87	118.60
1	B	2013	DC	O4'-C1'-N1	-5.43	104.20	108.00
1	B	2021	DC	N1-C1'-C2'	5.39	122.84	112.60
1	A	1012	DG	O4'-C1'-N9	-5.27	104.31	108.00
1	B	2017	DA	N9-C1'-C2'	5.08	122.26	112.60
1	B	2018	DA	C5-C6-N1	-5.07	115.16	117.70

There are no chirality outliers.

There are no planarity outliers.

5.2 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 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	243	0	136	1	0
1	B	243	0	136	3	0
2	B	35	0	18	0	0
3	A	1	0	0	0	0
4	A	62	0	0	0	0
4	B	55	0	0	1	0
All	All	639	0	290	5	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 6.

All (5) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:2015:DC:H2'	1:B:2016:DG:C8	2.48	0.49
1:A:1003:DC:H2'	1:A:1004:DG:C8	2.54	0.42
1:B:2014:DG:H2''	1:B:2015:DC:O5'	2.20	0.42

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

There are no protein chains in this entry.

5.3.2 Protein sidechains ⓘ

There are no protein chains in this entry.

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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$
2	CGQ	B	3025[A]	-	9,9,27	2.30	2 (22%)	10,11,35	1.06	1 (10%)
2	CGQ	B	3025[B]	-	9,9,27	2.34	3 (33%)	10,11,35	0.81	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
2	CGQ	B	3025[A]	-	-	0/4/4/20	0/1/1/2
2	CGQ	B	3025[B]	-	-	0/4/4/20	0/1/1/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3025[A]	CGQ	C28-N30	5.87	1.37	1.31
2	B	3025[B]	CGQ	C28-N30	5.57	1.36	1.31
2	B	3025[B]	CGQ	C26-C28	-3.31	1.45	1.48
2	B	3025[A]	CGQ	C26-C28	-3.30	1.45	1.48
2	B	3025[B]	CGQ	C28-N29	-2.20	1.28	1.31

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	3025[A]	CGQ	C25-C26-C28	2.41	122.22	120.39

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	12/12 (100%)	-0.29	0 100 100	20, 24, 29, 36	0
1	B	12/12 (100%)	-0.31	0 100 100	21, 26, 30, 34	0
All	All	24/24 (100%)	-0.30	0 100 100	20, 25, 30, 36	0

There are no RSRZ outliers to report.

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(Å ²)	Q<0.9
2	CGQ	B	3025[B]	9/26	0.23	29.57	42,54,68,72	9
2	CGQ	B	3025[A]	9/26	0.23	8.76	42,54,63,75	9
3	MG	A	4026	1/1	0.06	-2.57	21,21,21,21	0

6.5 Other polymers ⓘ

There are no such residues in this entry.