



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 16, 2017 – 07:30 am GMT

PDB ID : 3C1P
Title : Crystal Structure of an alternating D-Alanyl, L-Homoalanyl PNA
Authors : Cuesta-Seijo, J.A.; Sheldrick, G.M.; Zhang, J.; Diederichsen, U.
Deposited on : 2008-01-23
Resolution : 1.00 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 : **FAILED**
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : recalc28986
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28986

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 1.00 Å.

There are no overall percentile quality scores available for this entry.

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 814 atoms, of which 263 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 an unknown type called Peptide Nucleic Acid DLY-HGL-AGD-LHC-AGD-LHC-CUD-LYS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
1	A	8	Total	C	H	N	O	0	2
			172	56	70	33	13		
1	B	8	Total	C	H	N	O	0	0
			166	54	66	33	13		
1	C	8	Total	C	H	N	O	0	0
			166	54	66	33	13		
1	D	8	Total	C	H	N	O	0	4
			170	59	61	35	15		

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	44	Total	O	0	0
			44	44		
2	B	29	Total	O	0	0
			29	29		
2	C	34	Total	O	0	0
			34	34		
2	D	33	Total	O	0	0
			33	33		

3 Residue-property plots

There is no protein, DNA or RNA chain in this entry to show sequence plots.

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	26.31Å 30.73Å 33.55Å 90.00° 99.53° 90.00°	Depositor
Resolution (Å)	40.00 – 1.00 33.09 – 1.00	Depositor EDS
% Data completeness (in resolution range)	99.1 (40.00-1.00) 99.5 (33.09-1.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.20 (at 1.00Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.150 , 0.202 0.160 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	12.1	Xtriage
Anisotropy	0.472	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 55.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	814	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.93% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

5.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

5.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

5.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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](#)

There are no ligands in this entry.

5.7 Other polymers ⓘ

Of 37 such residues modelled in this entry, 3 are modelled with single atom - leaving 34 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
1	DLY	A	11	1	8,8,9	0.99	1 (12%)	5,8,10	1.74	2 (40%)
1	HGL	A	12	1	14,18,19	1.51	1 (7%)	9,25,27	1.46	2 (22%)
1	AGD	A	13	1	14,17,18	1.50	2 (14%)	8,24,26	1.89	4 (50%)
1	LHC	A	14	1	11,14,15	1.11	1 (9%)	9,18,20	1.37	0
1	AGD	A	15	1	14,17,18	1.56	3 (21%)	8,24,26	1.47	1 (12%)
1	LHC	A	16	1	11,14,15	1.15	1 (9%)	9,18,20	1.22	1 (11%)
1	CUD	A	17[A]	1	11,13,14	1.92	1 (9%)	8,17,19	1.47	1 (12%)
1	CUD	A	17[B]	-	9,12,14	1.17	0	8,16,19	1.09	0
1	DLY	B	21	1	8,8,9	1.04	1 (12%)	5,8,10	1.50	1 (20%)
1	HGL	B	22	1	14,18,19	2.35	6 (42%)	9,25,27	2.21	3 (33%)
1	AGD	B	23	1	14,17,18	1.95	5 (35%)	8,24,26	1.68	3 (37%)
1	LHC	B	24	1	11,14,15	1.41	2 (18%)	9,18,20	1.67	2 (22%)
1	AGD	B	25	1	14,17,18	1.46	1 (7%)	8,24,26	2.30	4 (50%)
1	LHC	B	26	1	11,14,15	1.49	2 (18%)	9,18,20	1.68	2 (22%)
1	CUD	B	27	1	11,13,14	1.04	1 (9%)	8,17,19	1.41	1 (12%)
1	DLY	C	31	1	8,8,9	0.79	0	5,8,10	1.60	1 (20%)
1	HGL	C	32	1	14,18,19	1.52	3 (21%)	9,25,27	1.55	2 (22%)
1	AGD	C	33	1	14,17,18	1.41	3 (21%)	8,24,26	1.19	0
1	LHC	C	34	1	11,14,15	1.04	1 (9%)	9,18,20	1.34	1 (11%)
1	AGD	C	35	1	14,17,18	1.56	2 (14%)	8,24,26	0.96	0
1	LHC	C	36	1	11,14,15	1.13	1 (9%)	9,18,20	0.87	1 (11%)
1	CUD	C	37	1	11,13,14	1.64	2 (18%)	8,17,19	1.82	4 (50%)
1	DLY	D	41[A]	1	4,4,9	1.30	1 (25%)	1,4,10	0.07	0
1	DLY	D	41[B]	1	4,4,9	1.20	1 (25%)	1,4,10	0.81	0
1	HGL	D	42[A]	1	14,18,19	1.34	3 (21%)	9,25,27	1.18	1 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HGL	D	42[B]	1	14,18,19	1.49	3 (21%)	9,25,27	1.24	1 (11%)
1	AGD	D	43	1	14,17,18	1.53	4 (28%)	8,24,26	1.80	4 (50%)
1	LHC	D	44	1	11,14,15	0.92	0	9,18,20	0.83	0
1	AGD	D	45	1	14,17,18	1.74	4 (28%)	8,24,26	1.14	1 (12%)
1	LHC	D	46	1	11,14,15	1.17	1 (9%)	9,18,20	1.01	0
1	CUD	D	47[A]	1	11,13,14	1.89	3 (27%)	8,17,19	1.99	3 (37%)
1	CUD	D	47[B]	1	11,13,14	2.07	3 (27%)	8,17,19	1.96	3 (37%)
1	LYS	D	48[A]	1	0,1,9	0.00	-	0,0,10	0.00	-
1	LYS	D	48[B]	1	0,1,9	0.00	-	0,0,10	0.00	-

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
1	DLY	A	11	1	-	0/5/7/9	0/0/0/0
1	HGL	A	12	1	-	0/5/7/9	0/2/2/2
1	AGD	A	13	1	-	0/1/6/8	0/2/2/2
1	LHC	A	14	1	-	0/5/7/9	0/1/1/1
1	AGD	A	15	1	-	0/1/6/8	0/2/2/2
1	LHC	A	16	1	-	0/5/7/9	0/1/1/1
1	CUD	A	17[A]	1	-	0/2/6/8	0/1/1/1
1	CUD	A	17[B]	-	-	0/3/4/8	0/1/1/1
1	DLY	B	21	1	-	0/5/7/9	0/0/0/0
1	HGL	B	22	1	-	0/5/7/9	0/2/2/2
1	AGD	B	23	1	-	0/1/6/8	0/2/2/2
1	LHC	B	24	1	-	0/5/7/9	0/1/1/1
1	AGD	B	25	1	-	0/1/6/8	0/2/2/2
1	LHC	B	26	1	-	0/5/7/9	0/1/1/1
1	CUD	B	27	1	-	0/2/6/8	0/1/1/1
1	DLY	C	31	1	-	0/5/7/9	0/0/0/0
1	HGL	C	32	1	-	0/5/7/9	0/2/2/2
1	AGD	C	33	1	-	0/1/6/8	0/2/2/2
1	LHC	C	34	1	-	0/5/7/9	0/1/1/1
1	AGD	C	35	1	-	0/1/6/8	0/2/2/2
1	LHC	C	36	1	-	0/5/7/9	0/1/1/1
1	CUD	C	37	1	-	0/2/6/8	0/1/1/1
1	DLY	D	41[A]	1	-	0/0/2/9	0/0/0/0
1	DLY	D	41[B]	1	-	0/0/2/9	0/0/0/0
1	HGL	D	42[A]	1	-	0/5/7/9	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HGL	D	42[B]	1	-	0/5/7/9	0/2/2/2
1	AGD	D	43	1	-	0/1/6/8	0/2/2/2
1	LHC	D	44	1	-	0/5/7/9	0/1/1/1
1	AGD	D	45	1	-	0/1/6/8	0/2/2/2
1	LHC	D	46	1	-	0/5/7/9	0/1/1/1
1	CUD	D	47[A]	1	-	0/2/6/8	0/1/1/1
1	CUD	D	47[B]	1	-	0/2/6/8	0/1/1/1
1	LYS	D	48[A]	1	-	0/0/0/9	0/0/0/0
1	LYS	D	48[B]	1	-	0/0/0/9	0/0/0/0

All (63) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	35	AGD	CB-N9	-3.85	1.44	1.48
1	B	25	AGD	CB-N9	-3.69	1.44	1.48
1	D	45	AGD	C8-N7	-3.50	1.28	1.34
1	D	45	AGD	CB-N9	-3.38	1.45	1.48
1	B	22	HGL	C8-N7	-3.34	1.28	1.34
1	D	47[A]	CUD	C6-C5	-3.26	1.31	1.38
1	D	47[B]	CUD	C6-C5	-3.26	1.31	1.38
1	C	37	CUD	CB-N1	-2.95	1.45	1.48
1	D	43	AGD	CB-N9	-2.93	1.45	1.48
1	B	23	AGD	C8-N7	-2.72	1.29	1.34
1	D	47[A]	CUD	CB-N1	-2.65	1.45	1.48
1	D	47[B]	CUD	CB-N1	-2.65	1.45	1.48
1	A	16	LHC	C4-N3	-2.61	1.30	1.35
1	D	43	AGD	C8-N7	-2.60	1.29	1.34
1	C	33	AGD	CB-N9	-2.58	1.45	1.48
1	B	22	HGL	C5-C4	-2.49	1.34	1.40
1	D	42[B]	HGL	CB-CA	-2.48	1.50	1.53
1	A	14	LHC	C6-C5	-2.46	1.32	1.38
1	D	42[B]	HGL	C8-N7	-2.42	1.30	1.34
1	D	42[A]	HGL	C8-N7	-2.42	1.30	1.34
1	B	22	HGL	C2-N3	-2.40	1.30	1.33
1	C	33	AGD	C8-N7	-2.36	1.30	1.34
1	B	23	AGD	CB-N9	-2.34	1.46	1.48
1	B	22	HGL	CG-N9	-2.32	1.44	1.49
1	C	32	HGL	C8-N7	-2.27	1.30	1.34
1	C	34	LHC	C6-C5	-2.23	1.33	1.38
1	B	24	LHC	C6-C5	-2.21	1.33	1.38
1	A	13	AGD	C8-N7	-2.21	1.30	1.34
1	A	15	AGD	CB-N9	-2.19	1.46	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	45	AGD	C2-N3	-2.18	1.31	1.33
1	B	26	LHC	C2-N3	-2.16	1.33	1.38
1	C	36	LHC	C6-C5	-2.06	1.33	1.38
1	B	24	LHC	C2-N3	-2.04	1.34	1.38
1	A	15	AGD	CB-CA	2.04	1.56	1.53
1	C	33	AGD	C6-N1	2.08	1.39	1.36
1	D	43	AGD	CA-C	2.14	1.53	1.50
1	D	42[B]	HGL	C2-N2	2.18	1.35	1.32
1	D	42[A]	HGL	C2-N2	2.18	1.35	1.32
1	D	41[B]	DLY	CA-C	2.19	1.53	1.50
1	D	43	AGD	C6-N1	2.19	1.39	1.36
1	D	42[A]	HGL	CA-C	2.20	1.53	1.50
1	B	27	CUD	CA-C	2.26	1.53	1.50
1	D	45	AGD	C2-N2	2.35	1.35	1.32
1	A	11	DLY	CA-C	2.36	1.53	1.50
1	D	41[A]	DLY	CA-C	2.37	1.53	1.50
1	B	26	LHC	CA-C	2.37	1.53	1.50
1	C	32	HGL	CA-C	2.41	1.53	1.50
1	D	46	LHC	CA-C	2.58	1.53	1.50
1	B	21	DLY	CA-C	2.61	1.53	1.50
1	A	13	AGD	C6-N1	2.87	1.40	1.36
1	C	32	HGL	C6-N1	2.87	1.40	1.36
1	B	23	AGD	CA-C	3.15	1.54	1.50
1	B	23	AGD	C2-N2	3.22	1.37	1.32
1	C	37	CUD	CA-C	3.29	1.54	1.50
1	A	15	AGD	C6-N1	3.32	1.41	1.36
1	A	12	HGL	CA-C	3.40	1.54	1.50
1	C	35	AGD	C6-N1	3.48	1.41	1.36
1	D	47[A]	CUD	CA-C	3.50	1.54	1.50
1	B	23	AGD	C6-N1	3.91	1.42	1.36
1	B	22	HGL	C2-N2	4.08	1.38	1.32
1	D	47[B]	CUD	CA-C	4.75	1.56	1.50
1	B	22	HGL	C6-N1	4.92	1.43	1.36
1	A	17[A]	CUD	CA-C	5.13	1.57	1.50

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	22	HGL	N2-C2-N1	-4.24	113.32	117.84
1	B	25	AGD	N2-C2-N1	-3.69	113.91	117.84
1	B	25	AGD	C2-N3-C4	-3.47	111.11	115.16
1	D	43	AGD	N2-C2-N1	-3.15	114.49	117.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	11	DLY	CB-CA-C	-3.08	106.58	111.65
1	A	12	HGL	C2-N3-C4	-3.07	111.57	115.16
1	C	37	CUD	O-C-CA	-2.93	116.94	125.02
1	C	31	DLY	O-C-CA	-2.88	117.08	125.02
1	B	22	HGL	C2-N3-C4	-2.81	111.88	115.16
1	A	13	AGD	C2-N3-C4	-2.55	112.18	115.16
1	C	32	HGL	N2-C2-N1	-2.45	115.23	117.84
1	B	26	LHC	C6-N1-C2	-2.44	118.19	122.14
1	A	13	AGD	O-C-CA	-2.38	118.45	125.02
1	B	23	AGD	C2-N3-C4	-2.30	112.47	115.16
1	B	21	DLY	CB-CA-C	-2.23	107.97	111.65
1	B	24	LHC	O-C-CA	-2.22	118.89	125.02
1	D	47[A]	CUD	C6-N1-C2	-2.22	118.56	122.14
1	D	47[B]	CUD	C6-N1-C2	-2.22	118.56	122.14
1	D	43	AGD	O-C-CA	-2.22	118.90	125.02
1	A	17[A]	CUD	O-C-CA	-2.21	118.91	125.02
1	D	42[B]	HGL	C2-N3-C4	-2.20	112.59	115.16
1	D	42[A]	HGL	C2-N3-C4	-2.20	112.59	115.16
1	C	37	CUD	C6-N1-C2	-2.18	118.62	122.14
1	C	32	HGL	C2-N3-C4	-2.17	112.62	115.16
1	A	13	AGD	N2-C2-N3	-2.17	117.60	120.26
1	A	11	DLY	O-C-CA	-2.16	119.07	125.02
1	B	23	AGD	N2-C2-N1	-2.14	115.55	117.84
1	D	43	AGD	C2-N3-C4	-2.13	112.67	115.16
1	C	36	LHC	O-C-CA	-2.07	119.29	125.02
1	D	45	AGD	O-C-CA	-2.05	119.37	125.02
1	A	15	AGD	N2-C2-N1	-2.01	115.70	117.84
1	A	16	LHC	C5-C6-N1	-2.00	119.64	121.35
1	D	43	AGD	N1-C2-N3	2.00	124.33	121.79
1	B	23	AGD	CB-N9-C8	2.02	129.65	125.70
1	C	37	CUD	C5-C6-N1	2.03	123.08	121.35
1	A	12	HGL	C4-C5-N7	2.09	111.43	109.41
1	B	25	AGD	N2-C2-N3	2.17	122.92	120.26
1	D	47[A]	CUD	C5-C6-N1	2.18	123.21	121.35
1	D	47[B]	CUD	C5-C6-N1	2.18	123.21	121.35
1	B	26	LHC	C5-C6-N1	2.21	123.23	121.35
1	A	13	AGD	C4-C5-N7	2.36	111.69	109.41
1	B	27	CUD	C5-C4-N3	2.64	124.82	121.68
1	C	37	CUD	CB-N1-C6	2.78	121.72	117.59
1	B	25	AGD	C4-C5-N7	3.08	112.39	109.41
1	C	34	LHC	CB-CG-N1	3.33	119.18	112.19
1	B	22	HGL	N1-C2-N3	3.84	126.67	121.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	24	LHC	CB-CG-N1	3.88	120.34	112.19
1	D	47[A]	CUD	CB-N1-C6	3.94	123.45	117.59
1	D	47[B]	CUD	CB-N1-C6	3.94	123.45	117.59

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

There are no RSRZ outliers to report within protein, DNA, RNA chains in this entry.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.