



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 11:10 AM GMT

PDB ID : 1ZTW
Title : d(CTTAATTCGAATTAAG) complexed with Moloney Murine Leukemia
Virus Reverse Transcriptase catalytic fragment
Authors : Goodwin, K.D.; Long, E.C.; Georgiadis, M.M.
Deposited on : 2005-05-27
Resolution : 1.80 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>

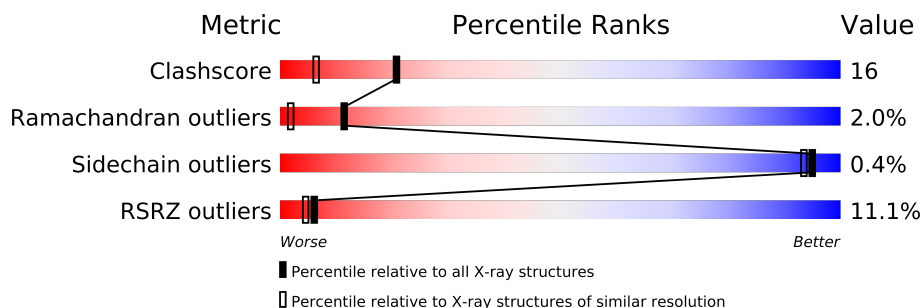
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.80 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	4461 (1.80-1.80)
Ramachandran outliers	78287	4404 (1.80-1.80)
Sidechain outliers	78261	4403 (1.80-1.80)
RSRZ outliers	66119	3515 (1.80-1.80)

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	B	8	
2	G	8	
3	A	255	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2603 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 CTTAATTC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	8	Total	C	N	O	P	0	0	0
			157	78	24	48	7			

- Molecule 2 is a DNA chain called GAATTAAG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	8	Total	C	N	O	P	0	0	0
			168	80	34	46	8			

- Molecule 3 is a protein called Reverse transcriptase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	255	Total	C	N	O	S	0	0	0
			2041	1311	356	367	7			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	229	Total	O	0	0
			229	229		
4	B	3	Total	O	0	0
			3	3		
4	G	5	Total	O	0	0
			5	5		

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: CTTAATTC

Chain B:

G1 T2 T3 A4 A5 T6 T7 C8

• Molecule 2: GAATTAAG

Chain G:

G9 A10 A11 T12 T13 A14 A15 G16

• Molecule 3: Reverse transcriptase

Chain A:

T24 W25 L26 T57 T61 K62 Q63 Y64 Q68 E69 A70 R71 L72 K75 P76 L99 P100 V101 K102 K103 P104 G105 T106 N107 D108 Y109 R110 E117 P132 L136 Q144 W145 H161 P162 T163 R173 D174 P175 E176 M177 G178 I179 S180 G181 D206 D209

Q213 I218 L219 L220 V223 L227 L228 A229 A230 T231 S232 E233 L234 Q237 Q238 R241 L250 L272 L273 K274 E275 Q276 Q277 R278

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	54.93Å 145.75Å 46.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.70 – 1.80 23.70 – 1.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (23.70-1.80) 95.7 (23.70-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.22 (at 1.80Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.227 , 0.264 0.240 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	21.3	Xtriage
Anisotropy	0.259	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 40.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 35406 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2603	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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	B	0.19	0/174	0.65	0/266
2	G	0.19	0/189	0.64	0/290
3	A	0.30	0/2097	0.59	0/2858
All	All	0.29	0/2460	0.60	0/3414

There are no bond length outliers.

There are no bond angle outliers.

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	B	157	0	94	12	1
2	G	168	0	91	18	1
3	A	2041	0	2056	46	0
4	A	229	0	0	3	0
4	B	3	0	0	0	0
4	G	5	0	0	0	0
All	All	2603	0	2241	72	1

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 16.

All (72) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:102:LYS:HD2	3:A:106:THR:HA	1.47	0.95
2:G:13:DT:H2"	2:G:14:DA:H5'	1.50	0.94
2:G:11:DA:H2"	2:G:12:DT:H5'	1.55	0.88
3:A:233:GLU:HG2	3:A:237:GLN:HE21	1.41	0.85
3:A:161:HIS:HD2	3:A:163:THR:H	1.26	0.80
3:A:68:GLN:O	3:A:72:LEU:HD13	1.90	0.71
1:B:4:DA:H2"	1:B:5:DA:H5"	1.73	0.69
1:B:8:DC:H42	2:G:9:DG:H1	1.39	0.69
3:A:103:LYS:HB2	3:A:104:PRO:HD3	1.72	0.69
3:A:274:LYS:HG2	3:A:275:GLU:HG3	1.78	0.64
2:G:14:DA:H2"	2:G:15:DA:H5'	1.80	0.62
3:A:61:ILE:HD11	3:A:117:GLU:HG3	1.80	0.62
2:G:12:DT:H1'	2:G:13:DT:H5"	1.82	0.62
3:A:234:LEU:HG	3:A:238:GLN:HE21	1.64	0.62
2:G:14:DA:H1'	2:G:15:DA:H5"	1.82	0.61
1:B:4:DA:C2'	1:B:5:DA:H5"	2.30	0.61
2:G:13:DT:H2"	2:G:14:DA:C5'	2.29	0.60
2:G:16:DG:C2	3:A:99:LEU:HD11	2.37	0.59
1:B:4:DA:H2"	1:B:5:DA:C5'	2.33	0.59
2:G:12:DT:H2"	2:G:13:DT:C5'	2.34	0.57
3:A:277:GLN:O	3:A:278:ARG:HB2	2.03	0.57
3:A:104:PRO:HA	4:A:409:HOH:O	2.05	0.57
3:A:233:GLU:HG2	3:A:237:GLN:NE2	2.16	0.56
3:A:233:GLU:O	3:A:237:GLN:HG3	2.06	0.56
3:A:104:PRO:HG2	3:A:107:ASN:HB2	1.87	0.55
3:A:220:LEU:HD22	3:A:227:LEU:HD23	1.88	0.55
3:A:102:LYS:HD2	3:A:106:THR:CA	2.31	0.55
3:A:161:HIS:CD2	3:A:163:THR:H	2.15	0.54
3:A:26:LEU:HD23	3:A:26:LEU:O	2.08	0.54
3:A:206:ASP:HB3	3:A:250:LEU:HD13	1.91	0.53
3:A:102:LYS:HD3	3:A:109:TYR:CZ	2.44	0.53
3:A:218:ILE:HB	3:A:229:ALA:HB3	1.91	0.52
3:A:179:ILE:HG22	3:A:180:SER:N	2.25	0.52
3:A:213:GLN:HA	3:A:213:GLN:HE21	1.74	0.52
2:G:14:DA:H2"	2:G:15:DA:C5'	2.40	0.51
1:B:6:DT:H2"	1:B:7:DT:H5"	1.92	0.51
3:A:173:ARG:HH11	3:A:173:ARG:HG2	1.76	0.51
3:A:277:GLN:NE2	3:A:277:GLN:HA	2.26	0.51
3:A:277:GLN:HE21	3:A:277:GLN:HA	1.74	0.51
3:A:213:GLN:HA	3:A:213:GLN:NE2	2.27	0.50
3:A:110:ARG:HG3	3:A:110:ARG:O	2.12	0.49
3:A:174:ASP:C	3:A:176:GLU:H	2.16	0.49
3:A:70:ALA:HB1	3:A:100:PRO:HB3	1.94	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:209:ASP:O	3:A:213:GLN:HG2	2.13	0.49
3:A:174:ASP:O	3:A:176:GLU:N	2.46	0.49
1:B:6:DT:C2'	1:B:7:DT:H5''	2.44	0.48
3:A:57:THR:HG22	4:A:348:HOH:O	2.13	0.48
3:A:272:LEU:H	3:A:278:ARG:HH11	1.61	0.48
1:B:8:DC:N4	2:G:9:DG:H1	2.11	0.47
3:A:234:LEU:HG	3:A:238:GLN:NE2	2.29	0.47
3:A:102:LYS:CD	3:A:106:THR:HA	2.32	0.47
2:G:12:DT:H2''	2:G:13:DT:H5'	1.95	0.47
2:G:12:DT:C2'	2:G:13:DT:H5''	2.46	0.46
2:G:11:DA:H2''	2:G:12:DT:C5'	2.38	0.46
3:A:237:GLN:O	3:A:241:ARG:HG3	2.14	0.46
1:B:6:DT:H2''	1:B:7:DT:C5'	2.46	0.45
3:A:132:PRO:O	3:A:136:LEU:HD23	2.17	0.45
1:B:4:DA:H1'	1:B:5:DA:H5''	1.98	0.44
3:A:174:ASP:C	3:A:176:GLU:N	2.70	0.44
1:B:6:DT:H1'	1:B:7:DT:H5''	2.00	0.44
2:G:12:DT:C1'	2:G:13:DT:H5''	2.48	0.44
2:G:12:DT:H2''	2:G:13:DT:H5''	2.00	0.43
3:A:75:LYS:HB3	3:A:76:PRO:HD3	2.01	0.42
3:A:104:PRO:CG	3:A:107:ASN:HB2	2.50	0.42
2:G:15:DA:H2''	2:G:16:DG:C8	2.55	0.42
3:A:278:ARG:HD2	4:A:452:HOH:O	2.20	0.42
1:B:1:DC:H2'	1:B:2:DT:H72	2.02	0.42
1:B:5:DA:H2'	1:B:6:DT:H72	2.01	0.41
3:A:99:LEU:HA	3:A:100:PRO:HD3	1.80	0.41
3:A:173:ARG:NH1	3:A:173:ARG:HG2	2.35	0.41
2:G:16:DG:N2	3:A:99:LEU:HD11	2.36	0.40
3:A:145:TRP:CH2	3:A:233:GLU:HB2	2.56	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:8:DC:O3'	2:G:9:DG:P[2_765]	1.60	0.60

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
3	A	253/255 (99%)	237 (94%)	11 (4%)	5 (2%)	11 2

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	104	PRO
3	A	107	ASN
3	A	223	VAL
3	A	181	GLY
3	A	175	PRO

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
3	A	224/224 (100%)	223 (100%)	1 (0%)	95 93

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	177	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	31	GLN
3	A	68	GLN
3	A	84	GLN
3	A	134	ASN
3	A	144	GLN
3	A	161	HIS
3	A	190	GLN
3	A	213	GLN
3	A	237	GLN

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Mol	Chain	Res	Type
3	A	238	GLN
3	A	245	GLN
3	A	277	GLN

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 ⓘ

There are no ligands in this entry.

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(Å²)	Q<0.9	
1	B	8/8 (100%)	0.56	0	100	100	40, 54, 64, 73	0
2	G	8/8 (100%)	0.88	0	100	100	23, 61, 72, 72	0
3	A	255/255 (100%)	0.75	30 (11%)	5	4	12, 24, 61, 78	0
All	All	271/271 (100%)	0.75	30 (11%)	6	4	12, 26, 68, 78	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	106	THR	9.4
3	A	105	GLY	8.4
3	A	179	ILE	8.3
3	A	177	MET	7.6
3	A	107	ASN	7.6
3	A	108	ASP	7.1
3	A	104	PRO	7.0
3	A	180	SER	6.7
3	A	175	PRO	6.6
3	A	178	GLY	5.2
3	A	174	ASP	5.0
3	A	176	GLU	4.7
3	A	234	LEU	4.5
3	A	103	LYS	4.4
3	A	100	PRO	3.9
3	A	99	LEU	3.5
3	A	173	ARG	3.4
3	A	26	LEU	3.3
3	A	101	VAL	3.3
3	A	109	TYR	3.2
3	A	64	TYR	2.9
3	A	275	GLU	2.7
3	A	231	THR	2.5

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Mol	Chain	Res	Type	RSRZ
3	A	110	ARG	2.5
3	A	102	LYS	2.4
3	A	62	LYS	2.2
3	A	24	THR	2.2
3	A	237	GLN	2.1
3	A	144	GLN	2.1
3	A	145	TRP	2.0

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 ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.