

Full wwPDB X-ray Structure Validation Report (i)

Aug 2, 2023 - 07:29 AM EDT

PDB ID : 1CL8 Title : A PRE-TRANSITION STATE ECO RI ENDONUCLEASE/COGNATE DNA (TCGCGAPTTCGCG) COMPLEX WITH DNA BASE ANALOG PURINE (P) Authors : Horvath, M.; Rosenberg, J.M. Deposited on : 1999-05-06 Resolution : 1.80 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 https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

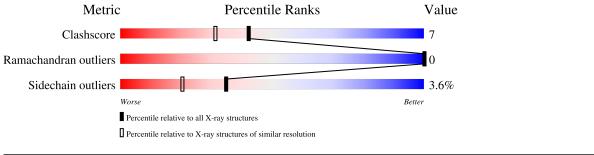
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.34

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\hbox{-}RAY\,DIFFRACTION$

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	Similar resolution
Metric	$(\# {\rm Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain			
1	В	13	69%	31%		
2	А	276	79%	14% • 5%		



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2471 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 DNA chain called DNA (5'-D(*TP*CP*GP*CP*GP*AP*(PRN)P*TP*TP* CP*GP*CP*G)-3').

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace			
1	В	13	Total 262		N 47	O 77	Р 12	0	0	0

• Molecule 2 is a protein called PROTEIN (ENDONUCLEASE).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	А	261	Total 2051	C 1294	N 356	0 394	${ m S} 7$	0	0	0

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	23	TotalO2525	0	2
3	А	132	Total O 133 133	0	1



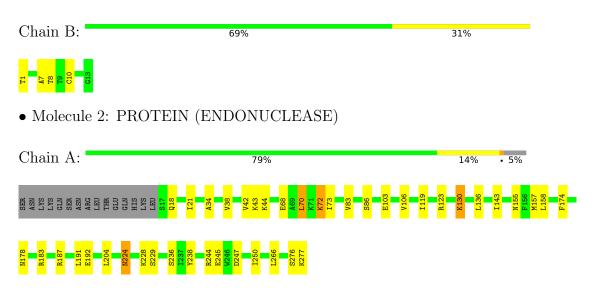


3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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. 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. 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: DNA (5'-D(*TP*CP*GP*CP*GP*AP*(PRN)P*TP*TP*CP*GP*CP*G)-3')





4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 3 2 1	Depositor	
Cell constants	117.83Å 117.83Å 48.99Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor	
Resolution (Å)	8.00 - 1.80	Depositor	
% Data completeness	98.3 (8.00-1.80)	Depositor	
(in resolution range)	50.5 (0.00-1.00)	Depositor	
R_{merge}	0.10	Depositor	
R _{sym}	(Not available)	Depositor	
Refinement program	X-PLOR 3.851	Depositor	
R, R_{free}	0.243 , 0.287	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	2471	wwPDB-VP	
Average B, all atoms $(Å^2)$	36.0	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: PRN

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		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	В	0.25	0/269	0.71	0/411	
2	А	0.26	0/2084	0.52	0/2805	
All	All	0.26	0/2353	0.54	0/3216	

There are no bond length outliers.

There are no bond angle outliers.

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	В	262	0	147	3	0
2	А	2051	0	2057	29	0
3	А	133	0	0	0	0
3	В	25	0	0	0	0
All	All	2471	0	2204	31	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 7.

All (31) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
2:A:143:ILE:HD11	2:A:204:LEU:HD11	1.69	0.74
2:A:143:ILE:HD12	2:A:174:PHE:CE1	2.25	0.70
2:A:247:ASP:HB3	2:A:250:ILE:HG12	1.75	0.69
2:A:143:ILE:HD12	2:A:174:PHE:CZ	2.31	0.66
1:B:10:DC:H3'	2:A:130:LYS:HD2	1.79	0.63
1:B:7:PRN:H4'	1:B:8:DT:H5'	1.82	0.61
2:A:130:LYS:HD3	2:A:130:LYS:H	1.71	0.55
2:A:178:ASN:ND2	2:A:192:GLU:HA	2.22	0.54
2:A:68:GLU:O	2:A:72:LYS:HD3	2.09	0.53
2:A:119:ILE:O	2:A:123:ARG:HG2	2.09	0.51
2:A:70:LEU:HD11	2:A:155:ASN:HB3	1.92	0.51
2:A:183:ARG:HG2	2:A:187:ARG:O	2.13	0.48
2:A:73:ILE:CD1	2:A:158:LEU:HB3	2.45	0.46
2:A:244:ARG:NH2	2:A:245:GLU:HG2	2.31	0.46
2:A:106:VAL:HG13	2:A:157:MET:CE	2.45	0.45
2:A:224:ASN:HD22	2:A:224:ASN:N	2.14	0.45
2:A:143:ILE:HG12	2:A:143:ILE:O	2.17	0.44
2:A:276:SER:O	2:A:277:LYS:HG2	2.18	0.43
2:A:38:VAL:O	2:A:42:VAL:HG23	2.18	0.43
2:A:136:LEU:HD21	2:A:191:LEU:HD21	2.00	0.43
2:A:73:ILE:HD13	2:A:158:LEU:HB3	2.00	0.43
2:A:236:SER:HB3	2:A:238:TYR:HE1	1.83	0.43
2:A:34:ALA:O	2:A:38:VAL:HG23	2.19	0.43
2:A:21:ILE:HD12	2:A:21:ILE:N	2.34	0.42
2:A:178:ASN:HD22	2:A:192:GLU:HA	1.85	0.42
2:A:228:LYS:O	2:A:229:SER:HB3	2.19	0.42
1:B:1:DT:H6	1:B:1:DT:HO5'	1.66	0.42
2:A:18:GLN:O	2:A:21:ILE:HD13	2.20	0.41
2:A:130:LYS:H	2:A:130:LYS:CD	2.28	0.41
2:A:244:ARG:HH22	2:A:245:GLU:HG2	1.84	0.41
2:A:83:VAL:HB	2:A:86:SER:HG	1.84	0.41

There are no symmetry-related clashes.

5.3 Torsion angles (i)

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	Percent	iles
2	А	259/276~(94%)	247~(95%)	12 (5%)	0	100 1	.00

There are no Ramachandran outliers to report.

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
2	А	225/240~(94%)	217~(96%)	8 (4%)	35 20

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	А	43	LYS
2	А	44	LYS
2	А	70	LEU
2	А	72	LYS
2	А	103	GLU
2	А	130	LYS
2	А	224	ASN
2	А	266	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type	
2	А	124	ASN	
2	А	178	ASN	
2	А	224	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)

1 non-standard protein/DNA/RNA residue is 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	Mol Type Chain		ain Res Li		Bond lengths			Bond angles		
	Moi Type Cham Re	nes	s Link	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2	
1	PRN	В	7	1	16,22,23	0.55	0	13,31,34	0.75	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
1	PRN	В	7	1	_	0/3/21/22	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	В	7	PRN	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.



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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

