

wwPDB X-ray Structure Validation Summary Report (i)

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PDB ID	:	1A73
Title	:	INTRON-ENCODED ENDONUCLEASE I-PPOI COMPLEXED WITH
		DNA
Authors	:	Flick, K.E.; Monnat Junior, R.J.; Stoddard, B.L.
Deposited on		
Resolution	:	1.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (1)) were used in the production of this report:

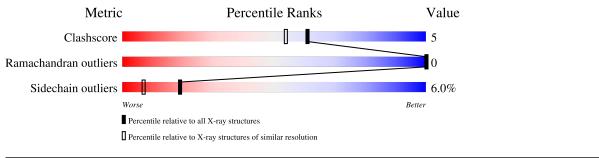
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

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	Qua	ality of chain	
1	С	13	38%	46%	15%
1	Е	13	859	%	15%
2	D	8	38%	50%	12%
2	F	8	8	8%	12%
3	А	163	8	39%	10% ••
3	В	163	86	%	12%



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 3743 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*TP*GP*AP*CP*TP*CP*TP*CP*TP* TP*AP*A)-3').

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	С	13	Total	С	Ν	Ο	Р	0	0	0
	U	10	259	127	41	79	12	0	0	0
1	F	13	Total	С	Ν	Ο	Р	0	0	0
	Ľ	15	259	127	41	79	12	0	U	0

• Molecule 2 is a DNA chain called DNA (5'-D(P*GP*AP*GP*AP*GP*TP*CP*A)-3').

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
0	Л	0	Total	С	Ν	Ο	Р	0	0	0
	D	0	169	79	35	47	8	0		
0	Б	0	Total	С	Ν	Ο	Р	0	0	0
	Г	8	169	79	35	47	8			

• Molecule 3 is a protein called INTRON 3 (I-PPO) ENCODED ENDONUCLEASE.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	Δ	162	Total	С	Ν	0	S	0	0	0
5	A	102	1245	786	232	219	8	0	0	0
2	P	162	Total	С	Ν	0	S	0	0	0
J	D	102	1245	786	232	219	8	0		U

• Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	Ε	1	Total Mg 1 1	0	0
4	В	1	Total Mg 1 1	0	0

• Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	2	Total Zn 2 2	0	0
5	В	2	Total Zn 2 2	0	0

• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	С	29	TotalO2929	0	0
6	D	14	Total O 14 14	0	0
6	Е	33	Total O 33 33	0	0
6	F	21	Total O 21 21	0	0
6	А	134	Total O 134 134	0	0
6	В	160	Total O 160 160	0	0



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*TP*GP*AP*CP*TP*CP*TP*CP*TP*TP*AP*A)-3')

Chain C:	38%	46%	15%
11 12 12 13 13 13 110 111 111 111 111			
• Molecule 1: I	DNA (5'-D(*TP*)	TP*GP*AP*CP*TP*CP*'	TP*CP*TP*TP*AP*A)-3'
Chain E:		85%	15%
11 18 13			
• Molecule 2: I	ONA (5'-D(P*GP))	*AP*GP*AP*GP*TP*CF	•*A)-3')
Chain D:	38%	50%	12%
614 A15 616 616 618 719 719 720 821			
• Molecule 2: I	DNA (5'-D(P*GP	*AP*GP*AP*GP*TP*CF	•*A)-3')
Chain F:		88%	12%
014 A21			
• Molecule 3: I	NTRON 3 (I-PPO	O) ENCODED ENDONU	CLEASE
Chain A:		89%	10%
MET A2 E17 V29 L39 N69 N69 N69	V/1 184 184 184 184 189 199 199 108 7125 7125 7126	4155 V162 V163	
• Molecule 3: I	NTRON 3 (I-PPO	O) ENCODED ENDONU	CLEASE
Chain B:		86%	12%
		WORLDWIDE	

PROTEIN DATA BANK





4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 31 2 1	Depositor	
Cell constants	113.70Å 113.70Å 88.40Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor	
Resolution (Å)	50.00 - 1.80	Depositor	
% Data completeness	99.4 (50.00-1.80)	Depositor	
(in resolution range)	55.4 (50.00-1.00)	Depositor	
R_{merge}	0.05	Depositor	
R _{sym}	0.05	Depositor	
Refinement program	X-PLOR 3.843	Depositor	
R, R_{free}	0.208 , 0.297	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	3743	wwPDB-VP	
Average B, all atoms $(Å^2)$	17.0	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: ZN, 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		Bo	nd angles
MOI		RMSZ	# Z > 5	RMSZ	# Z > 5
1	С	0.63	0/288	0.81	1/442~(0.2%)
1	Е	0.72	0/288	0.78	0/442
2	D	0.95	1/190~(0.5%)	0.85	1/290~(0.3%)
2	F	0.84	1/190~(0.5%)	0.77	0/290
3	А	0.42	0/1286	0.67	0/1760
3	В	0.43	0/1286	0.70	1/1760~(0.1%)
All	All	0.54	2/3528~(0.1%)	0.72	3/4984~(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	С	0	1
2	D	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
2	D	14	DG	OP3-P	-8.78	1.50	1.61
2	F	14	DG	OP3-P	-8.12	1.51	1.61

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
3	В	140	ARG	NE-CZ-NH2	-6.69	116.95	120.30
2	D	14	DG	OP1-P-OP2	-5.70	111.06	119.60
1	С	12	DA	C5'-C4'-C3'	-5.52	104.17	114.10



There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	С	10	DT	Sidechain
2	D	17	DA	Sidechain

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	С	259	0	151	6	0
1	Е	259	0	150	1	0
2	D	169	0	90	4	0
2	F	169	0	90	0	0
3	А	1245	0	1191	7	0
3	В	1245	0	1191	12	0
4	В	1	0	0	0	0
4	Ε	1	0	0	0	0
5	А	2	0	0	0	0
5	В	2	0	0	0	0
6	А	134	0	0	1	0
6	В	160	0	0	1	0
6	С	29	0	0	0	0
6	D	14	0	0	0	0
6	Е	33	0	0	0	0
6	F	21	0	0	0	0
All	All	3743	0	2863	28	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 5.

The worst 5 of 28 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:19:DT:H2"	2:D:20:DC:H5"	1.35	1.07
3:B:2:ALA:HB3	3:B:7:GLN:HB3	1.58	0.85
1:C:10:DT:H2"	1:C:11:DT:H5'	1.64	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:7:DC:H2"	1:E:8:DT:H5'	1.63	0.79
3:B:2:ALA:HB2	3:B:68:ILE:HG13	1.68	0.74

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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	Perce	ntiles
3	А	160/163~(98%)	159~(99%)	1 (1%)	0	100	100
3	В	160/163~(98%)	154 (96%)	6 (4%)	0	100	100
All	All	320/326~(98%)	313~(98%)	7~(2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	Percen	tiles
3	А	133/134~(99%)	125~(94%)	8 (6%)	19	7
3	В	133/134~(99%)	125~(94%)	8 (6%)	19	7
All	All	266/268~(99%)	250~(94%)	16 (6%)	19	7

5 of 16 residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
3	В	140	ARG
3	В	99	LEU
3	В	3	LEU
3	В	84	LEU
3	А	162	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
3	А	90	ASN
3	В	69	ASN
3	В	90	ASN
3	В	98	HIS

5.3.3 RNA (i)

There are no RNA molecules 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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.



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.

