

wwPDB X-ray Structure Validation Summary Report (i)

May 29, 2020 – 06:26 am BST

PDB ID : 4Y1O

Title : Oceanobacillus iheyensis group II intron domain 1 Authors : Zhao, C.; Rajashankar, K.R.; Marcia, M.; Pyle, A.M.

Deposited on : 2015-02-08

Resolution : 2.95 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 following versions of software and data (see references (1)) were used in the production of this report:

 $\begin{array}{ccc} Mol Probity & : & 4.02b\text{-}467 \\ Xtriage \ (Phenix) & : & 1.13 \end{array}$

EDS: 2.11

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac: 5.8.0158

CCP4 : 7.0.044 (Gargrove) oteins) : Engh & Huber (2001)

Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

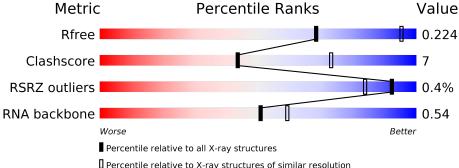
Validation Pipeline (wwPDB-VP) : 2.11

Overall quality at a glance (i) 1

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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.



Percentile relative to X-ray structures of similar resolution

Metric	Whole archive	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{resolution range}(ext{Å}))$
R_{free}	130704	3104 (3.00-2.92)
Clashscore	141614	3462 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)
RNA backbone	3102	1065 (3.22-2.70)

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 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\% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain			
1	A	275	54%	32%	6% • 6%	
1	В	275	60%	31%	• 7%	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MG	A	404	_	_	_	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MG	В	403	_	-	-	X
2	MG	В	405	-	-	-	X



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 11067 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 RNA chain called group II intron, domain 1.

Mol	Chain	Residues		Atoms			ZeroOcc	AltConf	Trace	
1	A	258	Total 5537	C 2474	N 1022	O 1783	P 258	23	0	0
1	В	256	Total 5507	C 2460	N 1027	O 1764	P 256	26	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	G	U	conflict	GB 42632302
A	91	A	С	conflict	GB 42632302
A	92	A	G	conflict	GB 42632302
A	269	U	G	conflict	GB 42632302
A	270	С	G	conflict	GB 42632302
В	-4	G	U	conflict	GB 42632302
В	91	A	С	conflict	GB 42632302
В	92	A	G	conflict	GB 42632302
В	269	U	G	conflict	GB 42632302
В	270	С	G	conflict	GB 42632302

• Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	12	Total Mg 12 12	0	0
2	A	7	Total Mg 7 7	0	0

• Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	Total K 1 1	0	0

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

• Molecule 4 is water.

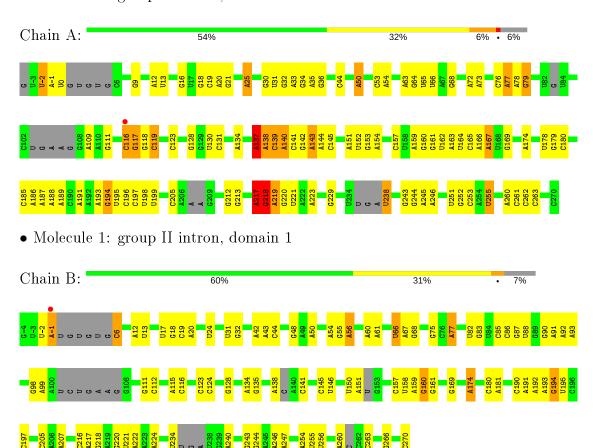
Mol	Chain	Residues	Residues Atoms		${f AltConf}$
4	A	1	Total O 1 1	0	0
4	В	1	Total O 1 1	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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 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: group II intron, domain 1





4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 1 21 1	Depositor	
Cell constants	84.34Å 132.25Å 84.56Å	D	
a, b, c, α , β , γ	90.00° 91.87° 90.00°	Depositor	
Resolution (Å)	40.25 - 2.95	Depositor	
Resolution (A)	40.25 - 2.95	EDS	
% Data completeness	98.6 (40.25-2.95)	Depositor	
(in resolution range)	98.7 (40.25-2.95)	EDS	
R_{merge}	(Not available)	Depositor	
R_{sum}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	1.30 (at 2.95Å)	Xtriage	
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor	
υ .	0.179 , 0.224	Depositor	
R, R_{free}	0.180 , 0.224	DCC	
R_{free} test set	1935 reflections (5.02%)	wwPDB-VP	
Wilson B-factor (Å ²)	91.3	Xtriage	
Anisotropy	0.180	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.27, 79.5	EDS	
L-test for twinning ²	$< L >=0.50, < L^2>=0.33$	Xtriage	
	0.000 for l,k,-h		
Estimated twinning fraction	0.026 for h,-k,-l	Xtriage	
	0.020 for $l,-k,h$		
F_o, F_c correlation	0.96	EDS	
Total number of atoms	11067	wwPDB-VP	
Average B, all atoms $(Å^2)$	107.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.69% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities estimated from amplitudes.

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: K, 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	Bo	nd lengths	Bond angles		
WIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z >5	
1	A	0.58	0/6199	1.12	18/9654 (0.2%)	
1	В	0.59	$1/6168 \; (0.0\%)$	1.13	21/9606 (0.2%)	
All	All	0.58	$1/12367 \ (0.0\%)$	1.12	39/19260 (0.2%)	

All (1) bond length outliers are listed below:

\mathbf{Mol}	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\mathbf{Ideal}(\mathbf{\AA})$
1	В	77	Α	N9-C4	5.80	1.41	1.37

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}(^o)$
1	В	6	С	N3-C2-O2	-10.89	114.28	121.90
1	В	116	С	N1-C2-O2	8.51	124.01	118.90
1	В	116	С	C2-N1-C1'	8.31	127.94	118.80
1	A	238	U	N3-C2-O2	-8.02	116.59	122.20
1	A	238	U	C5-C4-O4	7.45	130.37	125.90

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	A	5537	0	2788	59	0
1	В	5507	0	2770	46	0
2	A	7	0	0	0	0
2	В	12	0	0	0	0
3	A	1	0	0	0	0
3	В	1	0	0	0	0
4	A	1	0	0	0	0
4	В	1	0	0	0	0
All	All	11067	0	5558	105	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.

The worst 5 of 105 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{array}{l} ext{Interatomic} \ ext{distance } (ext{Å}) \end{array}$	Clash overlap (Å)	
1:A:218:G:H1'	1:A:219:A:H5'	1.51	0.93	
1:A:179:G:H5"	1:A:180:C:H5'	1.64	0.80	
1:A:65:U:OP1	1:A:116:C:N4	2.16	0.78	
1:A:50:A:N6	1:A:198:U:O4	2.16	0.78	
1:B:159:A:H2	1:B:218:G:H22	1.31	0.75	

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein molecules in this entry.

5.3.2 Protein sidechains (i)

There are no protein molecules in this entry.

5.3.3 RNA (i)

Mol	Chain	${f Analysed}$	Backbone Outliers	Pucker Outliers
1	A	252/275~(91%)	44 (17%)	6 (2%)
1	В	249/275~(90%)	28 (11%)	0
All	All	501/550 (91%)	72 (14%)	6 (1%)



5 of 72 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	-2	U
1	A	0	U
1	A	12	A
1	A	13	U
1	A	33	A

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	143	A
1	A	218	G
1	A	153	G
1	A	140	A
1	A	217	A

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)

Of 21 ligands modelled in this entry, 21 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)

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, 95^{th} 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	${f Analysed}$	<RSRZ $>$	$\#\mathrm{RSRZ}{>}2$		$OWAB(A^2)$	Q<0.9
1	A	258/275~(93%)	-0.24	1 (0%)	92 84	57, 100, 169, 266	4 (1%)
1	В	256/275~(93%)	-0.17	1 (0%)	92 84	59, 101, 168, 260	4 (1%)
All	All	514/550~(93%)	-0.20	2 (0%)	92 84	57, 100, 169, 266	8 (1%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	A	116	С	2.9	
1	В	-1	A	2.4	

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)

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. The B-factors column lists the minimum, median, 95^{th} 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	${f Res}$	Atoms	RSCC	RSR	${f B-factors}({f A}^2)$	Q<0.9
2	MG	В	408	1/1	0.76	0.35	106,106,106,106	0
2	MG	В	405	1/1	0.77	0.40	104,104,104,104	0
3	K	A	407	1/1	0.77	0.39	199,199,199,199	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	MG	A	404	1/1	0.78	0.98	87,87,87,87	0
2	MG	В	407	1/1	0.80	0.28	84,84,84,84	0
2	MG	В	403	1/1	0.80	0.45	91,91,91,91	0
2	MG	В	406	1/1	0.81	0.28	111,111,111,111	0
2	MG	В	410	1/1	0.84	0.20	98,98,98,98	0
2	MG	В	411	1/1	0.86	0.14	100,100,100,100	0
3	K	В	412	1/1	0.88	0.66	143,143,143,143	0
2	MG	В	404	1/1	0.88	0.23	76,76,76,76	0
2	MG	В	401	1/1	0.90	0.44	80,80,80,80	0
2	MG	A	405	1/1	0.91	0.17	86,86,86,86	0
2	MG	В	400	1/1	0.94	0.53	94,94,94,94	0
2	MG	A	401	1/1	0.95	0.84	84,84,84,84	0
2	MG	В	402	1/1	0.95	0.34	71,71,71,71	0
2	MG	В	409	1/1	0.96	0.23	90,90,90,90	0
2	MG	A	402	1/1	0.96	0.39	76,76,76,76	0
2	MG	A	403	1/1	0.96	0.44	73,73,73,73	0
2	MG	A	406	1/1	0.97	0.36	98,98,98,98	0
2	MG	A	400	1/1	0.97	0.30	70,70,70,70	0

6.5 Other polymers (i)

There are no such residues in this entry.

