

# Full wwPDB X-ray Structure Validation Report (i)

#### Nov 22, 2023 – 12:49 PM JST

PDB ID	:	7W9X
Title	:	Crystal structure of Bacillus subtilis YugJ in complex with nickel
Authors	:	Cho, H.Y.; Nam, M.S.; Hong, H.J.; Song, W.S.; Yoon, S.I.
Deposited on	:	2021-12-11
Resolution	:	2.15  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 (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
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 2.15 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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% 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	А	393	5% 94%	5% •
1	В	393	90%	6% •



#### 7W9X

## 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5835 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.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Λ	297	Total	С	Ν	0	$\mathbf{S}$	0	1	0
1	I A	307	2964	1895	494	561	14	0		0
1	Р	201	Total	С	Ν	0	S	0	0	0
I B	381	2753	1757	465	520	11	0	0	0	

• Molecule 1 is a protein called Iron-containing alcohol dehydrogenase.

Chain	Residue	Modelled	Actual	Comment	Reference
А	-5	GLY	-	expression tag	UNP A0A5F2KLJ3
А	-4	SER	-	expression tag	UNP A0A5F2KLJ3
А	-3	ALA	-	expression tag	UNP A0A5F2KLJ3
А	-2	LYS	-	expression tag	UNP A0A5F2KLJ3
A	-1	ASP	-	expression tag	UNP A0A5F2KLJ3
A	0	PRO	-	expression tag	UNP A0A5F2KLJ3
В	-5	GLY	-	expression tag	UNP A0A5F2KLJ3
В	-4	SER	-	expression tag	UNP A0A5F2KLJ3
В	-3	ALA	-	expression tag	UNP A0A5F2KLJ3
В	-2	LYS	-	expression tag	UNP A0A5F2KLJ3
В	-1	ASP	-	expression tag	UNP A0A5F2KLJ3
B	0	PRO	-	expression tag	UNP A0A5F2KLJ3

There are 12 discrepancies between the modelled and reference sequences:

• Molecule 2 is NICKEL (II) ION (three-letter code: NI) (formula: Ni) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total Ni 1 1	0	0
2	В	1	Total Ni 1 1	0	0

• Molecule 3 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	80	Total         O           80         80	0	0
3	В	36	Total O 36 36	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 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: Iron-containing alcohol dehydrogenase







## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	62.66Å 114.52Å 118.74Å	Deperitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
$\mathbf{P}_{\text{acclution}}(\hat{\mathbf{A}})$	29.29 - 2.15	Depositor
Resolution (A)	29.29 - 2.15	EDS
% Data completeness	99.7 (29.29-2.15)	Depositor
(in resolution range)	99.7 (29.29-2.15)	EDS
R <sub>merge</sub>	0.07	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.95 (at 2.16Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
D D.	0.203 , $0.241$	Depositor
$\mathbf{n}, \mathbf{n}_{free}$	0.203 , $0.241$	DCC
$R_{free}$ test set	2376 reflections $(5.05%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	33.4	Xtriage
Anisotropy	0.377	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.36 , 57.9	EDS
L-test for twinning <sup>2</sup>	$< L >=0.48, < L^2>=0.31$	Xtriage
Estimated twinning fraction	0.015 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5835	wwPDB-VP
Average B, all atoms $(Å^2)$	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.33% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities 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: NI

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).

Mal	Chain	Bond	lengths	Bond angles		
MIOI	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.42	0/3034	0.55	0/4132	
1	В	0.41	0/2814	0.54	0/3843	
All	All	0.41	0/5848	0.54	0/7975	

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	А	2964	0	2851	10	0
1	В	2753	0	2495	18	0
2	А	1	0	0	0	0
2	В	1	0	0	0	0
3	А	80	0	0	0	0
3	В	36	0	0	1	0
All	All	5835	0	5346	26	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 2.

All (26) close contacts within the same asymmetric unit are listed below, sorted by their clash



magnitude.

A + amo 1	A + 2	Interatomic	Clash
Atom-1	Atom-2	distance $(\text{\AA})$	overlap (Å)
1:B:205:HIS:HD2	1:B:207:VAL:H	1.28	0.81
1:A:205:HIS:HD2	1:A:207:VAL:H	1.35	0.74
1:A:215:ARG:NH2	1:B:226:GLU:OE2	2.32	0.61
1:A:226:GLU:OE2	1:B:215:ARG:NH2	2.32	0.59
1:B:145:GLU:OE2	1:B:249:THR:HG22	2.03	0.59
1:B:216:MET:HB3	1:B:256:LEU:HD21	1.83	0.59
1:B:205:HIS:CD2	1:B:207:VAL:H	2.15	0.58
1:B:205:HIS:HE1	3:B:507:HOH:O	1.88	0.56
1:B:94:ALA:HB1	1:B:100:VAL:HG12	1.90	0.53
1:A:205:HIS:CD2	1:A:207:VAL:H	2.22	0.51
1:B:352:ASP:HA	1:B:355:LEU:HG	1.91	0.51
1:B:247:THR:HA	1:B:251:ALA:HB3	1.94	0.50
1:A:118:TRP:CH2	1:A:154:ASN:HB2	2.48	0.48
1:A:299:GLU:HG3	1:A:372:LYS:HB2	1.96	0.48
1:B:201:GLU:OE2	1:B:267:HIS:ND1	2.34	0.48
1:B:74:VAL:HG11	1:B:118:TRP:HB2	1.96	0.47
1:A:84:CYS:HA	1:A:89:ILE:CG1	2.46	0.46
1:B:205:HIS:HD2	1:B:207:VAL:N	2.03	0.45
1:B:145:GLU:CD	1:B:249:THR:HG22	2.37	0.44
1:B:256:LEU:HA	1:B:256:LEU:HD23	1.74	0.43
1:B:37:TYR:CZ	1:B:66:ALA:HB2	2.55	0.42
1:B:303:ARG:HA	1:B:303:ARG:HD2	1.79	0.42
1:A:352:ASP:HA	1:A:355:LEU:HG	2.02	0.41
1:A:84:CYS:HA	1:A:89:ILE:HG12	2.02	0.41
1:B:148:SER:HB2	1:B:165:SER:O	2.20	0.41
1:A:183:VAL:HA	1:A:184:PRO:HD3	1.98	0.40

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
1	А	386/393~(98%)	378~(98%)	8 (2%)	0	100	100
1	В	373/393~(95%)	361~(97%)	12 (3%)	0	100	100
All	All	759/786~(97%)	739~(97%)	20~(3%)	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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
1	А	304/326~(93%)	299~(98%)	5(2%)	62 67		
1	В	253/326~(78%)	249~(98%)	4 (2%)	62 67		
All	All	557/652~(85%)	548 (98%)	9(2%)	62 67		

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	12	LEU
1	А	75	SER
1	А	258	MET
1	А	289	PHE
1	А	316	GLU
1	В	74	VAL
1	В	289	PHE
1	В	315	GLU
1	В	316	GLU

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

Mol	Chain	Res	Type
1	А	205	HIS
1	В	187	HIS
1	В	198	HIS
1	В	205	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 2 ligands modelled in this entry, 2 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	Analysed	<RSRZ $>$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	387/393~(98%)	0.21	18 (4%) 31 41	21, 43, 65, 79	0
1	В	381/393~(96%)	0.69	55 (14%) 2 3	23, 54, 87, 106	0
All	All	768/786~(97%)	0.45	73 (9%) 8 12	21, 48, 83, 106	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	349	ASP	5.4
1	В	360	ASP	5.2
1	А	93	LEU	4.9
1	В	252	LEU	4.3
1	А	36	VAL	4.3
1	В	364	ALA	4.2
1	А	94	ALA	4.2
1	В	357	THR	4.0
1	А	100	VAL	3.9
1	В	141	ALA	3.9
1	В	348	TYR	3.9
1	А	92	LEU	3.8
1	В	346	ALA	3.7
1	В	142	THR	3.7
1	В	317	ALA	3.6
1	В	161	TYR	3.6
1	А	95	VAL	3.5
1	В	353	GLU	3.5
1	А	155	TRP	3.5
1	В	200	PHE	3.4
1	В	28	SER	3.2
1	В	58	ALA	3.1
1	В	37	TYR	3.1
1	A	126	GLN	3.1

Continued on next page...



Mol	Chain	Res	Type	RSRZ
1	В	1	MET	3.0
1	А	96	GLY	3.0
1	В	199	VAL	3.0
1	А	134	GLY	3.0
1	А	35	LEU	3.0
1	В	87	HIS	3.0
1	А	136	VAL	2.9
1	А	101	ILE	2.9
1	В	155	TRP	2.8
1	В	122	THR	2.8
1	В	98	GLY	2.8
1	В	101	ILE	2.7
1	В	135	THR	2.7
1	В	198	HIS	2.7
1	В	140	ALA	2.7
1	В	111	ALA	2.6
1	В	347	ASP	2.6
1	В	276	VAL	2.6
1	А	104	THR	2.6
1	В	367	THR	2.6
1	А	34	LEU	2.6
1	А	88	HIS	2.5
1	В	59	GLY	2.5
1	В	137	LEU	2.5
1	В	289	PHE	2.5
1	В	362	ALA	2.4
1	В	49	ASP	2.4
1	В	197	SER	2.4
1	В	285	LEU	2.4
1	В	33	VAL	2.4
1	В	30	GLY	2.4
1	В	354	GLN	2.4
1	А	161	TYR	2.4
1	В	93	LEU	2.3
1	В	127	PRO	2.3
1	В	114	ASP	2.2
1	В	365	ASN	2.2
1	В	358	ILE	2.2
1	В	113	TYR	2.2
1	В	136	VAL	2.2
1	В	351	ASN	2.2
1	В	61	THR	2.2

Continued from previous page...

Continued on next page...



Mol	Chain	Res	Type	RSRZ
1	В	62	VAL	2.1
1	А	135	THR	2.1
1	В	266	THR	2.1
1	В	144	SER	2.1
1	В	117	ALA	2.1
1	В	253	ASN	2.0
1	В	277	TYR	2.0

Continued from previous page...

## 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 monosaccharides 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	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q<0.9
2	NI	В	401	1/1	0.97	0.10	72,72,72,72	0
2	NI	А	401	1/1	0.98	0.08	30,30,30,30	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.









## 6.5 Other polymers (i)

There are no such residues in this entry.

