



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:32 AM GMT

PDB ID : 2R5X  
Title : Crystal structure of uncharacterized conserved protein YugN from *Geobacillus kaustophilus* HTA426  
Authors : Ramagopal, U.A.; Patskovsky, Y.; Shi, W.; Toro, R.; Meyer, A.J.; Freeman, J.; Wu, B.; Koss, J.; Groshong, C.; Rodgers, L.; Wasserman, S.; Sauder, J.M.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)  
Deposited on : 2007-09-04  
Resolution : 2.04 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

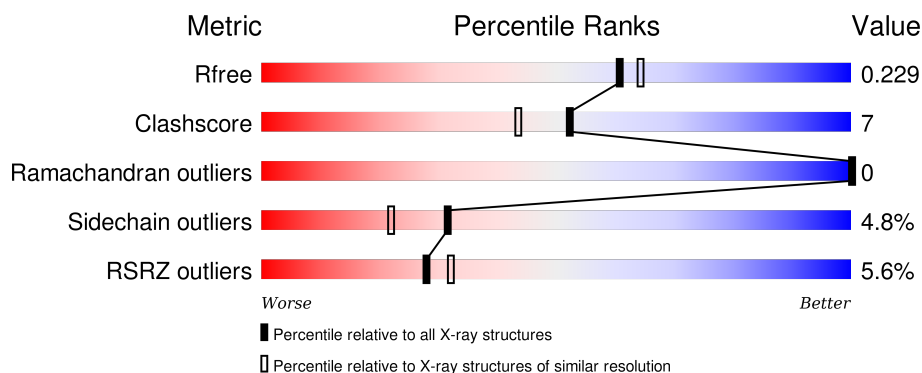
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.04 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))
$R_{free}$	91344	1192 (2.04-2.04)
Clashscore	102246	1269 (2.04-2.04)
Ramachandran outliers	100387	1258 (2.04-2.04)
Sidechain outliers	100360	1258 (2.04-2.04)
RSRZ outliers	91569	1194 (2.04-2.04)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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  $\leq 5\%$ . 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	129	<div> <div>3%</div> <div>79%</div> <div>10%</div> <div>11%</div> </div>
1	B	129	<div> <div>7%</div> <div>72%</div> <div>16%</div> <div>• • 9%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2140 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 protein called Uncharacterized conserved protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	115	Total	C	N	O	S	0	5	0
			978	622	167	186	3			
1	B	118	Total	C	N	O	S	0	9	0
			1029	657	171	198	3			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	EXPRESSION TAG	UNP Q5L106
A	0	SER	-	EXPRESSION TAG	UNP Q5L106
A	1	LEU	-	EXPRESSION TAG	UNP Q5L106
A	78	MET	LEU	ENGINEERED	UNP Q5L106
A	120	GLU	-	EXPRESSION TAG	UNP Q5L106
A	121	GLY	-	EXPRESSION TAG	UNP Q5L106
A	122	HIS	-	EXPRESSION TAG	UNP Q5L106
A	123	HIS	-	EXPRESSION TAG	UNP Q5L106
A	124	HIS	-	EXPRESSION TAG	UNP Q5L106
A	125	HIS	-	EXPRESSION TAG	UNP Q5L106
A	126	HIS	-	EXPRESSION TAG	UNP Q5L106
A	127	HIS	-	EXPRESSION TAG	UNP Q5L106
B	-1	MET	-	EXPRESSION TAG	UNP Q5L106
B	0	SER	-	EXPRESSION TAG	UNP Q5L106
B	1	LEU	-	EXPRESSION TAG	UNP Q5L106
B	78	MET	LEU	ENGINEERED	UNP Q5L106
B	120	GLU	-	EXPRESSION TAG	UNP Q5L106
B	121	GLY	-	EXPRESSION TAG	UNP Q5L106
B	122	HIS	-	EXPRESSION TAG	UNP Q5L106
B	123	HIS	-	EXPRESSION TAG	UNP Q5L106
B	124	HIS	-	EXPRESSION TAG	UNP Q5L106
B	125	HIS	-	EXPRESSION TAG	UNP Q5L106
B	126	HIS	-	EXPRESSION TAG	UNP Q5L106
B	127	HIS	-	EXPRESSION TAG	UNP Q5L106

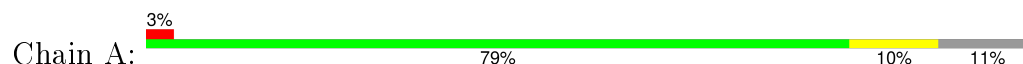
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	66	Total 66	O 66	0	0
2	B	67	Total 67	O 67	0	0

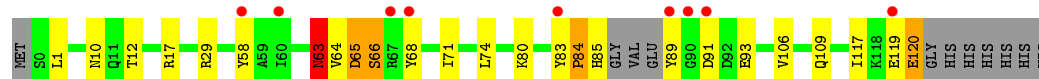
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Uncharacterized conserved protein



- Molecule 1: Uncharacterized conserved protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	79.16Å 92.32Å 33.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.04 31.78 – 2.04	Depositor EDS
% Data completeness (in resolution range)	99.8 (20.00-2.04) 99.6 (31.78-2.04)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.32 (at 2.05Å)	Xtrriage
Refinement program	REFMAC 5.3.0034	Depositor
R, $R_{free}$	0.198 , 0.233 0.200 , 0.229	Depositor DCC
$R_{free}$ test set	519 reflections (3.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	32.1	Xtrriage
Anisotropy	0.200	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 59.3	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Outliers	1 of 16456 reflections (0.006%)	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2140	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.04 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 6.1870e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup> Intensities estimated from amplitudes.

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

## 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	A	0.54	0/1011	0.59	0/1361
1	B	0.62	0/1076	0.68	4/1449 (0.3%)
All	All	0.58	0/2087	0.64	4/2810 (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	B	0	2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	29[A]	ARG	NE-CZ-NH1	5.84	123.22	120.30
1	B	29[B]	ARG	NE-CZ-NH1	5.84	123.22	120.30
1	B	29[A]	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	B	29[B]	ARG	NE-CZ-NH2	-5.64	117.48	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	63	ASN	Peptide
1	B	84	PRO	Peptide

## 5.2 Too-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 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	978	0	979	7	0
1	B	1029	0	1022	21	0
2	A	66	0	0	0	0
2	B	67	0	0	0	0
All	All	2140	0	2001	27	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 (27) 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)
1:B:63:ASN:ND2	1:B:66:SER:HB3	2.01	0.75
1:A:100:VAL:HG21	1:B:1:LEU:HD11	1.74	0.69
1:B:65:ASP:N	1:B:65:ASP:OD1	2.33	0.62
1:B:117:ILE:O	1:B:120:GLU:HB2	2.02	0.60
1:B:63:ASN:C	1:B:63:ASN:HD22	2.06	0.59
1:A:24[B]:ARG:HG2	1:A:24[B]:ARG:HH21	1.68	0.58
1:B:119:GLU:HA	1:B:119:GLU:OE1	2.06	0.55
1:B:106:VAL:HA	1:B:109:GLN:HE21	1.71	0.55
1:B:63:ASN:HD21	1:B:66:SER:HB3	1.72	0.54
1:B:119:GLU:O	1:B:120:GLU:C	2.45	0.54
1:A:3:PHE:HZ	1:A:78:MET:HE2	1.74	0.51
1:B:66:SER:O	1:B:68:TYR:N	2.47	0.48
1:B:83:TYR:CD1	1:B:84:PRO:HA	2.49	0.47
1:B:17:ARG:NH1	1:B:120:GLU:OE2	2.44	0.46
1:B:63:ASN:C	1:B:65:ASP:H	2.17	0.46
1:A:54:ARG:HB3	1:A:77:ILE:HG13	1.99	0.44
1:A:29[B]:ARG:HD3	1:A:40:TYR:CE1	2.52	0.44
1:B:85:HIS:N	1:B:85:HIS:CD2	2.85	0.44
1:A:24[A]:ARG:NH2	1:A:113:GLU:OE1	2.50	0.44
1:B:58[B]:TYR:CE2	1:B:74:LEU:HD21	2.53	0.44
1:B:12:THR:HA	1:B:71:ILE:O	2.18	0.44
1:A:27:PHE:HB3	1:A:40:TYR:HB3	2.01	0.42
1:B:64:VAL:CG1	1:B:64:VAL:O	2.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:80:LYS:HE3	1:B:93:GLU:HG3	2.02	0.41
1:B:63:ASN:ND2	1:B:65:ASP:OD1	2.54	0.41
1:B:66:SER:O	1:B:66:SER:OG	2.30	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	Percentiles	
1	A	115/129 (89%)	114 (99%)	1 (1%)	0	100	100
1	B	123/129 (95%)	119 (97%)	4 (3%)	0	100	100
All	All	238/258 (92%)	233 (98%)	5 (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 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	
1	A	109/115 (95%)	105 (96%)	4 (4%)	41	32
1	B	115/115 (100%)	108 (94%)	7 (6%)	23	13
All	All	224/230 (97%)	213 (95%)	11 (5%)	31	21

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0[A]	SER
1	A	0[B]	SER
1	A	61	GLU
1	A	99	LEU
1	B	10	ASN
1	B	63	ASN
1	B	65	ASP
1	B	66	SER
1	B	89	TYR
1	B	91	ASP
1	B	120	GLU

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

Mol	Chain	Res	Type
1	B	10	ASN
1	B	63	ASN
1	B	85	HIS
1	B	109	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules 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 [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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	115/129 (89%)	0.02	4 (3%)	48	54	23, 37, 87, 118	0
1	B	118/129 (91%)	0.16	9 (7%)	17	19	22, 34, 94, 114	1 (0%)
All	All	233/258 (90%)	0.09	13 (5%)	28	32	22, 36, 94, 118	1 (0%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	85	HIS	7.5
1	B	90	GLY	6.2
1	A	68	TYR	6.0
1	B	89	TYR	4.4
1	B	91	ASP	4.2
1	B	67[A]	ARG	3.9
1	A	67	ARG	3.7
1	B	68	TYR	3.5
1	B	83	TYR	2.8
1	B	60	ILE	2.6
1	B	58[A]	TYR	2.3
1	A	82	TYR	2.1
1	B	119	GLU	2.1

### 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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.