WORLDWIDE PDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 17, 2024 – 08:49 AM EDT

PDB ID	:	3KVP
Title	:	Crystal Structure of Uncharacterized protein ymzC Precursor from Bacillus subtilis, Northeast Structural Genomics Consortium Target SR378A
Authors	:	Kuzin, A.P.; Chen, Y.; Seetharaman, J.; Afonine, P.; Fang, F.; Xiao, R.; Cunningham, K.; Ma, L.; Chen, C.X.; Everett, J.K.; Nair, R.; Acton, T.B.; Rost, B.; Montelione, G.T.; Tong, L.; Hunt, J.F.; Northeast Structural Genomics Consortium (NESG)
Deposited on	:	2009-11-30
Resolution	:	2.40 Å(reported)

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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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
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)

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 2.40 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.
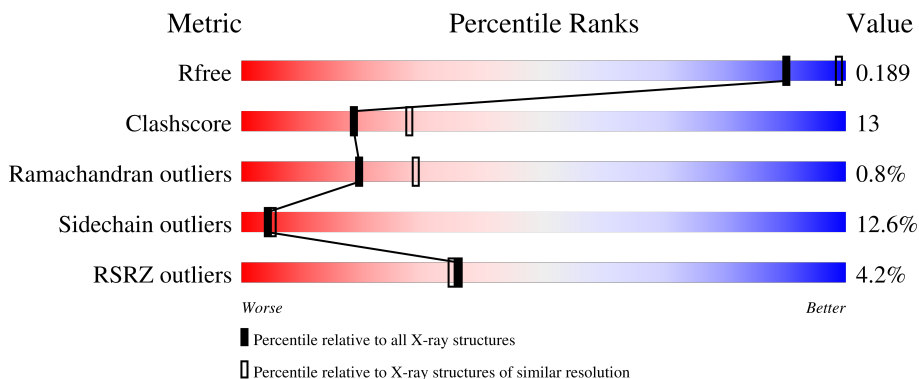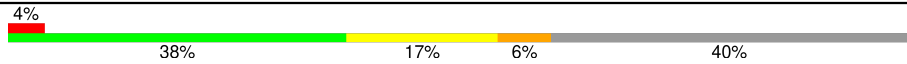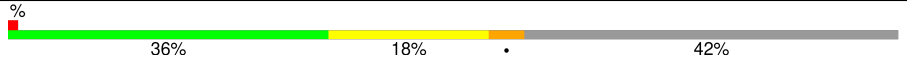

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	A	72	
1	B	72	
1	C	72	
1	D	72	

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Mol	Chain	Length	Quality of chain
1	E	72	4% ▬▬▬▬ 38% 17% 6% 40%
1	F	72	% ▬▬▬▬ 36% 18% • 42%

2   Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 2286 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 protein ymzC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	43	Total	C	N	O	Se	0	0	0
			364	231	58	74	1			
1	B	43	Total	C	N	O	Se	0	0	0
			363	231	58	73	1			
1	C	45	Total	C	N	O	Se	0	0	0
			382	243	60	78	1			
1	D	49	Total	C	N	O	Se	0	0	0
			421	266	70	84	1			
1	E	43	Total	C	N	O	Se	0	0	0
			364	232	58	73	1			
1	F	42	Total	C	N	O	Se	0	0	0
			354	226	57	70	1			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	expression tag	UNP O31797
A	65	LEU	-	expression tag	UNP O31797
A	66	GLU	-	expression tag	UNP O31797
A	67	HIS	-	expression tag	UNP O31797
A	68	HIS	-	expression tag	UNP O31797
A	69	HIS	-	expression tag	UNP O31797
A	70	HIS	-	expression tag	UNP O31797
A	71	HIS	-	expression tag	UNP O31797
A	72	HIS	-	expression tag	UNP O31797
B	1	MSE	-	expression tag	UNP O31797
B	65	LEU	-	expression tag	UNP O31797
B	66	GLU	-	expression tag	UNP O31797
B	67	HIS	-	expression tag	UNP O31797
B	68	HIS	-	expression tag	UNP O31797
B	69	HIS	-	expression tag	UNP O31797
B	70	HIS	-	expression tag	UNP O31797
B	71	HIS	-	expression tag	UNP O31797

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Chain	Residue	Modelled	Actual	Comment	Reference
B	72	HIS	-	expression tag	UNP O31797
C	1	MSE	-	expression tag	UNP O31797
C	65	LEU	-	expression tag	UNP O31797
C	66	GLU	-	expression tag	UNP O31797
C	67	HIS	-	expression tag	UNP O31797
C	68	HIS	-	expression tag	UNP O31797
C	69	HIS	-	expression tag	UNP O31797
C	70	HIS	-	expression tag	UNP O31797
C	71	HIS	-	expression tag	UNP O31797
C	72	HIS	-	expression tag	UNP O31797
D	1	MSE	-	expression tag	UNP O31797
D	65	LEU	-	expression tag	UNP O31797
D	66	GLU	-	expression tag	UNP O31797
D	67	HIS	-	expression tag	UNP O31797
D	68	HIS	-	expression tag	UNP O31797
D	69	HIS	-	expression tag	UNP O31797
D	70	HIS	-	expression tag	UNP O31797
D	71	HIS	-	expression tag	UNP O31797
D	72	HIS	-	expression tag	UNP O31797
E	1	MSE	-	expression tag	UNP O31797
E	65	LEU	-	expression tag	UNP O31797
E	66	GLU	-	expression tag	UNP O31797
E	67	HIS	-	expression tag	UNP O31797
E	68	HIS	-	expression tag	UNP O31797
E	69	HIS	-	expression tag	UNP O31797
E	70	HIS	-	expression tag	UNP O31797
E	71	HIS	-	expression tag	UNP O31797
E	72	HIS	-	expression tag	UNP O31797
F	1	MSE	-	expression tag	UNP O31797
F	65	LEU	-	expression tag	UNP O31797
F	66	GLU	-	expression tag	UNP O31797
F	67	HIS	-	expression tag	UNP O31797
F	68	HIS	-	expression tag	UNP O31797
F	69	HIS	-	expression tag	UNP O31797
F	70	HIS	-	expression tag	UNP O31797
F	71	HIS	-	expression tag	UNP O31797
F	72	HIS	-	expression tag	UNP O31797

- Molecule 2 is ACETIC ACID (three-letter code: ACY) (formula: $C_2H_4O_2$).

WORLDWIDE
PDB
PROTEIN DATA BANK
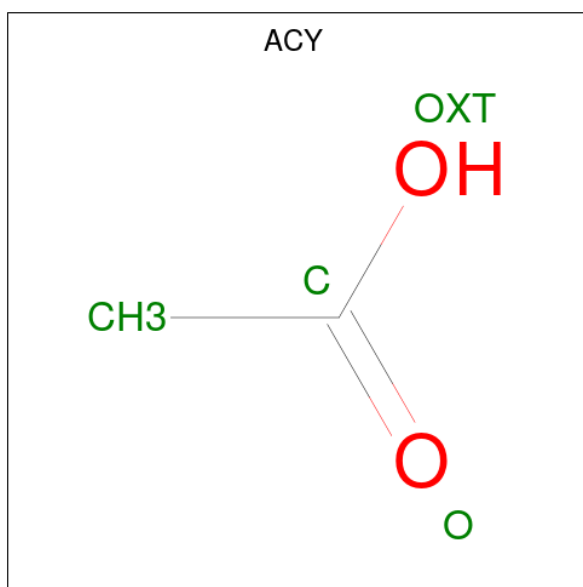
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0

• Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	12	Total 12	O 12	0	0
3	B	2	Total 2	O 2	0	0
3	C	2	Total 2	O 2	0	0
3	D	6	Total 6	O 6	0	0
3	E	1	Total 1	O 1	0	0
3	F	7	Total 7	O 7	0	0

3 Residue-property plots ⓘ

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: Uncharacterized protein ymzC

- Molecule 1: Uncharacterized protein ymzC

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- Molecule 1: Uncharacterized protein ymzC

- Molecule 1: Uncharacterized protein ymzC

%

Chain F:

36% 18% • 42%

MSE GLY ASN GLN ASP THR ILE ILE GLU THR ASP ASN GLY ASN SER ASP TYR GLU THR P20 Q21 H29 N30 V34 M35 E36 D37 G38 Y39 I40 K41 I42 Y43 E51 L54 K55 K56 E57 D61 GLU LEU GLU LEU GLU HIS HIS HIS HIS HIS

4   Data and refinement statistics   ⓘ

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	66.39Å 66.39Å 175.57Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.97 – 2.40 29.97 – 2.71	Depositor EDS
% Data completeness (in resolution range)	88.9 (29.97-2.40) 98.7 (29.97-2.71)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.17 (at 2.72Å)	Xtriage
Refinement program	PHENIX 1.5_2, CNS	Depositor
R, R_{free}	0.194 , 0.237 0.189 , 0.189	Depositor DCC
R_{free} test set	1118 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å^2)	60.6	Xtriage
Anisotropy	0.432	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 57.9	EDS
L-test for twinning[2]	$< \lvert L \rvert > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.043 for -h,-k,l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	2286	wwPDB-VP
Average B, all atoms (Å^2)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.68% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< \lvert L \rvert >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: ACY

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	0.52	0/373	0.62	0/500
1	B	0.38	0/372	0.55	0/499
1	C	0.40	0/390	0.54	0/523
1	D	0.48	0/432	0.57	0/580
1	E	0.41	0/372	0.55	0/498
1	F	0.52	0/363	0.60	0/486
All	All	0.46	0/2302	0.57	0/3086

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	A	364	0	333	12	0
1	B	363	0	333	3	0
1	C	382	0	353	20	0
1	D	421	0	380	19	0
1	E	364	0	336	11	0
1	F	354	0	327	14	0
2	B	8	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	12	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	6	0	0	0	0
3	E	1	0	0	0	0
3	F	7	0	0	0	0
All	All	2286	0	2070	57	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 13.

The worst 5 of 57 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:A:28:GLU:H	1:F:30:ASN:HD21	1.22	0.87
1:C:28:GLU:H	1:D:30:ASN:HD21	1.24	0.83
1:C:41:LYS:HG2	1:C:57:GLU:HG2	1.60	0.81
1:C:59:ALA:HB3	1:C:62:GLU:HG3	1.63	0.79
1:A:21:GLN:HB2	1:F:21:GLN:HE22	1.46	0.78

There are no symmetry-related clashes.

5.3   Torsion angles ⓘ

5.3.1   Protein backbone ⓘ

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	41/72 (57%)	40 (98%)	1 (2%)	0	100	100
1	B	41/72 (57%)	40 (98%)	1 (2%)	0	100	100
1	C	43/72 (60%)	40 (93%)	3 (7%)	0	100	100
1	D	47/72 (65%)	46 (98%)	1 (2%)	0	100	100
1	E	41/72 (57%)	38 (93%)	2 (5%)	1 (2%)	6	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	40/72 (56%)	37 (92%)	2 (5%)	1 (2%)	5	6
All	All	253/432 (59%)	241 (95%)	10 (4%)	2 (1%)	19	29

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	61	ASP
1	F	21	GLN

5.3.2   Protein sidechains ⓘ

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	40/65 (62%)	35 (88%)	5 (12%)	4	5
1	B	40/65 (62%)	37 (92%)	3 (8%)	13	21
1	C	42/65 (65%)	37 (88%)	5 (12%)	5	6
1	D	46/65 (71%)	39 (85%)	7 (15%)	3	3
1	E	40/65 (62%)	33 (82%)	7 (18%)	2	2
1	F	39/65 (60%)	35 (90%)	4 (10%)	7	10
All	All	247/390 (63%)	216 (87%)	31 (13%)	4	5

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	30	ASN
1	F	30	ASN
1	D	52	VAL
1	F	51	GLU
1	E	53	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	29	HIS
1	F	29	HIS
1	F	30	ASN
1	C	50	ASN
1	D	29	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 ligands are 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#|Z| > 2$	Counts	RMSZ	$\#|Z| > 2$
2	ACY	B	73	-	3,3,3	0.95	0	3,3,3	0.99	0
2	ACY	B	74	-	3,3,3	1.24	0	3,3,3	0.87	0

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 ⓘ

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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, 95th 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(Å²)	Q<0.9
1	A	42/72 (58%)	-0.06	0	100	100	36, 52, 85, 98	0
1	B	42/72 (58%)	0.51	4 (9%)	8	7	48, 78, 140, 160	0
1	C	44/72 (61%)	0.19	2 (4%)	33	31	44, 80, 115, 129	0
1	D	48/72 (66%)	0.11	1 (2%)	63	61	39, 68, 96, 108	0
1	E	42/72 (58%)	0.44	3 (7%)	16	14	47, 87, 131, 152	0
1	F	41/72 (56%)	0.06	1 (2%)	59	57	40, 57, 105, 118	0
All	All	259/432 (59%)	0.21	11 (4%)	36	35	36, 70, 121, 160	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	20	PRO	5.9
1	B	37	ASP	5.5
1	B	39	TYR	4.2
1	C	37	ASP	3.9
1	E	37	ASP	3.8

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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, 95th 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	ACY	B	74	4/4	0.80	0.32	60,69,73,76	0
2	ACY	B	73	4/4	0.83	0.27	116,120,121,125	0

6.5 Other polymers ⓘ

There are no such residues in this entry.