wwPDB X-ray Structure Validation Summary Report (i)

Sep 29, 2024 – 02:48 AM EDT

PDB ID	:	1ON0
Title	:	Crystal Structure of Putative Acetyltransferase (YycN) from Bacillus subtilis, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET SR144
Authors	:	Forouhar, F.; Shen, J.; Kuzin, A.; Chiang, Y.; Xiao, R.; Acton, T.B.; Rost, B.; Montelione, G.T.; Tong, L.; Northeast Structural Genomics Consortium (NESG)
Deposited on	:	2003-02-26
Resolution	:	2.20 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 (i)) were used in the production of this report:

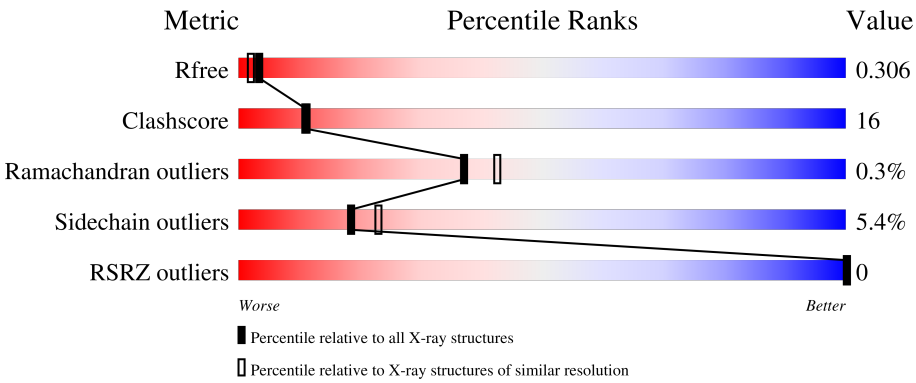
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.20 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}	164625	5791 (2.20-2.20)
Clashscore	180529	6634 (2.20-2.20)
Ramachandran outliers	177936	6560 (2.20-2.20)
Sidechain outliers	177891	6561 (2.20-2.20)
RSRZ outliers	164620	5791 (2.20-2.20)

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	158	84% 15%
1	B	158	68% 28%
1	C	158	61% 37%
1	D	158	56% 40%

Validation Pipeline (wwPDB-VP) : 2.39

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5528 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 YycN protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	156	1283	829	218	232	4	0	0	0
1	B	157	1292	834	219	235	4	0	0	0
1	C	156	1283	829	218	232	4	0	0	0
1	D	157	1292	834	219	235	4	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP O32293
A	4	MSE	MET	modified residue	UNP O32293
A	8	MSE	MET	modified residue	UNP O32293
A	120	MSE	MET	modified residue	UNP O32293
A	152	MSE	MET	modified residue	UNP O32293
A	157	LEU	-	cloning artifact	UNP O32293
A	158	GLU	-	cloning artifact	UNP O32293
B	1	MSE	MET	modified residue	UNP O32293
B	4	MSE	MET	modified residue	UNP O32293
B	8	MSE	MET	modified residue	UNP O32293
B	120	MSE	MET	modified residue	UNP O32293
B	152	MSE	MET	modified residue	UNP O32293
B	157	LEU	-	cloning artifact	UNP O32293
B	158	GLU	-	cloning artifact	UNP O32293
C	1	MSE	MET	modified residue	UNP O32293
C	4	MSE	MET	modified residue	UNP O32293
C	8	MSE	MET	modified residue	UNP O32293
C	120	MSE	MET	modified residue	UNP O32293
C	152	MSE	MET	modified residue	UNP O32293
C	157	LEU	-	cloning artifact	UNP O32293
C	158	GLU	-	cloning artifact	UNP O32293

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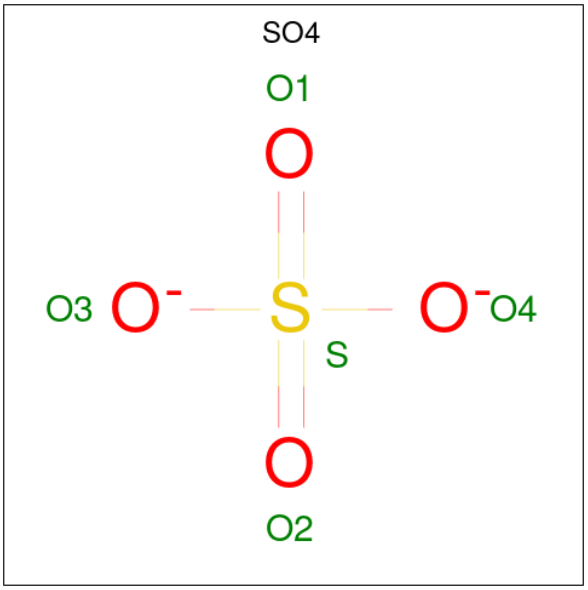
Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MSE	MET	modified residue	UNP O32293
D	4	MSE	MET	modified residue	UNP O32293
D	8	MSE	MET	modified residue	UNP O32293
D	120	MSE	MET	modified residue	UNP O32293
D	152	MSE	MET	modified residue	UNP O32293
D	157	LEU	-	cloning artifact	UNP O32293
D	158	GLU	-	cloning artifact	UNP O32293

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0
2	B	1	5	4	1	0	0
2	C	1	5	4	1	0	0
2	D	1	5	4	1	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 4 is water.

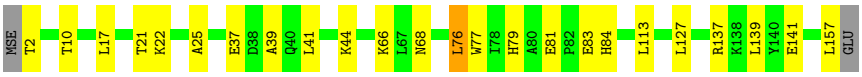
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	88	88	88	0	0
			Total	O		
4	B	96	96	96	0	0
			Total	O		
4	C	90	90	90	0	0
			Total	O		
4	D	83	83	83	0	0

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.

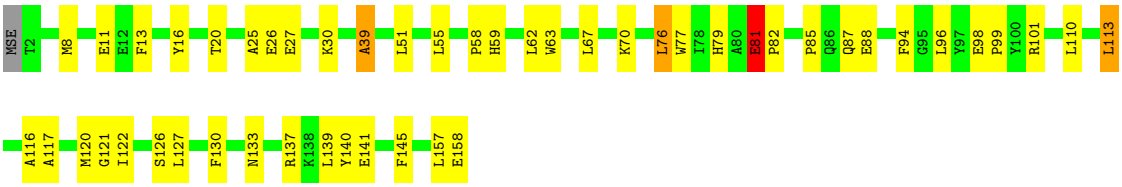
- Molecule 1: YycN protein

Chain A:



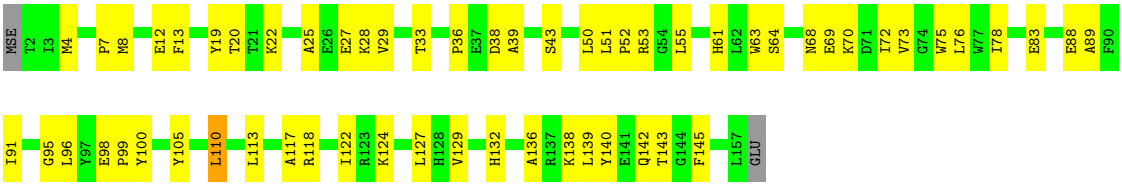
- Molecule 1: YycN protein

Chain B:



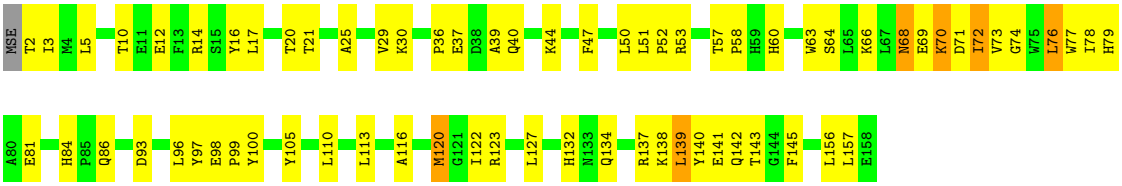
- Molecule 1: YycN protein

Chain C:



- Molecule 1: YycN protein

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	61.89Å 101.59Å 62.12Å 90.00° 97.00° 90.00°	Depositor
Resolution (Å)	29.68 – 2.20 29.68 – 2.20	Depositor EDS
% Data completeness (in resolution range)	9.9 (29.68-2.20) 97.0 (29.68-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	3.54 (at 2.20Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.225 , 0.289 0.241 , 0.306	Depositor DCC
R_{free} test set	3750 reflections (9.88%)	wwPDB-VP
Wilson B-factor (Å^2)	28.6	Xtriage
Anisotropy	0.266	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 19.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.25$	Xtriage
Estimated twinning fraction	0.278 for l,-k,h	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5528	wwPDB-VP
Average B, all atoms (Å^2)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.06% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical 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.

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: CL, SO4

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	0.38	0/1315	0.60	0/1775
1	B	0.39	0/1324	0.61	0/1787
1	C	0.37	0/1315	0.56	0/1775
1	D	0.37	0/1324	0.53	0/1787
All	All	0.38	0/5278	0.58	0/7124

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	1283	0	1266	20	0
1	B	1292	0	1272	40	0
1	C	1283	0	1266	60	0
1	D	1292	0	1272	53	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	88	0	0	3	0
4	B	96	0	0	5	0
4	C	90	0	0	3	0
4	D	83	0	0	2	0
All	All	5528	0	5076	166	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 16.

The worst 5 of 166 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:81:GLU:HB3	1:A:84:HIS:HB2	1.37	1.02
1:B:87:GLN:HG2	1:B:121:GLY:O	1.71	0.90
1:B:87:GLN:HB2	4:B:419:HOH:O	1.75	0.86
1:C:70:LYS:HG3	1:D:36:PRO:HB3	1.57	0.85
1:D:120:MSE:HG3	1:D:122:ILE:HD13	1.61	0.80

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	154/158 (98%)	143 (93%)	11 (7%)	0	100 100
1	B	155/158 (98%)	148 (96%)	5 (3%)	2 (1%)	10 8
1	C	154/158 (98%)	144 (94%)	10 (6%)	0	100 100
1	D	155/158 (98%)	141 (91%)	14 (9%)	0	100 100
All	All	618/632 (98%)	576 (93%)	40 (6%)	2 (0%)	37 42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	39	ALA
1	B	81	GLU

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	135/132 (102%)	130 (96%)	5 (4%)	29	39
1	B	136/132 (103%)	129 (95%)	7 (5%)	20	25
1	C	135/132 (102%)	127 (94%)	8 (6%)	16	20
1	D	136/132 (103%)	127 (93%)	9 (7%)	14	16
All	All	542/528 (103%)	513 (95%)	29 (5%)	18	23

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	38	ASP
1	D	120	MSE
1	C	83	GLU
1	D	70	LYS
1	C	69	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	146	GLN
1	D	84	HIS
1	D	142	GLN
1	D	133	ASN
1	B	61	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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 for Mogul analysis.

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	SO4	D	403	-	4,4,4	0.36	0	6,6,6	0.09	0
2	SO4	C	402	-	4,4,4	0.40	0	6,6,6	0.16	0
2	SO4	B	400	-	4,4,4	0.36	0	6,6,6	0.12	0
2	SO4	A	401	-	4,4,4	0.27	0	6,6,6	0.07	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 (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, 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(Å^2)	Q<0.9
1	A	152/158 (96%)	-1.48	0	100	100	16, 28, 49, 76	0
1	B	153/158 (96%)	-1.44	0	100	100	15, 29, 52, 83	0
1	C	152/158 (96%)	-1.37	0	100	100	17, 35, 64, 90	0
1	D	153/158 (96%)	-1.30	0	100	100	18, 38, 72, 92	0
All	All	610/632 (96%)	-1.40	0	100	100	15, 33, 64, 92	0

There are no RSRZ outliers to report.

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, 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	SO4	B	400	5/5	0.99	0.04	30,30,31,33	0
2	SO4	C	402	5/5	0.99	0.04	46,50,51,51	0
2	SO4	D	403	5/5	0.99	0.04	64,64,65,65	0
3	CL	A	405	1/1	0.99	0.03	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	SO4	A	401	5/5	1.00	0.02	25,26,30,31	0

6.5 Other polymers (i)

There are no such residues in this entry.