

wwPDB X-ray Structure Validation Summary Report (i)

Jan 15, 2024 – 02:43 pm GMT

PDB ID : 6YUB

Title : Crystal structure of Uba4 from Chaetomium thermophilum Authors : Grudnik, P.; Pabis, M.; Ethiraju Ravichandran, K.; Glatt, S.

Deposited on : 2020-04-26

Resolution : 2.19 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 (1)) were used in the production of this report:

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

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)

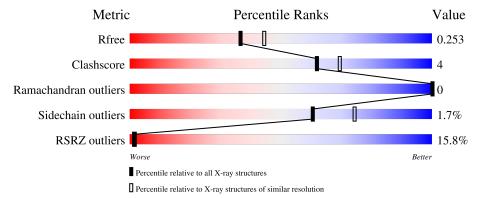
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.19 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(\mathring{A}))$
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (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	442	12%		10%	-
2	В	303	89%		6%	- 5%
3	С	127	55% 79%	9%	12%	6



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 12369 atoms, of which 6048 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 Adenylyltransferase and sulfurtransferase uba4.

Mol	Chain	Residues			Atom	S			ZeroOcc	AltConf	Trace
1	A	423	Total 6264	C 1982	H 3122	N 548	O 589	S 23	1	6	0

• Molecule 2 is a protein called Adenylyltransferase and sulfurtransferase uba4.

Mol	Chain	Residues			Atom	ıs			ZeroOcc	AltConf	Trace
2	В	289	Total 4328	C 1362	H 2183	N 371	O 394	S 18	0	6	0

• Molecule 3 is a protein called Adenylyltransferase and sulfurtransferase uba4.

Mol	Chain	Residues			Aton	ns			ZeroOcc	AltConf	Trace
3	С	112	Total 1553	C 510	H 743	N 146	O 151	S 3	0	0	0

• Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

\mathbf{Mol}	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Zn 1 1	0	0
4	В	1	Total Zn 1 1	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	93	Total O 93 93	0	0
5	В	116	Total O 116 116	0	0

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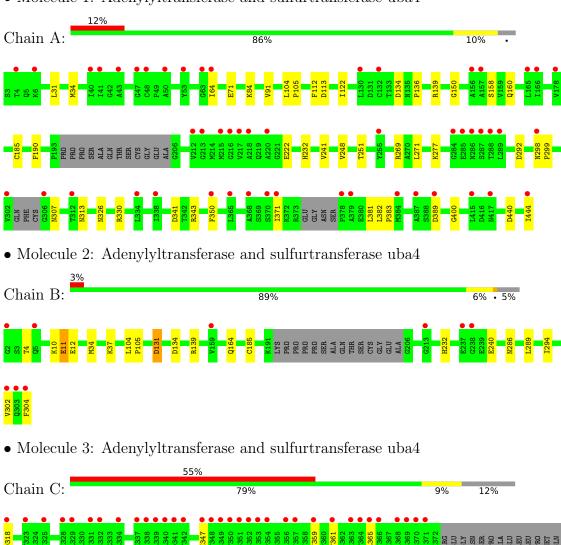
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	С	13	Total O 13 13	0	0



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: Adenylyltransferase and sulfurtransferase uba4





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	64.75Å 74.17Å 103.66Å	Donositon
a, b, c, α , β , γ	90.00° 106.36° 90.00°	Depositor
Resolution (Å)	47.63 - 2.19	Depositor
Resolution (A)	47.63 - 2.19	EDS
% Data completeness	99.5 (47.63-2.19)	Depositor
(in resolution range)	99.5 (47.63-2.19)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.21 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
D.D.	0.208 , 0.253	Depositor
R, R_{free}	0.208 , 0.253	DCC
R_{free} test set	2405 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	37.2	Xtriage
Anisotropy	0.618	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	$0.39\;,53.6$	EDS
L-test for twinning ²	$< L > = 0.46, < L^2> = 0.29$	Xtriage
Estimated twinning fraction	0.057 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12369	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.03% 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: ZN

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		
MIOI		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.31	0/3204	0.46	0/4350	
2	В	0.35	1/2193~(0.0%)	0.48	$1/2977 \ (0.0\%)$	
3	С	0.26	0/824	0.41	0/1117	
All	All	0.32	$1/6221 \ (0.0\%)$	0.46	1/8444 (0.0%)	

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
2	В	11	GLU	CG-CD	5.81	1.60	1.51

All (1) bond angle outliers are listed below:

\mathbf{Mol}	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$Ideal(^{o})$
2	В	11	GLU	OE1-CD-OE2	-6.30	115.73	123.30

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	3142	3122	3108	30	1
2	В	2145	2183	2166	11	1
3	С	810	743	740	12	0

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Continued	trom	mmoninonic	maaa
COHABABACA		DIEUIUU	DUIUE
0 0 1000100000			

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	1	0	0	0	0
4	В	1	0	0	0	0
5	A	93	0	0	9	2
5	В	116	0	0	5	1
5	С	13	0	0	3	0
All	All	6321	6048	6014	53	3

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 4.

The worst 5 of 53 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned} ext{Clash} \ ext{overlap } (ext{Å}) \end{aligned}$
2:B:34:MET:O	5:B:501:HOH:O	1.84	0.94
2:B:164:GLN:NE2	5:B:505:HOH:O	2.05	0.90
3:C:347:HIS:ND1	5:C:501:HOH:O	2.06	0.88
2:B:4:THR:O	5:B:502:HOH:O	1.94	0.86
1:A:400:GLY:O	5:A:601:HOH:O	1.96	0.83

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
5:A:682:HOH:O	5:A:693:HOH:O[1_455]	1.80	0.40
1:A:269[B]:ARG:NH2	2:B:286:ASN:OD1[2_646]	2.07	0.13
5:A:691:HOH:O	5:B:591:HOH:O[2_546]	2.08	0.12

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	A	417/442 (94%)	396 (95%)	21 (5%)	0	100	100
2	В	287/303 (95%)	277 (96%)	10 (4%)	0	100	100
3	С	108/127 (85%)	104 (96%)	4 (4%)	0	100	100
All	All	812/872 (93%)	777 (96%)	35 (4%)	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	334/369~(90%)	329 (98%)	5 (2%)	65	78	
2	В	232/250 (93%)	226 (97%)	6 (3%)	46	58	
3	С	76/108 (70%)	76 (100%)	0	100	100	
All	All	642/727 (88%)	631 (98%)	11 (2%)	60	74	

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	В	131	ASP
2	В	134	ASP
2	В	232	HIS
2	В	185[3]	CYS
1	A	440	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	В	164	GLN

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>	$\#\mathrm{RSRZ}{>}2$	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q<0.9
1	A	423/442~(95%)	0.96	51 (12%) 4 3	28, 49, 90, 144	2 (0%)
2	В	289/303 (95%)	0.55	9 (3%) 49 47	27, 39, 66, 120	0
3	С	112/127 (88%)	3.05	70 (62%) 0 0	59, 84, 116, 150	0
All	All	824/872 (94%)	1.10	130 (15%) 2 1	27, 46, 102, 150	2 (0%)

The worst 5 of 130 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	С	371	ILE	10.9
3	С	350	PHE	7.1
3	С	369	SER	7.1
3	С	334	LEU	7.0
3	С	414	GLY	7.0

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.

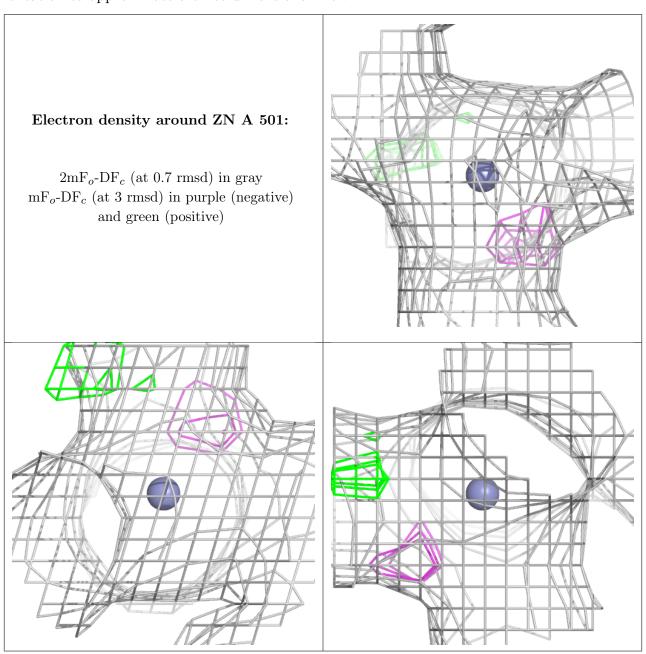
6.4 Ligands (i)

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.

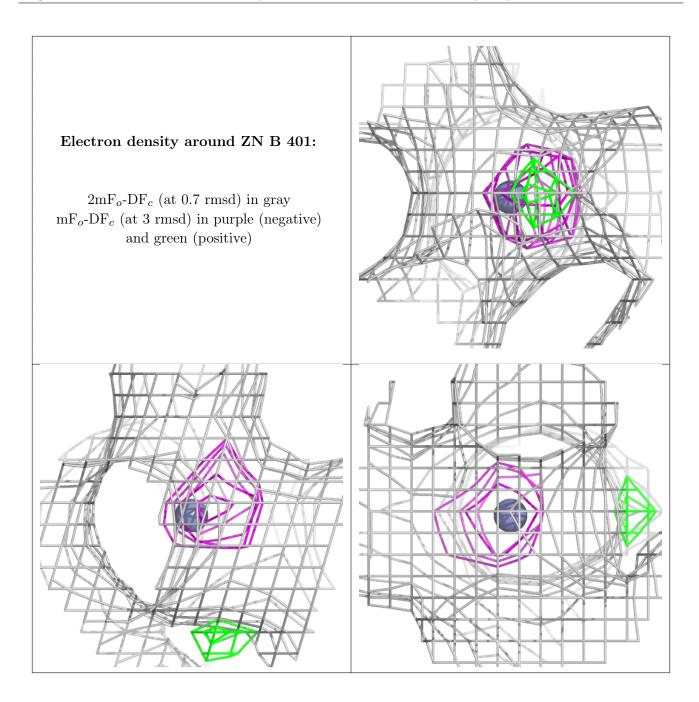


Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
4	ZN	A	501	1/1	0.99	0.10	44,44,44,44	0
4	ZN	В	401	1/1	0.99	0.08	38,38,38,38	0

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.

