Full wwPDB X-ray Structure Validation Report (i)

Jun 16, 2024 – 10:29 AM EDT

PDB ID	:	4ZOY
Title	:	Crystal structure of the Chaetomium thermophilum Sqt1
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Deposited on	:	2015-05-07
Resolution	:	1.50 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:

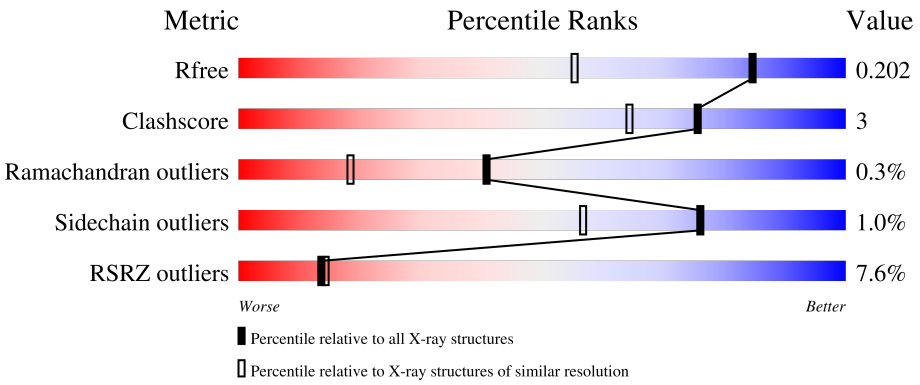
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

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

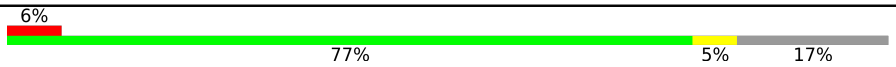
The reported resolution of this entry is 1.50 Å.

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	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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	491	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3569 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 Sqt1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	406	3009	1893	520	589	7	0	2	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	51	MET	-	initiating methionine	UNP G0S0R0
A	534	GLY	-	expression tag	UNP G0S0R0
A	535	SER	-	expression tag	UNP G0S0R0
A	536	HIS	-	expression tag	UNP G0S0R0
A	537	HIS	-	expression tag	UNP G0S0R0
A	538	HIS	-	expression tag	UNP G0S0R0
A	539	HIS	-	expression tag	UNP G0S0R0
A	540	HIS	-	expression tag	UNP G0S0R0
A	541	HIS	-	expression tag	UNP G0S0R0

- Molecule 2 is water.

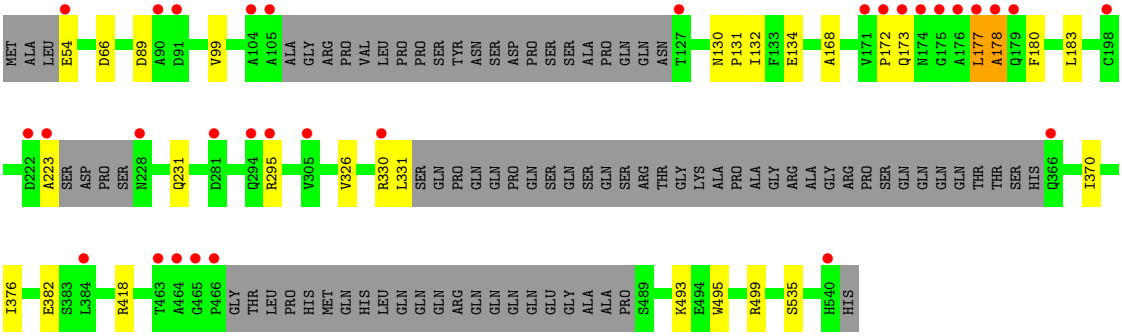
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	560	560	560	0	0

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: Sqt1

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	67.44Å 73.02Å 113.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.38 – 1.50 37.38 – 1.50	Depositor EDS
% Data completeness (in resolution range)	98.4 (37.38-1.50) 96.3 (37.38-1.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.52 (at 1.50Å)	Xtriage
Refinement program	PHENIX 1.9_1685	Depositor
R, R_{free}	0.184 , 0.202 0.185 , 0.202	Depositor DCC
R_{free} test set	4490 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	17.5	Xtriage
Anisotropy	0.189	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 52.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	3569	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.78% 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)

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	0.41	1/3076 (0.0%)	0.60	2/4189 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	376	ILE	C-O	-6.89	1.10	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	499	ARG	NE-CZ-NH2	-6.51	117.04	120.30
1	A	499	ARG	NE-CZ-NH1	6.39	123.50	120.30

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	3009	0	2891	18	2
2	A	560	0	0	8	2
All	All	3569	0	2891	18	2

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 3.

All (18) 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:172:PRO:HD2	1:A:177:LEU:HA	1.74	0.69
1:A:535:SER:OG	2:A:602:HOH:O	2.16	0.60
1:A:54:GLU:N	2:A:612:HOH:O	2.36	0.59
1:A:418:ARG:NH1	2:A:607:HOH:O	2.30	0.56
1:A:223:ALA:HB2	2:A:893:HOH:O	2.08	0.52
1:A:168:ALA:HB2	1:A:183:LEU:HD11	1.91	0.51
1:A:132:ILE:HD12	1:A:178:ALA:HB3	1.95	0.49
1:A:493:LYS:HG2	1:A:495:TRP:CZ2	2.49	0.48
1:A:178:ALA:HB1	1:A:180:PHE:CE1	2.50	0.46
1:A:99:VAL:HG11	1:A:180:PHE:CZ	2.51	0.45
1:A:295:ARG:HG3	1:A:370:ILE:HG13	1.99	0.43
1:A:134:GLU:OE1	2:A:604:HOH:O	2.21	0.43
1:A:326:VAL:HG22	1:A:370:ILE:HD13	2.02	0.41
1:A:130:ASN:HA	1:A:131:PRO:HD3	1.97	0.41
1:A:331:LEU:O	2:A:605:HOH:O	2.22	0.41
1:A:177:LEU:HB3	1:A:178:ALA:H	1.54	0.41
1:A:231:GLN:NE2	2:A:603:HOH:O	2.18	0.41
1:A:382:GLU:HG3	2:A:1027:HOH:O	2.21	0.40

All (2) 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	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:ASP:OD2	2:A:601:HOH:O[4_545]	2.04	0.16
1:A:89:ASP:OD2	2:A:601:HOH:O[4_545]	2.04	0.16

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	398/491 (81%)	384 (96%)	13 (3%)	1 (0%)	41 18

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	178	ALA

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	317/386 (82%)	314 (99%)	3 (1%)	78 61

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	173	GLN
1	A	177	LEU
1	A	330	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

There are no ligands in this entry.

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	406/491 (82%)	0.38	31 (7%) 13 14	13, 19, 41, 52	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	177	LEU	12.6
1	A	176	ALA	12.3
1	A	174	ASN	9.2
1	A	175	GLY	8.4
1	A	173	GLN	6.9
1	A	223	ALA	6.6
1	A	104	ALA	6.1
1	A	540	HIS	5.1
1	A	466	PRO	5.0
1	A	105	ALA	4.6
1	A	178	ALA	4.3
1	A	465	GLY	4.3
1	A	172	PRO	4.2
1	A	366	GLN	4.2
1	A	330	ARG	3.9
1	A	198	CYS	3.9
1	A	464	ALA	3.7
1	A	228	ASN	3.4
1	A	171	VAL	3.3
1	A	294	GLN	3.2
1	A	295	ARG	3.2
1	A	90	ALA	2.8
1	A	222	ASP	2.5
1	A	127	THR	2.4
1	A	91	ASP	2.4
1	A	305	VAL	2.3
1	A	281	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	384	LEU	2.2
1	A	179	GLN	2.1
1	A	54	GLU	2.1
1	A	463	THR	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 monosaccharides 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.