

Full wwPDB X-ray Structure Validation Report (i)

Oct 2, 2023 - 09:42 AM EDT

PDB ID	:	6MJE
Title	:	Structure of Candida glabrata Csm1: S. cerevisiae Dsn1 complex
Authors	:	Singh, N.; Corbett, K.D.
Deposited on		
Resolution	:	2.50 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:

:	FAILED
:	1.13
:	FAILED
:	20191225.v01 (using entries in the PDB archive December 25th 2019)
:	Engh & Huber (2001)
:	Parkinson et al. (1996)
:	2.35.1
	: : : :

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.50 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4561 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Δ	110	Total	С	Ν	0	\mathbf{S}	0	0	0
	А		897	578	144	172	3	0		
1	1 C	110	Total	С	Ν	0	S	0	0	0
			894	577	144	170	3			
1	Е	109	Total	С	Ν	0	S	0	0	0
	Ľ		889	574	143	169	3	0	0	0
1	1 G	109	Total	С	Ν	0	S	0	0	0
			889	574	143	169	3		0	U

• Molecule 1 is a protein called Monopolin complex subunit CSM1.

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	50	MET	-	expression tag	UNP A0A0W0CH22
А	51	LYS	-	expression tag	UNP A0A0W0CH22
А	52	SER	-	expression tag	UNP A0A0W0CH22
А	53	SER	-	expression tag	UNP A0A0W0CH22
А	54	HIS	-	expression tag	UNP A0A0W0CH22
А	55	HIS	-	expression tag	UNP A0A0W0CH22
А	56	HIS	-	expression tag	UNP A0A0W0CH22
А	57	HIS	-	expression tag	UNP A0A0W0CH22
А	58	HIS	-	expression tag	UNP A0A0W0CH22
A	59	HIS	-	expression tag	UNP A0A0W0CH22
А	60	GLU	-	expression tag	UNP A0A0W0CH22
А	61	ASN	-	expression tag	UNP A0A0W0CH22
A	62	LEU	-	expression tag	UNP A0A0W0CH22
А	63	TYR	-	expression tag	UNP A0A0W0CH22
А	64	PHE	-	expression tag	UNP A0A0W0CH22
А	65	GLN	-	expression tag	UNP A0A0W0CH22
А	66	SER	-	expression tag	UNP A0A0W0CH22
А	67	ASN	-	expression tag	UNP A0A0W0CH22
А	68	ALA	-	expression tag	UNP A0A0W0CH22
С	50	MET	-	expression tag	UNP A0A0W0CH22
С	51	LYS	-	expression tag	UNP A0A0W0CH22

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Continu	Continued from previous page							
Chain	Residue	Modelled	Actual	Comment	Reference			
С	52	SER	-	expression tag	UNP A0A0W0CH22			
С	53	SER	-	expression tag	UNP A0A0W0CH22			
С	54	HIS	-	expression tag	UNP A0A0W0CH22			
С	55	HIS	-	expression tag	UNP A0A0W0CH22			
С	56	HIS	-	expression tag	UNP A0A0W0CH22			
С	57	HIS	-	expression tag	UNP A0A0W0CH22			
С	58	HIS	-	expression tag	UNP A0A0W0CH22			
С	59	HIS	-	expression tag	UNP A0A0W0CH22			
С	60	GLU	-	expression tag	UNP A0A0W0CH22			
С	61	ASN	-	expression tag	UNP A0A0W0CH22			
С	62	LEU	-	expression tag	UNP A0A0W0CH22			
С	63	TYR	-	expression tag	UNP A0A0W0CH22			
С	64	PHE	-	expression tag	UNP A0A0W0CH22			
С	65	GLN	-	expression tag	UNP A0A0W0CH22			
С	66	SER	-	expression tag	UNP A0A0W0CH22			
С	67	ASN	-	expression tag	UNP A0A0W0CH22			
С	68	ALA	-	expression tag	UNP A0A0W0CH22			
Е	50	MET	-	expression tag	UNP A0A0W0CH22			
Е	51	LYS	-	expression tag	UNP A0A0W0CH22			
Е	52	SER	-	expression tag	UNP A0A0W0CH22			
Е	53	SER	-	expression tag	UNP A0A0W0CH22			
Е	54	HIS	-	expression tag	UNP A0A0W0CH22			
Ε	55	HIS	-	expression tag	UNP A0A0W0CH22			
E	56	HIS	-	expression tag	UNP A0A0W0CH22			
Ε	57	HIS	-	expression tag	UNP A0A0W0CH22			
Е	58	HIS	-	expression tag	UNP A0A0W0CH22			
Е	59	HIS	-	expression tag	UNP A0A0W0CH22			
Е	60	GLU	-	expression tag	UNP A0A0W0CH22			
E	61	ASN	-	expression tag	UNP A0A0W0CH22			
Е	62	LEU	-	expression tag	UNP A0A0W0CH22			
Е	63	TYR	-	expression tag	UNP A0A0W0CH22			
Е	64	PHE	-	expression tag	UNP A0A0W0CH22			
Ε	65	GLN	-	expression tag	UNP A0A0W0CH22			
Е	66	SER	-	expression tag	UNP A0A0W0CH22			
E	67	ASN	-	expression tag	UNP A0A0W0CH22			
Е	68	ALA	-	expression tag	UNP A0A0W0CH22			
G	50	MET	-	expression tag	UNP A0A0W0CH22			
G	51	LYS	-	expression tag	UNP A0A0W0CH22			
G	52	SER	-	expression tag	UNP A0A0W0CH22			
G	53	SER	-	expression tag	UNP A0A0W0CH22			
G	54	HIS	-	expression tag	UNP A0A0W0CH22			
G	55	HIS	-	expression tag	UNP A0A0W0CH22			

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	Continuea from previous page							
Chain	Residue	Modelled	Actual	Comment	Reference			
G	56	HIS	-	expression tag	UNP A0A0W0CH22			
G	57	HIS	-	expression tag	UNP A0A0W0CH22			
G	58	HIS	-	expression tag	UNP A0A0W0CH22			
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G	65	GLN	-	expression tag	UNP A0A0W0CH22			
G	66	SER	-	expression tag	UNP A0A0W0CH22			
G	67	ASN	-	expression tag	UNP A0A0W0CH22			
G	68	ALA	-	expression tag	UNP A0A0W0CH22			

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• Molecule 2 is a protein called Dsn1p.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
2	2 B	30	Total	С	Ν	0	0	0	0		
	D		248	156	49	43					
2	D	30	Total	С	Ν	0	0	0	0		
	D	- 50	248	156	49	43					
2	F	F 30	Total	С	Ν	0					
		Г	1	T,	- 50	248	156	49	43	0	0
0	2 H	Н 30	Total	С	Ν	0	0	0	0		
			248	156	49	43	U	0	U		

MolProbity and EDS failed to run properly - this section is therefore empty.



3 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	44.37\AA 203.75Å 44.26\AA	Depositor
a, b, c, α , β , γ	90.00° 90.36° 90.00°	Depositor
Resolution (Å)	43.35 - 2.50	Depositor
% Data completeness	94.2 (43.35-2.50)	Depositor
(in resolution range)	34.2 (40.00-2.00)	Depositor
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.07 (at 2.48 \text{\AA})$	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.240 , 0.297	Depositor
Wilson B-factor $(Å^2)$	56.2	Xtriage
Anisotropy	0.801	Xtriage
L-test for twinning ²	$< L > = 0.53, < L^2 > = 0.36$	Xtriage
	0.390 for -l,k,h	
Estimated twinning fraction	0.428 for -h,-k,l	Xtriage
	0.427 for l,-k,h	
Total number of atoms	4561	wwPDB-VP
Average B, all atoms $(Å^2)$	87.0	wwPDB-VP

EDS failed to run properly - this section is therefore incomplete.

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 10.14% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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.

4 Model quality (i)

4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains (i)

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

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

There are no ligands in this entry.

4.7 Other polymers (i)

There are no such residues in this entry.



4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



5 Fit of model and data (i)

5.1 Protein, DNA and RNA chains (i)

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

5.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.

