wwPDB X-ray Structure Validation Summary Report (i)

Jun 19, 2024 – 07:05 AM EDT

PDB ID	:	4JC8
Title	:	Crystal Structure of HOPS component Vps33 from Chaetomium thermophilum
Authors	:	Baker, R.W.; Jeffrey, P.D.; Hughson, F.M.
Deposited on	:	2013-02-21
Resolution	:	2.60 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:

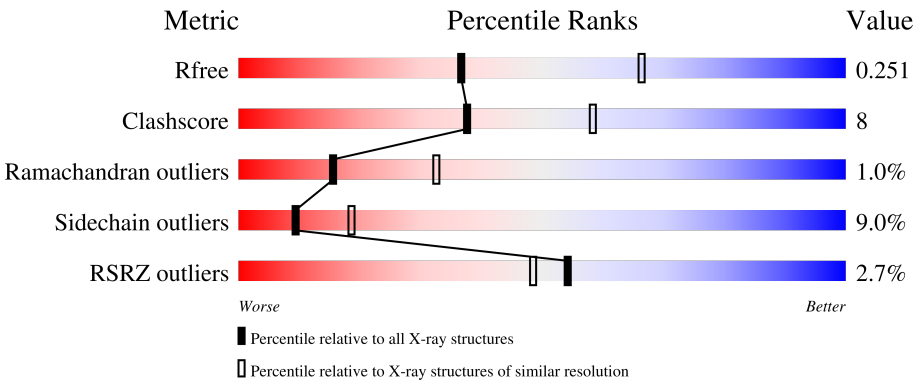
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	669	3% 68% 18% • 12%
1	B	669	2% 68% 17% • 12%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 9565 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 HOPS component Vps33.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	590	4665	2958	822	874	4	7	0	0	0
1	B	589	4675	2965	824	875	4	7	0	0	0

- Molecule 2 is water.

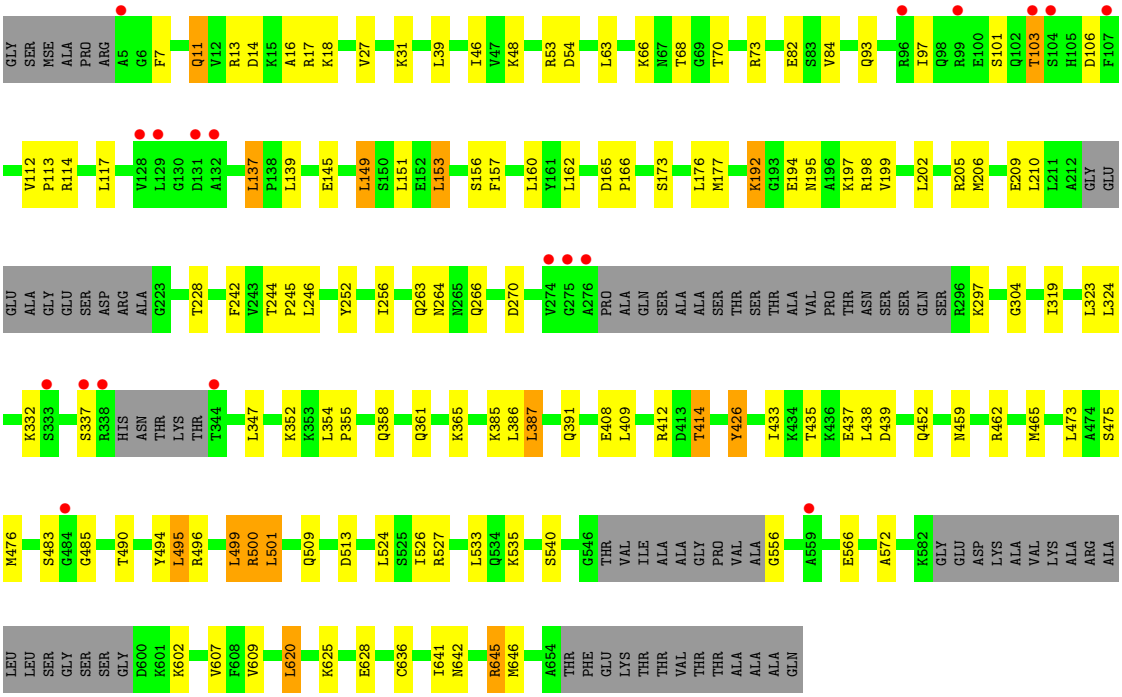
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	125	125	125	0	0
2	B	100	100	100	0	0

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.

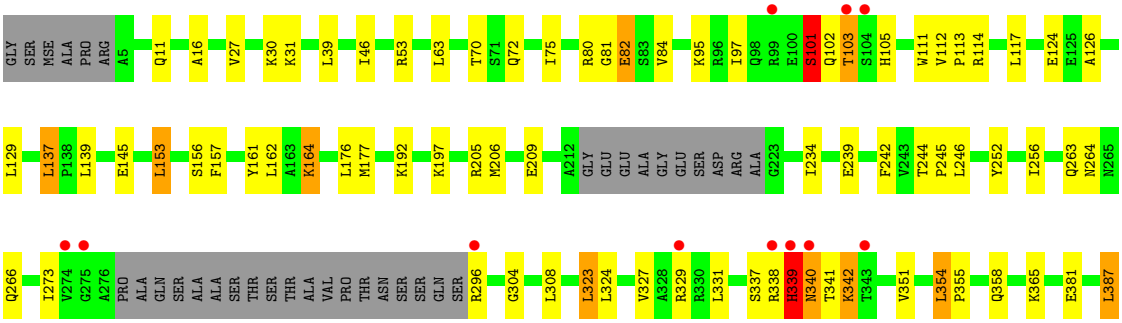
• Molecule 1: HOPS component Vps33

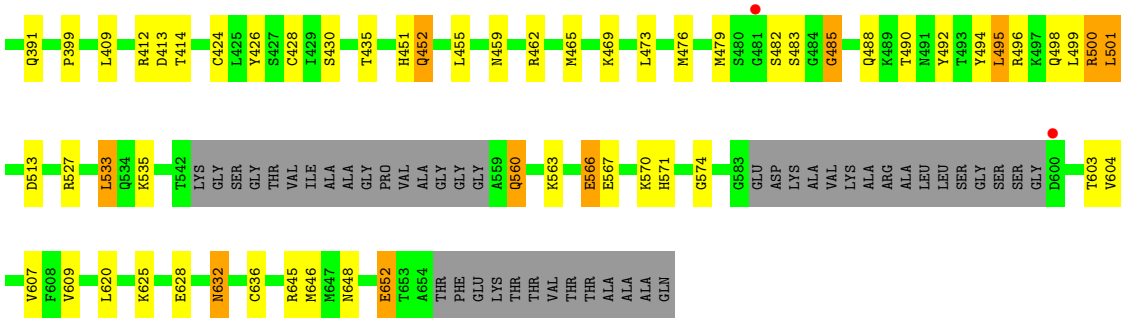
Chain A:



• Molecule 1: HOPS component Vps33

Chain B:




Q391
P399
L409
R412
D413
T414
C424
L425
Y426
S427
C428
I429
S430
T435
H451
Q452
L455
N459
R462
M465
K469
L473
M476
M479
S480
G481
S482
S483
G484
G485
Q488
K489
T490
N491
Y492
T493
Y494
L495
R496
K497
Q498
L499
R500
L501
D513
R527
L533
Q534
K535
T542
LYS
GLY
SER
GLY
THR
VAL
ILE
ALA
ALA
GLY
PRO
VAL
ALA
GLY
GLY
GLY
A559
Q560
K563
E566
E567
K570
H571
G574
G583
GLU
ASP
LYS
ALA
VAL
LYS
ALA
ARG
ALA
LEU
LEU
SER
GLY
SER
SER
GLY
D600
T603
V604
V607
F608
V609
L620
K625
E628
N632
C636
R645
M646
M647
N648
E652
T653
A654
THR
PHE
GLU
LYS
THR
THR
VAL
THR
THR
ALA
ALA
ALA
GLN

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	71.94Å 64.44Å 151.69Å 90.00° 91.77° 90.00°	Depositor
Resolution (Å)	35.95 – 2.60 49.10 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.7 (35.95-2.60) 99.7 (49.10-2.60)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	2.32 (at 2.61Å)	Xtriage
Refinement program	PHENIX dev_1144	Depositor
R, R_{free}	0.185 , 0.247 0.188 , 0.251	Depositor DCC
R_{free} test set	2153 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	46.7	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 42.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.108 for h,-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	9565	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.10% 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	0.45	0/4729	0.63	0/6363
1	B	0.40	0/4741	0.60	0/6384
All	All	0.42	0/9470	0.62	0/12747

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	4665	0	4745	70	0
1	B	4675	0	4756	80	0
2	A	125	0	0	15	0
2	B	100	0	0	9	0
All	All	9565	0	9501	145	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 8.

The worst 5 of 145 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:361:GLN:HG2	1:B:354:LEU:HG	1.58	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:82:GLU:OE1	2:B:704:HOH:O	2.00	0.77
1:A:426:TYR:OH	1:A:437:GLU:OE2	2.03	0.75
1:A:160:LEU:O	2:A:780:HOH:O	2.05	0.75
1:A:347:LEU:HD11	1:B:329:ARG:HG3	1.71	0.72

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	578/669 (86%)	554 (96%)	20 (4%)	4 (1%)	22	43
1	B	579/669 (86%)	548 (95%)	24 (4%)	7 (1%)	13	27
All	All	1157/1338 (86%)	1102 (95%)	44 (4%)	11 (1%)	15	32

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	101	SER
1	A	483	SER
1	B	101	SER
1	A	103	THR
1	B	103	THR

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	508/556 (91%)	460 (91%)	48 (9%)	8 17
1	B	511/556 (92%)	467 (91%)	44 (9%)	10 20
All	All	1019/1112 (92%)	927 (91%)	92 (9%)	9 18

5 of 92 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	105	HIS
1	B	342	LYS
1	B	117	LEU
1	B	197	LYS
1	B	426	TYR

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

Mol	Chain	Res	Type
1	B	72	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)

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	583/669 (87%)	-0.15	19 (3%)	46	39	3, 18, 60, 85	0
1	B	582/669 (86%)	-0.16	13 (2%)	62	56	7, 25, 55, 81	0
All	All	1165/1338 (87%)	-0.16	32 (2%)	54	48	3, 22, 57, 85	0

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	484	GLY	4.4
1	B	339	HIS	3.9
1	A	99	ARG	3.8
1	A	132	ALA	3.8
1	B	343	THR	3.8

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.