



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:00 PM GMT

PDB ID : 3VQK
Title : Small heat shock protein hsp14.0 of wild type
Authors : Hanazono, Y.; Takeda, K.; Miki, K.
Deposited on : 2012-03-26
Resolution : 4.50 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

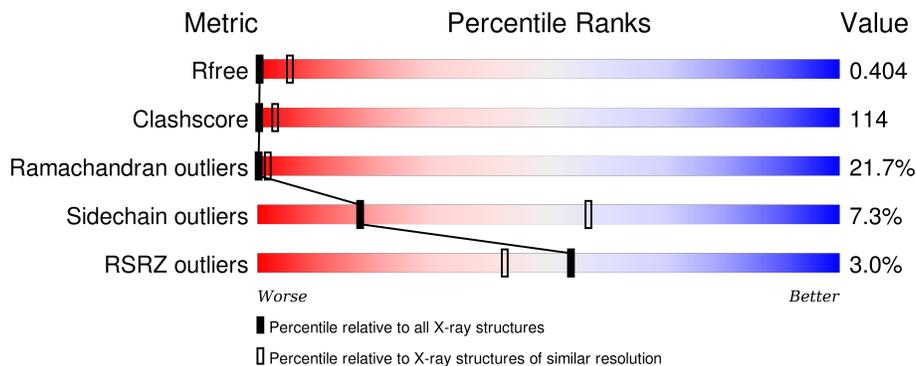
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.50 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}	91344	1071 (5.40-3.60)
Clashscore	102246	1003 (5.30-3.62)
Ramachandran outliers	100387	1117 (5.40-3.60)
Sidechain outliers	100360	1099 (5.40-3.60)
RSRZ outliers	91569	1075 (5.40-3.60)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$. 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	123	
1	B	123	
1	C	123	
1	D	123	
1	E	123	

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Mol	Chain	Length	Quality of chain
1	F	123	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into five segments with the following percentages from left to right: 2% (red), 14% (green), 59% (yellow), 14% (orange), and 13% (grey). A small red square is positioned above the 2% segment.</p>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5124 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.

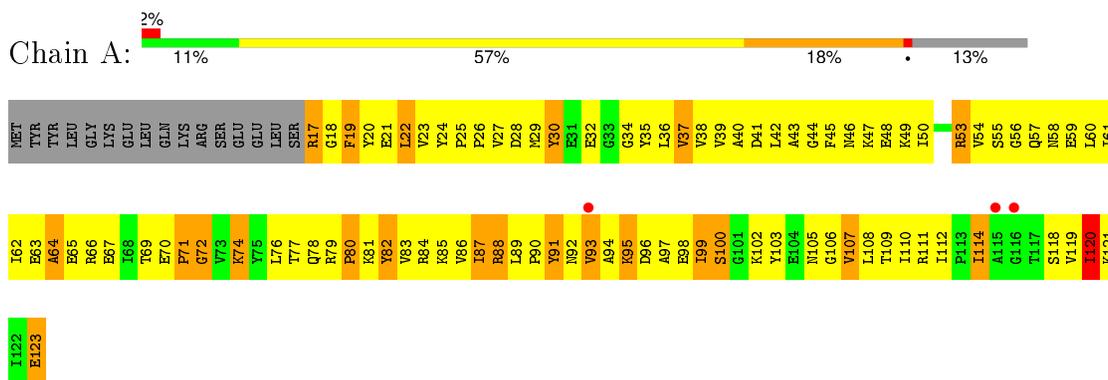
- Molecule 1 is a protein called Small heat shock protein StHsp14.0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	107	Total 854	C 551	N 143	O 159	S 1	0	0	0
1	B	107	Total 854	C 551	N 143	O 159	S 1	0	0	0
1	C	107	Total 854	C 551	N 143	O 159	S 1	0	0	0
1	D	107	Total 854	C 551	N 143	O 159	S 1	0	0	0
1	E	107	Total 854	C 551	N 143	O 159	S 1	0	0	0
1	F	107	Total 854	C 551	N 143	O 159	S 1	0	0	0

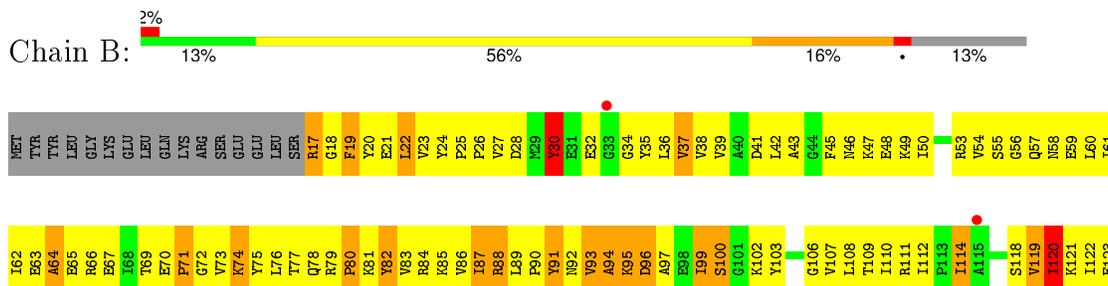
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

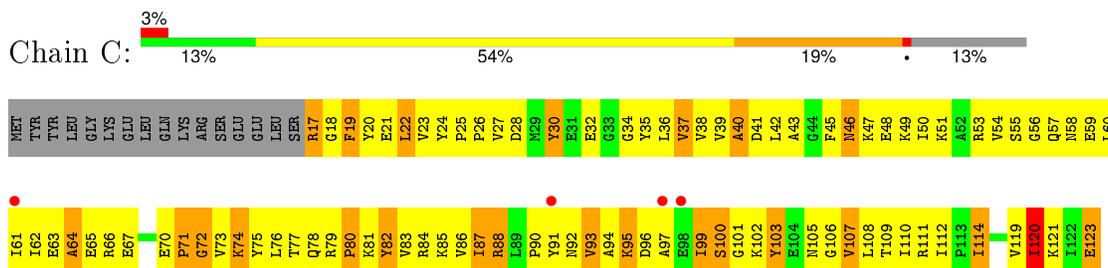
- Molecule 1: Small heat shock protein StHsp14.0



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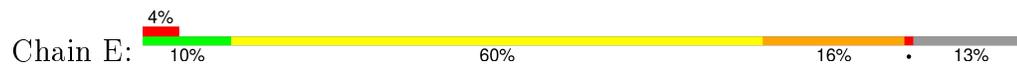


- Molecule 1: Small heat shock protein StHsp14.0

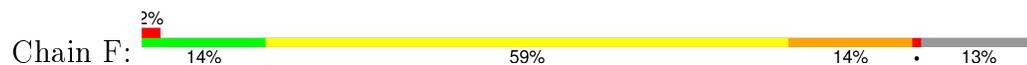




- Molecule 1: Small heat shock protein StHsp14.0



- Molecule 1: Small heat shock protein StHsp14.0



4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	117.43Å 117.43Å 115.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.13 – 4.50 37.13 – 4.50	Depositor EDS
% Data completeness (in resolution range)	87.1 (37.13-4.50) 87.1 (37.13-4.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.09 (at 4.44Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.333 , 0.404 0.333 , 0.404	Depositor DCC
R_{free} test set	216 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	210.3	Xtriage
Anisotropy	0.062	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.19 , 201.7	EDS
Estimated twinning fraction	0.116 for l,-k,h 0.138 for -l,-k,-h 0.136 for -h,-l,-k 0.117 for -h,l,k 0.195 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.35$, $\langle L^2 \rangle = 0.18$	Xtriage
Outliers	0 of 4120 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5124	wwPDB-VP
Average B, all atoms (Å ²)	287.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.53	0/869	0.71	0/1173
1	B	0.50	0/869	0.70	0/1173
1	C	0.53	0/869	0.71	0/1173
1	D	0.57	0/869	0.71	0/1173
1	E	0.57	0/869	0.72	0/1173
1	F	0.57	0/869	0.71	0/1173
All	All	0.55	0/5214	0.71	0/7038

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	854	0	883	232	0
1	B	854	0	883	224	0
1	C	854	0	883	202	0
1	D	854	0	883	198	0
1	E	854	0	883	224	0
1	F	854	0	883	209	0
All	All	5124	0	5298	1190	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 114.

The worst 5 of 1190 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:D:20:TYR:HA	1:D:23:VAL:HG22	1.24	1.12
1:C:42:LEU:HD11	1:C:45:PHE:HB3	1.22	1.10
1:F:110:ILE:HG22	1:F:111:ARG:H	1.15	1.10
1:D:55:SER:HB2	1:D:61:ILE:HD11	1.33	1.08
1:B:20:TYR:HA	1:B:23:VAL:HG22	1.31	1.08

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	105/123 (85%)	51 (49%)	32 (30%)	22 (21%)	0	2
1	B	105/123 (85%)	52 (50%)	30 (29%)	23 (22%)	0	1
1	C	105/123 (85%)	53 (50%)	27 (26%)	25 (24%)	0	1
1	D	105/123 (85%)	51 (49%)	32 (30%)	22 (21%)	0	2
1	E	105/123 (85%)	51 (49%)	31 (30%)	23 (22%)	0	1
1	F	105/123 (85%)	51 (49%)	32 (30%)	22 (21%)	0	2
All	All	630/738 (85%)	309 (49%)	184 (29%)	137 (22%)	0	2

5 of 137 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	37	VAL
1	A	64	ALA
1	A	93	VAL
1	A	100	SER
1	A	107	VAL

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	91/106 (86%)	84 (92%)	7 (8%)	16	55
1	B	91/106 (86%)	83 (91%)	8 (9%)	12	47
1	C	91/106 (86%)	85 (93%)	6 (7%)	21	60
1	D	91/106 (86%)	85 (93%)	6 (7%)	21	60
1	E	91/106 (86%)	84 (92%)	7 (8%)	16	55
1	F	91/106 (86%)	85 (93%)	6 (7%)	21	60
All	All	546/636 (86%)	506 (93%)	40 (7%)	17	57

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	91	TYR
1	D	22	LEU
1	F	91	TYR
1	C	123	GLU
1	D	82	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	58	ASN
1	C	105	ASN
1	E	105	ASN
1	C	46	ASN
1	E	46	ASN

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 carbohydrates 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	107/123 (86%)	-0.33	3 (2%) 56 46	204, 281, 360, 402	0
1	B	107/123 (86%)	-0.45	2 (1%) 70 61	204, 281, 359, 402	0
1	C	107/123 (86%)	-0.19	4 (3%) 45 36	201, 282, 359, 402	0
1	D	107/123 (86%)	-0.27	2 (1%) 70 61	202, 282, 360, 402	0
1	E	107/123 (86%)	-0.28	5 (4%) 35 28	201, 282, 360, 403	0
1	F	107/123 (86%)	-0.39	3 (2%) 56 46	203, 280, 361, 403	0
All	All	642/738 (86%)	-0.32	19 (2%) 54 42	201, 282, 365, 403	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	115	ALA	4.7
1	A	116	GLY	4.0
1	F	91	TYR	3.5
1	E	55	SER	3.5
1	E	97	ALA	3.1

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 carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.