



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:03 PM GMT

PDB ID : 3VQM  
Title : Small heat shock protein hsp14.0 of C-terminal deletion variant with C-terminal peptide  
Authors : Hanazono, Y.; Takeda, K.; Miki, K.  
Deposited on : 2012-03-26  
Resolution : 2.55 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](mailto: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.

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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

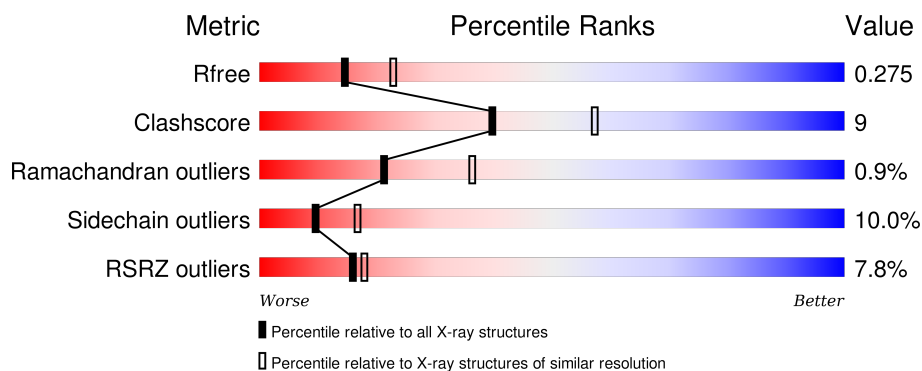
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.55 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	4549 (2.58-2.50)
Clashscore	102246	5292 (2.58-2.50)
Ramachandran outliers	100387	5194 (2.58-2.50)
Sidechain outliers	100360	5196 (2.58-2.50)
RSRZ outliers	91569	4561 (2.58-2.50)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	115	<div> <div>2%</div> <div>75% 19% . .</div> </div>
1	B	115	<div> <div>2%</div> <div>60% 24% 6% . 9%</div> </div>
1	C	115	<div> <div>68% 19% . 10%</div> </div>
1	D	115	<div> <div>3%</div> <div>73% 18% . .</div> </div>
1	E	115	<div> <div>5%</div> <div>74% 18% . 5%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	115	
1	G	115	
1	H	115	
1	I	115	
1	J	115	
1	K	115	
1	L	115	
1	M	115	
1	N	115	
2	O	5	
2	P	5	
2	Q	5	
2	R	5	
2	S	5	
2	T	5	
2	U	5	
2	V	5	
2	W	5	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12005 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
1	A	111	Total	C	N	O	S	0	0	0
			873	560	149	163	1			
1	B	105	Total	C	N	O	S	0	0	0
			821	530	140	150	1			
1	C	103	Total	C	N	O	S	0	0	0
			820	529	138	152	1			
1	D	110	Total	C	N	O	S	0	0	0
			864	553	145	165	1			
1	E	109	Total	C	N	O	S	0	0	0
			852	549	144	158	1			
1	F	101	Total	C	N	O	S	0	0	0
			791	512	131	147	1			
1	G	112	Total	C	N	O	S	0	0	0
			876	561	150	164	1			
1	H	102	Total	C	N	O	S	0	0	0
			789	512	133	143	1			
1	I	105	Total	C	N	O	S	0	0	0
			816	522	136	157	1			
1	J	112	Total	C	N	O	S	0	0	0
			856	551	146	158	1			
1	K	108	Total	C	N	O	S	0	0	0
			829	530	139	159	1			
1	L	98	Total	C	N	O		0	0	0
			715	462	123	130				
1	M	108	Total	C	N	O	S	0	0	0
			839	536	140	162	1			
1	N	99	Total	C	N	O	S	0	0	0
			774	500	128	145	1			

- Molecule 2 is a protein called C-terminal peptide from Small heat shock protein StHsp14.0.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	O	5	Total	C	N	O	0	0	0
			42	28	6	8			
2	P	5	Total	C	N	O	0	0	0
			42	28	6	8			
2	Q	5	Total	C	N	O	0	0	0
			42	28	6	8			
2	R	5	Total	C	N	O	0	0	0
			42	28	6	8			
2	S	5	Total	C	N	O	0	0	0
			42	28	6	8			
2	T	5	Total	C	N	O	0	0	0
			42	28	6	8			
2	U	5	Total	C	N	O	0	0	0
			38	25	5	8			
2	V	5	Total	C	N	O	0	0	0
			34	23	5	6			
2	W	5	Total	C	N	O	0	0	0
			38	25	5	8			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	12	Total	O	0	0
			12	12		
3	B	8	Total	O	0	0
			8	8		
3	C	16	Total	O	0	0
			16	16		
3	D	16	Total	O	0	0
			16	16		
3	E	6	Total	O	0	0
			6	6		
3	F	6	Total	O	0	0
			6	6		
3	G	16	Total	O	0	0
			16	16		
3	H	14	Total	O	0	0
			14	14		
3	I	8	Total	O	0	0
			8	8		
3	J	8	Total	O	0	0
			8	8		
3	K	9	Total	O	0	0
			9	9		

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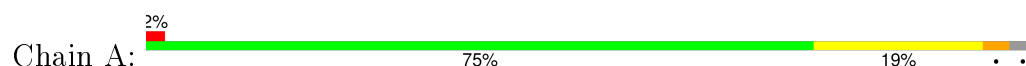
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	L	1	Total 1	O 1	0	0
3	M	3	Total 3	O 3	0	0
3	N	3	Total 3	O 3	0	0
3	Q	1	Total 1	O 1	0	0
3	S	1	Total 1	O 1	0	0

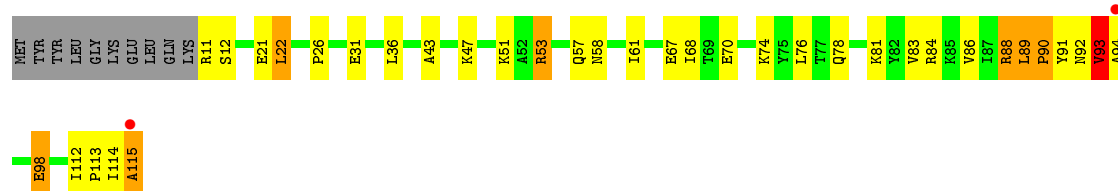
### 3 Residue-property plots [i](#)

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



- Molecule 1: Small heat shock protein StHsp14.0



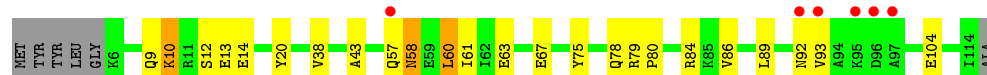
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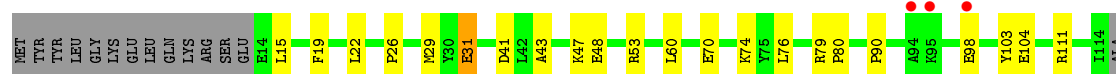
- Molecule 1: Small heat shock protein StHsp14.0



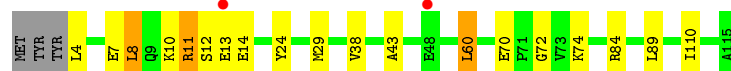
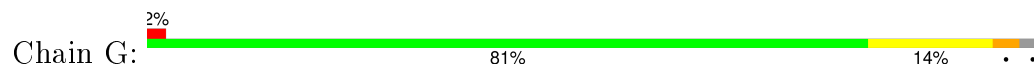
- Molecule 1: Small heat shock protein StHsp14.0



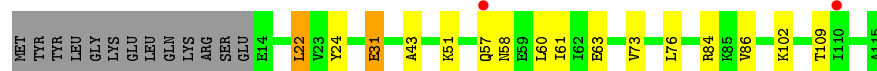
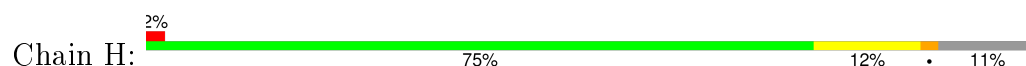
- Molecule 1: Small heat shock protein StHsp14.0



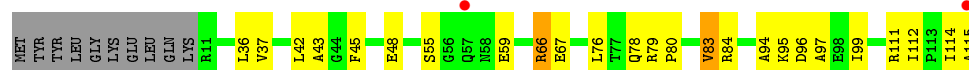
- Molecule 1: Small heat shock protein StHsp14.0



- Molecule 1: Small heat shock protein StHsp14.0



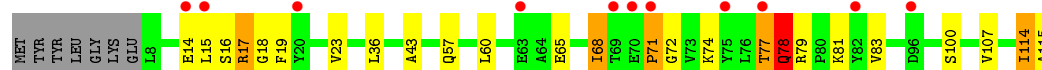
- Molecule 1: Small heat shock protein StHsp14.0



- Molecule 1: Small heat shock protein StHsp14.0



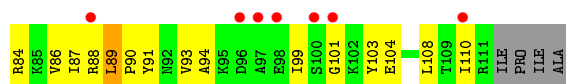
- Molecule 1: Small heat shock protein StHsp14.0



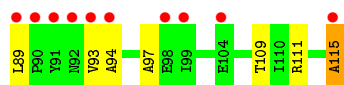
- Molecule 1: Small heat shock protein StHsp14.0



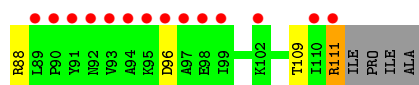
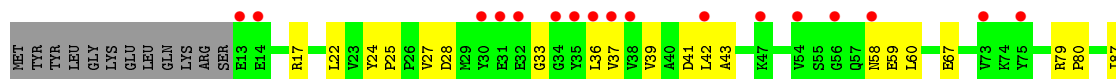




- Molecule 1: Small heat shock protein StHsp14.0



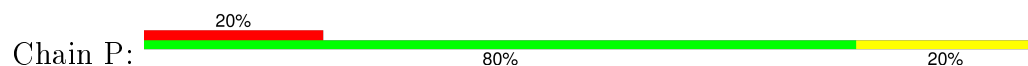
- Molecule 1: Small heat shock protein StHsp14.0



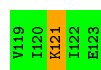
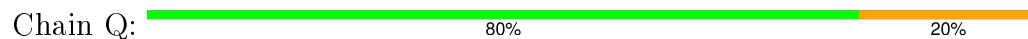
- Molecule 2: C-terminal peptide from Small heat shock protein StHsp14.0



- Molecule 2: C-terminal peptide from Small heat shock protein StHsp14.0



- Molecule 2: C-terminal peptide from Small heat shock protein StHsp14.0



- Molecule 2: C-terminal peptide from Small heat shock protein StHsp14.0



There are no outlier residues recorded for this chain.

- Molecule 2: C-terminal peptide from Small heat shock protein StHsp14.0

Chain S:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: C-terminal peptide from Small heat shock protein StHsp14.0

Chain T:  20% 100%



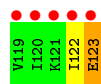
- Molecule 2: C-terminal peptide from Small heat shock protein StHsp14.0

Chain U:  20% 100%




- Molecule 2: C-terminal peptide from Small heat shock protein StHsp14.0

Chain V:  100% 60% 20% 20%



- Molecule 2: C-terminal peptide from Small heat shock protein StHsp14.0

Chain W:  40% 80% 20%



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	156.30Å 161.90Å 162.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.32 – 2.55 42.32 – 2.55	Depositor EDS
% Data completeness (in resolution range)	96.7 (42.32-2.55) 96.3 (42.32-2.55)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.37 (at 2.54Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, $R_{free}$	0.224 , 0.275 0.225 , 0.275	Depositor DCC
$R_{free}$ test set	3284 reflections (5.06%)	DCC
Wilson B-factor (Å <sup>2</sup> )	45.0	Xtriage
Anisotropy	0.197	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 73.0	EDS
Estimated twinning fraction	0.050 for -k,-h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 65215 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	12005	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.45% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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

### 5.1 Standard geometry

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	0.46	1/888 (0.1%)	0.46	0/1199
1	B	0.56	1/836 (0.1%)	0.59	0/1131
1	C	0.35	1/835 (0.1%)	0.46	0/1128
1	D	0.30	1/879 (0.1%)	0.43	0/1189
1	E	0.44	0/867	0.47	0/1174
1	F	0.29	0/806	0.44	0/1091
1	G	0.23	0/891	0.46	0/1203
1	H	0.23	0/804	0.42	0/1090
1	I	0.36	1/831 (0.1%)	0.45	0/1127
1	J	0.29	0/871	0.48	0/1180
1	K	0.54	1/844 (0.1%)	0.60	1/1143 (0.1%)
1	L	0.38	0/727	0.51	0/992
1	M	0.28	1/854 (0.1%)	0.39	0/1158
1	N	0.22	0/788	0.41	0/1067
2	O	0.17	0/41	0.39	0/52
2	P	0.19	0/41	0.42	0/52
2	Q	0.21	0/41	0.45	0/52
2	R	0.18	0/41	0.38	0/52
2	S	0.21	0/41	0.35	0/52
2	T	0.19	0/41	0.42	0/52
2	U	0.18	0/37	0.43	0/48
2	V	0.93	1/33 (3.0%)	0.42	0/43
2	W	0.89	1/37 (2.7%)	0.41	0/48
All	All	0.37	9/12074 (0.1%)	0.47	1/16323 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	K	0	1

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	K	115	ALA	C-OXT	5.59	1.33	1.23
1	A	115	ALA	C-OXT	5.58	1.33	1.23
1	D	115	ALA	C-OXT	5.40	1.33	1.23
1	I	115	ALA	C-OXT	5.28	1.33	1.23
1	M	115	ALA	C-OXT	5.26	1.33	1.23

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	78	GLN	N-CA-C	5.89	126.91	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	K	77	THR	Peptide

## 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	873	0	882	15	0
1	B	821	0	828	30	0
1	C	820	0	838	13	0
1	D	864	0	858	19	0
1	E	852	0	848	23	0
1	F	791	0	794	10	0
1	G	876	0	877	13	0
1	H	789	0	798	10	0
1	I	816	0	793	14	0
1	J	856	0	850	17	0
1	K	829	0	801	18	0
1	L	715	0	687	30	0
1	M	839	0	817	14	0
1	N	774	0	772	12	0
2	O	42	0	49	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	P	42	0	49	1	0
2	Q	42	0	49	3	0
2	R	42	0	49	0	0
2	S	42	0	49	0	0
2	T	42	0	49	0	0
2	U	38	0	38	0	0
2	V	34	0	34	1	0
2	W	38	0	38	0	0
3	A	12	0	0	1	0
3	B	8	0	0	1	0
3	C	16	0	0	1	0
3	D	16	0	0	0	0
3	E	6	0	0	0	0
3	F	6	0	0	2	0
3	G	16	0	0	1	0
3	H	14	0	0	0	0
3	I	8	0	0	0	0
3	J	8	0	0	0	0
3	K	9	0	0	2	0
3	L	1	0	0	0	0
3	M	3	0	0	1	0
3	N	3	0	0	0	0
3	Q	1	0	0	1	0
3	S	1	0	0	0	0
All	All	12005	0	11847	208	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 9.

The worst 5 of 208 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:E:10:LYS:HB2	1:E:10:LYS:HZ3	1.04	1.14
1:E:10:LYS:HB2	1:E:10:LYS:NZ	1.65	1.07
1:D:54:VAL:HG23	1:D:99:ILE:HD11	1.51	0.91
1:A:11:ARG:HB2	1:B:88:ARG:HH22	1.35	0.91
1:E:10:LYS:NZ	1:E:10:LYS:CB	2.30	0.89

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	109/115 (95%)	105 (96%)	4 (4%)	0	100	100
1	B	103/115 (90%)	98 (95%)	4 (4%)	1 (1%)	19	33
1	C	101/115 (88%)	98 (97%)	3 (3%)	0	100	100
1	D	108/115 (94%)	98 (91%)	8 (7%)	2 (2%)	10	15
1	E	107/115 (93%)	100 (94%)	7 (6%)	0	100	100
1	F	99/115 (86%)	94 (95%)	5 (5%)	0	100	100
1	G	110/115 (96%)	105 (96%)	4 (4%)	1 (1%)	21	36
1	H	100/115 (87%)	92 (92%)	8 (8%)	0	100	100
1	I	103/115 (90%)	96 (93%)	5 (5%)	2 (2%)	10	15
1	J	110/115 (96%)	101 (92%)	9 (8%)	0	100	100
1	K	106/115 (92%)	96 (91%)	7 (7%)	3 (3%)	6	8
1	L	96/115 (84%)	84 (88%)	11 (12%)	1 (1%)	19	33
1	M	106/115 (92%)	97 (92%)	8 (8%)	1 (1%)	21	36
1	N	97/115 (84%)	85 (88%)	10 (10%)	2 (2%)	9	13
2	O	3/5 (60%)	3 (100%)	0	0	100	100
2	P	3/5 (60%)	3 (100%)	0	0	100	100
2	Q	3/5 (60%)	3 (100%)	0	0	100	100
2	R	3/5 (60%)	3 (100%)	0	0	100	100
2	S	3/5 (60%)	3 (100%)	0	0	100	100
2	T	3/5 (60%)	3 (100%)	0	0	100	100
2	U	3/5 (60%)	1 (33%)	2 (67%)	0	100	100
2	V	3/5 (60%)	2 (67%)	1 (33%)	0	100	100
2	W	3/5 (60%)	3 (100%)	0	0	100	100
All	All	1482/1655 (90%)	1373 (93%)	96 (6%)	13 (1%)	21	36

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	93	VAL
1	K	71	PRO
1	G	10	LYS
1	I	96	ASP
1	I	97	ALA

### 5.3.2 Protein sidechains ⓘ

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	90/99 (91%)	80 (89%)	10 (11%)	8	13
1	B	83/99 (84%)	70 (84%)	13 (16%)	3	5
1	C	86/99 (87%)	77 (90%)	9 (10%)	8	15
1	D	89/99 (90%)	81 (91%)	8 (9%)	12	21
1	E	86/99 (87%)	80 (93%)	6 (7%)	19	33
1	F	81/99 (82%)	74 (91%)	7 (9%)	13	23
1	G	89/99 (90%)	84 (94%)	5 (6%)	26	45
1	H	80/99 (81%)	74 (92%)	6 (8%)	17	30
1	I	82/99 (83%)	76 (93%)	6 (7%)	17	31
1	J	85/99 (86%)	75 (88%)	10 (12%)	6	11
1	K	82/99 (83%)	71 (87%)	11 (13%)	5	8
1	L	66/99 (67%)	54 (82%)	12 (18%)	2	3
1	M	85/99 (86%)	75 (88%)	10 (12%)	6	11
1	N	79/99 (80%)	73 (92%)	6 (8%)	16	29
2	O	5/5 (100%)	5 (100%)	0	100	100
2	P	5/5 (100%)	5 (100%)	0	100	100
2	Q	5/5 (100%)	4 (80%)	1 (20%)	1	2
2	R	5/5 (100%)	5 (100%)	0	100	100
2	S	5/5 (100%)	5 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	T	5/5 (100%)	5 (100%)	0	100	100
2	U	4/5 (80%)	4 (100%)	0	100	100
2	V	3/5 (60%)	3 (100%)	0	100	100
2	W	4/5 (80%)	3 (75%)	1 (25%)	1	1
All	All	1204/1431 (84%)	1083 (90%)	121 (10%)	9	17

5 of 121 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	11	ARG
1	I	76	LEU
1	M	84	ARG
1	G	60	LEU
1	H	60	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	57	GLN
1	D	9	GLN
1	E	58	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	111/115 (96%)	0.12	2 (1%) 71 76	25, 43, 74, 81	0
1	B	105/115 (91%)	0.11	2 (1%) 70 74	24, 43, 96, 110	0
1	C	103/115 (89%)	-0.15	0 100 100	23, 39, 64, 82	0
1	D	110/115 (95%)	0.01	3 (2%) 58 63	24, 42, 80, 102	0
1	E	109/115 (94%)	0.22	6 (5%) 29 33	24, 48, 83, 93	0
1	F	101/115 (87%)	0.15	3 (2%) 54 60	24, 46, 91, 124	0
1	G	112/115 (97%)	0.02	2 (1%) 71 76	28, 44, 68, 82	0
1	H	102/115 (88%)	0.22	2 (1%) 68 73	28, 46, 68, 95	0
1	I	105/115 (91%)	0.26	2 (1%) 70 74	29, 54, 89, 99	0
1	J	112/115 (97%)	0.27	4 (3%) 46 53	28, 49, 93, 117	0
1	K	108/115 (93%)	0.72	11 (10%) 9 10	28, 71, 109, 121	0
1	L	98/115 (85%)	0.79	11 (11%) 7 8	26, 73, 111, 117	0
1	M	108/115 (93%)	1.48	29 (26%) 1 1	56, 88, 113, 123	0
1	N	99/115 (86%)	1.53	31 (31%) 1 0	54, 84, 129, 135	0
2	O	5/5 (100%)	0.28	1 (20%) 1 1	49, 55, 68, 75	0
2	P	5/5 (100%)	1.26	1 (20%) 1 1	48, 50, 76, 79	0
2	Q	5/5 (100%)	0.73	0 100 100	49, 55, 72, 73	0
2	R	5/5 (100%)	0.49	0 100 100	54, 67, 77, 78	0
2	S	5/5 (100%)	0.38	0 100 100	63, 72, 78, 88	0
2	T	5/5 (100%)	1.43	1 (20%) 1 1	56, 60, 82, 95	0
2	U	5/5 (100%)	0.86	1 (20%) 1 1	72, 72, 85, 91	0
2	V	5/5 (100%)	3.38	5 (100%) 0 0	88, 99, 103, 114	0
2	W	5/5 (100%)	2.31	2 (40%) 0 0	98, 99, 119, 122	0
All	All	1528/1655 (92%)	0.43	119 (7%) 16 18	23, 52, 104, 135	0

The worst 5 of 119 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	115	ALA	8.2
1	N	30	TYR	6.4
1	N	34	GLY	5.8
1	N	91	TYR	5.8
1	L	100	SER	5.7

## 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 [i](#)

There are no such residues in this entry.