



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2022 – 12:09 PM JST

PDB ID : 7CK4  
Title : Structural and functional analysis of small heat shock protein from *Synechococcus* phage S-ShM2  
Authors : Biswas, S.; Suguna, K.  
Deposited on : 2020-07-15  
Resolution : 7.00 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](mailto: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 ⓘ 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
Xtriage (Phenix)	:	1.13
EDS	:	2.27
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)	:	2.27

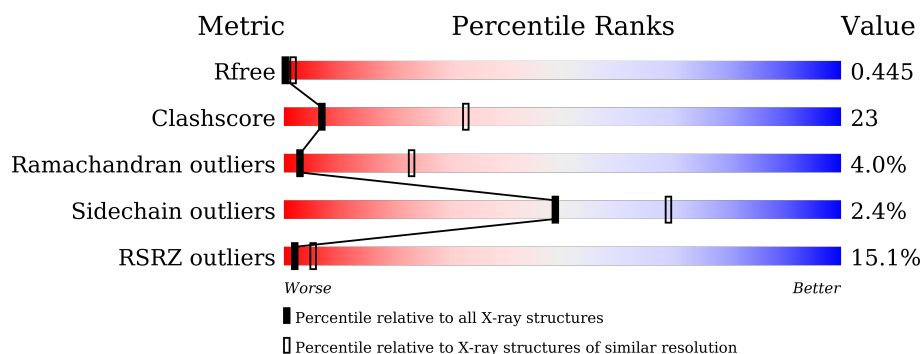
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 7.00 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	1004 (10.00-3.90)
Clashscore	141614	1069 (10.00-3.90)
Ramachandran outliers	138981	1002 (10.00-3.90)
Sidechain outliers	138945	1002 (10.00-3.86)
RSRZ outliers	127900	1004 (9.50-3.80)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	175	
1	B	175	
1	C	175	
1	D	175	
1	E	175	
1	F	175	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4678 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 Heat shock protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	106	Total	C	N	O	S	0	0	0
			840	536	144	159	1			
1	B	92	Total	C	N	O	S	0	0	0
			711	450	122	138	1			
1	C	102	Total	C	N	O	S	0	0	0
			805	518	136	150	1			
1	D	99	Total	C	N	O	S	0	0	0
			772	493	128	150	1			
1	E	102	Total	C	N	O	S	0	0	0
			813	518	138	156	1			
1	F	97	Total	C	N	O	S	0	0	0
			737	465	127	144	1			

There are 138 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	expression tag	UNP E3SJI7
A	-7	GLY	-	expression tag	UNP E3SJI7
A	-6	SER	-	expression tag	UNP E3SJI7
A	-5	SER	-	expression tag	UNP E3SJI7
A	-4	HIS	-	expression tag	UNP E3SJI7
A	-3	HIS	-	expression tag	UNP E3SJI7
A	-2	HIS	-	expression tag	UNP E3SJI7
A	-1	HIS	-	expression tag	UNP E3SJI7
A	0	HIS	-	expression tag	UNP E3SJI7
A	1	HIS	-	expression tag	UNP E3SJI7
A	2	SER	-	expression tag	UNP E3SJI7
A	3	SER	-	expression tag	UNP E3SJI7
A	4	GLY	-	expression tag	UNP E3SJI7
A	5	LEU	-	expression tag	UNP E3SJI7
A	6	VAL	-	expression tag	UNP E3SJI7
A	7	PRO	-	expression tag	UNP E3SJI7
A	8	ARG	-	expression tag	UNP E3SJI7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	9	GLY	-	expression tag	UNP E3SJI7
A	10	SER	-	expression tag	UNP E3SJI7
A	11	HIS	-	expression tag	UNP E3SJI7
A	12	MET	-	expression tag	UNP E3SJI7
A	13	ALA	-	expression tag	UNP E3SJI7
A	14	SER	-	expression tag	UNP E3SJI7
B	-8	MET	-	expression tag	UNP E3SJI7
B	-7	GLY	-	expression tag	UNP E3SJI7
B	-6	SER	-	expression tag	UNP E3SJI7
B	-5	SER	-	expression tag	UNP E3SJI7
B	-4	HIS	-	expression tag	UNP E3SJI7
B	-3	HIS	-	expression tag	UNP E3SJI7
B	-2	HIS	-	expression tag	UNP E3SJI7
B	-1	HIS	-	expression tag	UNP E3SJI7
B	0	HIS	-	expression tag	UNP E3SJI7
B	1	HIS	-	expression tag	UNP E3SJI7
B	2	SER	-	expression tag	UNP E3SJI7
B	3	SER	-	expression tag	UNP E3SJI7
B	4	GLY	-	expression tag	UNP E3SJI7
B	5	LEU	-	expression tag	UNP E3SJI7
B	6	VAL	-	expression tag	UNP E3SJI7
B	7	PRO	-	expression tag	UNP E3SJI7
B	8	ARG	-	expression tag	UNP E3SJI7
B	9	GLY	-	expression tag	UNP E3SJI7
B	10	SER	-	expression tag	UNP E3SJI7
B	11	HIS	-	expression tag	UNP E3SJI7
B	12	MET	-	expression tag	UNP E3SJI7
B	13	ALA	-	expression tag	UNP E3SJI7
B	14	SER	-	expression tag	UNP E3SJI7
C	-8	MET	-	expression tag	UNP E3SJI7
C	-7	GLY	-	expression tag	UNP E3SJI7
C	-6	SER	-	expression tag	UNP E3SJI7
C	-5	SER	-	expression tag	UNP E3SJI7
C	-4	HIS	-	expression tag	UNP E3SJI7
C	-3	HIS	-	expression tag	UNP E3SJI7
C	-2	HIS	-	expression tag	UNP E3SJI7
C	-1	HIS	-	expression tag	UNP E3SJI7
C	0	HIS	-	expression tag	UNP E3SJI7
C	1	HIS	-	expression tag	UNP E3SJI7
C	2	SER	-	expression tag	UNP E3SJI7
C	3	SER	-	expression tag	UNP E3SJI7
C	4	GLY	-	expression tag	UNP E3SJI7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	5	LEU	-	expression tag	UNP E3SJI7
C	6	VAL	-	expression tag	UNP E3SJI7
C	7	PRO	-	expression tag	UNP E3SJI7
C	8	ARG	-	expression tag	UNP E3SJI7
C	9	GLY	-	expression tag	UNP E3SJI7
C	10	SER	-	expression tag	UNP E3SJI7
C	11	HIS	-	expression tag	UNP E3SJI7
C	12	MET	-	expression tag	UNP E3SJI7
C	13	ALA	-	expression tag	UNP E3SJI7
C	14	SER	-	expression tag	UNP E3SJI7
D	-8	MET	-	expression tag	UNP E3SJI7
D	-7	GLY	-	expression tag	UNP E3SJI7
D	-6	SER	-	expression tag	UNP E3SJI7
D	-5	SER	-	expression tag	UNP E3SJI7
D	-4	HIS	-	expression tag	UNP E3SJI7
D	-3	HIS	-	expression tag	UNP E3SJI7
D	-2	HIS	-	expression tag	UNP E3SJI7
D	-1	HIS	-	expression tag	UNP E3SJI7
D	0	HIS	-	expression tag	UNP E3SJI7
D	1	HIS	-	expression tag	UNP E3SJI7
D	2	SER	-	expression tag	UNP E3SJI7
D	3	SER	-	expression tag	UNP E3SJI7
D	4	GLY	-	expression tag	UNP E3SJI7
D	5	LEU	-	expression tag	UNP E3SJI7
D	6	VAL	-	expression tag	UNP E3SJI7
D	7	PRO	-	expression tag	UNP E3SJI7
D	8	ARG	-	expression tag	UNP E3SJI7
D	9	GLY	-	expression tag	UNP E3SJI7
D	10	SER	-	expression tag	UNP E3SJI7
D	11	HIS	-	expression tag	UNP E3SJI7
D	12	MET	-	expression tag	UNP E3SJI7
D	13	ALA	-	expression tag	UNP E3SJI7
D	14	SER	-	expression tag	UNP E3SJI7
E	-8	MET	-	expression tag	UNP E3SJI7
E	-7	GLY	-	expression tag	UNP E3SJI7
E	-6	SER	-	expression tag	UNP E3SJI7
E	-5	SER	-	expression tag	UNP E3SJI7
E	-4	HIS	-	expression tag	UNP E3SJI7
E	-3	HIS	-	expression tag	UNP E3SJI7
E	-2	HIS	-	expression tag	UNP E3SJI7
E	-1	HIS	-	expression tag	UNP E3SJI7
E	0	HIS	-	expression tag	UNP E3SJI7

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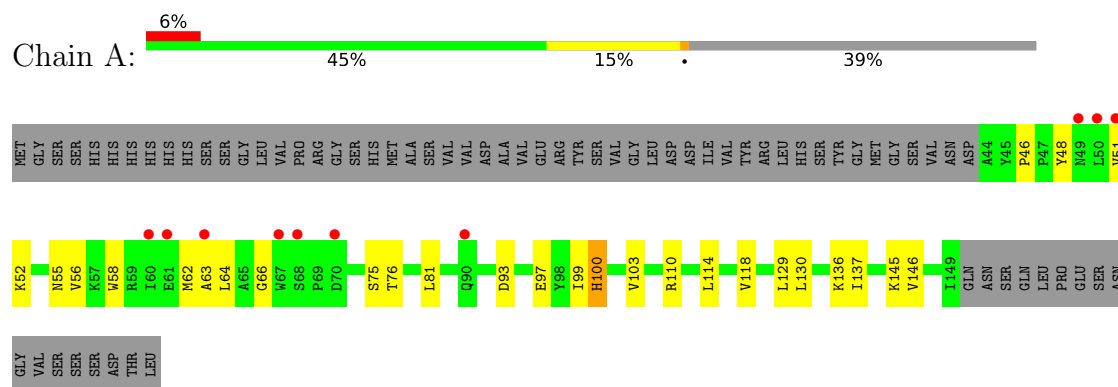
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Chain	Residue	Modelled	Actual	Comment	Reference
E	1	HIS	-	expression tag	UNP E3SJI7
E	2	SER	-	expression tag	UNP E3SJI7
E	3	SER	-	expression tag	UNP E3SJI7
E	4	GLY	-	expression tag	UNP E3SJI7
E	5	LEU	-	expression tag	UNP E3SJI7
E	6	VAL	-	expression tag	UNP E3SJI7
E	7	PRO	-	expression tag	UNP E3SJI7
E	8	ARG	-	expression tag	UNP E3SJI7
E	9	GLY	-	expression tag	UNP E3SJI7
E	10	SER	-	expression tag	UNP E3SJI7
E	11	HIS	-	expression tag	UNP E3SJI7
E	12	MET	-	expression tag	UNP E3SJI7
E	13	ALA	-	expression tag	UNP E3SJI7
E	14	SER	-	expression tag	UNP E3SJI7
F	-8	MET	-	expression tag	UNP E3SJI7
F	-7	GLY	-	expression tag	UNP E3SJI7
F	-6	SER	-	expression tag	UNP E3SJI7
F	-5	SER	-	expression tag	UNP E3SJI7
F	-4	HIS	-	expression tag	UNP E3SJI7
F	-3	HIS	-	expression tag	UNP E3SJI7
F	-2	HIS	-	expression tag	UNP E3SJI7
F	-1	HIS	-	expression tag	UNP E3SJI7
F	0	HIS	-	expression tag	UNP E3SJI7
F	1	HIS	-	expression tag	UNP E3SJI7
F	2	SER	-	expression tag	UNP E3SJI7
F	3	SER	-	expression tag	UNP E3SJI7
F	4	GLY	-	expression tag	UNP E3SJI7
F	5	LEU	-	expression tag	UNP E3SJI7
F	6	VAL	-	expression tag	UNP E3SJI7
F	7	PRO	-	expression tag	UNP E3SJI7
F	8	ARG	-	expression tag	UNP E3SJI7
F	9	GLY	-	expression tag	UNP E3SJI7
F	10	SER	-	expression tag	UNP E3SJI7
F	11	HIS	-	expression tag	UNP E3SJI7
F	12	MET	-	expression tag	UNP E3SJI7
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F	14	SER	-	expression tag	UNP E3SJI7

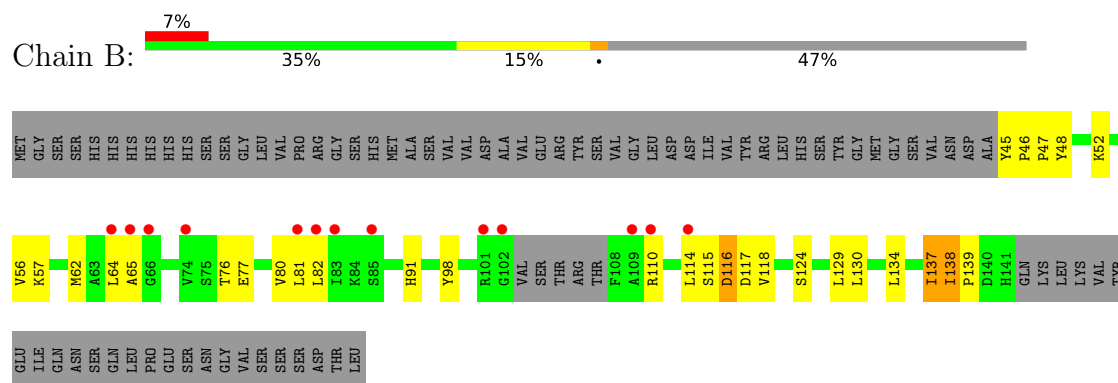
### 3 Residue-property plots [i](#)

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.

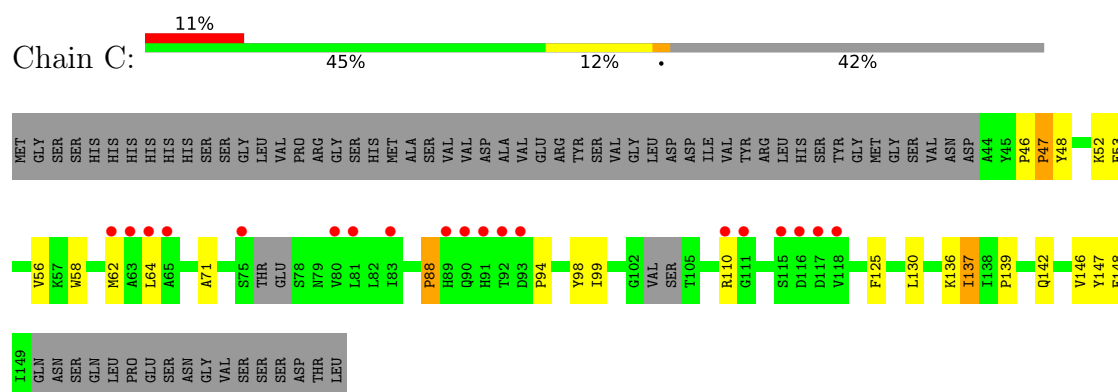
- Molecule 1: Heat shock protein



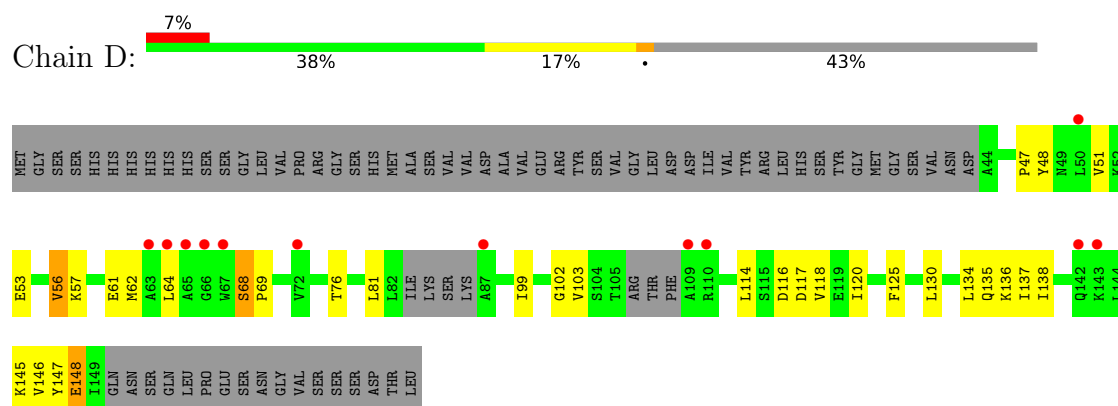
- Molecule 1: Heat shock protein



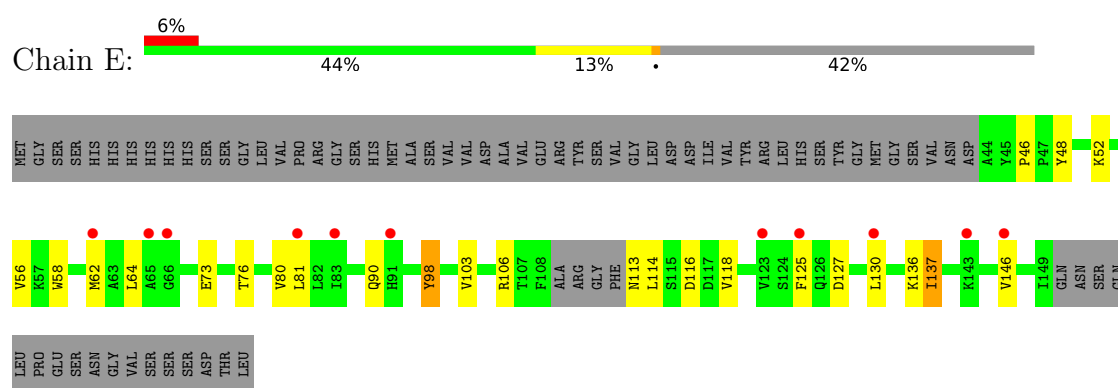
- Molecule 1: Heat shock protein



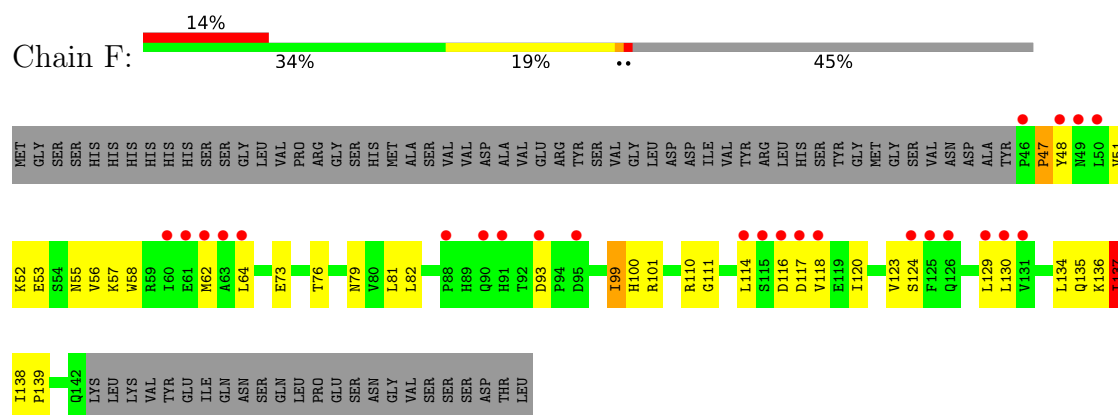
- Molecule 1: Heat shock protein



- Molecule 1: Heat shock protein



- Molecule 1: Heat shock protein





## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	126.15Å 126.15Å 152.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.65 – 7.00 48.65 – 7.00	Depositor EDS
% Data completeness (in resolution range)	99.2 (48.65-7.00) 99.5 (48.65-7.00)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.72 (at 7.37Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, $R_{free}$	0.346 , 0.433 0.360 , 0.445	Depositor DCC
$R_{free}$ test set	99 reflections (5.17%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	461.3	Xtriage
Anisotropy	0.324	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 542.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.068 for -h,k,-l	Xtriage
$F_o, F_c$ correlation	0.81	EDS
Total number of atoms	4678	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	500.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.13% 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, 0.333 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	0.36	0/859	0.57	0/1167
1	B	0.37	0/725	0.60	0/987
1	C	0.34	0/822	0.58	0/1114
1	D	0.38	0/790	0.60	0/1077
1	E	0.33	0/831	0.55	0/1130
1	F	0.41	0/752	0.58	0/1024
All	All	0.37	0/4779	0.58	0/6499

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	840	0	826	45	0
1	B	711	0	671	36	0
1	C	805	0	787	42	0
1	D	772	0	727	32	0
1	E	813	0	799	33	0
1	F	737	0	701	43	0
All	All	4678	0	4511	214	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 23.

All (214) 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:52:LYS:CB	1:E:58:TRP:HZ3	1.49	1.25
1:E:52:LYS:HD3	1:E:58:TRP:CZ3	1.74	1.22
1:E:52:LYS:HB3	1:E:58:TRP:HZ3	1.03	1.19
1:C:52:LYS:HB3	1:C:58:TRP:HZ3	1.07	1.14
1:C:52:LYS:CB	1:C:58:TRP:HZ3	1.59	1.14
1:A:52:LYS:HB3	1:A:58:TRP:CZ3	1.84	1.13
1:E:52:LYS:HB3	1:E:58:TRP:CZ3	1.88	1.07
1:F:137:ILE:CG2	1:F:138:ILE:H	1.65	1.06
1:E:52:LYS:CB	1:E:58:TRP:CZ3	2.38	1.05
1:F:137:ILE:HG22	1:F:138:ILE:N	1.55	1.04
1:C:52:LYS:HB3	1:C:58:TRP:CZ3	1.93	1.04
1:E:52:LYS:CD	1:E:58:TRP:CZ3	2.42	1.01
1:C:52:LYS:CB	1:C:58:TRP:CZ3	2.44	1.01
1:F:137:ILE:HG23	1:F:139:PRO:HD3	1.38	0.99
1:C:52:LYS:HD2	1:D:99:ILE:HD12	1.43	0.98
1:F:55:ASN:CA	1:F:137:ILE:HD11	1.97	0.94
1:E:52:LYS:CG	1:E:58:TRP:CZ3	2.50	0.94
1:A:52:LYS:CB	1:A:58:TRP:HZ3	1.82	0.93
1:E:52:LYS:HD2	1:F:99:ILE:HD11	1.49	0.93
1:F:137:ILE:HG22	1:F:138:ILE:H	0.78	0.93
1:A:52:LYS:HB3	1:A:58:TRP:HZ3	1.22	0.93
1:A:52:LYS:CB	1:A:58:TRP:CZ3	2.51	0.93
1:F:137:ILE:CG2	1:F:138:ILE:N	2.26	0.92
1:E:52:LYS:HD3	1:E:58:TRP:CH2	2.03	0.92
1:E:52:LYS:CG	1:E:58:TRP:HZ3	1.85	0.90
1:C:52:LYS:CG	1:C:58:TRP:CZ3	2.56	0.89
1:F:81:LEU:HG	1:F:114:LEU:HD11	1.56	0.86
1:B:56:VAL:HA	1:B:137:ILE:HG13	1.58	0.85
1:C:52:LYS:CD	1:C:58:TRP:CZ3	2.60	0.84
1:A:48:TYR:CZ	1:A:62:MET:HE1	2.14	0.83
1:D:53:GLU:HB2	1:D:57:LYS:CB	2.07	0.83
1:C:52:LYS:CG	1:C:58:TRP:HZ3	1.92	0.83
1:F:137:ILE:CG2	1:F:139:PRO:HD3	2.08	0.83
1:B:45:TYR:HB3	1:B:110:ARG:NH2	1.94	0.83
1:A:52:LYS:CD	1:A:58:TRP:CZ3	2.63	0.82
1:E:64:LEU:HD12	1:E:130:LEU:HD11	1.62	0.81
1:F:55:ASN:C	1:F:137:ILE:HD11	2.00	0.81
1:E:52:LYS:HA	1:E:58:TRP:CE3	2.17	0.79
1:A:52:LYS:CG	1:A:58:TRP:HZ3	1.95	0.79
1:A:52:LYS:CG	1:A:58:TRP:CZ3	2.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:LYS:CD	1:A:58:TRP:HZ3	1.97	0.78
1:C:52:LYS:HA	1:C:58:TRP:CE3	2.20	0.76
1:C:48:TYR:HE2	1:C:110:ARG:HH22	1.36	0.73
1:B:117:ASP:OD2	1:B:117:ASP:CB	2.37	0.72
1:B:117:ASP:CB	1:B:117:ASP:OD1	2.38	0.71
1:C:52:LYS:HD3	1:C:58:TRP:CZ3	2.25	0.71
1:D:81:LEU:HG	1:D:114:LEU:HD11	1.72	0.70
1:F:48:TYR:CD1	1:F:62:MET:SD	2.85	0.69
1:F:114:LEU:HD13	1:F:118:VAL:HB	1.72	0.69
1:A:52:LYS:HD3	1:A:58:TRP:CZ3	2.26	0.68
1:C:48:TYR:CE2	1:C:110:ARG:NH1	2.59	0.68
1:C:52:LYS:CD	1:D:99:ILE:HD12	2.20	0.68
1:D:56:VAL:HG13	1:D:136:LYS:C	2.14	0.67
1:A:52:LYS:HD3	1:A:58:TRP:HZ3	1.57	0.67
1:B:64:LEU:HD12	1:B:130:LEU:HD11	1.77	0.67
1:E:52:LYS:CD	1:F:99:ILE:HD11	2.23	0.66
1:A:129:LEU:HD21	1:B:65:ALA:HB1	1.77	0.65
1:F:55:ASN:C	1:F:137:ILE:CD1	2.65	0.65
1:D:48:TYR:CG	1:D:62:MET:SD	2.90	0.64
1:B:56:VAL:N	1:B:137:ILE:HD11	2.12	0.64
1:B:81:LEU:HG	1:B:114:LEU:HD11	1.79	0.64
1:A:52:LYS:HA	1:A:58:TRP:CE3	2.34	0.63
1:E:125:PHE:CD1	1:E:130:LEU:HD22	2.34	0.62
1:B:137:ILE:HG22	1:B:139:PRO:HD3	1.80	0.61
1:F:48:TYR:CG	1:F:62:MET:SD	2.92	0.61
1:F:55:ASN:O	1:F:137:ILE:HG13	2.00	0.60
1:C:52:LYS:HG2	1:C:58:TRP:CE3	2.36	0.60
1:D:62:MET:HB2	1:D:130:LEU:HB2	1.84	0.60
1:F:52:LYS:HE2	1:F:58:TRP:CH2	2.37	0.59
1:B:48:TYR:CG	1:B:62:MET:SD	2.95	0.59
1:F:99:ILE:HG22	1:F:100:HIS:N	2.17	0.59
1:A:62:MET:HB2	1:A:130:LEU:HB2	1.83	0.59
1:E:52:LYS:HA	1:E:58:TRP:HE3	1.67	0.59
1:A:46:PRO:HD2	1:A:110:ARG:HH21	1.68	0.58
1:B:117:ASP:OD2	1:B:117:ASP:OD1	2.20	0.58
1:E:114:LEU:HD13	1:E:118:VAL:HG21	1.86	0.58
1:F:64:LEU:HD12	1:F:130:LEU:HD11	1.85	0.58
1:F:55:ASN:O	1:F:137:ILE:CG1	2.52	0.58
1:A:51:VAL:HG13	1:B:98:TYR:CE1	2.39	0.57
1:F:52:LYS:HE2	1:F:58:TRP:CZ2	2.39	0.57
1:A:48:TYR:CE1	1:A:62:MET:HE1	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:56:VAL:HA	1:B:137:ILE:CG1	2.30	0.57
1:B:137:ILE:HG22	1:B:138:ILE:N	2.20	0.57
1:F:138:ILE:N	1:F:139:PRO:HD3	2.20	0.57
1:B:76:THR:HG22	1:B:81:LEU:HD23	1.86	0.57
1:F:120:ILE:HA	1:F:134:LEU:HD23	1.87	0.57
1:F:82:LEU:HD23	1:F:111:GLY:HA2	1.86	0.56
1:E:48:TYR:HD1	1:E:62:MET:HA	1.70	0.56
1:F:93:ASP:HB3	1:F:101:ARG:HH22	1.69	0.56
1:D:135:GLN:O	1:D:136:LYS:CG	2.53	0.56
1:D:147:TYR:O	1:D:148:GLU:HB2	2.05	0.56
1:E:98:TYR:CE1	1:F:51:VAL:HG22	2.41	0.56
1:C:52:LYS:HA	1:C:58:TRP:HE3	1.69	0.56
1:D:114:LEU:HD13	1:D:118:VAL:HB	1.88	0.55
1:F:135:GLN:O	1:F:136:LYS:CG	2.55	0.55
1:E:52:LYS:CA	1:E:58:TRP:CZ3	2.88	0.55
1:F:137:ILE:HG23	1:F:139:PRO:CD	2.26	0.55
1:B:76:THR:HG22	1:B:81:LEU:CD2	2.37	0.54
1:C:125:PHE:CD1	1:C:130:LEU:HD22	2.43	0.54
1:B:48:TYR:CD1	1:B:62:MET:SD	3.01	0.54
1:D:120:ILE:HA	1:D:134:LEU:HD23	1.90	0.54
1:C:52:LYS:HE2	1:C:58:TRP:CE3	2.43	0.54
1:C:64:LEU:HD12	1:C:130:LEU:HD11	1.89	0.54
1:C:98:TYR:CD1	1:D:51:VAL:HG21	2.42	0.53
1:A:52:LYS:CB	1:A:58:TRP:CE3	2.91	0.53
1:A:46:PRO:HB2	1:A:48:TYR:HE2	1.73	0.53
1:F:56:VAL:HA	1:F:137:ILE:HG13	1.91	0.53
1:A:76:THR:HG22	1:A:81:LEU:CD2	2.38	0.53
1:B:62:MET:HB2	1:B:130:LEU:HB2	1.92	0.52
1:A:52:LYS:CE	1:A:58:TRP:CZ3	2.92	0.52
1:C:52:LYS:CG	1:C:58:TRP:CE3	2.90	0.52
1:A:52:LYS:CG	1:A:58:TRP:CE3	2.94	0.51
1:C:148:GLU:HB2	1:F:123:VAL:O	2.10	0.51
1:C:48:TYR:CE2	1:C:110:ARG:NH2	2.76	0.50
1:C:52:LYS:HE2	1:C:58:TRP:CZ3	2.46	0.50
1:C:52:LYS:CA	1:C:58:TRP:CZ3	2.95	0.50
1:D:48:TYR:CD1	1:D:62:MET:SD	3.04	0.50
1:F:48:TYR:OH	1:F:110:ARG:HD2	2.11	0.50
1:A:52:LYS:HG2	1:A:58:TRP:CE3	2.47	0.49
1:A:62:MET:O	1:A:129:LEU:HA	2.12	0.49
1:E:46:PRO:HB2	1:E:48:TYR:CZ	2.47	0.49
1:F:62:MET:HB2	1:F:130:LEU:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:52:LYS:CE	1:C:58:TRP:CZ3	2.95	0.49
1:B:48:TYR:CZ	1:B:110:ARG:HD2	2.47	0.49
1:D:125:PHE:CE1	1:D:130:LEU:HD21	2.48	0.49
1:F:62:MET:O	1:F:129:LEU:HA	2.12	0.49
1:E:90:GLN:HE22	1:E:106:ARG:HG2	1.78	0.48
1:B:56:VAL:HG22	1:B:137:ILE:HD12	1.94	0.48
1:E:52:LYS:CG	1:E:58:TRP:CE3	2.96	0.48
1:D:48:TYR:CD2	1:D:62:MET:SD	3.07	0.48
1:A:103:VAL:HG22	1:B:47:PRO:HB2	1.96	0.48
1:B:46:PRO:CD	1:B:110:ARG:HH22	2.27	0.48
1:A:46:PRO:HD2	1:A:110:ARG:NH2	2.28	0.47
1:D:56:VAL:HG12	1:D:136:LYS:N	2.29	0.47
1:D:48:TYR:HA	1:D:62:MET:SD	2.54	0.47
1:F:53:GLU:HB2	1:F:57:LYS:HB2	1.97	0.47
1:C:47:PRO:HB2	1:D:103:VAL:HG22	1.97	0.47
1:B:48:TYR:CE2	1:B:110:ARG:CZ	2.98	0.47
1:A:66:GLY:CA	1:B:129:LEU:HD11	2.44	0.46
1:C:136:LYS:O	1:C:137:ILE:HB	2.15	0.46
1:F:76:THR:HG22	1:F:81:LEU:CD2	2.45	0.46
1:C:56:VAL:HG22	1:C:137:ILE:O	2.16	0.46
1:A:114:LEU:HD13	1:A:118:VAL:HG21	1.98	0.46
1:B:46:PRO:HD2	1:B:110:ARG:HH22	1.81	0.46
1:C:48:TYR:O	1:D:102:GLY:HA3	2.16	0.46
1:C:52:LYS:CD	1:C:58:TRP:HZ3	2.19	0.46
1:E:76:THR:HG22	1:E:81:LEU:CD2	2.47	0.45
1:B:56:VAL:HG22	1:B:137:ILE:CD1	2.46	0.45
1:E:90:GLN:HE22	1:E:106:ARG:CG	2.30	0.45
1:D:68:SER:HB2	1:D:69:PRO:CD	2.46	0.45
1:C:98:TYR:CG	1:D:51:VAL:HG11	2.52	0.44
1:F:56:VAL:O	1:F:135:GLN:HA	2.17	0.44
1:F:56:VAL:HB	1:F:57:LYS:HG3	1.99	0.44
1:A:97:GLU:HB3	1:B:52:LYS:HB2	1.99	0.44
1:E:52:LYS:HA	1:E:58:TRP:CZ3	2.47	0.44
1:A:48:TYR:CE1	1:A:110:ARG:CD	3.00	0.44
1:A:52:LYS:HE2	1:A:58:TRP:CZ3	2.51	0.44
1:B:48:TYR:CD2	1:B:62:MET:SD	3.11	0.44
1:B:48:TYR:HA	1:B:62:MET:SD	2.58	0.44
1:A:99:ILE:CG2	1:A:100:HIS:N	2.81	0.44
1:B:115:SER:O	1:B:116:ASP:O	2.36	0.44
1:A:63:ALA:HA	1:A:129:LEU:HD23	1.99	0.44
1:E:56:VAL:O	1:E:136:LYS:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:LYS:HA	1:A:58:TRP:HE3	1.81	0.43
1:E:130:LEU:HD23	1:E:130:LEU:N	2.34	0.43
1:E:103:VAL:HG11	1:F:47:PRO:CB	2.48	0.43
1:A:48:TYR:CZ	1:A:110:ARG:NE	2.86	0.43
1:A:46:PRO:CD	1:A:110:ARG:HH21	2.30	0.43
1:C:71:ALA:CB	1:C:88:PRO:HD3	2.49	0.43
1:C:139:PRO:CD	1:C:142:GLN:HE21	2.31	0.43
1:D:53:GLU:CB	1:D:57:LYS:CB	2.91	0.43
1:C:48:TYR:CD1	1:C:62:MET:SD	3.12	0.43
1:D:145:LYS:O	1:D:146:VAL:HG23	2.19	0.43
1:C:46:PRO:HD2	1:C:110:ARG:NH2	2.34	0.43
1:D:53:GLU:HG3	1:D:57:LYS:O	2.18	0.43
1:D:147:TYR:O	1:D:148:GLU:CB	2.66	0.43
1:D:76:THR:HG22	1:D:81:LEU:CD2	2.49	0.43
1:D:116:ASP:HA	1:D:117:ASP:HA	1.70	0.43
1:B:48:TYR:CE2	1:B:62:MET:CE	3.02	0.42
1:C:48:TYR:HD1	1:C:62:MET:HA	1.84	0.42
1:C:136:LYS:O	1:C:137:ILE:CB	2.66	0.42
1:D:68:SER:CB	1:D:69:PRO:CD	2.97	0.42
1:A:48:TYR:CE2	1:A:62:MET:HE1	2.54	0.42
1:A:52:LYS:CA	1:A:58:TRP:CE3	3.02	0.42
1:B:46:PRO:N	1:B:110:ARG:HH22	2.17	0.42
1:E:48:TYR:CD1	1:E:62:MET:HA	2.53	0.42
1:D:48:TYR:CE2	1:D:62:MET:CE	3.03	0.42
1:D:64:LEU:HD12	1:D:130:LEU:CD1	2.49	0.42
1:F:116:ASP:HA	1:F:117:ASP:HA	1.68	0.42
1:A:52:LYS:HE2	1:A:58:TRP:CE3	2.54	0.42
1:A:64:LEU:HD12	1:A:130:LEU:HD11	2.01	0.42
1:C:147:TYR:OH	1:F:73:GLU:HA	2.20	0.42
1:E:46:PRO:HB2	1:E:48:TYR:CE2	2.55	0.42
1:F:48:TYR:HA	1:F:62:MET:SD	2.60	0.42
1:B:77:GLU:O	1:B:80:VAL:HB	2.19	0.41
1:C:52:LYS:HA	1:C:58:TRP:CZ3	2.55	0.41
1:E:52:LYS:HG2	1:E:58:TRP:CE3	2.56	0.41
1:D:64:LEU:HD12	1:D:130:LEU:HD11	2.02	0.41
1:B:45:TYR:HB3	1:B:110:ARG:HH21	1.76	0.41
1:B:82:LEU:HA	1:B:110:ARG:O	2.20	0.41
1:E:56:VAL:HA	1:E:137:ILE:HB	2.03	0.41
1:A:56:VAL:O	1:A:136:LYS:N	2.51	0.41
1:A:145:LYS:O	1:A:146:VAL:HG23	2.20	0.41
1:B:57:LYS:HA	1:B:134:LEU:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:64:LEU:HD12	1:C:130:LEU:CD1	2.51	0.41
1:F:79:ASN:ND2	1:F:117:ASP:OD1	2.54	0.41
1:A:48:TYR:CZ	1:A:62:MET:CE	2.97	0.41
1:A:99:ILE:HG22	1:A:100:HIS:N	2.36	0.41
1:A:99:ILE:O	1:A:100:HIS:C	2.59	0.40
1:D:61:GLU:HA	1:D:130:LEU:O	2.20	0.40
1:E:80:VAL:HG22	1:E:113:ASN:HA	2.03	0.40
1:F:82:LEU:HD23	1:F:111:GLY:CA	2.51	0.40
1:C:52:LYS:CB	1:C:58:TRP:CE3	3.03	0.40
1:C:48:TYR:CD1	1:C:62:MET:HA	2.56	0.40

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	104/175 (59%)	90 (86%)	12 (12%)	2 (2%)	8	38
1	B	88/175 (50%)	75 (85%)	9 (10%)	4 (4%)	2	22
1	C	96/175 (55%)	81 (84%)	8 (8%)	7 (7%)	1	14
1	D	93/175 (53%)	78 (84%)	10 (11%)	5 (5%)	2	19
1	E	98/175 (56%)	86 (88%)	10 (10%)	2 (2%)	7	38
1	F	95/175 (54%)	84 (88%)	8 (8%)	3 (3%)	4	26
All	All	574/1050 (55%)	494 (86%)	57 (10%)	23 (4%)	3	23

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	100	HIS
1	A	137	ILE

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Mol	Chain	Res	Type
1	B	116	ASP
1	C	137	ILE
1	C	146	VAL
1	D	148	GLU
1	E	137	ILE
1	E	146	VAL
1	F	137	ILE
1	B	137	ILE
1	C	94	PRO
1	D	137	ILE
1	B	91	HIS
1	C	53	GLU
1	C	88	PRO
1	F	99	ILE
1	B	138	ILE
1	C	47	PRO
1	D	68	SER
1	D	138	ILE
1	D	47	PRO
1	C	99	ILE
1	F	47	PRO

### 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	92/155 (59%)	89 (97%)	3 (3%)	38	61
1	B	75/155 (48%)	73 (97%)	2 (3%)	44	65
1	C	86/155 (56%)	86 (100%)	0	100	100
1	D	83/155 (54%)	82 (99%)	1 (1%)	71	83
1	E	91/155 (59%)	87 (96%)	4 (4%)	28	53
1	F	78/155 (50%)	76 (97%)	2 (3%)	46	66
All	All	505/930 (54%)	493 (98%)	12 (2%)	49	69

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	ASN
1	A	75	SER
1	A	93	ASP
1	B	118	VAL
1	B	124	SER
1	D	56	VAL
1	E	73	GLU
1	E	98	TYR
1	E	116	ASP
1	E	127	ASP
1	F	124	SER
1	F	137	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	55	ASN
1	C	142	GLN
1	D	135	GLN
1	E	79	ASN
1	E	90	GLN
1	F	100	HIS

### 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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	106/175 (60%)	0.57	10 (9%) 8 11	312, 478, 682, 825	0
1	B	92/175 (52%)	0.73	13 (14%) 2 6	304, 484, 622, 775	0
1	C	102/175 (58%)	0.85	19 (18%) 1 4	341, 522, 679, 797	0
1	D	99/175 (56%)	0.58	12 (12%) 4 8	310, 485, 661, 734	0
1	E	102/175 (58%)	0.48	11 (10%) 5 9	327, 480, 626, 741	0
1	F	97/175 (55%)	0.97	25 (25%) 0 2	30, 483, 662, 738	0
All	All	598/1050 (56%)	0.69	90 (15%) 2 5	30, 491, 674, 825	0

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	115	SER	4.7
1	C	91	HIS	4.6
1	C	81	LEU	4.5
1	F	63	ALA	4.4
1	A	68	SER	4.4
1	B	64	LEU	4.3
1	F	91	HIS	4.3
1	C	111	GLY	4.1
1	A	49	ASN	4.0
1	C	118	VAL	4.0
1	C	63	ALA	4.0
1	F	129	LEU	3.9
1	F	117	ASP	3.9
1	B	65	ALA	3.8
1	A	51	VAL	3.8
1	D	65	ALA	3.7
1	A	50	LEU	3.7
1	D	87	ALA	3.7
1	A	90	GLN	3.7

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Mol	Chain	Res	Type	RSRZ
1	F	118	VAL	3.7
1	B	102	GLY	3.7
1	F	130	LEU	3.6
1	C	64	LEU	3.6
1	B	109	ALA	3.5
1	D	142	GLN	3.5
1	A	60	ILE	3.4
1	F	126	GLN	3.4
1	C	117	ASP	3.4
1	F	125	PHE	3.4
1	C	93	ASP	3.4
1	C	116	ASP	3.4
1	F	95	ASP	3.2
1	F	124	SER	3.2
1	A	61	GLU	3.2
1	C	90	GLN	3.1
1	F	64	LEU	3.1
1	F	60	ILE	3.0
1	B	101	ARG	3.0
1	B	110	ARG	3.0
1	B	83	ILE	3.0
1	F	116	ASP	3.0
1	C	62	MET	2.9
1	F	46	PRO	2.9
1	F	90	GLN	2.9
1	F	62	MET	2.9
1	C	92	THR	2.8
1	D	109	ALA	2.8
1	A	70	ASP	2.8
1	E	66	GLY	2.8
1	C	65	ALA	2.8
1	D	67	TRP	2.8
1	F	114	LEU	2.7
1	E	91	HIS	2.7
1	E	81	LEU	2.7
1	D	143	LYS	2.6
1	E	125	PHE	2.6
1	A	67	TRP	2.6
1	F	131	VAL	2.5
1	E	143	LYS	2.5
1	C	83	ILE	2.5
1	F	48	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	50	LEU	2.5
1	D	64	LEU	2.4
1	D	110	ARG	2.4
1	D	66	GLY	2.4
1	E	83	ILE	2.4
1	B	66	GLY	2.4
1	E	65	ALA	2.3
1	C	89	HIS	2.3
1	B	81	LEU	2.2
1	E	130	LEU	2.2
1	D	63	ALA	2.2
1	F	49	ASN	2.2
1	F	50	LEU	2.2
1	F	61	GLU	2.2
1	B	85	SER	2.2
1	C	115	SER	2.2
1	B	114	LEU	2.2
1	E	62	MET	2.1
1	B	82	LEU	2.1
1	C	80	VAL	2.1
1	E	146	VAL	2.1
1	C	75	SER	2.1
1	B	74	VAL	2.1
1	F	88	PRO	2.1
1	C	110	ARG	2.0
1	A	63	ALA	2.0
1	D	72	VAL	2.0
1	F	93	ASP	2.0
1	E	123	VAL	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 6.4 Ligands ⓘ

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.