



# Full wwPDB X-ray Structure Validation Report ⓘ

May 10, 2026 – 12:57 AM JST

PDB ID : 22HR / pdb\_000022hr  
Title : Crystal structure of Apo FtsZ from *Acinetobacter baumannii*  
Authors : Yadav, A.K.; Singh, A.; Madhuri, M.; Saini, C.; Kumar, M.; Kaur, P.; Singh, T.P.; Ethayathulla, A.S.  
Deposited on : 2026-01-11  
Resolution : 3.00 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

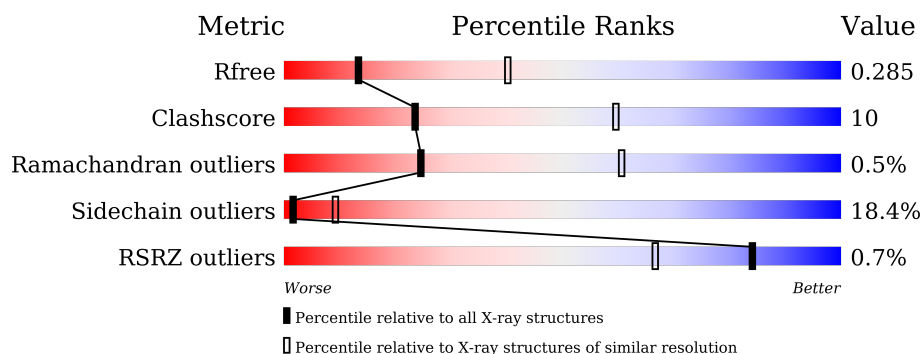
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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))
$R_{free}$	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	307	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>%</span> <span>67%</span> <span>24%</span> <span>6% ..</span> </div> </div>
1	B	307	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>%</span> <span>63%</span> <span>26%</span> <span>8% ..</span> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4496 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 Cell division protein FtsZ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	300	Total	C	N	O	S	0	1	0
			2236	1390	392	442	12			
1	B	299	Total	C	N	O	S	0	0	0
			2230	1388	394	437	11			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	324	LEU	-	expression tag	UNP V5V8B6
B	324	LEU	-	expression tag	UNP V5V8B6

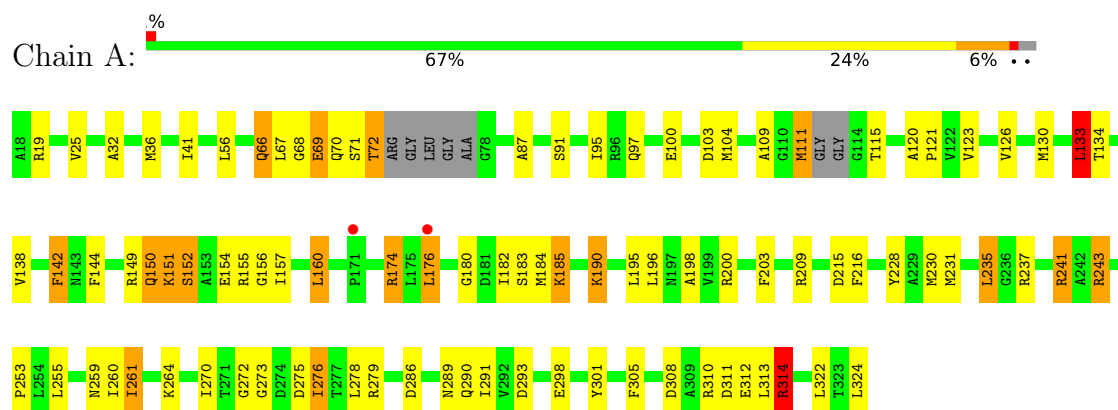
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	13	Total	O	0	0
			13	13		
2	B	17	Total	O	0	0
			17	17		

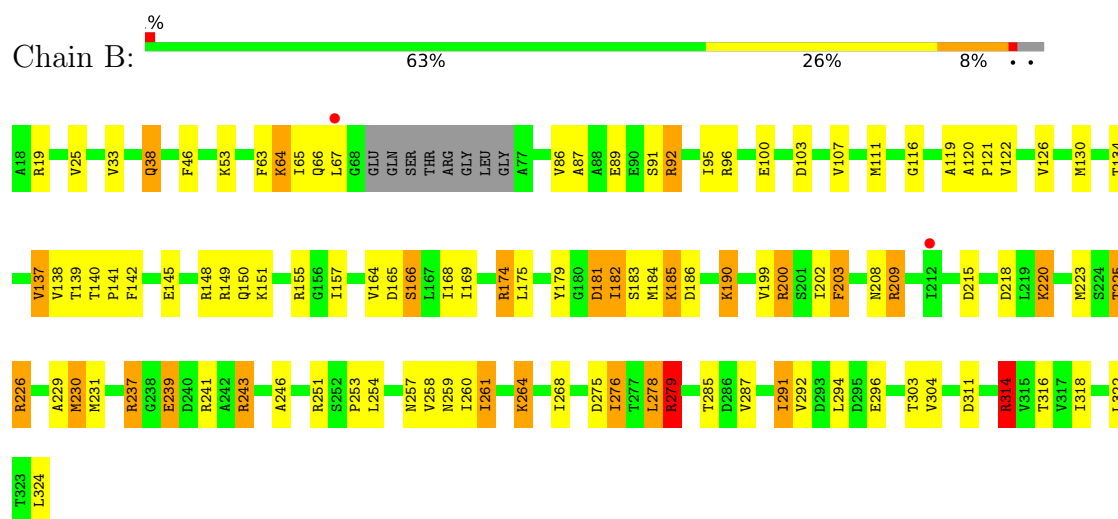
### 3 Residue-property plots

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: Cell division protein FtsZ



#### • Molecule 1: Cell division protein FtsZ



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	43.94Å 44.83Å 85.39Å 76.41° 81.31° 64.45°	Depositor
Resolution (Å)	39.61 – 3.00 39.61 – 3.00	Depositor EDS
% Data completeness (in resolution range)	92.7 (39.61-3.00) 92.7 (39.61-3.00)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.75 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0430	Depositor
R, $R_{free}$	0.245 , 0.285 0.247 , 0.285	Depositor DCC
$R_{free}$ test set	1011 reflections (8.86%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	73.5	Xtriage
Anisotropy	0.407	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 58.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4496	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.93% 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

### 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	0.49	0/2261	0.97	2/3057 (0.1%)
1	B	0.48	0/2254	0.95	2/3047 (0.1%)
All	All	0.49	0/4515	0.96	4/6104 (0.1%)

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	A	0	11
1	B	0	15
All	All	0	26

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	203	PHE	CA-CB-CG	7.66	121.46	113.80
1	A	203	PHE	CA-CB-CG	5.91	119.71	113.80
1	A	134	THR	CA-CB-OG1	-5.16	101.86	109.60
1	B	103	ASP	CA-CB-CG	5.09	117.69	112.60

There are no chirality outliers.

All (26) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	149	ARG	Sidechain
1	A	155	ARG	Sidechain
1	A	174	ARG	Sidechain
1	A	19	ARG	Sidechain
1	A	200	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	209	ARG	Sidechain
1	A	237	ARG	Sidechain
1	A	243	ARG	Sidechain
1	A	279	ARG	Sidechain
1	A	310	ARG	Sidechain
1	A	314	ARG	Sidechain
1	B	148	ARG	Sidechain
1	B	149	ARG	Sidechain
1	B	155	ARG	Sidechain
1	B	174	ARG	Sidechain
1	B	19	ARG	Sidechain
1	B	200	ARG	Sidechain
1	B	209	ARG	Sidechain
1	B	226	ARG	Sidechain
1	B	237	ARG	Sidechain
1	B	241	ARG	Sidechain
1	B	243	ARG	Sidechain
1	B	251	ARG	Sidechain
1	B	279	ARG	Sidechain
1	B	314	ARG	Sidechain
1	B	92	ARG	Sidechain

## 5.2 Too-close contacts ⓘ

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	2236	0	2224	44	2
1	B	2230	0	2230	47	0
2	A	13	0	0	0	0
2	B	17	0	0	0	0
All	All	4496	0	4454	91	2

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 10.

All (91) 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:174:ARG:HB3	1:A:253:PRO:HB2	1.61	0.81
1:B:278:LEU:HD12	1:B:278:LEU:O	1.84	0.78
1:B:231:MET:HE2	1:B:318:ILE:HG12	1.72	0.71
1:B:179:TYR:HB3	1:B:182:ILE:HG12	1.80	0.64
1:B:174:ARG:HB3	1:B:253:PRO:HB2	1.82	0.61
1:A:276:ILE:HD13	1:A:313:LEU:HD11	1.83	0.60
1:B:168:ILE:HD13	1:B:229:ALA:HB3	1.84	0.57
1:B:278:LEU:HD12	1:B:278:LEU:C	2.29	0.57
1:B:183:SER:H	1:B:186:ASP:HB2	1.70	0.56
1:B:257:ASN:O	1:B:259:ASN:N	2.38	0.56
1:A:104:MET:HB2	1:A:216:PHE:HZ	1.70	0.56
1:B:33:VAL:HG13	1:B:46:PHE:HB3	1.88	0.56
1:A:286:ASP:O	1:A:290:GLN:HG2	2.06	0.55
1:A:142:PHE:HB2	1:A:144:PHE:CD2	2.41	0.55
1:A:126:VAL:O	1:A:130:MET:HG3	2.06	0.55
1:B:126:VAL:O	1:B:130:MET:HG3	2.08	0.54
1:B:89:GLU:HA	1:B:92:ARG:HG3	1.89	0.54
1:B:259:ASN:HB2	1:B:261:ILE:HG13	1.90	0.53
1:A:121:PRO:HG3	1:A:160:LEU:HD12	1.89	0.53
1:A:259:ASN:HB3	1:A:322:LEU:HD22	1.89	0.53
1:A:322:LEU:HD13	1:A:324:LEU:HD21	1.91	0.53
1:A:104:MET:HB2	1:A:216:PHE:CZ	2.43	0.53
1:A:152:SER:HA	1:A:156:GLY:HA3	1.90	0.53
1:B:314:ARG:NH1	1:B:316:THR:OG1	2.42	0.52
1:A:120:ALA:HB3	1:A:121:PRO:HD3	1.90	0.52
1:B:141:PRO:HG2	1:B:150:GLN:HA	1.91	0.51
1:A:228:TYR:HB3	1:A:324:LEU:HD12	1.90	0.51
1:B:138:VAL:HG21	1:B:157:ILE:HG12	1.93	0.50
1:A:104:MET:HE3	1:A:133:LEU:HD13	1.92	0.50
1:B:116:GLY:HA2	1:B:119:ALA:HB3	1.93	0.50
1:A:312:GLU:HB3	1:A:314:ARG:HH12	1.77	0.49
1:A:235:LEU:HD11	1:A:314:ARG:HG2	1.94	0.49
1:A:111:MET:HE3	1:A:138:VAL:HG12	1.94	0.49
1:B:166:SER:HB3	1:B:223:MET:O	2.13	0.48
1:A:230:MET:HE2	1:A:324:LEU:HD13	1.95	0.47
1:B:120:ALA:N	1:B:121:PRO:HD2	2.30	0.47
1:B:142:PHE:HB2	1:B:145:GLU:HG3	1.96	0.47
1:A:151:LYS:O	1:A:156:GLY:N	2.48	0.47
1:A:190:LYS:HB3	1:A:190:LYS:HE3	1.41	0.47
1:B:174:ARG:O	1:B:175:LEU:C	2.58	0.47
1:A:231[A]:MET:HE3	1:A:231[A]:MET:HB3	1.62	0.46
1:B:181:ASP:O	1:B:182:ILE:C	2.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:291:ILE:H	1:B:291:ILE:HG13	1.55	0.46
1:A:32:ALA:O	1:A:36:MET:HG3	2.15	0.46
1:B:279:ARG:HB2	1:B:279:ARG:HH21	1.81	0.46
1:A:185:LYS:HB2	1:A:185:LYS:HE2	1.54	0.46
1:B:225:THR:O	1:B:226:ARG:C	2.59	0.46
1:B:208:ASN:HB2	1:B:304:VAL:HG13	1.98	0.46
1:A:184:MET:HE2	1:A:184:MET:HB3	1.78	0.45
1:B:183:SER:C	1:B:185:LYS:N	2.71	0.45
1:B:239:GLU:H	1:B:239:GLU:HG3	1.45	0.45
1:B:91:SER:O	1:B:92:ARG:C	2.60	0.45
1:B:151:LYS:HA	1:B:151:LYS:HD2	1.79	0.45
1:A:56:LEU:HD23	1:A:66:GLN:HG3	1.99	0.45
1:B:96:ARG:O	1:B:100:GLU:HG3	2.17	0.45
1:A:272:GLY:O	1:A:305:PHE:HA	2.18	0.44
1:B:137:VAL:HG21	1:B:199:VAL:HG22	1.99	0.44
1:B:183:SER:N	1:B:186:ASP:HB2	2.32	0.44
1:B:246:ALA:HB1	1:B:287:VAL:HG21	1.99	0.44
1:B:38:GLN:HE21	1:B:38:GLN:HB2	1.63	0.44
1:A:176:LEU:HG	1:A:182:ILE:HG21	2.00	0.43
1:A:180:GLY:C	1:A:182:ILE:H	2.26	0.43
1:B:264:LYS:HA	1:B:264:LYS:HD2	1.46	0.43
1:A:261:ILE:H	1:A:261:ILE:HG12	1.51	0.43
1:B:190:LYS:HD2	1:B:190:LYS:HA	1.69	0.43
1:A:150:GLN:O	1:A:154:GLU:N	2.52	0.43
1:B:230:MET:HG3	1:B:322:LEU:HD12	2.01	0.43
1:A:241:ARG:HH12	1:A:275:ASP:CG	2.26	0.43
1:A:198:ALA:HA	1:A:231[A]:MET:HE1	2.01	0.43
1:B:183:SER:O	1:B:184:MET:C	2.62	0.43
1:A:235:LEU:HD13	1:A:235:LEU:HA	1.82	0.42
1:A:235:LEU:HD12	1:A:312:GLU:HG2	2.01	0.42
1:B:63:PHE:C	1:B:64:LYS:HG2	2.45	0.42
1:B:202:ILE:HD11	1:B:231:MET:HE1	2.01	0.42
1:B:276:ILE:HD13	1:B:303:THR:HG23	2.02	0.42
1:A:67:LEU:HB3	1:A:87:ALA:HB1	2.01	0.42
1:A:68:GLY:O	1:A:69:GLU:C	2.63	0.42
1:B:65:ILE:HD12	1:B:95:ILE:HD13	2.01	0.42
1:A:109:ALA:HB3	1:A:111:MET:HE1	2.02	0.42
1:A:71:SER:O	1:A:72:THR:C	2.63	0.41
1:A:97:GLN:O	1:A:100:GLU:HG2	2.21	0.41
1:B:86:VAL:O	1:B:87:ALA:C	2.63	0.41
1:B:220:LYS:HB2	1:B:220:LYS:HE3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:GLY:HA2	1:A:305:PHE:CD1	2.56	0.41
1:B:122:VAL:O	1:B:126:VAL:HG23	2.21	0.41
1:B:179:TYR:HB3	1:B:182:ILE:CG1	2.50	0.41
1:A:314:ARG:NH2	1:A:314:ARG:HG3	2.34	0.41
1:B:200:ARG:HA	1:B:203:PHE:CZ	2.56	0.40
1:A:95:ILE:HD13	1:A:123:VAL:HG22	2.03	0.40
1:A:111:MET:SD	1:A:160:LEU:HD13	2.62	0.40
1:A:230:MET:HG2	1:A:324:LEU:HD11	2.03	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:PHE:C	1:A:301:TYR:OH[1_455]	2.01	0.19
1:A:144:PHE:O	1:A:301:TYR:OH[1_455]	2.14	0.06

## 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	295/307 (96%)	269 (91%)	24 (8%)	2 (1%)	18	53
1	B	295/307 (96%)	271 (92%)	23 (8%)	1 (0%)	36	70
All	All	590/614 (96%)	540 (92%)	47 (8%)	3 (0%)	24	60

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	142	PHE
1	A	133	LEU
1	B	258	VAL

### 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	235/240 (98%)	195 (83%)	40 (17%)	2	11
1	B	233/240 (97%)	187 (80%)	46 (20%)	1	8
All	All	468/480 (98%)	382 (82%)	86 (18%)	1	9

All (86) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	VAL
1	A	41	ILE
1	A	66	GLN
1	A	69	GLU
1	A	70	GLN
1	A	72	THR
1	A	91	SER
1	A	103	ASP
1	A	111	MET
1	A	115	THR
1	A	133	LEU
1	A	150	GLN
1	A	151	LYS
1	A	152	SER
1	A	157	ILE
1	A	160	LEU
1	A	176	LEU
1	A	183	SER
1	A	185	LYS
1	A	190	LYS
1	A	195	LEU
1	A	196	LEU
1	A	215	ASP
1	A	235	LEU
1	A	241	ARG
1	A	243	ARG
1	A	255	LEU

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Mol	Chain	Res	Type
1	A	260	ILE
1	A	261	ILE
1	A	264	LYS
1	A	270	ILE
1	A	276	ILE
1	A	278	LEU
1	A	289	ASN
1	A	291	ILE
1	A	293	ASP
1	A	298	GLU
1	A	308	ASP
1	A	311	ASP
1	A	314	ARG
1	B	25	VAL
1	B	38	GLN
1	B	53	LYS
1	B	64	LYS
1	B	66	GLN
1	B	67	LEU
1	B	107	VAL
1	B	111	MET
1	B	134	THR
1	B	137	VAL
1	B	139	THR
1	B	140	THR
1	B	164	VAL
1	B	165	ASP
1	B	166	SER
1	B	169	ILE
1	B	181	ASP
1	B	182	ILE
1	B	185	LYS
1	B	190	LYS
1	B	209	ARG
1	B	215	ASP
1	B	218	ASP
1	B	220	LYS
1	B	225	THR
1	B	230	MET
1	B	237	ARG
1	B	239	GLU
1	B	243	ARG

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Mol	Chain	Res	Type
1	B	254	LEU
1	B	260	ILE
1	B	261	ILE
1	B	264	LYS
1	B	268	ILE
1	B	275	ASP
1	B	276	ILE
1	B	278	LEU
1	B	279	ARG
1	B	285	THR
1	B	291	ILE
1	B	292	VAL
1	B	294	LEU
1	B	296	GLU
1	B	311	ASP
1	B	314	ARG
1	B	324	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	143	ASN
1	A	150	GLN
1	A	197	ASN
1	A	259	ASN
1	B	38	GLN
1	B	66	GLN
1	B	150	GLN
1	B	262	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	300/307 (97%)	0.08	2 (0%)	84 66	37, 68, 116, 144	1 (0%)
1	B	299/307 (97%)	0.22	2 (0%)	84 66	41, 75, 114, 132	0
All	All	599/614 (97%)	0.15	4 (0%)	84 66	37, 73, 114, 144	1 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	176	LEU	2.5
1	B	212	ILE	2.1
1	A	171	PRO	2.1
1	B	67	LEU	2.0

### 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 oligosaccharides 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.