



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 8, 2025 – 08:04 PM EST

PDB ID : 9CO2  
Title : Crystal structure of BamA in complex with the PTB2 open-state inhibitor  
(anisotropic data set)  
Authors : Sun, D.; Payandeh, J.  
Deposited on : 2024-07-16  
Resolution : 2.75 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

<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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

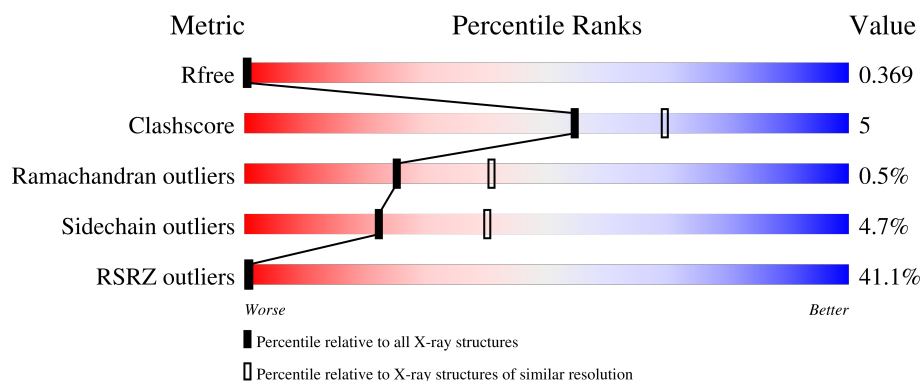
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.75 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))
$R_{free}$	164625	1606 (2.78-2.74)
Clashscore	180529	1689 (2.78-2.74)
Ramachandran outliers	177936	1665 (2.78-2.74)
Sidechain outliers	177891	1665 (2.78-2.74)
RSRZ outliers	164620	1606 (2.78-2.74)

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	382	<div> <div>37%</div> <div>87%</div> <div>12%</div> <div>..</div> </div>
1	B	382	<div> <div>31%</div> <div>87%</div> <div>12%</div> <div>.</div> </div>
1	C	382	<div> <div>50%</div> <div>88%</div> <div>10%</div> <div>.</div> </div>
1	D	382	<div> <div>44%</div> <div>87%</div> <div>12%</div> <div>..</div> </div>
2	E	17	<div> <div>29%</div> <div>76%</div> <div>18%</div> <div>6%</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	17	<div><div></div><div>65%</div><div>82%</div><div>18%</div></div>
2	G	17	<div><div></div><div>47%</div><div>71%</div><div>24%</div><div>6%</div></div>
2	I	17	<div><div></div><div>65%</div><div>76%</div><div>18%</div><div>6%</div></div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12648 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 Outer membrane protein assembly factor BamA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	382	Total	C	N	O	S	0	0	0
			3018	1918	484	606	10			
1	B	382	Total	C	N	O	S	0	0	0
			3018	1918	484	606	10			
1	C	382	Total	C	N	O	S	0	0	0
			3018	1918	484	606	10			
1	D	382	Total	C	N	O	S	0	0	0
			3018	1918	484	606	10			

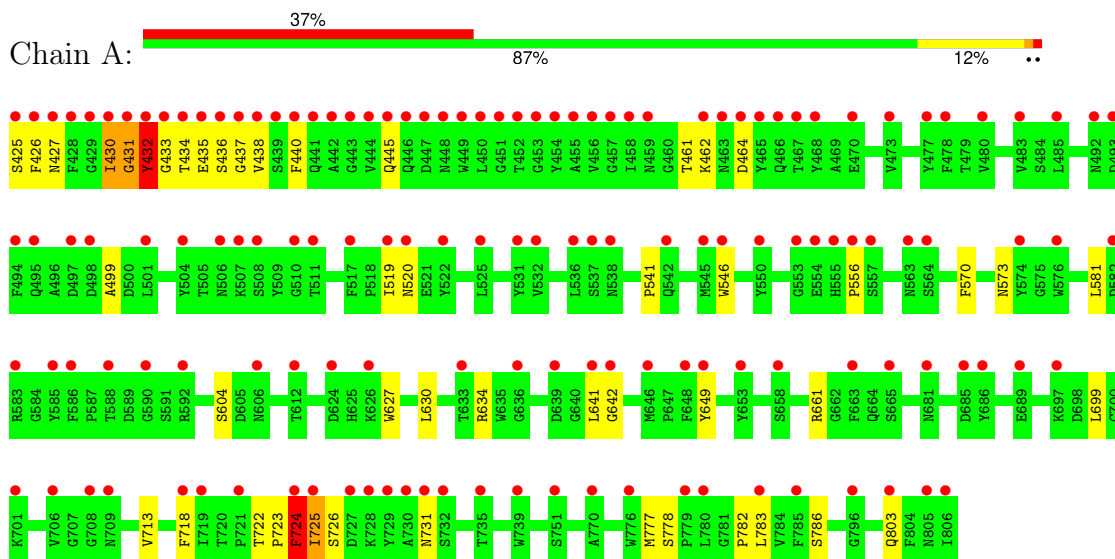
- Molecule 2 is a protein called PTB2 circular peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	17	Total	C	N	O	S	0	0	1
			144	96	29	18	1			
2	F	17	Total	C	N	O	S	0	0	1
			144	96	29	18	1			
2	G	17	Total	C	N	O	S	0	0	1
			144	96	29	18	1			
2	I	17	Total	C	N	O	S	0	0	1
			144	96	29	18	1			

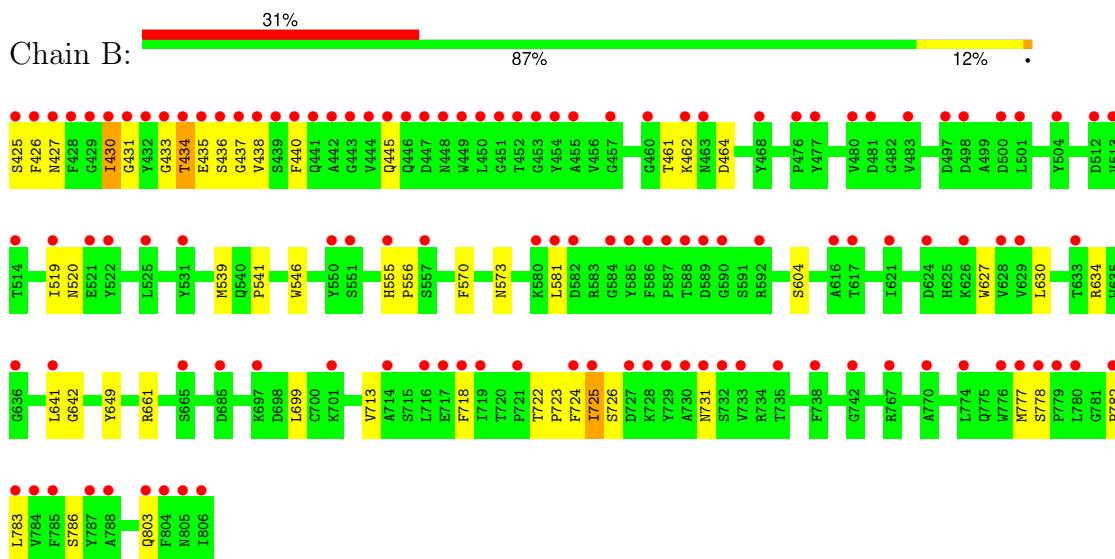
### 3 Residue-property plots

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.

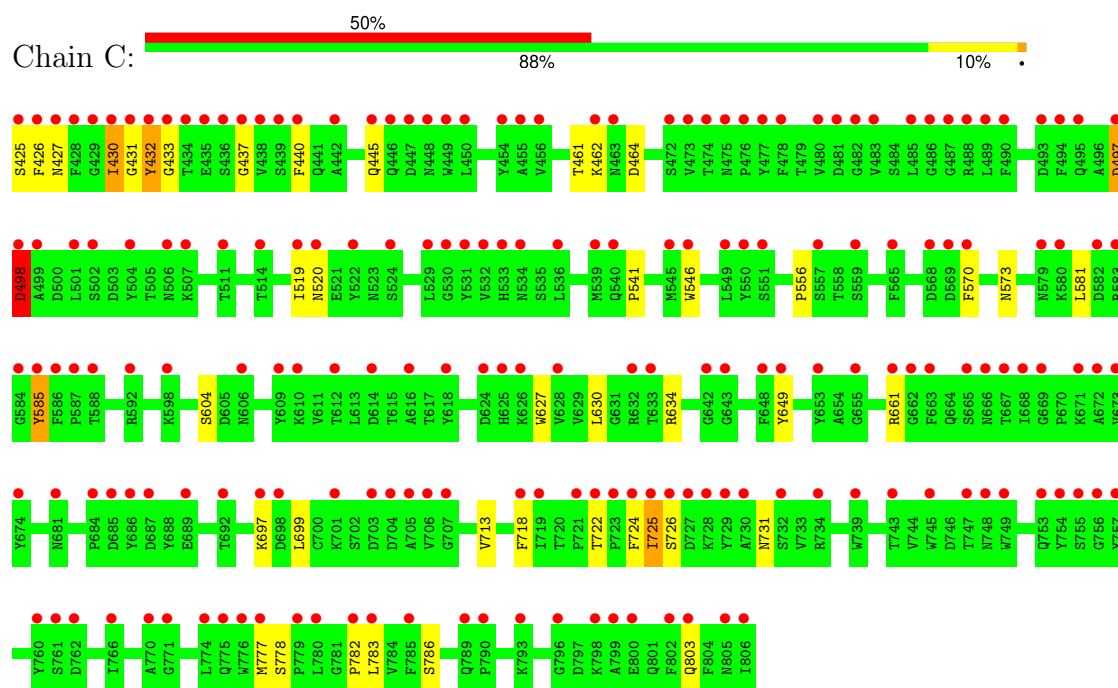
- Molecule 1: Outer membrane protein assembly factor BamA



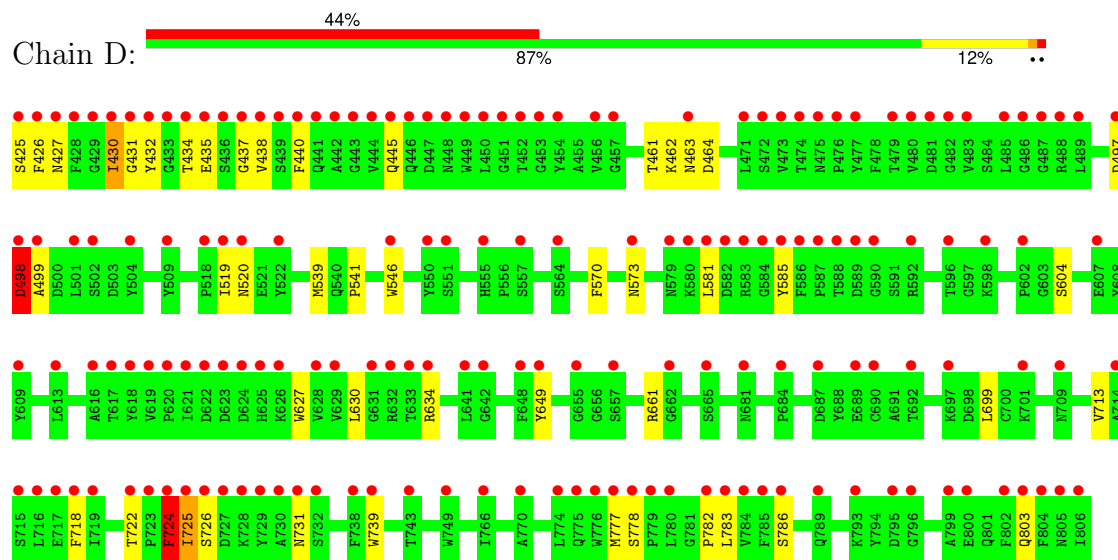
- Molecule 1: Outer membrane protein assembly factor BamA



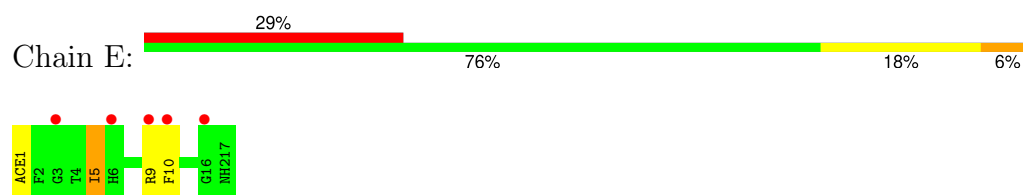
- Molecule 1: Outer membrane protein assembly factor BamA



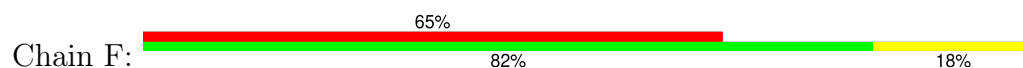
• Molecule 1: Outer membrane protein assembly factor BamA

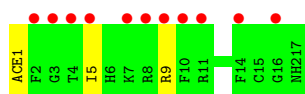


• Molecule 2: PTB2 circular peptide

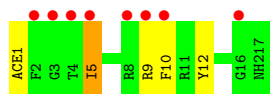


• Molecule 2: PTB2 circular peptide

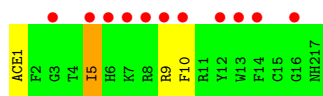
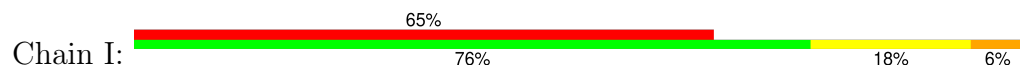




- Molecule 2: PTB2 circular peptide



- Molecule 2: PTB2 circular peptide



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	98.79Å 167.27Å 104.82Å 90.00° 110.99° 90.00°	Depositor
Resolution (Å)	29.59 – 2.75 29.59 – 2.75	Depositor EDS
% Data completeness (in resolution range)	57.3 (29.59-2.75) 57.4 (29.59-2.75)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.18 (at 2.76Å)	Xtriage
Refinement program	PHENIX (1.20rc3-4406_final: ???)	Depositor
R, $R_{free}$	0.336 , 0.368 0.336 , 0.369	Depositor DCC
$R_{free}$ test set	4112 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	52.9	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 41.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.58$ , $\langle L^2 \rangle = 0.43$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.86	EDS
Total number of atoms	12648	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 60.43 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.5235e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NH2, ACE

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	0.31	0/3111	0.60	1/4238 (0.0%)
1	B	0.33	0/3111	0.59	0/4238
1	C	0.38	1/3111 (0.0%)	0.63	3/4238 (0.1%)
1	D	0.40	3/3111 (0.1%)	0.61	1/4238 (0.0%)
2	E	0.43	0/147	0.80	1/195 (0.5%)
2	F	0.43	0/147	0.80	1/195 (0.5%)
2	G	0.43	0/147	0.80	1/195 (0.5%)
2	I	0.43	0/147	0.80	1/195 (0.5%)
All	All	0.36	4/13032 (0.0%)	0.62	9/17732 (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	1
1	B	0	2
1	C	0	1
1	D	0	2
All	All	0	6

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	724	PHE	CD2-CE2	-9.57	1.20	1.39
1	C	432	TYR	CB-CG	7.67	1.63	1.51
1	D	498	ASP	CB-CG	5.68	1.63	1.51
1	D	724	PHE	CB-CG	-5.67	1.41	1.51

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1	ACE	O-C-N	7.60	134.86	122.70
2	I	1	ACE	O-C-N	7.58	134.82	122.70
2	G	1	ACE	O-C-N	7.57	134.81	122.70
2	F	1	ACE	O-C-N	7.54	134.76	122.70
1	A	432	TYR	C-N-CA	7.29	137.61	122.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	431	GLY	Mainchain
1	B	433	GLY	Peptide
1	B	434	THR	Peptide
1	C	497	ASP	Peptide
1	D	434	THR	Peptide

## 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	3018	0	2740	33	0
1	B	3018	0	2740	29	0
1	C	3018	0	2740	25	0
1	D	3018	0	2740	27	0
2	E	144	0	136	1	0
2	F	144	0	136	0	0
2	G	144	0	136	2	0
2	I	144	0	136	1	0
All	All	12648	0	11504	113	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 5.

The worst 5 of 113 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:434:THR:O	1:A:436:SER:N	1.95	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:430:ILE:HG12	1:A:431:GLY:H	1.41	0.86
1:B:430:ILE:HG12	1:B:431:GLY:H	1.41	0.86
1:C:430:ILE:HG12	1:C:431:GLY:H	1.41	0.85
1:D:430:ILE:HG12	1:D:431:GLY:H	1.41	0.84

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	380/382 (100%)	358 (94%)	18 (5%)	4 (1%)	12	21
1	B	380/382 (100%)	358 (94%)	21 (6%)	1 (0%)	37	55
1	C	380/382 (100%)	362 (95%)	16 (4%)	2 (0%)	25	41
1	D	380/382 (100%)	361 (95%)	18 (5%)	1 (0%)	37	55
2	E	15/17 (88%)	15 (100%)	0	0	100	100
2	F	15/17 (88%)	15 (100%)	0	0	100	100
2	G	15/17 (88%)	15 (100%)	0	0	100	100
2	I	15/17 (88%)	15 (100%)	0	0	100	100
All	All	1580/1596 (99%)	1499 (95%)	73 (5%)	8 (0%)	25	41

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	432	TYR
1	A	435	GLU
1	B	435	GLU
1	C	498	ASP
1	A	499	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	320/320 (100%)	308 (96%)	12 (4%)	28	49
1	B	320/320 (100%)	309 (97%)	11 (3%)	32	54
1	C	320/320 (100%)	305 (95%)	15 (5%)	22	40
1	D	320/320 (100%)	304 (95%)	16 (5%)	20	37
2	E	13/13 (100%)	11 (85%)	2 (15%)	2	3
2	F	13/13 (100%)	11 (85%)	2 (15%)	2	3
2	G	13/13 (100%)	11 (85%)	2 (15%)	2	3
2	I	13/13 (100%)	11 (85%)	2 (15%)	2	3
All	All	1332/1332 (100%)	1270 (95%)	62 (5%)	22	40

5 of 62 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	581	LEU
2	E	9	ARG
1	C	725	ILE
2	E	5	ILE
2	G	9	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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	382/382 (100%)	1.88	141 (36%) <b>1</b> <b>1</b>	17, 51, 109, 172	0
1	B	382/382 (100%)	1.71	119 (31%) <b>1</b> <b>1</b>	16, 51, 107, 160	0
1	C	382/382 (100%)	2.45	190 (49%) <b>0</b> <b>0</b>	25, 53, 124, 185	0
1	D	382/382 (100%)	2.30	167 (43%) <b>1</b> <b>0</b>	27, 56, 118, 184	0
2	E	15/17 (88%)	2.07	5 (33%) <b>1</b> <b>1</b>	29, 50, 79, 79	7 (46%)
2	F	15/17 (88%)	3.11	11 (73%) <b>0</b> <b>0</b>	38, 66, 97, 97	0
2	G	15/17 (88%)	2.39	8 (53%) <b>0</b> <b>0</b>	39, 70, 106, 111	0
2	I	15/17 (88%)	3.25	11 (73%) <b>0</b> <b>0</b>	22, 35, 74, 79	7 (46%)
All	All	1588/1596 (99%)	2.11	652 (41%) <b>1</b> <b>0</b>	16, 53, 116, 185	14 (0%)

The worst 5 of 652 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	433	GLY	22.1
1	D	433	GLY	15.0
1	B	430	ILE	12.7
1	A	434	THR	11.5
1	C	432	TYR	11.1

### 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 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.