



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 22, 2020 – 01:06 am BST

PDB ID : 3KCV  
Title : Structure of formate channel  
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Deposited on : 2009-10-22  
Resolution : 3.20 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.

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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	:	2.11
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)	:	2.11

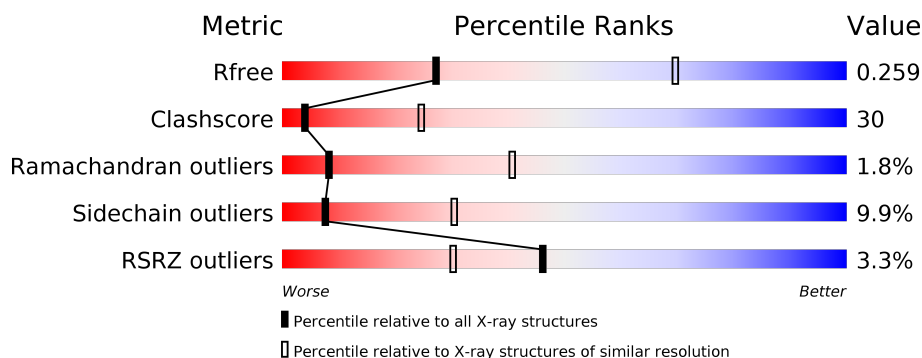
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 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	285	<div> <div>4%</div> <div> <div>41%</div> <div>42%</div> <div>•</div> <div>12%</div> </div> </div>
1	B	285	<div> <div>3%</div> <div> <div>47%</div> <div>34%</div> <div>6%</div> <div>12%</div> </div> </div>
1	C	285	<div> <div>6%</div> <div> <div>47%</div> <div>34%</div> <div>6%</div> <div>•</div> <div>12%</div> </div> </div>
1	D	285	<div> <div>4%</div> <div> <div>41%</div> <div>42%</div> <div>5%</div> <div>12%</div> </div> </div>
1	E	285	<div> <div>4%</div> <div> <div>41%</div> <div>41%</div> <div>6%</div> <div>12%</div> </div> </div>
1	F	285	<div> <div>2%</div> <div> <div>47%</div> <div>35%</div> <div>5%</div> <div>•</div> <div>12%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	285	<div><div><div></div><div></div><div></div><div></div><div></div></div><div>4%</div><div>46%</div><div>38%</div><div>5%</div><div>12%</div></div>
1	H	285	<div><div><div></div><div></div><div></div><div></div><div></div></div><div>3%</div><div>42%</div><div>39%</div><div>7%</div><div>12%</div></div>
1	I	285	<div><div><div></div><div></div><div></div><div></div><div></div></div><div>%</div><div>43%</div><div>39%</div><div>6%</div><div>12%</div></div>
1	J	285	<div><div><div></div><div></div><div></div><div></div><div></div></div><div>%</div><div>46%</div><div>36%</div><div>5%</div><div>13%</div></div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 19120 atoms, of which 0 are hydrogens and 0 are deuteriums.

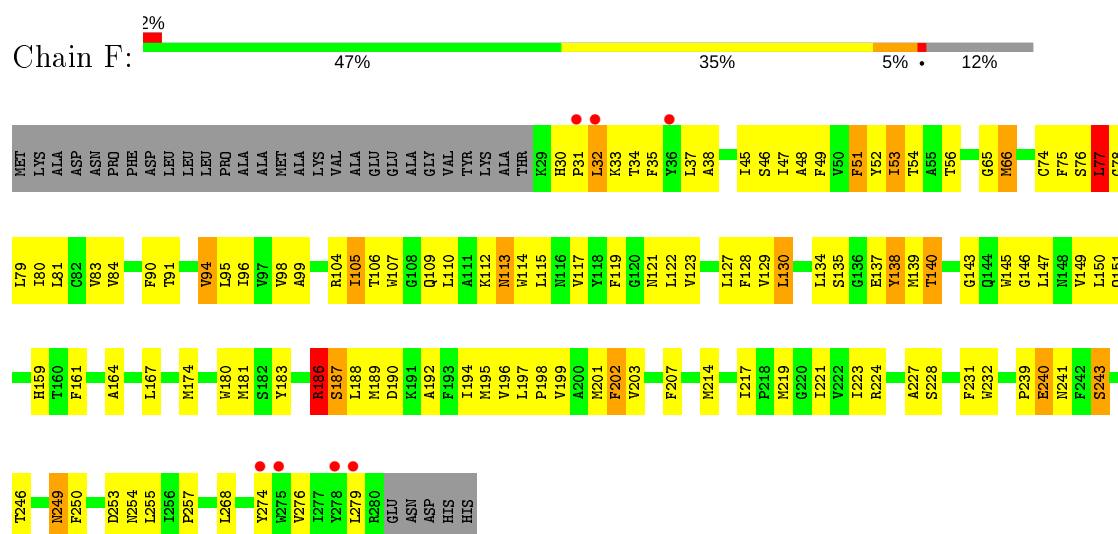
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Probable formate transporter 1.

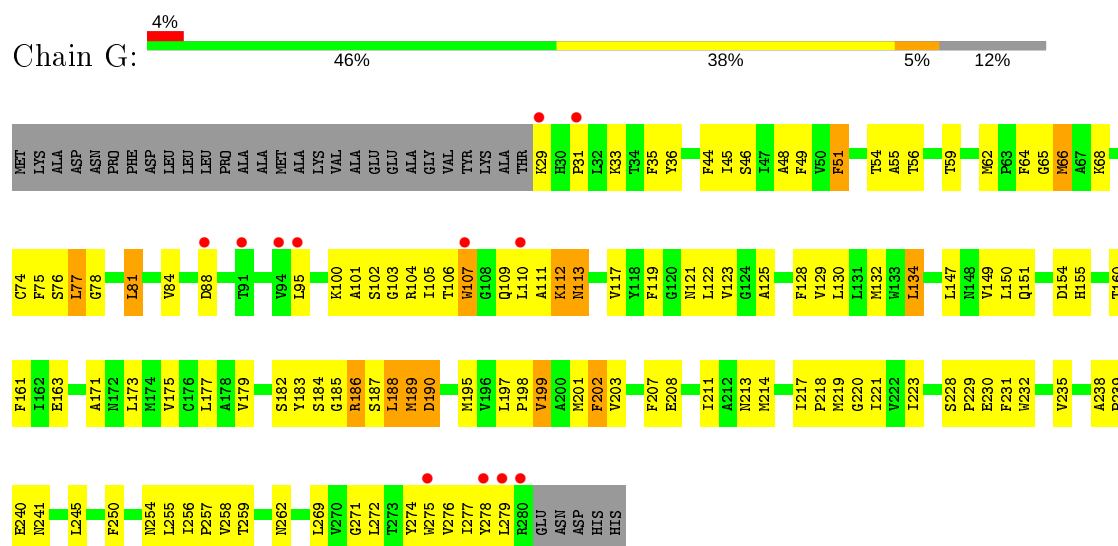
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1907	1269	298	322	18			
1	B	250	Total	C	N	O	S	0	0	0
			1907	1269	298	322	18			
1	C	250	Total	C	N	O	S	0	0	0
			1907	1269	298	322	18			
1	D	251	Total	C	N	O	S	0	0	0
			1912	1272	299	323	18			
1	E	252	Total	C	N	O	S	0	0	0
			1917	1275	300	324	18			
1	F	252	Total	C	N	O	S	0	0	0
			1917	1275	300	324	18			
1	G	252	Total	C	N	O	S	0	0	0
			1917	1275	300	324	18			
1	H	252	Total	C	N	O	S	0	0	0
			1917	1275	300	324	18			
1	I	252	Total	C	N	O	S	0	0	0
			1917	1275	300	324	18			
1	J	249	Total	C	N	O	S	0	0	0
			1902	1267	297	320	18			



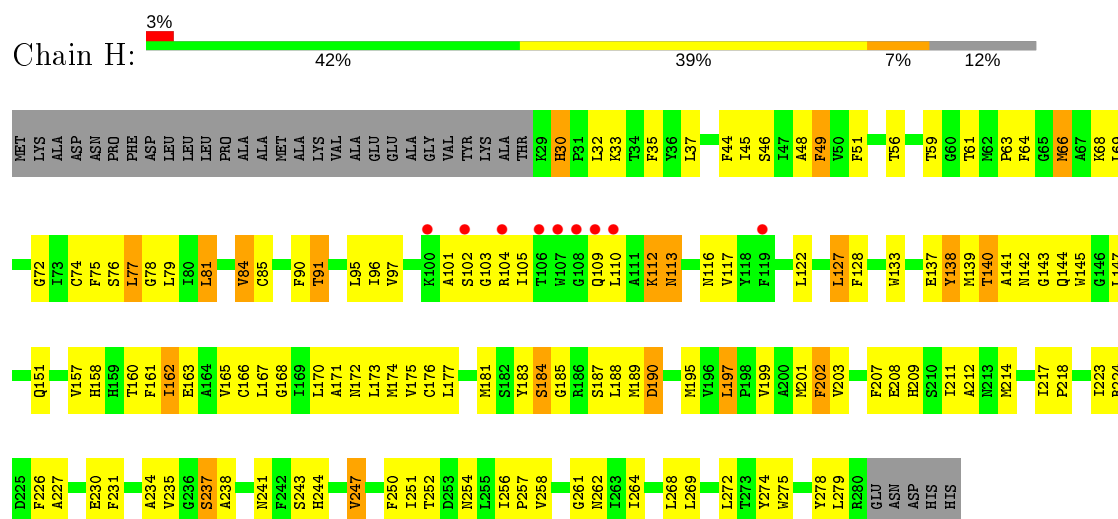




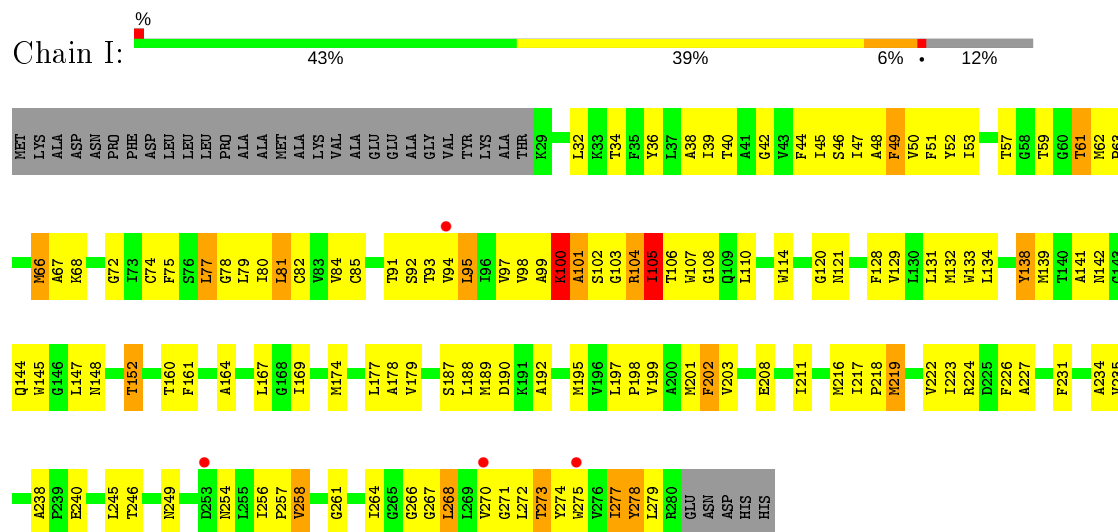
- Molecule 1: Probable formate transporter 1



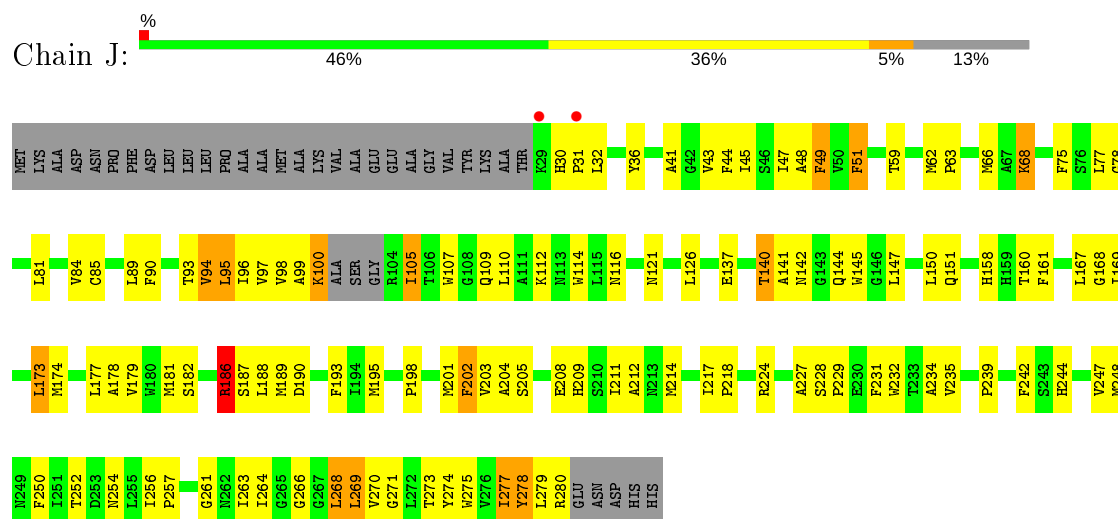
- Molecule 1: Probable formate transporter 1



- Molecule 1: Probable formate transporter 1



- Molecule 1: Probable formate transporter 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.03Å 107.03Å 285.45Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.61 – 3.20 48.61 – 3.20	Depositor EDS
% Data completeness (in resolution range)	90.4 (48.61-3.20) 99.6 (48.61-3.20)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.08 (at 3.19Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, $R_{free}$	0.193 , 0.260 0.195 , 0.259	Depositor DCC
$R_{free}$ test set	3238 reflections (5.37%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	84.0	Xtriage
Anisotropy	0.447	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 71.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,l 0.027 for h,-h-k,-l 0.009 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	19120	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.92% 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	0.42	0/1958	0.62	1/2670 (0.0%)
1	B	0.40	0/1958	0.57	0/2670
1	C	0.40	0/1958	0.56	0/2670
1	D	0.38	0/1963	0.57	0/2677
1	E	0.43	0/1968	0.60	0/2684
1	F	0.44	0/1968	0.58	1/2684 (0.0%)
1	G	0.43	0/1968	0.61	0/2684
1	H	0.42	0/1968	0.56	0/2684
1	I	0.46	0/1968	0.70	3/2684 (0.1%)
1	J	0.42	0/1952	0.61	0/2661
All	All	0.42	0/19629	0.60	5/26768 (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	I	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	100	LYS	N-CA-C	11.12	141.04	111.00
1	I	100	LYS	CB-CA-C	-8.88	92.63	110.40
1	I	100	LYS	C-N-CA	6.06	136.84	121.70
1	A	77	LEU	CA-CB-CG	5.48	127.90	115.30
1	F	77	LEU	CA-CB-CG	5.06	126.93	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	I	100	LYS	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	1907	0	1946	128	0
1	B	1907	0	1946	108	0
1	C	1907	0	1946	130	0
1	D	1912	0	1948	168	0
1	E	1917	0	1950	134	0
1	F	1917	0	1950	114	0
1	G	1917	0	1950	129	0
1	H	1917	0	1950	158	0
1	I	1917	0	1950	147	0
1	J	1902	0	1936	114	0
All	All	19120	0	19472	1160	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 30.

The worst 5 of 1160 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:C:223:ILE:O	1:C:227:ALA:HB2	1.39	1.23
1:D:101:ALA:O	1:D:104:ARG:HB2	1.45	1.13
1:H:95:LEU:HD21	1:H:269:LEU:HB3	1.37	1.05
1:I:271:GLY:O	1:I:275:TRP:HD1	1.38	1.04
1:C:274:TYR:O	1:C:278:TYR:HB3	1.59	1.02

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	248/285 (87%)	230 (93%)	15 (6%)	3 (1%)	13	49
1	B	248/285 (87%)	217 (88%)	26 (10%)	5 (2%)	7	38
1	C	248/285 (87%)	220 (89%)	23 (9%)	5 (2%)	7	38
1	D	249/285 (87%)	224 (90%)	20 (8%)	5 (2%)	7	38
1	E	250/285 (88%)	220 (88%)	23 (9%)	7 (3%)	5	29
1	F	250/285 (88%)	234 (94%)	12 (5%)	4 (2%)	9	43
1	G	250/285 (88%)	222 (89%)	25 (10%)	3 (1%)	13	49
1	H	250/285 (88%)	225 (90%)	19 (8%)	6 (2%)	6	34
1	I	250/285 (88%)	218 (87%)	28 (11%)	4 (2%)	9	43
1	J	245/285 (86%)	219 (89%)	22 (9%)	4 (2%)	9	43
All	All	2488/2850 (87%)	2229 (90%)	213 (9%)	46 (2%)	8	41

5 of 46 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	186	ARG
1	G	113	ASN
1	I	95	LEU
1	I	101	ALA
1	J	94	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	203/230 (88%)	183 (90%)	20 (10%)	8	30
1	B	203/230 (88%)	182 (90%)	21 (10%)	7	29
1	C	203/230 (88%)	177 (87%)	26 (13%)	4	20
1	D	203/230 (88%)	186 (92%)	17 (8%)	11	39
1	E	203/230 (88%)	184 (91%)	19 (9%)	8	33
1	F	203/230 (88%)	180 (89%)	23 (11%)	6	25
1	G	203/230 (88%)	186 (92%)	17 (8%)	11	39
1	H	203/230 (88%)	183 (90%)	20 (10%)	8	30
1	I	203/230 (88%)	184 (91%)	19 (9%)	8	33
1	J	202/230 (88%)	184 (91%)	18 (9%)	9	35
All	All	2029/2300 (88%)	1829 (90%)	200 (10%)	8	30

5 of 200 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	127	LEU
1	F	94	VAL
1	J	66	MET
1	E	173	LEU
1	E	259	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	151	GLN
1	G	116	ASN
1	J	151	GLN
1	F	159	HIS
1	G	213	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 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	250/285 (87%)	-0.35	2 (0%) 86 78	54, 78, 115, 178	0
1	B	250/285 (87%)	-0.33	8 (3%) 47 31	57, 88, 164, 301	0
1	C	250/285 (87%)	-0.07	16 (6%) 19 11	64, 98, 183, 259	0
1	D	251/285 (88%)	-0.15	11 (4%) 34 21	61, 91, 182, 314	0
1	E	252/285 (88%)	-0.12	12 (4%) 30 18	44, 83, 175, 306	0
1	F	252/285 (88%)	-0.27	7 (2%) 53 37	47, 79, 135, 210	0
1	G	252/285 (88%)	-0.10	12 (4%) 30 18	53, 84, 184, 236	0
1	H	252/285 (88%)	-0.15	9 (3%) 42 27	59, 90, 192, 316	0
1	I	252/285 (88%)	-0.28	4 (1%) 72 59	52, 85, 125, 224	0
1	J	249/285 (87%)	-0.28	2 (0%) 86 78	53, 84, 137, 223	0
All	All	2510/2850 (88%)	-0.21	83 (3%) 46 30	44, 86, 166, 316	0

The worst 5 of 83 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	279	LEU	6.5
1	C	110	LEU	6.4
1	G	279	LEU	6.1
1	G	278	TYR	5.8
1	B	110	LEU	5.4

### 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.