



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 10:59 PM BST

PDB ID : 6KRP  
Title : Peroxiredoxin from *Aeropyrum pernix* K1 (ApPrx) 0Cys W88A mutant  
Authors : Himiyama, T.; Nakamura, T.  
Deposited on : 2019-08-22  
Resolution : 1.89 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
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
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)	:	2.13.1

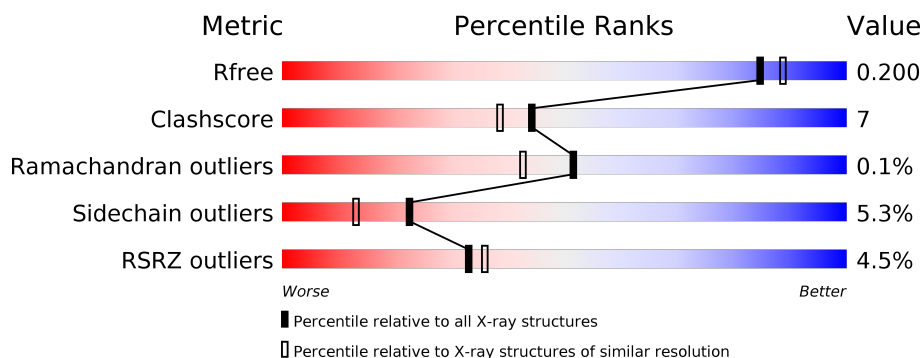
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.89 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	250	<div> <div>3%</div> <div> <div></div> <div>80%</div> <div>15%</div> <div>••</div> </div> </div>
1	B	250	<div> <div>5%</div> <div> <div></div> <div>83%</div> <div>13%</div> <div>••</div> </div> </div>
1	C	250	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>12%</div> <div>•••</div> </div> </div>
1	D	250	<div> <div>4%</div> <div> <div></div> <div>81%</div> <div>14%</div> <div>•••</div> </div> </div>
1	E	250	<div> <div>6%</div> <div> <div></div> <div>81%</div> <div>16%</div> <div>•</div> </div> </div>
1	F	250	<div> <div>3%</div> <div> <div></div> <div>78%</div> <div>17%</div> <div>••</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	250	<div><div></div><div>5%</div><div>78%</div><div>17%</div><div></div><div></div></div>
1	H	250	<div><div></div><div>6%</div><div>81%</div><div>15%</div><div></div><div></div></div>
1	I	250	<div><div></div><div>4%</div><div>80%</div><div>14%</div><div></div><div></div></div>
1	J	250	<div><div></div><div>4%</div><div>84%</div><div>12%</div><div></div><div></div></div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 21385 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 Peroxiredoxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	242	Total	C	N	O	S	0	0	0
			1953	1253	344	352	4			
1	B	244	Total	C	N	O	S	0	0	0
			1964	1260	346	354	4			
1	C	244	Total	C	N	O	S	0	0	0
			1964	1260	346	354	4			
1	D	244	Total	C	N	O	S	0	0	0
			1964	1260	346	354	4			
1	E	244	Total	C	N	O	S	0	0	0
			1964	1260	346	354	4			
1	F	243	Total	C	N	O	S	0	0	0
			1957	1255	345	353	4			
1	G	244	Total	C	N	O	S	0	0	0
			1964	1260	346	354	4			
1	H	244	Total	C	N	O	S	0	0	0
			1964	1260	346	354	4			
1	I	244	Total	C	N	O	S	0	0	0
			1964	1260	346	354	4			
1	J	244	Total	C	N	O	S	0	0	0
			1964	1260	346	354	4			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	SER	CYS	engineered mutation	UNP Q9Y9L0
A	88	ALA	TRP	engineered mutation	UNP Q9Y9L0
A	207	SER	CYS	engineered mutation	UNP Q9Y9L0
A	213	SER	CYS	engineered mutation	UNP Q9Y9L0
B	50	SER	CYS	engineered mutation	UNP Q9Y9L0
B	88	ALA	TRP	engineered mutation	UNP Q9Y9L0
B	207	SER	CYS	engineered mutation	UNP Q9Y9L0
B	213	SER	CYS	engineered mutation	UNP Q9Y9L0
C	50	SER	CYS	engineered mutation	UNP Q9Y9L0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	88	ALA	TRP	engineered mutation	UNP Q9Y9L0
C	207	SER	CYS	engineered mutation	UNP Q9Y9L0
C	213	SER	CYS	engineered mutation	UNP Q9Y9L0
D	50	SER	CYS	engineered mutation	UNP Q9Y9L0
D	88	ALA	TRP	engineered mutation	UNP Q9Y9L0
D	207	SER	CYS	engineered mutation	UNP Q9Y9L0
D	213	SER	CYS	engineered mutation	UNP Q9Y9L0
E	50	SER	CYS	engineered mutation	UNP Q9Y9L0
E	88	ALA	TRP	engineered mutation	UNP Q9Y9L0
E	207	SER	CYS	engineered mutation	UNP Q9Y9L0
E	213	SER	CYS	engineered mutation	UNP Q9Y9L0
F	50	SER	CYS	engineered mutation	UNP Q9Y9L0
F	88	ALA	TRP	engineered mutation	UNP Q9Y9L0
F	207	SER	CYS	engineered mutation	UNP Q9Y9L0
F	213	SER	CYS	engineered mutation	UNP Q9Y9L0
G	50	SER	CYS	engineered mutation	UNP Q9Y9L0
G	88	ALA	TRP	engineered mutation	UNP Q9Y9L0
G	207	SER	CYS	engineered mutation	UNP Q9Y9L0
G	213	SER	CYS	engineered mutation	UNP Q9Y9L0
H	50	SER	CYS	engineered mutation	UNP Q9Y9L0
H	88	ALA	TRP	engineered mutation	UNP Q9Y9L0
H	207	SER	CYS	engineered mutation	UNP Q9Y9L0
H	213	SER	CYS	engineered mutation	UNP Q9Y9L0
I	50	SER	CYS	engineered mutation	UNP Q9Y9L0
I	88	ALA	TRP	engineered mutation	UNP Q9Y9L0
I	207	SER	CYS	engineered mutation	UNP Q9Y9L0
I	213	SER	CYS	engineered mutation	UNP Q9Y9L0
J	50	SER	CYS	engineered mutation	UNP Q9Y9L0
J	88	ALA	TRP	engineered mutation	UNP Q9Y9L0
J	207	SER	CYS	engineered mutation	UNP Q9Y9L0
J	213	SER	CYS	engineered mutation	UNP Q9Y9L0

- Molecule 2 is CITRIC ACID (three-letter code: CIT) (formula: C<sub>6</sub>H<sub>8</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	6	7		
2	B	1	Total	C	O	0	0
			13	6	7		
2	C	1	Total	C	O	0	0
			13	6	7		
2	D	1	Total	C	O	0	0
			13	6	7		
2	E	1	Total	C	O	0	0
			13	6	7		
2	F	1	Total	C	O	0	0
			13	6	7		
2	G	1	Total	C	O	0	0
			13	6	7		
2	H	1	Total	C	O	0	0
			13	6	7		
2	I	1	Total	C	O	0	0
			13	6	7		
2	J	1	Total	C	O	0	0
			13	6	7		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	169	Total	O	0	0
			169	169		
3	B	169	Total	O	0	0
			169	169		

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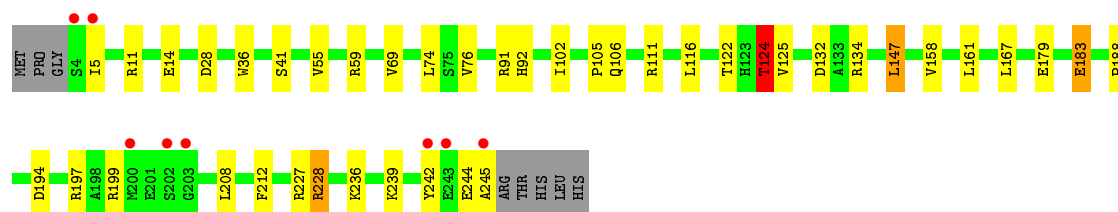
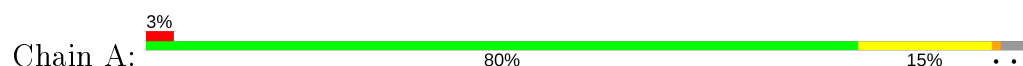
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	153	Total 153	O 153	0	0
3	D	156	Total 156	O 156	0	0
3	E	190	Total 190	O 190	0	0
3	F	167	Total 167	O 167	0	0
3	G	144	Total 144	O 144	0	0
3	H	175	Total 175	O 175	0	0
3	I	162	Total 162	O 162	0	0
3	J	148	Total 148	O 148	0	0

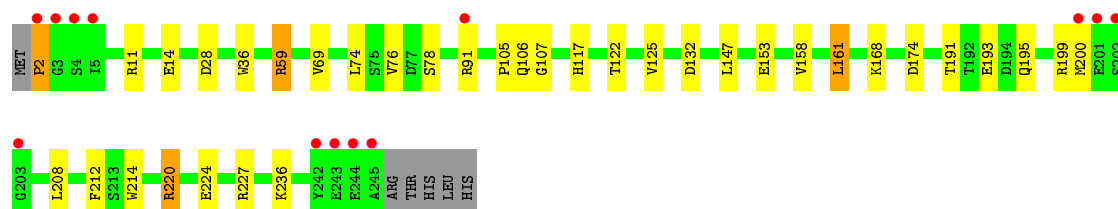
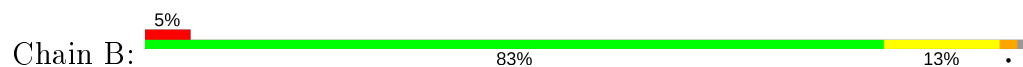
### 3 Residue-property plots [i](#)

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.

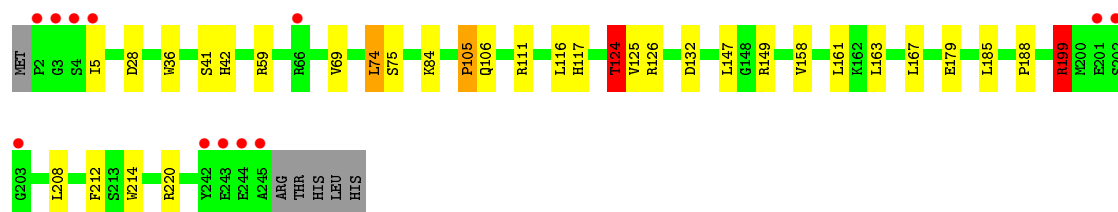
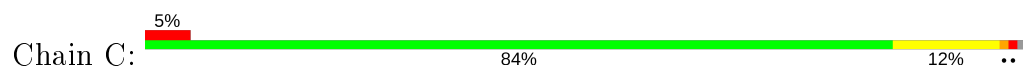
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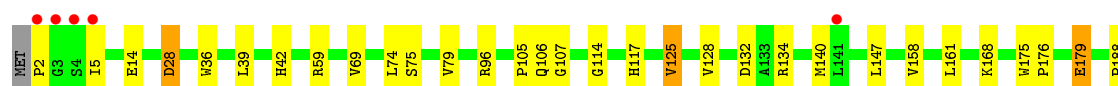
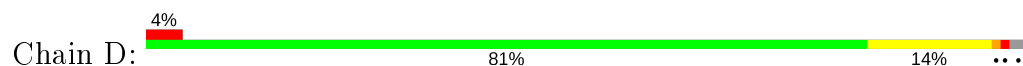
- Molecule 1: Peroxiredoxin



- Molecule 1: Peroxiredoxin



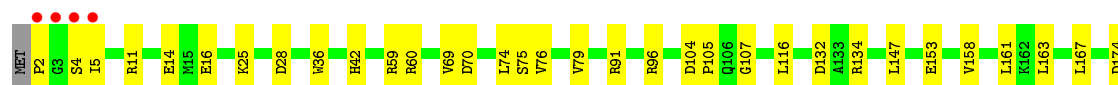
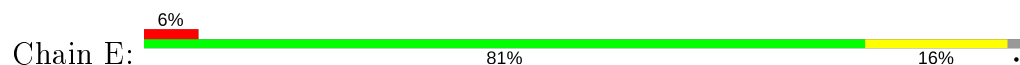
- Molecule 1: Peroxiredoxin



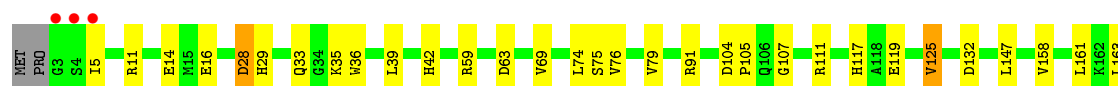
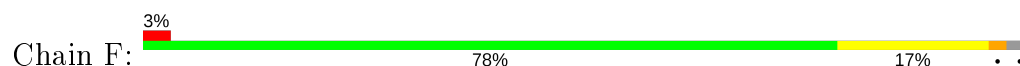




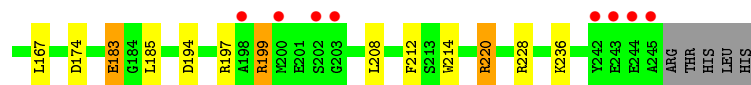
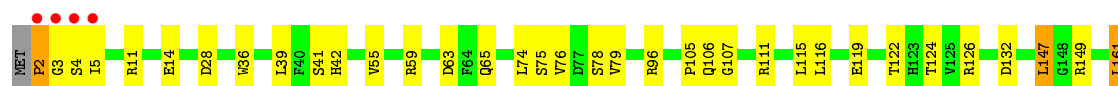
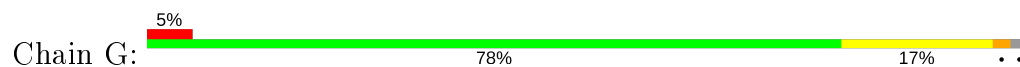
• Molecule 1: Peroxiredoxin



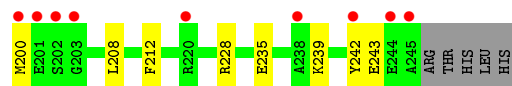
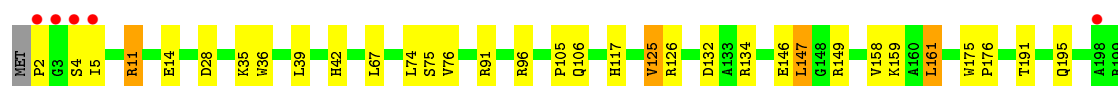
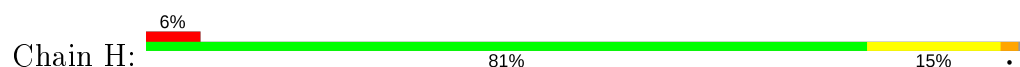
• Molecule 1: Peroxiredoxin



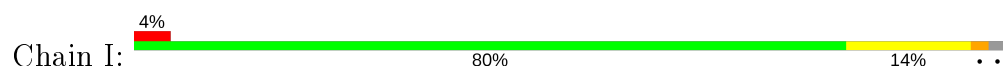
• Molecule 1: Peroxiredoxin

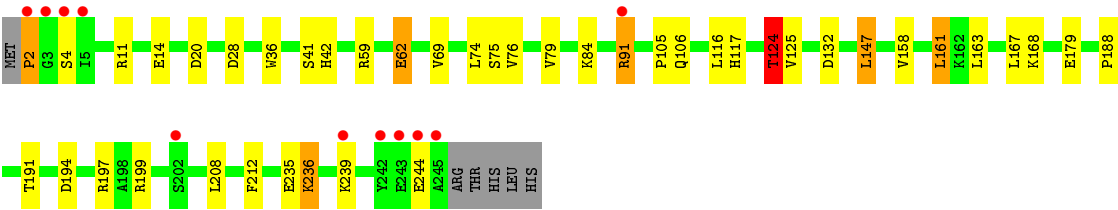


• Molecule 1: Peroxiredoxin

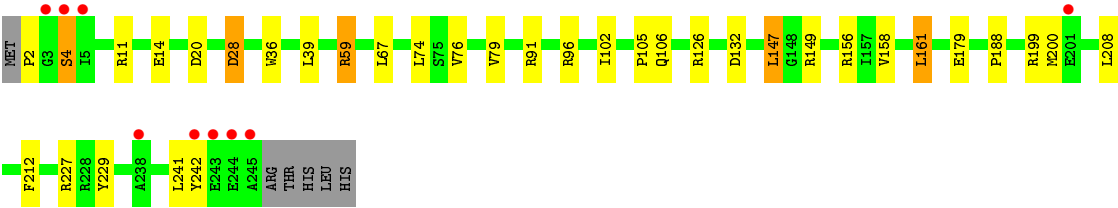
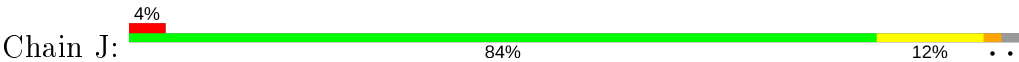


• Molecule 1: Peroxiredoxin





● Molecule 1: Peroxiredoxin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.24Å 103.28Å 105.13Å 105.78° 105.25° 92.45°	Depositor
Resolution (Å)	49.37 – 1.89 49.32 – 1.89	Depositor EDS
% Data completeness (in resolution range)	97.4 (49.37-1.89) 97.4 (49.32-1.89)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.63 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, $R_{free}$	0.164 , 0.188 0.179 , 0.200	Depositor DCC
$R_{free}$ test set	11796 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	22.5	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 50.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	21385	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.03% 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 ⓘ

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

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	0.90	2/2005 (0.1%)	0.99	5/2725 (0.2%)
1	B	0.78	0/2017	0.91	1/2741 (0.0%)
1	C	0.85	1/2017 (0.0%)	0.95	5/2741 (0.2%)
1	D	0.91	2/2017 (0.1%)	1.01	9/2741 (0.3%)
1	E	0.81	1/2017 (0.0%)	0.93	2/2741 (0.1%)
1	F	0.96	4/2009 (0.2%)	0.98	5/2730 (0.2%)
1	G	0.81	1/2017 (0.0%)	0.92	2/2741 (0.1%)
1	H	0.81	1/2017 (0.0%)	0.93	2/2741 (0.1%)
1	I	0.78	0/2017	0.91	2/2741 (0.1%)
1	J	0.78	0/2017	0.92	3/2741 (0.1%)
All	All	0.84	12/20150 (0.1%)	0.94	36/27383 (0.1%)

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	179	GLU	CD-OE2	16.59	1.44	1.25
1	C	179	GLU	CD-OE2	14.80	1.42	1.25
1	D	179	GLU	CD-OE2	14.45	1.41	1.25
1	A	179	GLU	CD-OE2	13.51	1.40	1.25
1	A	183	GLU	CD-OE1	7.00	1.33	1.25

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	199	ARG	NE-CZ-NH2	-11.33	114.64	120.30
1	D	199	ARG	NE-CZ-NH2	-9.70	115.45	120.30
1	D	231	ARG	NE-CZ-NH1	-9.62	115.49	120.30
1	D	96	ARG	CB-CG-CD	7.83	131.96	111.60
1	C	199	ARG	NE-CZ-NH2	-7.59	116.51	120.30

There are no chirality outliers.

There are no planarity outliers.

## 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	1953	0	1943	29	0
1	B	1964	0	1954	30	0
1	C	1964	0	1954	19	0
1	D	1964	0	1954	28	0
1	E	1964	0	1954	34	0
1	F	1957	0	1946	34	0
1	G	1964	0	1954	43	0
1	H	1964	0	1954	30	0
1	I	1964	0	1954	34	0
1	J	1964	0	1954	25	0
2	A	13	0	5	0	0
2	B	13	0	5	0	0
2	C	13	0	5	0	0
2	D	13	0	5	0	0
2	E	13	0	5	0	0
2	F	13	0	5	1	0
2	G	13	0	5	0	0
2	H	13	0	5	0	0
2	I	13	0	5	0	0
2	J	13	0	5	0	0
3	A	169	0	0	7	0
3	B	169	0	0	6	0
3	C	153	0	0	1	0
3	D	156	0	0	3	0
3	E	190	0	0	11	1
3	F	167	0	0	10	0
3	G	144	0	0	13	0
3	H	175	0	0	4	0
3	I	162	0	0	3	1
3	J	148	0	0	2	0
All	All	21385	0	19571	258	1

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 7.

The worst 5 of 258 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:F:76:VAL:HG12	3:F:498:HOH:O	1.26	1.30
1:E:76:VAL:HG12	3:E:515:HOH:O	1.39	1.19
1:E:16:GLU:HG2	3:E:554:HOH:O	1.42	1.19
1:G:76:VAL:HG12	3:G:495:HOH:O	1.49	1.09
1:A:236:LYS:HE2	3:A:458:HOH:O	1.50	1.08

All (1) 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)
3:E:477:HOH:O	3:I:477:HOH:O[1_554]	2.02	0.18

## 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	240/250 (96%)	235 (98%)	5 (2%)	0	100	100
1	B	242/250 (97%)	239 (99%)	3 (1%)	0	100	100
1	C	242/250 (97%)	239 (99%)	3 (1%)	0	100	100
1	D	242/250 (97%)	236 (98%)	5 (2%)	1 (0%)	34	24
1	E	242/250 (97%)	239 (99%)	3 (1%)	0	100	100
1	F	241/250 (96%)	235 (98%)	5 (2%)	1 (0%)	34	24
1	G	242/250 (97%)	238 (98%)	4 (2%)	0	100	100
1	H	242/250 (97%)	238 (98%)	3 (1%)	1 (0%)	34	24
1	I	242/250 (97%)	238 (98%)	4 (2%)	0	100	100
1	J	242/250 (97%)	238 (98%)	4 (2%)	0	100	100
All	All	2417/2500 (97%)	2375 (98%)	39 (2%)	3 (0%)	51	43

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	125	VAL
1	D	125	VAL
1	F	125	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	208/215 (97%)	198 (95%)	10 (5%)	25	16
1	B	209/215 (97%)	202 (97%)	7 (3%)	38	29
1	C	209/215 (97%)	197 (94%)	12 (6%)	20	11
1	D	209/215 (97%)	199 (95%)	10 (5%)	25	16
1	E	209/215 (97%)	197 (94%)	12 (6%)	20	11
1	F	208/215 (97%)	198 (95%)	10 (5%)	25	16
1	G	209/215 (97%)	198 (95%)	11 (5%)	22	13
1	H	209/215 (97%)	199 (95%)	10 (5%)	25	16
1	I	209/215 (97%)	191 (91%)	18 (9%)	10	4
1	J	209/215 (97%)	198 (95%)	11 (5%)	22	13
All	All	2088/2150 (97%)	1977 (95%)	111 (5%)	22	13

5 of 111 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	239	LYS
1	G	28	ASP
1	J	28	ASP
1	F	16	GLU
1	F	161	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	204	GLN
1	F	65	GLN
1	H	204	GLN
1	D	195	GLN
1	D	204	GLN

### 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 ⓘ

There are no monosaccharides in this entry.

### 5.6 Ligand geometry ⓘ

10 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	CIT	I	301	-	3,12,12	1.91	1 (33%)	3,17,17	1.64	1 (33%)
2	CIT	H	301	-	3,12,12	1.46	1 (33%)	3,17,17	1.04	0
2	CIT	J	301	-	3,12,12	1.77	1 (33%)	3,17,17	1.23	0
2	CIT	D	301	-	3,12,12	1.78	1 (33%)	3,17,17	1.74	1 (33%)
2	CIT	G	301	-	3,12,12	1.78	1 (33%)	3,17,17	1.68	1 (33%)
2	CIT	F	301	-	3,12,12	1.86	1 (33%)	3,17,17	1.72	2 (66%)
2	CIT	A	301	-	3,12,12	1.51	1 (33%)	3,17,17	1.29	0
2	CIT	C	301	-	3,12,12	1.77	1 (33%)	3,17,17	1.87	1 (33%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	CIT	B	301	-	3,12,12	1.34	1 (33%)	3,17,17	1.65	1 (33%)
2	CIT	E	301	-	3,12,12	2.18	1 (33%)	3,17,17	2.17	1 (33%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CIT	I	301	-	-	3/6/16/16	-
2	CIT	H	301	-	-	4/6/16/16	-
2	CIT	J	301	-	-	3/6/16/16	-
2	CIT	D	301	-	-	3/6/16/16	-
2	CIT	G	301	-	-	3/6/16/16	-
2	CIT	F	301	-	-	3/6/16/16	-
2	CIT	A	301	-	-	3/6/16/16	-
2	CIT	C	301	-	-	3/6/16/16	-
2	CIT	B	301	-	-	4/6/16/16	-
2	CIT	E	301	-	-	4/6/16/16	-

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	301	CIT	C4-C3	-3.64	1.49	1.54
2	I	301	CIT	C2-C3	-3.25	1.50	1.54
2	F	301	CIT	C2-C3	-3.14	1.50	1.54
2	D	301	CIT	C4-C3	-3.03	1.50	1.54
2	J	301	CIT	C2-C3	-2.89	1.50	1.54

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	301	CIT	C4-C3-C2	-3.64	99.58	109.33
2	I	301	CIT	C4-C3-C2	-2.67	102.18	109.33
2	G	301	CIT	C4-C3-C2	-2.55	102.50	109.33
2	C	301	CIT	C4-C3-C2	-2.55	102.52	109.33
2	B	301	CIT	C4-C3-C2	-2.54	102.53	109.33

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	I	301	CIT	C2-C3-C4-C5
2	I	301	CIT	O7-C3-C4-C5
2	I	301	CIT	C6-C3-C4-C5
2	H	301	CIT	C1-C2-C3-O7
2	H	301	CIT	C1-C2-C3-C4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	301	CIT	1	0

## 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	242/250 (96%)	-0.15	8 (3%) 46 49	18, 25, 48, 91	0
1	B	244/250 (97%)	-0.18	13 (5%) 26 29	18, 25, 56, 102	0
1	C	244/250 (97%)	-0.04	12 (4%) 29 33	19, 25, 55, 142	0
1	D	244/250 (97%)	-0.08	9 (3%) 41 44	19, 26, 52, 92	0
1	E	244/250 (97%)	-0.20	14 (5%) 23 26	16, 23, 56, 107	0
1	F	243/250 (97%)	-0.14	8 (3%) 46 49	16, 24, 49, 97	0
1	G	244/250 (97%)	-0.07	12 (4%) 29 33	19, 27, 54, 110	0
1	H	244/250 (97%)	-0.24	14 (5%) 23 26	18, 25, 54, 85	0
1	I	244/250 (97%)	-0.19	11 (4%) 33 36	19, 26, 52, 94	0
1	J	244/250 (97%)	-0.08	9 (3%) 41 44	19, 27, 55, 95	0
All	All	2437/2500 (97%)	-0.14	110 (4%) 33 36	16, 25, 55, 142	0

The worst 5 of 110 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	2	PRO	12.7
1	C	3	GLY	12.6
1	E	245	ALA	11.5
1	D	245	ALA	10.0
1	C	245	ALA	8.2

### 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 [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	CIT	B	301	13/13	0.91	0.11	24,33,40,45	0
2	CIT	E	301	13/13	0.92	0.10	18,28,38,40	0
2	CIT	J	301	13/13	0.93	0.10	23,36,44,49	0
2	CIT	C	301	13/13	0.93	0.10	20,31,39,39	0
2	CIT	F	301	13/13	0.94	0.09	19,30,39,43	0
2	CIT	A	301	13/13	0.94	0.10	21,32,41,44	0
2	CIT	I	301	13/13	0.94	0.09	22,31,39,40	0
2	CIT	D	301	13/13	0.94	0.10	21,29,40,42	0
2	CIT	G	301	13/13	0.94	0.09	23,30,40,40	0
2	CIT	H	301	13/13	0.95	0.10	22,32,45,50	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.