



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 11:46 PM GMT

PDB ID : 1YF1  
Title : Structural and biochemical analysis of the link between enzymatic activity and oligomerization in AhpC, a bacterial peroxiredoxin.  
Authors : Parsonage, D.; Youngblood, D.S.; Sarma, G.N.; Wood, Z.A.; Karplus, P.A.; Poole, L.B.  
Deposited on : 2004-12-29  
Resolution : 2.60 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

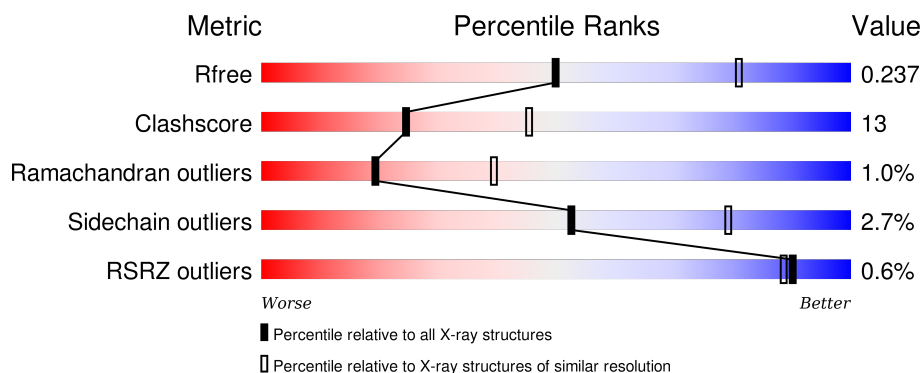
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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))
$R_{free}$	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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. 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	186	<div> <div> <div></div> <div>68%</div> <div>20%</div> <div>•</div> <div>11%</div> </div> </div>
1	B	186	<div> <div> <div></div> <div>65%</div> <div>23%</div> <div>•</div> <div>11%</div> </div> </div>
1	C	186	<div> <div> <div></div> <div>64%</div> <div>23%</div> <div>•</div> <div>12%</div> </div> </div>
1	D	186	<div> <div> <div></div> <div>55%</div> <div>33%</div> <div>•</div> <div>11%</div> </div> </div>
1	E	186	<div> <div> <div></div> <div>63%</div> <div>23%</div> <div>••</div> <div>11%</div> </div> </div>

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	186	<div><div><div>%</div><div><div></div><div></div><div></div></div><div>68%20%11%</div><div>..</div></div></div>
1	G	186	<div><div><div>%</div><div><div></div><div></div><div></div></div><div>71%16%11%</div><div>.</div></div></div>
1	H	186	<div><div><div></div><div><div></div><div></div><div></div></div><div>64%23%12%</div><div>.</div></div></div>
1	I	186	<div><div><div>%</div><div><div></div><div></div><div></div></div><div>72%17%11%</div><div>.</div></div></div>
1	J	186	<div><div><div>%</div><div><div></div><div></div><div></div></div><div>64%23%11%</div><div>.</div></div></div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13819 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 Alkyl hydroperoxide reductase subunit C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	166	Total	C	N	O	S	0	0	0
			1306	832	217	253	4			
1	B	165	Total	C	N	O	S	0	0	0
			1299	827	216	252	4			
1	C	163	Total	C	N	O	S	0	0	0
			1286	819	214	250	3			
1	D	166	Total	C	N	O	S	0	0	0
			1306	832	217	253	4			
1	E	165	Total	C	N	O	S	0	0	0
			1299	827	216	252	4			
1	F	166	Total	C	N	O	S	0	0	0
			1306	832	217	253	4			
1	G	165	Total	C	N	O	S	0	0	0
			1299	827	216	252	4			
1	H	163	Total	C	N	O	S	0	0	0
			1286	819	214	250	3			
1	I	166	Total	C	N	O	S	0	0	0
			1306	832	217	253	4			
1	J	165	Total	C	N	O	S	0	0	0
			1299	827	216	252	4			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	77	VAL	THR	ENGINEERED	UNP P0A251
B	77	VAL	THR	ENGINEERED	UNP P0A251
C	77	VAL	THR	ENGINEERED	UNP P0A251
D	77	VAL	THR	ENGINEERED	UNP P0A251
E	77	VAL	THR	ENGINEERED	UNP P0A251
F	77	VAL	THR	ENGINEERED	UNP P0A251
G	77	VAL	THR	ENGINEERED	UNP P0A251
H	77	VAL	THR	ENGINEERED	UNP P0A251
I	77	VAL	THR	ENGINEERED	UNP P0A251

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
J	77	VAL	THR	ENGINEERED	UNP P0A251

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Na 1 1	0	0

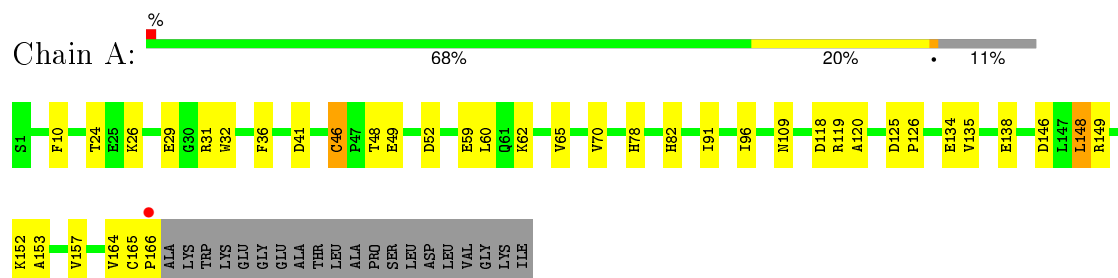
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	112	Total O 112 112	0	0
3	B	95	Total O 95 95	0	0
3	C	94	Total O 94 94	0	0
3	D	67	Total O 67 67	0	0
3	E	32	Total O 32 32	0	0
3	F	100	Total O 100 100	0	0
3	G	101	Total O 101 101	0	0
3	H	96	Total O 96 96	0	0
3	I	89	Total O 89 89	0	0
3	J	40	Total O 40 40	0	0

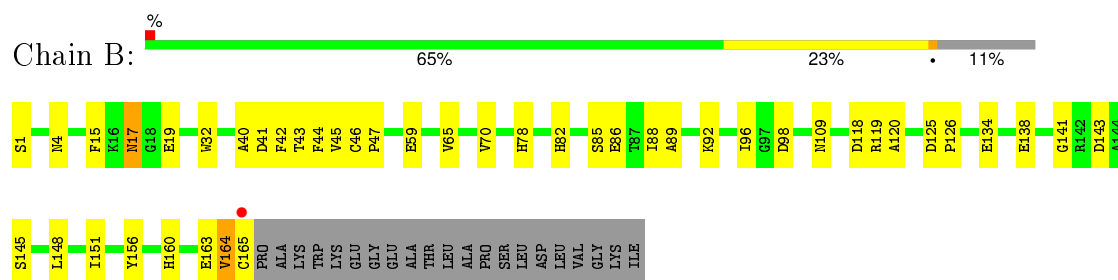
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ( $\text{RSRZ} > 2$ ). 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.

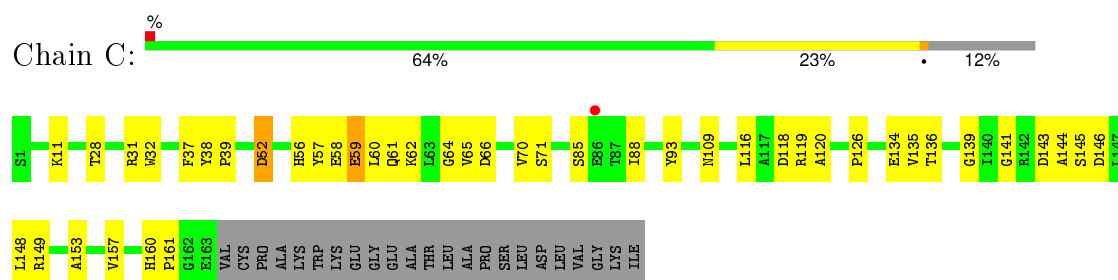
- Molecule 1: Alkyl hydroperoxide reductase subunit C



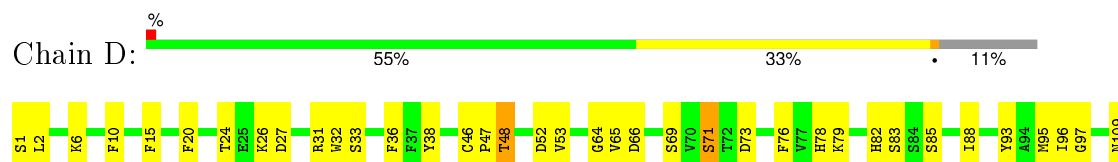
- Molecule 1: Alkyl hydroperoxide reductase subunit C



- Molecule 1: Alkyl hydroperoxide reductase subunit C

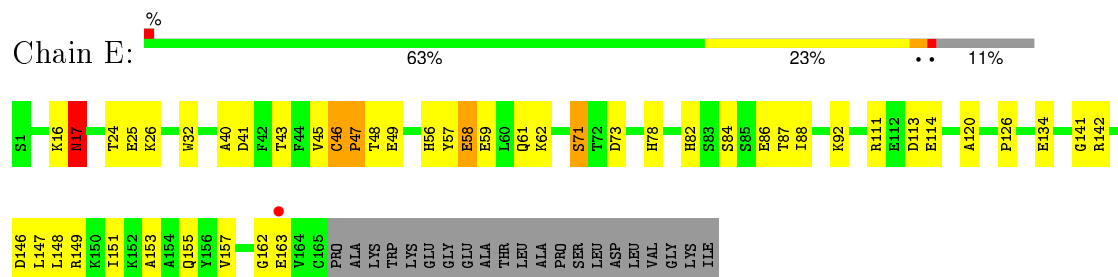


- Molecule 1: Alkyl hydroperoxide reductase subunit C

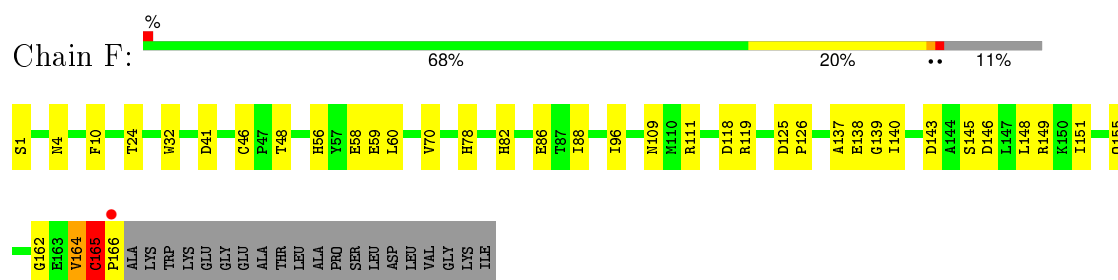




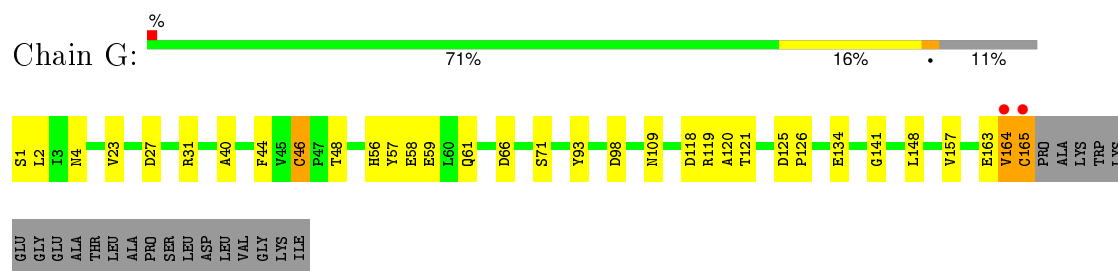
- Molecule 1: Alkyl hydroperoxide reductase subunit C



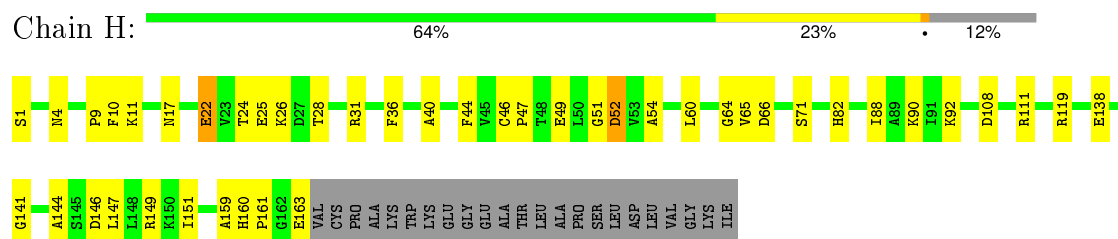
- Molecule 1: Alkyl hydroperoxide reductase subunit C



- Molecule 1: Alkyl hydroperoxide reductase subunit C

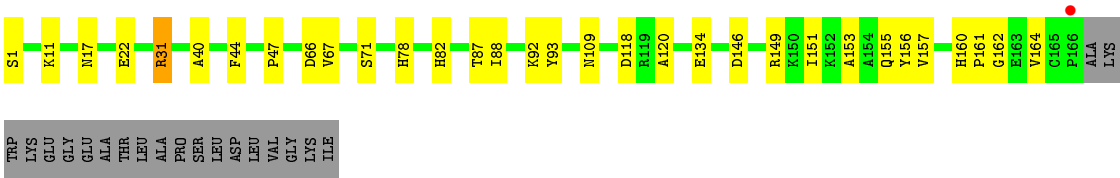


- Molecule 1: Alkyl hydroperoxide reductase subunit C

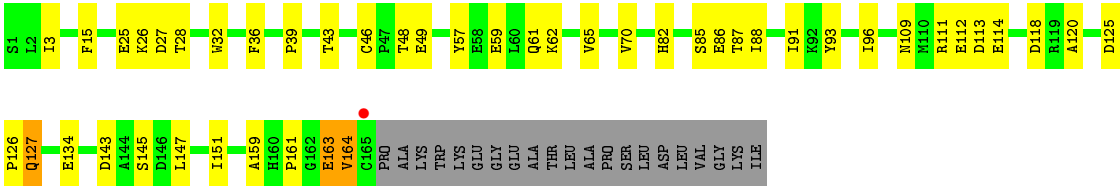


- Molecule 1: Alkyl hydroperoxide reductase subunit C





● Molecule 1: Alkyl hydroperoxide reductase subunit C





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 <sub>1</sub> 2 <sub>1</sub> 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	136.35Å 169.96Å 117.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 2.60 63.27 – 2.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) (100.00-2.60) 93.5 (63.27-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.93 (at 2.61Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.181 , 0.237 0.181 , 0.237	Depositor DCC
$R_{free}$ test set	7964 reflections (10.06%)	DCC
Wilson B-factor (Å <sup>2</sup> )	40.8	Xtriage
Anisotropy	0.269	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 64.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 83818 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	13819	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	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 41.66 % 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 2.2860e-04. 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, 0.375 respectively for untwinned datasets, and 0.333, 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:  
NA

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	0.55	0/1337	0.74	0/1813
1	B	0.54	0/1329	0.70	0/1801
1	C	0.54	0/1316	0.72	0/1783
1	D	0.45	0/1337	0.67	0/1813
1	E	0.44	0/1329	0.67	0/1801
1	F	0.51	0/1337	0.70	0/1813
1	G	0.53	0/1329	0.69	0/1801
1	H	0.50	0/1316	0.71	1/1783 (0.1%)
1	I	0.51	0/1337	0.71	0/1813
1	J	0.45	0/1329	0.67	0/1801
All	All	0.50	0/13296	0.70	1/18022 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	111	ARG	N-CA-C	-5.07	97.32	111.00

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	1306	0	1261	31	0
1	B	1299	0	1254	48	0
1	C	1286	0	1240	31	0
1	D	1306	0	1261	50	0
1	E	1299	0	1255	38	0
1	F	1306	0	1260	31	0
1	G	1299	0	1253	30	0
1	H	1286	0	1240	31	0
1	I	1306	0	1261	22	0
1	J	1299	0	1255	40	0
2	A	1	0	0	0	0
3	A	112	0	0	1	0
3	B	95	0	0	4	0
3	C	94	0	0	4	0
3	D	67	0	0	3	0
3	E	32	0	0	1	0
3	F	100	0	0	4	0
3	G	101	0	0	6	0
3	H	96	0	0	6	0
3	I	89	0	0	3	0
3	J	40	0	0	1	0
All	All	13819	0	12540	330	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 13.

The worst 5 of 330 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:B:119:ARG:HD3	3:B:2004:HOH:O	1.79	0.81
1:C:52:ASP:HB3	1:C:144:ALA:HB2	1.63	0.80
1:F:164:VAL:HG12	1:F:165:CYS:H	1.47	0.79
1:J:111:ARG:HH11	1:J:118:ASP:HA	1.50	0.77
1:F:164:VAL:HG12	1:F:165:CYS:N	2.02	0.74

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	164/186 (88%)	158 (96%)	6 (4%)	0	100	100
1	B	163/186 (88%)	154 (94%)	6 (4%)	3 (2%)	11	21
1	C	161/186 (87%)	156 (97%)	5 (3%)	0	100	100
1	D	164/186 (88%)	152 (93%)	11 (7%)	1 (1%)	30	56
1	E	163/186 (88%)	144 (88%)	14 (9%)	5 (3%)	5	8
1	F	164/186 (88%)	157 (96%)	4 (2%)	3 (2%)	11	21
1	G	163/186 (88%)	156 (96%)	6 (4%)	1 (1%)	30	56
1	H	161/186 (87%)	153 (95%)	8 (5%)	0	100	100
1	I	164/186 (88%)	156 (95%)	6 (4%)	2 (1%)	16	33
1	J	163/186 (88%)	146 (90%)	15 (9%)	2 (1%)	16	33
All	All	1630/1860 (88%)	1532 (94%)	81 (5%)	17 (1%)	19	39

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	164	VAL
1	F	165	CYS
1	G	164	VAL
1	J	164	VAL
1	B	164	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	139/154 (90%)	136 (98%)	3 (2%)	60	83
1	B	138/154 (90%)	136 (99%)	2 (1%)	74	90
1	C	136/154 (88%)	134 (98%)	2 (2%)	72	90
1	D	139/154 (90%)	135 (97%)	4 (3%)	50	77
1	E	138/154 (90%)	133 (96%)	5 (4%)	42	71
1	F	139/154 (90%)	134 (96%)	5 (4%)	42	71
1	G	138/154 (90%)	133 (96%)	5 (4%)	42	71
1	H	136/154 (88%)	132 (97%)	4 (3%)	50	77
1	I	139/154 (90%)	138 (99%)	1 (1%)	88	96
1	J	138/154 (90%)	132 (96%)	6 (4%)	35	64
All	All	1380/1540 (90%)	1343 (97%)	37 (3%)	52	79

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	4	ASN
1	F	165	CYS
1	J	87	THR
1	F	46	CYS
1	F	48	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	109	ASN
1	G	82	HIS
1	J	109	ASN
1	G	61	GLN
1	G	109	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	166/186 (89%)	-0.44	1 (0%) 90 88	18, 34, 65, 106	0
1	B	165/186 (88%)	-0.43	1 (0%) 90 88	18, 35, 62, 115	0
1	C	163/186 (87%)	-0.38	1 (0%) 90 88	21, 38, 65, 88	0
1	D	166/186 (89%)	-0.29	1 (0%) 90 88	30, 50, 73, 101	0
1	E	165/186 (88%)	-0.13	1 (0%) 90 88	36, 59, 95, 141	0
1	F	166/186 (89%)	-0.53	1 (0%) 90 88	18, 32, 62, 119	0
1	G	165/186 (88%)	-0.46	2 (1%) 81 77	21, 35, 67, 115	0
1	H	163/186 (87%)	-0.41	0 100 100	21, 40, 66, 99	0
1	I	166/186 (89%)	-0.47	1 (0%) 90 88	24, 37, 60, 99	0
1	J	165/186 (88%)	-0.23	1 (0%) 90 88	30, 48, 82, 121	0
All	All	1650/1860 (88%)	-0.38	10 (0%) 90 88	18, 41, 76, 141	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	164	VAL	3.6
1	G	165	CYS	3.5
1	F	166	PRO	3.1
1	A	166	PRO	3.0
1	I	166	PRO	2.7

### 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NA	A	6001	1/1	0.78	0.26	-	14,14,14,14	1

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

There are no such residues in this entry.