



# Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 04:54 PM GMT

PDB ID : 2BMX  
Title : MYCOBACTERIUM TUBERCULOSIS AHPC  
Authors : Guimaraes, B.G.; Alzari, P.M.  
Deposited on : 2005-03-16  
Resolution : 2.40 Å(reported)

This is a full wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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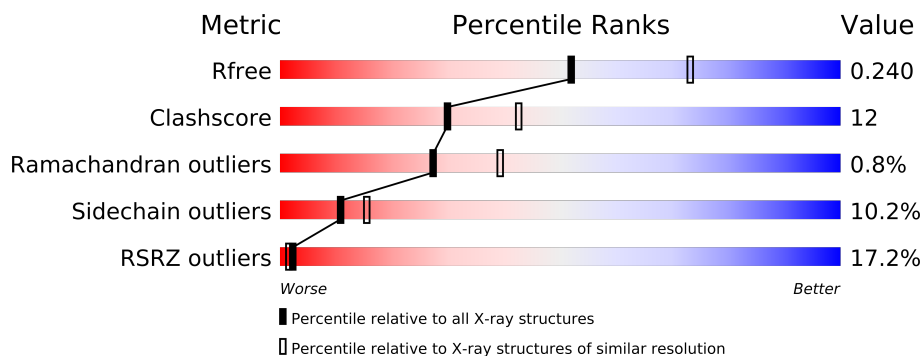
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.40 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))
$R_{free}$	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	195	
1	B	195	
1	C	195	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4247 atoms, of which 0 are hydrogen and 0 are deuterium.

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 HYDROPEROXIDASE C.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	169	Total	C	N	O	S	Se	0	0	0
			1292	829	214	247	1	1			
1	B	178	Total	C	N	O	S	Se	0	0	0
			1373	875	229	266	2	1			
1	C	169	Total	C	N	O	S	Se	0	0	0
			1298	830	215	251	1	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	176	SER	CYS	ENGINEERED MUTATION	UNP Q7BHK8

- Molecule 2 is water.

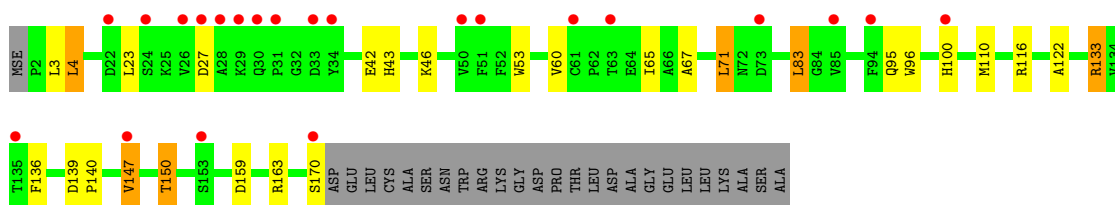
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	86	Total	O	0	0
			86	86		
2	B	95	Total	O	0	0
			95	95		
2	C	103	Total	O	0	0
			103	103		

### 3 Residue-property plots

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 ( $RSRZ > 2$ ). 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.

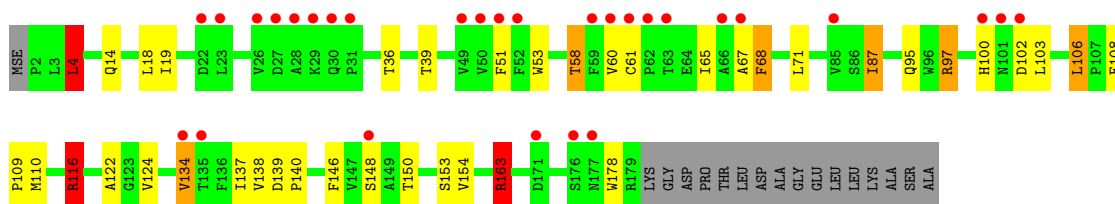
#### • Molecule 1: ALKYL HYDROPEROXIDASE C

Chain A: 



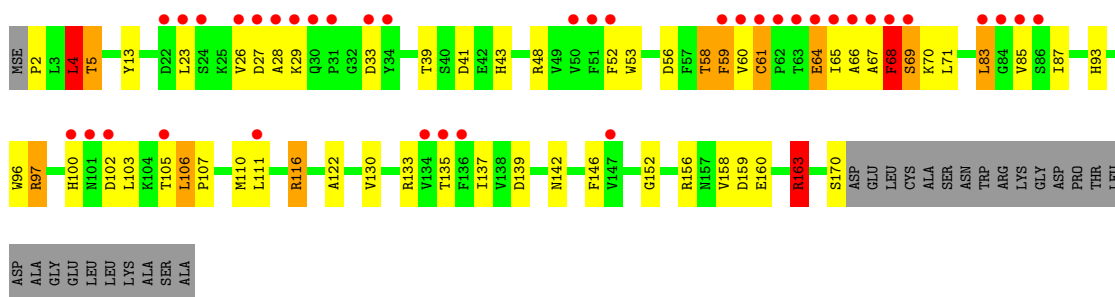
#### • Molecule 1: ALKYL HYDROPEROXIDASE C

Chain B: 



#### • Molecule 1: ALKYL HYDROPEROXIDASE C

Chain C: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 6 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	139.26Å 139.26Å 148.53Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	141.42 – 2.40 29.71 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (141.42-2.40) 100.0 (29.71-2.40)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	9.31 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.195 , 0.236 0.201 , 0.240	Depositor DCC
$R_{free}$ test set	1712 reflections (5.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	38.8	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 38.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 33794 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4247	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.94% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 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	0.85	0/1323	0.91	6/1805 (0.3%)
1	B	0.88	0/1406	1.02	7/1919 (0.4%)
1	C	0.97	2/1329 (0.2%)	0.99	6/1814 (0.3%)
All	All	0.90	2/4058 (0.0%)	0.98	19/5538 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	13	TYR	CD1-CE1	5.39	1.47	1.39
1	C	68	PHE	N-CA	5.25	1.56	1.46

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	163	ARG	NE-CZ-NH2	-11.95	114.32	120.30
1	B	116	ARG	NE-CZ-NH1	10.46	125.53	120.30
1	B	116	ARG	NE-CZ-NH2	-9.87	115.36	120.30
1	C	163	ARG	NE-CZ-NH2	-9.18	115.71	120.30
1	B	97	ARG	NE-CZ-NH2	-9.14	115.73	120.30
1	B	163	ARG	NE-CZ-NH1	8.25	124.42	120.30
1	C	163	ARG	NE-CZ-NH1	7.92	124.26	120.30
1	A	163	ARG	NE-CZ-NH2	-7.45	116.57	120.30
1	A	83	LEU	CA-CB-CG	6.71	130.73	115.30
1	A	163	ARG	NE-CZ-NH1	6.63	123.62	120.30
1	C	83	LEU	CB-CG-CD1	6.47	122.00	111.00
1	B	4	LEU	CB-CG-CD1	6.39	121.86	111.00
1	A	147	VAL	CB-CA-C	-6.34	99.35	111.40
1	C	4	LEU	CB-CG-CD1	6.17	121.50	111.00
1	B	106	LEU	CA-CB-CG	5.78	128.59	115.30
1	C	139	ASP	CB-CG-OD1	5.77	123.49	118.30
1	A	3	LEU	CB-CG-CD2	-5.43	101.77	111.00
1	C	5	THR	CB-CA-C	-5.22	97.51	111.60
1	A	83	LEU	CB-CG-CD1	5.01	119.52	111.00

There are no chirality outliers.

There are no planarity outliers.

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1292	0	1214	24	0
1	B	1373	0	1280	21	0
1	C	1298	0	1216	48	1
2	A	86	0	0	6	0
2	B	95	0	0	3	0
2	C	103	0	0	7	0
All	All	4247	0	3710	93	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 12.

All (93) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:133:ARG:NH1	1:C:152:GLY:O	1.93	1.01
1:C:87:ILE:HD12	1:C:116:ARG:HH22	1.36	0.90
1:C:39:THR:HG22	1:C:41:ASP:H	1.35	0.89
1:C:60:VAL:HB	2:C:2051:HOH:O	1.74	0.87
1:C:61:CYS:HB2	2:C:2052:HOH:O	1.77	0.83
1:C:87:ILE:HD12	1:C:116:ARG:NH2	1.97	0.79
1:C:87:ILE:CD1	1:C:116:ARG:NH2	2.46	0.78
1:C:56:ASP:OD2	1:C:93:HIS:HD2	1.73	0.71
1:A:4:LEU:HD22	1:A:122:ALA:HA	1.71	0.70
1:A:96:TRP:CD1	1:A:100:HIS:HD2	2.09	0.70
1:C:69:SER:HB2	1:C:107:PRO:HD3	1.72	0.70
1:A:133:ARG:HG3	1:A:133:ARG:NH1	2.07	0.69
1:C:87:ILE:CD1	1:C:116:ARG:HH22	2.03	0.68
1:C:59:PHE:HD2	2:C:2050:HOH:O	1.76	0.68
1:A:133:ARG:HG3	1:A:133:ARG:HH11	1.59	0.67
1:C:48:ARG:HH22	1:C:142:ASN:HD22	1.42	0.66
1:C:4:LEU:HD22	1:C:122:ALA:HA	1.77	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:150:THR:HG21	1:B:154:VAL:HB	1.79	0.65
1:C:39:THR:CG2	1:C:41:ASP:H	2.10	0.64
1:C:59:PHE:CD2	2:C:2050:HOH:O	2.50	0.64
1:B:60:VAL:HG11	1:B:65:ILE:HD11	1.80	0.63
1:A:136:PHE:CE2	1:A:147:VAL:HG13	2.33	0.63
1:C:87:ILE:HD13	1:C:116:ARG:NH2	2.14	0.62
1:C:69:SER:HB3	1:C:106:LEU:HD23	1.80	0.62
1:B:4:LEU:HD22	1:B:122:ALA:HA	1.82	0.62
1:C:96:TRP:CD1	1:C:100:HIS:HD2	2.19	0.60
1:C:69:SER:HB3	1:C:106:LEU:CD2	2.32	0.60
1:A:53:TRP:CZ2	1:A:110:MSE:HE3	2.37	0.60
1:B:58:THR:HG21	2:B:2045:HOH:O	2.02	0.59
1:A:95:GLN:HG3	2:A:2050:HOH:O	2.03	0.58
1:A:96:TRP:HD1	1:A:100:HIS:HD2	1.51	0.58
1:B:163:ARG:HG3	1:B:178:TRP:CG	2.39	0.57
1:A:43:HIS:HB3	1:A:46:LYS:CG	2.35	0.56
1:C:58:THR:HG21	2:C:2046:HOH:O	2.04	0.56
1:C:48:ARG:HH22	1:C:142:ASN:ND2	2.02	0.56
1:B:14:GLN:HG3	1:B:39:THR:HG22	1.86	0.55
1:C:53:TRP:CZ2	1:C:110:MSE:HE3	2.42	0.55
1:B:87:ILE:HG12	1:B:116:ARG:HG3	1.89	0.55
1:A:43:HIS:HB3	1:A:46:LYS:HG3	1.90	0.54
1:C:66:ALA:O	1:C:70:LYS:CB	2.56	0.54
1:C:69:SER:CB	1:C:106:LEU:HD23	2.38	0.54
1:C:69:SER:CB	1:C:106:LEU:CD2	2.86	0.53
1:B:137:ILE:HB	1:B:146:PHE:HB3	1.90	0.53
1:C:61:CYS:SG	1:C:64:GLU:HG2	2.49	0.52
1:B:87:ILE:HG12	1:B:116:ARG:CG	2.39	0.52
1:C:39:THR:HG22	1:C:41:ASP:N	2.16	0.52
1:C:96:TRP:CD1	1:C:100:HIS:CD2	2.97	0.52
1:C:68:PHE:HA	1:C:158:VAL:HG11	1.91	0.52
1:C:43:HIS:HD2	2:C:2028:HOH:O	1.94	0.51
1:C:97:ARG:HD2	1:C:103:LEU:O	2.11	0.50
1:C:67:ALA:O	1:C:71:LEU:N	2.31	0.50
1:A:133:ARG:CG	1:A:133:ARG:NH1	2.74	0.50
1:C:96:TRP:NE1	1:C:100:HIS:HD2	2.10	0.49
1:A:67:ALA:O	1:A:71:LEU:HB2	2.13	0.49
1:A:60:VAL:HG11	1:A:65:ILE:HD11	1.95	0.48
1:C:64:GLU:O	1:C:68:PHE:N	2.46	0.47
1:A:136:PHE:CD2	1:A:147:VAL:HG13	2.49	0.46
1:B:146:PHE:CZ	1:B:148:SER:HB2	2.50	0.46
1:A:42:GLU:HG2	2:A:2026:HOH:O	2.14	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:150:THR:HG21	2:A:2075:HOH:O	2.17	0.45
1:B:124:VAL:HG22	1:B:134:VAL:HG11	1.99	0.45
1:C:93:HIS:HE1	1:C:111:LEU:O	2.00	0.45
1:B:53:TRP:CZ2	1:B:110:MSE:HE3	2.52	0.45
1:C:96:TRP:NE1	1:C:100:HIS:CD2	2.85	0.44
1:A:150:THR:HG23	2:A:2073:HOH:O	2.16	0.44
1:C:160:GLU:OE2	1:C:163:ARG:NH1	2.51	0.44
1:B:87:ILE:CG1	1:B:116:ARG:HG3	2.47	0.44
1:C:135:THR:OG1	1:C:156:ARG:HD3	2.18	0.44
1:A:139:ASP:HB2	1:A:140:PRO:CD	2.48	0.43
1:A:139:ASP:HB2	1:A:140:PRO:HD2	1.99	0.43
1:B:67:ALA:O	1:B:71:LEU:HB2	2.19	0.43
1:C:48:ARG:NH2	1:C:142:ASN:HD22	2.14	0.42
1:A:150:THR:CG2	2:A:2073:HOH:O	2.66	0.42
1:C:93:HIS:CD2	1:C:110:MSE:HE2	2.54	0.42
1:C:69:SER:HB2	1:C:107:PRO:CD	2.47	0.42
1:B:95:GLN:NE2	2:B:2057:HOH:O	2.53	0.42
1:C:53:TRP:HZ2	1:C:110:MSE:HE3	1.84	0.42
1:A:43:HIS:HB3	1:A:46:LYS:HG2	2.02	0.41
1:B:116:ARG:NH2	2:B:2065:HOH:O	2.51	0.41
1:C:67:ALA:O	1:C:68:PHE:C	2.58	0.41
1:A:96:TRP:HD1	1:A:100:HIS:CD2	2.33	0.41
1:A:116:ARG:NH2	2:A:2056:HOH:O	2.51	0.41
1:C:43:HIS:CD2	2:C:2028:HOH:O	2.72	0.41
1:C:137:ILE:HB	1:C:146:PHE:HB3	2.02	0.41
1:B:18:LEU:HD23	1:B:97:ARG:HD3	2.03	0.41
1:B:108:PHE:HB2	1:B:109:PRO:CD	2.50	0.41
1:B:100:HIS:CD2	1:B:103:LEU:HD12	2.56	0.41
1:C:52:PHE:HA	1:C:85:VAL:O	2.21	0.41
1:B:51:PHE:CE1	1:B:68:PHE:HE1	2.38	0.41
1:B:139:ASP:HB2	1:B:140:PRO:CD	2.51	0.40
1:C:87:ILE:HD11	1:C:130:VAL:HG12	2.03	0.40
1:A:96:TRP:HE3	1:A:110:MSE:HE1	1.86	0.40
1:C:27:ASP:O	1:C:29:LYS:N	2.50	0.40

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	Distance(Å)	Clash(Å)
1:C:116:ARG:NH1	1:C:116:ARG:NH2[12_556]	1.95	0.25

## 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	167/195 (86%)	160 (96%)	6 (4%)	1 (1%)	33	47
1	B	176/195 (90%)	166 (94%)	9 (5%)	1 (1%)	33	47
1	C	167/195 (86%)	154 (92%)	11 (7%)	2 (1%)	19	26
All	All	510/585 (87%)	480 (94%)	26 (5%)	4 (1%)	27	39

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	68	PHE
1	C	28	ALA
1	A	27	ASP
1	C	26	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	133/162 (82%)	125 (94%)	8 (6%)	27	41
1	B	143/162 (88%)	130 (91%)	13 (9%)	14	20
1	C	135/162 (83%)	114 (84%)	21 (16%)	4	4
All	All	411/486 (85%)	369 (90%)	42 (10%)	11	15

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	23	LEU

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Mol	Chain	Res	Type
1	A	71	LEU
1	A	83	LEU
1	A	133	ARG
1	A	150	THR
1	A	159	ASP
1	A	170	SER
1	B	4	LEU
1	B	19	ILE
1	B	36	THR
1	B	58	THR
1	B	61	CYS
1	B	87	ILE
1	B	102	ASP
1	B	106	LEU
1	B	116	ARG
1	B	134	VAL
1	B	138	VAL
1	B	153	SER
1	B	163	ARG
1	C	2	PRO
1	C	4	LEU
1	C	5	THR
1	C	23	LEU
1	C	33	ASP
1	C	58	THR
1	C	59	PHE
1	C	61	CYS
1	C	64	GLU
1	C	65	ILE
1	C	68	PHE
1	C	69	SER
1	C	83	LEU
1	C	97	ARG
1	C	102	ASP
1	C	105	THR
1	C	106	LEU
1	C	116	ARG
1	C	159	ASP
1	C	163	ARG
1	C	170	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	100	HIS
1	B	43	HIS
1	B	100	HIS
1	C	43	HIS
1	C	93	HIS
1	C	100	HIS
1	C	142	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	169/195 (86%)	0.54	22 (13%) 4 4	28, 39, 52, 59	0
1	B	178/195 (91%)	0.70	29 (16%) 2 2	27, 38, 58, 64	0
1	C	169/195 (86%)	0.98	38 (22%) 1 1	24, 39, 60, 64	0
All	All	516/585 (88%)	0.74	89 (17%) 2 1	24, 39, 57, 64	0

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	28	ALA	8.2
1	C	63	THR	6.5
1	C	59	PHE	6.0
1	B	28	ALA	5.9
1	C	61	CYS	5.6
1	C	26	VAL	5.6
1	B	62	PRO	5.4
1	B	61	CYS	5.4
1	C	33	ASP	5.1
1	C	31	PRO	5.0
1	A	31	PRO	4.8
1	A	29	LYS	4.8
1	C	67	ALA	4.6
1	B	63	THR	4.5
1	C	27	ASP	4.5
1	C	62	PRO	4.5
1	C	24	SER	4.2
1	A	61	CYS	4.2
1	B	100	HIS	4.2
1	C	101	ASN	4.2
1	A	27	ASP	4.1
1	C	23	LEU	4.0
1	A	28	ALA	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	22	ASP	3.9
1	B	50	VAL	3.9
1	B	59	PHE	3.8
1	C	69	SER	3.7
1	B	60	VAL	3.6
1	C	60	VAL	3.5
1	C	29	LYS	3.4
1	B	177	ASN	3.3
1	C	34	TYR	3.3
1	C	135	THR	3.2
1	A	63	THR	3.1
1	B	67	ALA	3.1
1	C	51	PHE	3.1
1	C	136	PHE	3.0
1	B	102	ASP	3.0
1	A	135	THR	3.0
1	C	50	VAL	3.0
1	B	135	THR	2.9
1	B	31	PRO	2.9
1	B	26	VAL	2.9
1	C	30	GLN	2.9
1	C	52	PHE	2.8
1	A	51	PHE	2.8
1	B	51	PHE	2.8
1	C	85	VAL	2.7
1	B	171	ASP	2.7
1	C	22	ASP	2.6
1	C	100	HIS	2.6
1	A	100	HIS	2.6
1	A	34	TYR	2.6
1	A	33	ASP	2.6
1	A	26	VAL	2.6
1	C	105	THR	2.6
1	C	65	ILE	2.6
1	B	85	VAL	2.5
1	A	73	ASP	2.5
1	B	27	ASP	2.5
1	C	134	VAL	2.5
1	C	147	VAL	2.5
1	A	147	VAL	2.4
1	B	49	VAL	2.4
1	A	50	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	30	GLN	2.4
1	C	66	ALA	2.4
1	C	84	GLY	2.4
1	C	102	ASP	2.4
1	B	101	ASN	2.3
1	B	66	ALA	2.3
1	B	29	LYS	2.3
1	B	134	VAL	2.3
1	B	52	PHE	2.3
1	B	176	SER	2.3
1	A	24	SER	2.2
1	C	83	LEU	2.2
1	C	64	GLU	2.2
1	B	148	SER	2.2
1	B	22	ASP	2.2
1	A	153	SER	2.2
1	A	170	SER	2.2
1	B	23	LEU	2.1
1	C	68	PHE	2.1
1	C	111	LEU	2.1
1	A	85	VAL	2.1
1	C	86	SER	2.1
1	B	30	GLN	2.0
1	A	94	PHE	2.0

## 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 ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.