



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:48 AM GMT

PDB ID : 3Q1T  
Title : Crystal structure of enoyl-coA hydratase from Mycobacterium avium  
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)  
Deposited on : 2010-12-17  
Resolution : 2.35 Å(reported)

This is a Full wwPDB X-ray Structure 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/validation/2016/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 : 1.7 (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

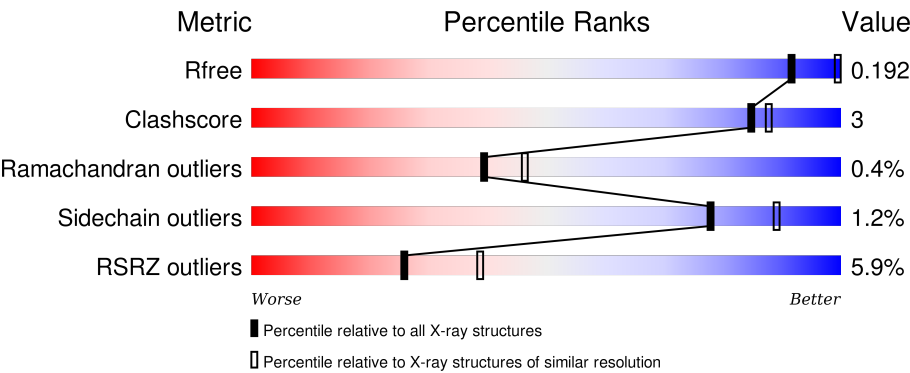
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.35 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 <sub>free</sub>	91344	1352 (2.38-2.34)
Clashscore	102246	1456 (2.38-2.34)
Ramachandran outliers	100387	1435 (2.38-2.34)
Sidechain outliers	100360	1436 (2.38-2.34)
RSRZ outliers	91569	1358 (2.38-2.34)

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 >=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 <=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	278	<div><div>6%</div><div>85%6%9%</div></div>
1	B	278	<div><div>4%</div><div>83%6%10%</div></div>
1	C	278	<div><div>6%</div><div>87%8%</div></div>
1	D	278	<div><div>5%</div><div>87%6%6%</div></div>
1	E	278	<div><div>5%</div><div>82%8%9%</div></div>

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Mol	Chain	Length	Quality of chain
1	F	278	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: a red segment at the beginning labeled '6%', a long green segment in the middle labeled '90%', and a small yellow segment at the end labeled '7%'. The total length of the bar represents 100%.

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11681 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 Enoyl-CoA hydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	253	Total	C	N	O	S	0	0	0
			1873	1179	325	358	11			
1	B	251	Total	C	N	O	S	0	0	0
			1846	1158	322	355	11			
1	C	257	Total	C	N	O	S	0	0	0
			1900	1197	330	362	11			
1	D	261	Total	C	N	O	S	0	2	0
			1942	1220	340	371	11			
1	E	252	Total	C	N	O	S	0	0	0
			1851	1163	321	356	11			
1	F	259	Total	C	N	O	S	0	1	0
			1921	1206	337	367	11			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	EXPRESSION TAG	UNP A0QIL3
A	-2	PRO	-	EXPRESSION TAG	UNP A0QIL3
A	-1	GLY	-	EXPRESSION TAG	UNP A0QIL3
A	0	SER	-	EXPRESSION TAG	UNP A0QIL3
A	1	MET	-	EXPRESSION TAG	UNP A0QIL3
A	2	VAL	-	EXPRESSION TAG	UNP A0QIL3
A	92	ILE	VAL	CONFLICT	UNP A0QIL3
A	232	MET	THR	CONFLICT	UNP A0QIL3
B	-3	GLY	-	EXPRESSION TAG	UNP A0QIL3
B	-2	PRO	-	EXPRESSION TAG	UNP A0QIL3
B	-1	GLY	-	EXPRESSION TAG	UNP A0QIL3
B	0	SER	-	EXPRESSION TAG	UNP A0QIL3
B	1	MET	-	EXPRESSION TAG	UNP A0QIL3
B	2	VAL	-	EXPRESSION TAG	UNP A0QIL3
B	92	ILE	VAL	CONFLICT	UNP A0QIL3
B	232	MET	THR	CONFLICT	UNP A0QIL3
C	-3	GLY	-	EXPRESSION TAG	UNP A0QIL3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	PRO	-	EXPRESSION TAG	UNP A0QIL3
C	-1	GLY	-	EXPRESSION TAG	UNP A0QIL3
C	0	SER	-	EXPRESSION TAG	UNP A0QIL3
C	1	MET	-	EXPRESSION TAG	UNP A0QIL3
C	2	VAL	-	EXPRESSION TAG	UNP A0QIL3
C	92	ILE	VAL	CONFLICT	UNP A0QIL3
C	232	MET	THR	CONFLICT	UNP A0QIL3
D	-3	GLY	-	EXPRESSION TAG	UNP A0QIL3
D	-2	PRO	-	EXPRESSION TAG	UNP A0QIL3
D	-1	GLY	-	EXPRESSION TAG	UNP A0QIL3
D	0	SER	-	EXPRESSION TAG	UNP A0QIL3
D	1	MET	-	EXPRESSION TAG	UNP A0QIL3
D	2	VAL	-	EXPRESSION TAG	UNP A0QIL3
D	92	ILE	VAL	CONFLICT	UNP A0QIL3
D	232	MET	THR	CONFLICT	UNP A0QIL3
E	-3	GLY	-	EXPRESSION TAG	UNP A0QIL3
E	-2	PRO	-	EXPRESSION TAG	UNP A0QIL3
E	-1	GLY	-	EXPRESSION TAG	UNP A0QIL3
E	0	SER	-	EXPRESSION TAG	UNP A0QIL3
E	1	MET	-	EXPRESSION TAG	UNP A0QIL3
E	2	VAL	-	EXPRESSION TAG	UNP A0QIL3
E	92	ILE	VAL	CONFLICT	UNP A0QIL3
E	232	MET	THR	CONFLICT	UNP A0QIL3
F	-3	GLY	-	EXPRESSION TAG	UNP A0QIL3
F	-2	PRO	-	EXPRESSION TAG	UNP A0QIL3
F	-1	GLY	-	EXPRESSION TAG	UNP A0QIL3
F	0	SER	-	EXPRESSION TAG	UNP A0QIL3
F	1	MET	-	EXPRESSION TAG	UNP A0QIL3
F	2	VAL	-	EXPRESSION TAG	UNP A0QIL3
F	92	ILE	VAL	CONFLICT	UNP A0QIL3
F	232	MET	THR	CONFLICT	UNP A0QIL3

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	52	Total O 52 52	0	0
2	B	79	Total O 79 79	0	0
2	C	71	Total O 71 71	0	0
2	D	63	Total O 63 63	0	0

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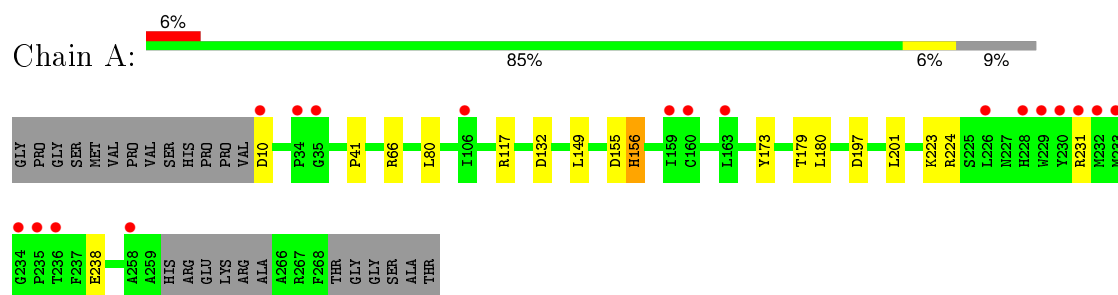
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	E	37	Total	O	0	0
			37	37		
2	F	46	Total	O	0	0
			46	46		

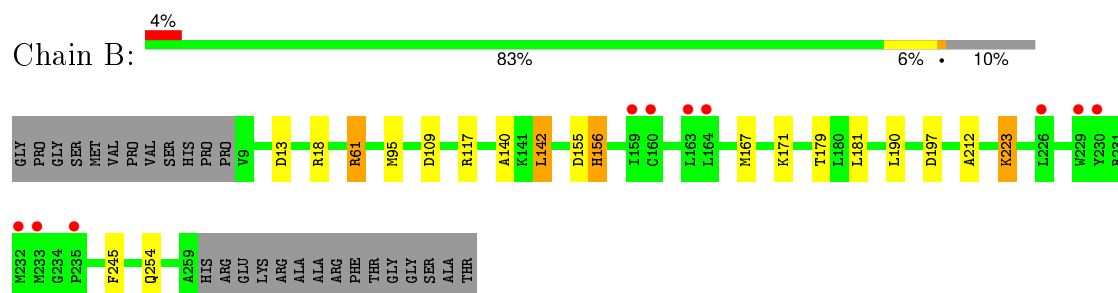
### 3 Residue-property plots [i](#)

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 ( $RSRZ > 2$ ). 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.

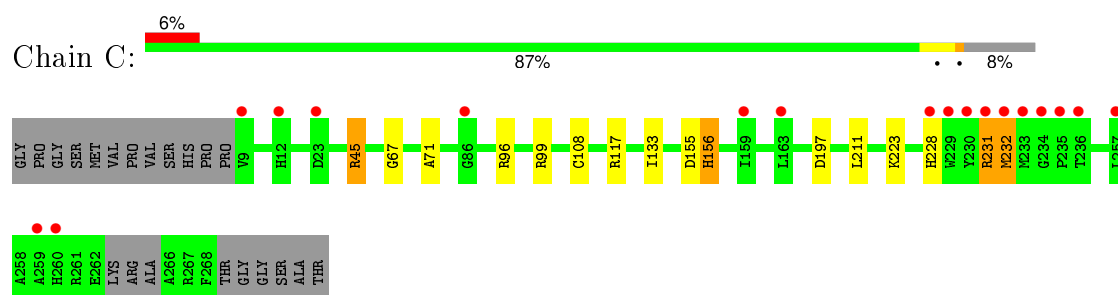
- Molecule 1: Enoyl-CoA hydratase



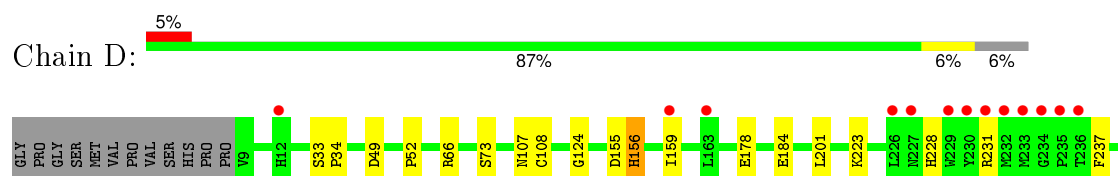
- Molecule 1: Enoyl-CoA hydratase



- Molecule 1: Enoyl-CoA hydratase

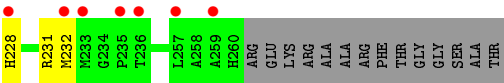
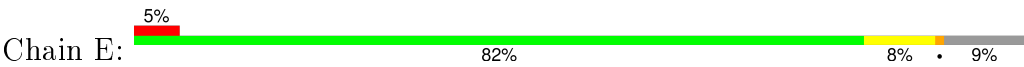


- Molecule 1: Enoyl-CoA hydratase

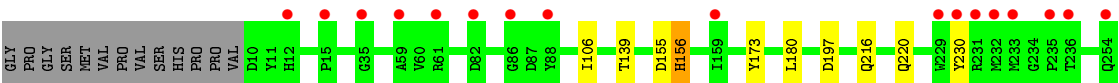
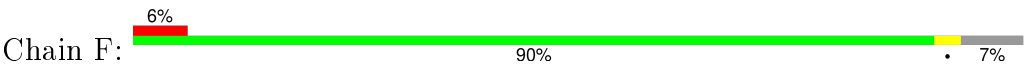




● Molecule 1: Enoyl-CoA hydratase



● Molecule 1: Enoyl-CoA hydratase





## 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, $\alpha$ , $\beta$ , $\gamma$	124.92Å 136.89Å 104.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.35 48.77 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.2 (50.00-2.35) 99.2 (48.77-2.35)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.83 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.189 , 0.227 0.190 , 0.192	Depositor DCC
$R_{free}$ test set	3756 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	39.4	Xtriage
Anisotropy	0.151	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 38.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 74523 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	11681	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.92% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.64	0/1907	0.71	0/2593
1	B	0.67	0/1880	0.71	0/2561
1	C	0.65	0/1934	0.73	1/2629 (0.0%)
1	D	0.66	0/1984	0.71	0/2699
1	E	0.64	0/1884	0.69	0/2567
1	F	0.63	0/1959	0.67	0/2665
All	All	0.65	0/11548	0.70	1/15714 (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	C	231	ARG	NE-CZ-NH2	5.62	123.11	120.30

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	1873	0	1838	10	0
1	B	1846	0	1796	9	0
1	C	1900	0	1866	15	0
1	D	1942	0	1899	14	0
1	E	1851	0	1809	14	0
1	F	1921	0	1877	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	52	0	0	2	0
2	B	79	0	0	1	0
2	C	71	0	0	1	0
2	D	63	0	0	1	0
2	E	37	0	0	1	0
2	F	46	0	0	0	0
All	All	11681	0	11085	65	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 3.

All (65) 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:108:CYS:O	1:C:223:LYS:HE2	1.85	0.77
1:A:155:ASP:O	1:A:156:HIS:HB3	1.92	0.69
1:A:238:GLU:OE2	1:C:231:ARG:NH1	2.29	0.64
1:C:96:ARG:NH2	2:C:325:HOH:O	2.34	0.61
1:C:228:HIS:HE1	1:C:231:ARG:NH1	1.99	0.61
1:C:228:HIS:CE1	1:C:231:ARG:HH11	2.19	0.60
1:B:18:ARG:NH2	2:B:333:HOH:O	2.37	0.58
1:C:155:ASP:O	1:C:156:HIS:HB3	2.04	0.56
1:E:9:VAL:HG22	1:E:10:ASP:H	1.72	0.55
1:A:224:ARG:NH2	1:C:99:ARG:HD2	2.21	0.55
1:E:37:ASN:ND2	1:E:71:ALA:O	2.39	0.55
1:C:228:HIS:CE1	1:C:231:ARG:NH1	2.76	0.54
1:E:66:ARG:HD3	1:E:201:LEU:HD11	1.91	0.53
1:F:139:THR:OG1	1:F:197:ASP:OD2	2.26	0.52
1:C:117:ARG:NE	1:C:197:ASP:HB3	2.25	0.52
1:F:155:ASP:O	1:F:156:HIS:HB3	2.10	0.51
1:C:228:HIS:HE1	1:C:231:ARG:HH11	1.54	0.51
1:E:108:CYS:O	1:E:223:LYS:HE2	2.11	0.51
1:D:228:HIS:HE1	1:D:231[B]:ARG:NH2	2.10	0.50
1:B:117:ARG:NH1	1:B:197:ASP:HB3	2.27	0.50
1:A:231:ARG:NH2	2:A:294:HOH:O	2.45	0.49
1:A:173:TYR:CZ	1:A:180:LEU:HD13	2.48	0.48
1:D:66:ARG:CD	1:D:201:LEU:HD11	2.43	0.48
1:D:66:ARG:HD2	1:D:201:LEU:HD11	1.94	0.48
1:E:61:ARG:HH21	1:E:213:GLN:NE2	2.11	0.48
1:D:228:HIS:CE1	1:D:231[B]:ARG:NH2	2.82	0.48
1:D:108:CYS:O	1:D:223:LYS:HE2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:142:LEU:HD12	1:B:190:LEU:HD23	1.96	0.47
1:E:231:ARG:NH2	2:E:291:HOH:O	2.48	0.47
2:A:287:HOH:O	1:C:232:MET:HB2	2.15	0.46
1:A:132:ASP:OD1	1:A:223:LYS:HE3	2.17	0.45
1:D:73:SER:HB3	1:D:124:GLY:HA3	1.99	0.45
1:E:61:ARG:HH21	1:E:213:GLN:HE22	1.65	0.45
1:C:67:GLY:HA3	1:C:71:ALA:O	2.16	0.45
1:C:133:ILE:HD12	1:C:211:LEU:HD11	1.97	0.45
1:B:167:MET:HG3	1:B:171:LYS:HD2	1.99	0.45
1:E:167:MET:O	1:E:171:LYS:HG3	2.17	0.45
1:E:228:HIS:ND1	1:E:231:ARG:NH1	2.65	0.44
1:D:231[A]:ARG:NH2	2:D:311:HOH:O	2.43	0.44
1:D:159:ILE:HB	1:D:237:PHE:HB2	1.98	0.44
1:B:95:MET:HG3	1:B:245:PHE:CD2	2.52	0.44
1:D:228:HIS:CE1	1:D:231[B]:ARG:HH21	2.35	0.44
1:A:66:ARG:HD3	1:A:201:LEU:HD11	2.00	0.43
1:E:33:SER:HB2	1:E:34:PRO:CD	2.48	0.43
1:A:117:ARG:HE	1:A:197:ASP:HB3	1.83	0.43
1:D:33:SER:HB2	1:D:34:PRO:HD2	2.01	0.43
1:F:106:ILE:HD12	1:F:230:TYR:HD2	1.83	0.43
1:C:45:ARG:HD3	1:C:45:ARG:C	2.39	0.43
1:D:49:ASP:O	1:D:52:PRO:HD2	2.19	0.43
1:B:155:ASP:O	1:B:156:HIS:HB3	2.18	0.43
1:E:183:GLU:HA	1:E:194:CYS:SG	2.59	0.42
1:E:126:VAL:HG22	1:E:156:HIS:HB3	2.00	0.42
1:D:184:GLU:OE1	1:D:184:GLU:HA	2.18	0.42
1:E:167:MET:HG3	1:E:171:LYS:HD2	2.02	0.42
1:F:173:TYR:CZ	1:F:180:LEU:HD13	2.55	0.42
1:F:216:GLN:O	1:F:220:GLN:HG3	2.18	0.42
1:D:107:ASN:HA	1:D:231[A]:ARG:HH21	1.85	0.42
1:A:149:LEU:O	1:A:149:LEU:HG	2.20	0.42
1:B:140:ALA:O	1:B:181:LEU:HA	2.20	0.41
1:E:73:SER:HB3	1:E:124:GLY:HA3	2.03	0.41
1:A:41:PRO:HA	1:A:80:LEU:HD13	2.02	0.41
1:B:109:ASP:O	1:B:223:LYS:HD3	2.21	0.41
1:D:155:ASP:O	1:D:156:HIS:HB3	2.21	0.41
1:C:117:ARG:HE	1:C:197:ASP:HB3	1.85	0.40
1:B:61:ARG:HD3	1:B:212:ALA:O	2.21	0.40

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	249/278 (90%)	241 (97%)	7 (3%)	1 (0%)	39	46
1	B	249/278 (90%)	245 (98%)	3 (1%)	1 (0%)	39	46
1	C	253/278 (91%)	247 (98%)	5 (2%)	1 (0%)	39	46
1	D	261/278 (94%)	253 (97%)	7 (3%)	1 (0%)	39	46
1	E	250/278 (90%)	242 (97%)	7 (3%)	1 (0%)	39	46
1	F	258/278 (93%)	252 (98%)	5 (2%)	1 (0%)	39	46
All	All	1520/1668 (91%)	1480 (97%)	34 (2%)	6 (0%)	39	46

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	156	HIS
1	C	156	HIS
1	D	156	HIS
1	F	156	HIS
1	B	156	HIS
1	E	156	HIS

### 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	193/217 (89%)	191 (99%)	2 (1%)	82	91
1	B	189/217 (87%)	183 (97%)	6 (3%)	46	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	195/217 (90%)	193 (99%)	2 (1%)	82	91
1	D	199/217 (92%)	198 (100%)	1 (0%)	92	97
1	E	190/217 (88%)	187 (98%)	3 (2%)	70	83
1	F	196/217 (90%)	196 (100%)	0	100	100
All	All	1162/1302 (89%)	1148 (99%)	14 (1%)	78	89

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ASP
1	A	179	THR
1	B	13	ASP
1	B	61	ARG
1	B	142	LEU
1	B	179	THR
1	B	223	LYS
1	B	254	GLN
1	C	45	ARG
1	C	232	MET
1	D	178	GLU
1	E	201	LEU
1	E	216	GLN
1	E	232	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	228	HIS
1	D	103	HIS
1	E	213	GLN
1	E	216	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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 ⓘ

### 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	253/278 (91%)	0.24	18 (7%)	19 28	22, 39, 56, 65	0
1	B	251/278 (90%)	0.13	10 (3%)	42 56	20, 34, 52, 66	0
1	C	257/278 (92%)	0.23	18 (7%)	19 29	22, 35, 54, 79	0
1	D	261/278 (93%)	0.12	14 (5%)	29 44	21, 35, 51, 68	0
1	E	252/278 (90%)	0.29	13 (5%)	31 46	24, 41, 59, 75	0
1	F	259/278 (93%)	0.30	18 (6%)	20 30	22, 41, 60, 73	0
All	All	1533/1668 (91%)	0.22	91 (5%)	26 39	20, 37, 57, 79	0

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	232	MET	4.5
1	C	9	VAL	4.3
1	E	9	VAL	4.1
1	F	12	HIS	4.1
1	F	35	GLY	4.0
1	C	232	MET	3.9
1	D	232	MET	3.7
1	C	260	HIS	3.7
1	F	232	MET	3.7
1	A	10	ASP	3.6
1	C	86	GLY	3.5
1	B	229	TRP	3.5
1	D	233	MET	3.4
1	F	231[A]	ARG	3.3
1	B	232	MET	3.2
1	F	229	TRP	3.2
1	C	233	MET	3.2
1	C	12	HIS	3.2
1	C	257	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	229	TRP	3.1
1	B	163	LEU	3.1
1	B	160	CYS	3.1
1	D	269	THR	3.0
1	A	235	PRO	3.0
1	E	198	ASP	3.0
1	C	23	ASP	3.0
1	D	226	LEU	2.9
1	D	231[A]	ARG	2.9
1	A	226	LEU	2.9
1	C	163	LEU	2.9
1	C	229	TRP	2.8
1	D	229	TRP	2.8
1	B	233	MET	2.8
1	C	235	PRO	2.8
1	E	235	PRO	2.8
1	E	257	LEU	2.8
1	F	233	MET	2.7
1	D	235	PRO	2.7
1	E	23	ASP	2.7
1	A	236	THR	2.7
1	A	159	ILE	2.7
1	B	159	ILE	2.7
1	A	233	MET	2.7
1	E	259	ALA	2.7
1	A	34	PRO	2.7
1	E	233	MET	2.6
1	F	159	ILE	2.6
1	E	236	THR	2.6
1	A	35	GLY	2.6
1	F	15	PRO	2.6
1	F	59	ALA	2.5
1	F	82	ASP	2.5
1	A	160	CYS	2.5
1	F	86	GLY	2.5
1	B	235	PRO	2.4
1	D	236	THR	2.4
1	E	159	ILE	2.4
1	A	230	TYR	2.4
1	E	10	ASP	2.4
1	F	265	ALA	2.4
1	E	232	MET	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	228	HIS	2.3
1	C	228	HIS	2.3
1	A	231	ARG	2.3
1	A	258	ALA	2.3
1	E	162	PRO	2.3
1	A	106	ILE	2.3
1	C	230	TYR	2.3
1	F	254	GLN	2.3
1	C	159	ILE	2.2
1	B	230	TYR	2.2
1	E	228	HIS	2.2
1	D	234	GLY	2.2
1	C	259	ALA	2.2
1	C	234	GLY	2.2
1	F	235	PRO	2.2
1	C	236	THR	2.2
1	A	234	GLY	2.2
1	D	230	TYR	2.2
1	C	231	ARG	2.1
1	D	159	ILE	2.1
1	F	236	THR	2.1
1	A	163	LEU	2.1
1	B	226	LEU	2.1
1	D	163	LEU	2.1
1	F	88	TYR	2.1
1	F	230	TYR	2.1
1	D	227	ASN	2.0
1	D	12	HIS	2.0
1	F	61	ARG	2.0
1	B	164	LEU	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 [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.