



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 03:25 am BST

PDB ID : 5O81  
Title : Crystal Structure of R67A/E173A Mutant of alpha-L-arabinofuranosidase Ara51 from Clostridium thermocellum  
Authors : Lafite, P.; Daniellou, R.  
Deposited on : 2017-06-12  
Resolution : 2.50 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

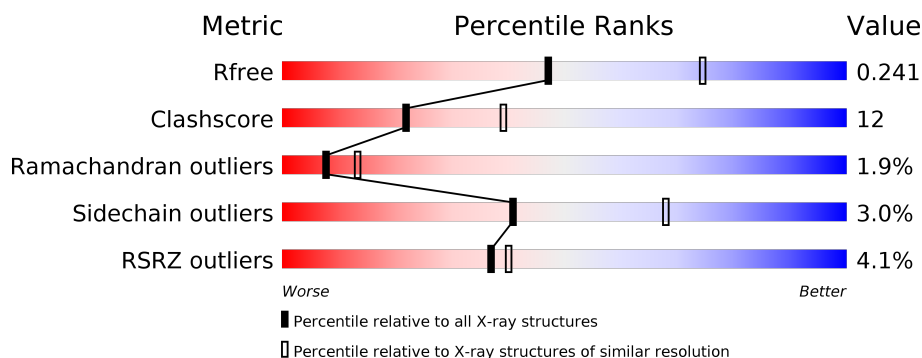
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	501	<div> <div>6%</div> <div> <div></div> <div>73%</div> <div>23%</div> <div>..</div> </div> </div>
1	B	501	<div> <div>4%</div> <div> <div></div> <div>74%</div> <div>23%</div> <div>..</div> </div> </div>
1	C	501	<div> <div>3%</div> <div> <div></div> <div>74%</div> <div>23%</div> <div>..</div> </div> </div>
1	D	501	<div> <div>4%</div> <div> <div></div> <div>71%</div> <div>26%</div> <div>..</div> </div> </div>
1	E	501	<div> <div>4%</div> <div> <div></div> <div>78%</div> <div>20%</div> <div>..</div> </div> </div>
1	F	501	<div> <div>3%</div> <div> <div></div> <div>77%</div> <div>20%</div> <div>..</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 23743 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 Intracellular exo-alpha-(1->5)-L-arabinofuranosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	496	Total	C	N	O	S	0	0	0
			3961	2518	673	748	22			
1	B	496	Total	C	N	O	S	0	0	0
			3953	2515	670	746	22			
1	C	496	Total	C	N	O	S	0	0	0
			3950	2508	673	747	22			
1	D	495	Total	C	N	O	S	0	0	0
			3950	2509	670	749	22			
1	E	496	Total	C	N	O	S	0	0	0
			3955	2513	672	748	22			
1	F	496	Total	C	N	O	S	0	0	0
			3941	2503	670	746	22			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	67	ALA	ARG	engineered mutation	UNP A3DIH0
A	173	ALA	GLU	engineered mutation	UNP A3DIH0
B	67	ALA	ARG	engineered mutation	UNP A3DIH0
B	173	ALA	GLU	engineered mutation	UNP A3DIH0
C	67	ALA	ARG	engineered mutation	UNP A3DIH0
C	173	ALA	GLU	engineered mutation	UNP A3DIH0
D	67	ALA	ARG	engineered mutation	UNP A3DIH0
D	173	ALA	GLU	engineered mutation	UNP A3DIH0
E	67	ALA	ARG	engineered mutation	UNP A3DIH0
E	173	ALA	GLU	engineered mutation	UNP A3DIH0
F	67	ALA	ARG	engineered mutation	UNP A3DIH0
F	173	ALA	GLU	engineered mutation	UNP A3DIH0

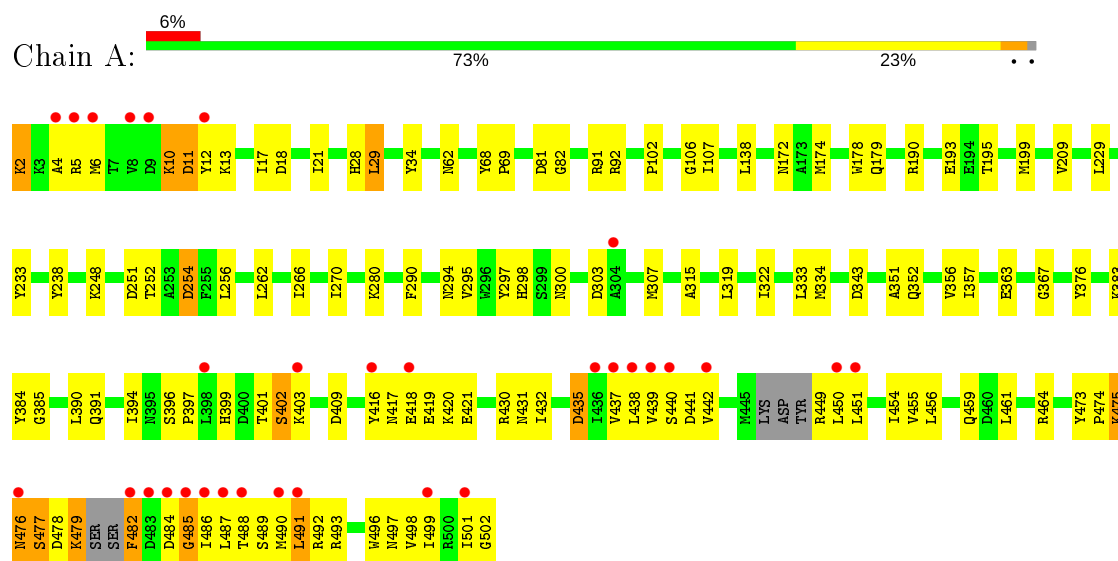
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	7	Total 7	O 7	0	0
2	B	3	Total 3	O 3	0	0
2	C	5	Total 5	O 5	0	0
2	D	9	Total 9	O 9	0	0
2	E	6	Total 6	O 6	0	0
2	F	3	Total 3	O 3	0	0

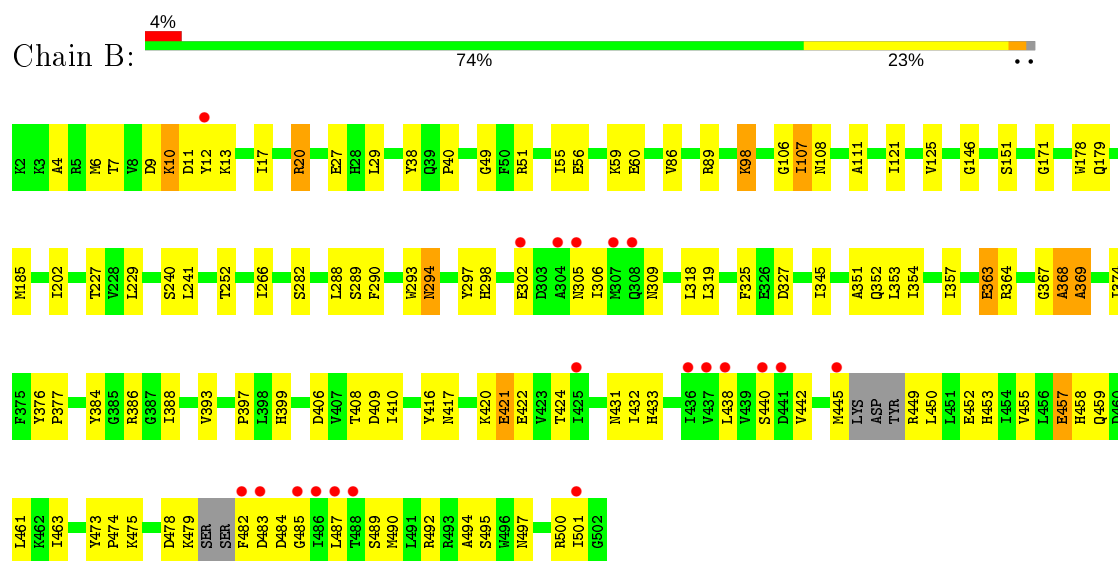
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

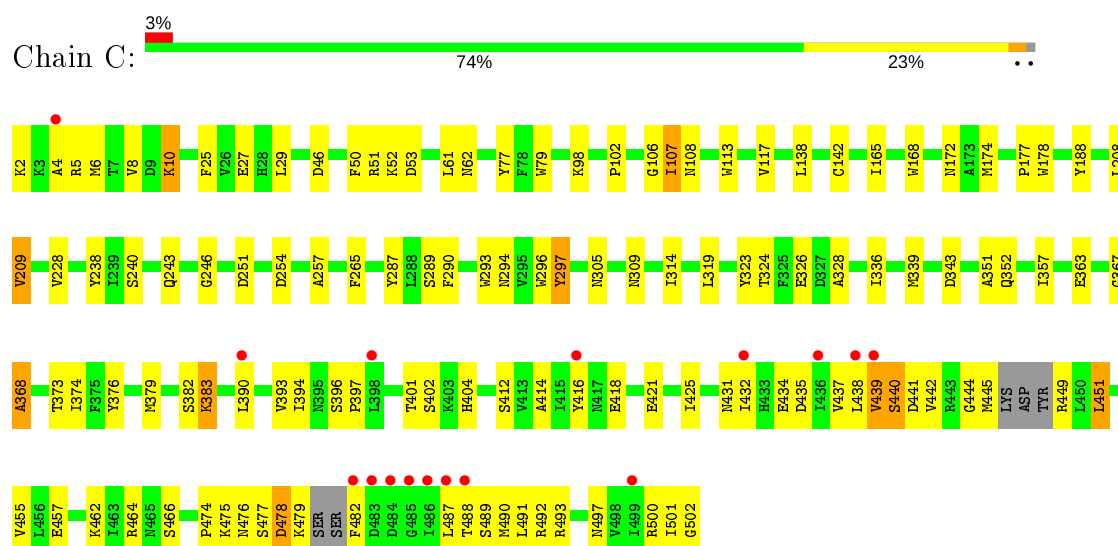
- Molecule 1: Intracellular exo-alpha-(1->5)-L-arabinofuranosidase



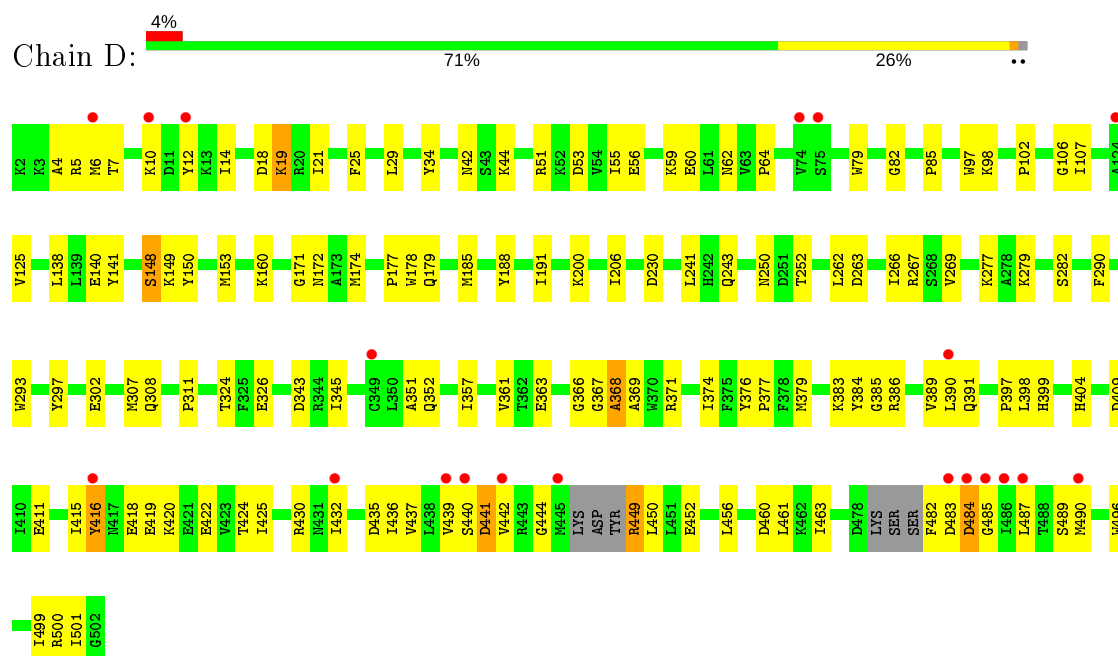
- Molecule 1: Intracellular exo-alpha-(1->5)-L-arabinofuranosidase



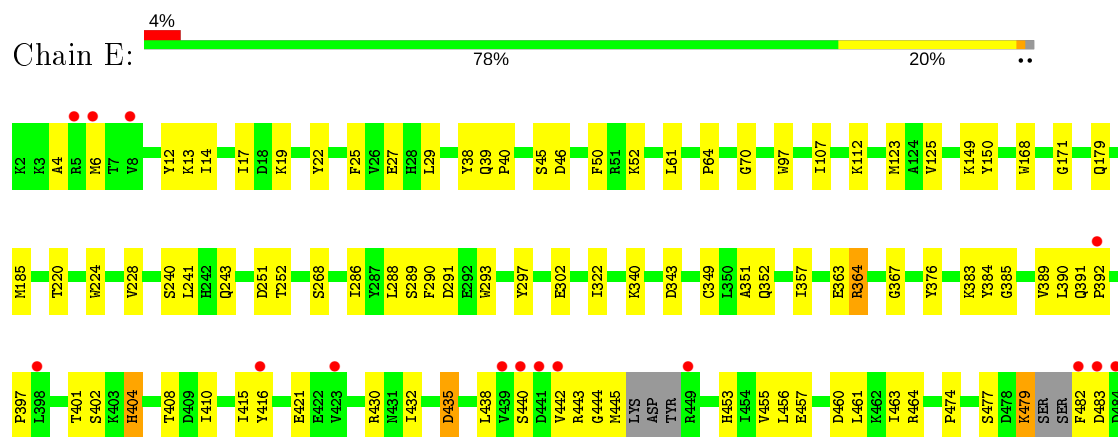
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• Molecule 1: Intracellular exo-alpha-(1->5)-L-arabinofuranosidase

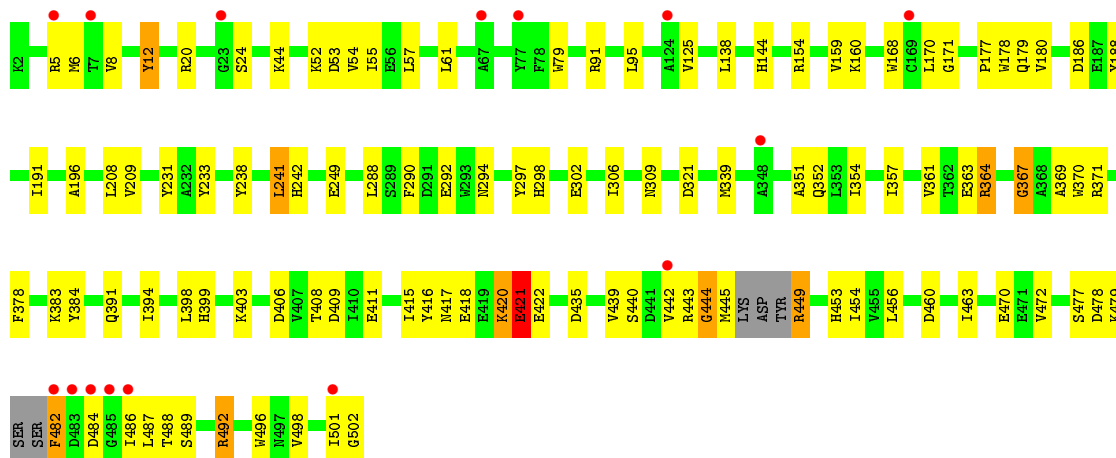
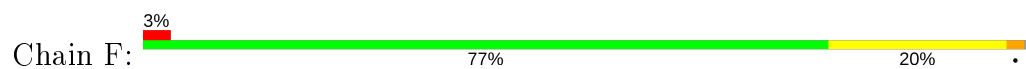


• Molecule 1: Intracellular exo-alpha-(1->5)-L-arabinofuranosidase





- Molecule 1: Intracellular exo- $\alpha$ -(1->5)-L-arabinofuranosidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	173.07Å 173.07Å 271.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.67 – 2.50 48.67 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.67-2.50) 99.8 (48.67-2.50)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.45 (at 2.51Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.193 , 0.241 0.194 , 0.241	Depositor DCC
$R_{free}$ test set	7122 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	52.6	Xtriage
Anisotropy	0.205	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 39.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	23743	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.35% 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 [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	0.52	0/4051	0.68	0/5487
1	B	0.48	0/4043	0.64	0/5477
1	C	0.50	0/4039	0.66	0/5470
1	D	0.47	0/4040	0.65	0/5474
1	E	0.49	0/4044	0.63	0/5477
1	F	0.49	0/4030	0.64	0/5461
All	All	0.49	0/24247	0.65	0/32846

There are no bond length outliers.

There are no bond angle outliers.

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	3961	0	3855	121	0
1	B	3953	0	3845	87	0
1	C	3950	0	3836	111	1
1	D	3950	0	3828	101	0
1	E	3955	0	3849	67	1
1	F	3941	0	3817	69	0
2	A	7	0	0	0	0
2	B	3	0	0	0	0
2	C	5	0	0	0	0
2	D	9	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	6	0	0	0	0
2	F	3	0	0	0	0
All	All	23743	0	23030	553	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 12.

The worst 5 of 553 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:D:12:TYR:CE1	1:D:391:GLN:NE2	1.68	1.61
1:D:12:TYR:CD1	1:D:391:GLN:NE2	1.80	1.46
1:E:479:LYS:NZ	1:E:488:THR:O	1.61	1.30
1:C:4:ALA:O	1:C:5:ARG:NH2	1.75	1.19
1:E:383:LYS:NZ	1:E:384:TYR:CZ	2.16	1.13

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)
1:C:52:LYS:NZ	1:E:363:GLU:OE1[6_447]	2.01	0.19

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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	490/501 (98%)	443 (90%)	38 (8%)	9 (2%)	8	14
1	B	490/501 (98%)	447 (91%)	32 (6%)	11 (2%)	6	10
1	C	490/501 (98%)	447 (91%)	33 (7%)	10 (2%)	7	12
1	D	489/501 (98%)	456 (93%)	27 (6%)	6 (1%)	13	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	490/501 (98%)	453 (92%)	30 (6%)	7 (1%)	11	20
1	F	490/501 (98%)	451 (92%)	26 (5%)	13 (3%)	5	7
All	All	2939/3006 (98%)	2697 (92%)	186 (6%)	56 (2%)	8	13

5 of 56 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	421	GLU
1	A	477	SER
1	B	107	ILE
1	B	369	ALA
1	C	368	ALA

### 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	426/438 (97%)	409 (96%)	17 (4%)	31	56
1	B	424/438 (97%)	414 (98%)	10 (2%)	49	74
1	C	423/438 (97%)	414 (98%)	9 (2%)	53	78
1	D	424/438 (97%)	410 (97%)	14 (3%)	38	64
1	E	425/438 (97%)	413 (97%)	12 (3%)	43	70
1	F	421/438 (96%)	407 (97%)	14 (3%)	38	64
All	All	2543/2628 (97%)	2467 (97%)	76 (3%)	41	68

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	466	SER
1	D	404	HIS
1	F	421	GLU
1	C	497	ASN
1	D	148	SER

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

Mol	Chain	Res	Type
1	B	453	HIS
1	B	497	ASN
1	C	404	HIS
1	E	300	ASN

### 5.3.3 RNA [i](#)

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 [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	496/501 (99%)	0.10	31 (6%) 20 21	34, 53, 96, 117	0
1	B	496/501 (99%)	0.13	20 (4%) 38 41	36, 54, 94, 118	0
1	C	496/501 (99%)	0.15	16 (3%) 47 51	36, 54, 92, 114	0
1	D	495/501 (98%)	0.15	20 (4%) 38 41	33, 54, 95, 115	0
1	E	496/501 (99%)	0.01	21 (4%) 36 39	34, 50, 85, 116	0
1	F	496/501 (99%)	0.11	15 (3%) 50 53	35, 53, 90, 117	0
All	All	2975/3006 (98%)	0.11	123 (4%) 37 40	33, 53, 92, 118	0

The worst 5 of 123 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	501	ILE	7.1
1	E	486	ILE	6.5
1	E	485	GLY	6.1
1	A	488	THR	6.0
1	F	483	ASP	5.6

### 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.