



# wwPDB X-ray Structure Validation Summary Report

Jul 6, 2022 – 01:07 pm BST

PDB ID : 6QPM  
Title : Adenovirus serotype 10 Fiber-Knob  
Authors : Baker, A.T.; Rizkallah, P.J.  
Deposited on : 2019-02-14  
Resolution : 3.39 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.

The types of validation reports are described at <http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 2.29  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.29

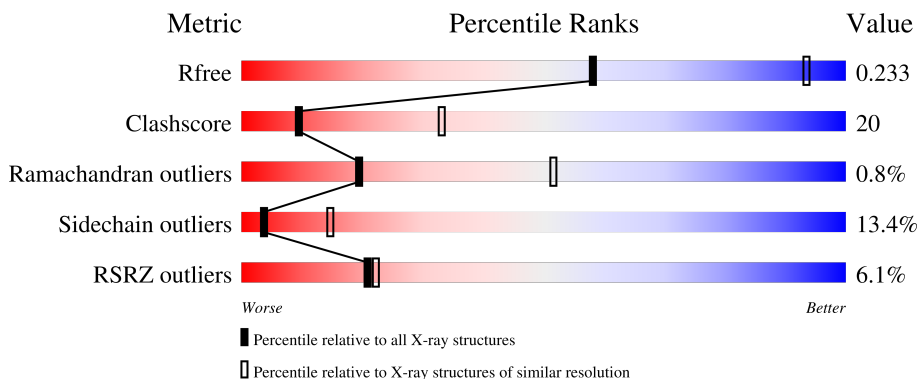
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



The reported resolution of this entry is 3.39 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.



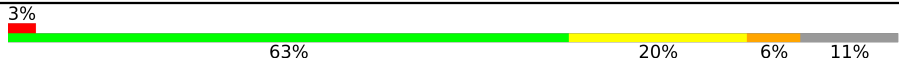
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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 of 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	205	
1	B	205	
1	C	205	
1	D	205	
1	E	205	

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Mol	Chain	Length	Quality of chain
1	F	205	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into five segments: a small red segment (3%), a large green segment (63%), a yellow segment (20%), a small orange segment (6%), and a grey segment (11%).</p>

## 2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 8631 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 Fiber protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	183	1449	929	233	283	4	0	0	0
1	B	183	1449	929	233	283	4	0	0	0
1	C	183	1449	929	233	283	4	0	0	0
1	D	175	1386	890	223	269	4	0	0	0
1	E	183	1449	929	233	283	4	0	0	0
1	F	183	1449	929	233	283	4	0	0	0

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	165	MET	-	initiating methionine	UNP B5BQ05
A	166	ARG	-	expression tag	UNP B5BQ05
A	167	GLY	-	expression tag	UNP B5BQ05
A	168	HIS	-	expression tag	UNP B5BQ05
A	169	HIS	-	expression tag	UNP B5BQ05
A	170	HIS	-	expression tag	UNP B5BQ05
A	171	HIS	-	expression tag	UNP B5BQ05
A	172	HIS	-	expression tag	UNP B5BQ05
A	173	HIS	-	expression tag	UNP B5BQ05
A	174	GLY	-	expression tag	UNP B5BQ05
A	175	SER	-	expression tag	UNP B5BQ05
B	165	MET	-	initiating methionine	UNP B5BQ05
B	166	ARG	-	expression tag	UNP B5BQ05
B	167	GLY	-	expression tag	UNP B5BQ05
B	168	HIS	-	expression tag	UNP B5BQ05
B	169	HIS	-	expression tag	UNP B5BQ05
B	170	HIS	-	expression tag	UNP B5BQ05

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Chain	Residue	Modelled	Actual	Comment	Reference
B	171	HIS	-	expression tag	UNP B5BQ05
B	172	HIS	-	expression tag	UNP B5BQ05
B	173	HIS	-	expression tag	UNP B5BQ05
B	174	GLY	-	expression tag	UNP B5BQ05
B	175	SER	-	expression tag	UNP B5BQ05
C	165	MET	-	initiating methionine	UNP B5BQ05
C	166	ARG	-	expression tag	UNP B5BQ05
C	167	GLY	-	expression tag	UNP B5BQ05
C	168	HIS	-	expression tag	UNP B5BQ05
C	169	HIS	-	expression tag	UNP B5BQ05
C	170	HIS	-	expression tag	UNP B5BQ05
C	171	HIS	-	expression tag	UNP B5BQ05
C	172	HIS	-	expression tag	UNP B5BQ05
C	173	HIS	-	expression tag	UNP B5BQ05
C	174	GLY	-	expression tag	UNP B5BQ05
C	175	SER	-	expression tag	UNP B5BQ05
D	165	MET	-	initiating methionine	UNP B5BQ05
D	166	ARG	-	expression tag	UNP B5BQ05
D	167	GLY	-	expression tag	UNP B5BQ05
D	168	HIS	-	expression tag	UNP B5BQ05
D	169	HIS	-	expression tag	UNP B5BQ05
D	170	HIS	-	expression tag	UNP B5BQ05
D	171	HIS	-	expression tag	UNP B5BQ05
D	172	HIS	-	expression tag	UNP B5BQ05
D	173	HIS	-	expression tag	UNP B5BQ05
D	174	GLY	-	expression tag	UNP B5BQ05
D	175	SER	-	expression tag	UNP B5BQ05
E	165	MET	-	initiating methionine	UNP B5BQ05
E	166	ARG	-	expression tag	UNP B5BQ05
E	167	GLY	-	expression tag	UNP B5BQ05
E	168	HIS	-	expression tag	UNP B5BQ05
E	169	HIS	-	expression tag	UNP B5BQ05
E	170	HIS	-	expression tag	UNP B5BQ05
E	171	HIS	-	expression tag	UNP B5BQ05
E	172	HIS	-	expression tag	UNP B5BQ05
E	173	HIS	-	expression tag	UNP B5BQ05
E	174	GLY	-	expression tag	UNP B5BQ05
E	175	SER	-	expression tag	UNP B5BQ05
F	165	MET	-	initiating methionine	UNP B5BQ05
F	166	ARG	-	expression tag	UNP B5BQ05
F	167	GLY	-	expression tag	UNP B5BQ05
F	168	HIS	-	expression tag	UNP B5BQ05

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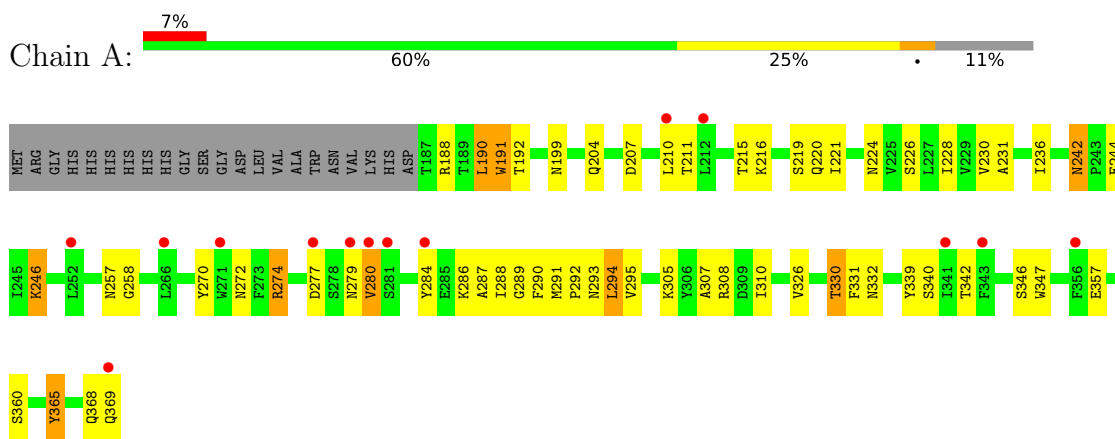
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<b>Chain</b>	<b>Residue</b>	<b>Modelled</b>	<b>Actual</b>	<b>Comment</b>	<b>Reference</b>
F	169	HIS	-	expression tag	UNP B5BQ05
F	170	HIS	-	expression tag	UNP B5BQ05
F	171	HIS	-	expression tag	UNP B5BQ05
F	172	HIS	-	expression tag	UNP B5BQ05
F	173	HIS	-	expression tag	UNP B5BQ05
F	174	GLY	-	expression tag	UNP B5BQ05
F	175	SER	-	expression tag	UNP B5BQ05

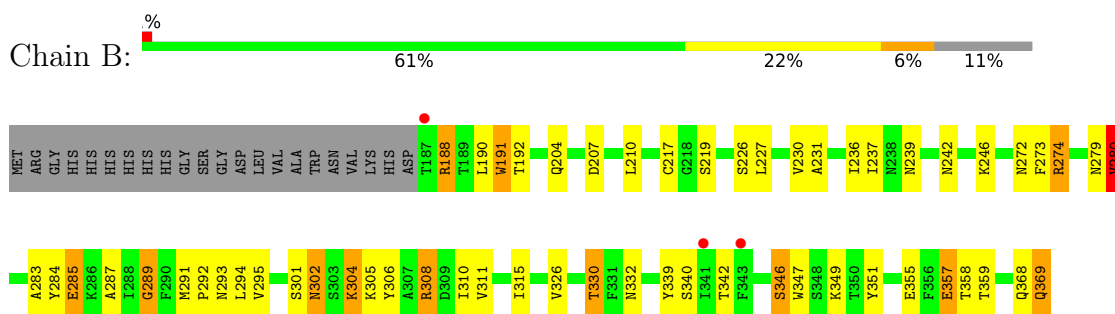
### 3 Residue-property plots [i](#)

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.

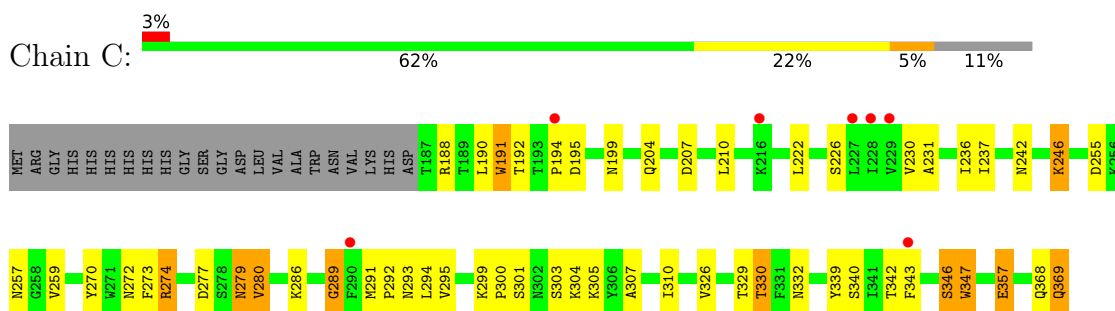
- Molecule 1: Fiber protein



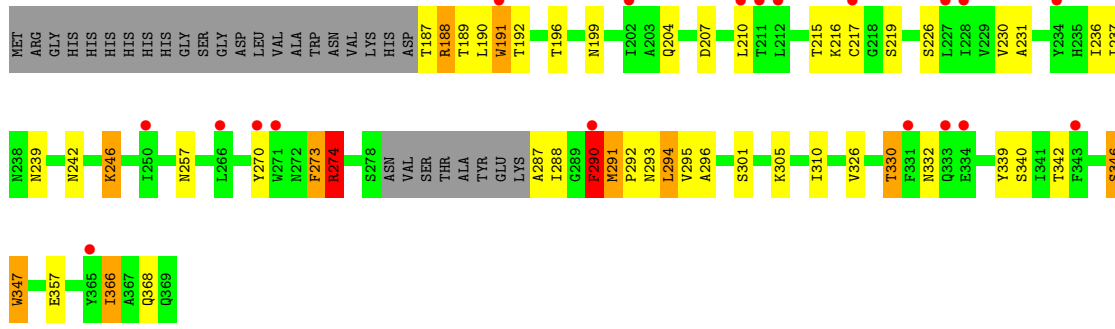
- Molecule 1: Fiber protein



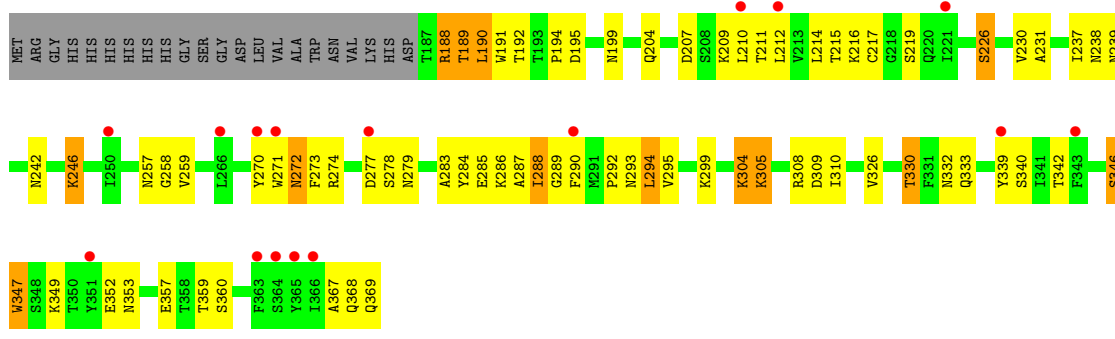
- Molecule 1: Fiber protein



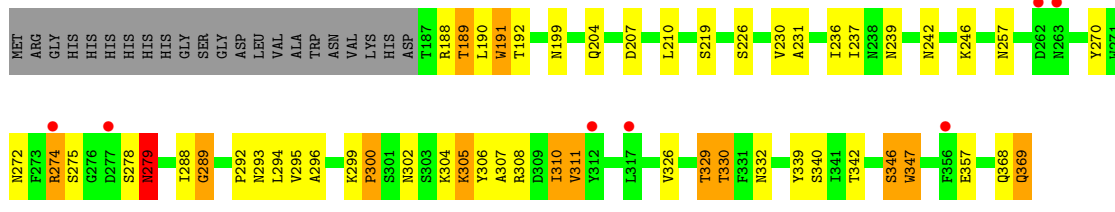
- Molecule 1: Fiber protein



• Molecule 1: Fiber protein



• Molecule 1: Fiber protein





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	183.57Å 183.57Å 94.88Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	79.49 – 3.39 79.49 – 3.39	Depositor EDS
% Data completeness (in resolution range)	98.9 (79.49-3.39) 99.0 (79.49-3.39)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.47 (at 3.41Å)	Xtrriage
Refinement program	REFMAC 5.8.0238	Depositor
R, $R_{free}$	0.199 , 0.232 0.200 , 0.233	Depositor DCC
$R_{free}$ test set	1235 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	153.6	Xtrriage
Anisotropy	0.118	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	0.097 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	8631	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	186.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% 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	0.69	0/1483	0.94	1/2014 (0.0%)
1	B	0.70	0/1483	0.94	1/2014 (0.0%)
1	C	0.67	0/1483	0.90	0/2014
1	D	0.67	0/1418	0.92	2/1924 (0.1%)
1	E	0.68	0/1483	0.96	0/2014
1	F	0.68	0/1483	0.96	1/2014 (0.0%)
All	All	0.68	0/8833	0.94	5/11994 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	F	0	1
All	All	0	4

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	369	GLN	CA-C-O	-5.97	107.56	120.10
1	B	302	ASN	CB-CA-C	5.95	122.30	110.40
1	D	274	ARG	CG-CD-NE	5.38	123.11	111.80
1	F	279	ASN	CB-CA-C	5.24	120.88	110.40
1	D	274	ARG	NE-CZ-NH2	-5.24	117.68	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	289	GLY	Peptide
1	B	289	GLY	Peptide
1	C	289	GLY	Peptide
1	F	289	GLY	Peptide

## 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	1449	0	1429	65	0
1	B	1449	0	1429	72	0
1	C	1449	0	1429	49	0
1	D	1386	0	1368	50	0
1	E	1449	0	1424	94	0
1	F	1449	0	1429	38	0
All	All	8631	0	8508	336	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 20.

The worst 5 of 336 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:272:ASN:C	1:B:279:ASN:HD21	1.20	1.40
1:E:272:ASN:ND2	1:E:279:ASN:OD1	1.58	1.33
1:B:272:ASN:O	1:B:279:ASN:ND2	1.66	1.24
1:E:258:GLY:N	1:E:286:LYS:CE	2.03	1.19
1:E:258:GLY:N	1:E:286:LYS:HE3	1.57	1.18

There are no symmetry-related clashes.

## 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	181/205 (88%)	162 (90%)	18 (10%)	1 (1%)	25	57
1	B	181/205 (88%)	161 (89%)	19 (10%)	1 (1%)	25	57
1	C	181/205 (88%)	159 (88%)	21 (12%)	1 (1%)	25	57
1	D	171/205 (83%)	152 (89%)	17 (10%)	2 (1%)	13	41
1	E	181/205 (88%)	156 (86%)	22 (12%)	3 (2%)	9	34
1	F	181/205 (88%)	163 (90%)	17 (9%)	1 (1%)	25	57
All	All	1076/1230 (88%)	953 (89%)	114 (11%)	9 (1%)	19	51

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	280	VAL
1	B	280	VAL
1	C	280	VAL
1	D	301	SER
1	E	284	TYR

### 5.3.2 Protein sidechains [i](#)

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	163/182 (90%)	142 (87%)	21 (13%)	4	16
1	B	163/182 (90%)	140 (86%)	23 (14%)	3	13
1	C	163/182 (90%)	144 (88%)	19 (12%)	5	20
1	D	156/182 (86%)	133 (85%)	23 (15%)	3	12
1	E	163/182 (90%)	144 (88%)	19 (12%)	5	20
1	F	163/182 (90%)	138 (85%)	25 (15%)	2	11
All	All	971/1092 (89%)	841 (87%)	130 (13%)	4	15

5 of 130 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	274	ARG
1	F	305	LYS
1	C	204	GLN
1	C	195	ASP
1	F	311	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	333	GLN
1	F	239	ASN
1	D	239	ASN
1	F	332	ASN
1	E	368	GLN

### 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 monosaccharides 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

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	183/205 (89%)	0.41	14 (7%) 13 15	110, 166, 232, 305	0
1	B	183/205 (89%)	0.21	3 (1%) 72 70	119, 158, 224, 285	0
1	C	183/205 (89%)	0.20	7 (3%) 40 39	134, 187, 246, 290	0
1	D	175/205 (85%)	0.45	19 (10%) 5 6	163, 226, 263, 309	0
1	E	183/205 (89%)	0.34	16 (8%) 10 12	138, 191, 263, 309	0
1	F	183/205 (89%)	0.37	7 (3%) 40 39	127, 165, 222, 285	0
All	All	1090/1230 (88%)	0.33	66 (6%) 21 22	110, 181, 257, 309	0

The worst 5 of 66 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	271	TRP	5.1
1	D	227	LEU	4.3
1	C	229	VAL	4.2
1	D	234	TYR	4.2
1	D	210	LEU	4.0

### 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 monosaccharides 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.