



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 3, 2024 – 10:23 am GMT

PDB ID : 4UW8  
Title : Structure of the carboxy-terminal domain of the bacteriophage T5 L- shaped tail fiber with its intra-molecular chaperone domain  
Authors : Garcia-Doval, C.; Luque, D.; Caston, J.R.; Otero, J.M.; Llamas-Saiz, A.L.; Boulanger, P.; van Raaij, M.J.  
Deposited on : 2014-08-08  
Resolution : 2.52 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  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

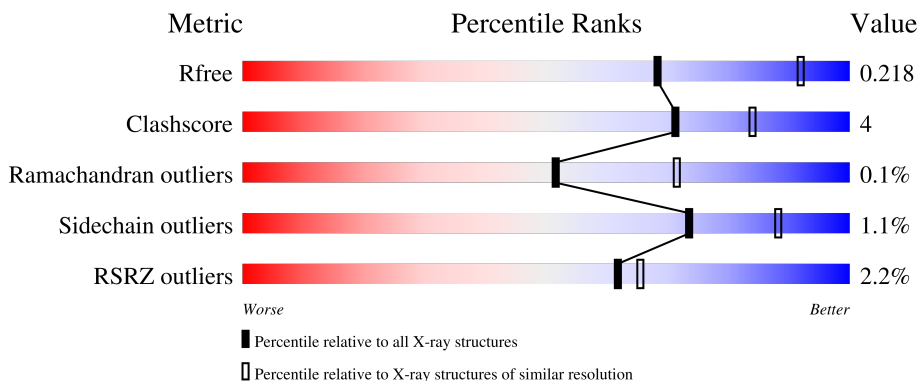
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.52 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	5743 (2.54-2.50)
Clashscore	141614	6463 (2.54-2.50)
Ramachandran outliers	138981	6335 (2.54-2.50)
Sidechain outliers	138945	6337 (2.54-2.50)
RSRZ outliers	127900	5630 (2.54-2.50)

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 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	427	 87% 7% 6%
1	B	427	 87% 6% 6%
1	C	427	 87% 7% 6%
1	D	427	 89% 5% 6%
1	E	427	 87% 6% 6%

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Mol	Chain	Length	Quality of chain
1	F	427	 3% 86% 7% • 6%
1	G	427	 3% 87% 6% • 6%
1	H	427	 4% 87% 6% • 6%
1	I	427	 % 88% 5% • 6%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FLC	C	2397	-	-	X	-

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 28644 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 L-SHAPED TAIL FIBER PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	401	3066	1925	542	586	13	0	2	0
1	B	401	3066	1925	542	586	13	0	2	0
1	C	401	3066	1925	542	586	13	0	2	0
1	D	401	3066	1925	542	586	13	0	2	0
1	E	401	3066	1925	542	586	13	0	2	0
1	F	401	3066	1925	542	586	13	0	2	0
1	G	400	3058	1919	541	585	13	0	2	0
1	H	401	3071	1928	542	588	13	0	3	0
1	I	401	3066	1925	542	586	13	0	2	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1264	ALA	SER	engineered mutation	UNP P13390
B	1264	ALA	SER	engineered mutation	UNP P13390
C	1264	ALA	SER	engineered mutation	UNP P13390
D	1264	ALA	SER	engineered mutation	UNP P13390
E	1264	ALA	SER	engineered mutation	UNP P13390
F	1264	ALA	SER	engineered mutation	UNP P13390
G	1264	ALA	SER	engineered mutation	UNP P13390
H	1264	ALA	SER	engineered mutation	UNP P13390
I	1264	ALA	SER	engineered mutation	UNP P13390

- Molecule 2 is CITRATE ANION (three-letter code: FLC) (formula: C<sub>6</sub>H<sub>5</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 13 6 7	0	0
2	B	1	Total C O 13 6 7	0	0
2	C	1	Total C O 13 6 7	0	0
2	D	1	Total C O 13 6 7	0	0
2	E	1	Total C O 13 6 7	0	0
2	F	1	Total C O 13 6 7	0	0
2	G	1	Total C O 13 6 7	0	0
2	H	1	Total C O 13 6 7	0	0
2	I	1	Total C O 13 6 7	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	154	Total O 154 154	0	0
3	B	128	Total O 128 128	0	0
3	C	108	Total O 108 108	0	0

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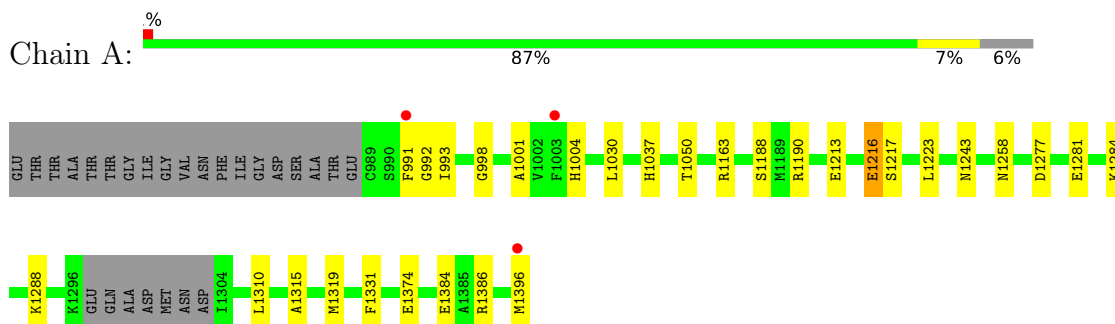
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	D	136	Total 136	O 136	0	0
3	E	122	Total 122	O 122	0	0
3	F	65	Total 65	O 65	0	0
3	G	90	Total 90	O 90	0	0
3	H	63	Total 63	O 63	0	0
3	I	70	Total 70	O 70	0	0

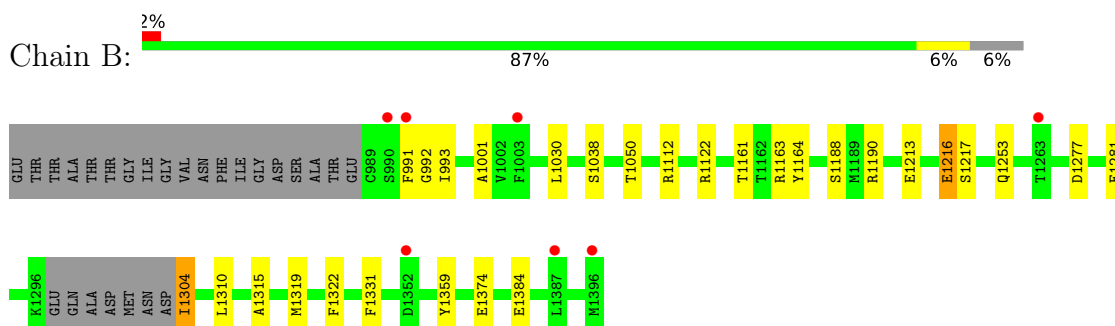
### 3 Residue-property plots [i](#)

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.

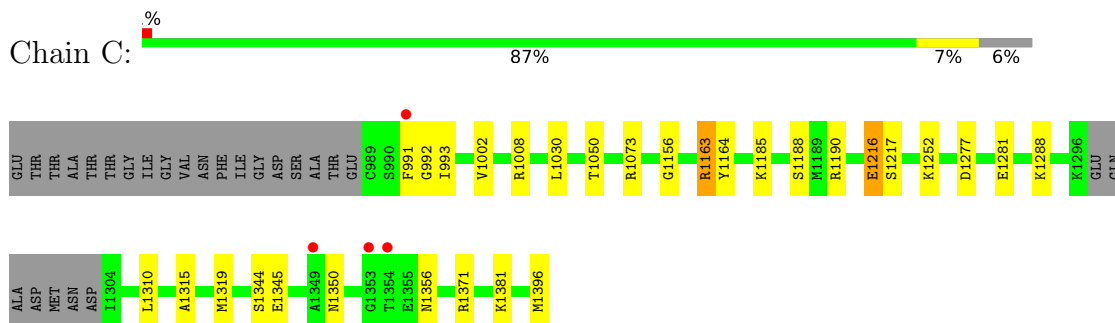
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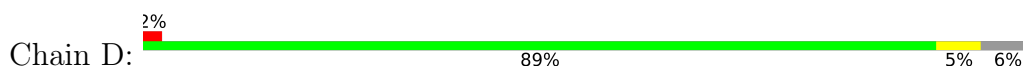
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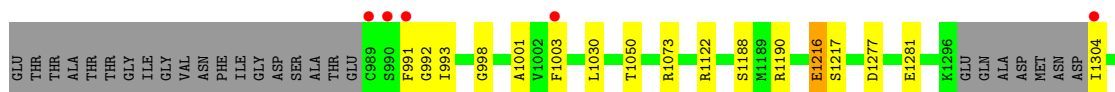


- Molecule 1: L-SHAPED TAIL FIBER PROTEIN

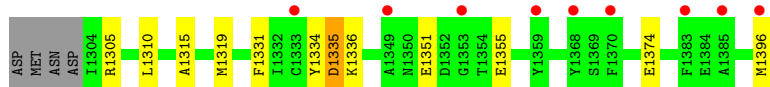
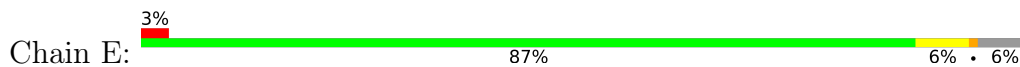


- Molecule 1: L-SHAPED TAIL FIBER PROTEIN

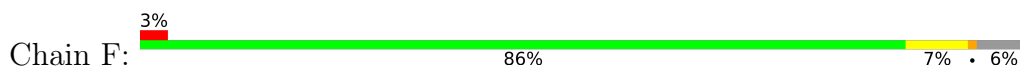




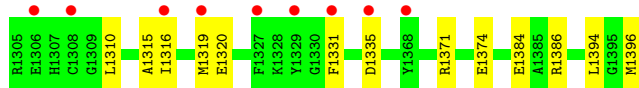
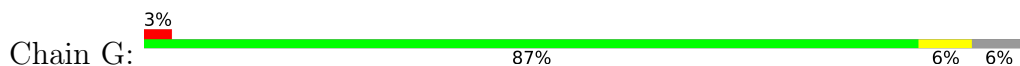
• Molecule 1: L-SHAPED TAIL FIBER PROTEIN



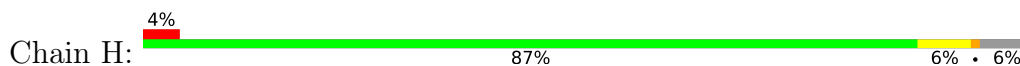
• Molecule 1: L-SHAPED TAIL FIBER PROTEIN



• Molecule 1: L-SHAPED TAIL FIBER PROTEIN



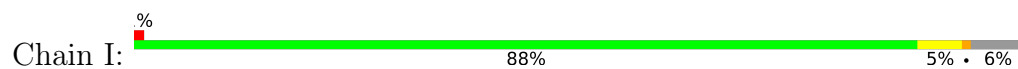
• Molecule 1: L-SHAPED TAIL FIBER PROTEIN







- Molecule 1: L-SHAPED TAIL FIBER PROTEIN



## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	160.85Å 99.29Å 286.23Å 90.00° 91.51° 90.00°	Depositor
Resolution (Å)	95.38 – 2.52 95.38 – 2.52	Depositor EDS
% Data completeness (in resolution range)	98.5 (95.38-2.52) 98.5 (95.38-2.52)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.30 (at 2.51Å)	Xtrriage
Refinement program	REFMAC 5.8.0049	Depositor
R, $R_{free}$	0.185 , 0.213 0.190 , 0.218	Depositor DCC
$R_{free}$ test set	2064 reflections (1.37%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.3	Xtrriage
Anisotropy	0.132	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 47.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.017 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	28644	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.54% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FLC

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	2/3147 (0.1%)	0.72	1/4269 (0.0%)
1	B	0.57	2/3147 (0.1%)	0.74	1/4269 (0.0%)
1	C	0.56	0/3147	0.73	0/4269
1	D	0.52	0/3147	0.72	0/4269
1	E	0.56	2/3147 (0.1%)	0.74	1/4269 (0.0%)
1	F	0.55	0/3147	0.76	4/4269 (0.1%)
1	G	0.50	0/3139	0.76	3/4258 (0.1%)
1	H	0.50	0/3155	0.71	0/4280
1	I	0.54	1/3147 (0.0%)	0.73	3/4269 (0.1%)
All	All	0.54	7/28323 (0.0%)	0.73	13/38421 (0.0%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1213	GLU	CD-OE1	-5.92	1.19	1.25
1	B	1213	GLU	CD-OE1	-5.86	1.19	1.25
1	E	1355	GLU	CD-OE2	-5.42	1.19	1.25
1	A	1213	GLU	CD-OE2	-5.24	1.19	1.25
1	B	1213	GLU	CD-OE2	-5.21	1.20	1.25

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	1335	ASP	CB-CG-OD2	9.50	126.85	118.30
1	I	1335	ASP	CB-CG-OD2	9.34	126.70	118.30
1	G	1122[A]	ARG	CG-CD-NE	8.76	130.19	111.80
1	G	1122[B]	ARG	CG-CD-NE	8.76	130.19	111.80
1	E	1335	ASP	CB-CG-OD2	8.70	126.13	118.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-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 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	3066	0	2963	26	0
1	B	3066	0	2963	29	0
1	C	3066	0	2963	29	0
1	D	3066	0	2963	24	0
1	E	3066	0	2963	25	0
1	F	3066	0	2963	32	0
1	G	3058	0	2952	26	0
1	H	3071	0	2967	25	0
1	I	3066	0	2963	23	0
2	A	13	0	5	2	0
2	B	13	0	5	2	0
2	C	13	0	5	4	0
2	D	13	0	5	2	0
2	E	13	0	5	0	0
2	F	13	0	5	1	0
2	G	13	0	5	0	0
2	H	13	0	5	1	0
2	I	13	0	5	0	0
3	A	154	0	0	0	0
3	B	128	0	0	5	0
3	C	108	0	0	1	0
3	D	136	0	0	2	0
3	E	122	0	0	1	0
3	F	65	0	0	3	0
3	G	90	0	0	3	0
3	H	63	0	0	2	0
3	I	70	0	0	0	0
All	All	28644	0	26705	191	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 4.

The worst 5 of 191 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:1331:PHE:HB3	1:B:1374:GLU:HG2	1.28	1.15
1:F:989:CYS:SG	3:F:2002:HOH:O	2.25	0.92
1:D:1304:ILE:N	3:D:2119:HOH:O	2.08	0.86
1:H:1281:GLU:HB3	1:H:1322:PHE:CE2	2.16	0.80
1:B:1281:GLU:HB3	1:B:1322:PHE:CE2	2.17	0.79

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	399/427 (93%)	390 (98%)	9 (2%)	0	100	100
1	B	399/427 (93%)	389 (98%)	10 (2%)	0	100	100
1	C	399/427 (93%)	390 (98%)	9 (2%)	0	100	100
1	D	399/427 (93%)	390 (98%)	9 (2%)	0	100	100
1	E	399/427 (93%)	390 (98%)	9 (2%)	0	100	100
1	F	399/427 (93%)	390 (98%)	9 (2%)	0	100	100
1	G	398/427 (93%)	389 (98%)	9 (2%)	0	100	100
1	H	400/427 (94%)	388 (97%)	10 (2%)	2 (0%)	29	47
1	I	399/427 (93%)	390 (98%)	9 (2%)	0	100	100
All	All	3591/3843 (93%)	3506 (98%)	83 (2%)	2 (0%)	51	71

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	1390	ILE
1	H	1391	GLU

### 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	318/336 (95%)	315 (99%)	3 (1%)	78	91
1	B	318/336 (95%)	315 (99%)	3 (1%)	78	91
1	C	318/336 (95%)	314 (99%)	4 (1%)	69	86
1	D	318/336 (95%)	316 (99%)	2 (1%)	86	94
1	E	318/336 (95%)	313 (98%)	5 (2%)	62	82
1	F	318/336 (95%)	313 (98%)	5 (2%)	62	82
1	G	317/336 (94%)	315 (99%)	2 (1%)	86	94
1	H	319/336 (95%)	315 (99%)	4 (1%)	69	86
1	I	318/336 (95%)	314 (99%)	4 (1%)	69	86
All	All	2862/3024 (95%)	2830 (99%)	32 (1%)	73	88

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	1163	ARG
1	I	1216	GLU
1	E	1163	ARG
1	D	1310	LEU
1	I	1310	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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](#)

9 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	FLC	A	2397	-	12,12,12	1.32	1 (8%)	17,17,17	1.32	4 (23%)
2	FLC	D	2397	-	12,12,12	1.38	1 (8%)	17,17,17	1.83	4 (23%)
2	FLC	H	2397	-	12,12,12	1.48	1 (8%)	17,17,17	1.23	1 (5%)
2	FLC	C	2397	-	12,12,12	1.61	1 (8%)	17,17,17	1.23	2 (11%)
2	FLC	G	2397	-	12,12,12	1.40	1 (8%)	17,17,17	1.30	2 (11%)
2	FLC	I	2397	-	12,12,12	1.02	0	17,17,17	1.41	1 (5%)
2	FLC	F	2397	-	12,12,12	1.43	1 (8%)	17,17,17	1.48	3 (17%)
2	FLC	B	2397	-	12,12,12	1.27	1 (8%)	17,17,17	1.17	2 (11%)
2	FLC	E	2397	-	12,12,12	1.36	1 (8%)	17,17,17	1.32	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FLC	A	2397	-	-	8/16/16/16	-
2	FLC	D	2397	-	-	6/16/16/16	-
2	FLC	H	2397	-	-	2/16/16/16	-
2	FLC	C	2397	-	-	4/16/16/16	-
2	FLC	G	2397	-	-	5/16/16/16	-
2	FLC	I	2397	-	-	7/16/16/16	-
2	FLC	F	2397	-	-	2/16/16/16	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FLC	B	2397	-	-	9/16/16/16	-
2	FLC	E	2397	-	-	2/16/16/16	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2397	FLC	CB-CBC	-3.89	1.49	1.53
2	H	2397	FLC	CB-CBC	-3.85	1.49	1.53
2	F	2397	FLC	CB-CBC	-3.69	1.49	1.53
2	D	2397	FLC	CB-CBC	-3.67	1.49	1.53
2	G	2397	FLC	CB-CBC	-3.52	1.49	1.53

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2397	FLC	OB1-CBC-CB	-4.81	115.45	122.25
2	I	2397	FLC	OB2-CBC-CB	4.10	120.17	113.05
2	D	2397	FLC	OB2-CBC-CB	3.84	119.71	113.05
2	F	2397	FLC	OB1-CBC-CB	-3.61	117.15	122.25
2	C	2397	FLC	OB1-CBC-CB	-3.13	117.82	122.25

There are no chirality outliers.

5 of 45 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	2397	FLC	CG-CB-CBC-OB1
2	A	2397	FLC	CG-CB-CBC-OB2
2	A	2397	FLC	OHB-CB-CBC-OB1
2	A	2397	FLC	OHB-CB-CBC-OB2
2	B	2397	FLC	CA-CB-CBC-OB1

There are no ring outliers.

6 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2397	FLC	2	0
2	D	2397	FLC	2	0
2	H	2397	FLC	1	0
2	C	2397	FLC	4	0
2	F	2397	FLC	1	0
2	B	2397	FLC	2	0



## 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 [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	401/427 (93%)	0.14	3 (0%) 87 89	19, 34, 68, 91	0
1	B	401/427 (93%)	0.12	7 (1%) 70 73	20, 34, 73, 93	0
1	C	401/427 (93%)	0.09	4 (0%) 82 84	20, 33, 68, 94	0
1	D	401/427 (93%)	0.13	10 (2%) 57 61	21, 36, 83, 115	0
1	E	401/427 (93%)	0.26	12 (2%) 50 54	20, 36, 86, 111	0
1	F	401/427 (93%)	0.15	11 (2%) 54 58	21, 36, 72, 106	0
1	G	400/427 (93%)	0.23	12 (3%) 50 54	25, 40, 85, 105	0
1	H	401/427 (93%)	0.35	16 (3%) 38 42	24, 42, 90, 120	0
1	I	401/427 (93%)	0.15	5 (1%) 79 81	27, 40, 74, 121	0
All	All	3608/3843 (93%)	0.18	80 (2%) 62 65	19, 37, 82, 121	0

The worst 5 of 80 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	991[A]	PHE	5.8
1	I	1396	MET	4.9
1	F	1396	MET	4.6
1	D	1396	MET	4.5
1	F	1264	ALA	4.4

### 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](#)

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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
2	FLC	I	2397	13/13	0.89	0.31	69,75,88,90	0
2	FLC	C	2397	13/13	0.90	0.28	66,79,90,90	0
2	FLC	H	2397	13/13	0.91	0.25	74,88,92,94	0
2	FLC	F	2397	13/13	0.91	0.32	58,78,90,95	0
2	FLC	B	2397	13/13	0.92	0.26	62,74,87,87	0
2	FLC	A	2397	13/13	0.94	0.38	80,87,97,101	0
2	FLC	G	2397	13/13	0.94	0.32	71,76,96,98	0
2	FLC	D	2397	13/13	0.94	0.19	61,79,88,88	0
2	FLC	E	2397	13/13	0.94	0.26	53,72,81,85	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.