



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 31, 2021 – 10:12 AM EDT

PDB ID : 1J1D  
Title : Crystal structure of the 46kDa domain of human cardiac troponin in the Ca<sup>2+</sup> saturated form  
Authors : Takeda, S.; Yamashita, A.; Maeda, K.; Maeda, Y.  
Deposited on : 2002-12-03  
Resolution : 2.61 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 : 2.23.2  
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) : 2.23.2

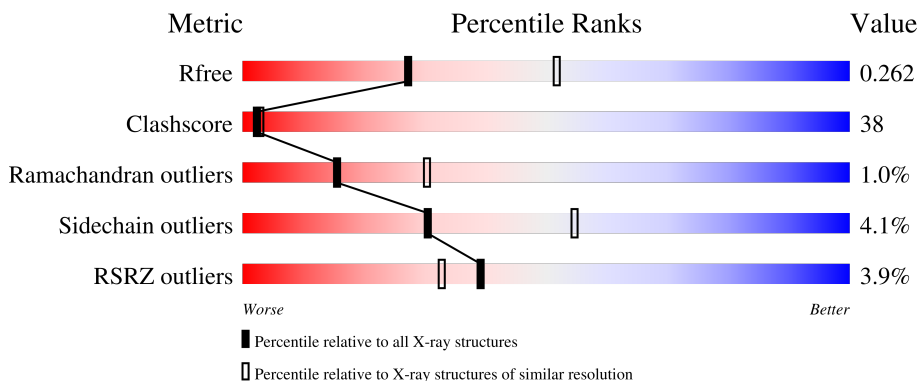
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.61 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.



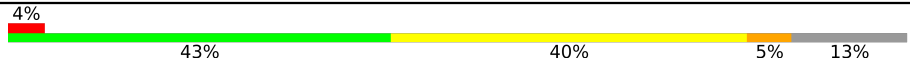
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

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	161	
1	D	161	
2	B	106	
2	E	106	
3	C	133	

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Mol	Chain	Length	Quality of chain												
3	F	133	 <p>A horizontal bar chart showing the quality distribution of chain F. The bar is divided into five segments: a small red segment (4%), a large green segment (43%), a large yellow segment (40%), a small orange segment (5%), and a grey segment (13%).</p> <table border="1"><thead><tr><th>Quality Category</th><th>Percentage</th></tr></thead><tbody><tr><td>Red</td><td>4%</td></tr><tr><td>Green</td><td>43%</td></tr><tr><td>Yellow</td><td>40%</td></tr><tr><td>Orange</td><td>5%</td></tr><tr><td>Grey</td><td>13%</td></tr></tbody></table>	Quality Category	Percentage	Red	4%	Green	43%	Yellow	40%	Orange	5%	Grey	13%
Quality Category	Percentage														
Red	4%														
Green	43%														
Yellow	40%														
Orange	5%														
Grey	13%														

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5777 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 Troponin C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	159	1269	786	193	279	11	0	0	0
1	D	160	1274	789	195	280	10	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	35	SER	CYS	engineered mutation	UNP P63316
A	84	SER	CYS	engineered mutation	UNP P63316
D	35	SER	CYS	engineered mutation	UNP P63316
D	84	SER	CYS	engineered mutation	UNP P63316

- Molecule 2 is a protein called Troponin T.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	70	611	383	114	114	0	0	0
2	E	75	656	411	125	120	0	0	0

- Molecule 3 is a protein called Troponin I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	118	942	584	180	176	2	0	0	0
3	F	116	917	569	172	174	2	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	31	MET	THR	engineered mutation	UNP P19429
C	80	ALA	CYS	engineered mutation	UNP P19429
C	97	ALA	CYS	engineered mutation	UNP P19429
F	31	MET	THR	engineered mutation	UNP P19429
F	80	ALA	CYS	engineered mutation	UNP P19429
F	97	ALA	CYS	engineered mutation	UNP P19429

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	3	Total Ca 3 3	0	0
4	D	3	Total Ca 3 3	0	0

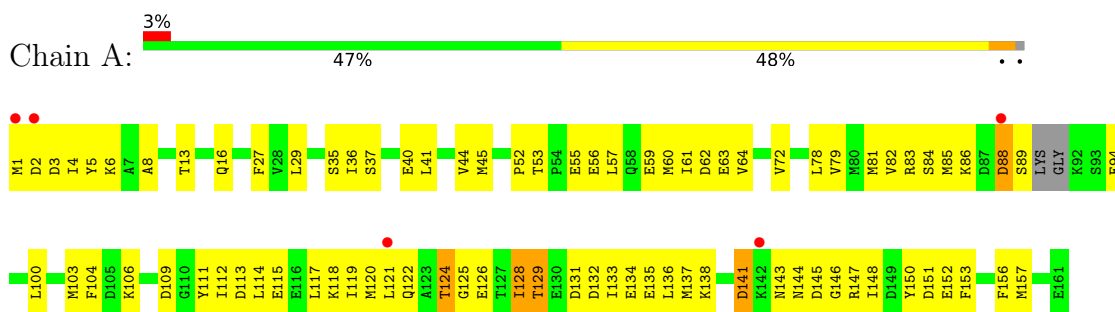
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	18	Total O 18 18	0	0
5	B	21	Total O 21 21	0	0
5	C	15	Total O 15 15	0	0
5	D	14	Total O 14 14	0	0
5	E	20	Total O 20 20	0	0
5	F	14	Total O 14 14	0	0

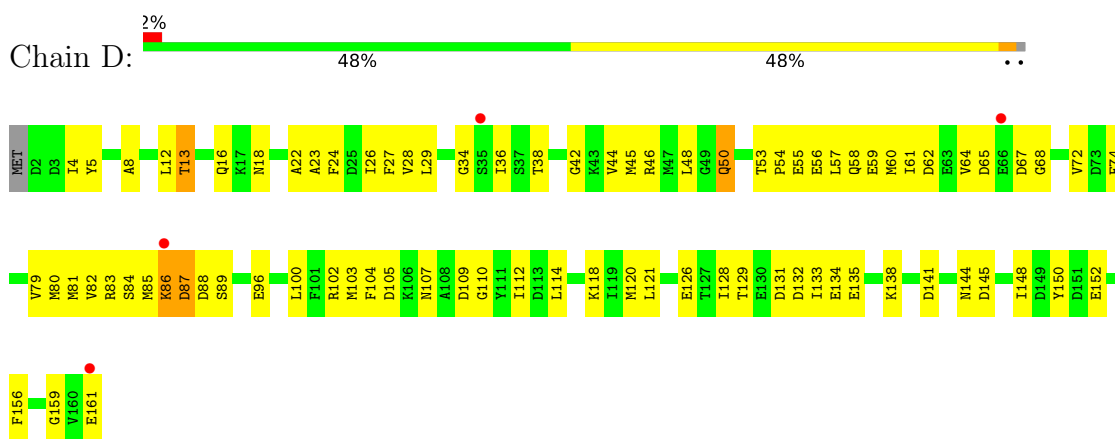
### 3 Residue-property plots [i](#)

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.

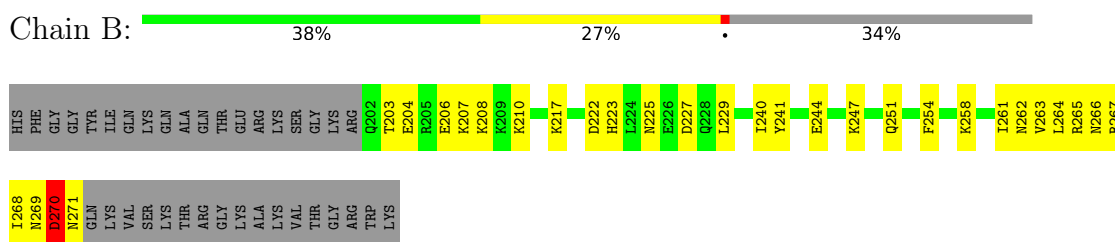
- Molecule 1: Troponin C



- Molecule 1: Troponin C

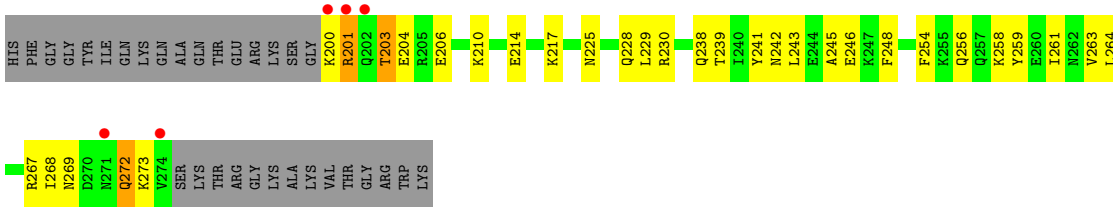


- Molecule 2: Troponin T

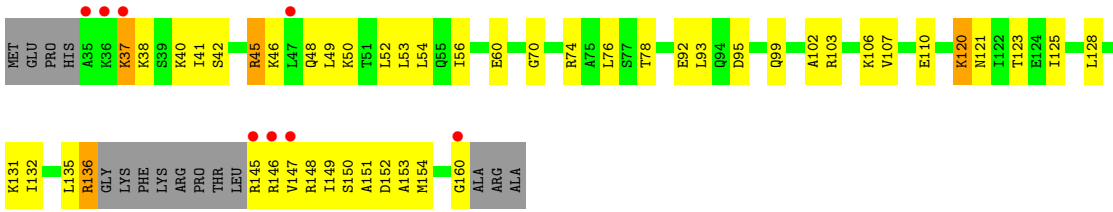


- Molecule 2: Troponin T

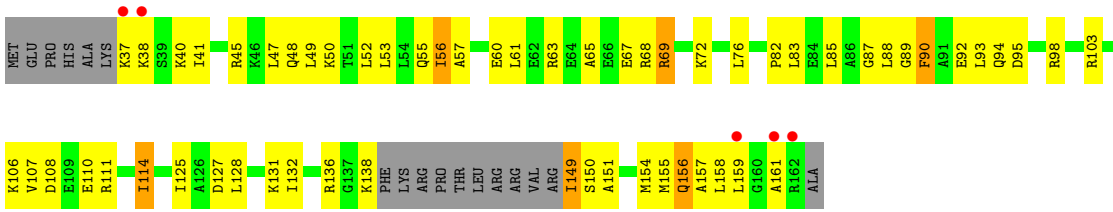
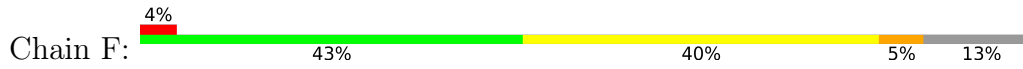




• Molecule 3: Troponin I



• Molecule 3: Troponin I



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	42.35Å 167.86Å 69.71Å 90.00° 101.35° 90.00°	Depositor
Resolution (Å)	40.00 – 2.61 38.04 – 2.61	Depositor EDS
% Data completeness (in resolution range)	96.3 (40.00-2.61) 96.3 (38.04-2.61)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.09 (at 2.61Å)	Xtrriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.264 , 0.298 0.264 , 0.262	Depositor DCC
$R_{free}$ test set	948 reflections (3.40%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	63.3	Xtrriage
Anisotropy	0.471	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 51.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	5777	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	72.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.84% 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:  
CA

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	0.46	0/1281	0.67	0/1711
1	D	0.38	0/1287	0.68	2/1720 (0.1%)
2	B	0.49	0/617	0.64	1/821 (0.1%)
2	E	0.45	0/662	0.64	0/879
3	C	0.42	0/945	0.68	0/1257
3	F	0.42	0/920	0.67	0/1224
All	All	0.43	0/5712	0.67	3/7612 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	D	88	ASP	N-CA-C	-5.98	94.86	111.00
1	D	87	ASP	N-CA-C	5.75	126.51	111.00
2	B	222	ASP	N-CA-C	5.23	125.12	111.00

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	1269	0	1197	125	0
1	D	1274	0	1202	135	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	611	0	628	38	0
2	E	656	0	684	57	0
3	C	942	0	1002	92	0
3	F	917	0	970	109	0
4	A	3	0	0	0	0
4	D	3	0	0	0	0
5	A	18	0	0	3	0
5	B	21	0	0	1	0
5	C	15	0	0	2	0
5	D	14	0	0	1	0
5	E	20	0	0	1	0
5	F	14	0	0	0	0
All	All	5777	0	5683	433	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 38.

The worst 5 of 433 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:4:ILE:HD11	1:D:159:GLY:HA3	1.28	1.09
1:A:135:GLU:HG3	3:C:41:ILE:HG22	1.37	1.03
3:F:88:LEU:HD22	3:F:92:GLU:HB2	1.41	1.02
1:A:104:PHE:HA	1:A:120:MET:HE3	1.39	1.01
1:D:121:LEU:HB3	1:D:128:ILE:CD1	1.89	1.01

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	155/161 (96%)	141 (91%)	11 (7%)	3 (2%)	8	14
1	D	158/161 (98%)	135 (85%)	22 (14%)	1 (1%)	25	45
2	B	68/106 (64%)	62 (91%)	5 (7%)	1 (2%)	10	19
2	E	73/106 (69%)	68 (93%)	5 (7%)	0	100	100
3	C	114/133 (86%)	104 (91%)	10 (9%)	0	100	100
3	F	112/133 (84%)	101 (90%)	9 (8%)	2 (2%)	8	15
All	All	680/800 (85%)	611 (90%)	62 (9%)	7 (1%)	15	30

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	125	GLY
1	A	63	GLU
2	B	270	ASP
1	A	141	ASP
1	D	86	LYS

### 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	141/142 (99%)	136 (96%)	5 (4%)	36	60
1	D	141/142 (99%)	139 (99%)	2 (1%)	67	84
2	B	66/95 (70%)	64 (97%)	2 (3%)	41	66
2	E	71/95 (75%)	68 (96%)	3 (4%)	30	53
3	C	98/110 (89%)	92 (94%)	6 (6%)	18	36
3	F	95/110 (86%)	88 (93%)	7 (7%)	13	26
All	All	612/694 (88%)	587 (96%)	25 (4%)	30	55

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	50	GLN

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Mol	Chain	Res	Type
2	E	272	GLN
3	F	156	GLN
2	E	203	THR
3	F	56	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	99	GLN
3	C	156	GLN
3	F	55	GLN
2	E	238	GLN
2	E	242	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	159/161 (98%)	0.24	5 (3%) 49 42	44, 73, 95, 114	0
1	D	160/161 (99%)	0.24	4 (2%) 57 51	51, 85, 106, 111	0
2	B	70/106 (66%)	-0.12	0 100 100	42, 55, 77, 85	0
2	E	75/106 (70%)	0.15	5 (6%) 17 13	38, 61, 103, 108	0
3	C	118/133 (88%)	0.37	8 (6%) 17 13	43, 72, 104, 110	0
3	F	116/133 (87%)	0.29	5 (4%) 35 29	41, 72, 101, 113	0
All	All	698/800 (87%)	0.23	27 (3%) 39 33	38, 73, 103, 114	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	35	ALA	7.3
3	F	161	ALA	5.7
1	A	1	MET	5.2
1	D	86	LYS	5.0
3	F	38	LYS	4.6

### 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 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(Å <sup>2</sup> )	Q<0.9
4	CA	A	203	1/1	0.90	0.09	95,95,95,95	0
4	CA	D	203	1/1	0.91	0.06	79,79,79,79	0
4	CA	D	201	1/1	0.92	0.08	92,92,92,92	0
4	CA	A	201	1/1	0.93	0.24	68,68,68,68	0
4	CA	A	202	1/1	0.94	0.13	67,67,67,67	0
4	CA	D	202	1/1	0.96	0.11	79,79,79,79	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.