



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 24, 2024 – 09:30 AM EDT

PDB ID : 6KDV  
Title : Crystal structure of TtCas1-DNA complex  
Authors : Wang, Y.L.; Li, J.Z.; Yang, J.; Wang, J.Y.  
Deposited on : 2019-07-02  
Resolution : 3.11 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>.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.37.1  
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) : 2.37.1

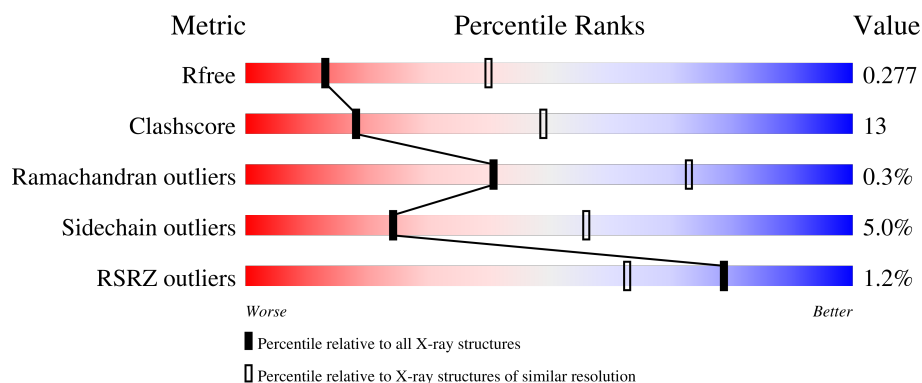
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.11 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	1292 (3.14-3.10)
Clashscore	141614	1389 (3.14-3.10)
Ramachandran outliers	138981	1337 (3.14-3.10)
Sidechain outliers	138945	1337 (3.14-3.10)
RSRZ outliers	127900	1260 (3.14-3.10)

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	325	<div> <div>58%</div> <div>20%</div> <div>•</div> <div>19%</div> </div>
1	B	325	<div> <div>4%</div> <div>62%</div> <div>24%</div> <div>•</div> <div>13%</div> </div>
1	C	325	<div> <div>4%</div> <div>63%</div> <div>17%</div> <div>•</div> <div>19%</div> </div>
1	D	325	<div> <div>66%</div> <div>19%</div> <div>•</div> <div>14%</div> </div>
2	E	23	<div> <div>4%</div> <div>43%</div> <div>22%</div> <div>35%</div> </div>

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	G	23	<div><div></div><div></div><div></div><div>30%</div><div>35%</div><div>35%</div></div>
3	F	23	<div><div></div><div></div><div></div><div>4%</div><div>39%</div><div>9%</div><div>52%</div></div>
3	H	23	<div><div></div><div></div><div></div><div>9%</div><div>22%</div><div>35%</div><div>43%</div></div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 9174 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 CRISPR-associated endonuclease Cas1 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	283	Total	C	N	O	S	Se	0	0	0
			2086	1336	383	362	1	4			
1	A	263	Total	C	N	O	S	Se	0	0	0
			1991	1270	371	345	1	4			
1	D	280	Total	C	N	O	S	Se	0	0	0
			2076	1330	379	362	1	4			
1	C	264	Total	C	N	O	S	Se	0	0	0
			1954	1243	364	342	1	4			

- Molecule 2 is a DNA chain called DNA (5'-D(\*GP\*AP\*GP\*TP\*CP\*GP\*AP\*TP\*GP\*CP\*TP\*GP\*GP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	15	Total	C	N	O	P	0	0	0
			296	139	43	99	15			
2	G	15	Total	C	N	O	P	0	0	0
			296	139	43	99	15			

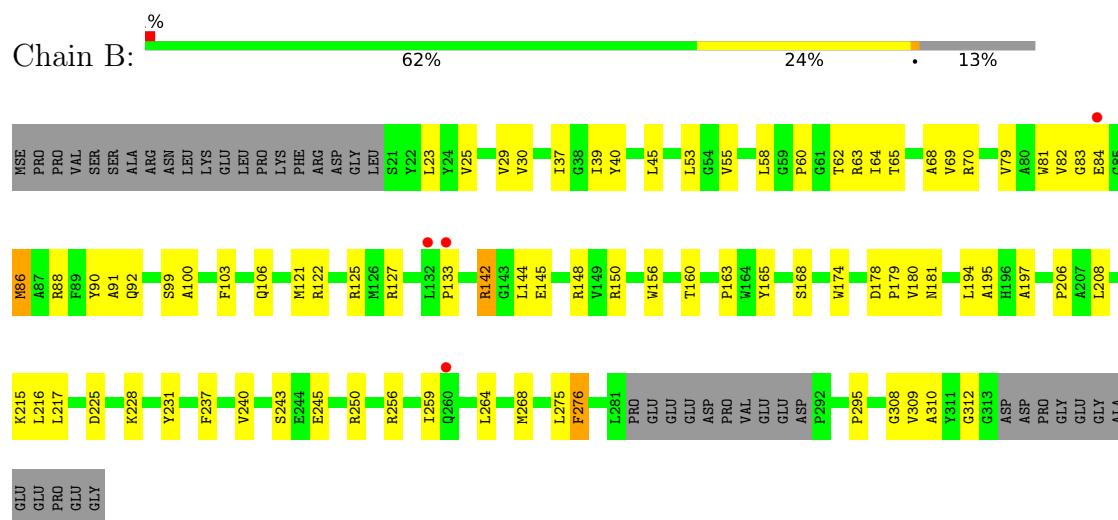
- Molecule 3 is a DNA chain called DNA (5'-D(\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*CP\*CP\*AP\*GP\*CP\*AP\*TP\*CP\*GP\*AP\*CP\*TP\*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	11	Total	C	N	O	P	0	0	0
			218	104	35	68	11			
3	H	13	Total	C	N	O	P	0	0	0
			257	123	39	82	13			

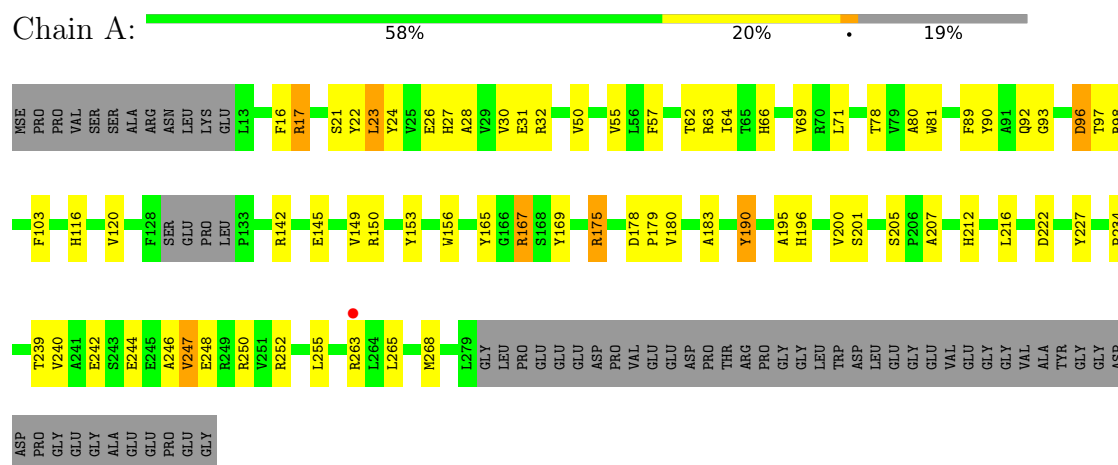
### 3 Residue-property plots [i](#)

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.

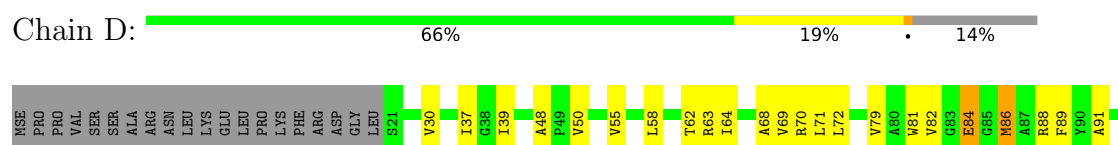
- Molecule 1: CRISPR-associated endonuclease Cas1 2

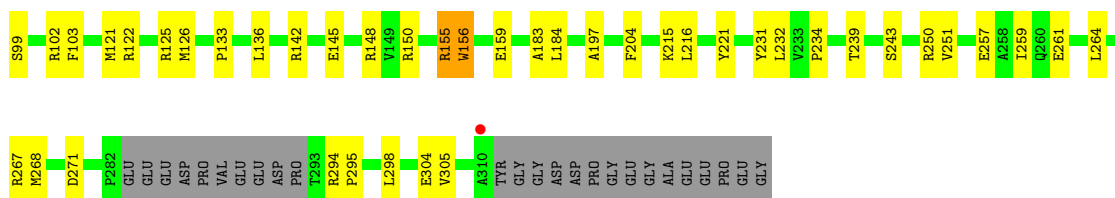


- Molecule 1: CRISPR-associated endonuclease Cas1 2

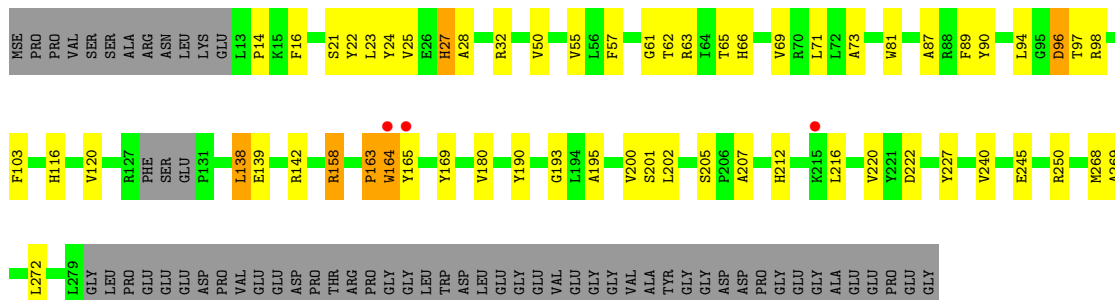


- Molecule 1: CRISPR-associated endonuclease Cas1 2

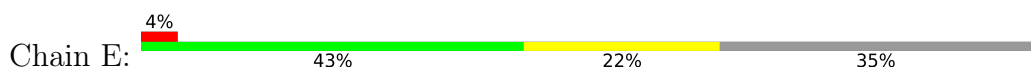




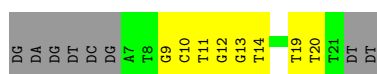
- Molecule 1: CRISPR-associated endonuclease Cas1 2



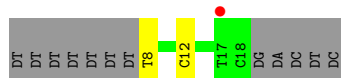
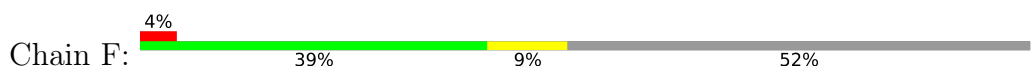
- Molecule 2: DNA (5'-D(\*GP\*AP\*GP\*TP\*CP\*GP\*AP\*TP\*GP\*CP\*TP\*GP\*GP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*T)-3')



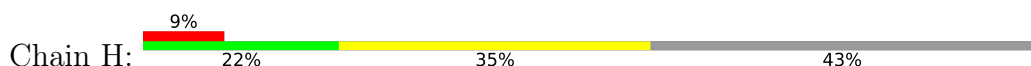
- Molecule 2: DNA (5'-D(\*GP\*AP\*GP\*TP\*CP\*GP\*AP\*TP\*GP\*CP\*TP\*GP\*GP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*T)-3')



- Molecule 3: DNA (5'-D(\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*CP\*CP\*AP\*GP\*CP\*AP\*TP\*CP\*GP\*AP\*CP\*TP\*C)-3')



- Molecule 3: DNA (5'-D(\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*CP\*CP\*AP\*GP\*CP\*AP\*TP\*CP\*GP\*AP\*CP\*TP\*C)-3')





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	116.55Å 201.20Å 77.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.89 – 3.11 19.89 – 3.11	Depositor EDS
% Data completeness (in resolution range)	99.2 (19.89-3.11) 99.2 (19.89-3.11)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.13	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.01 (at 3.09Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472, PHENIX 1.15.2_3472	Depositor
R, $R_{free}$	0.239 , 0.279 0.239 , 0.277	Depositor DCC
$R_{free}$ test set	1698 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	115.5	Xtriage
Anisotropy	0.300	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 82.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	9174	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	121.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% 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	0.36	0/2031	0.54	0/2748
1	B	0.41	0/2131	0.56	0/2892
1	C	0.45	0/1992	0.61	1/2699 (0.0%)
1	D	0.36	0/2121	0.52	0/2881
2	E	0.73	0/329	1.21	0/502
2	G	0.64	0/329	1.23	0/502
3	F	0.53	0/242	0.97	0/369
3	H	0.66	0/285	1.10	0/435
All	All	0.44	0/9460	0.67	1/13028 (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	14	PRO	N-CA-CB	5.68	110.11	103.30

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	1991	0	1929	77	1
1	B	2086	0	1976	75	0
1	C	1954	0	1848	56	0
1	D	2076	0	1972	61	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	296	0	146	6	0
2	G	296	0	146	12	0
3	F	218	0	120	4	0
3	H	257	0	141	10	0
All	All	9174	0	8278	233	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 13.

The worst 5 of 233 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:174:TRP:CH2	1:D:63:ARG:CB	2.21	1.23
1:D:221:TYR:OH	1:C:96:ASP:OD2	1.54	1.23
1:B:174:TRP:CZ3	1:D:63:ARG:CB	2.29	1.14
1:A:239:THR:O	1:A:250:ARG:NH2	1.83	1.10
1:D:86:MSE:CE	1:C:66:HIS:CE1	2.34	1.10

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:A:175:ARG:NH2	1:A:244:GLU:OE2[2_655]	2.14	0.06

## 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	259/325 (80%)	249 (96%)	10 (4%)	0	100	100
1	B	279/325 (86%)	260 (93%)	18 (6%)	1 (0%)	34	68

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	260/325 (80%)	247 (95%)	11 (4%)	2 (1%)	19	53
1	D	276/325 (85%)	264 (96%)	12 (4%)	0	100	100
All	All	1074/1300 (83%)	1020 (95%)	51 (5%)	3 (0%)	41	73

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	163	PRO
1	C	165	TYR
1	B	295	PRO

### 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	179/243 (74%)	168 (94%)	11 (6%)	18	49
1	B	179/243 (74%)	168 (94%)	11 (6%)	18	49
1	C	168/243 (69%)	161 (96%)	7 (4%)	30	62
1	D	181/243 (74%)	175 (97%)	6 (3%)	38	68
All	All	707/972 (73%)	672 (95%)	35 (5%)	24	56

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	27	HIS
1	C	96	ASP
1	C	158	ARG
1	A	23	LEU
1	A	17	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	173	ASN
1	A	27	HIS

### 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 [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	259/325 (79%)	-0.24	1 (0%) 92 85	81, 114, 148, 168	0
1	B	279/325 (85%)	-0.08	4 (1%) 75 58	76, 112, 155, 175	0
1	C	260/325 (80%)	-0.09	3 (1%) 79 63	74, 131, 184, 209	0
1	D	276/325 (84%)	-0.11	1 (0%) 92 85	74, 107, 150, 177	0
2	E	15/23 (65%)	0.48	1 (6%) 17 7	126, 150, 193, 202	0
2	G	15/23 (65%)	0.18	0 100 100	104, 138, 189, 194	0
3	F	11/23 (47%)	0.45	1 (9%) 9 3	99, 114, 179, 185	0
3	H	13/23 (56%)	0.47	2 (15%) 2 1	90, 118, 190, 199	0
All	All	1128/1392 (81%)	-0.11	13 (1%) 79 63	74, 114, 170, 209	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	260	GLN	4.2
2	E	21	DT	3.9
1	B	84	GLU	3.2
1	B	132	LEU	3.0
1	C	164	TRP	2.8

### 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.