



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 13, 2020 – 12:33 am BST

PDB ID : 3EK6  
Title : Unique GTP-binding Pocket and Allostery of UMP Kinase from a Gram-Negative Phytopathogen Bacterium  
Authors : Tu, J.-L.; Chin, K.-H.; Wang, A.H.-J.; Chou, S.-H.  
Deposited on : 2008-09-18  
Resolution : 2.34 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  
Xtrriage (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

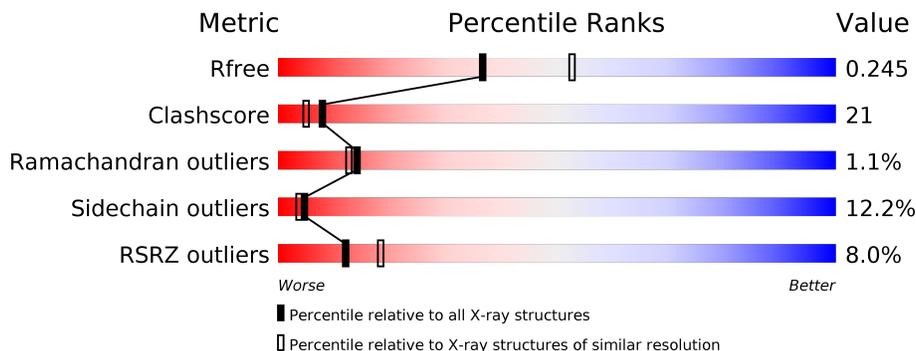
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.34 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	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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	243	
1	B	243	
1	C	243	
1	D	243	
1	E	243	
1	F	243	

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 11284 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 Uridylate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	243	Total 1823	C 1141	N 328	O 343	S 11	0	0	0
1	B	240	Total 1804	C 1131	N 324	O 338	S 11	0	0	0
1	C	238	Total 1790	C 1123	N 322	O 335	S 10	0	0	0
1	D	240	Total 1804	C 1131	N 324	O 338	S 11	0	0	0
1	E	238	Total 1784	C 1120	N 322	O 332	S 10	0	0	1
1	F	238	Total 1790	C 1123	N 322	O 335	S 10	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	EXPRESSION TAG	UNP P59009
A	-1	ASN	-	EXPRESSION TAG	UNP P59009
A	0	ALA	-	EXPRESSION TAG	UNP P59009
B	-2	SER	-	EXPRESSION TAG	UNP P59009
B	-1	ASN	-	EXPRESSION TAG	UNP P59009
B	0	ALA	-	EXPRESSION TAG	UNP P59009
C	-2	SER	-	EXPRESSION TAG	UNP P59009
C	-1	ASN	-	EXPRESSION TAG	UNP P59009
C	0	ALA	-	EXPRESSION TAG	UNP P59009
D	-2	SER	-	EXPRESSION TAG	UNP P59009
D	-1	ASN	-	EXPRESSION TAG	UNP P59009
D	0	ALA	-	EXPRESSION TAG	UNP P59009
E	-2	SER	-	EXPRESSION TAG	UNP P59009
E	-1	ASN	-	EXPRESSION TAG	UNP P59009
E	0	ALA	-	EXPRESSION TAG	UNP P59009
F	-2	SER	-	EXPRESSION TAG	UNP P59009
F	-1	ASN	-	EXPRESSION TAG	UNP P59009

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Chain	Residue	Modelled	Actual	Comment	Reference
F	0	ALA	-	EXPRESSION TAG	UNP P59009

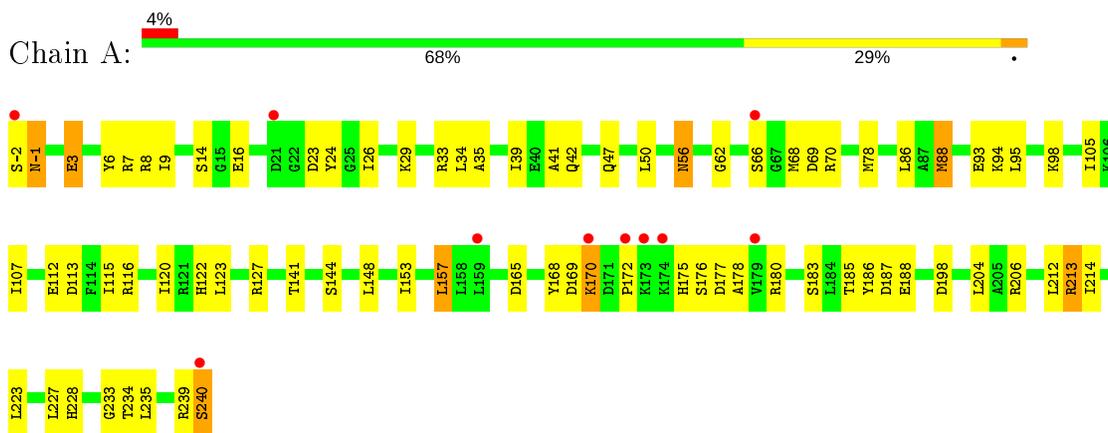
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	102	Total O 102 102	0	0
2	B	90	Total O 90 90	0	0
2	C	110	Total O 110 110	0	0
2	D	69	Total O 69 69	0	0
2	E	54	Total O 54 54	0	0
2	F	64	Total O 64 64	0	0

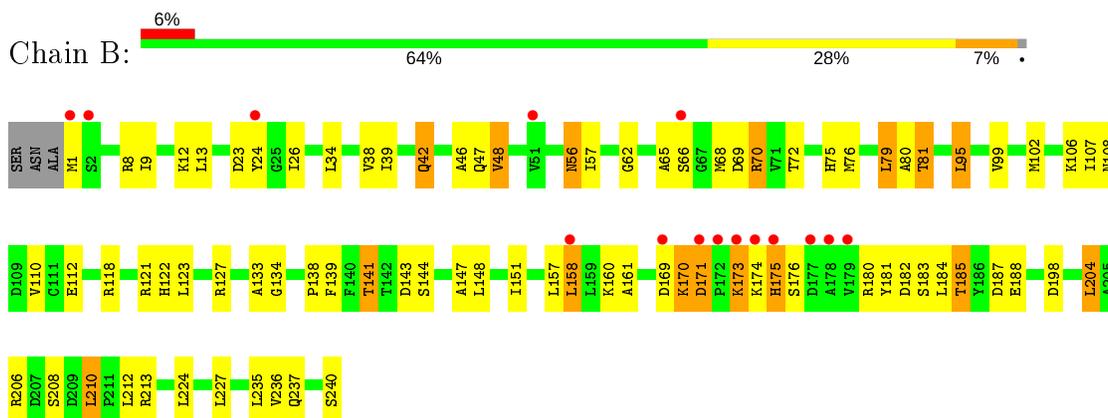
### 3 Residue-property plots [i](#)

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.

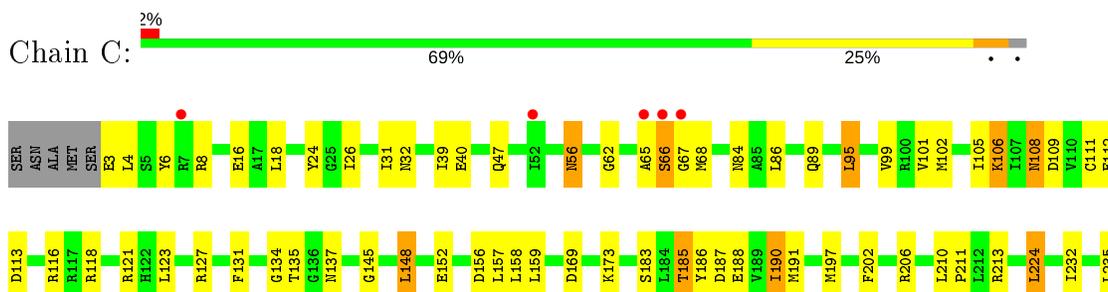
- Molecule 1: Uridylate kinase

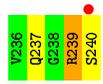


- Molecule 1: Uridylate kinase

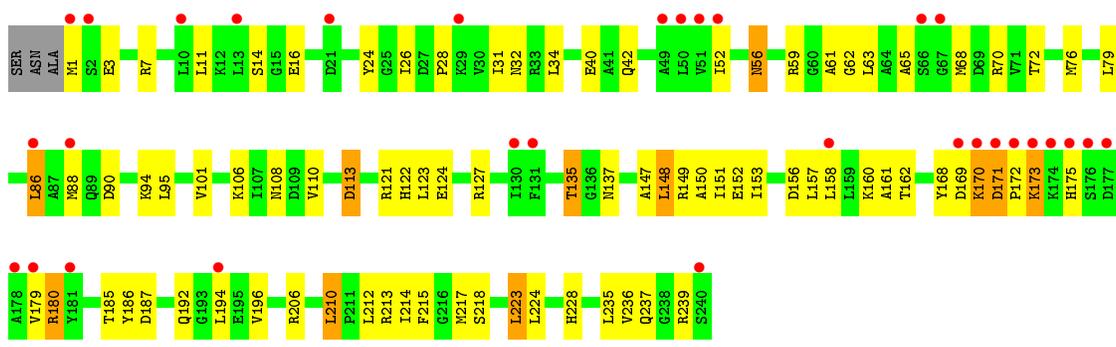


- Molecule 1: Uridylate kinase

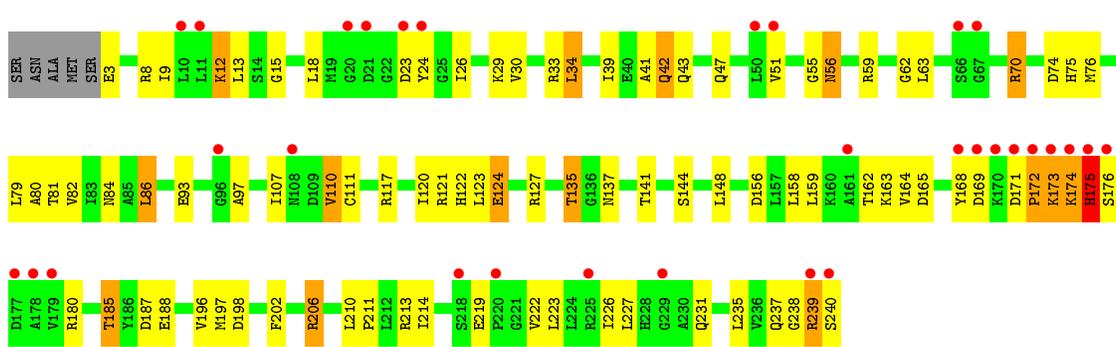




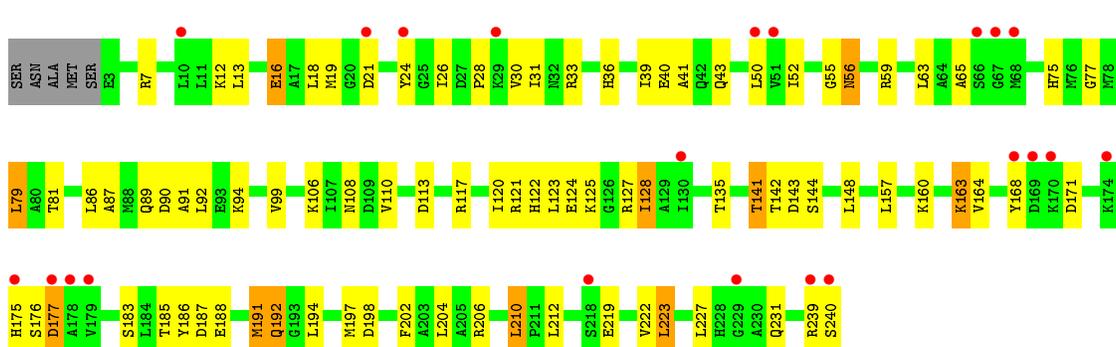
• Molecule 1: Uridylate kinase



• Molecule 1: Uridylate kinase



• Molecule 1: Uridylate kinase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	111.47Å 120.10Å 125.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.35 – 2.34 29.35 – 2.34	Depositor EDS
% Data completeness (in resolution range)	98.8 (29.35-2.34) 98.8 (29.35-2.34)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.53 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.207 , 0.246 0.207 , 0.245	Depositor DCC
$R_{free}$ test set	3603 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	41.4	Xtriage
Anisotropy	0.150	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 41.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.016 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	11284	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% 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	0.55	0/1844	0.71	0/2480
1	B	0.56	0/1825	0.72	0/2454
1	C	0.55	0/1811	0.71	0/2436
1	D	0.49	0/1825	0.66	0/2454
1	E	0.45	0/1805	0.60	0/2430
1	F	0.43	0/1811	0.65	0/2436
All	All	0.51	0/10921	0.67	0/14690

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	1823	0	1868	75	0
1	B	1804	0	1852	79	0
1	C	1790	0	1835	87	1
1	D	1804	0	1852	77	1
1	E	1784	0	1830	99	0
1	F	1790	0	1835	73	0
2	A	102	0	0	20	0
2	B	90	0	0	10	0
2	C	110	0	0	24	0
2	D	69	0	0	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	54	0	0	10	0
2	F	64	0	0	10	0
All	All	11284	0	11072	470	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 21.

The worst 5 of 470 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:C:169:ASP:HB3	2:C:1061:HOH:O	1.22	1.29
1:B:1:MET:HE2	2:B:1438:HOH:O	1.28	1.27
1:C:101:VAL:HB	2:C:1471:HOH:O	1.16	1.26
1:A:3:GLU:HG3	2:A:1440:HOH:O	1.40	1.21
2:A:1451:HOH:O	1:C:68:MET:CE	1.91	1.16

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:66:SER:OG	1:D:228:HIS:O[2_565]	2.17	0.03

## 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	241/243 (99%)	232 (96%)	7 (3%)	2 (1%)	19 20
1	B	238/243 (98%)	229 (96%)	7 (3%)	2 (1%)	19 20
1	C	236/243 (97%)	229 (97%)	6 (2%)	1 (0%)	34 38
1	D	238/243 (98%)	228 (96%)	8 (3%)	2 (1%)	19 20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	236/243 (97%)	220 (93%)	10 (4%)	6 (2%)	5	3
1	F	236/243 (97%)	225 (95%)	9 (4%)	2 (1%)	19	20
All	All	1425/1458 (98%)	1363 (96%)	47 (3%)	15 (1%)	14	13

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	-1	ASN
1	B	170	LYS
1	B	171	ASP
1	E	172	PRO
1	E	173	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	186/186 (100%)	165 (89%)	21 (11%)	6	5
1	B	184/186 (99%)	158 (86%)	26 (14%)	3	3
1	C	182/186 (98%)	165 (91%)	17 (9%)	9	8
1	D	184/186 (99%)	158 (86%)	26 (14%)	3	3
1	E	181/186 (97%)	160 (88%)	21 (12%)	5	4
1	F	182/186 (98%)	159 (87%)	23 (13%)	4	3
All	All	1099/1116 (98%)	965 (88%)	134 (12%)	5	4

5 of 134 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	210	LEU
1	D	110	VAL
1	F	163	LYS
1	C	235	LEU
1	D	56	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	137	ASN
1	D	84	ASN
1	F	84	ASN
1	C	192	GLN
1	C	237	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 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	243/243 (100%)	0.25	10 (4%) 37 48	24, 40, 58, 65	0
1	B	240/243 (98%)	0.45	15 (6%) 20 28	26, 41, 61, 71	0
1	C	238/243 (97%)	0.13	6 (2%) 57 66	25, 40, 56, 65	0
1	D	240/243 (98%)	0.64	31 (12%) 3 6	31, 49, 67, 73	0
1	E	238/243 (97%)	0.83	31 (13%) 3 6	36, 52, 68, 76	0
1	F	238/243 (97%)	0.46	22 (9%) 9 14	35, 51, 69, 75	0
All	All	1437/1458 (98%)	0.46	115 (8%) 12 18	24, 45, 65, 76	0

The worst 5 of 115 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	240	SER	10.0
1	E	168	TYR	9.2
1	E	176	SER	7.4
1	E	175	HIS	6.2
1	E	173	LYS	6.1

### 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

There are no such residues in this entry.