



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 16, 2023 – 12:45 pm GMT

PDB ID : 4AXG  
Title : Structure of eIF4E-Cup complex  
Authors : Kinkelin, K.; Veith, K.; Gruenwald, M.; Bono, F.  
Deposited on : 2012-06-12  
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 : 2.36  
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

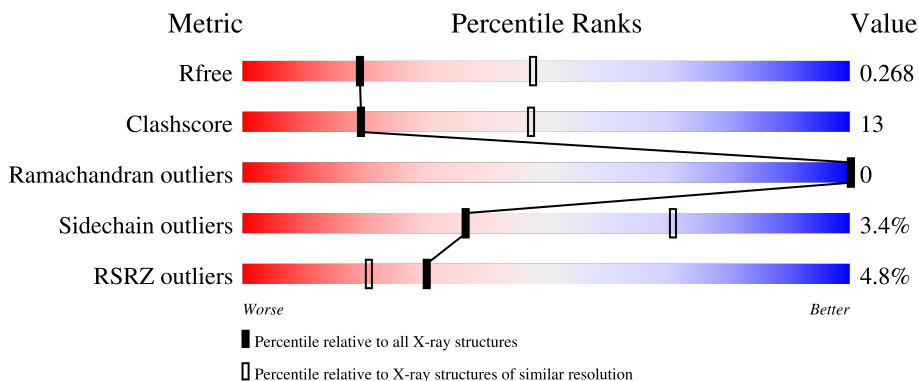
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	248	
1	B	248	
2	C	130	
2	D	130	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3047 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 EUKARYOTIC TRANSLATION INITIATION FACTOR 4E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	181	1439	912	245	276	6	0	0	0
1	B	167	1205	769	204	230	2	0	0	0

- Molecule 2 is a protein called PROTEIN CUP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	37	288	176	59	50	3	0	0	0
2	D	15	101	63	18	19	1	0	0	0

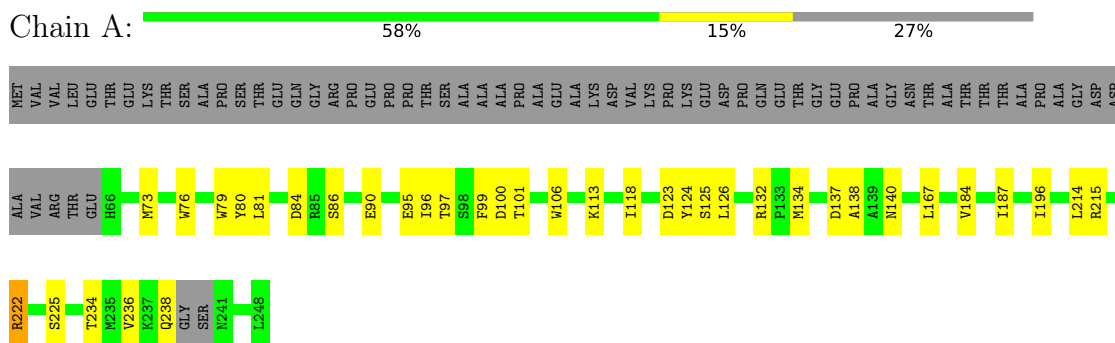
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	13	Total	O	0	0
			13	13		
3	B	1	Total	O	0	0
			1	1		

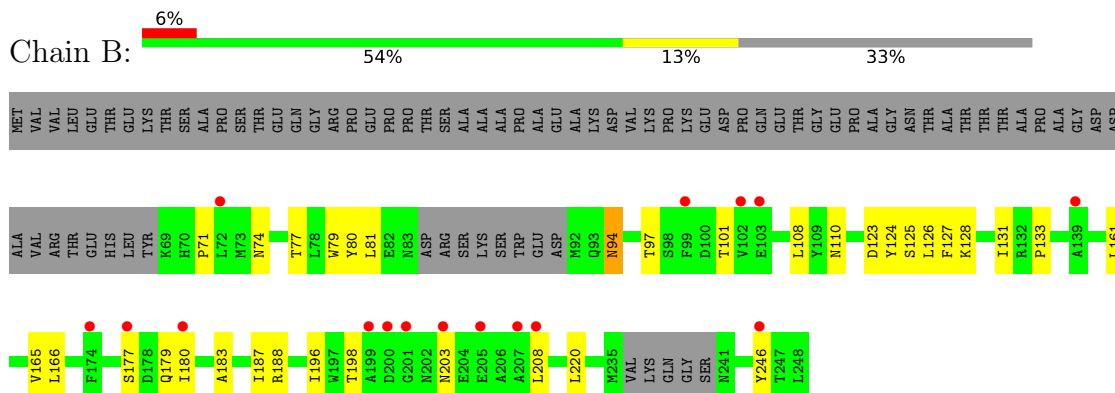
### 3 Residue-property plots [\(i\)](#)

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.

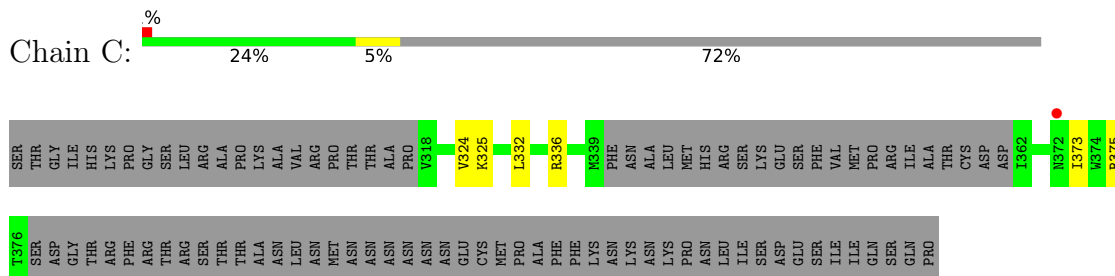
#### • Molecule 1: EUKARYOTIC TRANSLATION INITIATION FACTOR 4E



#### • Molecule 1: EUKARYOTIC TRANSLATION INITIATION FACTOR 4E



#### • Molecule 2: PROTEIN CUP



#### • Molecule 2: PROTEIN CUP



SER	LEU	GLN
THR	GLU	PRO
GLY	GLY	
ILE	ARG	
HIS	LEU	
LYS	ARG	
PRO	ARG	
GLY	MET	
SER	ASN	
LEU	ILE	
ARG	TRP	
ALA	ARG	
PRO	THR	
LYS	SER	
ALA	ASP	
VAL	GLY	
ARG	THR	
PRO	ARG	
THR	PHE	
THR	ARG	
ALA	THR	
PRO	ARG	
VAL	SER	
VAL	THR	
SER	THR	
SER	ALA	
LYS	ASN	
PRO	LEU	
VAL	ASN	
K325	MET	
S326	ASN	
Y327	ASN	
	ASN	
	ASN	
	ASN	
	ASN	
	ASN	
	GLU	
	CYS	
	MET	
	PRO	
	ALA	
	ALA	
	PHE	
	LYS	
	SER	
	LYS	
	GLU	
	SER	
	SER	
	PHE	
	VAL	
	VAL	
	MET	
	PRO	
	ARG	
	ILE	
	ILE	
	ALA	
	THR	
	CYS	
	ASP	
	ASP	
	ILE	
	GLN	
	SER	

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	142.58Å 142.58Å 108.05Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	81.31 – 2.80 81.31 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (81.31-2.80) 100.0 (81.31-2.80)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.01 (at 2.82Å)	Xtrriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.228 , 0.244 0.254 , 0.268	Depositor DCC
$R_{free}$ test set	825 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	67.1	Xtrriage
Anisotropy	0.409	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 65.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	3047	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	77.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.27% 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	0.30	0/1472	0.41	0/2002
1	B	0.28	0/1230	0.41	0/1686
2	C	0.24	0/290	0.41	0/386
2	D	0.22	0/101	0.32	0/136
All	All	0.29	0/3093	0.41	0/4210

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	1439	0	1347	49	0
1	B	1205	0	1042	25	0
2	C	288	0	280	18	0
2	D	101	0	80	1	0
3	A	13	0	0	0	0
3	B	1	0	0	0	0
All	All	3047	0	2749	74	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 13.

All (74) 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:A:73:MET:CE	2:C:324:VAL:HA	1.36	1.54
1:A:73:MET:CE	2:C:324:VAL:CA	2.28	1.11
1:A:73:MET:HE1	2:C:324:VAL:CA	1.81	1.10
1:A:222:ARG:HD2	1:A:222:ARG:H	1.35	0.90
1:A:73:MET:HE2	2:C:325:LYS:H	1.37	0.88
1:A:73:MET:CE	2:C:325:LYS:H	1.87	0.87
1:A:73:MET:HE1	2:C:324:VAL:HA	0.87	0.86
1:A:222:ARG:HD2	1:A:222:ARG:N	1.90	0.86
1:B:97:THR:CG2	1:B:108:LEU:HD22	2.09	0.83
1:A:222:ARG:HH11	1:A:222:ARG:HA	1.47	0.79
1:A:132:ARG:NH1	1:A:134:MET:SD	2.56	0.78
1:A:73:MET:HE2	2:C:324:VAL:HA	1.63	0.77
1:A:81:LEU:HB3	1:A:123:ASP:HB2	1.65	0.77
1:A:73:MET:HE2	2:C:325:LYS:N	2.01	0.74
1:A:73:MET:HE3	2:C:324:VAL:HA	1.65	0.74
1:A:236:VAL:CG1	1:A:238:GLN:O	2.36	0.73
1:A:118:ILE:HD11	1:A:187:ILE:HD13	1.72	0.72
1:A:73:MET:CE	2:C:325:LYS:N	2.53	0.71
1:A:99:PHE:CZ	1:A:126:LEU:HD11	2.26	0.70
1:A:234:THR:HG22	1:A:234:THR:O	1.95	0.66
1:B:94:ASN:N	1:B:94:ASN:OD1	2.30	0.64
1:B:97:THR:HG21	1:B:108:LEU:HD22	1.80	0.64
1:B:208:LEU:HD21	1:B:246:TYR:CD2	2.33	0.63
1:A:222:ARG:HG3	1:A:222:ARG:NH1	2.12	0.63
1:A:99:PHE:HZ	1:A:126:LEU:HD11	1.62	0.62
1:A:234:THR:O	1:A:234:THR:CG2	2.48	0.62
1:A:134:MET:O	1:A:140:ASN:ND2	2.30	0.62
1:A:222:ARG:HH11	1:A:222:ARG:CG	2.14	0.61
1:A:222:ARG:HH11	1:A:222:ARG:CA	2.14	0.60
1:A:196:ILE:HG13	1:A:214:LEU:HD11	1.86	0.58
1:A:222:ARG:HH11	1:A:222:ARG:HG3	1.67	0.58
1:B:81:LEU:HB3	1:B:123:ASP:HB2	1.86	0.57
1:A:125:SER:OG	1:A:184:VAL:HG23	2.04	0.57
1:A:76:TRP:HB2	1:A:99:PHE:CZ	2.41	0.56
1:B:80:TYR:O	1:B:94:ASN:OD1	2.24	0.56
1:A:73:MET:HE3	2:C:325:LYS:H	1.70	0.55
1:A:236:VAL:HG11	1:A:238:GLN:O	2.05	0.55
1:A:106:TRP:CE2	2:C:336:ARG:HB2	2.42	0.55
1:A:167:LEU:HD22	2:C:332:LEU:HD13	1.89	0.55
1:B:97:THR:HG22	1:B:108:LEU:HD22	1.86	0.55
1:A:76:TRP:HB2	1:A:99:PHE:CE2	2.42	0.54
1:A:222:ARG:HA	1:A:222:ARG:NH1	2.19	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:TRP:HB2	1:A:125:SER:HB2	1.91	0.53
1:B:179:GLN:NE2	1:B:203:ASN:HD22	2.07	0.53
1:A:222:ARG:NH1	1:A:222:ARG:CG	2.73	0.51
1:B:110:ASN:OD1	2:D:336:ARG:NH1	2.42	0.51
1:B:79:TRP:HB2	1:B:125:SER:HB2	1.93	0.51
1:B:79:TRP:CZ3	1:B:127:PHE:HB2	2.46	0.51
1:B:161:LEU:HD11	1:B:220:LEU:HD21	1.92	0.50
1:B:74:ASN:HD22	1:B:128:LYS:HD3	1.77	0.50
1:A:215:ARG:HH21	1:A:222:ARG:NH2	2.10	0.49
1:A:86:SER:HB2	1:A:90:GLU:HB2	1.95	0.49
1:A:73:MET:HE3	2:C:324:VAL:HG13	1.94	0.48
1:B:179:GLN:HE22	1:B:203:ASN:HD22	1.61	0.48
1:B:127:PHE:CE2	1:B:133:PRO:HA	2.47	0.48
1:B:71:PRO:HA	1:B:101:THR:HG22	1.95	0.47
1:A:80:TYR:HB2	1:A:96:ILE:HD11	1.96	0.47
1:B:180:ILE:HG22	1:B:198:THR:HG22	1.96	0.47
1:A:137:ASP:OD1	1:A:138:ALA:N	2.48	0.46
1:A:222:ARG:N	1:A:222:ARG:CD	2.73	0.46
1:B:128:LYS:HE2	1:B:180:ILE:O	2.15	0.46
1:A:73:MET:HE3	2:C:324:VAL:CA	2.34	0.45
1:B:128:LYS:HB2	1:B:131:ILE:HD12	1.97	0.45
1:B:126:LEU:HD22	1:B:166:LEU:HD22	1.98	0.44
1:B:187:ILE:O	1:B:188:ARG:HD3	2.17	0.44
1:A:100:ASP:OD1	1:A:101:THR:HG23	2.18	0.43
1:A:73:MET:HE3	2:C:325:LYS:N	2.29	0.42
1:A:81:LEU:HD21	1:A:84:ASP:HA	2.01	0.42
1:A:80:TYR:CD2	2:C:373:ILE:HD11	2.55	0.41
1:B:208:LEU:HD21	1:B:246:TYR:HD2	1.82	0.41
1:B:183:ALA:HB2	1:B:196:ILE:HD13	2.02	0.41
1:B:180:ILE:HA	1:B:198:THR:HA	2.02	0.41
1:A:113:LYS:HG3	2:C:373:ILE:O	2.21	0.41
1:B:165:VAL:HG13	1:B:196:ILE:HD11	2.01	0.40

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	177/248 (71%)	173 (98%)	4 (2%)	0	100	100
1	B	161/248 (65%)	160 (99%)	1 (1%)	0	100	100
2	C	33/130 (25%)	33 (100%)	0	0	100	100
2	D	13/130 (10%)	13 (100%)	0	0	100	100
All	All	384/756 (51%)	379 (99%)	5 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 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	152/215 (71%)	147 (97%)	5 (3%)	38	72
1	B	108/215 (50%)	104 (96%)	4 (4%)	34	68
2	C	29/118 (25%)	28 (97%)	1 (3%)	37	71
2	D	7/118 (6%)	7 (100%)	0	100	100
All	All	296/666 (44%)	286 (97%)	10 (3%)	37	71

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	95	GLU
1	A	97	THR
1	A	124	TYR
1	A	222	ARG
1	A	225	SER
1	B	77	THR
1	B	94	ASN
1	B	124	TYR

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Mol	Chain	Res	Type
1	B	177	SER
2	C	375	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	142	GLN
1	B	179	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 [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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	181/248 (72%)	0.10	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	31, 55, 106, 155	0
1	B	167/248 (67%)	0.51	16 (9%) <span style="border: 1px solid red; padding: 2px;">8</span> <span style="border: 1px solid red; padding: 2px;">4</span>	44, 95, 140, 154	0
2	C	37/130 (28%)	0.09	1 (2%) <span style="border: 1px solid gray; padding: 2px;">54</span> <span style="border: 1px solid gray; padding: 2px;">44</span>	36, 82, 116, 127	0
2	D	15/130 (11%)	-0.03	2 (13%) <span style="border: 1px solid red; padding: 2px;">3</span> <span style="border: 1px solid red; padding: 2px;">2</span>	86, 111, 133, 133	0
All	All	400/756 (52%)	0.26	19 (4%) <span style="border: 1px solid red; padding: 2px;">30</span> <span style="border: 1px solid red; padding: 2px;">21</span>	31, 75, 134, 155	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	208	LEU	4.7
1	B	174	PHE	4.2
1	B	102	VAL	3.7
2	D	326	SER	3.4
1	B	203	ASN	3.4
1	B	205	GLU	3.2
1	B	180	ILE	3.0
1	B	246	TYR	3.0
1	B	99	PHE	2.8
1	B	103	GLU	2.7
1	B	177	SER	2.6
1	B	72	LEU	2.5
2	C	372	ASN	2.5
1	B	201	GLY	2.4
2	D	327	TYR	2.4
1	B	200	ASP	2.3
1	B	139	ALA	2.1
1	B	207	ALA	2.1
1	B	199	ALA	2.0

## 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.