



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:26 AM GMT

PDB ID : 3ENP  
Title : Crystal structure of human cgi121  
Authors : Haffani, Y.Z.; Ceccarelli, D.F.; Neculai, D.; Mao, D.Y.; Sicheri, F.  
Deposited on : 2008-09-25  
Resolution : 2.48 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  
<http://wwpdb.org/validation/2016/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  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

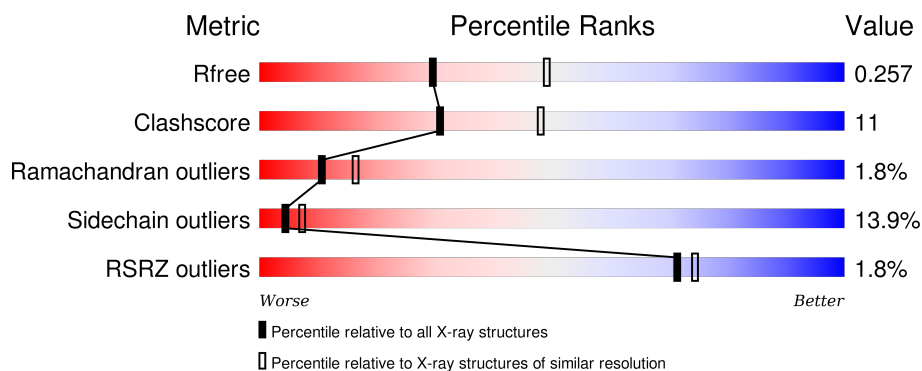
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*



The reported resolution of this entry is 2.48 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))
$R_{free}$	91344	4309 (2.50-2.46)
Clashscore	102246	5050 (2.50-2.46)
Ramachandran outliers	100387	4961 (2.50-2.46)
Sidechain outliers	100360	4963 (2.50-2.46)
RSRZ outliers	91569	4319 (2.50-2.46)

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. 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	177	 2% 71% 15% 7% . .
1	B	177	 2% 71% 18% 7% . .

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2654 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 TP53RK-binding protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	172	Total	C	N	O	S	Se	0	0	0
			1320	843	217	253	2	5			
1	B	172	Total	C	N	O	S	Se	0	0	0
			1316	838	218	253	2	5			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP Q9Y3C4
A	0	ALA	-	EXPRESSION TAG	UNP Q9Y3C4
B	-1	GLY	-	EXPRESSION TAG	UNP Q9Y3C4
B	0	ALA	-	EXPRESSION TAG	UNP Q9Y3C4

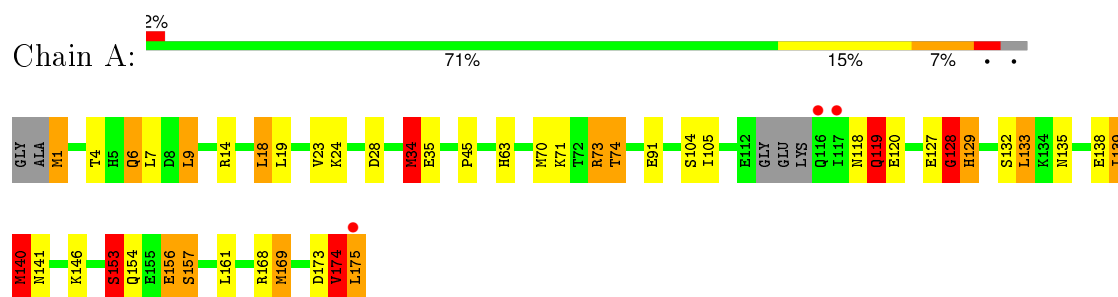
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	O	0	0
			4	4		
2	B	14	Total	O	0	0
			14	14		

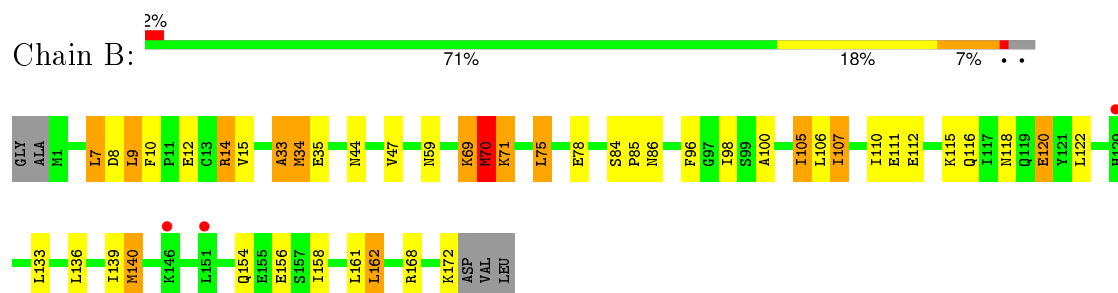
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: TP53RK-binding protein



- Molecule 1: TP53RK-binding protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 62	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	93.52Å 93.52Å 87.16Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.61 – 2.48 30.61 – 2.48	Depositor EDS
% Data completeness (in resolution range)	99.8 (30.61-2.48) 99.8 (30.61-2.48)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.21 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.4.0066	Depositor
R, $R_{free}$	0.211 , 0.257 0.215 , 0.257	Depositor DCC
$R_{free}$ test set	779 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	61.2	Xtriage
Anisotropy	0.251	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 50.2	EDS
Estimated twinning fraction	0.057 for h,-h-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 15398 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	2654	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.88% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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	1.00	10/1330 (0.8%)	1.31	10/1794 (0.6%)
1	B	0.82	3/1328 (0.2%)	1.02	5/1793 (0.3%)
All	All	0.91	13/2658 (0.5%)	1.18	15/3587 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7
1	B	0	6
All	All	0	13

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	157	SER	CB-OG	11.78	1.57	1.42
1	A	129	HIS	N-CA	11.08	1.68	1.46
1	A	156	GLU	CD-OE1	9.12	1.35	1.25
1	B	120	GLU	CB-CG	7.96	1.67	1.52
1	A	127	GLU	C-N	7.03	1.45	1.33
1	B	120	GLU	CG-CD	6.96	1.62	1.51
1	A	70	MSE	C-N	6.70	1.49	1.34
1	A	153	SER	C-N	5.91	1.47	1.34
1	A	128	GLY	C-O	-5.70	1.14	1.23
1	B	100	ALA	C-O	5.70	1.34	1.23
1	A	154	GLN	CA-CB	5.49	1.66	1.53
1	A	128	GLY	N-CA	5.12	1.53	1.46
1	A	127	GLU	N-CA	5.08	1.56	1.46

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	34	MSE	O-C-N	-30.96	73.16	122.70
1	A	1	MSE	O-C-N	-20.15	90.47	122.70
1	B	34	MSE	O-C-N	-18.43	93.21	122.70
1	B	34	MSE	CA-C-N	13.80	147.57	117.20
1	A	34	MSE	CA-C-N	13.50	146.90	117.20
1	B	70	MSE	C-N-CA	-8.77	99.78	121.70
1	A	140	MSE	O-C-N	-8.22	109.55	122.70
1	A	1	MSE	C-N-CA	7.78	141.14	121.70
1	B	34	MSE	C-N-CA	7.36	140.10	121.70
1	A	169	MSE	O-C-N	-7.35	110.94	122.70
1	B	140	MSE	O-C-N	-6.93	111.61	122.70
1	A	34	MSE	C-N-CA	6.60	138.21	121.70
1	A	70	MSE	C-N-CA	-6.58	105.24	121.70
1	A	174	VAL	C-N-CA	5.43	135.28	121.70
1	A	18	LEU	CA-CB-CG	5.21	127.28	115.30

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1	MSE	Mainchain
1	A	128	GLY	Mainchain
1	A	140	MSE	Mainchain
1	A	168	ARG	Mainchain
1	A	169	MSE	Mainchain
1	A	34	MSE	Mainchain,Peptide
1	B	139	ILE	Mainchain
1	B	140	MSE	Mainchain
1	B	168	ARG	Mainchain
1	B	33	ALA	Mainchain
1	B	69	LYS	Mainchain
1	B	70	MSE	Mainchain

## 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	1320	0	1356	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1316	0	1340	28	0
2	A	4	0	0	0	0
2	B	14	0	0	1	0
All	All	2654	0	2696	58	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 11.

All (58) 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:129:HIS:N	1:A:129:HIS:CA	1.68	1.54
1:A:118:ASN:HA	1:A:119:GLN:HB2	1.23	1.11
1:B:98:ILE:HG21	1:B:105:ILE:HD13	1.21	1.09
1:B:70:MSE:HE1	1:B:75:LEU:HA	1.12	1.09
1:B:98:ILE:CG2	1:B:105:ILE:HD13	1.90	1.00
1:A:6:GLN:HA	1:A:6:GLN:HE21	1.29	0.94
1:B:98:ILE:HG21	1:B:105:ILE:CD1	2.01	0.91
1:B:70:MSE:CE	1:B:75:LEU:HA	2.01	0.90
1:B:70:MSE:HE2	1:B:78:GLU:CB	2.05	0.87
1:A:118:ASN:CA	1:A:119:GLN:HB2	2.06	0.84
1:B:105:ILE:HD12	1:B:106:LEU:H	1.42	0.82
1:B:158:ILE:HG22	1:B:162:LEU:HD22	1.60	0.82
1:B:70:MSE:HE1	1:B:75:LEU:CA	2.05	0.82
1:A:175:LEU:HD23	1:A:175:LEU:H	1.47	0.78
1:A:9:LEU:HD22	1:A:63:HIS:CE1	2.22	0.75
1:A:146:LYS:NZ	1:A:153:SER:O	2.20	0.74
1:A:6:GLN:CA	1:A:6:GLN:HE21	2.00	0.74
1:B:70:MSE:HE2	1:B:78:GLU:HB3	1.71	0.71
1:B:105:ILE:HD12	1:B:106:LEU:N	2.06	0.70
1:A:118:ASN:HA	1:A:119:GLN:CB	2.15	0.68
1:A:118:ASN:ND2	1:A:120:GLU:OE2	2.23	0.67
1:B:14:ARG:HD2	2:B:189:HOH:O	1.96	0.65
1:A:128:GLY:C	1:A:129:HIS:CA	2.59	0.62
1:B:98:ILE:CG2	1:B:105:ILE:CD1	2.68	0.60
1:A:175:LEU:H	1:A:175:LEU:CD2	2.09	0.59
1:A:23:VAL:HG11	1:A:105:ILE:HD12	1.86	0.57
1:B:70:MSE:CE	1:B:75:LEU:HD23	2.35	0.57
1:B:33:ALA:O	1:B:34:MSE:C	2.44	0.56
1:A:156:GLU:HB2	1:A:161:LEU:HD12	1.87	0.56
1:B:71:LYS:HB2	1:B:71:LYS:NZ	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:70:MSE:HE1	1:B:75:LEU:HD23	1.87	0.55
1:B:7:LEU:HG	1:B:59:ASN:HD22	1.72	0.55
1:A:45:PRO:HG2	1:A:104:SER:HB3	1.90	0.53
1:A:156:GLU:HB2	1:A:161:LEU:CD1	2.38	0.53
1:A:133:LEU:C	1:A:135:ASN:H	2.11	0.53
1:A:6:GLN:HE22	1:A:14:ARG:HG3	1.74	0.52
1:A:73:ARG:HB3	1:A:74:THR:HG22	1.93	0.51
1:B:107:ILE:HD11	1:B:122:LEU:HD21	1.95	0.49
1:A:129:HIS:N	1:A:129:HIS:CB	2.67	0.48
1:B:70:MSE:HE2	1:B:78:GLU:CG	2.44	0.47
1:B:14:ARG:NH2	1:B:111:GLU:OE1	2.47	0.47
1:B:70:MSE:HE2	1:B:78:GLU:HB2	1.91	0.47
1:A:135:ASN:O	1:A:138:GLU:HG2	2.15	0.47
1:A:19:LEU:HD21	1:A:139:ILE:HD11	1.97	0.47
1:A:133:LEU:C	1:A:135:ASN:N	2.68	0.47
1:A:174:VAL:H	1:A:175:LEU:C	2.19	0.46
1:A:6:GLN:NE2	1:A:6:GLN:HA	2.11	0.46
1:B:107:ILE:CD1	1:B:122:LEU:HD21	2.45	0.46
1:B:85:PRO:O	1:B:172:LYS:HA	2.16	0.45
1:A:132:SER:O	1:A:135:ASN:HB2	2.16	0.45
1:A:9:LEU:O	1:B:69:LYS:HE3	2.19	0.43
1:A:6:GLN:NE2	1:A:6:GLN:CA	2.73	0.43
1:B:44:ASN:HD22	1:B:47:VAL:HG22	1.84	0.43
1:B:84:SER:HA	1:B:96:PHE:CE2	2.53	0.42
1:A:118:ASN:ND2	1:A:120:GLU:H	2.18	0.42
1:B:9:LEU:HD13	1:B:10:PHE:CE2	2.55	0.41
1:A:7:LEU:HD23	1:A:7:LEU:HA	1.90	0.41
1:A:6:GLN:NE2	1:A:14:ARG:HG3	2.35	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	168/177 (95%)	161 (96%)	2 (1%)	5 (3%)	5	7
1	B	170/177 (96%)	166 (98%)	3 (2%)	1 (1%)	30	48
All	All	338/354 (96%)	327 (97%)	5 (2%)	6 (2%)	11	16

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	MSE
1	A	35	GLU
1	A	119	GLN
1	A	141	ASN
1	A	173	ASP
1	B	154	GLN

### 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	149/154 (97%)	131 (88%)	18 (12%)	6	10
1	B	147/154 (96%)	124 (84%)	23 (16%)	3	5
All	All	296/308 (96%)	255 (86%)	41 (14%)	4	7

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	THR
1	A	6	GLN
1	A	9	LEU
1	A	18	LEU
1	A	24	LYS
1	A	28	ASP
1	A	71	LYS
1	A	73	ARG
1	A	74	THR
1	A	91	GLU

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Mol	Chain	Res	Type
1	A	119	GLN
1	A	133	LEU
1	A	139	ILE
1	A	140	MSE
1	A	153	SER
1	A	157	SER
1	A	174	VAL
1	A	175	LEU
1	B	7	LEU
1	B	8	ASP
1	B	9	LEU
1	B	12	GLU
1	B	14	ARG
1	B	15	VAL
1	B	35	GLU
1	B	71	LYS
1	B	75	LEU
1	B	86	ASN
1	B	105	ILE
1	B	107	ILE
1	B	110	ILE
1	B	112	GLU
1	B	115	LYS
1	B	116	GLN
1	B	118	ASN
1	B	120	GLU
1	B	133	LEU
1	B	136	LEU
1	B	156	GLU
1	B	161	LEU
1	B	162	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	63	HIS
1	A	101	ASN
1	A	119	GLN
1	B	44	ASN
1	B	59	ASN
1	B	86	ASN

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Mol	Chain	Res	Type
1	B	87	ASN
1	B	116	GLN
1	B	118	ASN
1	B	119	GLN
1	B	141	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 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	167/177 (94%)	0.13	3 (1%) 71 74	46, 56, 66, 72	0
1	B	167/177 (94%)	-0.03	3 (1%) 71 74	45, 55, 65, 67	0
All	All	334/354 (94%)	0.05	6 (1%) 71 74	45, 56, 66, 72	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	117	ILE	4.1
1	A	116	GLN	3.7
1	B	151	LEU	3.0
1	B	129	HIS	2.3
1	B	146	LYS	2.2
1	A	175	LEU	2.1

### 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.