



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 12, 2020 – 11:10 pm BST

PDB ID : 2V64  
Title : Crystallographic structure of the conformational dimer of the Spindle Assembly Checkpoint protein Mad2.  
Authors : Mapelli, M.; Massimiliano, L.; Santaguida, S.; Musacchio, A.  
Deposited on : 2007-07-13  
Resolution : 2.90 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	:	2.11
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

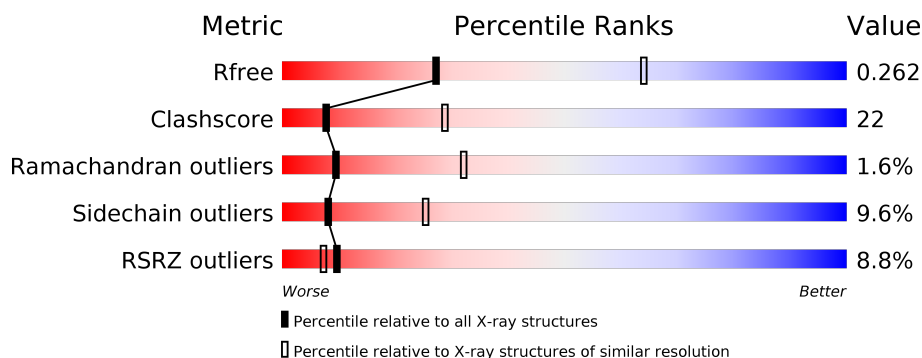
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	213	<div> <div>6%</div> <div> <div></div> <div>67%</div> <div>26%</div> <div>6%</div> </div> </div>
1	C	213	<div> <div>7%</div> <div> <div></div> <div>63%</div> <div>28%</div> <div>8%</div> </div> </div>
1	F	213	<div> <div>5%</div> <div> <div></div> <div>69%</div> <div>22%</div> <div>8%</div> </div> </div>
2	B	12	<div> <div></div> <div> <div></div> <div>75%</div> <div>17%</div> <div>8%</div> </div> </div>
2	G	12	<div> <div>17%</div> <div> <div></div> <div>83%</div> <div>8%</div> <div>8%</div> </div> </div>
2	I	12	<div> <div></div> <div> <div></div> <div>75%</div> <div>25%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	D	207	<div><div></div><div>9%</div><div>47%</div><div>29%</div><div>5%</div><div>17%</div></div>
3	E	207	<div><div></div><div>12%</div><div>44%</div><div>29%</div><div>9%</div><div>15%</div></div>
3	H	207	<div><div></div><div>12%</div><div>47%</div><div>30%</div><div>10%</div><div>13%</div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9648 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 MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	211	Total	C	N	O	S	0	0	1
			1700	1085	287	324	4			
1	C	211	Total	C	N	O	S	0	0	1
			1700	1085	287	324	4			
1	F	211	Total	C	N	O	S	0	0	1
			1700	1085	287	324	4			

- Molecule 2 is a protein called MBP1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	11	Total	C	N	O	0	0	1
			92	61	16	15			
2	G	11	Total	C	N	O	0	0	1
			92	61	16	15			
2	I	12	Total	C	N	O	0	0	1
			97	64	17	16			

- Molecule 3 is a protein called MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	172	Total	C	N	O	S	0	0	1
			1383	887	226	267	3			
3	E	176	Total	C	N	O	S	0	0	1
			1423	916	231	273	3			
3	H	181	Total	C	N	O	S	0	0	1
			1455	934	237	281	3			

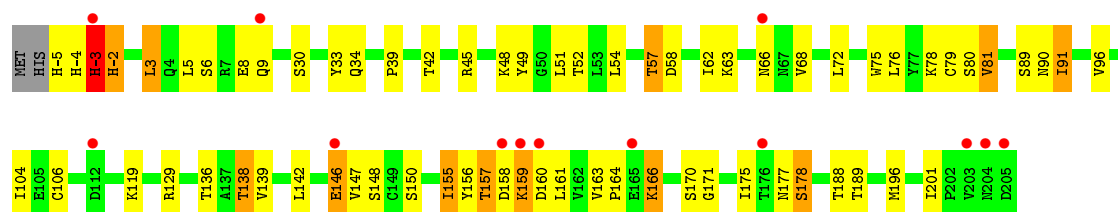
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	3	Total 3	O 3	0	0
4	F	2	Total 2	O 2	0	0
4	H	1	Total 1	O 1	0	0

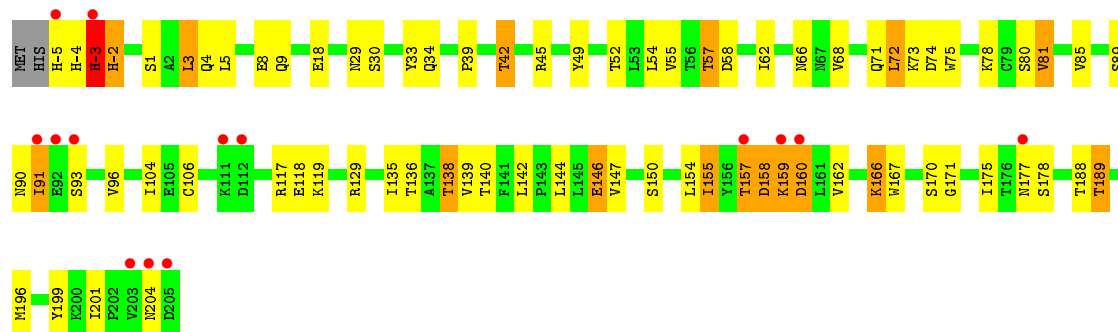
### 3 Residue-property plots [i](#)

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.

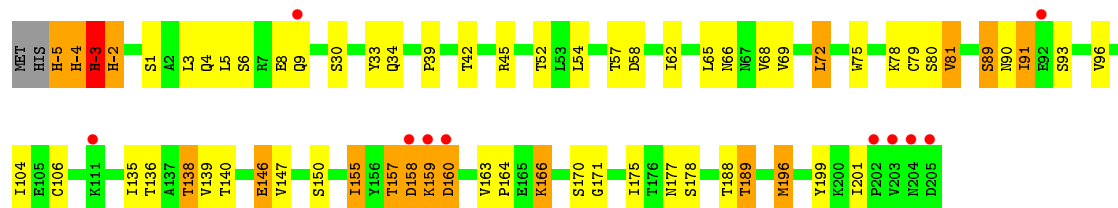
#### • Molecule 1: MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A



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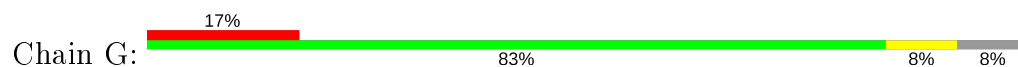


#### • Molecule 2: MBP1





- Molecule 2: MBP1



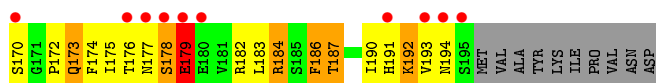
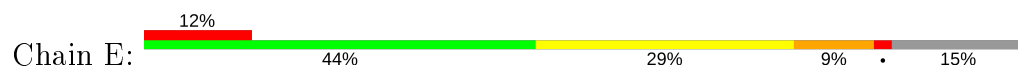
- Molecule 2: MBP1



- Molecule 3: MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A

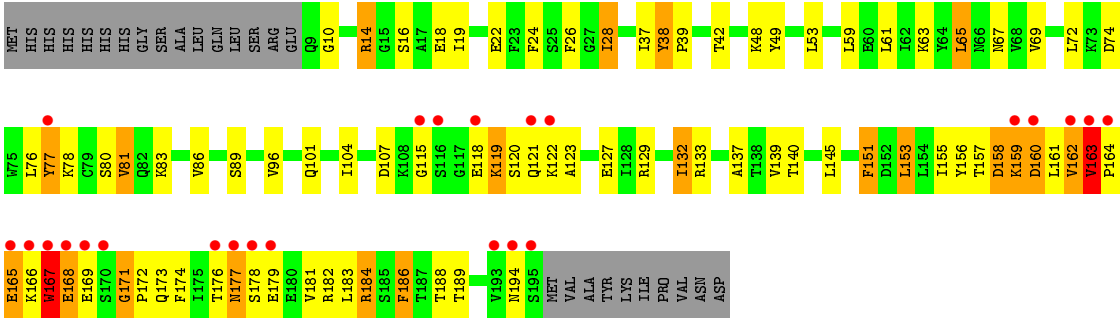


- Molecule 3: MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A



- Molecule 3: MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	112.58Å 111.88Å 131.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.44 – 2.90 29.44 – 2.90	Depositor EDS
% Data completeness (in resolution range)	94.8 (29.44-2.90) 94.9 (29.44-2.90)	Depositor EDS
$R_{merge}$	0.01	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.60 (at 2.90Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.233 , 0.273 0.221 , 0.262	Depositor DCC
$R_{free}$ test set	1766 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.8	Xtriage
Anisotropy	0.176	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 53.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.014 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	9648	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% 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 ⓘ

### 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	0.70	1/1733 (0.1%)	0.90	4/2350 (0.2%)
1	C	0.72	2/1733 (0.1%)	0.94	7/2350 (0.3%)
1	F	0.71	2/1733 (0.1%)	0.96	5/2350 (0.2%)
2	B	0.69	0/98	0.63	0/136
2	G	0.73	0/98	0.68	0/136
2	I	0.73	0/103	0.71	0/143
3	D	0.97	11/1404 (0.8%)	1.09	10/1899 (0.5%)
3	E	1.00	10/1447 (0.7%)	1.11	11/1962 (0.6%)
3	H	0.97	8/1480 (0.5%)	1.11	9/2006 (0.4%)
All	All	0.84	34/9829 (0.3%)	1.01	46/13332 (0.3%)

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	2
1	C	0	1
1	F	1	3
3	E	0	1
3	H	0	4
All	All	1	11

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	18	GLU	CB-CG	-10.80	1.31	1.52
3	E	77	TYR	CD1-CE1	-10.62	1.23	1.39
3	E	70	GLU	CG-CD	-8.74	1.38	1.51
3	D	77	TYR	CD1-CE1	-8.49	1.26	1.39
1	F	-3	HIS	C-O	-8.42	1.07	1.23

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	158	ASP	CB-CG-OD1	-19.52	100.73	118.30
1	F	-3	HIS	N-CA-C	15.57	153.03	111.00
3	E	160	ASP	CB-CG-OD1	-14.85	104.94	118.30
1	C	-3	HIS	N-CA-C	14.55	150.28	111.00
3	D	158	ASP	CB-CG-OD1	-14.49	105.26	118.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	F	-3	HIS	CA

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	-3	HIS	Sidechain,Mainchain
1	C	-3	HIS	Mainchain
3	E	184	ARG	Sidechain
1	F	-3	HIS	Mainchain
1	F	-5	HIS	Sidechain

## 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	1700	0	1707	61	0
1	C	1700	0	1707	61	2
1	F	1700	0	1707	59	0
2	B	92	0	82	1	0
2	G	92	0	82	1	0
2	I	97	0	87	5	0
3	D	1383	0	1399	75	0
3	E	1423	0	1438	96	2
3	H	1455	0	1469	88	0
4	C	3	0	0	0	0
4	F	2	0	0	0	0
4	H	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	9648	0	9678	420	2

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 22.

The worst 5 of 420 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)
3:H:184:ARG:HH11	3:H:184:ARG:CB	1.39	1.34
3:H:184:ARG:HB3	3:H:184:ARG:NH1	1.44	1.28
1:A:-3:HIS:NE2	1:F:-3:HIS:CE1	2.16	1.14
1:A:-3:HIS:CE1	1:C:-5:HIS:HE1	1.67	1.12
3:D:14:ARG:HH21	3:D:14:ARG:HB3	1.10	1.09

All (2) 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:204:ASN:N	3:E:78:LYS:NZ[4_545]	2.13	0.07
1:C:74:ASP:OD1	3:E:63:LYS:NZ[2_455]	2.16	0.04

## 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	209/213 (98%)	199 (95%)	9 (4%)	1 (0%)	29	61
1	C	209/213 (98%)	200 (96%)	8 (4%)	1 (0%)	29	61
1	F	209/213 (98%)	199 (95%)	9 (4%)	1 (0%)	29	61
2	B	9/12 (75%)	7 (78%)	2 (22%)	0	100	100
2	G	9/12 (75%)	7 (78%)	2 (22%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	I	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
3	D	168/207 (81%)	149 (89%)	14 (8%)	5 (3%)	4	17
3	E	172/207 (83%)	147 (86%)	19 (11%)	6 (4%)	3	14
3	H	179/207 (86%)	160 (89%)	14 (8%)	5 (3%)	5	19
All	All	1174/1296 (91%)	1077 (92%)	78 (7%)	19 (2%)	9	32

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	159	LYS
1	C	159	LYS
3	D	179	GLU
3	D	194	ASN
3	E	167	TRP

### 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	194/197 (98%)	180 (93%)	14 (7%)	14	39
1	C	194/197 (98%)	177 (91%)	17 (9%)	10	30
1	F	194/197 (98%)	178 (92%)	16 (8%)	11	32
2	B	10/11 (91%)	9 (90%)	1 (10%)	7	23
2	G	10/11 (91%)	10 (100%)	0	100	100
2	I	10/11 (91%)	10 (100%)	0	100	100
3	D	159/191 (83%)	145 (91%)	14 (9%)	10	30
3	E	164/191 (86%)	140 (85%)	24 (15%)	3	9
3	H	167/191 (87%)	147 (88%)	20 (12%)	5	15
All	All	1102/1197 (92%)	996 (90%)	106 (10%)	8	25

5 of 106 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	E	19	ILE
3	E	158	ASP
3	H	153	LEU
3	E	42	THR
3	E	81	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	194	ASN
3	E	82	GLN
3	H	121	GLN
3	E	66	ASN
3	E	101	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 ⓘ

### 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	211/213 (99%)	0.26	13 (6%) 20 16	16, 31, 61, 100	0
1	C	211/213 (99%)	0.30	14 (6%) 18 14	16, 32, 61, 100	0
1	F	211/213 (99%)	0.19	10 (4%) 31 28	16, 30, 61, 100	0
2	B	11/12 (91%)	0.37	0 100 100	36, 43, 67, 69	0
2	G	11/12 (91%)	0.62	2 (18%) 1 1	37, 43, 66, 68	0
2	I	12/12 (100%)	0.38	0 100 100	38, 42, 69, 69	0
3	D	172/207 (83%)	0.38	18 (10%) 6 5	14, 37, 88, 96	0
3	E	176/207 (85%)	0.41	24 (13%) 3 2	17, 38, 94, 98	0
3	H	181/207 (87%)	0.53	24 (13%) 3 2	15, 37, 92, 99	0
All	All	1196/1296 (92%)	0.34	105 (8%) 10 7	14, 34, 84, 100	0

The worst 5 of 105 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	205	ASP	15.9
1	A	205	ASP	9.1
1	C	204	ASN	9.0
1	A	204	ASN	8.1
1	F	204	ASN	8.1

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.