



# Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 08:54 am BST

PDB ID : 4OII  
Title : West Nile Virus NS1 in complex with neutralizing 22NS1 antibody Fab  
Authors : Edeling, M.A.; Fremont, D.H.; Center for Structural Genomics of Infectious Diseases (CSGID)  
Deposited on : 2014-01-19  
Resolution : 3.00 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.

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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

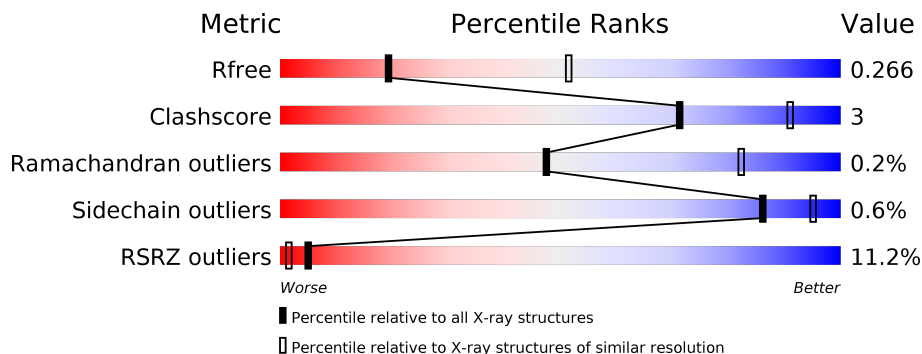
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	185	
1	B	185	
2	L	213	
2	M	213	
3	H	217	
3	I	217	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9455 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 NON-STRUCTURAL PROTEIN NS1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	177	1398	865	250	274	9	0	0	0
1	B	177	1398	865	250	274	9	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	168	MET	-	EXPRESSION TAG	UNP U3N977
A	169	ALA	-	EXPRESSION TAG	UNP U3N977
A	170	SER	-	EXPRESSION TAG	UNP U3N977
A	171	MET	-	EXPRESSION TAG	UNP U3N977
B	168	MET	-	EXPRESSION TAG	UNP U3N977
B	169	ALA	-	EXPRESSION TAG	UNP U3N977
B	170	SER	-	EXPRESSION TAG	UNP U3N977
B	171	MET	-	EXPRESSION TAG	UNP U3N977

- Molecule 2 is a protein called Light Chain of Fab fragment of 22NS1 Antibody.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	213	1655	1031	283	335	6	0	0	0
2	M	213	1655	1031	283	335	6	0	0	0

- Molecule 3 is a protein called Heavy Chain of Fab fragment of 22NS1 Antibody.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	H	217	1641	1041	268	325	7	0	0	0
3	I	217	1641	1041	268	325	7	0	0	0

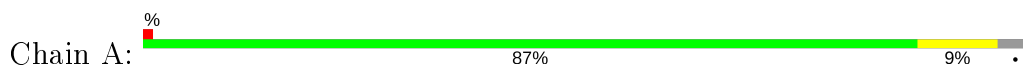
- Molecule 4 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	A	19	Total 19	O 19	0	0
4	B	16	Total 16	O 16	0	0
4	L	15	Total 15	O 15	0	0
4	H	15	Total 15	O 15	0	0
4	M	1	Total 1	O 1	0	0
4	I	1	Total 1	O 1	0	0

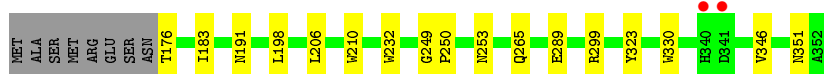
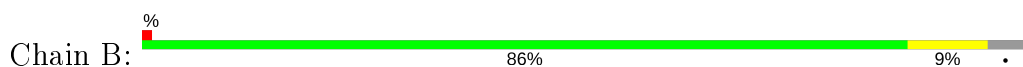
### 3 Residue-property plots [i](#)

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.

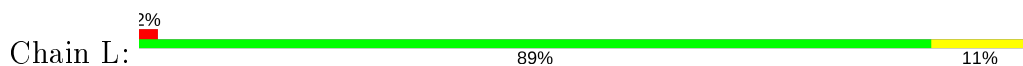
- Molecule 1: NON-STRUCTURAL PROTEIN NS1



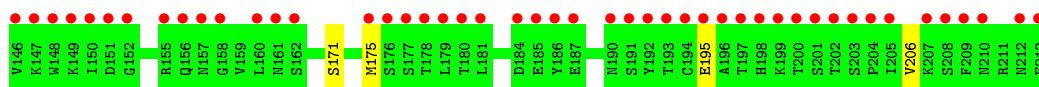
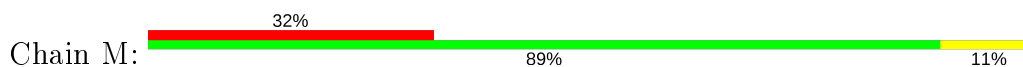
- Molecule 1: NON-STRUCTURAL PROTEIN NS1



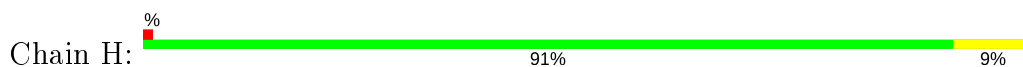
- Molecule 2: Light Chain of Fab fragment of 22NS1 Antibody



- Molecule 2: Light Chain of Fab fragment of 22NS1 Antibody

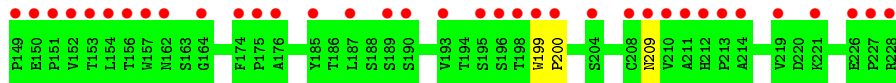
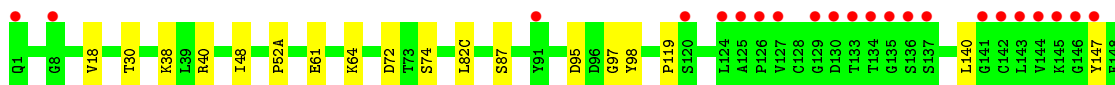
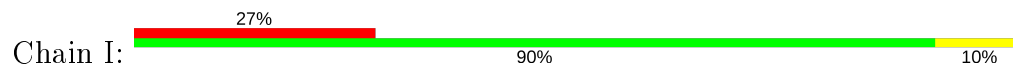


- Molecule 3: Heavy Chain of Fab fragment of 22NS1 Antibody





- Molecule 3: Heavy Chain of Fab fragment of 22NS1 Antibody



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	215.87Å 49.55Å 130.07Å 90.00° 91.21° 90.00°	Depositor
Resolution (Å)	49.47 – 3.00 49.47 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.47-3.00) 99.9 (49.47-3.00)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.52 (at 3.01Å)	Xtrriage
Refinement program	PHENIX 1.7.2_869	Depositor
R, $R_{free}$	0.214 , 0.265 0.216 , 0.266	Depositor DCC
$R_{free}$ test set	1428 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	59.4	Xtrriage
Anisotropy	0.224	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 60.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.018 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	9455	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	81.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.69% 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	0.22	0/1432	0.42	0/1952
1	B	0.21	0/1432	0.42	0/1952
2	L	0.24	0/1694	0.42	0/2300
2	M	0.24	0/1694	0.42	0/2300
3	H	0.22	0/1686	0.41	0/2306
3	I	0.22	0/1686	0.41	0/2306
All	All	0.22	0/9624	0.42	0/13116

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	1398	0	1335	8	0
1	B	1398	0	1335	10	0
2	L	1655	0	1582	15	0
2	M	1655	0	1582	14	0
3	H	1641	0	1596	10	0
3	I	1641	0	1596	10	0
4	A	19	0	0	0	0
4	B	16	0	0	0	0
4	H	15	0	0	0	0
4	I	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	L	15	0	0	0	0
4	M	1	0	0	0	0
All	All	9455	0	9026	64	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 3.

All (64) 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:323:TYR:HB2	1:B:330:TRP:HB2	1.68	0.75
1:A:323:TYR:HB2	1:A:330:TRP:HB2	1.68	0.74
2:M:21:ILE:HD11	2:M:73:LEU:HD23	1.77	0.67
2:L:21:ILE:HD11	2:L:73:LEU:HD23	1.77	0.67
1:A:289:GLU:HG3	2:L:56:ASP:HB2	1.83	0.61
2:M:37:GLN:HB2	2:M:47:LEU:HD11	1.82	0.59
2:M:108:ARG:HD2	2:M:171:SER:HB2	1.84	0.59
2:L:108:ARG:HD2	2:L:171:SER:HB2	1.84	0.59
2:L:37:GLN:HB2	2:L:47:LEU:HD11	1.83	0.59
2:M:195:GLU:HG2	2:M:206:VAL:HG22	1.90	0.54
2:L:195:GLU:HG2	2:L:206:VAL:HG22	1.90	0.54
2:L:136:LEU:HB2	2:L:175:MET:HG3	1.92	0.52
2:L:108:ARG:HH12	2:L:111:ALA:HB2	1.75	0.52
2:M:136:LEU:HB2	2:M:175:MET:HG3	1.92	0.52
2:L:136:LEU:HD23	2:L:144:ILE:HD13	1.92	0.51
2:M:136:LEU:HD23	2:M:144:ILE:HD13	1.91	0.51
1:B:232:TRP:CD2	1:B:253:ASN:HB2	2.46	0.51
2:M:108:ARG:HH12	2:M:111:ALA:HB2	1.76	0.50
1:A:232:TRP:CD2	1:A:253:ASN:HB2	2.46	0.50
3:I:199:TRP:CG	3:I:200:PRO:HA	2.47	0.50
2:L:61:ARG:HB2	2:L:76:ASN:O	2.12	0.50
2:M:12:SER:HA	2:M:105:GLU:HB2	1.94	0.49
2:M:61:ARG:HB2	2:M:76:ASN:O	2.12	0.49
1:A:206:LEU:HB2	1:A:210:TRP:CE2	2.48	0.49
1:B:206:LEU:HB2	1:B:210:TRP:CE2	2.48	0.49
2:L:12:SER:HA	2:L:105:GLU:HB2	1.95	0.49
3:I:119:PRO:HB3	3:I:147:TYR:HB3	1.94	0.48
3:H:119:PRO:HB3	3:H:147:TYR:HB3	1.94	0.48
3:H:38:LYS:HB2	3:H:48:ILE:HD11	1.96	0.48
3:I:38:LYS:HB2	3:I:48:ILE:HD11	1.96	0.48
3:H:95:ASP:OD1	3:H:98:TYR:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:108:ARG:NH1	2:M:109:ALA:O	2.48	0.46
3:H:56:GLY:HA2	3:H:57:PRO:HD3	1.80	0.46
3:I:95:ASP:OD1	3:I:98:TYR:N	2.48	0.46
2:L:108:ARG:NH1	2:L:109:ALA:O	2.49	0.46
3:H:30:THR:HA	3:H:52(A):PRO:HB2	1.99	0.45
3:I:30:THR:HA	3:I:52(A):PRO:HB2	1.98	0.45
3:I:140:LEU:HD11	3:I:199:TRP:CD1	2.52	0.45
2:L:108:ARG:NH2	2:L:109:ALA:HB3	2.32	0.45
3:H:61:GLU:HA	3:H:64:LYS:HG3	2.00	0.44
1:A:183:ILE:HB	1:A:198:LEU:HD13	2.00	0.44
3:I:61:GLU:HA	3:I:64:LYS:HG3	2.00	0.43
3:H:18:VAL:HG12	3:H:82(C):LEU:HD11	2.01	0.43
3:H:40:ARG:NH1	3:H:87:SER:O	2.52	0.43
2:M:113:PRO:HG3	2:M:144:ILE:HD11	2.00	0.43
1:B:183:ILE:HB	1:B:198:LEU:HD13	2.00	0.43
2:L:113:PRO:HG3	2:L:144:ILE:HD11	2.00	0.43
3:I:18:VAL:HG12	3:I:82(C):LEU:HD11	2.01	0.43
1:B:249:GLY:HA2	1:B:250:PRO:HD3	1.91	0.42
2:M:107:LYS:HA	2:M:140:TYR:OH	2.20	0.42
1:A:299:ARG:NH2	1:A:346:VAL:HG21	2.34	0.42
1:B:299:ARG:NH2	1:B:346:VAL:HG21	2.34	0.42
1:B:191:ASN:OD1	1:B:191:ASN:N	2.53	0.42
3:I:40:ARG:NH1	3:I:87:SER:O	2.52	0.42
1:A:265:GLN:HE21	1:A:351:ASN:ND2	2.18	0.42
1:B:232:TRP:CH2	2:M:30:HIS:HE1	2.38	0.42
3:I:72:ASP:OD2	3:I:74:SER:OG	2.34	0.41
2:L:107:LYS:HA	2:L:140:TYR:OH	2.20	0.41
1:B:289:GLU:HG3	2:M:56:ASP:HB2	2.03	0.41
3:H:199:TRP:CG	3:H:200:PRO:HA	2.55	0.41
1:B:265:GLN:HE21	1:B:351:ASN:ND2	2.18	0.40
3:H:12:VAL:HG11	3:H:82(C):LEU:HD13	2.03	0.40
2:L:28:ASN:OD1	2:L:30:HIS:HD2	2.04	0.40
1:A:191:ASN:OD1	1:A:191:ASN:N	2.54	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	175/185 (95%)	161 (92%)	14 (8%)	0	100	100
1	B	175/185 (95%)	160 (91%)	15 (9%)	0	100	100
2	L	211/213 (99%)	204 (97%)	7 (3%)	0	100	100
2	M	211/213 (99%)	203 (96%)	8 (4%)	0	100	100
3	H	215/217 (99%)	210 (98%)	4 (2%)	1 (0%)	29	68
3	I	215/217 (99%)	210 (98%)	4 (2%)	1 (0%)	29	68
All	All	1202/1230 (98%)	1148 (96%)	52 (4%)	2 (0%)	47	82

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	H	97	GLY
3	I	97	GLY

### 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	157/164 (96%)	155 (99%)	2 (1%)	69	89
1	B	157/164 (96%)	156 (99%)	1 (1%)	86	95
2	L	187/187 (100%)	186 (100%)	1 (0%)	88	96
2	M	187/187 (100%)	186 (100%)	1 (0%)	88	96
3	H	186/186 (100%)	186 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	I	186/186 (100%)	185 (100%)	1 (0%)	88	96
All	All	1060/1074 (99%)	1054 (99%)	6 (1%)	86	95

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	176	THR
1	A	269	ASP
1	B	176	THR
2	L	81	GLU
2	M	81	GLU
3	I	209	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	265	GLN
1	B	265	GLN
2	L	30	HIS
2	M	30	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 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	177/185 (95%)	-0.28	1 (0%) 89 72	27, 44, 81, 133	0
1	B	177/185 (95%)	-0.18	2 (1%) 80 56	29, 52, 97, 172	0
2	L	213/213 (100%)	-0.05	4 (1%) 66 37	30, 62, 126, 152	0
2	M	213/213 (100%)	1.68	69 (32%) 0 0	52, 134, 183, 196	0
3	H	217/217 (100%)	-0.12	2 (0%) 84 63	38, 61, 91, 158	0
3	I	217/217 (100%)	1.32	58 (26%) 0 0	54, 117, 176, 190	0
All	All	1214/1230 (98%)	0.43	136 (11%) 5 1	27, 69, 167, 196	0

All (136) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	M	155	ARG	12.2
2	M	209	PHE	8.9
2	M	157	ASN	8.2
2	M	194	CYS	8.2
2	M	200	THR	8.1
3	I	144	VAL	7.8
2	M	146	VAL	7.8
2	M	212	ASN	7.0
2	M	145	ASN	7.0
2	M	150	ILE	6.7
3	I	133	THR	6.6
3	I	204	SER	6.4
2	M	156	GLN	6.4
2	M	149	LYS	6.0
2	M	201	SER	5.8
2	M	161	ASN	5.5
2	M	190	ASN	5.4
3	I	142	CYS	5.4
3	I	189	SER	5.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	M	119	PRO	5.3
2	M	148	TRP	5.3
2	M	208	SER	5.2
2	M	113	PRO	5.0
2	M	179	LEU	5.0
2	M	210	ASN	4.8
3	I	141	GLY	4.7
2	M	134	CYS	4.6
2	M	198	HIS	4.6
2	M	151	ASP	4.6
2	L	202	THR	4.6
2	M	197	THR	4.6
3	I	130	ASP	4.5
2	M	186	TYR	4.5
3	I	187	LEU	4.5
2	M	130	ALA	4.5
2	M	180	THR	4.3
2	M	135	PHE	4.2
2	M	118	PHE	4.1
2	M	178	THR	4.1
3	I	157	TRP	4.1
2	M	196	ALA	4.1
3	I	154	LEU	4.0
3	I	208	CYS	4.0
2	M	147	LYS	4.0
2	M	181	LEU	4.0
2	M	205	ILE	4.0
2	M	152	GLY	3.9
3	I	226	GLU	3.9
3	I	134	THR	3.9
2	M	132	VAL	3.9
3	I	143	LEU	3.8
2	M	192	TYR	3.8
2	M	129	GLY	3.8
2	M	207	LYS	3.8
3	I	213	PRO	3.8
3	I	214	ALA	3.7
2	L	200	THR	3.7
2	M	193	THR	3.7
3	I	129	GLY	3.7
2	M	185	GLU	3.6
3	I	147	TYR	3.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
3	I	145	LYS	3.5
3	I	199	TRP	3.5
2	M	199	LYS	3.5
3	I	152	VAL	3.4
2	M	158	GLY	3.3
2	M	114	THR	3.3
3	I	198	THR	3.3
2	M	133	VAL	3.3
2	M	144	ILE	3.3
3	I	190	SER	3.3
3	I	149	PRO	3.2
2	M	131	SER	3.2
3	I	126	PRO	3.2
3	I	150	GLU	3.2
3	H	134	THR	3.2
2	M	162	SER	3.2
2	M	175	MET	3.2
2	M	125	LEU	3.1
1	B	340	HIS	3.0
2	M	184	ASP	3.0
3	I	162	ASN	3.0
3	I	219	VAL	3.0
2	M	136	LEU	2.9
1	A	340	HIS	2.9
2	L	157	ASN	2.9
2	M	204	PRO	2.9
3	I	1	GLN	2.9
3	I	127	VAL	2.9
3	I	151	PRO	2.8
2	M	213	GLU	2.8
2	M	124	GLN	2.8
3	I	120	SER	2.8
3	I	153	THR	2.8
2	M	176	SER	2.8
3	I	135	GLY	2.8
3	I	193	VAL	2.8
3	I	175	PRO	2.7
3	I	156	THR	2.7
2	M	195	GLU	2.7
2	M	177	SER	2.6
2	M	203	SER	2.6
3	I	211	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
2	M	120	PRO	2.6
1	B	341	ASP	2.6
3	I	8	GLY	2.5
2	M	187	GLU	2.5
3	I	176	ALA	2.5
3	I	164	GLY	2.4
2	M	115	VAL	2.4
2	M	160	LEU	2.4
3	I	146	GLY	2.4
3	H	133	THR	2.4
2	M	121	SER	2.3
3	I	174	PHE	2.3
3	I	185	TYR	2.3
3	I	124	LEU	2.3
3	I	212	HIS	2.3
3	I	228	ARG	2.2
3	I	136	SER	2.2
2	M	191	SER	2.2
3	I	227	PRO	2.2
2	L	198	HIS	2.1
3	I	195	SER	2.1
2	M	103	LYS	2.1
3	I	221	LYS	2.1
3	I	200	PRO	2.1
3	I	210	VAL	2.1
3	I	91	TYR	2.1
3	I	196	SER	2.1
3	I	125	ALA	2.1
2	M	117	ILE	2.1
3	I	209	ASN	2.0
3	I	137	SER	2.0
2	M	142	LYS	2.0
2	M	202	THR	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 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.