



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 31, 2023 – 11:56 AM JST

PDB ID : 5CP7  
Title : Crystal Structure of an Antigen-Binding Fragment of Monoclonal Antibody against Sulfonamides  
Authors : Wang, Z.; Shen, J.; Li, C.; Li, Y.; Wen, K.; Yu, X.; Zhang, X.  
Deposited on : 2015-07-21  
Resolution : 3.01 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

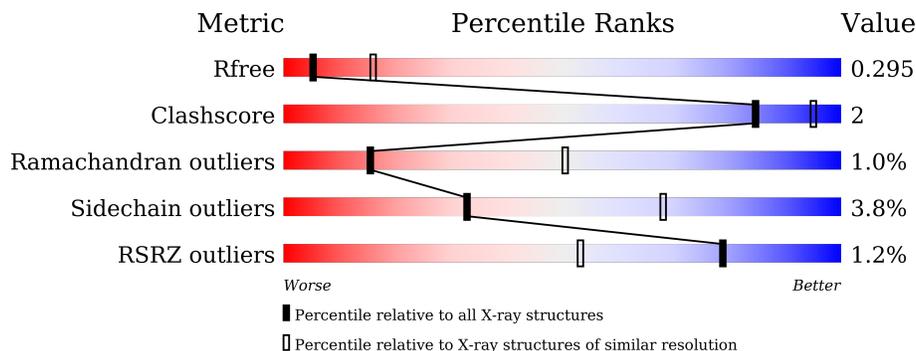
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.01 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.



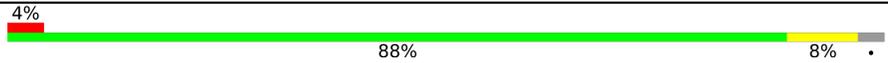
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2399 (3.04-3.00)
Clashscore	141614	2734 (3.04-3.00)
Ramachandran outliers	138981	2640 (3.04-3.00)
Sidechain outliers	138945	2643 (3.04-3.00)
RSRZ outliers	127900	2287 (3.04-3.00)

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 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	218	91% 8%
1	C	218	89% 11%
1	E	218	3% 91% 8% .
1	G	218	93% 6%
2	B	214	93% 6% .
2	D	214	% 87% 8% 5%

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Mol	Chain	Length	Quality of chain
2	F	214	 4% 88% 8% •
2	H	214	 85% 13% ••

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13178 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 Light Chain of Antigen-Binding Fragment of Monoclonal Antibody of 4C7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	218	Total 1700	C 1061	N 288	O 345	S 6	0	1	0
1	C	218	Total 1702	C 1062	N 288	O 346	S 6	0	1	0
1	E	218	Total 1686	C 1052	N 285	O 343	S 6	0	0	0
1	G	218	Total 1702	C 1062	N 289	O 345	S 6	0	1	0

- Molecule 2 is a protein called Heavy Chain of Antigen-Binding Fragment of Monoclonal Antibody of 4C7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	214	Total 1628	C 1027	N 272	O 323	S 6	0	0	0
2	D	204	Total 1573	C 999	N 260	O 308	S 6	0	1	0
2	F	207	Total 1576	C 995	N 264	O 311	S 6	0	0	0
2	H	212	Total 1610	C 1017	N 268	O 319	S 6	0	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total 1	O 1	0	0

### 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: Light Chain of Antigen-Binding Fragment of Monoclonal Antibody of 4C7

Chain A:  91% 8%



- Molecule 1: Light Chain of Antigen-Binding Fragment of Monoclonal Antibody of 4C7

Chain C:  89% 11%



- Molecule 1: Light Chain of Antigen-Binding Fragment of Monoclonal Antibody of 4C7

Chain E:  3% 91% 8%



- Molecule 1: Light Chain of Antigen-Binding Fragment of Monoclonal Antibody of 4C7

Chain G:  93% 6%

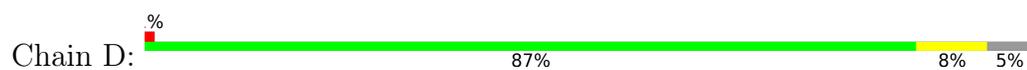


- Molecule 2: Heavy Chain of Antigen-Binding Fragment of Monoclonal Antibody of 4C7

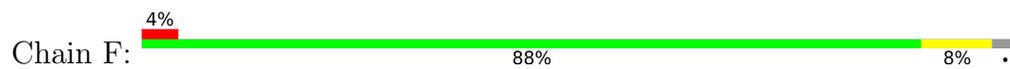
Chain B:  93% 6%



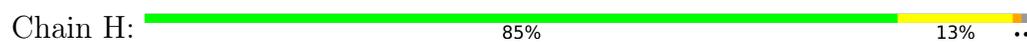
- Molecule 2: Heavy Chain of Antigen-Binding Fragment of Monoclonal Antibody of 4C7



- Molecule 2: Heavy Chain of Antigen-Binding Fragment of Monoclonal Antibody of 4C7



- Molecule 2: Heavy Chain of Antigen-Binding Fragment of Monoclonal Antibody of 4C7



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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	176.10Å 96.51Å 138.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.88 – 3.01 29.86 – 3.01	Depositor EDS
% Data completeness (in resolution range)	94.6 (29.88-3.01) 94.7 (29.86-3.01)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.42 (at 3.00Å)	Xtrriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.260 , 0.302 0.257 , 0.295	Depositor DCC
$R_{free}$ test set	2274 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	41.6	Xtrriage
Anisotropy	0.129	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 23.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.85	EDS
Total number of atoms	13178	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.55% 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	0/1735	0.51	0/2356
1	C	0.30	0/1737	0.52	0/2357
1	E	0.29	0/1721	0.49	0/2338
1	G	0.29	0/1737	0.48	0/2357
2	B	0.29	0/1675	0.52	0/2297
2	D	0.29	0/1619	0.50	0/2220
2	F	0.30	0/1622	0.49	0/2224
2	H	0.31	0/1655	0.53	0/2270
All	All	0.30	0/13501	0.51	0/18419

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	1700	0	1655	8	0
1	C	1702	0	1659	8	0
1	E	1686	0	1634	9	0
1	G	1702	0	1661	6	0
2	B	1628	0	1566	8	0
2	D	1573	0	1515	7	0
2	F	1576	0	1506	4	0
2	H	1610	0	1549	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	1	0	0	0	0
All	All	13178	0	12745	59	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 2.

All (59) 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:55:LEU:O	1:A:57:SER:N	2.23	0.70
1:C:55:LEU:O	1:C:57:SER:N	2.25	0.69
1:G:55:LEU:O	1:G:57:SER:N	2.28	0.66
2:H:14:PRO:O	2:H:86:VAL:O	2.14	0.66
1:E:55:LEU:O	1:E:57:SER:N	2.30	0.64
1:C:91:TYR:CE1	1:C:109:LEU:HD12	2.33	0.64
2:F:18:LEU:HD11	2:F:109:VAL:HG11	1.85	0.58
1:G:41:LEU:HD23	1:G:51:ARG:HA	1.88	0.54
2:H:91:THR:HG23	2:H:110:THR:HA	1.88	0.54
2:H:3:GLN:C	2:H:4:LEU:HD23	2.29	0.53
2:B:41:PHE:O	2:B:43:GLY:O	2.26	0.53
2:H:82:GLN:NE2	2:H:84:ASN:OD1	2.41	0.52
2:D:30:THR:HG21	2:D:74:THR:HG23	1.92	0.52
2:B:91:THR:HG23	2:B:110:THR:HA	1.93	0.51
2:F:147:GLU:HB3	2:F:148:PRO:HA	1.93	0.50
2:D:4:LEU:HD22	2:D:24:VAL:HG12	1.94	0.49
1:E:66:ARG:NH2	1:E:87:ASP:OD2	2.43	0.49
2:D:91:THR:HG23	2:D:110:THR:HA	1.95	0.48
2:F:162:VAL:O	2:F:162:VAL:HG13	2.13	0.48
1:C:42:LEU:HD13	1:C:91:TYR:CE1	2.49	0.47
1:A:84:GLU:HG2	2:B:31:SER:CB	2.46	0.46
2:D:32:GLY:O	2:D:54:TYR:CD1	2.69	0.46
1:G:38:LEU:HD22	1:G:76:PHE:CG	2.51	0.46
1:C:38:LEU:HD13	1:C:76:PHE:CD1	2.51	0.46
1:E:42:LEU:HB2	1:E:52:LEU:HD11	1.97	0.46
1:E:94:TRP:CD1	1:E:94:TRP:C	2.89	0.46
1:G:29:LEU:HD12	1:G:76:PHE:CE1	2.51	0.45
2:B:3:GLN:C	2:B:4:LEU:HD12	2.37	0.45
1:C:83:VAL:HG23	1:C:83:VAL:O	2.15	0.45
1:A:84:GLU:HG2	2:B:31:SER:HB3	1.98	0.45
2:B:176:LEU:C	2:B:176:LEU:HD12	2.37	0.45
1:E:187:THR:HB	1:E:190:GLU:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:151:VAL:HG11	2:H:178:SER:HB3	2.00	0.44
2:H:4:LEU:HD22	2:H:24:VAL:HB	2.00	0.43
1:E:50:LYS:NZ	1:E:60:ASP:OD2	2.51	0.43
1:C:194:HIS:O	1:C:216:ARG:NH1	2.52	0.42
1:A:38:LEU:HD22	1:A:76:PHE:CG	2.54	0.42
2:B:14:PRO:O	2:B:86:VAL:O	2.37	0.42
2:H:43:GLY:O	2:H:44:ASN:HB2	2.20	0.42
2:B:52:ILE:HG23	2:B:52:ILE:O	2.19	0.42
1:G:2:VAL:HG21	1:G:98:HIS:HB2	2.02	0.42
2:F:119:PRO:HD2	2:F:203:THR:HG21	2.00	0.42
2:H:151:VAL:HG11	2:H:178:SER:CB	2.49	0.42
1:E:42:LEU:HD13	1:E:91:TYR:CZ	2.55	0.41
2:H:137:LEU:HD12	2:H:192:VAL:HG11	2.02	0.41
1:A:155:ILE:HD11	1:A:184:LEU:HD21	2.01	0.41
1:A:38:LEU:HD22	1:A:76:PHE:CD2	2.54	0.41
1:E:62:ARG:O	1:E:62:ARG:HG3	2.19	0.41
1:A:110:GLU:HG3	1:A:178:TYR:OH	2.21	0.41
1:G:94:TRP:CH2	1:G:96:GLY:HA3	2.55	0.41
2:H:119:PRO:HB3	2:H:144:TYR:HB3	2.03	0.41
2:D:176:LEU:HD12	2:D:176:LEU:C	2.41	0.41
1:C:56:VAL:HG23	1:C:57:SER:N	2.36	0.40
2:D:211:PRO:O	2:D:212:ARG:HB3	2.21	0.40
1:A:29:LEU:HD12	1:A:76:PHE:CE1	2.56	0.40
1:C:13:VAL:HG21	1:C:83:VAL:HG11	2.01	0.40
2:D:4:LEU:HD12	2:D:97:ALA:HA	2.04	0.40
2:H:4:LEU:HD12	2:H:97:ALA:HA	2.03	0.40
1:E:55:LEU:O	1:E:56:VAL:C	2.59	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	217/218 (100%)	209 (96%)	7 (3%)	1 (0%)	29	66
1	C	217/218 (100%)	208 (96%)	8 (4%)	1 (0%)	29	66
1	E	216/218 (99%)	197 (91%)	15 (7%)	4 (2%)	8	34
1	G	217/218 (100%)	204 (94%)	11 (5%)	2 (1%)	17	53
2	B	212/214 (99%)	195 (92%)	16 (8%)	1 (0%)	29	66
2	D	201/214 (94%)	184 (92%)	15 (8%)	2 (1%)	15	50
2	F	203/214 (95%)	178 (88%)	21 (10%)	4 (2%)	7	32
2	H	210/214 (98%)	189 (90%)	19 (9%)	2 (1%)	15	50
All	All	1693/1728 (98%)	1564 (92%)	112 (7%)	17 (1%)	15	50

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	56	VAL
1	C	56	VAL
1	E	56	VAL
1	E	101	GLN
1	G	56	VAL
2	B	65	ARG
2	D	14	PRO
2	D	171	SER
2	F	132	ASN
2	F	133	SER
2	H	160	GLY
2	F	180	VAL
1	G	143	ASN
2	H	131	THR
2	F	126	PRO
1	E	73	GLY
1	E	100	PRO

### 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	195/195 (100%)	186 (95%)	9 (5%)	27	62
1	C	196/195 (100%)	182 (93%)	14 (7%)	14	44
1	E	193/195 (99%)	189 (98%)	4 (2%)	53	81
1	G	196/195 (100%)	193 (98%)	3 (2%)	65	86
2	B	186/186 (100%)	180 (97%)	6 (3%)	39	73
2	D	181/186 (97%)	177 (98%)	4 (2%)	52	80
2	F	180/186 (97%)	173 (96%)	7 (4%)	32	67
2	H	185/186 (100%)	173 (94%)	12 (6%)	17	48
All	All	1512/1524 (99%)	1453 (96%)	59 (4%)	33	67

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	THR
1	A	24	LYS
1	A	62	ARG
1	A	86	GLU
1	A	109	LEU
1	A	110	GLU
1	A	113	ARG
1	A	180	MET
1	A	181	SER
2	B	5	ARG
2	B	31	SER
2	B	65	ARG
2	B	67	ARG
2	B	88	THR
2	B	110	THR
1	C	24	LYS
1	C	61	SER
1	C	62	ARG
1	C	68	THR
1	C	84	GLU
1	C	112	LYS
1	C	162	ASN
1	C	180	MET
1	C	181	SER
1	C	190[A]	GLU
1	C	190[B]	GLU
1	C	196	THR

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Mol	Chain	Res	Type
1	C	212	LYS
1	C	217	ASN
2	D	5	ARG
2	D	6	GLU
2	D	68	ILE
2	D	77	ASN
1	E	75	ASP
1	E	94	TRP
1	E	113	ARG
1	E	161	GLN
2	F	12	VAL
2	F	59	ASN
2	F	65	ARG
2	F	84	ASN
2	F	99	TYR
2	F	105	GLN
2	F	117	THR
1	G	38	LEU
1	G	79	LYS
1	G	148	ASP
2	H	3	GLN
2	H	7	SER
2	H	24	VAL
2	H	45	LYS
2	H	65	ARG
2	H	76	LYS
2	H	89	GLU
2	H	139	CYS
2	H	184	SER
2	H	194	CYS
2	H	195	ASN
2	H	203	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	GLN
2	B	105	GLN
2	B	198	HIS
2	D	16	GLN
1	E	47	GLN
1	E	101	GLN

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Mol	Chain	Res	Type
1	E	161	GLN
2	F	59	ASN
2	F	82	GLN
2	F	84	ASN
2	H	16	GLN
2	H	40	GLN
2	H	82	GLN
2	H	84	ASN
2	H	105	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	218/218 (100%)	-0.47	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	12, 16, 22, 31	0
1	C	218/218 (100%)	-0.45	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	13, 18, 23, 26	0
1	E	218/218 (100%)	0.22	7 (3%) <span style="border: 1px solid gray; padding: 2px;">47</span> <span style="border: 1px solid red; padding: 2px;">20</span>	16, 44, 68, 72	0
1	G	218/218 (100%)	0.11	1 (0%) <span style="border: 1px solid blue; padding: 2px;">91</span> <span style="border: 1px solid blue; padding: 2px;">75</span>	23, 46, 59, 69	0
2	B	214/214 (100%)	-0.24	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	14, 23, 41, 58	0
2	D	204/214 (95%)	0.12	3 (1%) <span style="border: 1px solid gray; padding: 2px;">73</span> <span style="border: 1px solid gray; padding: 2px;">46</span>	9, 32, 71, 84	0
2	F	207/214 (96%)	0.55	9 (4%) <span style="border: 1px solid red; padding: 2px;">35</span> <span style="border: 1px solid red; padding: 2px;">13</span>	31, 52, 77, 80	0
2	H	212/214 (99%)	-0.37	1 (0%) <span style="border: 1px solid blue; padding: 2px;">91</span> <span style="border: 1px solid blue; padding: 2px;">75</span>	6, 16, 36, 55	0
All	All	1709/1728 (98%)	-0.07	21 (1%) <span style="border: 1px solid blue; padding: 2px;">79</span> <span style="border: 1px solid gray; padding: 2px;">53</span>	6, 26, 67, 84	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	131	THR	3.9
2	D	191	THR	3.6
1	E	217	ASN	3.4
1	E	85	ALA	3.4
2	F	155	SER	3.2
2	F	112	SER	3.1
2	F	199	PRO	2.9
1	E	199	CYS	2.9
2	H	1	ASP	2.8
1	E	209	PRO	2.7
2	F	32	GLY	2.6
2	F	161	GLY	2.4
1	E	207	THR	2.2
2	F	136	THR	2.2
2	D	159	SER	2.2
1	G	207	THR	2.1

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Mol	Chain	Res	Type	RSRZ
2	F	133	SER	2.1
1	E	208	SER	2.1
2	D	183	PRO	2.0
2	F	75	SER	2.0
1	E	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 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.