



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 12, 2026 – 10:53 PM JST

PDB ID : 9UE0 / pdb_00009ue0
Title : Crystal structure of MPXV A35R in complex with a neutralizing antibody MA49
Authors : Sun, D.; Zhang, N.; Guo, Y.
Deposited on : 2025-04-07
Resolution : 2.70 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

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>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.48.1

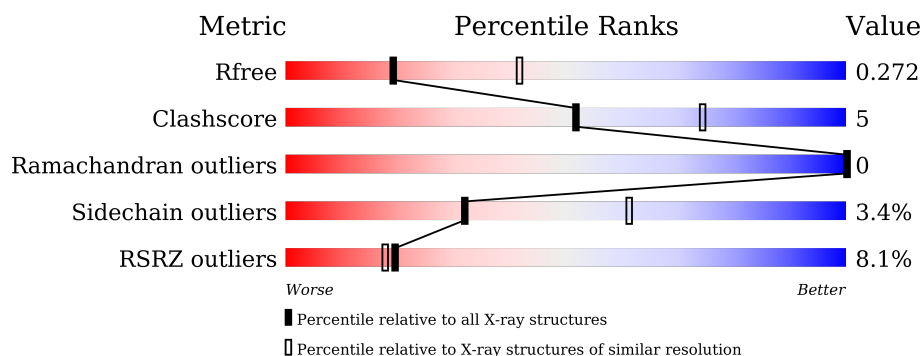
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	164625	3333 (2.70-2.70)
Clashscore	180529	3684 (2.70-2.70)
Ramachandran outliers	177936	3633 (2.70-2.70)
Sidechain outliers	177891	3633 (2.70-2.70)
RSRZ outliers	164620	3333 (2.70-2.70)

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 ≥ 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	223	<div> <div>4%</div> <div>85%</div> <div>13%</div> <div>.</div> </div>
2	B	214	<div> <div>5%</div> <div>86%</div> <div>10%</div> <div>.</div> </div>
3	C	124	<div> <div>11%</div> <div>54%</div> <div>13%</div> <div>.</div> <div>32%</div> </div>
3	D	124	<div> <div>12%</div> <div>53%</div> <div>14%</div> <div>.</div> <div>32%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4682 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 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	223	Total	C	N	O	S	0	0	0
			1691	1073	283	328	7			

- Molecule 2 is a protein called Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	214	Total	C	N	O	S	0	0	0
			1643	1027	279	332	5			

- Molecule 3 is a protein called Protein OPG161.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	84	Total	C	N	O	S	0	0	0
			665	412	103	146	4			
3	D	84	Total	C	N	O	S	0	0	0
			665	412	103	146	4			

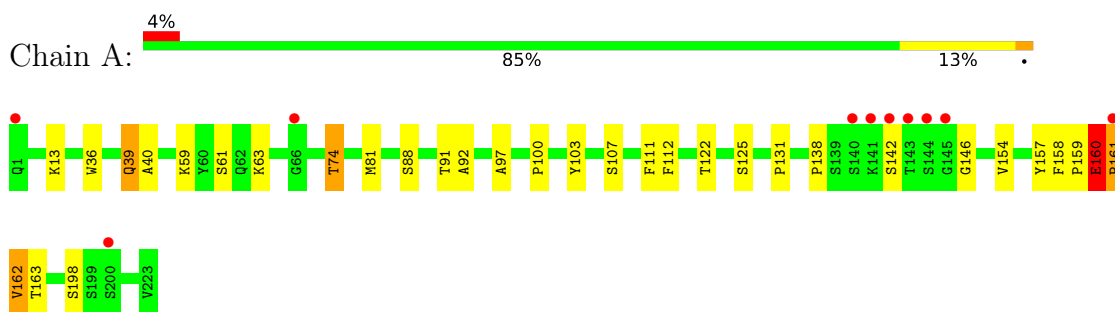
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	9	Total	O	0	0
			9	9		
4	B	5	Total	O	0	0
			5	5		
4	C	3	Total	O	0	0
			3	3		
4	D	1	Total	O	0	0
			1	1		

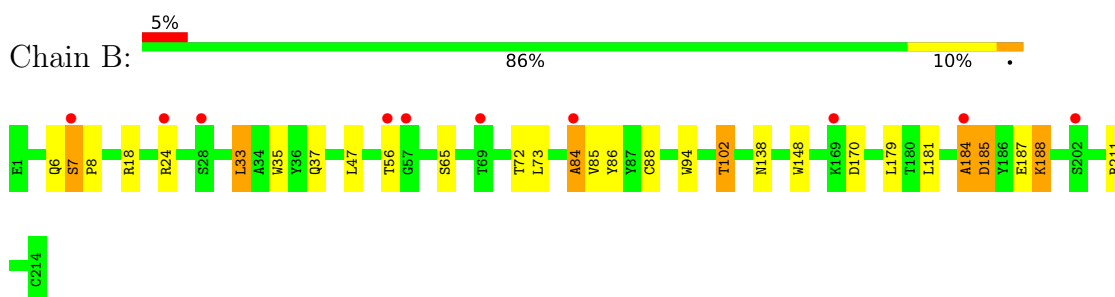
3 Residue-property plots [i](#)

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.

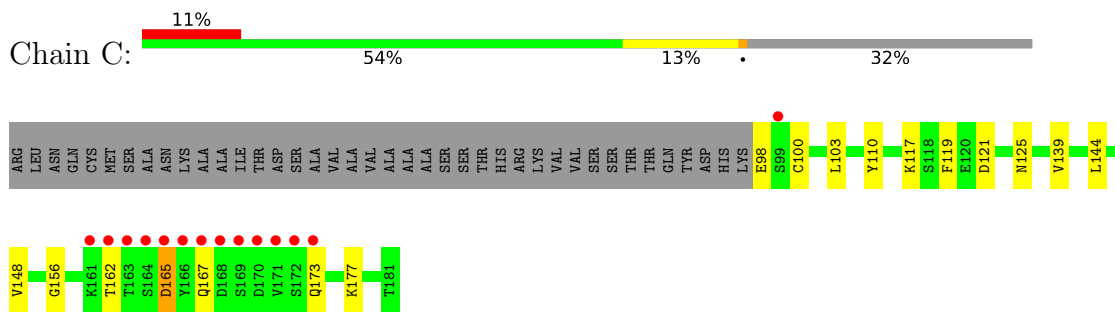
• Molecule 1: Heavy Chain



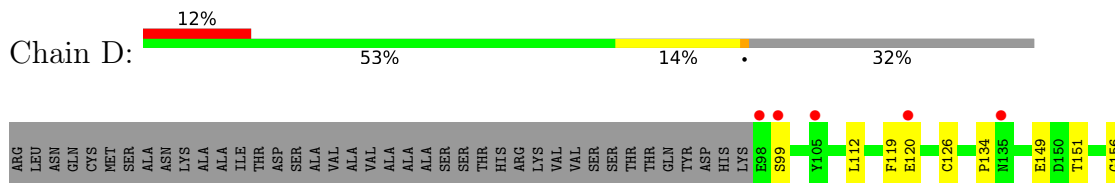
• Molecule 2: Light Chain

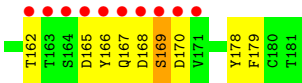


• Molecule 3: Protein OPG161



• Molecule 3: Protein OPG161





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.77Å 82.53Å 107.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.95 – 2.70 44.95 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.8 (44.95-2.70) 99.5 (44.95-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.81 (at 2.69Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.214 , 0.267 0.224 , 0.272	Depositor DCC
R_{free} test set	2011 reflections (9.79%)	wwPDB-VP
Wilson B-factor (Å ²)	44.3	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 33.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.014 for k,h,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4682	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.24% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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	0.41	1/1738 (0.1%)	0.66	10/2367 (0.4%)
2	B	0.13	0/1679	0.50	5/2281 (0.2%)
3	C	0.42	0/680	0.67	0/924
3	D	0.11	0/680	0.52	3/924 (0.3%)
All	All	0.31	1/4777 (0.0%)	0.59	18/6496 (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
3	D	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	161	PRO	N-CD	-15.30	1.26	1.47

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	161	PRO	CA-N-CD	14.20	131.38	111.50
1	A	161	PRO	N-CA-CB	-11.23	90.25	102.60
2	B	84	ALA	CB-CA-C	-9.11	95.12	110.43
1	A	39	GLN	CB-CA-C	8.03	125.59	109.68
1	A	39	GLN	N-CA-C	-7.69	95.60	108.75
2	B	185	ASP	N-CA-C	-7.67	103.72	113.23
1	A	40	ALA	N-CA-C	-7.40	99.25	110.50
2	B	85	VAL	N-CA-C	7.38	121.44	109.78
1	A	160	GLU	CB-CA-C	7.32	122.64	109.61
1	A	161	PRO	N-CD-CG	-7.21	95.14	103.80
1	A	160	GLU	N-CA-C	-6.79	100.17	110.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	161	PRO	N-CA-C	6.56	129.15	112.10
1	A	160	GLU	C-N-CD	-6.45	106.41	120.60
2	B	184	ALA	N-CA-C	6.29	119.43	111.69
3	D	169	SER	CB-CA-C	-5.88	100.15	111.78
3	D	170	ASP	N-CA-C	5.83	118.94	107.98
2	B	184	ALA	CB-CA-C	-5.59	100.47	110.70
3	D	170	ASP	N-CA-CB	-5.34	102.59	110.49

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	D	120	GLU	Peptide

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	1691	0	1642	17	1
2	B	1643	0	1597	15	4
3	C	665	0	596	10	3
3	D	665	0	596	8	0
4	A	9	0	0	0	0
4	B	5	0	0	0	0
4	C	3	0	0	1	0
4	D	1	0	0	0	0
All	All	4682	0	4431	45	4

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 5.

All (45) 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:39:GLN:O	1:A:92:ALA:HB1	1.38	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:167:GLN:NE2	3:D:169:SER:O	1.95	1.00
1:A:39:GLN:O	1:A:92:ALA:CB	2.25	0.83
2:B:56:THR:OG1	3:C:173:GLN:NE2	2.11	0.82
3:C:121:ASP:O	3:C:125:ASN:ND2	2.19	0.74
3:C:98:GLU:HG3	3:C:100:CYS:H	1.58	0.69
2:B:184:ALA:O	2:B:188:LYS:HE3	1.99	0.63
2:B:187:GLU:O	2:B:211:ARG:NH2	2.24	0.63
1:A:131:PRO:HB3	1:A:157:TYR:HB3	1.83	0.60
2:B:37:GLN:HB2	2:B:47:LEU:HD11	1.84	0.60
2:B:84:ALA:O	2:B:86:TYR:CE1	2.56	0.59
3:C:162:THR:OG1	3:C:165:ASP:HB3	2.03	0.59
2:B:6:GLN:HB3	2:B:102:THR:HG22	1.84	0.58
3:C:139:VAL:HG11	3:C:148:VAL:HG21	1.85	0.57
3:C:103:LEU:HB2	3:C:110:TYR:HB2	1.91	0.52
1:A:100:PRO:HG3	1:A:111:PHE:CZ	2.45	0.51
1:A:146:GLY:O	1:A:198:SER:N	2.43	0.51
2:B:181:LEU:HD12	2:B:185:ASP:HB2	1.93	0.50
1:A:91:THR:HG23	1:A:122:THR:HA	1.94	0.49
1:A:36:TRP:CE2	1:A:81:MET:HB2	2.49	0.47
2:B:184:ALA:O	2:B:188:LYS:HG2	2.15	0.47
2:B:8:PRO:O	2:B:102:THR:HB	2.15	0.46
2:B:138:ASN:ND2	2:B:170:ASP:OD2	2.49	0.45
3:C:139:VAL:HG13	3:C:144:LEU:HB3	1.99	0.45
1:A:97:ALA:HB1	1:A:112:PHE:HB3	1.98	0.44
2:B:33:LEU:HD11	2:B:88:CYS:HB2	1.98	0.44
1:A:61:SER:OG	1:A:63:LYS:HG3	2.18	0.44
1:A:13:LYS:HD2	1:A:125:SER:HA	2.01	0.43
2:B:94:TRP:HB2	3:D:165:ASP:HB2	2.00	0.43
1:A:154:VAL:HG11	1:A:162:VAL:HG11	2.01	0.42
1:A:103:TYR:CD2	3:C:177:LYS:HE2	2.55	0.42
1:A:160:GLU:HA	1:A:161:PRO:HA	1.78	0.42
3:C:117:LYS:NZ	4:C:201:HOH:O	2.52	0.41
3:C:119:PHE:CE1	3:C:156:GLY:HA2	2.55	0.41
3:D:134:PRO:HD3	3:D:179:PHE:O	2.20	0.41
1:A:138:PRO:HA	1:A:142:SER:OG	2.21	0.41
2:B:148:TRP:CG	2:B:179:LEU:HD13	2.55	0.41
3:D:112:LEU:HD13	3:D:179:PHE:CZ	2.55	0.41
3:D:119:PHE:CE1	3:D:156:GLY:HA2	2.56	0.41
1:A:59:LYS:NZ	3:D:168:ASP:HB2	2.35	0.41
2:B:184:ALA:O	2:B:188:LYS:CG	2.69	0.41
1:A:107:SER:HA	3:D:149:GLU:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:151:THR:HB	3:D:178:TYR:HA	2.02	0.41
2:B:35:TRP:CE2	2:B:73:LEU:HB2	2.56	0.40
1:A:158:PHE:HA	1:A:159:PRO:HA	1.76	0.40

All (4) 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)
2:B:7:SER:OG	3:C:165:ASP:O[3_555]	1.05	1.15
2:B:7:SER:CB	3:C:165:ASP:O[3_555]	1.37	0.83
2:B:7:SER:OG	3:C:165:ASP:C[3_555]	1.58	0.62
1:A:74:THR:OG1	2:B:18:ARG:NH2[3_545]	2.09	0.11

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	221/223 (99%)	212 (96%)	9 (4%)	0	100	100
2	B	212/214 (99%)	204 (96%)	8 (4%)	0	100	100
3	C	82/124 (66%)	77 (94%)	5 (6%)	0	100	100
3	D	82/124 (66%)	77 (94%)	5 (6%)	0	100	100
All	All	597/685 (87%)	570 (96%)	27 (4%)	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	187/187 (100%)	182 (97%)	5 (3%)	40	69
2	B	185/185 (100%)	178 (96%)	7 (4%)	28	56
3	C	76/108 (70%)	74 (97%)	2 (3%)	41	70
3	D	76/108 (70%)	72 (95%)	4 (5%)	19	43
All	All	524/588 (89%)	506 (97%)	18 (3%)	32	61

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	74	THR
1	A	88	SER
1	A	160	GLU
1	A	162	VAL
1	A	163	THR
2	B	7	SER
2	B	24	ARG
2	B	33	LEU
2	B	65	SER
2	B	72	THR
2	B	102	THR
2	B	188	LYS
3	C	165	ASP
3	C	167	GLN
3	D	99	SER
3	D	126	CYS
3	D	162	THR
3	D	166	TYR

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

Mol	Chain	Res	Type
1	A	65	GLN
2	B	42	GLN
3	C	173	GLN
3	D	125	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 oligosaccharides 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, 95th 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 ²)	Q<0.9
1	A	223/223 (100%)	0.12	10 (4%) 39 37	22, 35, 69, 97	0
2	B	214/214 (100%)	0.21	10 (4%) 37 35	25, 39, 61, 111	0
3	C	84/124 (67%)	0.89	14 (16%) 5 5	29, 41, 92, 106	0
3	D	84/124 (67%)	0.94	15 (17%) 4 5	32, 46, 92, 115	0
All	All	605/685 (88%)	0.37	49 (8%) 19 18	22, 39, 79, 115	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	167	GLN	8.8
3	C	173	GLN	6.6
3	C	166	TYR	6.2
3	C	168	ASP	6.1
3	C	165	ASP	5.6
3	D	166	TYR	5.6
2	B	24	ARG	5.4
3	D	167	GLN	5.0
3	D	164	SER	4.9
3	C	162	THR	4.7
3	C	164	SER	4.5
3	C	163	THR	4.5
3	C	170	ASP	4.4
3	D	120	GLU	4.4
1	A	142	SER	4.4
3	D	165	ASP	4.2
3	C	169	SER	4.2
3	C	171	VAL	4.1
3	D	168	ASP	4.0
1	A	143	THR	4.0
1	A	141	LYS	3.9

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Mol	Chain	Res	Type	RSRZ
3	D	169	SER	3.9
1	A	145	GLY	3.9
3	C	172	SER	3.7
3	D	163	THR	3.6
1	A	1	GLN	3.3
1	A	144	SER	3.2
2	B	184	ALA	3.1
1	A	161	PRO	3.1
2	B	84	ALA	3.1
2	B	56	THR	3.0
1	A	140	SER	3.0
2	B	169	LYS	3.0
3	C	99	SER	2.9
3	D	99	SER	2.9
2	B	7	SER	2.8
2	B	57	GLY	2.7
3	C	161	LYS	2.7
1	A	200	SER	2.5
3	D	162	THR	2.5
3	D	135	ASN	2.5
3	D	170	ASP	2.4
3	D	171	VAL	2.3
1	A	66	GLY	2.3
2	B	202	SER	2.2
2	B	28	SER	2.2
3	D	98	GLU	2.2
3	D	105	TYR	2.1
2	B	69	THR	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 oligosaccharides 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.