



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 05:56 AM UTC

PDB ID : 6WXY / pdb_00006wxy
Title : crystal structure of cA6-bound Card1
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Deposited on : 2020-05-12
Resolution : 2.10 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	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
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)	:	2.49

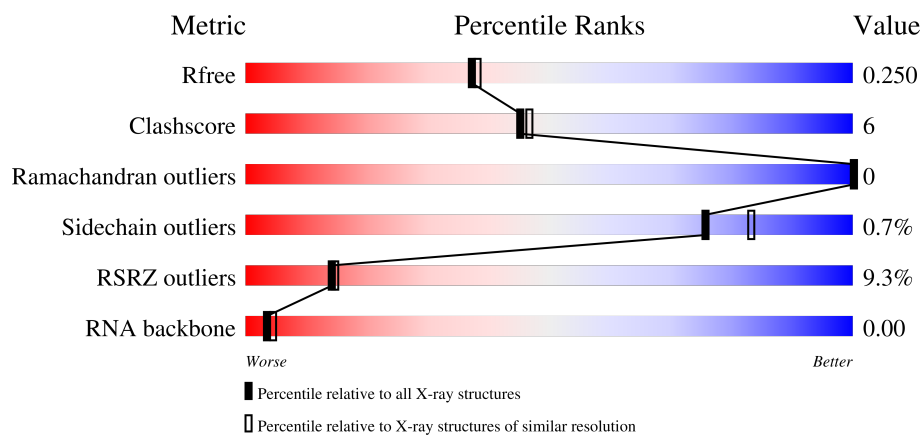
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)
RNA backbone	3983	1006 (2.42-1.78)

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	6	17% 33% 33% 33%
2	B	382	12% 84% 13% . .
2	C	382	6% 85% 12% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6534 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 RNA chain called cA6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	6	Total	C	N	O	P	0	0	0
			132	60	30	36	6			

- Molecule 2 is a protein called Card1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	372	Total	C	N	O	S	0	0	0
			3092	1991	506	585	10			
2	C	372	Total	C	N	O	S	0	0	0
			3092	1991	506	585	10			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	374	GLY	-	expression tag	UNP F2NWD3
B	375	SER	-	expression tag	UNP F2NWD3
B	376	GLY	-	expression tag	UNP F2NWD3
B	377	HIS	-	expression tag	UNP F2NWD3
B	378	HIS	-	expression tag	UNP F2NWD3
B	379	HIS	-	expression tag	UNP F2NWD3
B	380	HIS	-	expression tag	UNP F2NWD3
B	381	HIS	-	expression tag	UNP F2NWD3
B	382	HIS	-	expression tag	UNP F2NWD3
C	374	GLY	-	expression tag	UNP F2NWD3
C	375	SER	-	expression tag	UNP F2NWD3
C	376	GLY	-	expression tag	UNP F2NWD3
C	377	HIS	-	expression tag	UNP F2NWD3
C	378	HIS	-	expression tag	UNP F2NWD3
C	379	HIS	-	expression tag	UNP F2NWD3
C	380	HIS	-	expression tag	UNP F2NWD3
C	381	HIS	-	expression tag	UNP F2NWD3
C	382	HIS	-	expression tag	UNP F2NWD3

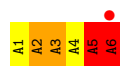
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	O 1	0	0
3	B	92	Total 92	O 92	0	0
3	C	125	Total 125	O 125	0	0

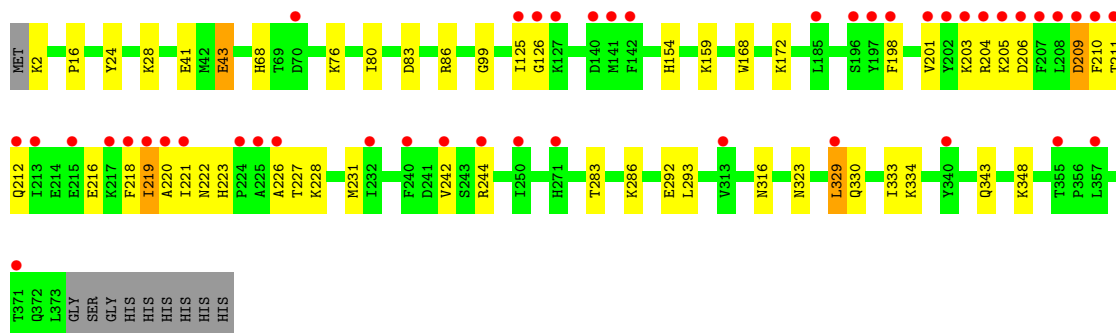
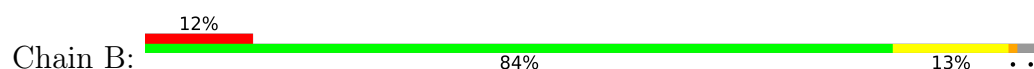
3 Residue-property plots [i](#)

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.

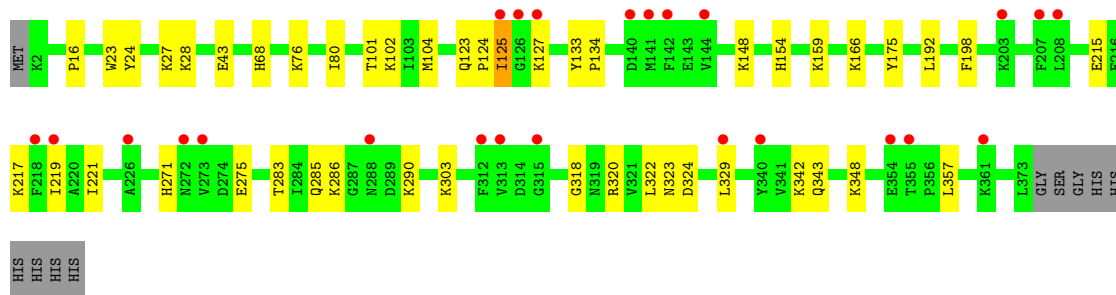
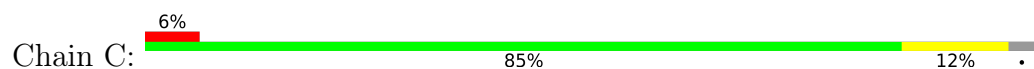
- Molecule 1: cA6



- Molecule 2: Card1



- Molecule 2: Card1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	172.91Å 124.76Å 42.26Å 90.00° 96.79° 90.00°	Depositor
Resolution (Å)	85.85 – 2.10 85.85 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.4 (85.85-2.10) 98.4 (85.85-2.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.34 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.18_3855	Depositor
R, R_{free}	0.206 , 0.245 0.210 , 0.250	Depositor DCC
R_{free} test set	2520 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	42.1	Xtriage
Anisotropy	0.194	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6534	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.43% 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 [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	0.82	0/149	1.29	3/230 (1.3%)
2	B	0.42	1/3157 (0.0%)	0.58	5/4257 (0.1%)
2	C	0.32	0/3157	0.49	0/4257
All	All	0.39	1/6463 (0.0%)	0.57	8/8744 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	43	GLU	C-O	-5.03	1.17	1.24

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	222	ASN	N-CA-C	10.63	122.73	108.38
1	A	6	A	C4'-C3'-O3'	6.64	122.96	113.00
2	B	223	HIS	N-CA-C	-6.17	102.30	110.07
2	B	221	ILE	CB-CA-C	-6.15	105.28	111.80
1	A	5	A	C1'-C2'-O2'	-5.77	103.15	111.80
2	B	329	LEU	CA-CB-CG	-5.57	96.80	116.30
2	B	222	ASN	O-C-N	5.43	128.80	122.99
1	A	6	A	C2'-C3'-O3'	5.37	121.75	113.70

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	132	0	66	11	0
2	B	3092	0	3063	39	0
2	C	3092	0	3063	35	0
3	A	1	0	0	0	0
3	B	92	0	0	5	0
3	C	125	0	0	7	0
All	All	6534	0	6192	74	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 6.

All (74) 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)
2:C:101:THR:H	2:C:104:MET:HE3	1.24	0.99
2:C:285:GLN:HB2	2:C:290:LYS:HE3	1.67	0.77
1:A:6:A:H1'	2:B:125:ILE:HD13	1.67	0.76
1:A:5:A:O2'	2:B:125:ILE:HG23	1.89	0.72
2:C:101:THR:N	2:C:104:MET:HE3	2.04	0.69
2:B:203:LYS:HB2	2:B:206:ASP:O	1.95	0.66
2:B:219:ILE:HG22	2:B:226:ALA:O	1.98	0.63
2:B:293:LEU:HD11	2:B:333:ILE:HD11	1.80	0.62
2:C:166:LYS:NZ	3:C:404:HOH:O	2.36	0.59
2:B:43:GLU:HG3	2:B:68:HIS:NE2	2.18	0.59
1:A:5:A:C5	2:B:16:PRO:HG3	2.38	0.58
2:B:329:LEU:HD22	2:B:343:GLN:CD	2.28	0.58
2:C:271:HIS:HA	3:C:438:HOH:O	2.03	0.58
1:A:1:A:C2	2:C:104:MET:HE1	2.40	0.57
2:B:283:THR:HG22	2:B:292:GLU:HG2	1.86	0.56
2:B:323:ASN:HD21	2:C:322:LEU:HD23	1.70	0.56
2:C:123:GLN:HG2	3:C:508:HOH:O	2.05	0.56
2:C:124:PRO:HB2	2:C:127:LYS:HB2	1.87	0.55
1:A:5:A:C4	2:B:125:ILE:HG22	2.42	0.55
2:C:192:LEU:HA	2:C:221:ILE:HD13	1.89	0.55
2:C:329:LEU:HD13	2:C:343:GLN:HB2	1.88	0.55
2:C:43:GLU:HG3	2:C:68:HIS:NE2	2.23	0.54
2:B:218:PHE:C	2:B:220:ALA:H	2.15	0.54
1:A:3:A:H3'	1:A:3:A:C8	2.43	0.54
2:B:125:ILE:HG13	2:B:126:GLY:H	1.73	0.54
2:B:329:LEU:HD22	2:B:343:GLN:OE1	2.08	0.53
2:C:342:LYS:HD2	3:C:424:HOH:O	2.08	0.52
2:C:215:GLU:O	2:C:219:ILE:HG13	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:275:GLU:OE1	3:C:401:HOH:O	2.19	0.52
1:A:3:A:O4'	2:C:125:ILE:HG12	2.09	0.52
2:B:99:GLY:O	2:C:102:LYS:NZ	2.43	0.52
2:B:212:GLN:HB2	2:B:242:VAL:HG13	1.91	0.52
1:A:5:A:C4	2:B:16:PRO:HG3	2.45	0.51
2:B:209:ASP:HB3	2:B:244:ARG:HG3	1.93	0.51
2:B:316:ASN:OD1	2:B:316:ASN:N	2.41	0.51
2:B:24:TYR:CZ	2:B:28:LYS:HG3	2.45	0.50
2:B:2:LYS:NZ	3:B:407:HOH:O	2.40	0.49
1:A:2:A:C4	2:C:16:PRO:HG3	2.47	0.49
2:B:348:LYS:NZ	3:B:406:HOH:O	2.36	0.49
1:A:1:A:H5'	1:A:6:A:H5'	1.95	0.48
2:C:148:LYS:NZ	3:C:406:HOH:O	2.38	0.48
2:C:24:TYR:CZ	2:C:28:LYS:HG3	2.49	0.47
2:C:23:TRP:CZ2	2:C:27:LYS:HE3	2.49	0.47
2:C:303:LYS:HG3	3:C:418:HOH:O	2.14	0.47
2:B:198:PHE:HA	2:B:201:VAL:HG12	1.97	0.46
2:C:320:ARG:NH1	2:C:324:ASP:OD2	2.47	0.46
2:B:168:TRP:O	2:B:172:LYS:HG3	2.16	0.46
2:C:101:THR:HG23	2:C:104:MET:CE	2.47	0.45
2:C:133:TYR:CD1	2:C:134:PRO:HA	2.51	0.45
2:B:204:ARG:NH2	3:B:408:HOH:O	2.48	0.45
2:B:154:HIS:O	2:B:286:LYS:HE3	2.16	0.45
2:B:219:ILE:HG21	2:B:227:THR:C	2.41	0.45
2:B:83:ASP:OD1	2:B:86:ARG:NH2	2.48	0.45
2:C:124:PRO:HB2	2:C:127:LYS:HD3	1.99	0.44
2:B:41:GLU:H	2:B:41:GLU:CD	2.26	0.44
2:C:76:LYS:O	2:C:80:ILE:HG23	2.18	0.44
2:B:159:LYS:HB2	2:B:159:LYS:HE3	1.66	0.44
2:B:219:ILE:HG13	2:B:228:LYS:HB2	1.99	0.44
2:B:218:PHE:C	2:B:220:ALA:N	2.70	0.44
2:B:226:ALA:HA	2:B:231:MET:HE3	1.99	0.44
2:C:217:LYS:HA	2:C:217:LYS:HE2	2.00	0.43
3:B:403:HOH:O	2:C:323:ASN:CG	2.61	0.43
2:C:154:HIS:O	2:C:286:LYS:HE3	2.18	0.42
2:B:201:VAL:HG13	2:B:210:PHE:CZ	2.55	0.41
2:B:205:LYS:HD3	2:B:205:LYS:HA	1.90	0.41
1:A:5:A:C8	2:B:125:ILE:HA	2.55	0.41
2:B:330:GLN:O	2:B:334:LYS:HB3	2.20	0.41
2:B:329:LEU:HA	2:B:329:LEU:HD12	1.81	0.41
2:C:318:GLY:HA2	2:C:357:LEU:HD23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:159:LYS:HG2	2:C:283:THR:HB	2.03	0.41
2:C:175:TYR:CD2	2:C:348:LYS:HE2	2.56	0.41
2:B:76:LYS:O	2:B:80:ILE:HG23	2.21	0.40
3:B:452:HOH:O	2:C:101:THR:HB	2.22	0.40
2:C:198:PHE:CE2	2:C:221:ILE:HD11	2.57	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	
2	B	370/382 (97%)	354 (96%)	16 (4%)	0	100	100
2	C	370/382 (97%)	361 (98%)	9 (2%)	0	100	100
All	All	740/764 (97%)	715 (97%)	25 (3%)	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	
2	B	344/352 (98%)	340 (99%)	4 (1%)	63	72
2	C	344/352 (98%)	343 (100%)	1 (0%)	86	91
All	All	688/704 (98%)	683 (99%)	5 (1%)	76	83

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	209	ASP
2	B	211	THR
2	B	216	GLU
2	B	219	ILE
2	C	125	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	8	ASN
2	B	13	GLN
2	B	92	ASN
2	B	96	ASN
2	B	137	GLN
2	B	195	ASN
2	B	223	HIS
2	B	291	ASN
2	B	319	ASN
2	B	372	GLN
2	C	137	GLN
2	C	194	ASN
2	C	195	ASN
2	C	319	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	5/6 (83%)	5 (100%)	0

All (5) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	A
1	A	3	A
1	A	4	A
1	A	5	A
1	A	6	A

There are no RNA pucker outliers to report.

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	6/6 (100%)	1.57	1 (16%) 4 4	52, 71, 91, 113	0
2	B	372/382 (97%)	0.83	45 (12%) 8 9	31, 50, 93, 110	0
2	C	372/382 (97%)	0.55	24 (6%) 25 26	27, 47, 70, 92	0
All	All	750/770 (97%)	0.70	70 (9%) 14 15	27, 48, 87, 113	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	210	PHE	8.2
2	B	208	LEU	5.9
2	C	125	ILE	4.7
2	C	126	GLY	4.7
2	B	126	GLY	4.5
2	B	219	ILE	4.4
2	B	202	TYR	4.4
2	B	207	PHE	4.4
2	B	221	ILE	3.9
2	B	142	PHE	3.8
2	B	127	LYS	3.7
2	C	142	PHE	3.7
2	B	125	ILE	3.6
1	A	6	A	3.6
2	B	215	GLU	3.3
2	B	242	VAL	3.2
2	B	329	LEU	3.2
2	B	203	LYS	3.2
2	B	213	ILE	3.1
2	B	340	TYR	3.1
2	C	207	PHE	3.0
2	C	140	ASP	3.0
2	B	211	THR	3.0

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Mol	Chain	Res	Type	RSRZ
2	B	225	ALA	2.9
2	C	127	LYS	2.9
2	C	329	LEU	2.8
2	B	197	TYR	2.8
2	B	206	ASP	2.7
2	B	209	ASP	2.7
2	B	218	PHE	2.7
2	B	220	ALA	2.7
2	C	354	GLU	2.6
2	C	288	ASN	2.6
2	B	355	THR	2.6
2	C	226	ALA	2.6
2	B	140	ASP	2.5
2	B	371	THR	2.5
2	B	224	PRO	2.5
2	B	357	LEU	2.4
2	B	204	ARG	2.4
2	C	313	VAL	2.4
2	C	355	THR	2.4
2	B	201	VAL	2.3
2	C	219	ILE	2.3
2	C	315	GLY	2.3
2	B	205	LYS	2.3
2	B	217	LYS	2.3
2	C	203	LYS	2.3
2	B	196	SER	2.3
2	C	141	MET	2.2
2	B	313	VAL	2.2
2	B	198	PHE	2.1
2	B	250	ILE	2.1
2	B	226	ALA	2.1
2	C	272	ASN	2.1
2	C	340	TYR	2.1
2	B	70	ASP	2.1
2	B	232	ILE	2.1
2	C	312	PHE	2.1
2	B	271	HIS	2.1
2	C	273	VAL	2.1
2	C	361	LYS	2.1
2	C	144	VAL	2.1
2	B	141	MET	2.1
2	B	212	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	240	PHE	2.0
2	C	218	PHE	2.0
2	B	185	LEU	2.0
2	C	208	LEU	2.0
2	B	244	ARG	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 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.