



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:24 PM UTC

PDB ID : 2O8A / pdb_00002o8a
Title : rat PP1cgamma complexed with mouse inhibitor-2
Authors : Hurley, T.D.
Deposited on : 2006-12-12
Resolution : 2.61 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

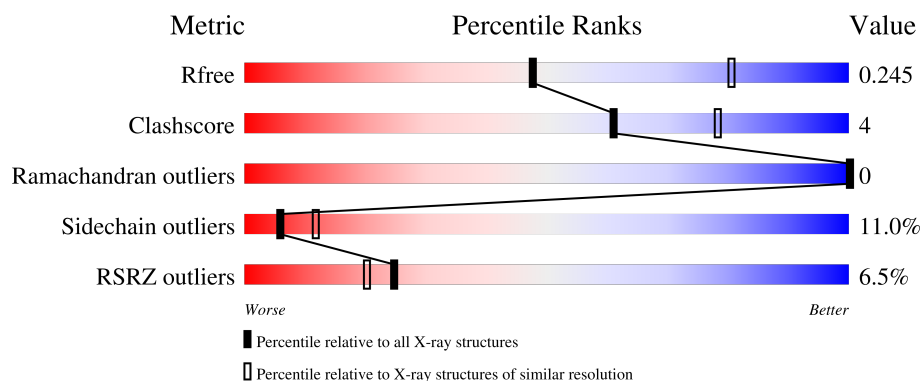
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)

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	329	2% 75% 13% 10%
1	B	329	% 76% 13% 10%
2	I	206	10% 17% 10% 71%
2	J	206	7% 21% 7% 72%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5842 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 Serine/threonine-protein phosphatase PP1-gamma catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	S	0	0	0
			2380	1527	399	436	18			
1	B	295	Total	C	N	O	S	0	0	0
			2380	1527	399	436	18			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	initiating methionine	UNP P63088
A	-4	HIS	-	expression tag	UNP P63088
A	-3	HIS	-	expression tag	UNP P63088
A	-2	HIS	-	expression tag	UNP P63088
A	-1	HIS	-	expression tag	UNP P63088
A	0	HIS	-	expression tag	UNP P63088
A	1	HIS	-	expression tag	UNP P63088
B	-5	MET	-	initiating methionine	UNP P63088
B	-4	HIS	-	expression tag	UNP P63088
B	-3	HIS	-	expression tag	UNP P63088
B	-2	HIS	-	expression tag	UNP P63088
B	-1	HIS	-	expression tag	UNP P63088
B	0	HIS	-	expression tag	UNP P63088
B	1	HIS	-	expression tag	UNP P63088

- Molecule 2 is a protein called Protein phosphatase inhibitor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	59	Total	C	N	O	S	0	0	0
			495	309	93	91	2			
2	J	58	Total	C	N	O	S	0	0	0
			487	305	92	88	2			

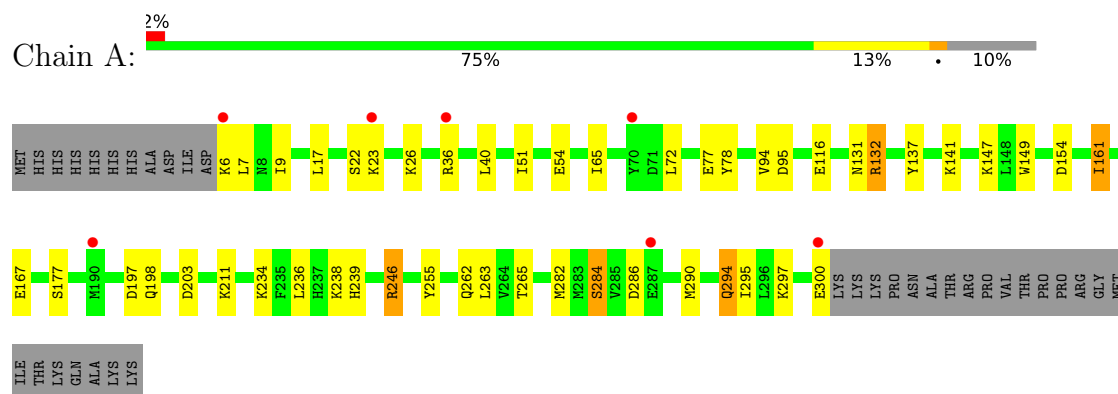
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	47	Total 47	O 47	0	0
3	I	5	Total 5	O 5	0	0
3	B	38	Total 38	O 38	0	0
3	J	10	Total 10	O 10	0	0

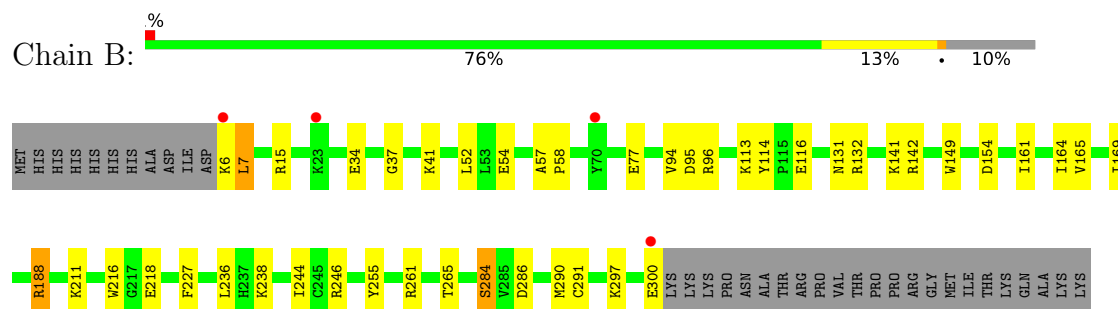
3 Residue-property plots

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: Serine/threonine-protein phosphatase PP1-gamma catalytic subunit



- Molecule 1: Serine/threonine-protein phosphatase PP1-gamma catalytic subunit



- Molecule 2: Protein phosphatase inhibitor 2



LEU
GLN
HIS
LYS
SER
GLN
SER
SER

● Molecule 2: Protein phosphatase inhibitor 2



MET
ALA
ALA
SER
THR
ALA
SER
HIS
ARG
PRO
ILE
K12
K16
N17
LYS
THR
SER
ALA
ALA
SER
PRO
PRO
VAL
VAL
PRO
SER
ALA
GLU
GLN
PRO
ARG
PRO
ILE
VAL
GLU
GLU
LEU
SER
LYS
K44
K47
T56
TYR
HIS
PRO
ALA
ASP
LYS
TYR
GLY
LEU
MET
LYS
ILE
ASP

GLU
PRO
ASN
THR
PRO
TYR
HIS
ASN
MET
ILE
GLY
ASP
ASP
GLU
ASP
ALA
TYR
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SER
GLU
GLY
ASN
GLU
VAL
MET
THR
PRO
ASP
ILE
LEU
ALA
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ALA
ALA
GLU
GLY
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GLU
PRO
LYS
TYR
ARG
THR
SER
GLU
GLN
GLU
SER
SER
GLY
GLU
GLU
ASP
ASN
ASP
L130

S131
P132
E133
E134
R135
E136
K137
Q140
F141
E142
M143
K144
L153
K156
K164
D165
L166
H167
D168
ASP
ASP
GLU
GLU
GLU
MET
ALA
GLU
THR
ALA
ASP
GLY
ASP
SER
MET
ASN
VAL
GLU
GLU
SER
SER
GLN
GLY
THR
THR
SER
ASP
HIS
LEU
GLN
HIS
LYS
SER
GLN
SER

SER

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.46Å 103.81Å 151.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.70 – 2.61 41.70 – 2.61	Depositor EDS
% Data completeness (in resolution range)	95.4 (41.70-2.61) 95.6 (41.70-2.61)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.00 (at 2.61Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.216 , 0.254 0.208 , 0.245	Depositor DCC
R_{free} test set	2248 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	45.7	Xtriage
Anisotropy	0.387	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 21.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5842	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.36% 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	0.55	0/2434	0.87	1/3286 (0.0%)
1	B	0.55	0/2434	0.87	0/3286
2	I	0.64	0/499	0.90	0/658
2	J	0.62	0/491	1.00	0/647
All	All	0.56	0/5858	0.89	1/7877 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	22	SER	N-CA-C	5.07	116.88	110.33

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	2380	0	2351	18	0
1	B	2380	0	2351	16	0
2	I	495	0	507	10	0
2	J	487	0	503	8	0
3	A	47	0	0	1	0
3	B	38	0	0	0	0
3	I	5	0	0	0	0
3	J	10	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5842	0	5712	48	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 4.

All (48) 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:J:131:SER:HB3	2:J:134:GLU:HB2	1.73	0.69
1:B:286:ASP:OD1	1:B:290:MET:HB3	1.97	0.65
1:A:284:SER:HB2	1:A:294:GLN:HE22	1.61	0.64
2:I:131:SER:HB2	2:I:134:GLU:HB2	1.78	0.64
2:I:52:ASN:O	2:I:56:THR:HG23	1.99	0.61
2:I:131:SER:HB3	2:I:134:GLU:H	1.65	0.61
1:B:15:ARG:HH22	1:B:34:GLU:CD	2.13	0.56
2:I:131:SER:O	2:I:135:ARG:HB2	2.05	0.56
1:B:236:LEU:HD21	1:B:244:ILE:HG13	1.88	0.55
1:A:131:ASN:HB3	1:A:149:TRP:HE1	1.73	0.54
1:B:15:ARG:NH2	1:B:34:GLU:OE2	2.42	0.53
2:I:136:GLU:OE1	2:I:139:ARG:NH1	2.37	0.53
2:I:131:SER:CB	2:I:134:GLU:HB2	2.39	0.52
2:J:47:LYS:HD3	3:J:216:HOH:O	2.09	0.52
2:J:131:SER:HB3	2:J:134:GLU:H	1.75	0.51
1:B:131:ASN:HB3	1:B:149:TRP:HE1	1.77	0.49
2:J:131:SER:CB	2:J:134:GLU:HB2	2.41	0.49
1:A:132:ARG:NH2	1:A:137:TYR:CE2	2.82	0.48
1:A:286:ASP:OD1	1:A:290:MET:HB3	2.13	0.48
1:B:113:LYS:HG2	1:B:114:TYR:CE1	2.49	0.47
1:B:94:VAL:O	1:B:95:ASP:HB2	2.14	0.47
1:B:57:ALA:HB1	1:B:58:PRO:HA	1.97	0.46
1:A:65:ILE:HD13	1:A:72:LEU:HD13	1.99	0.45
1:A:94:VAL:O	1:A:95:ASP:HB2	2.15	0.45
1:A:54:GLU:HG3	2:I:17:ASN:ND2	2.31	0.45
1:A:36:ARG:O	1:A:40:LEU:HG	2.17	0.45
1:A:239:HIS:HE1	3:A:326:HOH:O	2.00	0.45
1:B:188:ARG:HA	1:B:188:ARG:HD3	1.74	0.45
1:A:177:SER:HB2	1:A:203:ASP:HB2	2.00	0.44
1:B:255:TYR:HA	1:B:265:THR:O	2.16	0.44
2:J:131:SER:HB2	2:J:134:GLU:CD	2.42	0.44
1:A:284:SER:HB2	1:A:294:GLN:NE2	2.29	0.44
1:B:54:GLU:HG3	2:J:17:ASN:ND2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:216:TRP:CZ3	1:B:227:PHE:HB3	2.54	0.43
1:A:255:TYR:HA	1:A:265:THR:O	2.19	0.43
1:A:246:ARG:HD2	1:A:263:LEU:HD21	2.00	0.43
1:A:132:ARG:NH1	2:I:161:LEU:HD13	2.35	0.42
1:A:78:TYR:CE2	1:A:294:GLN:HG2	2.54	0.42
1:A:197:ASP:CG	2:I:159:ARG:HH12	2.26	0.42
1:A:236:LEU:CD1	1:A:262:GLN:HB3	2.50	0.42
2:I:139:ARG:HH21	2:I:143:MET:HE1	1.85	0.41
1:B:165:VAL:HB	1:B:169:ILE:HB	2.03	0.41
2:J:144:LYS:HD2	3:J:208:HOH:O	2.19	0.41
1:A:51:ILE:HD11	1:A:161:ILE:CD1	2.51	0.41
2:J:131:SER:O	2:J:135:ARG:HB2	2.21	0.41
1:B:52:LEU:HD11	1:B:164:ILE:HG13	2.03	0.41
1:B:284:SER:O	1:B:291:CYS:HA	2.20	0.41
1:B:7:LEU:HD13	1:B:37:GLY:HA3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	293/329 (89%)	277 (94%)	16 (6%)	0	100	100
1	B	293/329 (89%)	276 (94%)	17 (6%)	0	100	100
2	I	53/206 (26%)	51 (96%)	2 (4%)	0	100	100
2	J	52/206 (25%)	52 (100%)	0	0	100	100
All	All	691/1070 (65%)	656 (95%)	35 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	261/291 (90%)	236 (90%)	25 (10%)	8	16
1	B	261/291 (90%)	241 (92%)	20 (8%)	12	25
2	I	54/181 (30%)	38 (70%)	16 (30%)	0	0
2	J	53/181 (29%)	45 (85%)	8 (15%)	3	5
All	All	629/944 (67%)	560 (89%)	69 (11%)	6	12

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LYS
1	A	7	LEU
1	A	9	ILE
1	A	17	LEU
1	A	23	LYS
1	A	26	LYS
1	A	77	GLU
1	A	116	GLU
1	A	132	ARG
1	A	141	LYS
1	A	147	LYS
1	A	154	ASP
1	A	161	ILE
1	A	167	GLU
1	A	198	GLN
1	A	211	LYS
1	A	234	LYS
1	A	238	LYS
1	A	246	ARG
1	A	282	MET
1	A	284	SER
1	A	294	GLN
1	A	295	ILE
1	A	297	LYS

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Mol	Chain	Res	Type
1	A	300	GLU
2	I	12	LYS
2	I	45	SER
2	I	47	LYS
2	I	53	ILE
2	I	131	SER
2	I	133	GLU
2	I	134	GLU
2	I	137	LYS
2	I	138	LYS
2	I	142	GLU
2	I	143	MET
2	I	163	SER
2	I	166	LEU
2	I	167	HIS
2	I	168	ASP
2	I	169	ASP
1	B	6	LYS
1	B	7	LEU
1	B	41	LYS
1	B	77	GLU
1	B	96	ARG
1	B	116	GLU
1	B	132	ARG
1	B	141	LYS
1	B	142	ARG
1	B	154	ASP
1	B	161	ILE
1	B	188	ARG
1	B	211	LYS
1	B	218	GLU
1	B	238	LYS
1	B	246	ARG
1	B	261	ARG
1	B	284	SER
1	B	297	LYS
1	B	300	GLU
2	J	12	LYS
2	J	16	LYS
2	J	137	LYS
2	J	142	GLU
2	J	156	LYS

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Mol	Chain	Res	Type
2	J	164	LYS
2	J	166	LEU
2	J	167	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	239	HIS
1	B	27	ASN
1	B	117	ASN
1	B	145	ASN
1	B	239	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 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	295/329 (89%)	-0.03	7 (2%) 59 54	30, 42, 59, 73	0
1	B	295/329 (89%)	-0.04	4 (1%) 73 70	30, 42, 59, 73	0
2	I	59/206 (28%)	1.54	20 (33%) 1 1	36, 62, 82, 85	0
2	J	58/206 (28%)	1.45	15 (25%) 1 1	35, 63, 82, 85	0
All	All	707/1070 (66%)	0.22	46 (6%) 25 20	30, 44, 71, 85	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	I	130	LEU	6.1
2	J	130	LEU	5.7
2	J	167	HIS	5.6
2	J	133	GLU	4.8
2	J	168	ASP	4.7
2	J	131	SER	4.3
2	I	166	LEU	4.2
2	I	55	ALA	4.1
2	I	53	ILE	4.1
1	A	6	LYS	4.0
2	J	132	PRO	4.0
2	I	51	MET	4.0
2	I	132	PRO	3.9
2	J	134	GLU	3.8
1	B	23	LYS	3.8
2	I	56	THR	3.7
2	I	167	HIS	3.7
2	I	169	ASP	3.6
2	J	12	LYS	3.6
1	B	300	GLU	3.5
2	I	165	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	6	LYS	3.1
2	I	131	SER	3.1
2	J	135	ARG	3.0
1	A	70	TYR	3.0
2	I	45	SER	2.9
2	I	12	LYS	2.9
2	J	166	LEU	2.9
2	J	17	ASN	2.9
2	I	54	LEU	2.8
2	I	135	ARG	2.7
2	I	153	LEU	2.6
1	A	36	ARG	2.6
1	A	300	GLU	2.6
2	I	133	GLU	2.6
2	J	56	THR	2.5
2	J	165	ASP	2.5
2	I	44	LYS	2.5
2	J	153	LEU	2.5
2	I	52	ASN	2.3
2	I	168	ASP	2.3
1	A	190	MET	2.2
2	J	140	GLN	2.2
1	B	70	TYR	2.2
1	A	23	LYS	2.1
1	A	287	GLU	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.