



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 09:34 AM UTC

PDB ID : 8QAC / pdb_00008qac
Title : X-ray crystal structure of a de novo designed antiparallel coiled-coil 8-helix bundle with 4 heptad repeats, antiparallel 8-helix bundle-GLIA
Authors : Albanese, K.I.; Dawson, W.M.; Petrenas, R.; Woolfson, D.N.
Deposited on : 2023-08-22
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

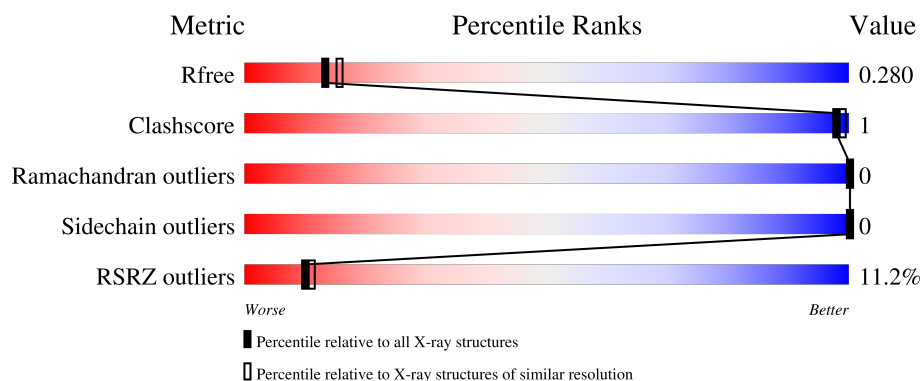
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	B	33	6% 91% 9%
1	C	33	9% 91% 9%
1	D	33	6% 85% 15%
1	E	33	9% 91% 9%
1	F	33	6% 85% 12%

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Mol	Chain	Length	Quality of chain
1	G	33	
1	H	33	
1	I	33	
1	J	33	
1	K	33	
1	L	33	
1	M	33	
1	N	33	
1	O	33	
1	P	33	
1	R	33	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5826 atoms, of which 2857 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 antiparallel 8-helix bundle-GLIA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	30	Total	C	H	N	O	0	0	1
			370	124	182	30	34			
1	C	30	Total	C	H	N	O	0	0	0
			377	127	183	32	35			
1	D	28	Total	C	H	N	O	0	0	0
			369	124	184	29	32			
1	E	30	Total	C	H	N	O	0	0	1
			371	124	183	30	34			
1	F	29	Total	C	H	N	O	0	0	0
			377	126	185	31	35			
1	G	29	Total	C	H	N	O	0	0	0
			411	133	211	33	34			
1	H	27	Total	C	H	N	O	0	0	0
			342	115	170	30	27			
1	I	28	Total	C	H	N	O	0	0	0
			375	124	186	32	33			
1	J	27	Total	C	H	N	O	0	0	0
			350	114	173	29	34			
1	K	28	Total	C	H	N	O	0	0	1
			360	122	176	29	33			
1	L	29	Total	C	H	N	O	0	2	0
			295	102	133	29	31			
1	N	28	Total	C	H	N	O	0	0	0
			355	118	173	31	33			
1	O	28	Total	C	H	N	O	0	0	0
			366	122	183	31	30			
1	P	28	Total	C	H	N	O	0	0	0
			322	111	152	31	28			
1	R	29	Total	C	H	N	O	0	0	0
			403	133	207	32	31			
1	M	28	Total	C	H	N	O	0	0	0
			363	121	176	31	35			

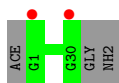
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total O 1 1	0	0
2	C	2	Total O 2 2	0	0
2	D	3	Total O 3 3	0	2
2	E	1	Total O 1 1	0	0
2	F	2	Total O 2 2	0	0
2	G	2	Total O 2 2	0	0
2	H	2	Total O 2 2	0	0
2	I	1	Total O 1 1	0	0
2	K	1	Total O 1 1	0	0
2	N	1	Total O 1 1	0	0
2	O	1	Total O 1 1	0	0
2	R	3	Total O 3 3	0	0

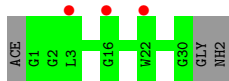
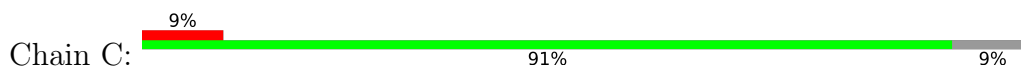
3 Residue-property plots [i](#)

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.

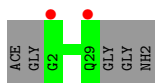
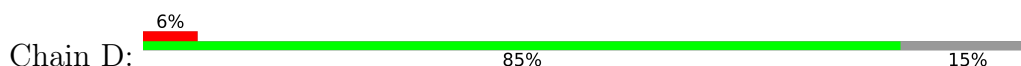
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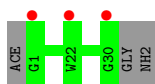
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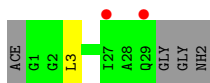
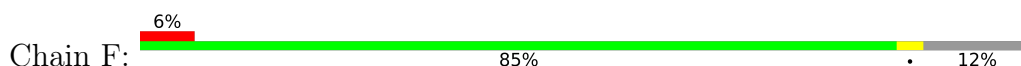
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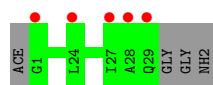
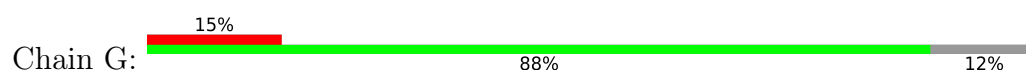
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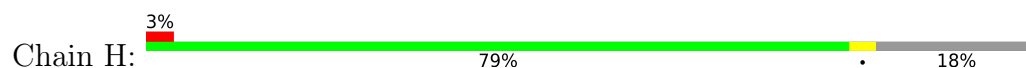
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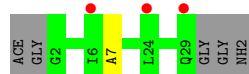
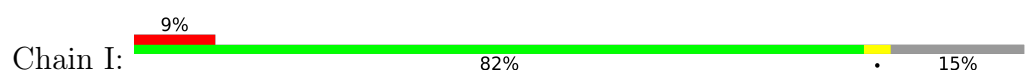
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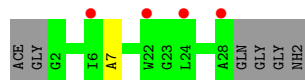
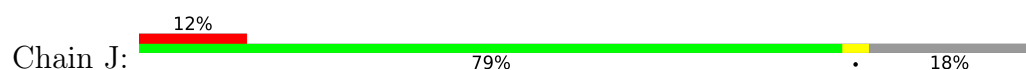
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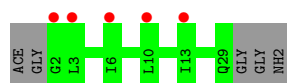
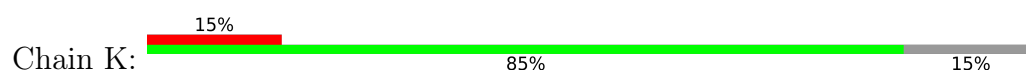
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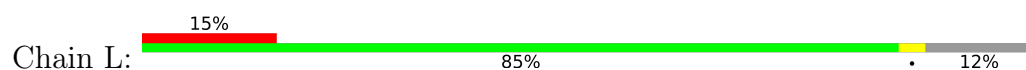
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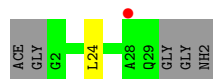
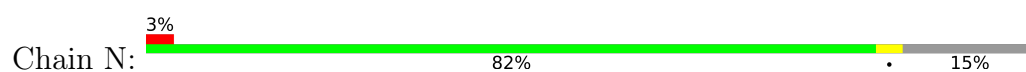
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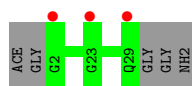
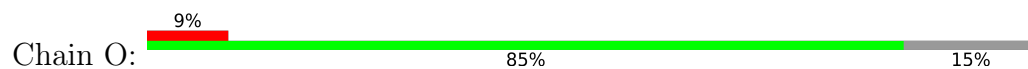
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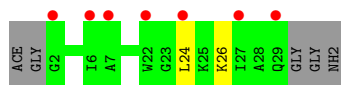
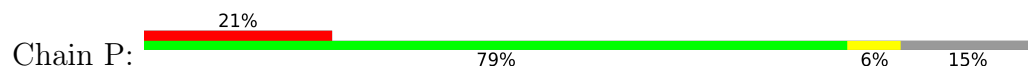
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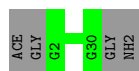
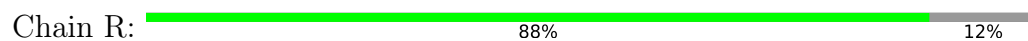
- Molecule 1: antiparallel 8-helix bundle-GLIA



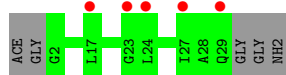
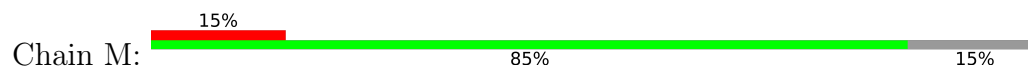
- Molecule 1: antiparallel 8-helix bundle-GLIA



- Molecule 1: antiparallel 8-helix bundle-GLIA



- Molecule 1: antiparallel 8-helix bundle-GLIA



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.27Å 45.87Å 72.88Å 90.00° 103.94° 90.00°	Depositor
Resolution (Å)	35.68 – 2.30 35.68 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.6 (35.68-2.30) 99.9 (35.68-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.12 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.227 , 0.283 0.227 , 0.280	Depositor DCC
R_{free} test set	1577 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	42.9	Xtriage
Anisotropy	0.507	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 82.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.039 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5826	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.71% 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	B	0.07	0/189	0.18	0/255
1	C	0.19	0/195	0.16	0/263
1	D	0.05	0/186	0.13	0/251
1	E	0.07	0/189	0.18	0/255
1	F	0.19	0/193	0.16	0/259
1	G	0.19	0/201	0.18	0/268
1	H	0.06	0/173	0.15	0/234
1	I	0.06	0/190	0.15	0/256
1	J	0.08	0/176	0.18	0/234
1	K	0.07	0/185	0.15	0/249
1	L	0.20	0/168	0.15	0/228
1	M	0.07	0/188	0.15	0/254
1	N	0.05	0/183	0.14	0/247
1	O	0.07	0/184	0.17	0/248
1	P	0.05	0/171	0.14	0/231
1	R	0.06	0/197	0.15	0/262
All	All	0.11	0/2968	0.16	0/3994

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	B	188	182	173	0	0
1	C	194	183	184	0	0
1	D	185	184	175	0	0
1	E	188	183	173	0	0
1	F	192	185	183	1	0
1	G	200	211	207	0	0
1	H	172	170	165	1	0
1	I	189	186	181	1	0
1	J	177	173	169	1	0
1	K	184	176	170	0	0
1	L	162	133	127	1	0
1	M	187	176	173	0	0
1	N	182	173	164	1	0
1	O	183	183	181	0	0
1	P	170	152	150	2	0
1	R	196	207	202	0	0
2	B	1	0	0	0	0
2	C	2	0	0	0	0
2	D	3	0	0	0	0
2	E	1	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	1	0	0	0	0
2	K	1	0	0	0	0
2	N	1	0	0	0	0
2	O	1	0	0	0	0
2	R	3	0	0	0	0
All	All	2969	2857	2777	4	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 1.

All (4) 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:F:3:LEU:HD23	1:H:27:ILE:HD11	1.84	0.59
1:L:5:GLU:OE1	1:P:26:LYS:NZ	2.36	0.45
1:I:7:ALA:HB3	1:N:24:LEU:HD21	2.01	0.41
1:J:7:ALA:HB1	1:P:24:LEU:HD21	2.03	0.41

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	B	28/33 (85%)	28 (100%)	0	0	100	100
1	C	28/33 (85%)	28 (100%)	0	0	100	100
1	D	26/33 (79%)	26 (100%)	0	0	100	100
1	E	28/33 (85%)	28 (100%)	0	0	100	100
1	F	27/33 (82%)	27 (100%)	0	0	100	100
1	G	27/33 (82%)	27 (100%)	0	0	100	100
1	H	25/33 (76%)	24 (96%)	1 (4%)	0	100	100
1	I	26/33 (79%)	26 (100%)	0	0	100	100
1	J	25/33 (76%)	25 (100%)	0	0	100	100
1	K	26/33 (79%)	26 (100%)	0	0	100	100
1	L	29/33 (88%)	29 (100%)	0	0	100	100
1	M	26/33 (79%)	26 (100%)	0	0	100	100
1	N	26/33 (79%)	26 (100%)	0	0	100	100
1	O	26/33 (79%)	25 (96%)	1 (4%)	0	100	100
1	P	26/33 (79%)	26 (100%)	0	0	100	100
1	R	27/33 (82%)	27 (100%)	0	0	100	100
All	All	426/528 (81%)	424 (100%)	2 (0%)	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	B	11/20 (55%)	11 (100%)	0	100	100
1	C	12/20 (60%)	12 (100%)	0	100	100
1	D	11/20 (55%)	11 (100%)	0	100	100
1	E	11/20 (55%)	11 (100%)	0	100	100
1	F	12/20 (60%)	12 (100%)	0	100	100
1	G	14/20 (70%)	14 (100%)	0	100	100
1	H	10/20 (50%)	10 (100%)	0	100	100
1	I	13/20 (65%)	13 (100%)	0	100	100
1	J	12/20 (60%)	12 (100%)	0	100	100
1	K	11/20 (55%)	11 (100%)	0	100	100
1	L	6/20 (30%)	6 (100%)	0	100	100
1	M	13/20 (65%)	13 (100%)	0	100	100
1	N	11/20 (55%)	11 (100%)	0	100	100
1	O	12/20 (60%)	12 (100%)	0	100	100
1	P	8/20 (40%)	8 (100%)	0	100	100
1	R	12/20 (60%)	12 (100%)	0	100	100
All	All	179/320 (56%)	179 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	B	30/33 (90%)	0.61	2 (6%) 24 26	42, 51, 69, 75	0
1	C	30/33 (90%)	0.65	3 (10%) 12 14	46, 54, 73, 85	0
1	D	28/33 (84%)	0.65	2 (7%) 22 24	45, 53, 71, 75	0
1	E	30/33 (90%)	0.61	3 (10%) 12 14	40, 50, 70, 79	0
1	F	29/33 (87%)	0.82	2 (6%) 23 25	41, 54, 90, 96	0
1	G	29/33 (87%)	0.90	5 (17%) 4 4	38, 53, 88, 93	0
1	H	27/33 (81%)	0.36	1 (3%) 45 48	40, 50, 72, 78	0
1	I	28/33 (84%)	0.78	3 (10%) 11 12	46, 52, 74, 94	0
1	J	27/33 (81%)	0.91	4 (14%) 5 6	48, 60, 84, 103	0
1	K	28/33 (84%)	0.97	5 (17%) 3 4	52, 65, 95, 106	0
1	L	29/33 (87%)	1.15	5 (17%) 4 4	51, 67, 93, 99	1 (3%)
1	M	28/33 (84%)	1.03	5 (17%) 3 4	55, 64, 84, 93	0
1	N	28/33 (84%)	0.46	1 (3%) 46 48	47, 57, 65, 85	0
1	O	28/33 (84%)	0.80	3 (10%) 11 12	51, 60, 83, 95	0
1	P	28/33 (84%)	1.26	7 (25%) 2 2	60, 71, 95, 102	0
1	R	29/33 (87%)	0.38	0 100 100	38, 49, 64, 75	0
All	All	456/528 (86%)	0.77	51 (11%) 10 11	38, 58, 90, 106	1 (0%)

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	29	GLN	4.6
1	G	24	LEU	4.4
1	K	3	LEU	4.0
1	B	1	GLY	3.9
1	P	6	ILE	3.9

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.