Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:50 AM GMT

PDB ID	:	2IZM
Title	:	MS2-RNA HAIRPIN (C-10) COMPLEX
Authors	:	Helgstrand, C.; Grahn, E.; Moss, T.; Stonehouse, N.J.; Tars, K.; Stockley, P.G.; Liljas, L.
Deposited on	:	2006-07-25
Resolution	:	2.70 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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.
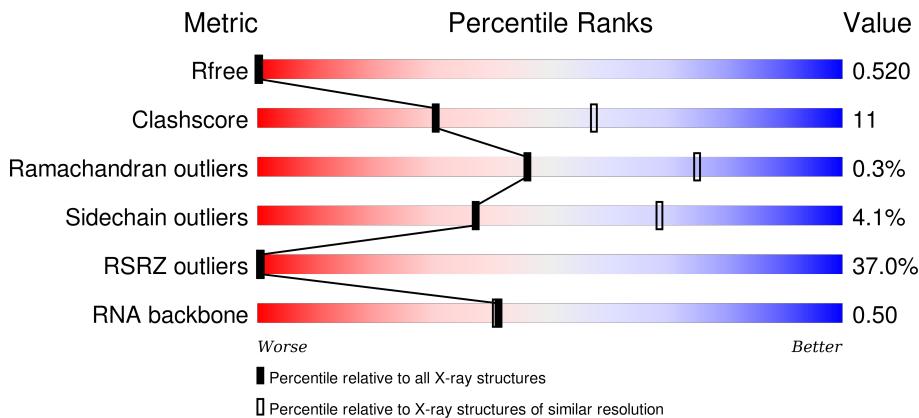
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)
RNA backbone	2183	1069 (3.10-2.30)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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 <=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	129	
1	B	129	
1	C	129	
2	R	19	

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Mol	Chain	Length	Quality of chain
2	S	19	
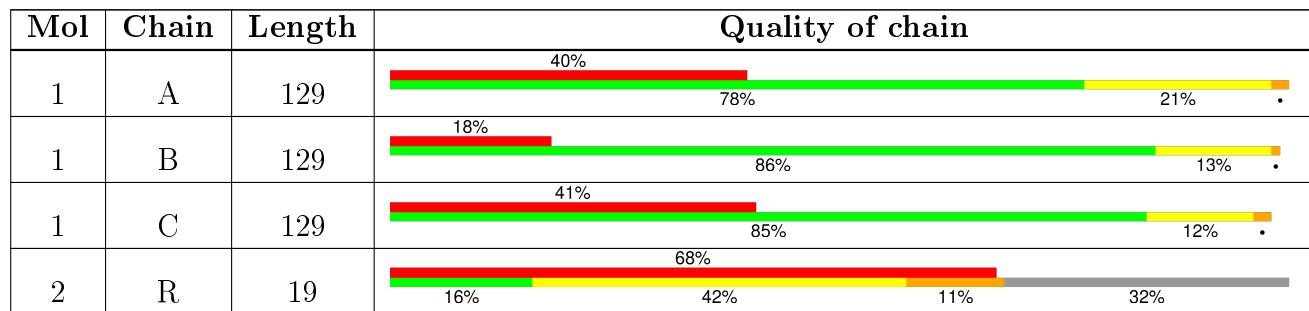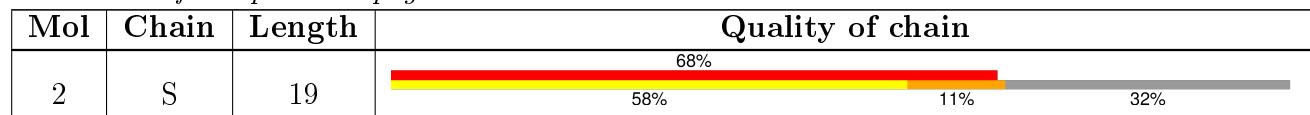
2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3591 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 MS2 COAT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	129	Total 965	C 606	N 165	O 190	S 4	0	0	0
1	B	129	Total 965	C 606	N 165	O 190	S 4	0	0	0
1	C	129	Total 965	C 606	N 165	O 190	S 4	0	0	0

- Molecule 2 is a RNA chain called 5'-R(*AP*CP*AP*UP*GP*CP*GP*GP*AP*UP *CP*AP*CP*CP*CP*AP*UP*GP*U)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	R	13	Total 272	C 123	N 49	O 88	P 12	0	0	0
2	S	13	Total 272	C 123	N 49	O 88	P 12	0	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	51	Total 51	O 51	0	0
3	B	60	Total 60	O 60	0	0
3	C	39	Total 39	O 39	0	0
3	R	2	Total 2	O 2	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: MS2 COAT PROTEIN
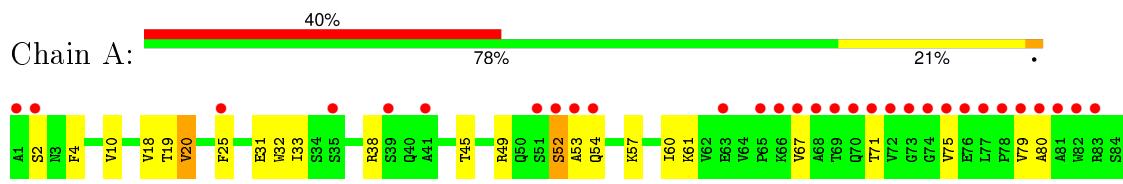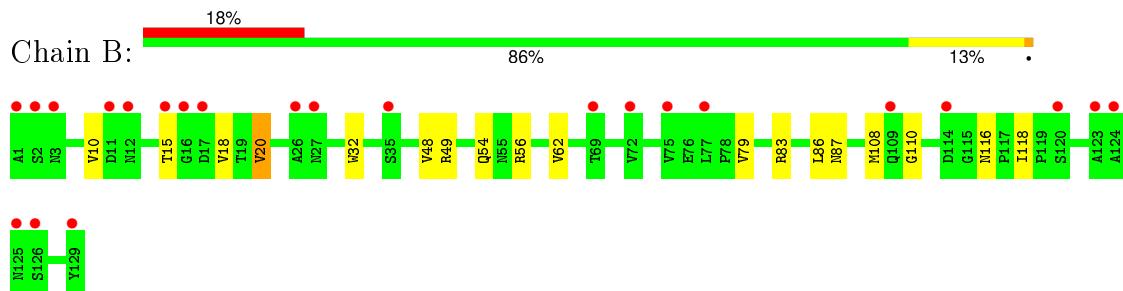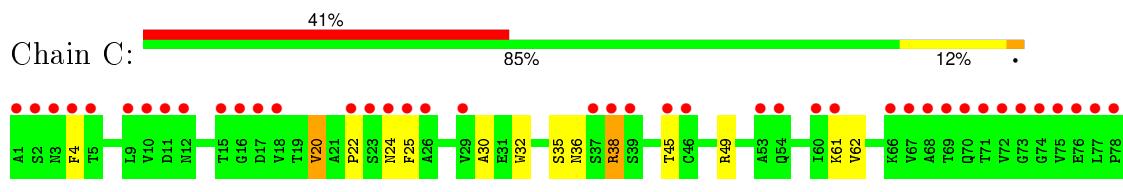
Chain A:

- Molecule 1: MS2 COAT PROTEIN

Chain B:

- Molecule 1: MS2 COAT PROTEIN

Chain C:

- Molecule 2: 5'-R(*AP*CP*AP*UP*GP*CP*GP*GP*AP*UP *CP*AP*CP*CP*CP*AP*UP* GP*U)-3'

Chain R:

• Molecule 2: 5'-R(*AP*CP*AP*UP*GP*CP*GP*GP*AP*UP *CP*AP*CP*CP*CP*AP*UP* GP*U)-3'

Chain S:
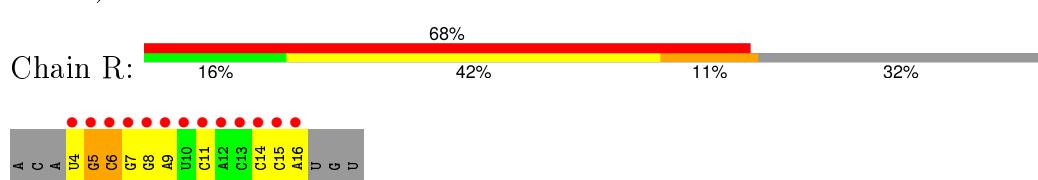
4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α, β, γ	288.00Å 288.00Å 653.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.24 – 2.70 94.27 – 6.65	Depositor EDS
% Data completeness (in resolution range)	48.3 (38.24-2.70) 57.9 (94.27-6.65)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.66 (at 6.72Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.246 , 0.243 0.544 , 0.520	Depositor DCC
R_{free} test set	549 reflections (4.95%)	DCC
Wilson B-factor (Å^2)	213.2	Xtriage
Anisotropy	0.951	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 3770.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< |L| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 12186 reflections	Xtriage
F_o,F_c correlation	0.62	EDS
Total number of atoms	3591	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 5.52% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.42	0/982	0.68	0/1337
1	B	0.42	0/982	0.67	0/1337
1	C	0.42	0/982	0.68	0/1337
2	R	0.41	0/303	0.68	0/470
2	S	0.51	0/303	0.70	0/470
All	All	0.43	0/3552	0.68	0/4951

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	965	0	964	23	0
1	B	965	0	964	16	0
1	C	965	0	964	14	0
2	R	272	0	143	11	0
2	S	272	0	143	15	0
3	A	51	0	0	3	0
3	B	60	0	0	3	0
3	C	39	0	0	1	0
3	R	2	0	0	2	0
All	All	3591	0	3178	73	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 11.

All (73) 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:C:20:VAL:HG13	1:C:32:TRP:HB3	1.38	1.05
1:A:20:VAL:HG13	1:A:32:TRP:HB3	1.52	0.91
1:A:79:VAL:HG22	1:A:80:ALA:H	1.43	0.83
1:C:20:VAL:CG1	1:C:32:TRP:HB3	2.12	0.77
1:C:111:LEU:HD11	1:C:118:ILE:HD12	1.69	0.73
2:R:4:U:H2'	2:R:5:G:C5'	2.23	0.69
2:R:4:U:H2'	2:R:5:G:H5"	1.75	0.69
1:B:20:VAL:HG13	1:B:32:TRP:HB3	1.79	0.63
1:A:79:VAL:HG22	1:A:80:ALA:N	2.14	0.63
2:R:4:U:C2'	2:R:5:G:H5"	2.29	0.62
1:B:10:VAL:HB	1:B:18:VAL:HB	1.82	0.61
1:C:61:LYS:HE2	1:C:87:ASN:HD21	1.63	0.61
2:S:6:C:H5'	2:S:7:G:H5"	1.82	0.61
2:S:4:U:C2'	2:S:5:G:H5"	2.32	0.59
1:A:61:LYS:HG2	1:A:87:ASN:ND2	2.18	0.59
2:S:4:U:H2'	2:S:5:G:C5'	2.34	0.58
2:S:4:U:H2'	2:S:5:G:H5"	1.86	0.56
1:A:60:ILE:HB	1:A:88:MET:HG3	1.87	0.56
1:B:15:THR:HG23	1:B:15:THR:O	2.08	0.54
1:B:83:ARG:HD2	3:B:2016:HOH:O	2.07	0.54
1:A:19:THR:HG22	3:A:2006:HOH:O	2.08	0.53
2:R:4:U:H2'	2:R:5:G:H5'	1.90	0.53
1:C:61:LYS:HD2	2:S:12:A:N7	2.24	0.53
1:A:20:VAL:CG1	1:A:32:TRP:HB3	2.33	0.53
2:S:6:C:H5'	2:S:7:G:C5'	2.38	0.52
2:R:15:C:H2'	2:R:16:A:C8	2.44	0.52
1:A:52:SER:OG	1:A:53:ALA:N	2.43	0.52
1:A:10:VAL:HB	1:A:18:VAL:HB	1.92	0.51
2:S:15:C:H2'	2:S:16:A:H8	1.75	0.50
2:R:8:G:O2'	2:R:9:A:H5'	2.11	0.50
1:B:62:VAL:HB	1:B:86:LEU:HB3	1.93	0.49
2:R:6:C:H5'	2:R:7:G:C5'	2.42	0.49
2:R:15:C:H2'	2:R:16:A:H8	1.76	0.49
1:A:112:LEU:HD13	1:B:108:MET:HB3	1.95	0.48
1:C:4:PHE:CZ	1:C:22:PRO:HB3	2.48	0.48
1:B:49:ARG:NE	3:R:2001:HOH:O	2.46	0.48
1:B:49:ARG:CD	3:R:2001:HOH:O	2.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:83:ARG:HG2	1:B:83:ARG:HH11	1.79	0.47
2:R:6:C:H5'	2:R:7:G:H5"	1.96	0.46
1:A:33:ILE:HD13	1:A:38:ARG:NH1	2.31	0.46
2:R:4:U:C2'	2:R:5:G:C5'	2.90	0.46
2:S:9:A:HO2'	2:S:10:U:H6	1.63	0.46
2:S:13:C:H2'	2:S:14:C:C6	2.52	0.45
1:A:57:LYS:HE3	1:A:89:GLU:HB3	1.98	0.45
1:A:88:MET:HA	1:B:87:ASN:O	2.17	0.45
1:C:49:ARG:HG2	1:C:49:ARG:HH11	1.81	0.45
2:R:14:C:O2'	2:R:15:C:H5'	2.16	0.44
1:B:56:ARG:NH2	3:B:2021:HOH:O	2.46	0.44
2:S:15:C:H2'	2:S:16:A:C8	2.52	0.44
1:C:35:SER:O	1:C:36:ASN:HB2	2.16	0.44
1:A:45:THR:OG1	1:A:61:LYS:HB2	2.18	0.44
2:S:4:U:O2'	2:S:5:G:H5"	2.17	0.43
2:S:8:G:O2'	2:S:9:A:H5'	2.18	0.43
1:C:62:VAL:HB	1:C:86:LEU:HB3	2.00	0.43
2:S:4:U:H2'	2:S:5:G:H5'	2.00	0.43
1:C:49:ARG:NH1	1:C:49:ARG:HG2	2.33	0.43
1:C:85:TYR:CE2	2:S:11:C:H2'	2.54	0.43
1:B:79:VAL:HG13	3:B:2016:HOH:O	2.18	0.42
1:A:67:VAL:HG22	3:A:2029:HOH:O	2.19	0.42
2:S:4:U:C2'	2:S:5:G:C5'	2.97	0.42
1:A:49:ARG:HB2	3:A:2021:HOH:O	2.19	0.42
1:C:38:ARG:NH1	3:C:2016:HOH:O	2.53	0.42
1:B:83:ARG:HG2	1:B:83:ARG:NH1	2.35	0.42
1:A:61:LYS:HE2	1:A:61:LYS:HB3	1.73	0.42
1:B:110:GLY:O	1:B:116:ASN:ND2	2.53	0.41
1:A:57:LYS:CE	1:A:89:GLU:HB3	2.50	0.41
1:A:60:ILE:HD13	1:B:118:ILE:HG21	2.02	0.41
1:C:30:ALA:O	1:C:45:THR:HA	2.21	0.41
1:C:111:LEU:CD1	1:C:118:ILE:HD12	2.45	0.40
1:A:86:LEU:HD22	1:B:108:MET:HG2	2.03	0.40
1:A:31:GLU:HG2	1:A:32:TRP:N	2.36	0.40
1:A:60:ILE:HB	1:A:88:MET:CG	2.51	0.40
1:A:71:THR:HA	1:A:75:VAL:O	2.21	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	127/129 (98%)	123 (97%)	3 (2%)	1 (1%)	24	51
1	B	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
1	C	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
All	All	381/387 (98%)	363 (95%)	17 (4%)	1 (0%)	46	75

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	SER

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	106/106 (100%)	101 (95%)	5 (5%)	32	63
1	B	106/106 (100%)	103 (97%)	3 (3%)	51	81
1	C	106/106 (100%)	101 (95%)	5 (5%)	32	63
All	All	318/318 (100%)	305 (96%)	13 (4%)	37	69

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	PHE
1	A	20	VAL

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Mol	Chain	Res	Type
1	A	25	PHE
1	A	52	SER
1	A	54	GLN
1	B	20	VAL
1	B	48	VAL
1	B	54	GLN
1	C	20	VAL
1	C	24	ASN
1	C	25	PHE
1	C	38	ARG
1	C	87	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	ASN
1	A	87	ASN
1	B	54	GLN
1	B	87	ASN
1	C	24	ASN
1	C	87	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	R	12/19 (63%)	3 (25%)	0
2	S	12/19 (63%)	2 (16%)	0
All	All	24/38 (63%)	5 (20%)	0

All (5) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	R	5	G
2	R	6	C
2	R	11	C
2	S	5	G
2	S	6	C

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 carbohydrates 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(Å²)	Q<0.9
1	A	129/129 (100%)	3.34	51 (39%)	0	0	26, 38, 60, 75	0
1	B	129/129 (100%)	0.77	23 (17%)	2	1	27, 34, 57, 75	0
1	C	129/129 (100%)	2.95	53 (41%)	0	0	30, 40, 59, 82	0
2	R	13/19 (68%)	27.05	13 (100%)	0	0	17, 40, 65, 75	13 (100%)
2	S	13/19 (68%)	26.18	13 (100%)	0	0	47, 62, 98, 116	13 (100%)
All	All	413/425 (97%)	3.88	153 (37%)	0	0	17, 38, 66, 116	26 (6%)

All (153) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	R	7	G	48.9
2	R	5	G	42.0
2	R	14	C	41.7
2	S	7	G	41.6
2	S	15	C	41.3
2	R	15	C	36.8
2	S	5	G	36.7
2	R	16	A	33.6
2	R	13	C	33.3
1	C	2	SER	33.0
2	S	14	C	30.5
2	S	16	A	30.0
2	S	13	C	28.8
2	S	8	G	26.5
1	A	81	ALA	26.5
2	R	11	C	24.3
1	A	71	THR	24.2
1	A	73	GLY	23.7
1	A	72	VAL	23.4
2	S	9	A	23.2

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Mol	Chain	Res	Type	RSRZ
1	A	75	VAL	22.2
2	R	8	G	22.1
1	A	74	GLY	22.1
1	C	3	ASN	21.4
2	S	4	U	20.6
2	R	4	U	20.3
1	A	76	GLU	18.8
2	S	12	A	17.9
2	R	10	U	17.6
1	B	1	ALA	17.3
2	S	11	C	16.2
1	A	80	ALA	15.8
1	A	1	ALA	15.6
1	C	1	ALA	15.1
1	A	77	LEU	14.8
1	A	70	GLN	14.7
2	R	9	A	14.6
2	S	10	U	14.3
1	A	69	THR	14.1
1	C	16	GLY	13.3
2	S	6	C	12.9
1	C	4	PHE	12.3
1	C	72	VAL	12.0
2	R	6	C	11.8
1	C	75	VAL	11.2
1	C	77	LEU	11.1
1	C	76	GLU	10.8
1	A	79	VAL	10.8
1	A	120	SER	10.5
1	C	10	VAL	10.4
1	B	15	THR	10.4
1	B	16	GLY	10.3
1	C	129	TYR	10.1
1	A	68	ALA	9.9
1	C	71	THR	9.6
1	A	115	GLY	9.5
1	C	74	GLY	9.4
1	B	124	ALA	9.2
1	C	112	LEU	9.0
1	C	73	GLY	8.9
1	C	70	GLN	8.9
1	B	2	SER	8.7

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Mol	Chain	Res	Type	RSRZ
1	B	129	TYR	8.5
1	A	114	ASP	8.5
1	A	129	TYR	8.1
1	C	25	PHE	7.9
1	C	78	PRO	7.9
1	C	9	LEU	7.4
1	C	12	ASN	7.0
1	B	12	ASN	6.9
1	A	112	LEU	6.6
1	C	18	VAL	6.4
1	A	98	ASN	6.2
1	A	2	SER	6.2
1	A	82	TRP	6.1
1	C	69	THR	5.9
1	A	102	GLU	5.7
1	C	88	MET	5.7
1	C	46	CYS	5.6
1	A	78	PRO	5.6
1	C	5	THR	5.5
1	C	24	ASN	5.4
1	A	67	VAL	5.3
1	A	119	PRO	5.1
1	C	15	THR	5.0
1	B	125	ASN	4.9
2	R	12	A	4.8
1	B	27	ASN	4.7
1	C	53	ALA	4.7
1	B	35	SER	4.7
1	A	95	PHE	4.6
1	A	106	LYS	4.6
1	C	17	ASP	4.6
1	A	54	GLN	4.6
1	B	69	THR	4.6
1	C	79	VAL	4.5
1	B	75	VAL	4.5
1	A	83	ARG	4.4
1	A	53	ALA	4.4
1	A	66	LYS	4.3
1	A	113	LYS	4.2
1	B	3	ASN	4.0
1	A	109	GLN	4.0
1	C	39	SER	4.0

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Mol	Chain	Res	Type	RSRZ
1	C	87	ASN	3.9
1	C	23	SER	3.9
1	C	67	VAL	3.8
1	A	97	THR	3.7
1	C	95	PHE	3.7
1	A	99	SER	3.6
1	C	128	ILE	3.6
1	B	77	LEU	3.5
1	A	124	ALA	3.5
1	A	116	ASN	3.5
1	A	65	PRO	3.4
1	C	26	ALA	3.4
1	B	72	VAL	3.4
1	A	39	SER	3.3
1	B	126	SER	3.3
1	C	22	PRO	3.3
1	C	60	ILE	3.3
1	B	123	ALA	3.3
1	A	85	TYR	3.2
1	C	37	SER	3.1
1	A	35	SER	3.0
1	C	11	ASP	3.0
1	C	68	ALA	3.0
1	C	29	VAL	2.9
1	A	105	VAL	2.8
1	A	110	GLY	2.8
1	C	61	LYS	2.8
1	C	125	ASN	2.7
1	A	126	SER	2.7
1	A	94	ILE	2.7
1	B	26	ALA	2.7
1	A	51	SER	2.7
1	A	25	PHE	2.6
1	B	109	GLN	2.6
1	C	54	GLN	2.6
1	B	114	ASP	2.5
1	C	38	ARG	2.5
1	B	120	SER	2.5
1	B	17	ASP	2.4
1	B	11	ASP	2.3
1	C	111	LEU	2.3
1	A	41	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	66	LYS	2.3
1	C	110	GLY	2.2
1	C	114	ASP	2.2
1	A	63	GLU	2.2
1	C	45	THR	2.1
1	C	108	MET	2.1
1	A	52	SER	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 carbohydrates 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.