Full wwPDB X-ray Structure Validation Report ⓘ

Nov 1, 2023 – 12:11 AM EDT

PDB ID	:	3RPK
Title	:	Structure of the Full-Length Major Pilin RrgB from Streptococcus pneumoniae
Authors	:	Paterson, N.G.; Baker, E.N.
Deposited on	:	2011-04-26
Resolution	:	2.80 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:

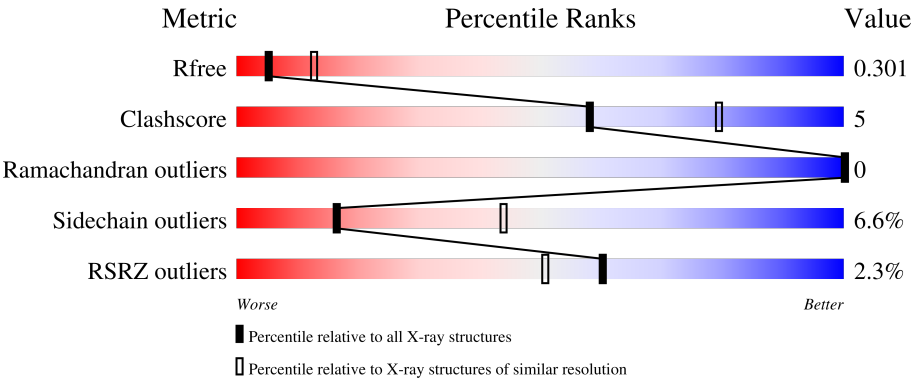
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.80 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}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 <=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	603	2% 81% 16%
1	B	603	2% 80% 17%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 8986 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 Backbone pilus subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	590	Total	C	N	O	Se	0	2	0
			4493	2817	749	922	5			
1	B	590	Total	C	N	O	Se	0	2	0
			4493	2817	749	922	5			

There are 6 discrepancies between the modelled and reference sequences:

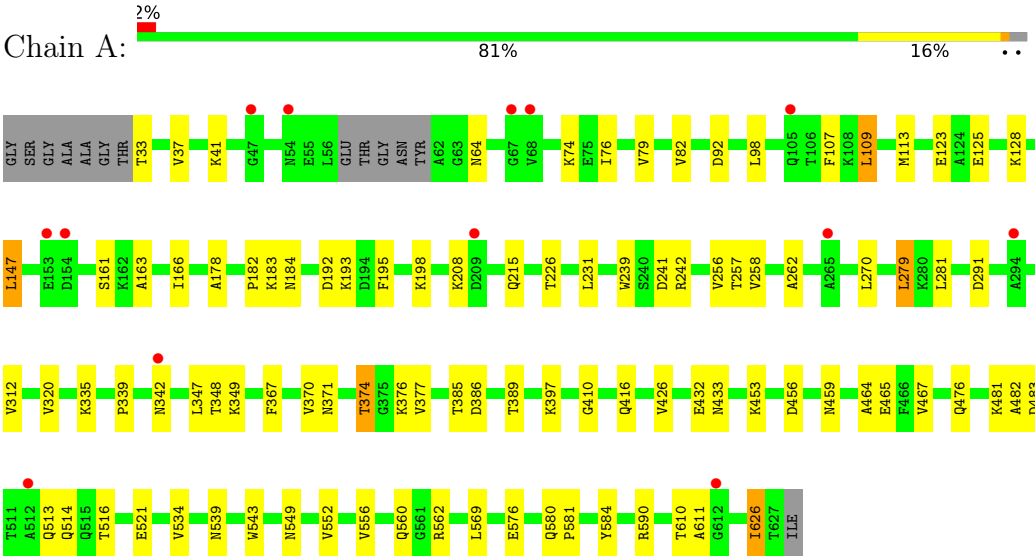
Chain	Residue	Modelled	Actual	Comment	Reference
A	26	GLY	-	expression tag	UNP A7KT39
A	27	SER	-	expression tag	UNP A7KT39
A	28	GLY	-	expression tag	UNP A7KT39
B	26	GLY	-	expression tag	UNP A7KT39
B	27	SER	-	expression tag	UNP A7KT39
B	28	GLY	-	expression tag	UNP A7KT39

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.

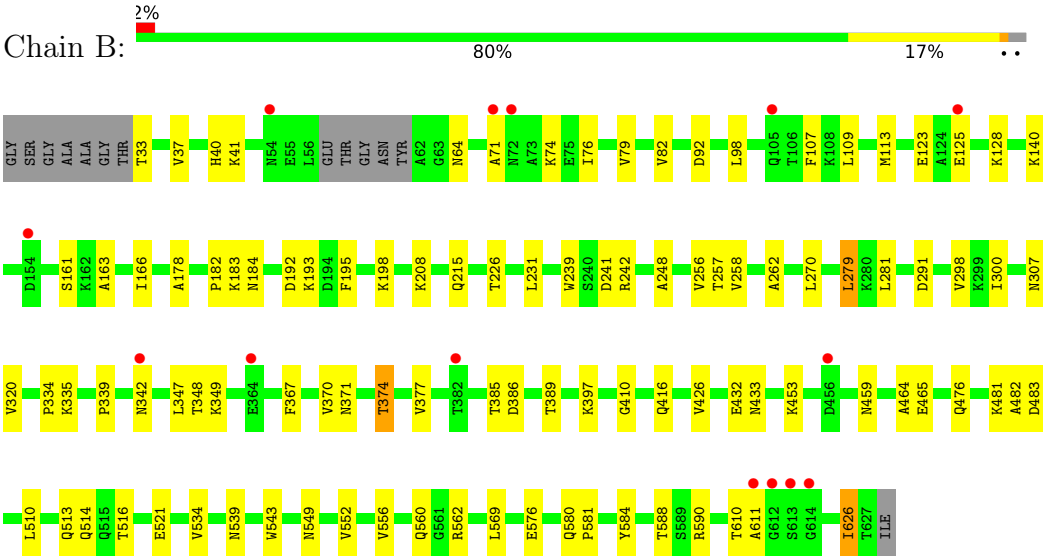
• Molecule 1: Backbone pilus subunit

Chain A:



• Molecule 1: Backbone pilus subunit

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	84.37Å 107.93Å 142.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.47 – 2.80 19.74 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (19.47-2.80) 94.5 (19.74-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.20	Depositor
$< I/\sigma(I) >$ [1]	2.08 (at 2.79Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.217 , 0.281 0.237 , 0.301	Depositor DCC
R_{free} test set	1570 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å^2)	31.4	Xtriage
Anisotropy	0.808	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 49.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	8986	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 46.07 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2067e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.56	1/4566 (0.0%)	0.77	0/6203
1	B	0.57	1/4566 (0.0%)	0.78	1/6203 (0.0%)
All	All	0.56	2/9132 (0.0%)	0.78	1/12406 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	433	ASN	CG-OD1	5.16	1.35	1.24
1	B	433	ASN	CG-OD1	5.03	1.35	1.24

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	71	ALA	CB-CA-C	-5.98	101.13	110.10

There are no chirality outliers.

There are no planarity outliers.

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	4493	0	4442	42	0
1	B	4493	0	4442	44	0
All	All	8986	0	8884	85	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 5.

All (85) 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:41:LYS:HG2	1:A:79:VAL:HG21	1.72	0.72
1:B:41:LYS:HG2	1:B:79:VAL:HG21	1.72	0.72
1:B:193:LYS:HD2	1:B:320:VAL:HG23	1.82	0.62
1:A:193:LYS:HD2	1:A:320:VAL:HG23	1.82	0.62
1:A:258:VAL:HG22	1:A:298:VAL:HG22	1.84	0.60
1:B:258:VAL:HG22	1:B:298:VAL:HG22	1.84	0.59
1:B:610:THR:HG22	1:B:611:ALA:H	1.68	0.58
1:A:610:THR:HG22	1:A:611:ALA:H	1.69	0.58
1:B:560:GLN:HG3	1:B:562:ARG:HH11	1.69	0.57
1:A:560:GLN:HG3	1:A:562:ARG:HH11	1.68	0.57
1:A:256:VAL:HG13	1:A:300:ILE:HG12	1.89	0.55
1:A:109:LEU:HD11	1:B:588:THR:HG21	1.88	0.55
1:B:256:VAL:HG13	1:B:300:ILE:HG12	1.89	0.55
1:B:215:GLN:HB3	1:B:569:LEU:HG	1.89	0.55
1:B:270:LEU:HD13	1:B:279:LEU:HD12	1.89	0.55
1:A:163:ALA:HA	1:A:184:ASN:HA	1.89	0.54
1:A:270:LEU:HD13	1:A:279:LEU:HD12	1.90	0.54
1:B:163:ALA:HA	1:B:184:ASN:HA	1.90	0.53
1:A:82:VAL:HG21	1:A:113:MSE:HE1	1.90	0.53
1:A:215:GLN:HB3	1:A:569:LEU:HG	1.91	0.53
1:B:242:ARG:HG3	1:B:335:LYS:HG3	1.92	0.52
1:A:242:ARG:HG3	1:A:335:LYS:HG3	1.92	0.52
1:B:239:TRP:HZ3	1:B:281:LEU:HG	1.75	0.52
1:A:339:PRO:HG2	1:A:397:LYS:HA	1.92	0.52
1:A:239:TRP:HZ3	1:A:281:LEU:HG	1.76	0.51
1:B:195:PHE:HB2	1:B:198:LYS:HD2	1.93	0.51
1:B:465:GLU:HG2	1:B:556:VAL:HG22	1.91	0.51
1:A:195:PHE:HB2	1:A:198:LYS:HD2	1.93	0.51
1:B:82:VAL:HG21	1:B:113:MSE:HE1	1.91	0.51
1:B:248:ALA:HB2	1:B:307:ASN:HD22	1.74	0.51
1:A:549:ASN:HB3	1:A:552:VAL:HG23	1.92	0.50
1:A:371:ASN:HB3	1:A:374:THR:HG22	1.91	0.50
1:B:371:ASN:HB3	1:B:374:THR:HG22	1.92	0.50
1:B:549:ASN:HB3	1:B:552:VAL:HG23	1.93	0.49
1:A:140:LYS:HA	1:A:166:ILE:O	2.12	0.49
1:B:257:THR:HG22	1:B:262:ALA:HA	1.95	0.49
1:B:339:PRO:HG2	1:B:397:LYS:HA	1.95	0.49
1:A:349:LYS:HD2	1:A:367:PHE:HZ	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:465:GLU:HG2	1:A:556:VAL:HG22	1.93	0.49
1:B:140:LYS:HA	1:B:166:ILE:O	2.13	0.49
1:A:257:THR:HG22	1:A:262:ALA:HA	1.95	0.48
1:B:349:LYS:HD2	1:B:367:PHE:HZ	1.78	0.48
1:A:347:LEU:HD11	1:A:426:VAL:HG23	1.96	0.47
1:A:144:ILE:HG21	1:A:147:LEU:HD22	1.97	0.47
1:A:482:ALA:HA	1:A:485:VAL:HG12	1.97	0.47
1:A:192:ASP:OD1	1:A:208:LYS:NZ	2.39	0.47
1:B:123:GLU:C	1:B:125:GLU:H	2.18	0.47
1:B:370:VAL:HG22	1:B:377:VAL:HG22	1.97	0.47
1:A:37:VAL:HG22	1:A:178:ALA:HB3	1.98	0.46
1:A:410:GLY:HA2	1:A:432:GLU:HA	1.97	0.46
1:B:347:LEU:HD11	1:B:426:VAL:HG23	1.97	0.46
1:A:510:LEU:HD22	1:A:514:GLN:HB3	1.97	0.46
1:B:144:ILE:HG21	1:B:147:LEU:HD22	1.98	0.46
1:A:464:ALA:HB2	1:A:581:PRO:HG3	1.97	0.45
1:A:123:GLU:C	1:A:125:GLU:H	2.19	0.45
1:B:166:ILE:CG1	1:B:182:PRO:HB3	2.47	0.45
1:B:192:ASP:OD1	1:B:208:LYS:NZ	2.40	0.45
1:A:166:ILE:CG1	1:A:182:PRO:HB3	2.47	0.45
1:B:464:ALA:HB2	1:B:581:PRO:HG3	1.98	0.45
1:B:560:GLN:HG3	1:B:562:ARG:NH1	2.32	0.45
1:A:370:VAL:HG22	1:A:377:VAL:HG22	1.99	0.44
1:B:166:ILE:HD11	1:B:182:PRO:HG3	1.99	0.44
1:B:510:LEU:HD22	1:B:514:GLN:HB3	1.99	0.44
1:B:37:VAL:HG22	1:B:178:ALA:HB3	2.00	0.44
1:B:231:LEU:HA	1:B:291:ASP:HA	2.00	0.44
1:B:410:GLY:HA2	1:B:432:GLU:HA	1.99	0.43
1:A:231:LEU:HA	1:A:291:ASP:HA	2.00	0.43
1:B:482:ALA:HA	1:B:485:VAL:HG12	2.01	0.43
1:A:626:ILE:H	1:A:626:ILE:HG13	1.65	0.43
1:A:560:GLN:HG3	1:A:562:ARG:NH1	2.34	0.43
1:B:626:ILE:H	1:B:626:ILE:HG13	1.64	0.41
1:A:576:GLU:HG3	1:A:590:ARG:HG2	2.02	0.41
1:B:40:HIS:O	1:B:182:PRO:HD2	2.21	0.41
1:A:476:GLN:HB2	1:A:543:TRP:HB3	2.01	0.41
1:A:92:ASP:HB2	1:A:98:LEU:HD21	2.02	0.41
1:A:166:ILE:HD11	1:A:182:PRO:HG3	2.02	0.41
1:B:319:ASP:OD1	1:B:334:PRO:HD2	2.20	0.41
1:B:507:TYR:HA	1:B:510:LEU:HD12	2.03	0.41
1:B:576:GLU:HG3	1:B:590:ARG:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:580:GLN:HG3	1:A:584:TYR:O	2.21	0.41
1:B:580:GLN:HG3	1:B:584:TYR:O	2.22	0.40
1:A:374:THR:HG23	1:A:376:LYS:HG3	2.03	0.40
1:A:467:VAL:HG23	1:A:576:GLU:HB3	2.04	0.40
1:B:92:ASP:HB2	1:B:98:LEU:HD21	2.02	0.40
1:B:476:GLN:HB2	1:B:543:TRP:HB3	2.02	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	588/603 (98%)	561 (95%)	27 (5%)	0	100	100
1	B	588/603 (98%)	560 (95%)	28 (5%)	0	100	100
All	All	1176/1206 (98%)	1121 (95%)	55 (5%)	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	482/482 (100%)	450 (93%)	32 (7%)	16	44
1	B	482/482 (100%)	451 (94%)	31 (6%)	17	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	964/964 (100%)	901 (94%)	63 (6%)	16 44

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	THR
1	A	64	ASN
1	A	74	LYS
1	A	76	ILE
1	A	107	PHE
1	A	109	LEU
1	A	128	LYS
1	A	147	LEU
1	A	161	SER
1	A	183	LYS
1	A	226	THR
1	A	241	ASP
1	A	279	LEU
1	A	312	VAL
1	A	342	ASN
1	A	348	THR
1	A	374	THR
1	A	385	THR
1	A	386	ASP
1	A	389	THR
1	A	416	GLN
1	A	453	LYS
1	A	456	ASP
1	A	459	ASN
1	A	481	LYS
1	A	483	ASP
1	A	513	GLN
1	A	516	THR
1	A	521	GLU
1	A	534	VAL
1	A	539	ASN
1	A	626	ILE
1	B	33	THR
1	B	64	ASN
1	B	74	LYS
1	B	76	ILE
1	B	107	PHE

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Mol	Chain	Res	Type
1	B	109	LEU
1	B	128	LYS
1	B	147	LEU
1	B	161	SER
1	B	183	LYS
1	B	226	THR
1	B	241	ASP
1	B	279	LEU
1	B	312	VAL
1	B	342	ASN
1	B	348	THR
1	B	374	THR
1	B	385	THR
1	B	386	ASP
1	B	389	THR
1	B	416	GLN
1	B	453	LYS
1	B	459	ASN
1	B	481	LYS
1	B	483	ASP
1	B	513	GLN
1	B	516	THR
1	B	521	GLU
1	B	534	VAL
1	B	539	ASN
1	B	626	ILE

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

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 monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95^{th} 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	585/603 (97%)	-0.09	13 (2%)	62	52	5, 26, 46, 72	0
1	B	585/603 (97%)	-0.04	14 (2%)	59	49	6, 28, 49, 73	0
All	All	1170/1206 (97%)	-0.06	27 (2%)	60	51	5, 27, 48, 73	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	613	SER	9.2
1	B	611	ALA	7.9
1	B	612	GLY	5.3
1	A	612	GLY	4.8
1	A	105	GLN	3.6
1	B	54	ASN	3.1
1	B	71	ALA	2.9
1	B	72	ASN	2.9
1	B	154	ASP	2.8
1	B	125	GLU	2.8
1	B	614	GLY	2.7
1	B	105	GLN	2.7
1	A	47	GLY	2.6
1	A	68	VAL	2.6
1	A	67	GLY	2.5
1	A	342	ASN	2.5
1	A	294	ALA	2.5
1	A	154	ASP	2.5
1	A	54	ASN	2.4
1	B	364	GLU	2.2
1	A	512	ALA	2.2
1	B	456	ASP	2.2
1	A	153	GLU	2.2
1	B	382	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	209	ASP	2.1
1	B	342	ASN	2.1
1	A	265	ALA	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 monosaccharides 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.