



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 9, 2020 – 12:05 PM GMT

PDB ID : 6RC9
Title : P1 Mycoplasma pneumoniae
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Deposited on : 2019-04-11
Resolution : 1.94 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.14.6
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) : 2.14.6

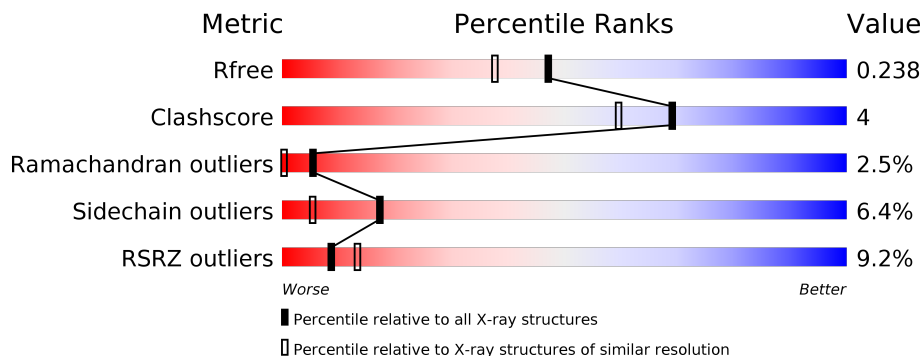
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.94 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	4310 (1.96-1.92)
Clashscore	141614	1023 (1.94-1.94)
Ramachandran outliers	138981	1007 (1.94-1.94)
Sidechain outliers	138945	1007 (1.94-1.94)
RSRZ outliers	127900	4250 (1.96-1.92)

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 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	1469	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10929 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 Adhesin P1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1339	10523	6642	1838	2033	10	0	7	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1522	LYS	-	expression tag	UNP P11311
A	1523	HIS	-	expression tag	UNP P11311
A	1524	HIS	-	expression tag	UNP P11311
A	1525	HIS	-	expression tag	UNP P11311
A	1526	HIS	-	expression tag	UNP P11311
A	1527	HIS	-	expression tag	UNP P11311
A	1528	HIS	-	expression tag	UNP P11311

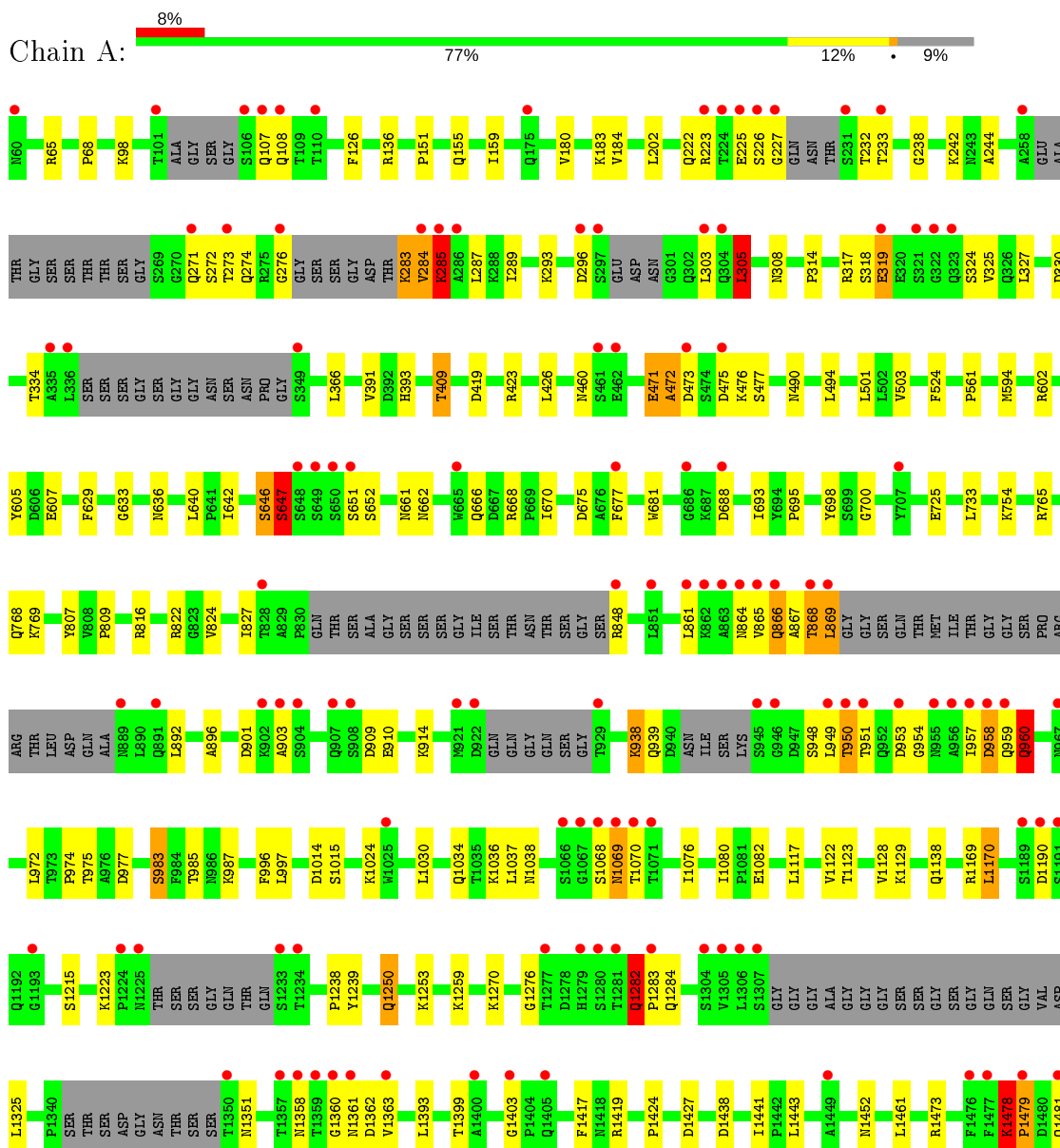
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	406	Total	O	0	0
			406	406		

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: Adhesin P1



D1482	THR		
	GLN		
	PRO		
	ASN		
	ASN		
	ASN		
	VAL		
	GLN		
	VAL		
	ASN		
	PRO		
	ASN		
	ASN		
G1496			
D1497			
P1500			
L1501			
W1519			
P1520			
D1521			
K1522			
H1523			
H1526			
H1527			
H1528			

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	132.90Å 115.64Å 96.34Å 90.00° 117.67° 90.00°	Depositor
Resolution (Å)	72.20 – 1.94 72.20 – 1.94	Depositor EDS
% Data completeness (in resolution range)	96.3 (72.20-1.94) 96.3 (72.20-1.94)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 1.94Å)	Xtrriage
Refinement program	BUSTER 2.10.3, REFMAC	Depositor
R, R_{free}	0.187 , 0.229 0.195 , 0.238	Depositor DCC
R_{free} test set	4593 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	32.2	Xtrriage
Anisotropy	0.580	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 55.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10929	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.32% 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	0.50	0/10794	0.70	2/14714 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	271	GLN	C-N-CA	5.07	134.38	121.70
1	A	283	LYS	C-N-CA	5.04	134.30	121.70

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	10523	0	10127	77	0
2	A	406	0	0	2	0
All	All	10929	0	10127	77	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 (77) 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:227:GLY:HA3	1:A:1259:LYS:HD2	1.66	0.77
1:A:1282:GLN:HB3	1:A:1283:PRO:HA	1.67	0.75
1:A:903:ALA:HB2	1:A:910:GLU:HG2	1.73	0.69
1:A:180:VAL:HG11	1:A:391:VAL:HG11	1.75	0.68
1:A:661:ASN:HD21	1:A:700:GLY:H	1.43	0.67
1:A:136:ARG:HG3	1:A:1399:THR:HG21	1.80	0.64
1:A:1038:ASN:HA	1:A:1080:ILE:HG12	1.82	0.61
1:A:646:SER:O	1:A:647:SER:HB3	2.01	0.61
1:A:957:ILE:HG13	1:A:960:GLN:HE22	1.66	0.60
1:A:1424:PRO:HD2	1:A:1427:ASP:OD2	2.02	0.59
1:A:1068:SER:O	1:A:1069:ASN:HB2	2.02	0.58
1:A:314:PRO:HD2	1:A:642:ILE:HG22	1.86	0.57
1:A:765:ARG:O	1:A:768:GLN:HB2	2.03	0.57
1:A:222:GLN:HB2	1:A:238:GLY:HA2	1.84	0.57
1:A:865:VAL:HG21	1:A:892:LEU:HD12	1.87	0.57
1:A:285:LYS:H	1:A:681:TRP:HZ2	1.52	0.56
1:A:1419:ARG:HE	1:A:1443:LEU:HD21	1.71	0.55
1:A:816:ARG:HH22	1:A:1360:GLY:HA3	1.72	0.55
1:A:1403:GLY:HA3	1:A:1501:LEU:HD13	1.89	0.55
1:A:244:ALA:HB3	1:A:605:TYR:HB2	1.90	0.54
1:A:183:LYS:HB3	1:A:202:LEU:HB3	1.89	0.53
1:A:807:TYR:OH	1:A:1360:GLY:HA2	2.08	0.53
1:A:636:ASN:HA	1:A:661:ASN:HD22	1.74	0.53
1:A:126:PHE:CD1	1:A:184:VAL:HG11	2.44	0.53
1:A:1024:LYS:HB2	1:A:1036:LYS:HB3	1.92	0.52
1:A:284:VAL:HG23	1:A:285:LYS:HG2	1.91	0.52
1:A:1403:GLY:HA3	1:A:1501:LEU:CD1	2.40	0.52
1:A:809:PRO:HA	1:A:816:ARG:HA	1.92	0.51
1:A:276:GLY:H	1:A:285:LYS:HB2	1.75	0.51
1:A:319:GLU:HA	1:A:324:SER:HA	1.91	0.51
1:A:317:ARG:HD2	1:A:325:VAL:O	2.10	0.51
1:A:426:LEU:CD1	1:A:602:ARG:HG2	2.41	0.49
1:A:950:THR:HG22	1:A:951:THR:H	1.78	0.49
1:A:975:THR:HA	1:A:987:LYS:HE3	1.94	0.49
1:A:636:ASN:HB2	1:A:698:TYR:O	2.13	0.49
1:A:997:LEU:HD12	1:A:1117:LEU:HD21	1.94	0.48
1:A:68:PRO:HB3	2:A:1784:HOH:O	2.12	0.48
1:A:561:PRO:HG2	1:A:594:MET:HB3	1.95	0.48
1:A:284:VAL:HB	1:A:285:LYS:HE2	1.95	0.47
1:A:283:LYS:O	1:A:284:VAL:HG22	2.13	0.47
1:A:1417:PHE:CD1	1:A:1521:ASP:HB2	2.50	0.47
1:A:180:VAL:HG21	1:A:393:HIS:HE1	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:668:ARG:HG3	1:A:670:ILE:HG12	1.98	0.46
1:A:1478:LYS:CB	1:A:1479:PRO:HD3	2.46	0.46
1:A:285:LYS:HG3	1:A:695:PRO:HG3	1.98	0.46
1:A:503:VAL:HB	1:A:524:PHE:HB2	1.97	0.46
1:A:1076:ILE:HD11	1:A:1270:LYS:HD3	1.97	0.45
1:A:977:ASP:HA	1:A:985:THR:HG23	1.97	0.45
1:A:677:PHE:O	1:A:695:PRO:HD2	2.15	0.45
1:A:1123:THR:HB	1:A:1138:GLN:HB2	1.99	0.45
1:A:409:THR:O	1:A:409:THR:CG2	2.65	0.45
1:A:666:GLN:HE22	1:A:983:SER:HB3	1.81	0.45
1:A:305:LEU:HD12	1:A:308:ASN:HB2	1.98	0.45
1:A:232:THR:HA	1:A:1250:GLN:HG3	1.99	0.44
1:A:629:PHE:CG	1:A:974:PRO:HG3	2.53	0.44
1:A:868:THR:HG23	1:A:869:LEU:H	1.83	0.44
1:A:896:ALA:HB1	1:A:1037:LEU:HD21	2.00	0.43
1:A:409:THR:O	1:A:409:THR:HG23	2.18	0.43
1:A:607:GLU:HG2	1:A:633:GLY:CA	2.49	0.43
1:A:1473:ARG:HD3	1:A:1500:PRO:HB3	2.01	0.42
1:A:733:LEU:HD22	1:A:996:PHE:HE2	1.84	0.42
1:A:939:GLN:HB3	1:A:949:LEU:HB2	2.01	0.42
1:A:471:GLU:HB3	1:A:472:ALA:H	1.68	0.42
1:A:733:LEU:HD21	1:A:1122:VAL:HG11	2.02	0.42
1:A:289:ILE:HD11	1:A:693:ILE:HD11	2.02	0.41
1:A:1282:GLN:HB3	1:A:1283:PRO:CA	2.46	0.41
1:A:1170:LEU:HA	1:A:1170:LEU:HD12	1.97	0.41
1:A:1238:PRO:HG2	1:A:1239:TYR:CE2	2.55	0.41
1:A:494:LEU:HB3	1:A:501:LEU:HD11	2.02	0.41
1:A:1169:ARG:HD2	2:A:1961:HOH:O	2.21	0.41
1:A:274:GLN:CD	1:A:938:LYS:HG2	2.41	0.41
1:A:1128:VAL:HG12	1:A:1129:LYS:HG2	2.03	0.41
1:A:1438:ASP:HA	1:A:1441:ILE:HD12	2.03	0.41
1:A:640:LEU:HD22	1:A:693:ILE:HD13	2.03	0.41
1:A:242:LYS:HD3	1:A:318:SER:HB2	2.02	0.41
1:A:419:ASP:OD2	1:A:423:ARG:HD2	2.20	0.40
1:A:151:PRO:HG2	1:A:159:ILE:HD12	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	1316/1469 (90%)	1208 (92%)	75 (6%)	33 (2%)	5 0

All (33) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	284	VAL
1	A	647	SER
1	A	959	GLN
1	A	1069	ASN
1	A	1276	GLY
1	A	1351	ASN
1	A	1363	VAL
1	A	1478	LYS
1	A	1479	PRO
1	A	1497	ASP
1	A	1523	HIS
1	A	226	SER
1	A	866	GLN
1	A	868	THR
1	A	1015	SER
1	A	1070	THR
1	A	233	THR
1	A	272	SER
1	A	303	LEU
1	A	867	ALA
1	A	958	ASP
1	A	960	GLN
1	A	1361	ASN
1	A	285	LYS
1	A	472	ALA
1	A	948	SER
1	A	950	THR
1	A	1284	GLN

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Mol	Chain	Res	Type
1	A	108	GLN
1	A	225	GLU
1	A	305	LEU
1	A	1282	GLN
1	A	954	GLY

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	1139/1227 (93%)	1067 (94%)	72 (6%)	18 5

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	ARG
1	A	98	LYS
1	A	107	GLN
1	A	155	GLN
1	A	223	ARG
1	A	273	THR
1	A	285	LYS
1	A	287	LEU
1	A	293	LYS
1	A	296	ASP
1	A	305	LEU
1	A	319	GLU
1	A	327	LEU
1	A	330	ASP
1	A	334	THR
1	A	366	LEU
1	A	409	THR
1	A	460	ASN
1	A	471	GLU
1	A	473	ASP
1	A	475	ASP

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Mol	Chain	Res	Type
1	A	476	LYS
1	A	477	SER
1	A	490	ASN
1	A	646	SER
1	A	647	SER
1	A	651	SER
1	A	652	SER
1	A	662	ASN
1	A	675	ASP
1	A	688	ASP
1	A	725	GLU
1	A	754	LYS
1	A	769	LYS
1	A	822	ARG
1	A	824	VAL
1	A	827	ILE
1	A	848	ARG
1	A	861	LEU
1	A	864	ASN
1	A	866	GLN
1	A	869	LEU
1	A	901	ASP
1	A	909	ASP
1	A	914	LYS
1	A	938	LYS
1	A	953	ASP
1	A	958	ASP
1	A	960	GLN
1	A	972	LEU
1	A	983	SER
1	A	1014	ASP
1	A	1030	LEU
1	A	1034	GLN
1	A	1082	GLU
1	A	1170	LEU
1	A	1190	ASP
1	A	1215	SER
1	A	1223	LYS
1	A	1250	GLN
1	A	1253	LYS
1	A	1282	GLN
1	A	1325	LEU

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Mol	Chain	Res	Type
1	A	1358	ASN
1	A	1362	ASP
1	A	1393	LEU
1	A	1452	ASN
1	A	1461	LEU
1	A	1478	LYS
1	A	1481	GLN
1	A	1522	LYS
1	A	1523	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	304	GLN
1	A	460	ASN
1	A	661	ASN
1	A	662	ASN
1	A	685	ASN
1	A	864	ASN
1	A	960	GLN
1	A	1031	HIS
1	A	1266	GLN
1	A	1301	ASN

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 [i](#)

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 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	A	1339/1469 (91%)	0.38	123 (9%) 9 13	25, 52, 124, 174	0

All (123) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1068	SER	12.1
1	A	107	GLN	9.3
1	A	226	SER	8.3
1	A	227	GLY	8.3
1	A	284	VAL	8.0
1	A	869	LEU	8.0
1	A	336	LEU	7.4
1	A	224	THR	7.4
1	A	1359	THR	7.0
1	A	1360	GLY	6.9
1	A	1281	THR	6.9
1	A	950	THR	6.5
1	A	1350	THR	6.5
1	A	1190	ASP	6.3
1	A	108	GLN	6.0
1	A	1496	GLY	6.0
1	A	1193	GLY	5.9
1	A	1069	ASN	5.8
1	A	908	SER	5.2
1	A	1225	ASN	5.1
1	A	955	ASN	5.0
1	A	475	ASP	4.8
1	A	1519[A]	TRP	4.7
1	A	233	THR	4.6
1	A	1305	VAL	4.5
1	A	1025[A]	TRP	4.5
1	A	686	GLY	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	60	ASN	4.3
1	A	921	MET	4.3
1	A	231	SER	4.2
1	A	322	GLY	4.1
1	A	945	SER	4.1
1	A	1189	SER	4.1
1	A	1191	SER	4.1
1	A	225	GLU	4.1
1	A	258	ALA	4.0
1	A	1277	THR	4.0
1	A	1479	PRO	3.9
1	A	648	SER	3.9
1	A	1357	THR	3.8
1	A	889	ASN	3.8
1	A	297	SER	3.8
1	A	828	THR	3.7
1	A	953	ASP	3.7
1	A	1071	THR	3.7
1	A	286	ALA	3.6
1	A	902	LYS	3.6
1	A	106	SER	3.6
1	A	956	ALA	3.6
1	A	1405	GLN	3.6
1	A	929	THR	3.5
1	A	223	ARG	3.5
1	A	957	ILE	3.5
1	A	304	GLN	3.5
1	A	903	ALA	3.5
1	A	1234	THR	3.5
1	A	651	SER	3.4
1	A	1280	SER	3.4
1	A	864	ASN	3.3
1	A	922	ASP	3.3
1	A	1233	SER	3.3
1	A	891	GLN	3.3
1	A	907	GLN	3.3
1	A	649	SER	3.2
1	A	1528	HIS	3.2
1	A	865	VAL	3.2
1	A	349	SER	3.1
1	A	949	LEU	3.1
1	A	904	SER	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	959	GLN	3.0
1	A	473	ASP	3.0
1	A	110	THR	2.9
1	A	276	GLY	2.9
1	A	1358	ASN	2.8
1	A	323	GLN	2.8
1	A	951	THR	2.8
1	A	707	TYR	2.8
1	A	1361	ASN	2.8
1	A	101	THR	2.8
1	A	1477	PHE	2.8
1	A	1066	SER	2.7
1	A	1067	GLY	2.7
1	A	688	ASP	2.6
1	A	175	GLN	2.6
1	A	1070	THR	2.6
1	A	296	ASP	2.6
1	A	1403	GLY	2.6
1	A	848	ARG	2.6
1	A	1307	SER	2.6
1	A	303	LEU	2.5
1	A	1304	SER	2.5
1	A	863	ALA	2.5
1	A	665	TRP	2.5
1	A	866	GLN	2.5
1	A	958	ASP	2.5
1	A	1279	HIS	2.4
1	A	285	LYS	2.4
1	A	1481	GLN	2.4
1	A	461	SER	2.4
1	A	1476	PHE	2.4
1	A	1363	VAL	2.4
1	A	1224	PRO	2.3
1	A	321	SER	2.3
1	A	861	LEU	2.3
1	A	1449	ALA	2.3
1	A	677	PHE	2.2
1	A	1283	PRO	2.2
1	A	1523	HIS	2.2
1	A	650	SER	2.2
1	A	1482	ASP	2.2
1	A	1400	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1526	HIS	2.1
1	A	335	ALA	2.1
1	A	319	GLU	2.1
1	A	273	THR	2.1
1	A	868	THR	2.1
1	A	967	ASN	2.1
1	A	1306	LEU	2.1
1	A	862	LYS	2.0
1	A	946	GLY	2.0
1	A	271	GLN	2.0
1	A	462	GLU	2.0
1	A	851	LEU	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.