



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:43 PM UTC

PDB ID : 6RC9 / pdb_00006rc9
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 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

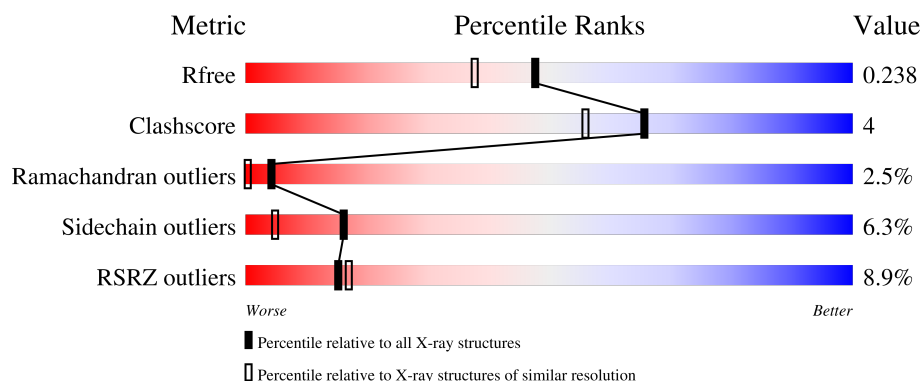
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (1.94-1.94)

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	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.

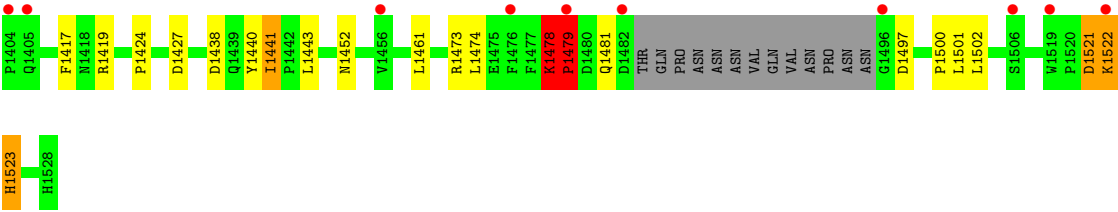
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1339	Total	C	N	O	S	0	7	0
			10523	6642	1838	2033	10			

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		



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)	Xtriage
Refinement program	BUSTER 2.10.3, REFMAC	Depositor
R, R_{free}	0.187 , 0.229 0.196 , 0.238	Depositor DCC
R_{free} test set	4593 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	32.2	Xtriage
Anisotropy	0.580	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 56.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
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

Xtriage'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

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	0.85	4/10794 (0.0%)	1.24	54/14714 (0.4%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	409	THR	CA-C	6.93	1.61	1.52
1	A	1441	ILE	CA-CB	6.81	1.57	1.54
1	A	1478	LYS	CA-C	6.24	1.60	1.52
1	A	285	LYS	CA-C	5.64	1.60	1.52

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	132	ASP	CA-CB-CG	7.40	120.00	112.60
1	A	283	LYS	CA-C-N	6.85	134.30	121.97
1	A	283	LYS	C-N-CA	6.85	134.30	121.97
1	A	271	GLN	CA-C-N	6.72	134.38	121.54
1	A	271	GLN	C-N-CA	6.72	134.38	121.54
1	A	409	THR	CB-CA-C	6.54	119.77	111.21
1	A	232	THR	CA-C-N	6.12	133.24	121.54
1	A	232	THR	C-N-CA	6.12	133.24	121.54
1	A	480	ILE	N-CA-C	-6.00	101.79	109.30
1	A	284	VAL	N-CA-CB	5.95	121.05	111.23
1	A	1522	LYS	CA-C-N	5.92	132.85	121.54
1	A	1522	LYS	C-N-CA	5.92	132.85	121.54
1	A	1440	TYR	CA-C-N	5.87	126.06	120.43
1	A	1440	TYR	C-N-CA	5.87	126.06	120.43
1	A	667	ASP	CA-CB-CG	5.84	118.44	112.60
1	A	83	GLY	CA-C-N	5.83	128.56	120.29
1	A	83	GLY	C-N-CA	5.83	128.56	120.29
1	A	1350	THR	CA-C-N	5.76	132.55	121.54
1	A	1350	THR	C-N-CA	5.76	132.55	121.54
1	A	763	TYR	CA-C-N	5.70	127.92	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	763	TYR	C-N-CA	5.70	127.92	120.28
1	A	272	SER	N-CA-C	-5.58	98.90	110.80
1	A	1521	ASP	CA-CB-CG	5.50	118.10	112.60
1	A	526	VAL	N-CA-CB	5.43	118.51	111.67
1	A	1479	PRO	N-CA-C	5.38	123.54	112.47
1	A	1367	GLY	N-CA-C	5.36	118.55	110.18
1	A	330	ASP	CA-CB-CG	5.36	117.96	112.60
1	A	365	ASP	CA-C-N	5.32	126.74	120.09
1	A	365	ASP	C-N-CA	5.32	126.74	120.09
1	A	575	ALA	N-CA-C	-5.31	97.87	107.75
1	A	865	VAL	CA-C-N	5.28	131.62	121.54
1	A	865	VAL	C-N-CA	5.28	131.62	121.54
1	A	958	ASP	CA-C-N	5.21	131.49	121.54
1	A	958	ASP	C-N-CA	5.21	131.49	121.54
1	A	635	ALA	N-CA-C	-5.21	102.77	110.48
1	A	60	ASN	CA-C-N	5.20	127.24	120.28
1	A	60	ASN	C-N-CA	5.20	127.24	120.28
1	A	1014	ASP	CA-C-N	5.19	131.45	121.54
1	A	1014	ASP	C-N-CA	5.19	131.45	121.54
1	A	223	ARG	CA-C-N	5.18	131.44	121.54
1	A	223	ARG	C-N-CA	5.18	131.44	121.54
1	A	1168	ASN	CA-CB-CG	5.18	117.78	112.60
1	A	922	ASP	CA-CB-CG	5.17	117.77	112.60
1	A	86	PRO	N-CA-C	5.16	118.71	110.40
1	A	1068	SER	CA-C-N	5.16	131.40	121.54
1	A	1068	SER	C-N-CA	5.16	131.40	121.54
1	A	546	PHE	CA-CB-CG	5.14	118.94	113.80
1	A	646	SER	CA-C-N	5.10	131.28	121.54
1	A	646	SER	C-N-CA	5.10	131.28	121.54
1	A	389	ASP	CA-CB-CG	5.09	117.69	112.60
1	A	959	GLN	CA-C-N	5.09	131.26	121.54
1	A	959	GLN	C-N-CA	5.09	131.26	121.54
1	A	154	ASP	CA-CB-CG	5.04	117.64	112.60
1	A	409	THR	N-CA-CB	-5.03	102.85	110.75

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	10523	0	10127	78	0
2	A	406	0	0	2	0
All	All	10929	0	10127	78	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 (78) 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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:668:ARG:HG3	1:A:670:ILE:HG12	1.98	0.46
1:A:285:LYS:HG3	1:A:695:PRO:HG3	1.98	0.46
1:A:1478:LYS:CB	1:A:1479:PRO:HD3	2.46	0.46
1:A:503:VAL:HB	1:A:524:PHE:HB2	1.97	0.46
1:A:274:GLN:CD	1:A:938:LYS:HG2	2.41	0.45
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:409:THR:O	1:A:409:THR:CG2	2.65	0.45
1:A:1123:THR:HB	1:A:1138:GLN:HB2	1.99	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:409:THR:O	1:A:409:THR:HG23	2.18	0.43
1:A:896:ALA:HB1	1:A:1037:LEU:HD21	2.00	0.43
1:A:607:GLU:HG2	1:A:633:GLY:CA	2.49	0.43
1:A:733:LEU:HD22	1:A:996:PHE:HE2	1.84	0.42
1:A:1473:ARG:HD3	1:A:1500:PRO:HB3	2.01	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:494:LEU:HB3	1:A:501:LEU:HD11	2.02	0.41
1:A:1170:LEU:HD12	1:A:1170:LEU:HA	1.97	0.41
1:A:1238:PRO:HG2	1:A:1239:TYR:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1169:ARG:HD2	2:A:1961:HOH:O	2.21	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
1:A:694:TYR:C	1:A:696:TYR:H	2.30	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	1316/1469 (90%)	1208 (92%)	75 (6%)	33 (2%)	4 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

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Mol	Chain	Res	Type
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
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 ⓘ

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%)	1068 (94%)	71 (6%)	16 5

All (71) 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	273	THR
1	A	285	LYS

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Mol	Chain	Res	Type
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	374	LEU
1	A	409	THR
1	A	460	ASN
1	A	471	GLU
1	A	473	ASP
1	A	475	ASP
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	675	ASP
1	A	688	ASP
1	A	754	LYS
1	A	769	LYS
1	A	824	VAL
1	A	827	ILE
1	A	861	LEU
1	A	864	ASN
1	A	866	GLN
1	A	869	LEU
1	A	901	ASP
1	A	914	LYS
1	A	938	LYS
1	A	950	THR
1	A	953	ASP
1	A	957	ILE
1	A	958	ASP
1	A	960	GLN
1	A	961	GLU
1	A	968	LEU

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Mol	Chain	Res	Type
1	A	1030	LEU
1	A	1034	GLN
1	A	1082	GLU
1	A	1170	LEU
1	A	1190	ASP
1	A	1223	LYS
1	A	1250	GLN
1	A	1253	LYS
1	A	1282	GLN
1	A	1325	LEU
1	A	1339	LEU
1	A	1358	ASN
1	A	1359	THR
1	A	1362	ASP
1	A	1393	LEU
1	A	1452	ASN
1	A	1461	LEU
1	A	1474	LEU
1	A	1478	LYS
1	A	1481	GLN
1	A	1502	LEU
1	A	1522	LYS
1	A	1523	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	108	GLN
1	A	155	GLN
1	A	178	ASN
1	A	182	ASN
1	A	304	GLN
1	A	308	ASN
1	A	415	HIS
1	A	460	ASN
1	A	469	GLN
1	A	661	ASN
1	A	685	ASN
1	A	716	GLN
1	A	782	HIS
1	A	856	ASN
1	A	891	GLN

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Mol	Chain	Res	Type
1	A	939	GLN
1	A	960	GLN
1	A	1031	HIS
1	A	1186	GLN
1	A	1266	GLN
1	A	1282	GLN
1	A	1301	ASN
1	A	1338	GLN
1	A	1361	ASN
1	A	1378	ASN
1	A	1405	GLN
1	A	1481	GLN
1	A	1525	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	1339/1469 (91%)	0.52	119 (8%) 15 17	23, 51, 124, 174	7 (0%)

All (119) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	227	GLY	6.5
1	A	1025[A]	TRP	6.2
1	A	1519[A]	TRP	5.9
1	A	284	VAL	5.5
1	A	1067	GLY	5.1
1	A	869	LEU	5.0
1	A	956	ALA	4.9
1	A	949	LEU	4.7
1	A	951	THR	4.5
1	A	258	ALA	4.5
1	A	233	THR	4.4
1	A	336	LEU	4.2
1	A	1068	SER	4.2
1	A	950	THR	4.1
1	A	686	GLY	3.9
1	A	276	GLY	3.8
1	A	225	GLU	3.8
1	A	101	THR	3.8
1	A	1479	PRO	3.7
1	A	867	ALA	3.7
1	A	1360	GLY	3.7
1	A	903	ALA	3.7
1	A	472	ALA	3.6
1	A	827	ILE	3.6
1	A	232	THR	3.5
1	A	959	GLN	3.5
1	A	1496	GLY	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	1071	THR	3.4
1	A	1234	THR	3.4
1	A	1193	GLY	3.4
1	A	953	ASP	3.4
1	A	297	SER	3.4
1	A	226	SER	3.3
1	A	945	SER	3.3
1	A	272	SER	3.2
1	A	1305	VAL	3.2
1	A	303	LEU	3.2
1	A	929	THR	3.1
1	A	1350	THR	3.1
1	A	1359	THR	3.1
1	A	475	ASP	3.0
1	A	955	ASN	3.0
1	A	224	THR	3.0
1	A	1281	THR	3.0
1	A	830	PRO	3.0
1	A	1276	GLY	3.0
1	A	305	LEU	3.0
1	A	1225	ASN	3.0
1	A	868	THR	3.0
1	A	322	GLY	3.0
1	A	957	ILE	3.0
1	A	921	MET	2.9
1	A	1277	THR	2.9
1	A	1189	SER	2.9
1	A	286	ALA	2.9
1	A	296	ASP	2.9
1	A	904	SER	2.9
1	A	1065	GLY	2.8
1	A	828	THR	2.8
1	A	649	SER	2.8
1	A	861	LEU	2.7
1	A	1482	ASP	2.7
1	A	865	VAL	2.7
1	A	954	GLY	2.6
1	A	908	SER	2.6
1	A	109	THR	2.6
1	A	1405	GLN	2.6
1	A	1325	LEU	2.5
1	A	285	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	687	LYS	2.5
1	A	1357	THR	2.5
1	A	850	PHE	2.5
1	A	1522	LYS	2.5
1	A	1224	PRO	2.5
1	A	1506	SER	2.4
1	A	223	ARG	2.4
1	A	107	GLN	2.4
1	A	650	SER	2.4
1	A	1476	PHE	2.4
1	A	1069	ASN	2.4
1	A	1403	GLY	2.4
1	A	476	LYS	2.3
1	A	349	SER	2.3
1	A	323	GLN	2.3
1	A	1361	ASN	2.3
1	A	707	TYR	2.3
1	A	962	ALA	2.3
1	A	648	SER	2.2
1	A	1307	SER	2.2
1	A	1456	VAL	2.2
1	A	947	ASP	2.2
1	A	958	ASP	2.2
1	A	1066	SER	2.2
1	A	679	LYS	2.2
1	A	1070	THR	2.2
1	A	851	LEU	2.2
1	A	231	SER	2.2
1	A	1404	PRO	2.2
1	A	1166	TRP	2.2
1	A	458	VAL	2.2
1	A	273	THR	2.2
1	A	940	ASP	2.2
1	A	906	GLY	2.2
1	A	684	LYS	2.1
1	A	468	PHE	2.1
1	A	670	ILE	2.1
1	A	907	GLN	2.1
1	A	1358	ASN	2.1
1	A	473	ASP	2.1
1	A	1027	TYR	2.0
1	A	1378	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	890	LEU	2.0
1	A	863	ALA	2.0
1	A	292	LYS	2.0
1	A	470	LYS	2.0
1	A	321	SER	2.0
1	A	1028	THR	2.0
1	A	60	ASN	2.0
1	A	367	PRO	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 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.