



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 01:54 am GMT

PDB ID : 1Q8I
Title : Crystal structure of ESCHERICHIA coli DNA Polymerase II
Authors : Brunzelle, J.S.; Muchmore, C.R.A.; Mashhoon, N.; Blair-Johnson, M.; Shuvalova, L.; Goodman, M.F.; Anderson, W.F.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2003-08-21
Resolution : 2.00 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

<http://wwpdb.org/validation/2016/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)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

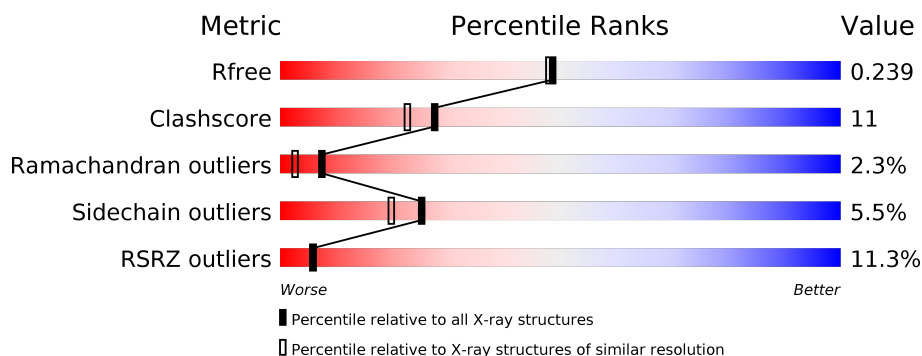
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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 $\leq 5\%$. 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	783	<div> <div>10%</div> <div> <div></div> <div>70%</div> <div>16%</div> <div>• •</div> <div>10%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6152 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 DNA polymerase II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	708	Total	C	N	O	S	0	8	0
			5736	3671	1002	1039	24			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	428	VAL	ILE	ENGINEERED	UNP P21189

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	416	Total	O	0	0
			416	416		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	92.38Å 116.60Å 82.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 29.74 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (20.00-2.00) 99.8 (29.74-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	10.89 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5	Depositor
R, R_{free}	0.197 , 0.236 0.200 , 0.239	Depositor DCC
R_{free} test set	3067 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.448	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 60.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6152	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.54% 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	0.73	0/5927	0.93	21/8038 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	113	ARG	NE-CZ-NH1	14.70	127.65	120.30
1	A	113	ARG	NE-CZ-NH2	-14.60	113.00	120.30
1	A	118[A]	ARG	NE-CZ-NH2	-7.63	116.49	120.30
1	A	118[B]	ARG	NE-CZ-NH2	-7.63	116.49	120.30
1	A	512	ASP	CB-CG-OD2	7.53	125.07	118.30
1	A	522	ARG	NE-CZ-NH1	7.05	123.82	120.30
1	A	364	ASP	CB-CG-OD2	6.34	124.01	118.30
1	A	113	ARG	CD-NE-CZ	6.20	132.27	123.60
1	A	367	GLY	N-CA-C	6.16	128.50	113.10
1	A	770	ASP	CB-CG-OD2	6.13	123.82	118.30
1	A	610	ASP	CB-CG-OD2	6.09	123.78	118.30
1	A	522	ARG	NE-CZ-NH2	-6.07	117.26	120.30
1	A	28	ASP	CB-CG-OD2	5.68	123.41	118.30
1	A	156	ASP	CB-CG-OD2	5.54	123.29	118.30
1	A	318	ASP	CB-CG-OD2	5.44	123.19	118.30
1	A	640	ASP	CB-CG-OD2	5.42	123.18	118.30
1	A	446	ASP	CB-CG-OD2	5.39	123.16	118.30
1	A	129	ASP	CB-CG-OD2	5.25	123.02	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	251	SER	N-CA-C	5.19	125.01	111.00
1	A	625	ASP	CB-CG-OD2	5.17	122.95	118.30
1	A	286	TRP	N-CA-C	5.09	124.75	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	182	GLY	Mainchain,Peptide

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	5736	0	5621	128	2
2	A	416	0	0	16	2
All	All	6152	0	5621	128	2

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 (128) 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:613:SER:HB2	1:A:616:ARG:HD3	1.16	1.11
1:A:281:LEU:HD21	1:A:346:THR:HG21	1.43	0.99
1:A:314:MET:O	1:A:316:GLU:N	1.97	0.96
1:A:232:MET:HG2	1:A:235:LYS:HZ1	1.30	0.95
1:A:645:ALA:HB2	1:A:756:GLN:HG3	1.49	0.95
1:A:232:MET:CG	1:A:235:LYS:HZ1	1.88	0.86
1:A:176:ARG:NH2	1:A:192:ASP:O	2.10	0.85
1:A:185:ASN:HD21	1:A:325:LYS:H	1.25	0.83
1:A:196:GLU:OE1	2:A:856:HOH:O	1.98	0.81
1:A:613:SER:HB2	1:A:616:ARG:CD	2.05	0.80
1:A:248:ARG:O	1:A:251:SER:OG	1.98	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:PRO:HD3	2:A:1062:HOH:O	1.81	0.79
1:A:113:ARG:HD2	2:A:833:HOH:O	1.84	0.77
1:A:24:TRP:HE1	1:A:270[A]:LYS:HE3	1.49	0.76
1:A:272:ARG:NH2	2:A:1162:HOH:O	2.17	0.75
1:A:196:GLU:OE2	1:A:207:LYS:HE3	1.87	0.75
1:A:206:GLU:OE1	2:A:908:HOH:O	2.05	0.75
1:A:223:TRP:CD1	1:A:293:LEU:HD23	2.21	0.74
1:A:299:GLU:O	1:A:300:LEU:HB2	1.87	0.73
1:A:232:MET:HA	1:A:235:LYS:CE	2.18	0.73
1:A:223:TRP:HZ2	1:A:291:PHE:O	1.72	0.73
1:A:127:GLU:OE2	1:A:139:ARG:NH2	2.22	0.72
1:A:24:TRP:HE1	1:A:270[A]:LYS:CE	2.01	0.71
1:A:226[B]:VAL:HG23	1:A:227:GLN:H	1.55	0.71
1:A:232:MET:HA	1:A:235:LYS:HE3	1.71	0.71
1:A:290:SER:O	1:A:291:PHE:HB3	1.91	0.71
1:A:635:GLU:O	1:A:641:TRP:CD2	2.45	0.69
1:A:446:ASP:OD1	1:A:449:HIS:HD2	1.76	0.69
1:A:175:GLN:HE22	1:A:177:ILE:HG22	1.57	0.69
1:A:228:PHE:O	1:A:232:MET:HG3	1.92	0.68
1:A:11:HIS:CE1	1:A:270[B]:LYS:HG2	2.30	0.67
1:A:429:ARG:NH2	2:A:876:HOH:O	2.27	0.67
1:A:384:ALA:HB1	1:A:463:LYS:HD2	1.77	0.66
1:A:123:PRO:HB2	1:A:143:HIS:O	1.97	0.64
1:A:226[B]:VAL:HG23	1:A:227:GLN:N	2.12	0.64
1:A:17:GLN:O	1:A:17:GLN:CG	2.45	0.63
1:A:645:ALA:HB2	1:A:756:GLN:CG	2.25	0.63
1:A:223:TRP:CZ2	1:A:291:PHE:O	2.52	0.63
1:A:288:PHE:O	1:A:289:SER:HB2	2.00	0.61
1:A:196:GLU:OE2	1:A:207:LYS:CE	2.48	0.61
1:A:185:ASN:HD22	1:A:185:ASN:C	2.02	0.61
1:A:633:GLY:O	1:A:634:LEU:HB2	2.01	0.61
1:A:232:MET:HG2	1:A:235:LYS:NZ	2.13	0.59
1:A:252:GLU:HB3	2:A:1095:HOH:O	2.01	0.59
1:A:617:TYR:CZ	1:A:632:LYS:HG3	2.38	0.59
1:A:175:GLN:HE22	1:A:177:ILE:CG2	2.16	0.58
1:A:290:SER:O	1:A:291:PHE:CB	2.52	0.58
1:A:232:MET:CG	1:A:235:LYS:NZ	2.66	0.57
1:A:258:HIS:CD2	1:A:365:ARG:HH22	2.22	0.57
1:A:301:LEU:HD13	1:A:341:GLN:HE21	1.70	0.57
1:A:185:ASN:ND2	1:A:325:LYS:H	1.99	0.56
1:A:232:MET:HA	1:A:235:LYS:NZ	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:600:ARG:NH2	1:A:659:ASN:OD1	2.39	0.55
1:A:185:ASN:HD21	1:A:325:LYS:HG3	1.71	0.55
1:A:249:ASP:CG	1:A:250:ASN:H	2.10	0.55
1:A:185:ASN:ND2	1:A:325:LYS:HG3	2.21	0.55
1:A:226[B]:VAL:HG23	1:A:227:GLN:HG2	1.89	0.55
1:A:93:GLU:OE2	1:A:97:ARG:NH1	2.40	0.55
1:A:255:TRP:O	1:A:256:ARG:HG3	2.06	0.54
1:A:281:LEU:CD2	1:A:346:THR:HG21	2.28	0.54
1:A:209:ASN:ND2	2:A:1159:HOH:O	2.40	0.54
1:A:497:ASN:ND2	2:A:972:HOH:O	2.30	0.53
1:A:175:GLN:NE2	1:A:211:TRP:HE1	2.05	0.53
1:A:642:THR:HG22	1:A:684:TYR:HB3	1.90	0.53
1:A:284:ALA:O	1:A:285:PHE:HB2	2.09	0.53
1:A:206:GLU:HA	2:A:1159:HOH:O	2.09	0.52
1:A:299:GLU:O	1:A:300:LEU:CB	2.58	0.52
1:A:758:GLN:HB3	1:A:759:PRO:HD3	1.92	0.52
1:A:223:TRP:NE1	1:A:278:ILE:HD11	2.26	0.51
1:A:17:GLN:O	1:A:17:GLN:HG3	2.10	0.51
1:A:232:MET:CB	1:A:235:LYS:NZ	2.74	0.51
1:A:140:LEU:N	1:A:140:LEU:HD12	2.26	0.50
1:A:258:HIS:HD2	1:A:365:ARG:HH22	1.58	0.49
1:A:440:GLU:HG3	1:A:463:LYS:HG2	1.93	0.49
1:A:288:PHE:O	1:A:289:SER:CB	2.60	0.49
1:A:364:ASP:O	1:A:365:ARG:HB3	2.13	0.49
1:A:768:ILE:O	1:A:769:GLU:HB3	2.13	0.49
1:A:682:LEU:HG	1:A:752:TYR:CD2	2.48	0.49
1:A:345:LYS:O	1:A:345:LYS:HD3	2.13	0.48
1:A:122:SER:H	1:A:123:PRO:CD	2.27	0.48
1:A:349:MET:HB2	1:A:350:PRO:HD3	1.96	0.48
1:A:364:ASP:O	1:A:365:ARG:CB	2.62	0.47
1:A:635:GLU:O	1:A:636:THR:OG1	2.31	0.47
1:A:76:GLN:HG2	2:A:943:HOH:O	2.13	0.47
1:A:411:LEU:HD21	1:A:600:ARG:NH1	2.29	0.47
1:A:635:GLU:O	1:A:641:TRP:CE2	2.68	0.47
1:A:431:PHE:CD2	1:A:522:ARG:HD3	2.50	0.47
1:A:257:GLU:CG	1:A:258:HIS:N	2.78	0.47
1:A:431:PHE:CE2	1:A:522:ARG:HD3	2.49	0.47
1:A:473[B]:ILE:CD1	1:A:499:PHE:HZ	2.28	0.47
1:A:419:ASP:OD2	1:A:595:GLU:OE2	2.32	0.47
1:A:345:LYS:HD3	1:A:345:LYS:C	2.36	0.46
1:A:531:LYS:HE2	1:A:535:GLU:OE2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:TRP:CZ2	1:A:292:SER:HA	2.50	0.46
1:A:446:ASP:HB2	1:A:448:GLU:OE1	2.16	0.46
1:A:183:PRO:CD	2:A:1062:HOH:O	2.54	0.45
1:A:455:LEU:CD2	1:A:455:LEU:N	2.79	0.45
1:A:635:GLU:OE1	1:A:641:TRP:HD1	1.99	0.45
1:A:277:GLY:O	1:A:281:LEU:HB2	2.16	0.45
1:A:232:MET:HA	1:A:235:LYS:HG2	1.99	0.45
1:A:314:MET:C	1:A:316:GLU:N	2.70	0.45
1:A:85:ALA:HB3	1:A:88:GLN:HB3	1.98	0.44
1:A:109:ARG:HE	1:A:109:ARG:HB2	1.55	0.44
1:A:232:MET:CA	1:A:235:LYS:HE3	2.46	0.44
1:A:301:LEU:HD13	1:A:341:GLN:NE2	2.31	0.44
1:A:250:ASN:HB3	1:A:251:SER:H	1.44	0.44
1:A:257:GLU:HG3	1:A:258:HIS:N	2.33	0.43
1:A:17:GLN:O	1:A:17:GLN:HG2	2.19	0.43
1:A:71[A]:LYS:HG3	2:A:942:HOH:O	2.17	0.43
1:A:756:GLN:HE21	1:A:756:GLN:HA	1.83	0.43
1:A:314:MET:C	1:A:316:GLU:H	2.13	0.43
1:A:24:TRP:HE1	1:A:270[A]:LYS:HE2	1.82	0.43
1:A:682:LEU:HG	1:A:752:TYR:CE2	2.54	0.43
1:A:52:ARG:HG2	1:A:101:VAL:CG2	2.48	0.42
1:A:616:ARG:O	1:A:617:TYR:HB3	2.19	0.42
1:A:83:CYS:HB3	1:A:88:GLN:HE21	1.85	0.42
1:A:437:GLY:HA3	2:A:802:HOH:O	2.19	0.41
1:A:403:TYR:HD2	1:A:545:ASP:O	2.02	0.41
1:A:270[A]:LYS:HE3	2:A:834:HOH:O	2.20	0.41
1:A:401:GLY:O	1:A:524:HIS:NE2	2.51	0.41
1:A:158:GLU:HG2	1:A:328:LEU:HD11	2.01	0.41
1:A:358:VAL:HG11	1:A:492:LEU:HD23	2.02	0.41
1:A:768:ILE:O	1:A:769:GLU:CB	2.68	0.41
1:A:232:MET:CA	1:A:235:LYS:NZ	2.84	0.40
1:A:550:PHE:N	1:A:550:PHE:CD1	2.89	0.40
1:A:552:TRP:CE2	1:A:554:LYS:HA	2.55	0.40
1:A:642:THR:HG23	1:A:756:GLN:OE1	2.19	0.40
1:A:258:HIS:HA	2:A:1161:HOH:O	2.20	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:231:ARG:NH1	2:A:1125:HOH:O[2_675]	2.01	0.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:ARG:NH1	2:A:1168:HOH:O[1_556]	2.13	0.07

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	708/783 (90%)	666 (94%)	26 (4%)	16 (2%)	7 3

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	182	GLY
1	A	183	PRO
1	A	250	ASN
1	A	251	SER
1	A	287	ASN
1	A	289	SER
1	A	291	PHE
1	A	315	ASP
1	A	365	ARG
1	A	634	LEU
1	A	367	GLY
1	A	285	PHE
1	A	286	TRP
1	A	399	SER
1	A	122	SER
1	A	260	PHE

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	608/670 (91%)	575 (95%)	33 (5%)	26	20

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	76	GLN
1	A	113	ARG
1	A	143	HIS
1	A	158	GLU
1	A	175	GLN
1	A	185	ASN
1	A	225	VAL
1	A	254	GLU
1	A	286	TRP
1	A	292	SER
1	A	293	LEU
1	A	298	GLN
1	A	316	GLU
1	A	332	ASN
1	A	334	LYS
1	A	345	LYS
1	A	364	ASP
1	A	365	ARG
1	A	405	MET
1	A	455	LEU
1	A	463	LYS
1	A	496	MET
1	A	522	ARG
1	A	614	LYS
1	A	639	THR
1	A	640	ASP
1	A	652	LEU
1	A	664	GLU
1	A	673	LEU
1	A	682	LEU
1	A	756	GLN
1	A	779	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	GLN
1	A	76	GLN
1	A	86	HIS
1	A	88	GLN
1	A	175	GLN
1	A	185	ASN
1	A	258	HIS
1	A	268	GLN
1	A	298	GLN
1	A	341	GLN
1	A	390	ASN
1	A	449	HIS
1	A	497	ASN
1	A	557	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 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 ⓘ

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	708/783 (90%)	0.59	80 (11%) 6 6	11, 21, 42, 73	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	611	THR	11.9
1	A	288	PHE	11.7
1	A	291	PHE	11.0
1	A	286	TRP	10.2
1	A	613	SER	10.0
1	A	639	THR	9.8
1	A	640	ASP	9.5
1	A	610	ASP	8.4
1	A	683	VAL	7.1
1	A	612	GLY	7.0
1	A	290	SER	6.7
1	A	684	TYR	6.6
1	A	300	LEU	6.4
1	A	264	VAL	6.3
1	A	609	ALA	6.2
1	A	634	LEU	6.2
1	A	636	THR	5.9
1	A	287	ASN	5.7
1	A	366	HIS	5.6
1	A	367	GLY	5.6
1	A	285	PHE	5.6
1	A	641	TRP	5.4
1	A	633	GLY	5.2
1	A	635	GLU	5.0
1	A	289	SER	4.9
1	A	223	TRP	4.8
1	A	265	PHE	4.8

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Mol	Chain	Res	Type	RSRZ
1	A	266	PHE	4.8
1	A	398	ALA	4.7
1	A	365	ARG	4.5
1	A	261	LYS	4.4
1	A	301	LEU	4.4
1	A	322	ALA	4.3
1	A	556	ALA	4.1
1	A	161	ARG	4.1
1	A	262	ASN	4.0
1	A	260	PHE	4.0
1	A	317	ILE	4.0
1	A	258	HIS	3.9
1	A	190	SER	3.9
1	A	399	SER	3.9
1	A	297	ALA	3.9
1	A	294	GLU	3.7
1	A	614	LYS	3.5
1	A	162	HIS	3.5
1	A	314	MET	3.4
1	A	295	THR	3.4
1	A	2	ALA	3.2
1	A	254	GLU	3.2
1	A	284	ALA	3.1
1	A	402	GLY	3.1
1	A	192	ASP	3.1
1	A	298	GLN	3.0
1	A	490	GLN	3.0
1	A	263	GLY	2.9
1	A	278	ILE	2.9
1	A	400	PRO	2.9
1	A	61	GLN	2.8
1	A	323	GLU	2.8
1	A	257	GLU	2.8
1	A	345	LYS	2.8
1	A	250	ASN	2.7
1	A	16	PRO	2.6
1	A	292	SER	2.6
1	A	315	ASP	2.6
1	A	680	ALA	2.6
1	A	745	SER	2.6
1	A	338	LEU	2.5
1	A	769	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	401	GLY	2.5
1	A	608	GLY	2.3
1	A	87	ARG	2.3
1	A	256	ARG	2.2
1	A	336	CYS	2.1
1	A	615	LYS	2.1
1	A	281	LEU	2.1
1	A	324	ASP	2.1
1	A	282	LYS	2.1
1	A	555	GLY	2.1
1	A	251	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.