



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:49 AM UTC

PDB ID : 1Q8I / pdb_00001q8i
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

<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

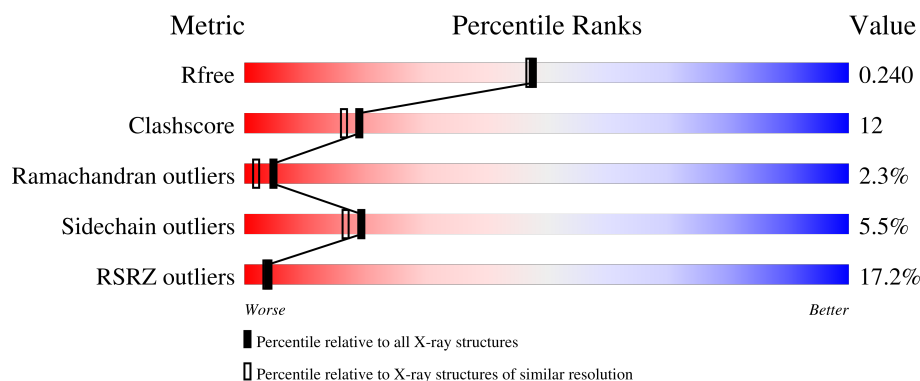
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (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 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	783	16% 70% 16% 10%

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 mutation	UNP P21189

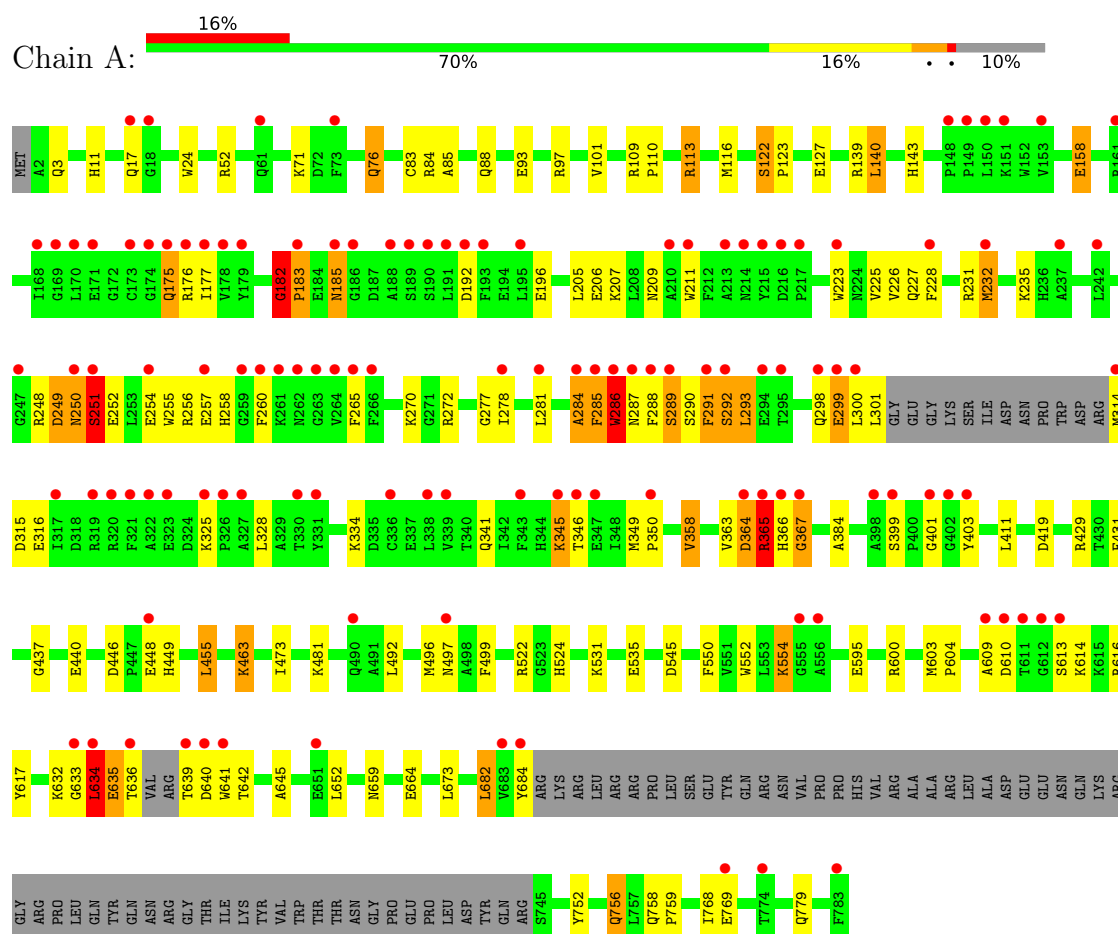
- Molecule 2 is water.

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

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: DNA polymerase II



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 20.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (20.00-2.00) 99.6 (20.00-2.00)	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 5.0	Depositor
R, R_{free}	0.197 , 0.236 0.200 , 0.240	Depositor DCC
R_{free} test set	3067 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.448	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 61.7	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	0.92	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

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	0.89	2/5927 (0.0%)	1.09	18/8038 (0.2%)

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	116	MET	SD-CE	-5.81	1.65	1.79
1	A	110	PRO	CA-C	5.45	1.57	1.52

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	113	ARG	NE-CZ-NH2	-6.89	113.00	119.20
1	A	284	ALA	N-CA-C	-6.70	105.26	113.50
1	A	610	ASP	N-CA-C	6.70	119.04	108.79
1	A	251	SER	N-CA-C	6.67	125.01	110.80
1	A	286	TRP	N-CA-C	6.55	124.75	110.80
1	A	367	GLY	N-CA-C	6.46	128.50	113.18
1	A	113	ARG	NE-CZ-NH1	6.15	127.65	121.50
1	A	110	PRO	N-CA-C	6.00	118.02	110.70
1	A	265	PHE	N-CA-C	5.96	119.79	110.32
1	A	358	VAL	CB-CA-C	-5.87	104.54	111.94
1	A	113	ARG	CD-NE-CZ	5.62	132.27	124.40
1	A	249	ASP	CB-CA-C	-5.47	108.68	116.34
1	A	299	GLU	N-CA-C	-5.45	101.65	110.32
1	A	609	ALA	N-CA-C	5.41	117.87	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	635	GLU	N-CA-C	-5.25	106.38	112.89
1	A	363	VAL	CA-C-N	5.03	127.73	120.38
1	A	363	VAL	C-N-CA	5.03	127.73	120.38
1	A	182	GLY	N-CA-C	5.01	122.56	112.34

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 [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	5736	0	5621	134	2
2	A	416	0	0	16	2
All	All	6152	0	5621	134	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 12.

All (134) 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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:ARG:O	1:A:251:SER:OG	1.98	0.80
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:603:MET:HE3	1:A:604:PRO:HD2	1.76	0.66
1:A:185:ASN:HD22	1:A:185:ASN:C	2.02	0.65
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:633:GLY:O	1:A:634:LEU:HB2	2.01	0.61
1:A:249:ASP:CG	1:A:250:ASN:H	2.10	0.60
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:314:MET:C	1:A:316:GLU:H	2.13	0.56
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: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:345:LYS:HD3	1:A:345:LYS:C	2.36	0.51
1:A:232:MET:CB	1:A:235:LYS:NZ	2.74	0.51
1:A:140:LEU:HD12	1:A:140:LEU:N	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:314:MET:C	1:A:316:GLU:N	2.70	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:HD3	1:A:345:LYS:O	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:76:GLN:HG2	2:A:943:HOH:O	2.13	0.47
1:A:635:GLU:O	1:A:636:THR:OG1	2.31	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:419:ASP:OD2	1:A:595:GLU:OE2	2.32	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:185:ASN:C	1:A:185:ASN:ND2	2.73	0.46
1:A:531:LYS:HE2	1:A:535:GLU:OE2	2.16	0.46
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: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:365:ARG:O	1:A:366:HIS:C	2.59	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: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:403:TYR:HD2	1:A:545:ASP:O	2.02	0.41
1:A:437:GLY:HA3	2:A:802:HOH:O	2.19	0.41
1:A:603:MET:HE3	1:A:604:PRO:CD	2.49	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:CD1	1:A:550:PHE:N	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:139:ARG:C	1:A:140:LEU:HD12	2.47	0.40
1:A:291:PHE:CD1	1:A:291:PHE:C	3.00	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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%)	5 2

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

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Mol	Chain	Res	Type
1	A	122	SER
1	A	260	PHE

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	608/670 (91%)	575 (95%)	33 (5%)	20	17

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	140	LEU
1	A	158	GLU
1	A	175	GLN
1	A	185	ASN
1	A	205	LEU
1	A	225	VAL
1	A	232	MET
1	A	254	GLU
1	A	286	TRP
1	A	292	SER
1	A	293	LEU
1	A	298	GLN
1	A	334	LYS
1	A	345	LYS
1	A	364	ASP
1	A	365	ARG
1	A	455	LEU
1	A	463	LYS
1	A	481	LYS
1	A	496	MET
1	A	554	LYS
1	A	614	LYS

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Mol	Chain	Res	Type
1	A	634	LEU
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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	17	GLN
1	A	33	GLN
1	A	74	HIS
1	A	76	GLN
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	332	ASN
1	A	341	GLN
1	A	390	ASN
1	A	449	HIS
1	A	490	GLN
1	A	497	ASN
1	A	557	HIS
1	A	572	HIS
1	A	779	GLN

5.3.3 RNA ⓘ

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	708/783 (90%)	0.78	122 (17%) 4 3	11, 21, 42, 73	8 (1%)

All (122) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	291	PHE	6.5
1	A	640	ASP	6.3
1	A	398	ALA	5.3
1	A	367	GLY	5.3
1	A	215	TYR	5.1
1	A	186	GLY	5.1
1	A	264	VAL	5.0
1	A	633	GLY	5.0
1	A	189	SER	4.8
1	A	366	HIS	4.7
1	A	636	THR	4.7
1	A	634	LEU	4.5
1	A	288	PHE	4.4
1	A	223	TRP	4.4
1	A	191	LEU	4.4
1	A	336	CYS	4.2
1	A	260	PHE	4.1
1	A	188	ALA	4.1
1	A	286	TRP	4.0
1	A	330	THR	4.0
1	A	613	SER	4.0
1	A	641	TRP	3.9
1	A	326	PRO	3.8
1	A	612	GLY	3.7
1	A	314	MET	3.7
1	A	783	PHE	3.7
1	A	177	ILE	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	285	PHE	3.7
1	A	173	CYS	3.6
1	A	174	GLY	3.6
1	A	250	ASN	3.6
1	A	365	ARG	3.6
1	A	61	GLN	3.6
1	A	214	ASN	3.5
1	A	287	ASN	3.5
1	A	259	GLY	3.5
1	A	213	ALA	3.5
1	A	251	SER	3.5
1	A	265	PHE	3.4
1	A	178	VAL	3.4
1	A	319	ARG	3.4
1	A	299	GLU	3.4
1	A	289	SER	3.3
1	A	556	ALA	3.3
1	A	261	LYS	3.3
1	A	325	LYS	3.3
1	A	611	THR	3.2
1	A	610	ASP	3.2
1	A	639	THR	3.1
1	A	183	PRO	3.1
1	A	237	ALA	3.1
1	A	150	LEU	3.1
1	A	300	LEU	3.1
1	A	402	GLY	3.1
1	A	192	ASP	3.1
1	A	401	GLY	3.1
1	A	216	ASP	3.0
1	A	769	GLU	3.0
1	A	217	PRO	3.0
1	A	195	LEU	3.0
1	A	254	GLU	3.0
1	A	364	ASP	2.9
1	A	148	PRO	2.9
1	A	211	TRP	2.9
1	A	339	VAL	2.9
1	A	190	SER	2.9
1	A	266	PHE	2.9
1	A	210	ALA	2.8
1	A	317	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	153	VAL	2.7
1	A	320	ARG	2.7
1	A	683	VAL	2.7
1	A	228	PHE	2.7
1	A	185	ASN	2.7
1	A	346	THR	2.6
1	A	171	GLU	2.6
1	A	350	PRO	2.6
1	A	151	LYS	2.6
1	A	651	GLU	2.6
1	A	168	ILE	2.5
1	A	149	PRO	2.5
1	A	175	GLN	2.5
1	A	343	PHE	2.5
1	A	684	TYR	2.5
1	A	345	LYS	2.5
1	A	322	ALA	2.4
1	A	295	THR	2.4
1	A	284	ALA	2.4
1	A	247	GLY	2.4
1	A	490	GLN	2.4
1	A	17	GLN	2.4
1	A	331	TYR	2.3
1	A	18	GLY	2.3
1	A	73	PHE	2.3
1	A	321	PHE	2.3
1	A	323	GLU	2.3
1	A	609	ALA	2.3
1	A	176	ARG	2.3
1	A	399	SER	2.3
1	A	193	PHE	2.3
1	A	232	MET	2.3
1	A	298	GLN	2.2
1	A	278	ILE	2.2
1	A	242	LEU	2.2
1	A	281	LEU	2.2
1	A	169	GLY	2.2
1	A	294	GLU	2.2
1	A	262	ASN	2.2
1	A	170	LEU	2.2
1	A	347	GLU	2.1
1	A	448	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	774	THR	2.1
1	A	292	SER	2.1
1	A	338	LEU	2.1
1	A	497	ASN	2.1
1	A	263	GLY	2.1
1	A	555	GLY	2.1
1	A	327	ALA	2.1
1	A	161	ARG	2.0
1	A	257	GLU	2.0
1	A	179	TYR	2.0
1	A	403	TYR	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.