



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 07:01 AM UTC

PDB ID : 1ZZD / pdb_00001zzd
Title : Structures of Yeast Ribonucleotide Reductase I
Authors : Xu, H.; Faber, C.; Uchiki, T.; Fairman, J.W.; Racca, J.; Dealwis, C.
Deposited on : 2005-06-13
Resolution : 2.60 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

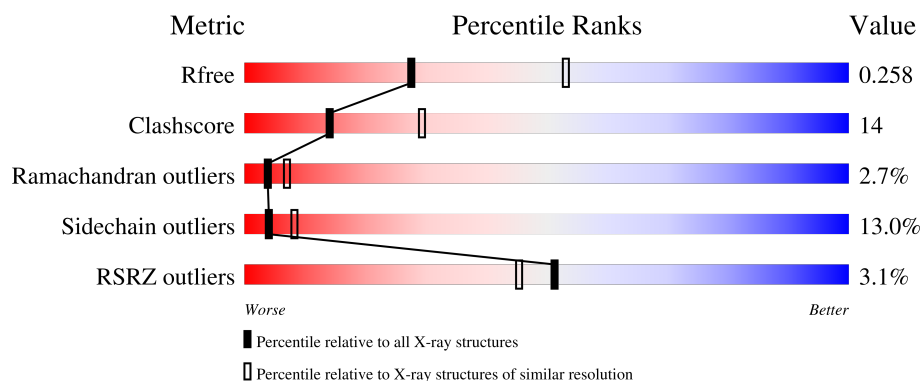
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	888	2% 46% 21% • 28%
2	B	9	11% 44% 22% 33%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5241 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 Ribonucleoside-diphosphate reductase large chain 1.

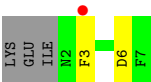
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	640	Total	C	N	O	S	0	0	0
			5128	3272	865	960	31			

- Molecule 2 is a protein called Ribonucleoside-diphosphate reductase small chain 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	6	Total	C	N	O	0	0	0
			55	34	7	14			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	58	Total	O	0	0
			58	58		



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	108.32Å 117.68Å 64.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.60 50.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.6 (50.00-2.60) 99.7 (50.00-2.60)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.61 (at 2.60Å)	Xtriage
Refinement program	REFMAC 5.2.0007	Depositor
R, R_{free}	0.201 , 0.260 0.199 , 0.258	Depositor DCC
R_{free} test set	2626 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å ²)	45.0	Xtriage
Anisotropy	0.570	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 41.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5241	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.82% 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	0.93	2/5247 (0.0%)	1.15	13/7103 (0.2%)
2	B	0.81	0/56	1.21	1/73 (1.4%)
All	All	0.93	2/5303 (0.0%)	1.15	14/7176 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	383	ILE	CG1-CD1	6.38	1.76	1.51
1	A	665	THR	CA-CB	5.20	1.59	1.53

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	326	ARG	N-CA-C	7.87	122.83	110.17
1	A	308	ILE	N-CA-C	6.73	117.49	110.62
1	A	334	ILE	N-CA-C	6.59	114.42	107.76
1	A	673	LEU	N-CA-C	-6.33	102.08	109.93
1	A	560	PHE	N-CA-C	6.21	118.56	111.11
1	A	352	SER	N-CA-C	-6.17	101.80	110.31
2	B	3	PHE	N-CA-C	5.79	123.14	110.80
1	A	265	THR	CA-C-N	5.58	128.52	120.38
1	A	265	THR	C-N-CA	5.58	128.52	120.38
1	A	267	GLY	N-CA-C	5.35	117.62	111.36
1	A	154	SER	N-CA-C	5.23	122.59	114.64
1	A	179	HIS	N-CA-C	5.18	119.75	113.38
1	A	703	SER	N-CA-C	5.17	118.69	112.38
1	A	206	PHE	CB-CA-C	-5.11	102.83	110.90

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	5128	0	5057	146	0
2	B	55	0	35	1	0
3	A	58	0	0	2	0
All	All	5241	0	5092	147	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 14.

All (147) 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:383:ILE:CD1	1:A:383:ILE:CG1	1.76	1.57
1:A:326:ARG:HH11	1:A:326:ARG:HG3	1.18	1.06
1:A:538:THR:HB	1:A:583:TRP:NE1	1.77	0.99
1:A:538:THR:HB	1:A:583:TRP:HE1	1.25	0.99
1:A:638:PHE:O	1:A:639:GLN:HB3	1.66	0.95
1:A:567:GLN:HE21	1:A:567:GLN:HA	1.34	0.92
1:A:567:GLN:HE21	1:A:567:GLN:CA	1.89	0.85
1:A:589:ARG:O	1:A:593:MET:HG3	1.76	0.85
1:A:557:TYR:CD1	1:A:559:THR:HG22	2.14	0.81
1:A:447:SER:HB3	1:A:606:MET:HE1	1.62	0.81
1:A:334:ILE:HD12	1:A:404:VAL:HG13	1.66	0.78
1:A:654:ILE:HG21	1:A:675:ASN:HD22	1.49	0.77
1:A:326:ARG:HH11	1:A:326:ARG:CG	1.97	0.77
1:A:639:GLN:NE2	1:A:660:LYS:HE3	2.00	0.77
1:A:101:LEU:HD22	1:A:115:MET:HE2	1.65	0.77
1:A:520:ARG:NH2	1:A:648:ASP:OD2	2.18	0.76
1:A:717:ARG:O	1:A:719:PRO:HD3	1.87	0.74
1:A:217:SER:HB3	1:A:445:LEU:HD12	1.69	0.74
1:A:217:SER:CB	1:A:445:LEU:HD12	2.18	0.74
1:A:482:ASN:OD1	1:A:503:ARG:NH1	2.20	0.73
1:A:666:GLN:O	1:A:667:ASN:HB2	1.90	0.70
1:A:427:LEU:HD12	1:A:427:LEU:O	1.92	0.70
1:A:657:GLU:C	1:A:659:MET:H	2.00	0.69
1:A:296:ALA:HB3	1:A:427:LEU:HD21	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259:GLY:HA2	1:A:268:THR:OG1	1.92	0.69
1:A:602:THR:N	1:A:707:ASP:OD2	2.25	0.69
1:A:326:ARG:HG3	1:A:326:ARG:NH1	1.93	0.69
1:A:557:TYR:CE1	1:A:559:THR:HG22	2.28	0.69
1:A:557:TYR:HD1	1:A:559:THR:HG22	1.59	0.68
1:A:530:LEU:O	1:A:534:GLN:HG2	1.94	0.67
1:A:127:ASN:HB2	1:A:131:LEU:HD22	1.75	0.67
1:A:426:ASN:ND2	1:A:428:CYS:H	1.93	0.67
1:A:481:LEU:HB3	1:A:505:ILE:HD12	1.76	0.67
1:A:166:ARG:HB2	1:A:169:HIS:CE1	2.31	0.65
1:A:688:TRP:HB3	1:A:717:ARG:HH11	1.62	0.64
1:A:388:LEU:O	1:A:392:ILE:HG12	1.97	0.64
1:A:445:LEU:HD23	1:A:506:ALA:HB3	1.78	0.64
1:A:170:LEU:HD22	1:A:173:ARG:NH2	2.14	0.62
1:A:445:LEU:HD23	1:A:506:ALA:CB	2.29	0.62
1:A:447:SER:HB3	1:A:606:MET:CE	2.30	0.62
1:A:560:PHE:CZ	1:A:596:GLY:HA2	2.35	0.61
1:A:745:THR:O	1:A:746:GLN:HB2	2.01	0.61
1:A:567:GLN:HA	1:A:567:GLN:NE2	2.11	0.60
1:A:538:THR:CB	1:A:583:TRP:HE1	2.10	0.59
1:A:383:ILE:HD12	1:A:384:LYS:H	1.67	0.59
1:A:510:GLN:HA	1:A:620:CYS:HA	1.83	0.59
1:A:660:LYS:O	1:A:664:ILE:HG12	2.01	0.59
1:A:242:SER:HB3	1:A:286:VAL:HG21	1.85	0.58
1:A:502:HIS:ND1	1:A:559:THR:HG21	2.18	0.58
1:A:719:PRO:HG3	1:A:745:THR:OG1	2.04	0.58
1:A:534:GLN:O	1:A:538:THR:HG22	2.03	0.57
1:A:654:ILE:HG21	1:A:675:ASN:ND2	2.16	0.57
1:A:320:LYS:HB2	1:A:320:LYS:NZ	2.20	0.57
1:A:324:ARG:O	1:A:325:ALA:HB2	2.04	0.57
1:A:444:ASN:HD21	1:A:499:ASN:HD21	1.53	0.56
1:A:534:GLN:O	1:A:538:THR:CG2	2.54	0.56
1:A:109:THR:HG23	1:A:111:LYS:HG3	1.86	0.55
1:A:299:LEU:HD11	1:A:328:LEU:HD12	1.87	0.55
1:A:120:VAL:O	1:A:124:VAL:HG23	2.07	0.55
1:A:116:ILE:HG22	1:A:117:SER:O	2.07	0.55
1:A:740:MET:HG2	1:A:741:TYR:O	2.05	0.55
1:A:486:ASP:OD1	1:A:503:ARG:NH2	2.39	0.55
1:A:140:ASP:OD1	1:A:166:ARG:NH1	2.40	0.55
1:A:686:THR:CG2	1:A:688:TRP:HD1	2.21	0.54
1:A:106:ASN:OD1	1:A:109:THR:CG2	2.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:368:GLU:O	1:A:372:THR:HB	2.08	0.54
1:A:211:PRO:O	1:A:212:LYS:HD3	2.08	0.53
1:A:539:ILE:HG22	1:A:603:MET:SD	2.49	0.53
1:A:484:VAL:O	1:A:488:ASN:HB2	2.09	0.53
1:A:520:ARG:HH22	1:A:648:ASP:CG	2.15	0.53
1:A:220:LEU:HD13	1:A:425:SER:O	2.09	0.53
1:A:300:TYR:OH	1:A:425:SER:HB3	2.10	0.51
1:A:170:LEU:C	1:A:170:LEU:CD1	2.83	0.51
1:A:203:PRO:HG2	1:A:217:SER:HA	1.93	0.51
1:A:686:THR:HG22	1:A:688:TRP:H	1.75	0.51
1:A:210:THR:HB	1:A:211:PRO:HD2	1.93	0.51
1:A:332:LEU:HD11	1:A:392:ILE:HD12	1.92	0.51
1:A:657:GLU:C	1:A:659:MET:N	2.69	0.50
1:A:662:TYR:CE1	1:A:666:GLN:HG3	2.46	0.50
1:A:688:TRP:HB3	1:A:717:ARG:NH1	2.26	0.50
1:A:654:ILE:C	1:A:656:ASP:H	2.19	0.50
1:A:428:CYS:O	1:A:429:CYS:HB2	2.11	0.49
1:A:731:GLY:HA3	3:A:939:HOH:O	2.12	0.49
1:A:257:SER:HA	1:A:307:ASP:OD2	2.13	0.48
1:A:438:ASP:OD1	1:A:497:LYS:NZ	2.44	0.48
1:A:217:SER:HB3	1:A:445:LEU:CD1	2.39	0.48
1:A:702:ARG:HH11	1:A:710:HIS:CE1	2.31	0.48
1:A:567:GLN:HE21	1:A:567:GLN:N	2.11	0.48
1:A:625:THR:HA	1:A:687:VAL:HG12	1.94	0.48
1:A:109:THR:HG23	1:A:111:LYS:H	1.79	0.48
1:A:662:TYR:CZ	1:A:666:GLN:HG3	2.48	0.48
1:A:306:ALA:HA	1:A:350:LEU:HB3	1.96	0.48
1:A:604:ALA:HB2	1:A:708:GLN:HB2	1.95	0.47
1:A:557:TYR:CE1	1:A:559:THR:CG2	2.96	0.47
1:A:436:ALA:HB1	1:A:437:PRO:HD2	1.95	0.47
1:A:101:LEU:HD22	1:A:115:MET:CE	2.39	0.47
1:A:351:PHE:HE1	1:A:371:TYR:CE1	2.33	0.47
1:A:628:MET:HE1	1:A:639:GLN:HG2	1.97	0.47
1:A:224:LYS:O	1:A:225:GLU:HB2	2.15	0.46
1:A:92:LYS:O	1:A:92:LYS:HG3	2.15	0.46
1:A:166:ARG:HB2	1:A:169:HIS:ND1	2.31	0.46
1:A:606:MET:HB2	1:A:607:PRO:CD	2.47	0.45
1:A:115:MET:HE3	1:A:157:LEU:HD22	1.97	0.45
1:A:324:ARG:O	1:A:325:ALA:CB	2.64	0.45
1:A:557:TYR:CE2	1:A:600:SER:HA	2.51	0.45
1:A:459:ASP:HB3	1:A:460:GLY:H	1.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:725:THR:O	1:A:729:PHE:HD1	2.00	0.45
1:A:691:SER:C	1:A:693:LYS:N	2.74	0.44
1:A:691:SER:C	1:A:693:LYS:H	2.25	0.44
1:A:567:GLN:CA	1:A:567:GLN:NE2	2.63	0.44
1:A:717:ARG:O	1:A:719:PRO:CD	2.62	0.44
1:A:220:LEU:HD13	1:A:425:SER:C	2.43	0.44
1:A:638:PHE:HB3	1:A:639:GLN:H	1.55	0.44
1:A:513:ALA:HB2	1:A:623:PRO:HA	2.00	0.44
1:A:662:TYR:C	1:A:662:TYR:CD1	2.96	0.44
1:A:312:ILE:HG22	1:A:402:PRO:HG3	1.99	0.43
1:A:557:TYR:HE1	1:A:559:THR:CG2	2.31	0.43
1:A:463:SER:HB3	1:A:519:LEU:HD23	2.01	0.43
1:A:273:ILE:HD12	1:A:314:ILE:HD11	2.01	0.43
1:A:315:ARG:HH12	1:A:327:ASP:HA	1.83	0.43
1:A:648:ASP:HB3	1:A:680:LEU:HD11	2.01	0.43
1:A:273:ILE:HB	1:A:274:PRO:HD3	2.01	0.43
1:A:316:LYS:HD3	1:A:318:HIS:HE2	1.84	0.42
1:A:505:ILE:HD13	1:A:505:ILE:HA	1.67	0.42
1:A:413:LYS:HE3	1:A:575:TRP:CE2	2.54	0.42
2:B:6:ASP:O	2:B:6:ASP:CG	2.63	0.42
1:A:728:HIS:CE1	1:A:740:MET:HE3	2.54	0.42
1:A:251:HIS:HB3	1:A:424:SER:HB3	2.00	0.42
1:A:483:ARG:HD2	3:A:906:HOH:O	2.19	0.42
1:A:431:ILE:HG13	1:A:443:CYS:SG	2.59	0.41
1:A:642:ASN:OD1	1:A:642:ASN:C	2.63	0.41
1:A:511:GLY:HA2	1:A:514:ASP:OD2	2.20	0.41
1:A:168:GLN:NE2	1:A:190:TYR:OH	2.43	0.41
1:A:582:MET:HE3	1:A:582:MET:HB2	1.83	0.41
1:A:657:GLU:OE2	1:A:660:LYS:HB3	2.21	0.41
1:A:520:ARG:HH12	1:A:680:LEU:CD2	2.33	0.41
1:A:526:GLU:OE2	1:A:529:ARG:NH1	2.54	0.41
1:A:314:ILE:HD13	1:A:314:ILE:HA	1.73	0.41
1:A:557:TYR:HB3	1:A:598:ARG:O	2.21	0.41
1:A:135:ILE:HG21	1:A:137:TYR:CZ	2.56	0.41
1:A:557:TYR:CZ	1:A:600:SER:HA	2.56	0.41
1:A:240:LEU:O	1:A:243:LYS:HB3	2.20	0.40
1:A:320:LYS:HB2	1:A:320:LYS:HZ2	1.84	0.40
1:A:466:ASN:C	1:A:466:ASN:OD1	2.64	0.40
1:A:686:THR:CG2	1:A:688:TRP:CD1	3.03	0.40
1:A:128:LYS:O	1:A:132:ASN:ND2	2.55	0.40
1:A:220:LEU:N	1:A:220:LEU:HD23	2.36	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	634/888 (71%)	568 (90%)	49 (8%)	17 (3%)	4	7
2	B	4/9 (44%)	3 (75%)	1 (25%)	0	100	100
All	All	638/897 (71%)	571 (90%)	50 (8%)	17 (3%)	4	7

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	321	GLU
1	A	325	ALA
1	A	458	GLU
1	A	459	ASP
1	A	639	GLN
1	A	319	GLY
1	A	619	GLU
1	A	92	LYS
1	A	246	GLY
1	A	620	CYS
1	A	707	ASP
1	A	741	TYR
1	A	655	TRP
1	A	93	GLN
1	A	609	ALA
1	A	718	ALA
1	A	658	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	557/761 (73%)	484 (87%)	73 (13%)	4	8
2	B	6/9 (67%)	6 (100%)	0	100	100
All	All	563/770 (73%)	490 (87%)	73 (13%)	4	8

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	109	THR
1	A	126	GLU
1	A	131	LEU
1	A	141	PHE
1	A	142	GLN
1	A	154	SER
1	A	159	ILE
1	A	162	GLN
1	A	166	ARG
1	A	170	LEU
1	A	176	LEU
1	A	187	LEU
1	A	194	SER
1	A	196	LYS
1	A	214	GLN
1	A	217	SER
1	A	220	LEU
1	A	266	ASN
1	A	268	THR
1	A	281	ASN
1	A	301	LEU
1	A	314	ILE
1	A	317	ASN
1	A	320	LYS
1	A	321	GLU
1	A	322	GLU
1	A	326	ARG
1	A	328	LEU
1	A	337	LEU
1	A	359	LEU
1	A	361	ASP

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Mol	Chain	Res	Type
1	A	372	THR
1	A	381	LYS
1	A	383	ILE
1	A	388	LEU
1	A	427	LEU
1	A	432	VAL
1	A	458	GLU
1	A	461	LYS
1	A	464	THR
1	A	469	LYS
1	A	496	ARG
1	A	505	ILE
1	A	507	LEU
1	A	512	LEU
1	A	518	LEU
1	A	530	LEU
1	A	534	GLN
1	A	538	THR
1	A	559	THR
1	A	567	GLN
1	A	590	LYS
1	A	594	LYS
1	A	606	MET
1	A	613	GLN
1	A	638	PHE
1	A	639	GLN
1	A	640	VAL
1	A	641	VAL
1	A	657	GLU
1	A	659	MET
1	A	660	LYS
1	A	661	GLN
1	A	673	LEU
1	A	679	GLU
1	A	680	LEU
1	A	686	THR
1	A	707	ASP
1	A	712	LEU
1	A	714	LEU
1	A	724	LEU
1	A	743	LEU
1	A	744	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	162	GLN
1	A	168	GLN
1	A	251	HIS
1	A	270	ASN
1	A	317	ASN
1	A	444	ASN
1	A	534	GLN
1	A	567	GLN
1	A	618	ASN
1	A	639	GLN
1	A	661	GLN
1	A	666	GLN
1	A	675	ASN
1	A	692	GLN
1	A	710	HIS
1	A	713	ASN
2	B	2	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 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 ⓘ

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	640/888 (72%)	-0.15	19 (2%) 52 47	26, 41, 81, 96	0
2	B	6/9 (66%)	0.93	1 (16%) 4 3	58, 74, 82, 83	0
All	All	646/897 (72%)	-0.14	20 (3%) 51 45	26, 41, 81, 96	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	146	PHE	4.4
1	A	323	ILE	3.8
1	A	609	ALA	3.2
1	A	321	GLU	3.1
1	A	638	PHE	3.1
1	A	457	SER	2.8
1	A	318	HIS	2.8
1	A	640	VAL	2.8
1	A	266	ASN	2.7
1	A	91	THR	2.7
1	A	629	TYR	2.7
1	A	460	GLY	2.4
1	A	658	GLY	2.4
1	A	742	TYR	2.3
1	A	390	TYR	2.2
1	A	320	LYS	2.1
2	B	3	PHE	2.1
1	A	610	SER	2.1
1	A	617	TYR	2.0
1	A	618	ASN	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.