



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:32 PM UTC

PDB ID : 2FGZ / pdb_00002fgz
Title : Crystal Structure Analysis of apo pullulanase from *Klebsiella pneumoniae*
Authors : Mikami, B.; Iwamoto, H.; Katsuya, Y.; Yoon, H.-J.; Demirkan-Sarikaya, E.; Malle, D.
Deposited on : 2005-12-23
Resolution : 1.75 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

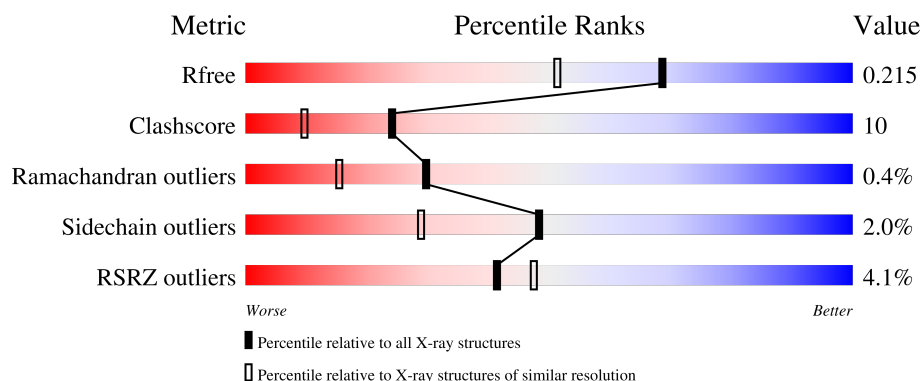
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	1083	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8383 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 Alpha-dextrin endo-1,6-alpha-glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	926	Total	C	N	O	S	0	13	0
			7168	4479	1226	1439	24			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	680	LEU	GLY	conflict	UNP W9BQ28

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	Ca	0	0
			4	4		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1211	Total	O	0	0
			1211	1211		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	148.98Å 60.21Å 132.79Å 90.00° 112.61° 90.00°	Depositor
Resolution (Å)	14.94 – 1.75 14.94 – 1.75	Depositor EDS
% Data completeness (in resolution range)	98.6 (14.94-1.75) 98.5 (14.94-1.75)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.99 (at 1.75Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.183 , 0.214 0.186 , 0.215	Depositor DCC
R_{free} test set	10814 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å ²)	14.9	Xtriage
Anisotropy	0.807	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 59.8	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	0.95	EDS
Total number of atoms	8383	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.03% 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

Bond lengths and bond angles in the following residue types are not validated in this section:
CA

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	0.33	0/7364	0.92	25/10010 (0.2%)

There are no bond length outliers.

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	555	TYR	N-CA-C	7.93	122.16	109.24
1	A	480	PHE	N-CA-C	-7.91	99.44	110.35
1	A	484	THR	N-CA-C	7.32	121.63	113.21
1	A	931	LYS	N-CA-C	6.93	119.42	111.11
1	A	426	ILE	N-CA-C	6.82	119.24	108.87
1	A	652	ARG	N-CA-C	6.77	119.24	111.11
1	A	289	ALA	N-CA-C	6.56	118.98	111.11
1	A	562	PHE	N-CA-C	-6.53	104.24	112.93
1	A	845	LYS	N-CA-C	6.50	121.34	113.41
1	A	520	SER	N-CA-C	-6.29	101.48	110.59
1	A	958	SER	N-CA-C	5.89	118.48	111.71
1	A	280	THR	N-CA-C	5.81	120.49	113.17
1	A	891	SER	N-CA-C	5.80	119.42	112.93
1	A	278	VAL	N-CA-C	5.79	116.28	108.17
1	A	297	TYR	N-CA-C	5.61	118.40	109.81
1	A	904	SER	N-CA-C	-5.50	106.33	113.16
1	A	477	LEU	N-CA-C	-5.47	102.07	110.01
1	A	441	VAL	N-CA-C	-5.40	101.67	108.05
1	A	885	LYS	N-CA-C	-5.33	105.48	112.41
1	A	523	THR	N-CA-C	-5.30	102.67	110.52
1	A	471	VAL	N-CA-C	-5.23	101.99	108.89
1	A	905	LEU	N-CA-C	5.19	118.88	112.24
1	A	1019	SER	N-CA-C	-5.14	102.08	110.20
1	A	718	ILE	N-CA-C	5.11	115.62	110.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	481	ASP	N-CA-C	5.03	116.67	108.63

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	7168	0	6904	141	0
2	A	4	0	0	0	0
3	A	1211	0	0	19	1
All	All	8383	0	6904	141	1

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 10.

All (141) 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:680:LEU:HD22	1:A:707:GLY:HA3	1.48	0.95
1:A:680:LEU:HG	1:A:710:SER:CB	2.01	0.90
1:A:680:LEU:HD13	1:A:708:TRP:H	1.39	0.88
1:A:978:ASN:HD21	1:A:984:GLN:H	1.19	0.86
1:A:680:LEU:HG	1:A:710:SER:HB3	1.61	0.83
1:A:606:ASN:HD21	1:A:607:HIS:HD2	1.25	0.82
1:A:680:LEU:HD11	1:A:710:SER:H	1.44	0.81
1:A:680:LEU:HD13	1:A:708:TRP:N	1.99	0.78
1:A:987:LEU:HD21	1:A:1022:LEU:HD21	1.65	0.78
1:A:722[B]:ILE:HD11	3:A:1809:HOH:O	1.83	0.77
1:A:680:LEU:HG	1:A:710:SER:HB2	1.67	0.77
1:A:654:PHE:O	1:A:658[B]:ILE:HG12	1.85	0.76
1:A:680:LEU:CD1	1:A:710:SER:H	2.00	0.73
1:A:680:LEU:HD11	1:A:709:ASP:H	1.52	0.72
1:A:1039:ALA:HB3	1:A:1043:SER:HB2	1.71	0.72
1:A:680:LEU:HD11	1:A:709:ASP:N	2.05	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1013[B]:ILE:HD13	1:A:1063:VAL:HG13	1.69	0.72
1:A:229:ASN:ND2	1:A:232:VAL:H	1.86	0.72
1:A:229:ASN:HD21	1:A:232:VAL:HG23	1.56	0.71
1:A:627:TYR:O	1:A:651:HIS:HD2	1.74	0.70
1:A:680:LEU:HD21	3:A:1411:HOH:O	1.91	0.70
1:A:606:ASN:ND2	1:A:607:HIS:HD2	1.89	0.70
1:A:722[B]:ILE:HG12	3:A:1584:HOH:O	1.92	0.69
1:A:680:LEU:CD2	1:A:707:GLY:HA3	2.24	0.67
1:A:229:ASN:HD21	1:A:232:VAL:H	1.41	0.66
1:A:605:TYR:CD1	1:A:658[B]:ILE:HD12	2.31	0.66
1:A:682:HIS:HD2	1:A:686:GLN:HE22	1.44	0.65
1:A:1030:LEU:HG	1:A:1066:LEU:HB3	1.78	0.65
1:A:1013[B]:ILE:CD1	1:A:1063:VAL:HG13	2.28	0.64
1:A:680:LEU:CG	1:A:710:SER:HB3	2.28	0.63
1:A:682:HIS:HD2	1:A:686:GLN:NE2	1.98	0.62
1:A:708:TRP:N	1:A:708:TRP:CE3	2.69	0.61
1:A:722[B]:ILE:HD12	3:A:2353:HOH:O	2.01	0.60
1:A:560:ASP:HB3	1:A:609:ASN:ND2	2.17	0.59
1:A:675[A]:ARG:HD3	1:A:732:PHE:HE2	1.67	0.59
1:A:251:VAL:HG12	3:A:2279:HOH:O	2.03	0.59
1:A:642:THR:O	1:A:643:CYS:HB3	2.03	0.58
1:A:322:ILE:HG22	1:A:330:ILE:HD11	1.83	0.58
1:A:680:LEU:CD2	1:A:680:LEU:H	2.15	0.58
1:A:223:LEU:CD2	1:A:247:LEU:HG	2.34	0.58
1:A:675[B]:ARG:NH1	1:A:677:ASP:HA	2.19	0.58
1:A:219:LYS:NZ	1:A:219:LYS:HB3	2.19	0.58
1:A:654:PHE:CZ	1:A:658[B]:ILE:HD11	2.39	0.57
1:A:750:ASP:O	1:A:754:GLN:HG3	2.05	0.57
1:A:495:ILE:HA	1:A:524:VAL:HB	1.87	0.56
1:A:219:LYS:HB3	1:A:219:LYS:HZ2	1.72	0.55
1:A:272:LEU:C	1:A:272:LEU:HD23	2.32	0.55
1:A:706:GLU:HG2	1:A:707:GLY:N	2.21	0.55
1:A:465:GLN:HG3	1:A:950:GLN:HE22	1.73	0.54
1:A:675[A]:ARG:HD3	1:A:732:PHE:CE2	2.43	0.54
1:A:680:LEU:H	1:A:680:LEU:HD23	1.72	0.53
1:A:680:LEU:HD23	1:A:680:LEU:N	2.23	0.53
1:A:430:HIS:CD2	1:A:432:ARG:H	2.26	0.53
1:A:222:LYS:NZ	1:A:222:LYS:HB3	2.23	0.53
1:A:682:HIS:CD2	1:A:686:GLN:HE22	2.24	0.53
1:A:430:HIS:HD2	1:A:433:ASP:H	1.55	0.53
1:A:642:THR:O	1:A:643:CYS:CB	2.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:MET:HE1	3:A:1395:HOH:O	2.09	0.52
1:A:996:MET:HE3	3:A:2193:HOH:O	2.09	0.52
1:A:1052:ALA:C	1:A:1054:GLY:H	2.18	0.52
1:A:258:GLN:HE22	1:A:316:GLN:HA	1.75	0.52
1:A:238:HIS:HE1	3:A:1438:HOH:O	1.92	0.51
1:A:387:ASN:ND2	1:A:487:GLU:H	2.07	0.51
1:A:197:ILE:HB	1:A:266:ALA:HB3	1.92	0.51
1:A:523:THR:OG1	1:A:526:GLU:HG3	2.11	0.51
1:A:246[B]:LYS:HD3	1:A:247:LEU:O	2.09	0.51
1:A:680:LEU:CD1	1:A:708:TRP:N	2.70	0.51
1:A:834:ASP:O	1:A:835:ASN:HB2	2.10	0.51
1:A:229:ASN:HD21	1:A:232:VAL:CG2	2.23	0.51
1:A:260:GLU:HB2	1:A:364:TYR:CE1	2.46	0.51
1:A:951[B]:GLU:OE1	1:A:1036:GLN:HG2	2.10	0.51
1:A:496:GLN:NE2	1:A:496:GLN:H	2.09	0.50
1:A:745:PRO:HA	3:A:2486:HOH:O	2.12	0.50
1:A:693[B]:ARG:NH2	3:A:1576:HOH:O	2.44	0.50
1:A:657:LEU:C	1:A:657:LEU:HD23	2.37	0.50
1:A:592:LYS:HE2	1:A:672:ASP:OD2	2.12	0.50
1:A:706:GLU:CG	1:A:707:GLY:N	2.74	0.49
1:A:606:ASN:ND2	1:A:607:HIS:CD2	2.75	0.49
1:A:411:MET:HG2	1:A:672:ASP:OD1	2.13	0.49
1:A:675[A]:ARG:HG2	1:A:704:PHE:CE2	2.48	0.49
1:A:886:SER:O	1:A:887:PHE:HB2	2.12	0.49
1:A:643:CYS:SG	1:A:644:CYS:N	2.86	0.49
1:A:978:ASN:ND2	1:A:984:GLN:H	2.00	0.49
1:A:317:GLN:HB2	1:A:362:THR:HB	1.95	0.48
1:A:377:THR:OG1	1:A:563:HIS:HE1	1.95	0.48
1:A:204:HIS:HE1	3:A:1651:HOH:O	1.96	0.48
1:A:229:ASN:C	1:A:229:ASN:HD22	2.21	0.47
1:A:797:LEU:HD12	1:A:797:LEU:C	2.38	0.47
1:A:222:LYS:HB3	1:A:222:LYS:HZ3	1.78	0.47
1:A:252:ASN:C	1:A:252:ASN:HD22	2.22	0.47
1:A:418:LYS:HD2	1:A:966[B]:ASP:OD1	2.15	0.47
1:A:465:GLN:HG3	1:A:950:GLN:NE2	2.28	0.47
1:A:680:LEU:CD2	1:A:680:LEU:N	2.78	0.47
1:A:543:GLN:HE21	1:A:916:ARG:HA	1.81	0.46
1:A:416:LYS:HE2	3:A:1649:HOH:O	2.15	0.46
1:A:38:PRO:HG2	1:A:172:PHE:CE2	2.51	0.46
1:A:785:ARG:NH2	3:A:1603:HOH:O	2.49	0.45
1:A:875:ASP:OD1	1:A:879:SER:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:413:HIS:HD2	3:A:1488:HOH:O	1.99	0.45
1:A:708:TRP:N	1:A:708:TRP:CD2	2.84	0.45
1:A:230:GLN:O	1:A:234:MET:HG2	2.17	0.45
1:A:1014:ASN:HD21	1:A:1020:ARG:HH11	1.64	0.45
1:A:272:LEU:HD23	1:A:273:SER:N	2.32	0.44
1:A:955:LEU:HD13	1:A:1065:VAL:HG21	1.99	0.44
1:A:229:ASN:ND2	1:A:229:ASN:C	2.74	0.44
1:A:183:ASP:OD2	1:A:183:ASP:C	2.61	0.44
1:A:238:HIS:H	1:A:238:HIS:CD2	2.36	0.44
1:A:226:THR:HG21	1:A:246[A]:LYS:HD3	1.99	0.44
1:A:708:TRP:HB2	3:A:1786:HOH:O	2.18	0.44
1:A:264:ILE:HG12	1:A:275:ALA:CB	2.48	0.43
1:A:195:LYS:HG2	1:A:265:ALA:HB1	2.01	0.43
1:A:977:ARG:NH2	3:A:1636:HOH:O	2.52	0.43
1:A:337:ARG:HD2	1:A:344:TRP:CZ2	2.54	0.43
1:A:841:MET:HE1	3:A:2018:HOH:O	2.17	0.43
1:A:708:TRP:CH2	1:A:731:THR:HB	2.54	0.43
1:A:555:TYR:C	1:A:555:TYR:CD1	2.97	0.42
1:A:366:PRO:HB2	1:A:626:TRP:CE2	2.55	0.42
1:A:481:ASP:OD2	1:A:563:HIS:HD2	2.02	0.42
1:A:1028:THR:O	1:A:1029:SER:HB2	2.19	0.42
1:A:1066:LEU:HD22	1:A:1066:LEU:N	2.35	0.42
1:A:199:ARG:HD3	1:A:220:TYR:CD2	2.54	0.42
1:A:384:LEU:HD23	1:A:391:SER:HA	2.00	0.42
1:A:1052:ALA:C	1:A:1054:GLY:N	2.78	0.42
1:A:392:GLN:HE22	1:A:577:GLY:HA2	1.85	0.42
1:A:168:PHE:O	1:A:171:ALA:HB3	2.19	0.42
1:A:388:SER:HB2	1:A:562:PHE:CE1	2.54	0.42
1:A:753:ARG:HD2	1:A:930:VAL:HG11	2.01	0.42
1:A:946:THR:O	1:A:950:GLN:HG3	2.20	0.41
1:A:973:ARG:HG2	1:A:998:ALA:HB1	2.01	0.41
1:A:267:GLU:HA	1:A:267:GLU:OE1	2.20	0.41
1:A:654:PHE:CE1	1:A:658[B]:ILE:HD11	2.55	0.41
1:A:465:GLN:NE2	3:A:2099:HOH:O	2.53	0.41
1:A:176:LEU:HA	3:A:1854:HOH:O	2.20	0.41
1:A:223:LEU:HD22	1:A:247:LEU:HG	2.03	0.41
1:A:682:HIS:CD2	1:A:686:GLN:NE2	2.83	0.41
1:A:890:ASP:HB3	1:A:916:ARG:HH21	1.86	0.41
1:A:690:ALA:O	1:A:694:ILE:HG12	2.21	0.41
1:A:222:LYS:NZ	1:A:222:LYS:CB	2.84	0.40
1:A:38:PRO:HG3	1:A:271:ILE:CG2	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:187:LEU:C	1:A:187:LEU:HD13	2.47	0.40
1:A:560:ASP:HB3	1:A:609:ASN:HD22	1.85	0.40

All (1) 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)
3:A:2098:HOH:O	3:A:2098:HOH:O[2_756]	1.96	0.24

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	935/1083 (86%)	912 (98%)	19 (2%)	4 (0%)	30 15

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	643	CYS
1	A	478	PRO
1	A	167	ALA
1	A	707	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	774/891 (87%)	759 (98%)	15 (2%)	50 31

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	184	LYS
1	A	229	ASN
1	A	374	TYR
1	A	387	ASN
1	A	391	SER
1	A	478	PRO
1	A	482	LEU
1	A	496	GLN
1	A	504	GLU
1	A	543	GLN
1	A	708	TRP
1	A	709	ASP
1	A	859	GLN
1	A	1037	GLN
1	A	1066	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	194	ASN
1	A	204	HIS
1	A	229	ASN
1	A	230	GLN
1	A	238	HIS
1	A	252	ASN
1	A	258	GLN
1	A	277	GLN
1	A	316	GLN
1	A	387	ASN
1	A	392	GLN
1	A	413	HIS
1	A	430	HIS
1	A	439	GLN
1	A	455	GLN
1	A	458	ASN
1	A	461	GLN
1	A	496	GLN

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Mol	Chain	Res	Type
1	A	533	GLN
1	A	534	ASN
1	A	541	GLN
1	A	543	GLN
1	A	551	GLN
1	A	563	HIS
1	A	606	ASN
1	A	607	HIS
1	A	609	ASN
1	A	629	GLN
1	A	651	HIS
1	A	682	HIS
1	A	686	GLN
1	A	712	GLN
1	A	723	ASN
1	A	859	GLN
1	A	899	ASN
1	A	906	GLN
1	A	911	ASN
1	A	944	GLN
1	A	950	GLN
1	A	978	ASN
1	A	984	GLN
1	A	1014	ASN
1	A	1023	GLN
1	A	1037	GLN
1	A	1049	GLN
1	A	1074	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

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	926/1083 (85%)	-0.05	38 (4%)	41 47	6, 17, 43, 70	13 (1%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	168	PHE	9.4
1	A	167	ALA	6.4
1	A	169	ARG	4.2
1	A	266	ALA	4.0
1	A	708	TRP	4.0
1	A	172	PHE	3.8
1	A	35	VAL	3.6
1	A	171	ALA	3.4
1	A	166	ASP	3.4
1	A	214	GLY	3.2
1	A	1052	ALA	3.2
1	A	170	ALA	3.1
1	A	34	VAL	3.1
1	A	746	PHE	3.0
1	A	707	GLY	2.9
1	A	33	VAL	2.9
1	A	39	ASP	2.7
1	A	173	GLY	2.7
1	A	268	SER	2.7
1	A	1027	GLY	2.7
1	A	213	ASN	2.6
1	A	303	ASP	2.5
1	A	1026	ALA	2.5
1	A	228	VAL	2.5
1	A	1051	ALA	2.4
1	A	212	SER	2.4
1	A	1028	THR	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	217	SER	2.4
1	A	1053	ASP	2.4
1	A	271	ILE	2.3
1	A	1030	LEU	2.3
1	A	37	LEU	2.2
1	A	247	LEU	2.2
1	A	208	VAL	2.2
1	A	267	GLU	2.1
1	A	230	GLN	2.1
1	A	1022	LEU	2.1
1	A	304	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CA	A	1193	1/1	0.95	0.07	38,38,38,38	0
2	CA	A	1192	1/1	0.97	0.17	32,32,32,32	0
2	CA	A	1194	1/1	0.99	0.06	16,16,16,16	0
2	CA	A	1191	1/1	1.00	0.03	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.