



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 05:07 AM UTC

PDB ID : 1WNS / pdb_00001wns
Title : Crystal structure of family B DNA polymerase from hyperthermophilic archaeon pyrococcus kodakaraensis KOD1
Authors : Hashimoto, H.; Inoue, T.; Kai, Y.; Fujiwara, S.; Takagi, M.; Nishioka, M.; Imanaka, T.
Deposited on : 2004-08-09
Resolution : 3.00 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

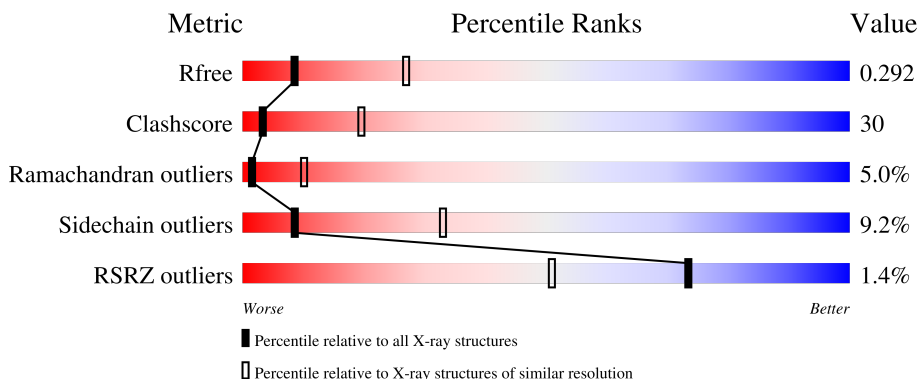
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	774	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5703 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.

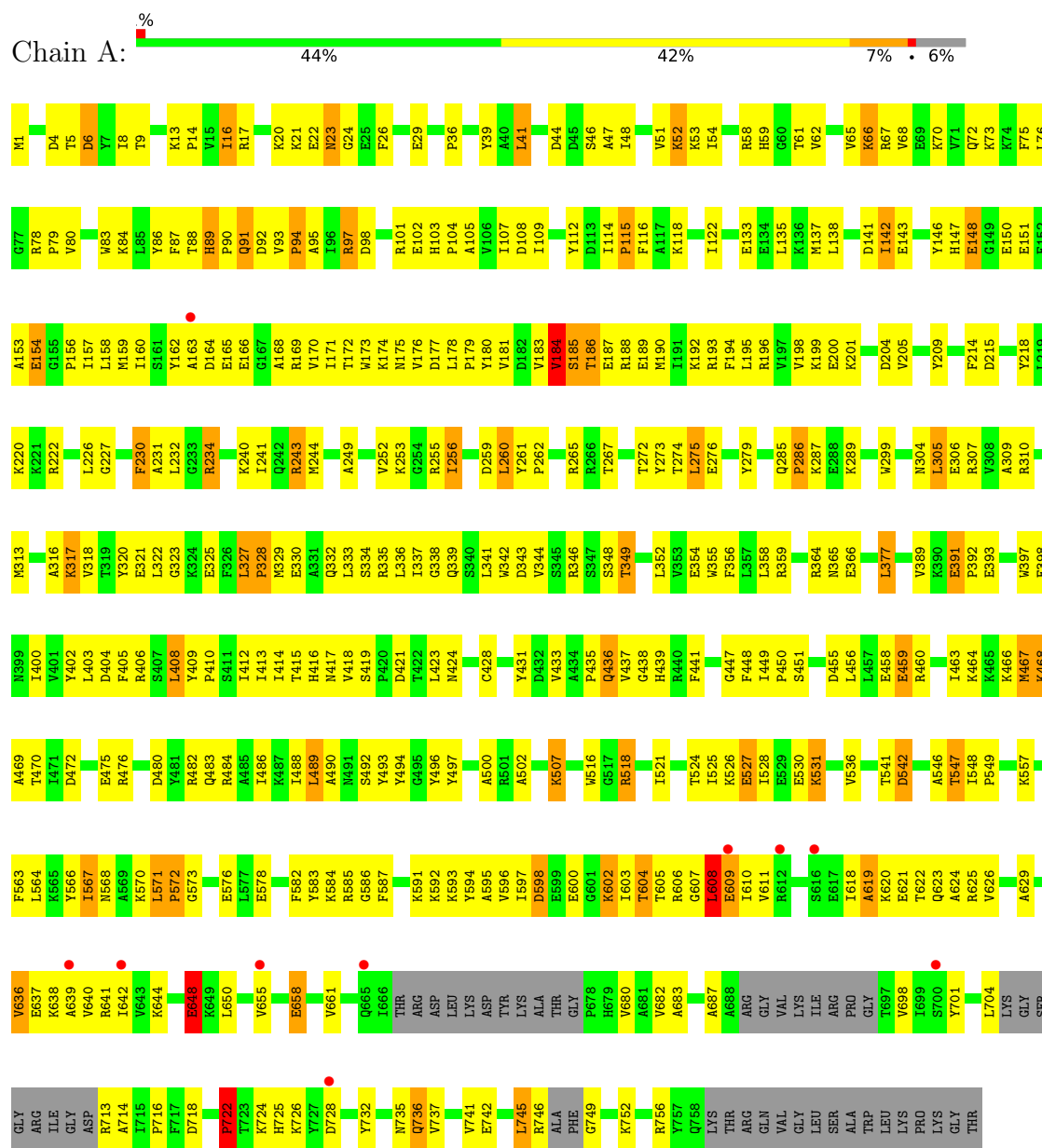
- Molecule 1 is a protein called DNA POLYMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	729	Total	C	N	O	S	0	0	0
			5703	3656	962	1069	16			

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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.64Å 111.38Å 111.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.24 – 3.00 35.24 – 3.00	Depositor EDS
% Data completeness (in resolution range)	89.2 (35.24-3.00) 89.2 (35.24-3.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.42 (at 2.81Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.231 , 0.313 0.209 , 0.292	Depositor DCC
R_{free} test set	737 reflections (3.63%)	wwPDB-VP
Wilson B-factor (Å ²)	48.9	Xtriage
Anisotropy	0.493	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 58.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.024 for -h,l,k	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5703	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.18% 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	0.45	0/5824	0.93	16/7885 (0.2%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	716	PRO	N-CA-CB	10.10	110.10	102.73
1	A	305	LEU	N-CA-C	-7.01	104.85	113.19
1	A	571	LEU	CA-C-N	6.74	128.27	119.84
1	A	571	LEU	C-N-CA	6.74	128.27	119.84
1	A	722	PRO	N-CA-CB	6.42	109.99	103.25
1	A	89	HIS	CA-C-N	6.25	125.99	119.05
1	A	89	HIS	C-N-CA	6.25	125.99	119.05
1	A	256	ILE	CB-CA-C	-6.16	104.25	111.09
1	A	352	LEU	N-CA-C	-5.82	104.57	111.03
1	A	648	GLU	N-CA-C	-5.76	105.91	113.17
1	A	260	LEU	N-CA-C	5.66	117.45	111.28
1	A	718	ASP	N-CA-C	-5.65	104.27	113.19
1	A	619	ALA	N-CA-C	-5.48	106.48	112.72
1	A	502	ALA	N-CA-C	5.41	118.17	110.10
1	A	460	ARG	N-CA-C	-5.41	104.79	111.33
1	A	321	GLU	N-CA-C	-5.07	105.44	110.97

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	5703	0	5398	337	0
All	All	5703	0	5398	337	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 30.

All (337) 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:150:GLU:HB2	1:A:154:GLU:HG3	1.42	1.00
1:A:276:GLU:HG3	1:A:287:LYS:HD2	1.44	0.99
1:A:636:VAL:HG23	1:A:637:GLU:H	1.27	0.98
1:A:188:ARG:HD2	1:A:226:LEU:HD22	1.52	0.89
1:A:619:ALA:HB1	1:A:737:VAL:HG22	1.58	0.85
1:A:103:HIS:ND1	1:A:104:PRO:HD2	1.91	0.84
1:A:174:LYS:HB2	1:A:299:TRP:CH2	2.13	0.83
1:A:159:MET:HE2	1:A:170:VAL:HG11	1.61	0.82
1:A:586:GLY:HA3	1:A:596:VAL:HG12	1.63	0.80
1:A:72:GLN:H	1:A:72:GLN:CD	1.90	0.80
1:A:1:MET:HE2	1:A:135:LEU:HD21	1.61	0.79
1:A:680:VAL:HA	1:A:683:ALA:HB3	1.64	0.79
1:A:118:LYS:HG3	1:A:339:GLN:HE22	1.46	0.78
1:A:567:ILE:O	1:A:571:LEU:HG	1.84	0.76
1:A:417:ASN:HD21	1:A:447:GLY:H	1.34	0.76
1:A:304:ASN:OD1	1:A:306:GLU:HB2	1.87	0.74
1:A:66:LYS:HD3	1:A:88:THR:HG22	1.69	0.73
1:A:157:ILE:O	1:A:190:MET:HE1	1.89	0.71
1:A:93:VAL:HB	1:A:94:PRO:HD3	1.71	0.71
1:A:449:ILE:HB	1:A:450:PRO:HD3	1.71	0.71
1:A:244:MET:HE2	1:A:249:ALA:HB2	1.72	0.71
1:A:682:VAL:HG22	1:A:713:ARG:O	1.91	0.71
1:A:118:LYS:HE3	1:A:343:ASP:OD2	1.92	0.70
1:A:464:LYS:O	1:A:467:MET:HB2	1.92	0.70
1:A:598:ASP:OD2	1:A:602:LYS:HB3	1.93	0.68
1:A:89:HIS:O	1:A:92:ASP:HB2	1.94	0.68
1:A:174:LYS:O	1:A:183:VAL:HG13	1.94	0.67
1:A:704:LEU:H	1:A:713:ARG:N	1.90	0.67
1:A:147:HIS:O	1:A:150:GLU:HG2	1.93	0.67
1:A:636:VAL:HG23	1:A:637:GLU:N	2.07	0.67
1:A:8:ILE:HD11	1:A:17:ARG:CZ	2.25	0.67
1:A:115:PRO:HB2	1:A:118:LYS:HD3	1.75	0.67
1:A:73:LYS:HA	1:A:365:ASN:ND2	2.11	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:VAL:O	1:A:95:ALA:N	2.29	0.66
1:A:417:ASN:HD22	1:A:450:PRO:HG2	1.58	0.66
1:A:428:CYS:HB2	1:A:431:TYR:CZ	2.31	0.66
1:A:466:LYS:O	1:A:470:THR:HG23	1.96	0.65
1:A:637:GLU:O	1:A:641:ARG:HG3	1.97	0.65
1:A:172:THR:O	1:A:183:VAL:HA	1.98	0.64
1:A:171:ILE:HG22	1:A:190:MET:HG3	1.79	0.64
1:A:334:SER:HA	1:A:344:VAL:HG21	1.78	0.64
1:A:70:LYS:HD3	1:A:83:TRP:CZ2	2.33	0.63
1:A:276:GLU:HG2	1:A:289:LYS:HB2	1.79	0.63
1:A:89:HIS:ND1	1:A:90:PRO:HD2	2.13	0.63
1:A:307:ARG:HG2	1:A:310:ARG:HH21	1.63	0.63
1:A:184:VAL:HG12	1:A:185:SER:H	1.64	0.63
1:A:118:LYS:HG3	1:A:339:GLN:NE2	2.12	0.63
1:A:97:ARG:HG3	1:A:98:ASP:H	1.64	0.63
1:A:622:THR:O	1:A:626:VAL:HG23	2.00	0.62
1:A:456:LEU:HD11	1:A:489:LEU:HD13	1.81	0.62
1:A:318:VAL:HG12	1:A:322:LEU:HD12	1.81	0.61
1:A:468:LYS:C	1:A:470:THR:H	2.08	0.61
1:A:196:ARG:O	1:A:200:GLU:HB2	1.99	0.60
1:A:332:GLN:HE22	1:A:335:ARG:HD3	1.64	0.60
1:A:159:MET:HE2	1:A:170:VAL:CG1	2.31	0.60
1:A:160:ILE:HB	1:A:171:ILE:HB	1.83	0.60
1:A:722:PRO:N	1:A:726:LYS:HE2	2.16	0.60
1:A:417:ASN:ND2	1:A:450:PRO:HG2	2.15	0.60
1:A:456:LEU:HD22	1:A:486:ILE:HG23	1.84	0.59
1:A:644:LYS:O	1:A:648:GLU:HB2	2.02	0.59
1:A:732:TYR:HA	1:A:736:GLN:HB2	1.84	0.59
1:A:98:ASP:O	1:A:102:GLU:HG3	2.02	0.59
1:A:122:ILE:CG2	1:A:359:ARG:HA	2.33	0.59
1:A:470:THR:OG1	1:A:476:ARG:HG2	2.02	0.59
1:A:285:GLN:HB3	1:A:286:PRO:HD2	1.84	0.59
1:A:472:ASP:O	1:A:476:ARG:HG3	2.03	0.59
1:A:638:LYS:O	1:A:642:ILE:HG13	2.02	0.59
1:A:58:ARG:HH12	1:A:91:GLN:NE2	2.01	0.59
1:A:103:HIS:ND1	1:A:104:PRO:CD	2.66	0.59
1:A:435:PRO:O	1:A:437:VAL:N	2.35	0.58
1:A:93:VAL:C	1:A:95:ALA:H	2.12	0.58
1:A:158:LEU:C	1:A:159:MET:HG3	2.29	0.58
1:A:97:ARG:HG3	1:A:98:ASP:N	2.19	0.58
1:A:409:TYR:O	1:A:413:ILE:HG13	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:602:LYS:HG2	1:A:604:THR:H	1.68	0.58
1:A:138:LEU:HD11	1:A:162:TYR:HB2	1.87	0.57
1:A:436:GLN:HG3	1:A:518:ARG:HH22	1.69	0.57
1:A:122:ILE:HG23	1:A:359:ARG:HA	1.86	0.57
1:A:79:PRO:O	1:A:80:VAL:HG13	2.04	0.57
1:A:619:ALA:CB	1:A:737:VAL:HG22	2.33	0.57
1:A:163:ALA:O	1:A:164:ASP:HB3	2.04	0.57
1:A:608:LEU:HD13	1:A:609:GLU:N	2.20	0.57
1:A:299:TRP:HA	1:A:305:LEU:HD21	1.87	0.57
1:A:557:LYS:HE2	1:A:582:PHE:CG	2.40	0.56
1:A:51:VAL:O	1:A:54:ILE:HG12	2.04	0.56
1:A:84:LYS:HD3	1:A:86:TYR:OH	2.05	0.56
1:A:377:LEU:HD23	1:A:500:ALA:HB1	1.87	0.56
1:A:447:GLY:O	1:A:450:PRO:HD2	2.06	0.56
1:A:521:ILE:O	1:A:524:THR:HG22	2.05	0.56
1:A:147:HIS:HB2	1:A:150:GLU:OE1	2.04	0.56
1:A:447:GLY:C	1:A:450:PRO:HD2	2.31	0.56
1:A:16:ILE:HD12	1:A:116:PHE:CE2	2.41	0.56
1:A:73:LYS:HA	1:A:365:ASN:HD21	1.70	0.56
1:A:405:PHE:HZ	1:A:524:THR:HG21	1.71	0.56
1:A:418:VAL:HG13	1:A:441:PHE:CE2	2.41	0.55
1:A:620:LYS:O	1:A:623:GLN:HB3	2.06	0.55
1:A:483:GLN:HE22	1:A:484:ARG:HG3	1.70	0.55
1:A:546:ALA:O	1:A:547:THR:HB	2.05	0.55
1:A:607:GLY:O	1:A:608:LEU:HB3	2.06	0.55
1:A:260:LEU:HD21	1:A:323:GLY:HA2	1.87	0.55
1:A:279:TYR:HD2	1:A:287:LYS:HB2	1.72	0.55
1:A:21:LYS:HD2	1:A:204:ASP:OD1	2.07	0.55
1:A:621:GLU:O	1:A:625:ARG:HG2	2.07	0.54
1:A:525:ILE:HG23	1:A:536:VAL:HG21	1.89	0.54
1:A:52:LYS:HG3	1:A:53:LYS:HE3	1.89	0.54
1:A:157:ILE:HG13	1:A:222:ARG:HG3	1.89	0.54
1:A:595:ALA:HA	1:A:605:THR:CB	2.38	0.54
1:A:198:VAL:HG11	1:A:232:LEU:HD22	1.90	0.54
1:A:67:ARG:HG2	1:A:68:VAL:N	2.23	0.53
1:A:137:MET:HG2	1:A:205:VAL:HB	1.90	0.53
1:A:397:TRP:O	1:A:585:ARG:HA	2.07	0.53
1:A:304:ASN:C	1:A:306:GLU:H	2.16	0.53
1:A:164:ASP:OD1	1:A:165:GLU:N	2.41	0.53
1:A:168:ALA:HB2	1:A:317:LYS:HG2	1.89	0.52
1:A:348:SER:O	1:A:349:THR:C	2.51	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:THR:OG1	1:A:187:GLU:N	2.43	0.52
1:A:464:LYS:HA	1:A:467:MET:HG3	1.91	0.52
1:A:745:LEU:O	1:A:746:ARG:HG2	2.10	0.52
1:A:567:ILE:HD12	1:A:568:ASN:N	2.25	0.52
1:A:279:TYR:CD2	1:A:287:LYS:HB2	2.44	0.52
1:A:480:ASP:O	1:A:483:GLN:HG3	2.09	0.52
1:A:47:ALA:CB	1:A:105:ALA:HB1	2.40	0.52
1:A:93:VAL:C	1:A:95:ALA:N	2.67	0.52
1:A:507:LYS:HA	1:A:507:LYS:HE2	1.92	0.51
1:A:530:GLU:O	1:A:531:LYS:HG3	2.10	0.51
1:A:158:LEU:HD22	1:A:299:TRP:CD2	2.44	0.51
1:A:160:ILE:HD12	1:A:190:MET:HG2	1.93	0.51
1:A:256:ILE:HG21	1:A:341:LEU:HD23	1.92	0.51
1:A:333:LEU:O	1:A:337:ILE:HG12	2.10	0.51
1:A:419:SER:HB3	1:A:421:ASP:OD1	2.10	0.51
1:A:89:HIS:CE1	1:A:90:PRO:HD2	2.46	0.51
1:A:272:THR:HG22	1:A:274:THR:HG23	1.93	0.51
1:A:287:LYS:HD3	1:A:287:LYS:C	2.35	0.51
1:A:48:ILE:HG12	1:A:83:TRP:CZ3	2.46	0.51
1:A:109:ILE:HG22	1:A:112:TYR:CD2	2.46	0.51
1:A:114:ILE:HD12	1:A:114:ILE:N	2.26	0.51
1:A:398:GLU:HA	1:A:584:LYS:O	2.11	0.50
1:A:26:PHE:CE1	1:A:234:ARG:HG2	2.47	0.50
1:A:596:VAL:HG22	1:A:605:THR:CB	2.42	0.50
1:A:625:ARG:HG3	1:A:625:ARG:HH11	1.76	0.50
1:A:752:LYS:O	1:A:756:ARG:HG3	2.11	0.50
1:A:175:ASN:OD1	1:A:183:VAL:HG21	2.11	0.50
1:A:75:PHE:O	1:A:76:LEU:HB2	2.12	0.50
1:A:195:LEU:HD12	1:A:230:PHE:CD2	2.47	0.50
1:A:563:PHE:O	1:A:564:LEU:C	2.55	0.50
1:A:603:ILE:O	1:A:604:THR:C	2.55	0.50
1:A:177:ASP:C	1:A:178:LEU:HG	2.38	0.49
1:A:409:TYR:HB2	1:A:410:PRO:HD3	1.95	0.49
1:A:423:LEU:C	1:A:423:LEU:HD13	2.37	0.49
1:A:602:LYS:C	1:A:604:THR:N	2.70	0.49
1:A:160:ILE:CD1	1:A:190:MET:HG2	2.42	0.49
1:A:524:THR:HG23	1:A:525:ILE:N	2.26	0.49
1:A:39:TYR:CZ	1:A:73:LYS:HE3	2.48	0.49
1:A:103:HIS:NE2	1:A:105:ALA:HB3	2.27	0.49
1:A:408:LEU:O	1:A:412:ILE:HG13	2.12	0.49
1:A:41:LEU:HB3	1:A:107:ILE:HB	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:THR:CG2	1:A:189:GLU:HG2	2.43	0.48
1:A:44:ASP:C	1:A:46:SER:H	2.21	0.48
1:A:65:VAL:HG22	1:A:87:PHE:HE2	1.79	0.48
1:A:626:VAL:HG13	1:A:639:ALA:HB1	1.95	0.48
1:A:14:PRO:HG3	1:A:90:PRO:HD3	1.94	0.48
1:A:198:VAL:HG11	1:A:232:LEU:CD2	2.42	0.48
1:A:330:GLU:HB3	1:A:341:LEU:HD11	1.96	0.48
1:A:408:LEU:HD22	1:A:542:ASP:HA	1.94	0.48
1:A:22:GLU:O	1:A:23:ASN:C	2.55	0.48
1:A:259:ASP:O	1:A:262:PRO:HD2	2.13	0.48
1:A:265:ARG:HD3	1:A:273:TYR:CE2	2.48	0.48
1:A:36:PRO:HG3	1:A:116:PHE:CE1	2.49	0.48
1:A:417:ASN:HD21	1:A:447:GLY:N	2.07	0.48
1:A:101:ARG:HG3	1:A:109:ILE:HD13	1.94	0.48
1:A:583:TYR:N	1:A:583:TYR:CD1	2.82	0.48
1:A:741:VAL:O	1:A:745:LEU:HG	2.13	0.48
1:A:564:LEU:HA	1:A:567:ILE:HD11	1.96	0.48
1:A:67:ARG:NH1	1:A:67:ARG:HB3	2.29	0.47
1:A:327:LEU:N	1:A:328:PRO:CD	2.76	0.47
1:A:22:GLU:O	1:A:24:GLY:N	2.47	0.47
1:A:468:LYS:C	1:A:470:THR:N	2.70	0.47
1:A:475:GLU:HA	1:A:475:GLU:OE1	2.14	0.47
1:A:489:LEU:HD22	1:A:493:TYR:CE1	2.50	0.47
1:A:356:PHE:CD1	1:A:489:LEU:HD11	2.50	0.47
1:A:608:LEU:HD22	1:A:608:LEU:O	2.15	0.47
1:A:20:LYS:NZ	1:A:29:GLU:OE2	2.46	0.47
1:A:265:ARG:HA	1:A:273:TYR:CE2	2.49	0.47
1:A:335:ARG:NE	1:A:482:ARG:NH2	2.63	0.47
1:A:527:GLU:OE2	1:A:570:LYS:HE2	2.14	0.47
1:A:184:VAL:HG12	1:A:185:SER:N	2.30	0.47
1:A:597:ILE:HG23	1:A:597:ILE:O	2.15	0.47
1:A:732:TYR:O	1:A:736:GLN:HB2	2.15	0.47
1:A:404:ASP:OD2	1:A:578:GLU:OE2	2.33	0.47
1:A:78:ARG:HG2	1:A:78:ARG:NH1	2.30	0.46
1:A:153:ALA:HA	1:A:218:TYR:CZ	2.51	0.46
1:A:450:PRO:O	1:A:451:SER:C	2.58	0.46
1:A:89:HIS:ND1	1:A:90:PRO:CD	2.77	0.46
1:A:608:LEU:HD22	1:A:608:LEU:C	2.41	0.46
1:A:70:LYS:HD3	1:A:83:TRP:CE2	2.49	0.46
1:A:93:VAL:CB	1:A:94:PRO:HD3	2.45	0.46
1:A:21:LYS:HE2	1:A:204:ASP:OD2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:ARG:NH1	1:A:192:LYS:HD2	2.30	0.46
1:A:746:ARG:HA	1:A:749:GLY:N	2.31	0.46
1:A:36:PRO:HD2	1:A:87:PHE:O	2.16	0.46
1:A:58:ARG:NH1	1:A:91:GLN:NE2	2.63	0.46
1:A:150:GLU:CB	1:A:154:GLU:HG3	2.30	0.46
1:A:159:MET:HE1	1:A:309:ALA:HB2	1.98	0.46
1:A:459:GLU:O	1:A:463:ILE:HG12	2.15	0.46
1:A:1:MET:CE	1:A:135:LEU:HD21	2.40	0.45
1:A:364:ARG:C	1:A:366:GLU:N	2.74	0.45
1:A:525:ILE:O	1:A:528:ILE:HG22	2.16	0.45
1:A:603:ILE:O	1:A:605:THR:N	2.49	0.45
1:A:722:PRO:C	1:A:724:LYS:H	2.24	0.45
1:A:79:PRO:O	1:A:80:VAL:CG1	2.65	0.45
1:A:455:ASP:HA	1:A:458:GLU:HB3	1.98	0.45
1:A:59:HIS:C	1:A:61:THR:H	2.25	0.45
1:A:252:VAL:O	1:A:253:LYS:C	2.59	0.45
1:A:146:TYR:CZ	1:A:148:GLU:HA	2.52	0.45
1:A:151:GLU:O	1:A:154:GLU:HB2	2.17	0.45
1:A:188:ARG:CD	1:A:226:LEU:HD22	2.35	0.45
1:A:209:TYR:CD2	1:A:275:LEU:HG	2.52	0.45
1:A:304:ASN:C	1:A:306:GLU:N	2.73	0.45
1:A:391:GLU:HA	1:A:392:PRO:HD3	1.83	0.45
1:A:521:ILE:HD11	1:A:542:ASP:H	1.81	0.44
1:A:571:LEU:HA	1:A:572:PRO:HD3	1.85	0.44
1:A:650:LEU:HA	1:A:655:VAL:HG12	1.98	0.44
1:A:159:MET:HA	1:A:171:ILE:O	2.17	0.44
1:A:405:PHE:CZ	1:A:524:THR:HG21	2.51	0.44
1:A:466:LYS:HA	1:A:469:ALA:HB3	1.99	0.44
1:A:342:TRP:CD1	1:A:346:ARG:NH1	2.86	0.44
1:A:402:TYR:O	1:A:403:LEU:HD23	2.18	0.44
1:A:67:ARG:HB3	1:A:67:ARG:CZ	2.47	0.44
1:A:141:ASP:OD2	1:A:142:ILE:N	2.50	0.44
1:A:163:ALA:HB2	1:A:316:ALA:C	2.43	0.44
1:A:158:LEU:O	1:A:159:MET:HG3	2.17	0.44
1:A:176:VAL:HG22	1:A:305:LEU:HB2	1.98	0.44
1:A:490:ALA:C	1:A:492:SER:H	2.25	0.44
1:A:406:ARG:HD3	1:A:576:GLU:OE1	2.18	0.44
1:A:602:LYS:C	1:A:604:THR:H	2.24	0.44
1:A:48:ILE:HD11	1:A:68:VAL:HG11	1.99	0.44
1:A:275:LEU:HD23	1:A:275:LEU:HA	1.82	0.43
1:A:433:VAL:HG12	1:A:438:GLY:HA2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:72:GLN:CD	1:A:72:GLN:N	2.64	0.43
1:A:118:LYS:HG2	1:A:355:TRP:CH2	2.54	0.43
1:A:252:VAL:HG11	1:A:255:ARG:HD2	2.01	0.43
1:A:587:PHE:H	1:A:587:PHE:HD2	1.65	0.43
1:A:26:PHE:CD1	1:A:234:ARG:HG2	2.52	0.43
1:A:97:ARG:HD3	1:A:112:TYR:CD1	2.53	0.43
1:A:175:ASN:HA	1:A:183:VAL:HG21	2.00	0.43
1:A:433:VAL:CG1	1:A:438:GLY:HA2	2.48	0.43
1:A:26:PHE:CD2	1:A:234:ARG:CZ	3.02	0.43
1:A:115:PRO:CB	1:A:118:LYS:HD3	2.48	0.43
1:A:158:LEU:HD22	1:A:299:TRP:CE2	2.54	0.43
1:A:624:ALA:O	1:A:625:ARG:C	2.62	0.43
1:A:4:ASP:CG	1:A:5:THR:H	2.27	0.43
1:A:195:LEU:O	1:A:199:LYS:HB2	2.18	0.43
1:A:410:PRO:O	1:A:414:ILE:HG22	2.18	0.43
1:A:466:LYS:NZ	1:A:466:LYS:HB3	2.33	0.43
1:A:65:VAL:HG22	1:A:87:PHE:CE2	2.53	0.43
1:A:196:ARG:NH1	1:A:196:ARG:HG2	2.33	0.43
1:A:526:LYS:O	1:A:530:GLU:HG2	2.18	0.43
1:A:746:ARG:HD3	1:A:749:GLY:HA2	2.01	0.43
1:A:41:LEU:HD22	1:A:107:ILE:HD12	2.01	0.43
1:A:168:ALA:CB	1:A:317:LYS:HG2	2.48	0.43
1:A:279:TYR:CE2	1:A:285:GLN:HB2	2.53	0.43
1:A:397:TRP:HB2	1:A:400:ILE:HD11	2.00	0.43
1:A:423:LEU:CD1	1:A:424:ASN:ND2	2.82	0.43
1:A:626:VAL:O	1:A:629:ALA:HB3	2.19	0.43
1:A:741:VAL:O	1:A:742:GLU:C	2.62	0.43
1:A:164:ASP:OD2	1:A:201:LYS:HD3	2.19	0.43
1:A:438:GLY:O	1:A:439:HIS:C	2.61	0.43
1:A:156:PRO:HA	1:A:222:ARG:CZ	2.49	0.43
1:A:165:GLU:OE1	1:A:165:GLU:HA	2.18	0.43
1:A:417:ASN:ND2	1:A:447:GLY:H	2.09	0.43
1:A:79:PRO:C	1:A:80:VAL:HG13	2.44	0.42
1:A:732:TYR:CA	1:A:736:GLN:HB2	2.48	0.42
1:A:118:LYS:HG2	1:A:355:TRP:CZ2	2.54	0.42
1:A:47:ALA:HB1	1:A:105:ALA:HB1	2.00	0.42
1:A:76:LEU:HD23	1:A:76:LEU:HA	1.87	0.42
1:A:147:HIS:O	1:A:148:GLU:C	2.62	0.42
1:A:541:THR:O	1:A:542:ASP:CB	2.68	0.42
1:A:102:GLU:O	1:A:103:HIS:C	2.63	0.42
1:A:261:TYR:N	1:A:262:PRO:HD2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:563:PHE:O	1:A:566:TYR:N	2.53	0.42
1:A:101:ARG:HA	1:A:109:ILE:CD1	2.48	0.42
1:A:404:ASP:O	1:A:578:GLU:HG2	2.18	0.42
1:A:483:GLN:NE2	1:A:484:ARG:N	2.68	0.42
1:A:591:LYS:C	1:A:593:LYS:H	2.28	0.42
1:A:752:LYS:CB	1:A:756:ARG:HH21	2.32	0.42
1:A:6:ASP:OD1	1:A:6:ASP:C	2.61	0.42
1:A:23:ASN:HA	1:A:133:GLU:CD	2.45	0.42
1:A:163:ALA:HB3	1:A:320:TYR:HB2	2.01	0.42
1:A:318:VAL:CG1	1:A:322:LEU:HD12	2.49	0.42
1:A:8:ILE:HG22	1:A:9:THR:N	2.34	0.42
1:A:51:VAL:C	1:A:53:LYS:H	2.27	0.42
1:A:196:ARG:HG2	1:A:196:ARG:HH11	1.85	0.42
1:A:214:PHE:O	1:A:215:ASP:C	2.61	0.42
1:A:488:ILE:O	1:A:489:LEU:C	2.63	0.42
1:A:661:VAL:HA	1:A:701:TYR:O	2.20	0.42
1:A:608:LEU:HD13	1:A:608:LEU:C	2.45	0.42
1:A:178:LEU:C	1:A:180:TYR:H	2.28	0.42
1:A:194:PHE:O	1:A:198:VAL:HG23	2.20	0.42
1:A:541:THR:O	1:A:541:THR:HG23	2.19	0.41
1:A:354:GLU:OE2	1:A:496:TYR:OH	2.36	0.41
1:A:335:ARG:NE	1:A:482:ARG:HH21	2.18	0.41
1:A:338:GLY:HA3	1:A:359:ARG:HE	1.86	0.41
1:A:636:VAL:CG2	1:A:637:GLU:H	2.10	0.41
1:A:84:LYS:HD3	1:A:86:TYR:CZ	2.55	0.41
1:A:159:MET:HE1	1:A:309:ALA:HA	2.02	0.41
1:A:195:LEU:HD12	1:A:230:PHE:HD2	1.85	0.41
1:A:334:SER:OG	1:A:341:LEU:HA	2.20	0.41
1:A:220:LYS:NZ	1:A:241:ILE:HD12	2.35	0.41
1:A:356:PHE:CG	1:A:489:LEU:HD11	2.56	0.41
1:A:548:ILE:O	1:A:549:PRO:C	2.63	0.41
1:A:101:ARG:CB	1:A:109:ILE:HD13	2.51	0.41
1:A:163:ALA:N	1:A:316:ALA:HB1	2.36	0.41
1:A:188:ARG:HH12	1:A:192:LYS:HD2	1.85	0.41
1:A:163:ALA:HA	1:A:168:ALA:HA	2.02	0.41
1:A:358:LEU:HA	1:A:358:LEU:HD23	1.80	0.41
1:A:433:VAL:HG13	1:A:438:GLY:O	2.20	0.41
1:A:174:LYS:HB2	1:A:299:TRP:CZ3	2.54	0.41
1:A:416:HIS:O	1:A:417:ASN:HB3	2.21	0.41
1:A:186:THR:HG22	1:A:189:GLU:HG2	2.02	0.41
1:A:61:THR:HG22	1:A:62:VAL:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:PRO:O	1:A:116:PHE:C	2.63	0.40
1:A:243:ARG:H	1:A:243:ARG:HG3	1.59	0.40
1:A:261:TYR:OH	1:A:265:ARG:NH2	2.53	0.40
1:A:418:VAL:HG13	1:A:441:PHE:CZ	2.56	0.40
1:A:606:ARG:HH11	1:A:606:ARG:HG2	1.86	0.40
1:A:159:MET:HG2	1:A:172:THR:HB	2.04	0.40
1:A:463:ILE:HG21	1:A:483:GLN:HB3	2.03	0.40
1:A:178:LEU:HB2	1:A:181:VAL:HG23	2.02	0.40
1:A:328:PRO:O	1:A:329:MET:C	2.64	0.40
1:A:494:TYR:O	1:A:497:TYR:HB2	2.22	0.40
1:A:658:GLU:CD	1:A:658:GLU:H	2.29	0.40
1:A:78:ARG:HG2	1:A:78:ARG:HH11	1.86	0.40
1:A:89:HIS:ND1	1:A:90:PRO:N	2.69	0.40
1:A:160:ILE:HG21	1:A:194:PHE:CG	2.57	0.40
1:A:175:ASN:HA	1:A:183:VAL:CG2	2.52	0.40
1:A:330:GLU:HB3	1:A:341:LEU:CD1	2.52	0.40
1:A:701:TYR:HB2	1:A:714:ALA:O	2.21	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	719/774 (93%)	591 (82%)	92 (13%)	36 (5%)	1 10

All (36) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	66	LYS
1	A	572	PRO
1	A	608	LEU
1	A	722	PRO

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Mol	Chain	Res	Type
1	A	728	ASP
1	A	23	ASN
1	A	227	GLY
1	A	531	LYS
1	A	598	ASP
1	A	735	ASN
1	A	94	PRO
1	A	231	ALA
1	A	286	PRO
1	A	389	VAL
1	A	415	THR
1	A	436	GLN
1	A	602	LYS
1	A	604	THR
1	A	609	GLU
1	A	687	ALA
1	A	698	VAL
1	A	52	LYS
1	A	448	PHE
1	A	547	THR
1	A	573	GLY
1	A	618	ILE
1	A	636	VAL
1	A	148	GLU
1	A	328	PRO
1	A	408	LEU
1	A	610	ILE
1	A	725	HIS
1	A	745	LEU
1	A	611	VAL
1	A	179	PRO
1	A	184	VAL

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	555/674 (82%)	504 (91%)	51 (9%)	8 33

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ASP
1	A	13	LYS
1	A	16	ILE
1	A	41	LEU
1	A	91	GLN
1	A	97	ARG
1	A	108	ASP
1	A	115	PRO
1	A	142	ILE
1	A	143	GLU
1	A	154	GLU
1	A	166	GLU
1	A	169	ARG
1	A	173	TRP
1	A	184	VAL
1	A	185	SER
1	A	186	THR
1	A	193	ARG
1	A	230	PHE
1	A	234	ARG
1	A	240	LYS
1	A	243	ARG
1	A	267	THR
1	A	275	LEU
1	A	313	MET
1	A	317	LYS
1	A	325	GLU
1	A	327	LEU
1	A	336	LEU
1	A	349	THR
1	A	377	LEU
1	A	391	GLU
1	A	393	GLU
1	A	459	GLU
1	A	467	MET
1	A	468	LYS
1	A	489	LEU
1	A	507	LYS

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Mol	Chain	Res	Type
1	A	516	TRP
1	A	518	ARG
1	A	527	GLU
1	A	542	ASP
1	A	567	ILE
1	A	592	LYS
1	A	594	TYR
1	A	600	GLU
1	A	608	LEU
1	A	640	VAL
1	A	648	GLU
1	A	658	GLU
1	A	736	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	91	GLN
1	A	147	HIS
1	A	242	GLN
1	A	332	GLN
1	A	339	GLN
1	A	365	ASN
1	A	416	HIS
1	A	417	ASN
1	A	424	ASN
1	A	483	GLN
1	A	491	ASN
1	A	736	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 [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	729/774 (94%)	0.20	10 (1%)	73 51	12, 53, 108, 130	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	728	ASP	3.5
1	A	163	ALA	3.3
1	A	655	VAL	3.0
1	A	665	GLN	2.4
1	A	639	ALA	2.4
1	A	616	SER	2.4
1	A	612	ARG	2.3
1	A	609	GLU	2.2
1	A	642	ILE	2.1
1	A	700	SER	2.1

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.