



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:37 AM UTC

PDB ID : 1ONN / pdb_00001onn
Title : IspC apo structure
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Deposited on : 2003-02-28
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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

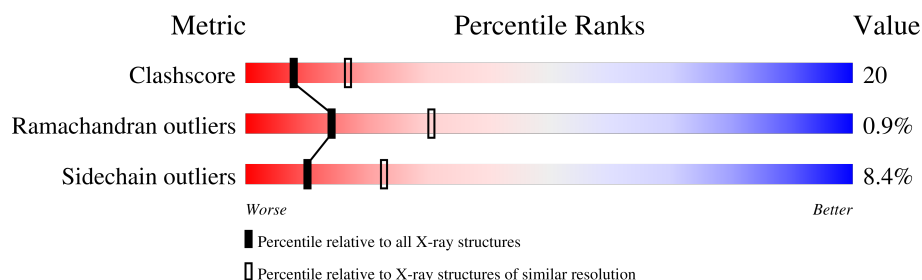
1 Overall quality at a glance

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))
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	398	 58% 35% 5% ..
1	B	398	 63% 30% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6226 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 1-deoxy-D-xylulose 5-phosphate reductoisomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	389	Total	C	N	O	S	0	0	0
			2955	1847	518	564	26			
1	B	389	Total	C	N	O	S	0	0	0
			2955	1847	518	564	26			

- Molecule 2 is water.

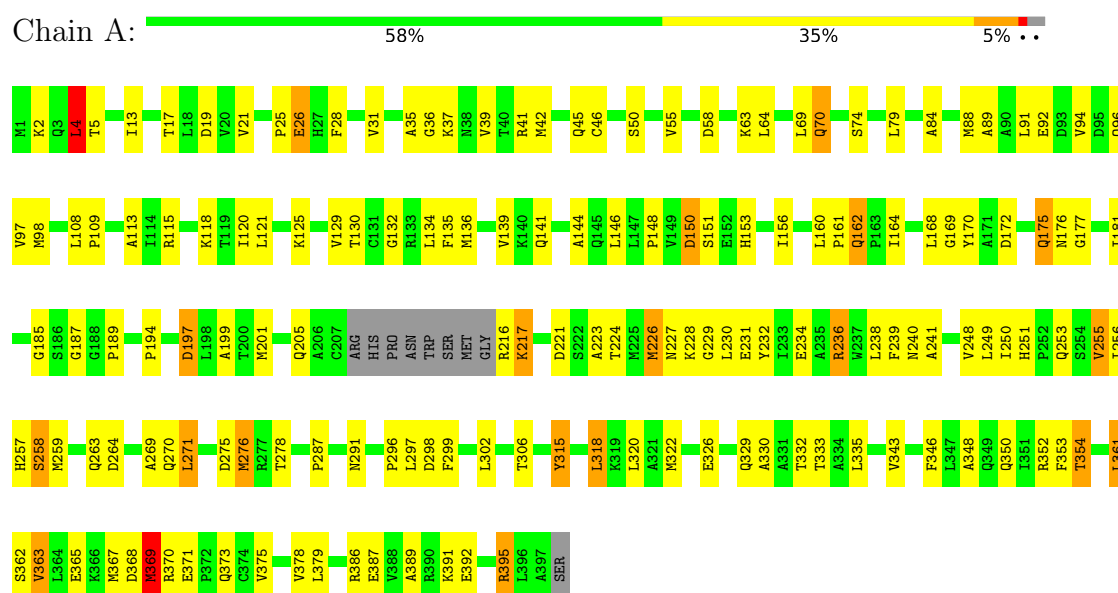
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	153	Total	O	0	0
			153	153		
2	B	163	Total	O	0	0
			163	163		

3 Residue-property plots

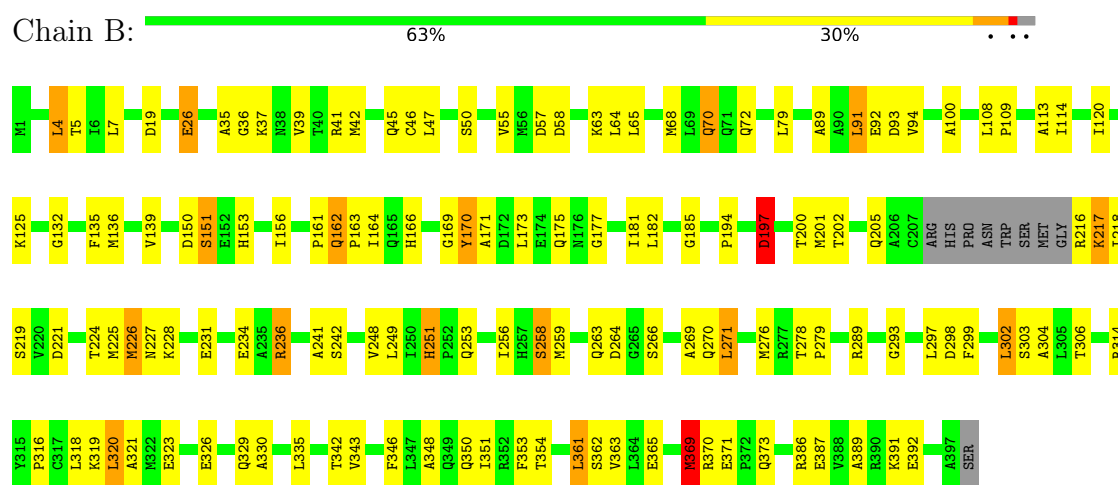
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: 1-deoxy-D-xylulose 5-phosphate reductoisomerase



• Molecule 1: 1-deoxy-D-xylulose 5-phosphate reductoisomerase



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	90.40Å 53.42Å 107.49Å 90.00° 92.85° 90.00°	Depositor
Resolution (Å)	20.00 – 2.60	Depositor
% Data completeness (in resolution range)	98.4 (20.00-2.60)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.244 , 0.298	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6226	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

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	0.64	0/2998	1.04	7/4062 (0.2%)
1	B	0.63	0/2998	1.01	8/4062 (0.2%)
All	All	0.64	0/5996	1.02	15/8124 (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	1

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	226	MET	N-CA-C	-7.24	103.42	111.82
1	A	226	MET	N-CA-C	-6.92	103.79	111.82
1	B	251	HIS	CA-C-N	6.86	126.38	119.24
1	B	251	HIS	C-N-CA	6.86	126.38	119.24
1	A	255	VAL	N-CA-C	-6.71	104.47	111.58
1	A	141	GLN	N-CA-C	6.43	117.95	111.07
1	B	330	ALA	N-CA-C	-6.19	104.61	111.36
1	B	4	LEU	N-CA-C	6.15	118.76	109.41
1	A	36	GLY	N-CA-C	5.45	115.17	110.21
1	B	293	GLY	N-CA-C	-5.27	108.04	115.32
1	A	330	ALA	N-CA-C	-5.23	105.66	111.36
1	A	4	LEU	N-CA-C	5.20	117.32	109.41
1	B	151	SER	N-CA-C	5.15	116.58	111.07
1	A	276	MET	N-CA-C	5.11	118.61	112.38
1	B	248	VAL	N-CA-C	-5.07	101.07	108.17

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	315	TYR	Sidechain

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	2955	0	2989	129	0
1	B	2955	0	2989	111	0
2	A	153	0	0	5	0
2	B	163	0	0	7	0
All	All	6226	0	5978	234	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 20.

All (234) 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:B:227:ASN:HB3	2:B:399:HOH:O	1.62	0.97
1:A:227:ASN:HB3	2:A:399:HOH:O	1.69	0.91
1:B:170:TYR:H	1:B:170:TYR:HD2	1.26	0.84
1:A:395:ARG:HH11	1:A:395:ARG:HB3	1.43	0.82
1:B:236:ARG:HD2	1:B:241:ALA:O	1.83	0.79
1:B:201:MET:HE2	1:B:201:MET:HA	1.66	0.77
1:B:221:ASP:HB3	1:B:227:ASN:HB2	1.67	0.75
1:A:156:ILE:HD13	1:A:181:ILE:CG2	2.19	0.71
1:B:216:ARG:HG3	1:B:217:LYS:H	1.55	0.71
1:B:156:ILE:HD13	1:B:181:ILE:HG21	1.72	0.70
1:A:256:ILE:HG12	1:A:271:LEU:HD22	1.74	0.69
1:B:182:LEU:HD23	1:B:259:MET:HE3	1.74	0.69
1:B:39:VAL:HG11	1:B:64:LEU:HD22	1.74	0.69
1:A:2:LYS:NZ	1:A:96:GLN:HE21	1.90	0.68
1:B:256:ILE:HG12	1:B:271:LEU:HD22	1.75	0.68
1:B:217:LYS:NZ	1:B:217:LYS:HB3	2.08	0.68
1:A:368:ASP:HA	1:A:369:MET:HE3	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:156:ILE:HD13	1:B:181:ILE:CG2	2.24	0.67
1:A:375:VAL:O	1:A:379:LEU:HG	1.94	0.67
1:A:217:LYS:NZ	1:A:217:LYS:HB3	2.09	0.67
1:B:35:ALA:HB3	1:B:42:MET:HE2	1.79	0.65
1:B:161:PRO:CG	1:B:164:ILE:HD12	2.27	0.65
1:B:299:PHE:HA	1:B:302:LEU:HD22	1.79	0.64
1:B:170:TYR:HD2	1:B:170:TYR:N	1.95	0.64
1:A:221:ASP:HB3	1:A:227:ASN:HB2	1.80	0.64
1:B:170:TYR:N	1:B:170:TYR:CD2	2.65	0.63
1:A:226:MET:HE2	1:A:230:LEU:HG	1.79	0.63
1:A:41:ARG:O	1:A:45:GLN:HG3	1.99	0.63
1:A:35:ALA:HB3	1:A:42:MET:HE2	1.80	0.63
1:A:153:HIS:HE1	1:A:234:GLU:OE1	1.82	0.63
1:A:132:GLY:H	1:A:329:GLN:NE2	1.96	0.62
1:A:201:MET:HA	1:A:201:MET:HE2	1.81	0.62
1:A:64:LEU:O	1:A:64:LEU:HD23	2.00	0.62
1:A:395:ARG:HB3	1:A:395:ARG:NH1	2.11	0.62
1:A:37:LYS:HE3	1:A:58:ASP:OD2	1.99	0.62
1:A:156:ILE:HD13	1:A:181:ILE:HG21	1.80	0.62
1:B:132:GLY:H	1:B:329:GLN:HE21	1.44	0.62
1:A:216:ARG:HG3	1:A:217:LYS:H	1.65	0.62
1:B:89:ALA:HB1	1:B:113:ALA:HB2	1.82	0.62
1:A:125:LYS:HB3	1:A:234:GLU:OE1	2.00	0.62
1:A:226:MET:O	1:A:226:MET:HE3	2.00	0.61
1:A:98:MET:HE2	1:A:121:LEU:HD12	1.81	0.61
1:A:35:ALA:CB	1:A:42:MET:HE2	2.30	0.61
1:A:227:ASN:O	1:A:231:GLU:HG3	2.01	0.61
1:A:136:MET:CE	1:A:169:GLY:HA3	2.31	0.60
1:A:148:PRO:HB3	1:A:238:LEU:HD21	1.84	0.60
1:B:226:MET:HE1	1:B:321:ALA:HB2	1.83	0.59
1:B:161:PRO:HG2	1:B:164:ILE:HD12	1.85	0.59
1:A:156:ILE:O	1:A:160:LEU:HG	2.02	0.59
1:B:39:VAL:HG13	1:B:65:LEU:HB2	1.83	0.59
1:B:185:GLY:HA3	1:B:228:LYS:HE3	1.85	0.59
1:B:136:MET:CE	1:B:169:GLY:HA3	2.32	0.58
1:A:270:GLN:C	1:A:271:LEU:HD23	2.28	0.58
1:B:270:GLN:C	1:B:271:LEU:HD23	2.27	0.58
1:B:47:LEU:HD11	1:B:72:GLN:HG3	1.86	0.58
1:A:177:GLY:HA3	1:B:289:ARG:HB2	1.85	0.58
1:A:21:VAL:HG13	1:A:28:PHE:HB2	1.85	0.58
1:A:369:MET:SD	1:A:369:MET:C	2.87	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:132:GLY:H	1:B:329:GLN:NE2	2.02	0.58
1:A:248:VAL:HG11	1:A:318:LEU:HD11	1.86	0.57
1:A:299:PHE:HA	1:A:302:LEU:HD22	1.87	0.57
1:B:35:ALA:CB	1:B:42:MET:HE2	2.34	0.57
1:A:136:MET:HE2	1:A:169:GLY:HA3	1.86	0.57
1:A:25:PRO:HD2	1:A:26:GLU:OE1	2.05	0.57
1:B:217:LYS:HB3	1:B:217:LYS:HZ3	1.68	0.57
1:B:171:ALA:HB3	2:B:488:HOH:O	2.05	0.56
1:B:278:THR:HB	1:B:279:PRO:CD	2.35	0.56
1:A:84:ALA:O	1:A:88:MET:HG2	2.05	0.56
1:B:201:MET:HA	1:B:205:GLN:OE1	2.06	0.56
1:A:236:ARG:HD2	1:A:241:ALA:O	2.05	0.56
1:B:108:LEU:HB2	1:B:109:PRO:HD3	1.86	0.55
1:A:392:GLU:OE1	1:A:392:GLU:HA	2.06	0.55
1:B:320:LEU:HD13	1:B:335:LEU:HD21	1.87	0.55
1:B:125:LYS:HG2	1:B:150:ASP:HB2	1.89	0.54
1:A:257:HIS:HE1	2:A:424:HOH:O	1.90	0.54
1:A:2:LYS:HZ3	1:A:96:GLN:HE21	1.54	0.54
1:A:91:LEU:HB3	1:A:94:VAL:HG23	1.88	0.54
1:A:387:GLU:O	1:A:391:LYS:HG2	2.08	0.54
1:B:278:THR:HB	1:B:279:PRO:HD3	1.89	0.54
1:B:342:THR:O	1:B:351:ILE:HD11	2.08	0.54
1:A:278:THR:HG23	1:B:264:ASP:O	2.08	0.53
1:A:217:LYS:HB3	1:A:217:LYS:HZ3	1.73	0.53
1:B:41:ARG:O	1:B:45:GLN:HG3	2.08	0.53
1:A:185:GLY:HA3	1:A:228:LYS:HE3	1.90	0.53
1:A:236:ARG:NH2	1:A:326:GLU:OE2	2.42	0.53
1:A:298:ASP:O	1:A:302:LEU:HD13	2.07	0.53
1:A:17:THR:O	1:A:21:VAL:HG23	2.09	0.53
1:A:253:GLN:CD	1:A:253:GLN:H	2.16	0.52
1:A:329:GLN:N	1:A:371:GLU:OE1	2.42	0.52
1:B:329:GLN:N	1:B:371:GLU:OE1	2.42	0.52
1:B:251:HIS:HD2	1:B:306:THR:O	1.92	0.52
1:B:253:GLN:H	1:B:253:GLN:CD	2.17	0.52
1:A:39:VAL:HG11	1:A:64:LEU:HD22	1.92	0.51
1:B:236:ARG:NH2	1:B:326:GLU:OE2	2.44	0.51
1:B:125:LYS:HB3	1:B:234:GLU:OE1	2.10	0.51
1:A:132:GLY:H	1:A:329:GLN:HE21	1.58	0.51
1:B:153:HIS:HE1	1:B:234:GLU:OE1	1.94	0.50
1:B:194:PRO:O	1:B:197:ASP:HB2	2.11	0.50
1:B:362:SER:O	1:B:363:VAL:C	2.52	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:369:MET:SD	1:B:369:MET:C	2.95	0.50
1:A:251:HIS:CE1	1:A:255:VAL:H	2.30	0.50
1:A:251:HIS:HE1	1:A:255:VAL:H	1.60	0.50
1:A:346:PHE:CE1	1:A:353:PHE:HB2	2.47	0.50
1:A:251:HIS:HD2	1:A:306:THR:O	1.95	0.49
1:B:236:ARG:CD	1:B:241:ALA:O	2.59	0.49
1:B:70:GLN:HE21	1:B:70:GLN:CA	2.25	0.49
1:B:136:MET:HE2	1:B:169:GLY:HA3	1.92	0.49
1:A:4:LEU:N	1:A:4:LEU:HD23	2.28	0.49
1:B:135:PHE:O	1:B:139:VAL:HG23	2.13	0.49
1:B:224:THR:O	1:B:225:MET:HB2	2.13	0.49
1:A:227:ASN:ND2	2:A:399:HOH:O	2.44	0.49
1:A:386:ARG:O	1:A:389:ALA:HB3	2.13	0.49
1:B:197:ASP:O	1:B:201:MET:HG2	2.13	0.49
1:A:70:GLN:HE21	1:A:70:GLN:CA	2.25	0.48
1:A:69:LEU:HB3	1:A:74:SER:HB3	1.94	0.48
1:B:392:GLU:OE1	1:B:392:GLU:HA	2.13	0.48
1:B:335:LEU:HD13	1:B:335:LEU:C	2.39	0.48
1:A:229:GLY:O	1:A:232:TYR:HB3	2.13	0.48
1:B:227:ASN:O	1:B:231:GLU:HG3	2.14	0.48
1:A:256:ILE:HG12	1:A:271:LEU:CD2	2.43	0.47
1:B:64:LEU:HD23	1:B:64:LEU:C	2.39	0.47
1:B:361:LEU:HD22	1:B:365:GLU:HG3	1.96	0.47
1:A:135:PHE:O	1:A:139:VAL:HG23	2.14	0.47
1:B:37:LYS:HE3	1:B:58:ASP:OD2	2.15	0.47
1:A:89:ALA:HB1	1:A:113:ALA:HB2	1.96	0.47
1:A:369:MET:SD	1:A:369:MET:N	2.87	0.47
1:A:88:MET:HE2	1:A:88:MET:HA	1.95	0.47
1:A:370:ARG:HD2	1:A:370:ARG:N	2.30	0.47
1:A:291:ASN:HB3	2:A:493:HOH:O	2.14	0.47
1:A:361:LEU:HD22	1:A:365:GLU:CD	2.39	0.47
1:A:2:LYS:NZ	1:A:96:GLN:NE2	2.62	0.46
1:B:177:GLY:HA2	1:B:263:GLN:NE2	2.30	0.46
1:A:108:LEU:HB2	1:A:109:PRO:HD3	1.96	0.46
1:A:346:PHE:CD1	1:A:353:PHE:HA	2.51	0.46
1:B:151:SER:HB2	1:B:276:MET:HE1	1.96	0.46
1:B:7:LEU:O	1:B:100:ALA:HB3	2.16	0.46
1:A:169:GLY:O	1:A:240:ASN:HB2	2.15	0.46
1:A:194:PRO:O	1:A:197:ASP:HB2	2.16	0.46
1:B:201:MET:HE2	1:B:201:MET:CA	2.42	0.46
1:A:164:ILE:HD11	1:A:176:ASN:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:PRO:HD2	1:A:223:ALA:HA	1.97	0.45
1:A:296:PRO:HG3	2:A:542:HOH:O	2.16	0.45
1:A:46:CYS:O	1:A:50:SER:HA	2.16	0.45
1:B:55:VAL:HA	1:B:79:LEU:O	2.15	0.45
1:B:170:TYR:CG	2:B:426:HOH:O	2.69	0.45
1:A:129:VAL:O	1:A:332:THR:OG1	2.31	0.45
1:A:168:LEU:O	1:A:170:TYR:CD2	2.70	0.45
1:B:278:THR:HG21	2:B:421:HOH:O	2.17	0.45
1:B:348:ALA:HB3	1:B:350:GLN:HE21	1.82	0.45
1:A:115:ARG:HG3	1:A:115:ARG:HH11	1.82	0.45
1:B:26:GLU:CD	1:B:26:GLU:H	2.24	0.45
1:B:114:ILE:HG12	1:B:120:ILE:HD13	1.98	0.45
1:A:177:GLY:HA2	1:A:263:GLN:NE2	2.32	0.45
1:B:217:LYS:HD2	1:B:343:VAL:CG1	2.47	0.45
1:A:130:THR:HB	1:A:378:VAL:CG1	2.46	0.45
1:A:151:SER:HB2	1:A:276:MET:HE1	1.98	0.44
1:A:31:VAL:HG11	1:A:91:LEU:HD23	2.00	0.44
1:B:91:LEU:HB3	1:B:94:VAL:HG23	1.99	0.44
1:A:226:MET:SD	1:A:335:LEU:HD11	2.58	0.44
1:B:177:GLY:HA2	1:B:263:GLN:HE21	1.83	0.44
1:A:217:LYS:HD2	1:A:343:VAL:CG1	2.47	0.44
1:A:335:LEU:C	1:A:335:LEU:HD13	2.43	0.44
1:B:202:THR:OG1	1:B:205:GLN:HG3	2.18	0.44
1:B:346:PHE:CD1	1:B:353:PHE:HA	2.53	0.44
1:A:387:GLU:OE2	1:A:391:LYS:HE3	2.17	0.44
1:A:130:THR:HG22	1:A:333:THR:HA	1.99	0.44
1:A:118:LYS:O	1:A:120:ILE:HD12	2.17	0.44
1:A:368:ASP:CA	1:A:369:MET:HE3	2.44	0.44
1:B:125:LYS:CG	1:B:150:ASP:HB2	2.48	0.44
1:A:162:GLN:HG3	1:B:162:GLN:HG3	2.00	0.44
1:B:259:MET:HG2	1:B:269:ALA:HB2	1.99	0.43
1:A:125:LYS:HD3	1:A:150:ASP:HB2	2.00	0.43
1:A:228:LYS:HD3	1:A:228:LYS:HA	1.77	0.43
1:B:316:PRO:HD2	2:B:506:HOH:O	2.17	0.43
1:B:64:LEU:O	1:B:68:MET:HG3	2.19	0.43
1:A:5:THR:HB	1:A:97:VAL:HG22	1.99	0.43
1:A:232:TYR:CZ	1:A:322:MET:HG2	2.54	0.43
1:A:201:MET:HA	1:A:205:GLN:OE1	2.18	0.43
1:B:93:ASP:OD1	1:B:93:ASP:N	2.48	0.43
1:A:187:GLY:HA2	1:A:250:ILE:HD12	1.99	0.43
1:A:264:ASP:OD1	1:B:289:ARG:NH1	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:335:LEU:HD13	1:B:335:LEU:O	2.19	0.43
1:B:114:ILE:HA	1:B:120:ILE:HD11	2.02	0.42
1:A:125:LYS:HB3	1:A:234:GLU:CD	2.43	0.42
1:A:348:ALA:HB3	1:A:350:GLN:HE21	1.84	0.42
1:A:369:MET:HB2	1:A:370:ARG:H	1.68	0.42
1:B:226:MET:CE	1:B:335:LEU:HD11	2.50	0.42
1:B:227:ASN:ND2	2:B:399:HOH:O	2.51	0.42
1:B:369:MET:SD	1:B:370:ARG:N	2.92	0.42
1:A:108:LEU:HD23	1:A:375:VAL:HG21	2.01	0.42
1:A:161:PRO:HD2	1:A:164:ILE:HD12	2.01	0.42
1:B:125:LYS:H	1:B:125:LYS:HG3	1.67	0.42
1:A:257:HIS:HD2	1:A:270:GLN:OE1	2.02	0.42
1:A:270:GLN:NE2	1:B:266:SER:OG	2.50	0.42
1:A:88:MET:HE2	1:A:91:LEU:HD13	2.00	0.42
1:B:173:LEU:N	2:B:417:HOH:O	2.52	0.42
1:B:226:MET:SD	1:B:335:LEU:HD11	2.60	0.42
1:A:91:LEU:HB3	1:A:94:VAL:CG2	2.49	0.41
1:B:259:MET:HG2	1:B:269:ALA:CB	2.50	0.41
1:B:387:GLU:O	1:B:391:LYS:HG2	2.20	0.41
1:A:170:TYR:CD2	1:A:170:TYR:N	2.88	0.41
1:A:275:ASP:C	1:A:275:ASP:OD2	2.63	0.41
1:B:278:THR:N	1:B:279:PRO:HD2	2.34	0.41
1:A:362:SER:O	1:A:363:VAL:C	2.64	0.41
1:B:217:LYS:HD2	1:B:343:VAL:HG12	2.02	0.41
1:A:259:MET:HG2	1:A:269:ALA:CB	2.50	0.41
1:B:314:ARG:C	1:B:316:PRO:HD3	2.46	0.41
1:A:270:GLN:HE21	1:B:266:SER:CB	2.33	0.41
1:B:46:CYS:O	1:B:50:SER:HA	2.20	0.41
1:B:162:GLN:N	1:B:163:PRO:HD2	2.35	0.41
1:B:253:GLN:CD	1:B:253:GLN:N	2.78	0.41
1:A:161:PRO:CG	1:A:164:ILE:HD12	2.50	0.41
1:B:36:GLY:HA2	1:B:57:ASP:CG	2.45	0.41
1:B:319:LYS:O	1:B:323:GLU:HG3	2.20	0.41
1:A:55:VAL:HG22	1:A:79:LEU:HB2	2.01	0.41
1:A:224:THR:HG22	1:A:353:PHE:CZ	2.55	0.41
1:A:256:ILE:HA	1:A:271:LEU:HD22	2.02	0.41
1:B:370:ARG:N	1:B:370:ARG:HD2	2.36	0.41
1:A:172:ASP:HB3	1:A:175:GLN:HB2	2.02	0.41
1:A:368:ASP:O	1:A:369:MET:HB3	2.21	0.41
1:B:162:GLN:O	1:B:166:HIS:HD2	2.04	0.41
1:B:236:ARG:NH1	1:B:242:SER:HA	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:LEU:HD23	1:A:146:LEU:HA	1.89	0.40
1:A:239:PHE:O	1:A:240:ASN:C	2.64	0.40
1:B:298:ASP:O	1:B:302:LEU:HD13	2.21	0.40
1:A:187:GLY:O	1:A:315:TYR:OH	2.35	0.40
1:B:39:VAL:HG11	1:B:64:LEU:CD2	2.48	0.40
1:B:319:LYS:HA	1:B:319:LYS:HD2	1.89	0.40
1:A:120:ILE:CD1	1:A:144:ALA:HB1	2.51	0.40
1:A:199:ALA:HA	1:A:354:THR:HB	2.03	0.40
1:A:251:HIS:CE1	1:A:256:ILE:H	2.40	0.40
1:A:352:ARG:HH21	1:A:354:THR:CG2	2.34	0.40
1:B:303:SER:O	1:B:304:ALA:C	2.61	0.40
1:B:386:ARG:O	1:B:389:ALA:HB3	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	385/398 (97%)	365 (95%)	16 (4%)	4 (1%)	12	28
1	B	385/398 (97%)	358 (93%)	24 (6%)	3 (1%)	16	34
All	All	770/796 (97%)	723 (94%)	40 (5%)	7 (1%)	14	30

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	369	MET
1	B	369	MET
1	A	258	SER
1	B	197	ASP
1	B	258	SER
1	A	197	ASP

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Mol	Chain	Res	Type
1	A	363	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	320/328 (98%)	294 (92%)	26 (8%)	11	24
1	B	320/328 (98%)	292 (91%)	28 (9%)	9	21
All	All	640/656 (98%)	586 (92%)	54 (8%)	10	23

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	13	ILE
1	A	19	ASP
1	A	26	GLU
1	A	63	LYS
1	A	70	GLN
1	A	92	GLU
1	A	134	LEU
1	A	150	ASP
1	A	162	GLN
1	A	175	GLN
1	A	217	LYS
1	A	236	ARG
1	A	249	LEU
1	A	258	SER
1	A	271	LEU
1	A	287	PRO
1	A	297	LEU
1	A	318	LEU
1	A	320	LEU
1	A	354	THR
1	A	361	LEU

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Mol	Chain	Res	Type
1	A	367	MET
1	A	369	MET
1	A	373	GLN
1	A	395	ARG
1	B	4	LEU
1	B	5	THR
1	B	19	ASP
1	B	26	GLU
1	B	63	LYS
1	B	70	GLN
1	B	91	LEU
1	B	92	GLU
1	B	162	GLN
1	B	170	TYR
1	B	175	GLN
1	B	197	ASP
1	B	200	THR
1	B	217	LYS
1	B	218	ILE
1	B	219	SER
1	B	236	ARG
1	B	249	LEU
1	B	258	SER
1	B	271	LEU
1	B	297	LEU
1	B	302	LEU
1	B	318	LEU
1	B	320	LEU
1	B	354	THR
1	B	361	LEU
1	B	369	MET
1	B	373	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	GLN
1	A	71	GLN
1	A	72	GLN
1	A	96	GLN
1	A	124	ASN
1	A	141	GLN

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Mol	Chain	Res	Type
1	A	145	GLN
1	A	153	HIS
1	A	162	GLN
1	A	165	GLN
1	A	175	GLN
1	A	227	ASN
1	A	251	HIS
1	A	257	HIS
1	A	263	GLN
1	A	291	ASN
1	A	329	GLN
1	A	350	GLN
1	B	70	GLN
1	B	71	GLN
1	B	72	GLN
1	B	96	GLN
1	B	141	GLN
1	B	145	GLN
1	B	153	HIS
1	B	162	GLN
1	B	165	GLN
1	B	166	HIS
1	B	167	ASN
1	B	227	ASN
1	B	251	HIS
1	B	257	HIS
1	B	263	GLN
1	B	270	GLN
1	B	329	GLN
1	B	350	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.