



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:58 AM UTC

PDB ID : 1IQ0 / pdb_00001iq0
Title : THERMUS THERMOPHILUS ARGINYL-TRNA SYNTHETASE
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Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2001-05-24
Resolution : 2.30 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

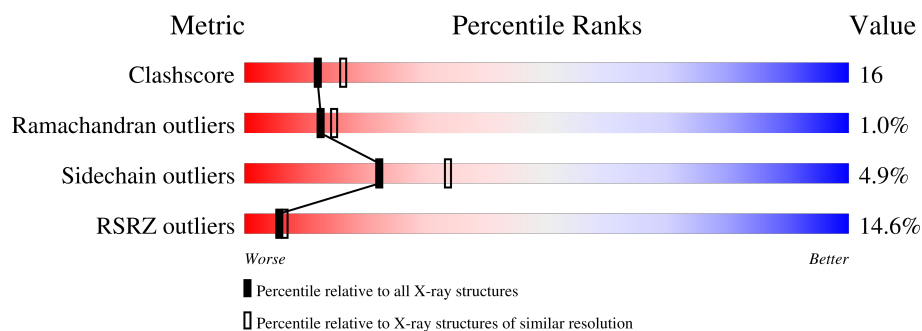
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	592	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4842 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 ARGINYL-TRNA SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	588	Total	C	N	O	S	0	0	0
			4646	2960	827	849	10			

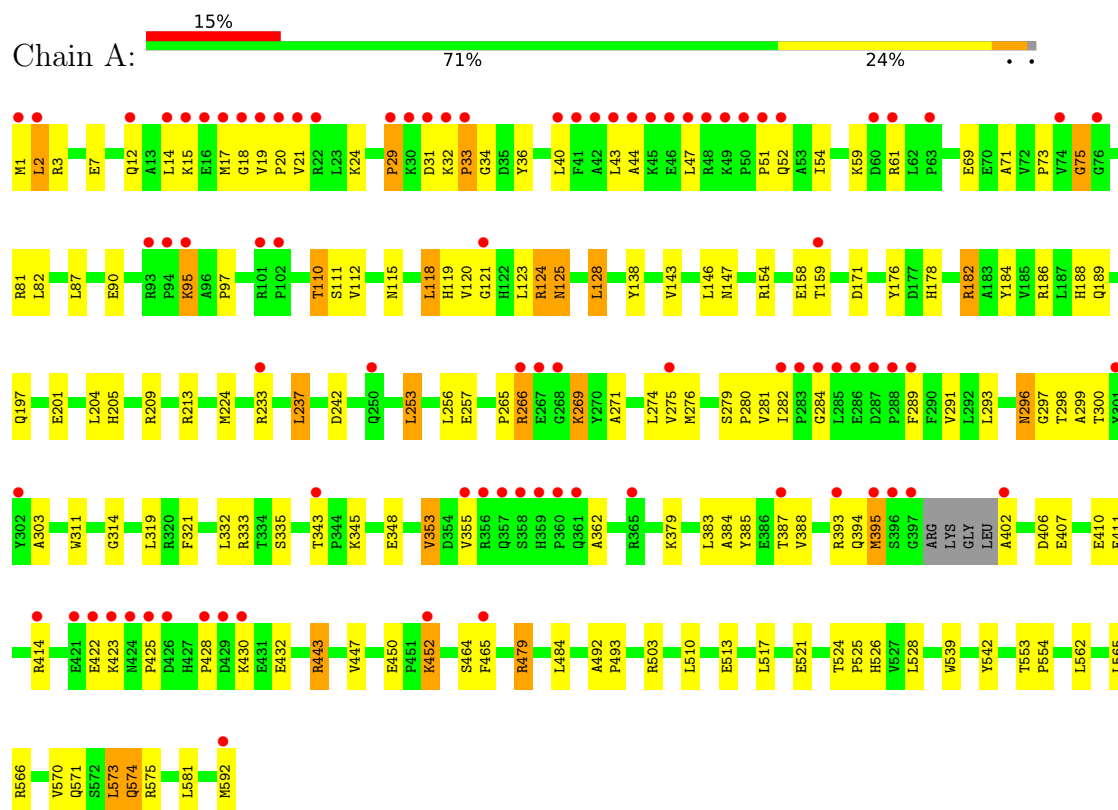
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	196	Total	O	0	0
			196	196		

3 Residue-property plots [i](#)

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: ARGINYL-TRNA SYNTHETASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	154.75Å 154.75Å 84.57Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.67 – 2.30 44.67 – 2.30	Depositor EDS
% Data completeness (in resolution range)	95.8 (44.67-2.30) 95.8 (44.67-2.30)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	9.03 (at 2.29Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.215 , 0.242 0.208 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	28.5	Xtriage
Anisotropy	0.397	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 34.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.027 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4842	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.06% 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	0.39	0/4751	0.85	7/6454 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	176	TYR	N-CA-C	6.43	119.11	111.33
1	A	34	GLY	N-CA-C	6.18	119.61	111.70
1	A	335	SER	N-CA-C	-5.99	102.05	110.50
1	A	143	VAL	N-CA-C	5.85	117.01	108.53
1	A	353	VAL	N-CA-C	5.57	117.84	108.81
1	A	189	GLN	N-CA-C	-5.32	106.81	113.72
1	A	464	SER	N-CA-C	5.29	118.02	110.24

There are no chirality outliers.

There are no planarity outliers.

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	4646	0	4667	145	0
2	A	196	0	0	6	0
All	All	4842	0	4667	145	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 16.

All (145) 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:314:GLY:HA2	1:A:343:THR:HG21	1.37	1.06
1:A:1:MET:HG2	1:A:2:LEU:H	1.27	0.97
1:A:110:THR:H	1:A:125:ASN:ND2	1.70	0.88
1:A:110:THR:H	1:A:125:ASN:HD21	1.18	0.87
1:A:542:TYR:O	1:A:553:THR:HG21	1.79	0.81
1:A:275:VAL:HG21	1:A:289:PHE:HB3	1.66	0.77
1:A:95:LYS:H	1:A:95:LYS:HD3	1.49	0.77
1:A:450:GLU:HG3	2:A:696:HOH:O	1.85	0.77
1:A:452:LYS:HZ2	1:A:452:LYS:HB2	1.52	0.75
1:A:154:ARG:HB2	1:A:154:ARG:HH11	1.54	0.73
1:A:291:VAL:O	1:A:300:THR:HG21	1.88	0.72
1:A:266:ARG:H	1:A:266:ARG:HE	1.36	0.71
1:A:21:VAL:HG11	1:A:43:LEU:HD21	1.73	0.70
1:A:300:THR:HG23	1:A:303:ALA:H	1.56	0.70
1:A:17:MET:HG2	1:A:61:ARG:HD2	1.73	0.70
1:A:450:GLU:HB3	1:A:452:LYS:NZ	2.07	0.70
1:A:387:THR:HG21	1:A:394:GLN:HE22	1.59	0.68
1:A:44:ALA:CB	1:A:51:PRO:HG3	2.24	0.68
1:A:44:ALA:HB1	1:A:51:PRO:HG3	1.76	0.67
1:A:265:PRO:O	1:A:271:ALA:HA	1.96	0.66
1:A:553:THR:HG22	2:A:595:HOH:O	1.95	0.66
1:A:59:LYS:HE2	1:A:71:ALA:O	1.98	0.64
1:A:343:THR:HG22	1:A:345:LYS:H	1.62	0.64
1:A:205:HIS:O	1:A:209:ARG:HG3	1.97	0.64
1:A:115:ASN:O	1:A:159:THR:HG21	1.97	0.63
1:A:321:PHE:HB2	1:A:333:ARG:NH2	2.14	0.63
1:A:311:TRP:O	1:A:343:THR:HG23	1.99	0.62
1:A:7:GLU:OE2	1:A:24:LYS:HE2	2.00	0.62
1:A:296:ASN:ND2	1:A:298:THR:H	1.97	0.62
1:A:1:MET:HG2	1:A:2:LEU:N	2.06	0.60
1:A:414:ARG:HH11	1:A:414:ARG:HG2	1.65	0.59
1:A:395:MET:HE3	1:A:395:MET:HA	1.83	0.59
1:A:447:VAL:CG2	1:A:525:PRO:HB2	2.32	0.59
1:A:159:THR:HG22	1:A:184:TYR:HB2	1.83	0.59
1:A:407:GLU:HA	1:A:410:GLU:HG2	1.83	0.59
1:A:296:ASN:HD22	1:A:297:GLY:N	2.01	0.58
1:A:493:PRO:HB3	1:A:565:LEU:HA	1.85	0.58
1:A:124:ARG:HD2	2:A:658:HOH:O	2.03	0.57
1:A:14:LEU:HD23	1:A:17:MET:CE	2.34	0.57
1:A:154:ARG:HB2	1:A:154:ARG:NH1	2.19	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:HIS:HE1	1:A:406:ASP:OD2	1.88	0.56
1:A:282:ILE:HD13	1:A:362:ALA:HB1	1.88	0.56
1:A:300:THR:CG2	1:A:303:ALA:H	2.19	0.56
1:A:125:ASN:C	1:A:125:ASN:HD22	2.12	0.56
1:A:40:LEU:HD23	1:A:54:ILE:HG22	1.88	0.55
1:A:12:GLN:HE22	1:A:15:LYS:NZ	2.04	0.55
1:A:269:LYS:HD3	1:A:269:LYS:O	2.07	0.55
1:A:115:ASN:HB2	1:A:159:THR:CG2	2.36	0.55
1:A:513:GLU:HG3	2:A:631:HOH:O	2.06	0.55
1:A:1:MET:HG3	1:A:513:GLU:OE1	2.07	0.54
1:A:128:LEU:HD22	1:A:383:LEU:HD21	1.90	0.54
1:A:32:LYS:HB3	1:A:33:PRO:CD	2.38	0.54
1:A:281:VAL:HG23	1:A:282:ILE:HG13	1.90	0.54
1:A:296:ASN:HD22	1:A:296:ASN:C	2.16	0.54
1:A:279:SER:N	1:A:280:PRO:HD2	2.22	0.53
1:A:233:ARG:HG3	1:A:233:ARG:HH11	1.73	0.53
1:A:31:ASP:O	1:A:32:LYS:HD2	2.08	0.53
1:A:353:VAL:O	1:A:384:ALA:HA	2.09	0.53
1:A:115:ASN:HB2	1:A:159:THR:HG21	1.90	0.53
1:A:197:GLN:O	1:A:201:GLU:HG2	2.09	0.53
1:A:90:GLU:HG3	1:A:510:LEU:HD22	1.89	0.52
1:A:275:VAL:CG2	1:A:289:PHE:HB3	2.39	0.52
1:A:450:GLU:HB3	1:A:452:LYS:HZ3	1.73	0.52
1:A:182:ARG:HG2	2:A:706:HOH:O	2.09	0.51
1:A:393:ARG:HG2	1:A:393:ARG:HH11	1.75	0.51
1:A:465:PHE:HE2	1:A:592:MET:HE2	1.74	0.51
1:A:574:GLN:HG3	1:A:575:ARG:N	2.25	0.51
1:A:182:ARG:HG2	1:A:182:ARG:HH11	1.75	0.51
1:A:112:VAL:HG21	1:A:118:LEU:HD22	1.92	0.51
1:A:573:LEU:O	1:A:573:LEU:HG	2.08	0.51
1:A:1:MET:HE2	1:A:513:GLU:HB3	1.93	0.50
1:A:422:GLU:HG3	1:A:423:LYS:N	2.28	0.49
1:A:425:PRO:C	1:A:430:LYS:HZ1	2.21	0.49
1:A:146:LEU:C	1:A:146:LEU:HD23	2.37	0.48
1:A:40:LEU:O	1:A:44:ALA:HB2	2.13	0.48
1:A:524:THR:HB	1:A:526:HIS:CE1	2.48	0.48
1:A:69:GLU:HG2	1:A:81:ARG:NH1	2.28	0.48
1:A:410:GLU:HG3	1:A:411:GLU:N	2.28	0.48
1:A:3:ARG:O	1:A:7:GLU:HG3	2.14	0.48
1:A:256:LEU:HD22	1:A:276:MET:HE2	1.96	0.48
1:A:465:PHE:CE2	1:A:592:MET:HE2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:MET:CG	1:A:2:LEU:H	2.09	0.47
1:A:517:LEU:O	1:A:521:GLU:HG3	2.13	0.47
1:A:119:HIS:HD2	1:A:121:GLY:N	2.12	0.47
1:A:571:GLN:O	1:A:574:GLN:HG3	2.14	0.47
1:A:186:ARG:HG2	2:A:682:HOH:O	2.13	0.47
1:A:293:LEU:HD23	1:A:299:ALA:HA	1.96	0.47
1:A:32:LYS:HB3	1:A:33:PRO:HD2	1.97	0.46
1:A:213:ARG:HH22	1:A:242:ASP:CG	2.23	0.46
1:A:484:LEU:HD11	1:A:574:GLN:HG2	1.98	0.46
1:A:275:VAL:HG22	1:A:276:MET:N	2.31	0.46
1:A:450:GLU:HB3	1:A:452:LYS:HZ1	1.77	0.46
1:A:59:LYS:HD2	1:A:73:PRO:HD3	1.98	0.46
1:A:269:LYS:HD3	1:A:269:LYS:C	2.41	0.46
1:A:492:ALA:HA	1:A:493:PRO:HD3	1.78	0.45
1:A:29:PRO:HB2	1:A:32:LYS:HB2	1.98	0.45
1:A:253:LEU:O	1:A:257:GLU:HG3	2.15	0.45
1:A:479:ARG:HH11	1:A:479:ARG:CB	2.29	0.45
1:A:119:HIS:HD2	1:A:121:GLY:H	1.64	0.45
1:A:40:LEU:HD23	1:A:54:ILE:CG2	2.47	0.45
1:A:158:GLU:OE1	1:A:188:HIS:HE1	1.98	0.45
1:A:19:VAL:HG11	1:A:47:LEU:HD11	1.99	0.45
1:A:452:LYS:HZ2	1:A:452:LYS:CB	2.26	0.45
1:A:52:GLN:HE22	1:A:75:GLY:H	1.63	0.44
1:A:87:LEU:HD13	1:A:503:ARG:NH1	2.32	0.44
1:A:296:ASN:ND2	1:A:296:ASN:C	2.75	0.44
1:A:31:ASP:C	1:A:32:LYS:HD2	2.43	0.44
1:A:125:ASN:ND2	1:A:125:ASN:C	2.74	0.44
1:A:553:THR:O	1:A:553:THR:HG23	2.18	0.43
1:A:566:ARG:O	1:A:570:VAL:HG23	2.18	0.43
1:A:19:VAL:O	1:A:19:VAL:HG23	2.18	0.43
1:A:443:ARG:HA	1:A:443:ARG:HD2	1.90	0.43
1:A:443:ARG:HH11	1:A:443:ARG:HB3	1.84	0.43
1:A:348:GLU:HG2	1:A:379:LYS:HD2	2.00	0.43
1:A:119:HIS:CD2	1:A:121:GLY:H	2.37	0.43
1:A:36:TYR:HE1	1:A:82:LEU:HD11	1.84	0.43
1:A:539:TRP:CE3	1:A:573:LEU:HD22	2.53	0.43
1:A:14:LEU:HA	1:A:17:MET:HE2	2.00	0.43
1:A:237:LEU:HD13	1:A:332:LEU:HD11	2.01	0.42
1:A:447:VAL:HG22	1:A:525:PRO:HB2	2.00	0.42
1:A:553:THR:N	1:A:554:PRO:CD	2.82	0.42
1:A:95:LYS:H	1:A:95:LYS:CD	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:THR:HG22	1:A:184:TYR:CD1	2.54	0.42
1:A:18:GLY:O	1:A:20:PRO:HD3	2.20	0.42
1:A:111:SER:H	1:A:147:ASN:ND2	2.17	0.41
1:A:120:VAL:O	1:A:123:LEU:HB2	2.20	0.41
1:A:479:ARG:HH11	1:A:479:ARG:HB2	1.85	0.41
1:A:111:SER:HA	1:A:147:ASN:HD21	1.86	0.41
1:A:147:ASN:C	1:A:147:ASN:HD22	2.28	0.41
1:A:97:PRO:HG3	1:A:138:TYR:CD1	2.56	0.41
1:A:355:VAL:HG22	1:A:385:TYR:O	2.20	0.41
1:A:414:ARG:HH11	1:A:414:ARG:CG	2.33	0.41
1:A:154:ARG:HH11	1:A:154:ARG:CB	2.29	0.41
1:A:275:VAL:HG21	1:A:289:PHE:HD2	1.85	0.41
1:A:348:GLU:HG2	1:A:379:LYS:HB3	2.03	0.41
1:A:432:GLU:HA	1:A:432:GLU:OE1	2.21	0.41
1:A:224:MET:HE3	1:A:224:MET:HB2	1.96	0.41
1:A:414:ARG:HG2	1:A:414:ARG:NH1	2.35	0.40
1:A:542:TYR:O	1:A:553:THR:CG2	2.62	0.40
1:A:387:THR:HG22	1:A:388:VAL:N	2.35	0.40
1:A:395:MET:HG3	1:A:402:ALA:HA	2.03	0.40
1:A:452:LYS:NZ	1:A:452:LYS:H	2.20	0.40
1:A:539:TRP:CD2	1:A:573:LEU:HD22	2.57	0.40
1:A:171:ASP:C	1:A:171:ASP:OD2	2.63	0.40
1:A:274:LEU:HB3	1:A:293:LEU:HB2	2.03	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	584/592 (99%)	564 (97%)	14 (2%)	6 (1%)	12 15

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	110	THR
1	A	428	PRO
1	A	284	GLY
1	A	33	PRO
1	A	75	GLY
1	A	29	PRO

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	473/476 (99%)	450 (95%)	23 (5%)	22	34

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LEU
1	A	95	LYS
1	A	118	LEU
1	A	124	ARG
1	A	125	ASN
1	A	128	LEU
1	A	182	ARG
1	A	204	LEU
1	A	237	LEU
1	A	253	LEU
1	A	266	ARG
1	A	269	LYS
1	A	296	ASN
1	A	319	LEU
1	A	395	MET
1	A	443	ARG
1	A	452	LYS
1	A	479	ARG
1	A	528	LEU
1	A	562	LEU
1	A	573	LEU

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Mol	Chain	Res	Type
1	A	574	GLN
1	A	581	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	GLN
1	A	119	HIS
1	A	125	ASN
1	A	147	ASN
1	A	165	HIS
1	A	178	HIS
1	A	188	HIS
1	A	261	HIS
1	A	296	ASN
1	A	351	ASN
1	A	361	GLN
1	A	424	ASN
1	A	497	GLN
1	A	548	ASN
1	A	550	GLN

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 [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	588/592 (99%)	0.65	86 (14%) 6 6	15, 30, 86, 131	0

All (86) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	397	GLY	8.7
1	A	402	ALA	7.7
1	A	357	GLN	7.1
1	A	396	SER	6.5
1	A	287	ASP	5.8
1	A	31	ASP	5.7
1	A	1	MET	5.6
1	A	266	ARG	5.4
1	A	19	VAL	5.4
1	A	32	LYS	5.3
1	A	45	LYS	5.2
1	A	426	ASP	5.1
1	A	30	LYS	5.0
1	A	422	GLU	4.9
1	A	286	GLU	4.8
1	A	282	ILE	4.7
1	A	18	GLY	4.7
1	A	285	LEU	4.6
1	A	361	GLN	4.5
1	A	452	LYS	4.4
1	A	33	PRO	4.3
1	A	395	MET	4.3
1	A	16	GLU	4.1
1	A	102	PRO	4.1
1	A	424	ASN	4.0
1	A	284	GLY	3.9
1	A	20	PRO	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	288	PRO	3.8
1	A	94	PRO	3.7
1	A	48	ARG	3.7
1	A	21	VAL	3.6
1	A	283	PRO	3.6
1	A	301	TYR	3.6
1	A	428	PRO	3.6
1	A	17	MET	3.6
1	A	358	SER	3.6
1	A	267	GLU	3.6
1	A	414	ARG	3.5
1	A	268	GLY	3.5
1	A	359	HIS	3.5
1	A	50	PRO	3.5
1	A	29	PRO	3.4
1	A	52	GLN	3.3
1	A	289	PHE	3.3
1	A	430	LYS	3.3
1	A	43	LEU	3.3
1	A	22	ARG	3.2
1	A	343	THR	3.2
1	A	47	LEU	3.2
1	A	425	PRO	3.1
1	A	356	ARG	3.0
1	A	393	ARG	2.9
1	A	360	PRO	2.9
1	A	41	PHE	2.9
1	A	46	GLU	2.9
1	A	44	ALA	2.8
1	A	121	GLY	2.8
1	A	42	ALA	2.8
1	A	40	LEU	2.7
1	A	15	LYS	2.6
1	A	2	LEU	2.6
1	A	159	THR	2.6
1	A	74	VAL	2.5
1	A	275	VAL	2.5
1	A	429	ASP	2.5
1	A	233	ARG	2.4
1	A	355	VAL	2.4
1	A	14	LEU	2.4
1	A	387	THR	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	592	MET	2.3
1	A	51	PRO	2.3
1	A	95	LYS	2.3
1	A	63	PRO	2.3
1	A	49	LYS	2.3
1	A	365	ARG	2.2
1	A	61	ARG	2.2
1	A	421	GLU	2.2
1	A	76	GLY	2.2
1	A	250	GLN	2.2
1	A	60	ASP	2.1
1	A	93	ARG	2.1
1	A	302	TYR	2.1
1	A	101	ARG	2.1
1	A	423	LYS	2.1
1	A	465	PHE	2.1
1	A	12	GLN	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.