



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:33 PM UTC

PDB ID : 2GGO / pdb_00002ggo
Title : Crystal Structure of glucose-1-phosphate thymidyltransferase from *Sulfolobus tokodaii*
Authors : Rajakannan, V.; Mizushima, T.; Suzuki, A.; Masui, R.; Kuramitsu, S.; Yamane, T.
Deposited on : 2006-03-24
Resolution : 1.80 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

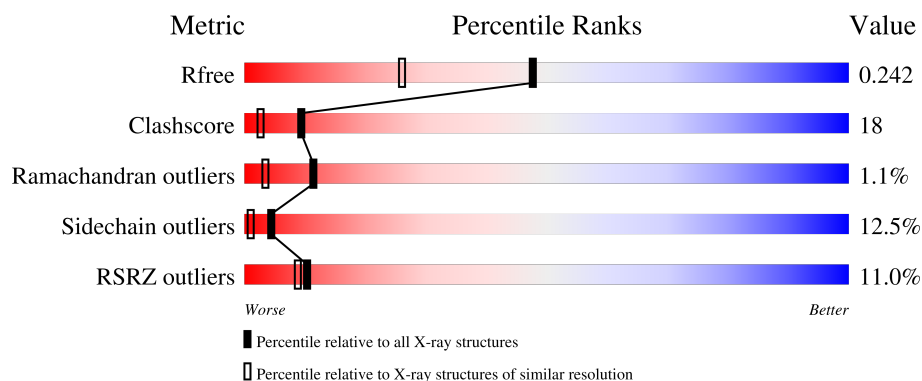
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	401	11% 60% 29% 9%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3332 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 401aa long hypothetical glucose-1-phosphate thymidyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	401	Total	C	N	O	S	0	0	0
			3141	2021	524	590	6			

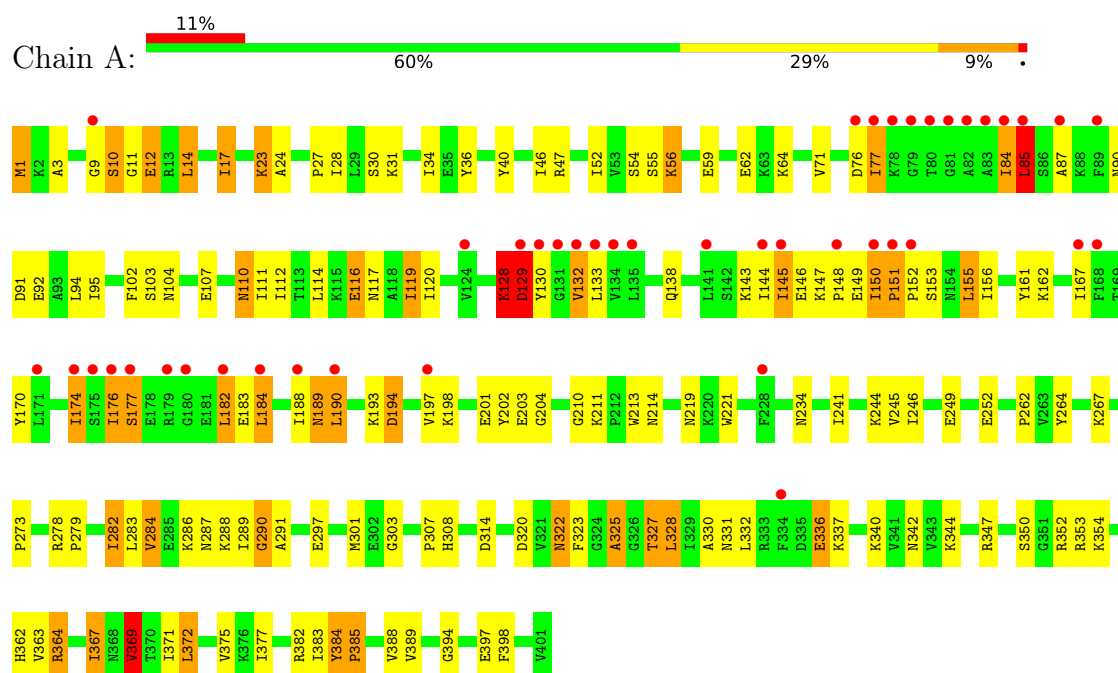
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	191	Total	O	0	0
			191	191		

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: 401aa long hypothetical glucose-1-phosphate thymidyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	123.00Å 123.00Å 94.88Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.00 – 1.80 19.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	96.6 (19.00-1.80) 96.6 (19.00-1.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.222 , 0.267 (Not available) , 0.242	Depositor DCC
R_{free} test set	2438 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	19.4	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 69.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.031 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3332	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.11% 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	1.19	13/3195 (0.4%)	1.26	30/4311 (0.7%)

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	2

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	322	ASN	C-O	-7.21	1.15	1.24
1	A	290	GLY	N-CA	6.76	1.51	1.44
1	A	369	VAL	CB-CG2	6.61	1.74	1.52
1	A	325	ALA	CA-C	-6.55	1.44	1.52
1	A	323	PHE	CA-C	-6.12	1.45	1.52
1	A	282	ILE	CA-CB	6.03	1.61	1.53
1	A	308	HIS	C-O	-5.88	1.17	1.23
1	A	367	ILE	N-CA	5.83	1.53	1.46
1	A	369	VAL	CA-C	5.31	1.58	1.52
1	A	388	VAL	CA-CB	5.27	1.60	1.53
1	A	330	ALA	CA-CB	-5.21	1.45	1.53
1	A	363	VAL	CA-CB	5.17	1.59	1.54
1	A	369	VAL	C-O	5.13	1.30	1.24

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	323	PHE	CA-C-N	-6.48	113.94	120.10
1	A	323	PHE	C-N-CA	-6.48	113.94	120.10
1	A	308	HIS	CB-CA-C	-6.47	98.80	109.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	129	ASP	CA-C-N	6.03	132.56	121.70
1	A	129	ASP	C-N-CA	6.03	132.56	121.70
1	A	203	GLU	N-CA-C	5.97	120.62	112.68
1	A	328	LEU	CB-CG-CD2	-5.89	93.04	110.70
1	A	328	LEU	N-CA-C	-5.88	98.28	108.69
1	A	384	TYR	CA-C-N	5.83	125.85	119.90
1	A	384	TYR	C-N-CA	5.83	125.85	119.90
1	A	371	ILE	N-CA-C	5.82	116.24	107.80
1	A	336	GLU	N-CA-C	5.80	119.67	112.47
1	A	369	VAL	CB-CA-C	5.68	119.89	111.26
1	A	372	LEU	CA-C-N	-5.57	114.19	119.76
1	A	372	LEU	C-N-CA	-5.57	114.19	119.76
1	A	364	ARG	CA-C-N	-5.51	114.44	122.65
1	A	364	ARG	C-N-CA	-5.51	114.44	122.65
1	A	85	LEU	N-CA-C	-5.44	106.71	113.19
1	A	12	GLU	N-CA-C	5.42	116.86	111.07
1	A	377	ILE	CA-C-N	5.36	125.19	120.10
1	A	377	ILE	C-N-CA	5.36	125.19	120.10
1	A	363	VAL	N-CA-C	5.33	117.31	109.63
1	A	327	THR	CA-C-O	-5.27	115.41	121.47
1	A	369	VAL	CA-C-N	5.26	130.58	123.11
1	A	369	VAL	C-N-CA	5.26	130.58	123.11
1	A	289	ILE	CA-C-N	5.24	127.09	122.43
1	A	289	ILE	C-N-CA	5.24	127.09	122.43
1	A	128	LYS	N-CA-C	5.14	121.76	110.80
1	A	284	VAL	N-CA-C	5.13	115.90	110.72
1	A	327	THR	N-CA-CB	-5.03	102.64	110.29

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	128	LYS	Peptide
1	A	9	GLY	Peptide

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	3141	0	3244	115	0
2	A	191	0	0	15	0
All	All	3332	0	3244	115	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 18.

All (115) 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:320:ASP:HB3	2:A:559:HOH:O	1.49	1.11
1:A:84:ILE:HG22	1:A:87:ALA:HB2	1.38	1.06
1:A:176:ILE:HG12	1:A:182:LEU:HD13	1.47	0.93
1:A:128:LYS:N	1:A:129:ASP:HB2	1.96	0.81
1:A:107:GLU:HG3	1:A:202:TYR:CD1	2.16	0.80
1:A:84:ILE:HD11	1:A:184:LEU:HD22	1.65	0.76
1:A:129:ASP:O	1:A:129:ASP:OD1	2.03	0.75
1:A:107:GLU:HG3	1:A:202:TYR:HD1	1.51	0.74
1:A:394:GLY:N	1:A:397:GLU:OE1	2.20	0.73
1:A:40:TYR:CD2	1:A:102:PHE:CE1	2.76	0.73
1:A:1:MET:HE1	1:A:162:LYS:HD3	1.74	0.69
1:A:148:PRO:HG2	1:A:150:ILE:O	1.93	0.69
1:A:147:LYS:HB3	2:A:590:HOH:O	1.93	0.68
1:A:128:LYS:O	1:A:148:PRO:HD2	1.93	0.67
1:A:40:TYR:HD2	1:A:102:PHE:CE1	2.14	0.66
1:A:327:THR:HA	1:A:369:VAL:O	1.96	0.65
1:A:353:ARG:HD3	2:A:499:HOH:O	1.97	0.64
1:A:286:LYS:O	1:A:303:GLY:HA2	1.99	0.63
1:A:119:ILE:HD11	1:A:188:ILE:HD13	1.80	0.62
1:A:1:MET:CE	1:A:162:LYS:HD3	2.31	0.59
1:A:342:ASN:OD1	1:A:347:ARG:HD2	2.02	0.59
1:A:288:LYS:HE2	2:A:439:HOH:O	2.02	0.59
1:A:249:GLU:HG2	2:A:527:HOH:O	2.02	0.58
1:A:54:SER:OG	1:A:56:LYS:HG3	2.03	0.58
1:A:40:TYR:CE2	1:A:102:PHE:O	2.57	0.58
1:A:143:LYS:HA	1:A:189:ASN:HD21	1.68	0.58
1:A:336:GLU:OE1	1:A:353:ARG:NH2	2.38	0.57
1:A:129:ASP:OD1	1:A:129:ASP:C	2.48	0.57
1:A:150:ILE:O	1:A:152:PRO:HD3	2.05	0.57
1:A:336:GLU:HB3	1:A:353:ARG:HH21	1.70	0.56
1:A:340:LYS:HB2	1:A:347:ARG:NH2	2.20	0.56
1:A:3:ALA:HB2	1:A:46:ILE:HG21	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:241:ILE:HG23	1:A:245:VAL:HG21	1.88	0.56
1:A:145:ILE:CD1	1:A:152:PRO:HG2	2.35	0.56
1:A:320:ASP:CB	2:A:559:HOH:O	2.28	0.56
1:A:194:ASP:N	1:A:194:ASP:OD1	2.39	0.55
1:A:119:ILE:HG12	1:A:161:TYR:CD2	2.41	0.55
1:A:40:TYR:HE2	1:A:102:PHE:O	1.89	0.55
1:A:244:LYS:O	1:A:262:PRO:HA	2.07	0.54
1:A:290:GLY:HA3	1:A:307:PRO:O	2.07	0.54
1:A:352:ARG:HD2	2:A:563:HOH:O	2.08	0.54
1:A:76:ASP:HA	2:A:461:HOH:O	2.08	0.53
1:A:325:ALA:O	1:A:367:ILE:HA	2.08	0.53
1:A:47:ARG:HD3	2:A:405:HOH:O	2.09	0.53
1:A:143:LYS:HA	1:A:189:ASN:ND2	2.25	0.52
1:A:77:ILE:CD1	1:A:85:LEU:HD12	2.40	0.52
1:A:128:LYS:CA	1:A:129:ASP:HB2	2.40	0.52
1:A:133:LEU:HD12	1:A:155:LEU:HD13	1.92	0.51
1:A:110:ASN:HD22	1:A:110:ASN:C	2.18	0.51
1:A:219:ASN:HB3	1:A:282:ILE:HD13	1.92	0.51
1:A:145:ILE:HD13	1:A:152:PRO:HG2	1.92	0.50
1:A:210:GLY:O	1:A:211:LYS:HG3	2.12	0.50
1:A:114:LEU:HD13	1:A:198:LYS:HD3	1.94	0.49
1:A:119:ILE:HG12	1:A:161:TYR:HD2	1.77	0.49
1:A:84:ILE:HD11	1:A:184:LEU:CD2	2.39	0.49
1:A:30:SER:HB3	1:A:264:TYR:OH	2.13	0.48
1:A:384:TYR:CD1	1:A:385:PRO:HD2	2.48	0.48
1:A:150:ILE:HD13	1:A:151:PRO:HD2	1.95	0.48
1:A:155:LEU:HD21	1:A:201:GLU:HG3	1.95	0.48
1:A:297:GLU:O	1:A:314:ASP:HA	2.13	0.48
1:A:246:ILE:HD12	1:A:246:ILE:N	2.28	0.48
1:A:84:ILE:CG2	1:A:87:ALA:HB2	2.27	0.48
1:A:52:ILE:HA	1:A:71:VAL:O	2.13	0.47
1:A:322:ASN:ND2	2:A:410:HOH:O	2.46	0.47
1:A:23:LYS:HG3	2:A:404:HOH:O	2.14	0.47
1:A:241:ILE:CG2	1:A:245:VAL:HG21	2.45	0.46
1:A:364:ARG:HD3	2:A:477:HOH:O	2.15	0.46
1:A:174:ILE:HG12	1:A:190:LEU:HD11	1.98	0.46
1:A:234:ASN:HD22	1:A:252:GLU:HG3	1.79	0.45
1:A:128:LYS:N	1:A:129:ASP:CB	2.75	0.45
1:A:27:PRO:HD2	1:A:301:MET:HE2	1.99	0.45
1:A:24:ALA:HB1	1:A:34:ILE:HB	1.98	0.45
1:A:283:LEU:HB3	1:A:287:ASN:ND2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:GLU:HB3	2:A:418:HOH:O	2.16	0.45
1:A:23:LYS:HG3	1:A:23:LYS:H	1.57	0.45
1:A:211:LYS:H	1:A:214:ASN:HD22	1.65	0.44
1:A:278:ARG:HB3	1:A:279:PRO:HD2	1.99	0.44
1:A:1:MET:HG3	1:A:112:ILE:HB	2.00	0.44
1:A:174:ILE:HG23	1:A:176:ILE:HG23	2.00	0.44
1:A:146:GLU:OE2	1:A:147:LYS:HG3	2.17	0.44
1:A:372:LEU:HD12	1:A:372:LEU:N	2.32	0.44
1:A:369:VAL:HG21	1:A:383:ILE:HG22	1.99	0.44
1:A:10:SER:HA	1:A:11:GLY:HA3	1.66	0.43
1:A:103:SER:HB3	1:A:221:TRP:CH2	2.53	0.43
1:A:320:ASP:O	1:A:362:HIS:HA	2.17	0.43
1:A:1:MET:HE1	1:A:92:GLU:HB3	1.99	0.43
1:A:77:ILE:HD12	1:A:85:LEU:HD12	2.00	0.43
1:A:170:TYR:HB3	1:A:190:LEU:HD12	2.01	0.43
1:A:331:ASN:O	1:A:354:LYS:HA	2.18	0.43
1:A:17:ILE:N	1:A:17:ILE:CD1	2.81	0.43
1:A:129:ASP:HB3	1:A:130:TYR:HB2	1.99	0.43
1:A:193:LYS:HA	1:A:193:LYS:HD3	1.81	0.42
1:A:111:ILE:HG12	1:A:162:LYS:HB2	2.01	0.42
1:A:116:GLU:OE2	1:A:198:LYS:HG3	2.19	0.42
1:A:161:TYR:HE1	1:A:184:LEU:HD23	1.85	0.42
1:A:332:LEU:HD13	1:A:354:LYS:HE3	2.00	0.42
1:A:3:ALA:HA	1:A:94:LEU:O	2.20	0.42
1:A:120:ILE:CG2	1:A:202:TYR:HB2	2.50	0.42
1:A:167:ILE:HD12	1:A:167:ILE:HA	1.93	0.42
1:A:14:LEU:HD12	1:A:14:LEU:HA	1.93	0.42
1:A:176:ILE:HG22	1:A:177:SER:OG	2.19	0.42
1:A:328:LEU:HD23	1:A:328:LEU:HA	1.80	0.42
1:A:148:PRO:C	1:A:150:ILE:H	2.27	0.41
1:A:336:GLU:HB3	1:A:353:ARG:NH2	2.33	0.41
1:A:213:TRP:CZ2	1:A:350:SER:HA	2.55	0.41
1:A:31:LYS:NZ	2:A:565:HOH:O	2.53	0.41
1:A:273:PRO:O	1:A:291:ALA:HA	2.21	0.41
1:A:12:GLU:HB3	1:A:344:LYS:HG2	2.03	0.41
1:A:128:LYS:HB3	2:A:570:HOH:O	2.21	0.41
1:A:394:GLY:CA	1:A:397:GLU:OE1	2.68	0.41
1:A:132:VAL:HG12	1:A:153:SER:HB3	2.02	0.41
1:A:382:ARG:O	1:A:398:PHE:HA	2.20	0.41
1:A:117:ASN:O	1:A:197:VAL:HA	2.21	0.41
1:A:176:ILE:HA	1:A:177:SER:HA	1.93	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:ILE:HB	1:A:36:TYR:CE1	2.56	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	363/401 (90%)	331 (91%)	28 (8%)	4 (1%)	11 3

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	149	GLU
1	A	129	ASP
1	A	204	GLY
1	A	151	PRO

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	344/344 (100%)	301 (88%)	43 (12%)	4 1

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	10	SER
1	A	14	LEU
1	A	17	ILE
1	A	23	LYS
1	A	55	SER
1	A	56	LYS
1	A	59	GLU
1	A	62	GLU
1	A	64	LYS
1	A	77	ILE
1	A	84	ILE
1	A	85	LEU
1	A	90	ASN
1	A	91	ASP
1	A	95	ILE
1	A	104	ASN
1	A	110	ASN
1	A	116	GLU
1	A	119	ILE
1	A	128	LYS
1	A	132	VAL
1	A	138	GLN
1	A	144	ILE
1	A	145	ILE
1	A	150	ILE
1	A	155	LEU
1	A	156	ILE
1	A	174	ILE
1	A	176	ILE
1	A	177	SER
1	A	182	LEU
1	A	184	LEU
1	A	189	ASN
1	A	190	LEU
1	A	194	ASP
1	A	267	LYS
1	A	284	VAL
1	A	337	LYS
1	A	369	VAL
1	A	375	VAL
1	A	385	PRO
1	A	389	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	GLN
1	A	104	ASN
1	A	110	ASN
1	A	140	ASN
1	A	154	ASN
1	A	189	ASN
1	A	195	HIS
1	A	214	ASN
1	A	225	ASN
1	A	230	GLN
1	A	234	ASN
1	A	287	ASN
1	A	308	HIS

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 ⓘ

There are no ligands in this entry.

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	401/401 (100%)	0.24	44 (10%) 10 9	5, 37, 97, 122	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	77	ILE	5.8
1	A	150	ILE	4.8
1	A	89	PHE	3.9
1	A	182	LEU	3.8
1	A	174	ILE	3.8
1	A	334	PHE	3.6
1	A	141	LEU	3.4
1	A	167	ILE	3.4
1	A	83	ALA	3.3
1	A	84	ILE	3.2
1	A	82	ALA	3.2
1	A	130	TYR	3.1
1	A	145	ILE	3.1
1	A	129	ASP	3.1
1	A	134	VAL	3.0
1	A	79	GLY	3.0
1	A	180	GLY	3.0
1	A	176	ILE	2.7
1	A	184	LEU	2.7
1	A	76	ASP	2.6
1	A	135	LEU	2.6
1	A	144	ILE	2.6
1	A	87	ALA	2.6
1	A	80	THR	2.6
1	A	133	LEU	2.6
1	A	85	LEU	2.5
1	A	152	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	177	SER	2.4
1	A	148	PRO	2.4
1	A	175	SER	2.4
1	A	9	GLY	2.4
1	A	151	PRO	2.4
1	A	131	GLY	2.4
1	A	132	VAL	2.4
1	A	188	ILE	2.3
1	A	78	LYS	2.3
1	A	179	ARG	2.3
1	A	124	VAL	2.2
1	A	171	LEU	2.2
1	A	168	PHE	2.2
1	A	190	LEU	2.2
1	A	81	GLY	2.2
1	A	228	PHE	2.1
1	A	197	VAL	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.