



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:44 AM GMT

PDB ID : 2IHR
Title : RF2 of Thermus thermophilus
Authors : Dobbek, H.; Voertler, C.S.; Sprinzl, M.
Deposited on : 2006-09-27
Resolution : 2.50 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

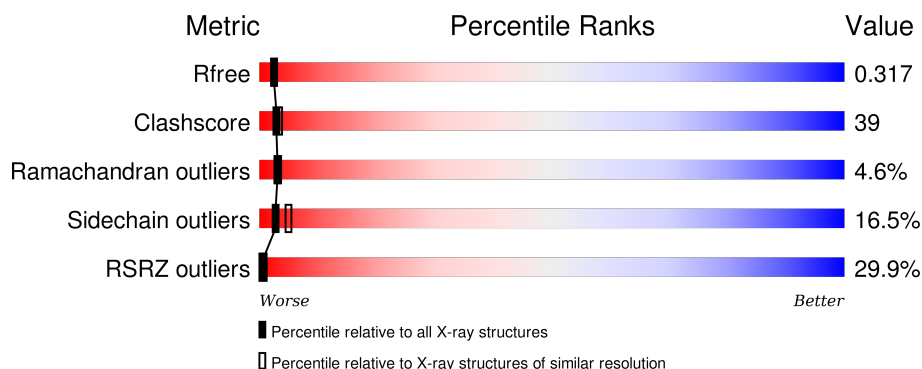
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	1	365	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2823 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 Peptide chain release factor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	351	Total	C	N	O	S	0	0	0
			2792	1748	503	533	8			

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	-4	MET	-	CLONING ARTIFACT	UNP Q5SM01
1	-3	ASP	-	CLONING ARTIFACT	UNP Q5SM01
1	-2	LEU	-	CLONING ARTIFACT	UNP Q5SM01
1	-1	GLU	-	CLONING ARTIFACT	UNP Q5SM01
1	0	ARG	-	CLONING ARTIFACT	UNP Q5SM01
1	1	LEU	-	CLONING ARTIFACT	UNP Q5SM01
1	2	ALA	-	CLONING ARTIFACT	UNP Q5SM01
1	3	GLN	-	CLONING ARTIFACT	UNP Q5SM01
1	4	ARG	-	CLONING ARTIFACT	UNP Q5SM01
1	5	LEU	-	CLONING ARTIFACT	UNP Q5SM01
1	6	GLU	-	CLONING ARTIFACT	UNP Q5SM01
1	7	GLY	-	CLONING ARTIFACT	UNP Q5SM01
1	8	LEU	-	CLONING ARTIFACT	UNP Q5SM01

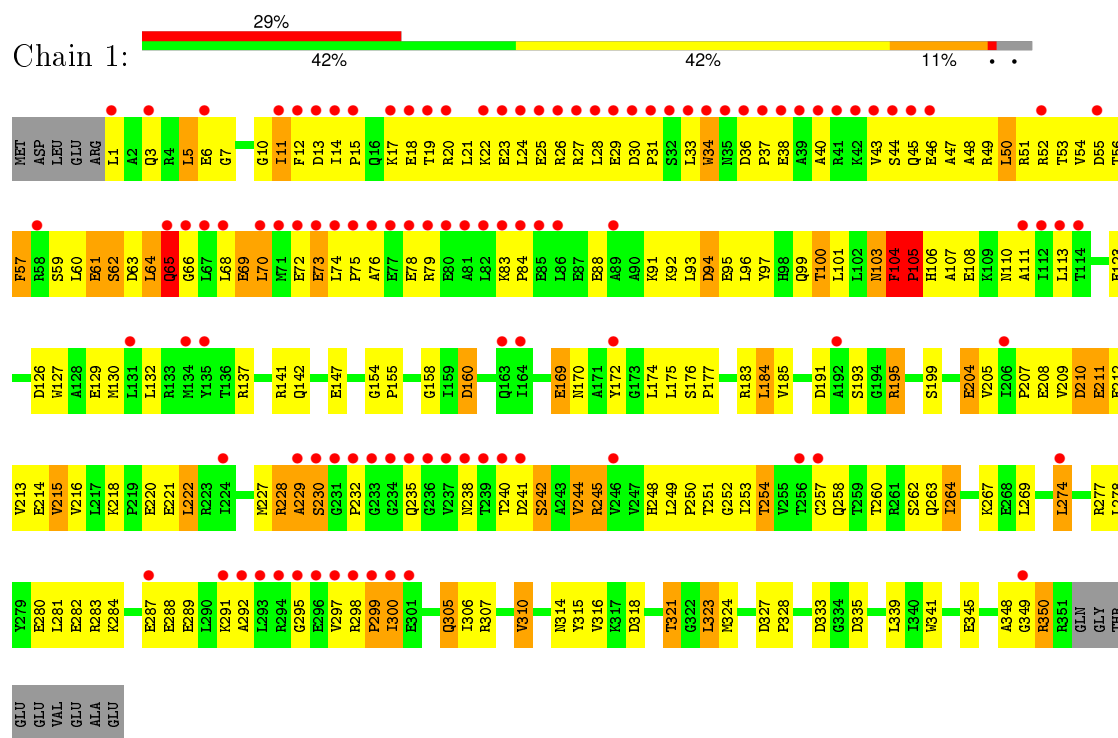
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	1	31	Total	O	0	0
			31	31		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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: Peptide chain release factor 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	144.65Å 144.65Å 54.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 24.81 – 2.37	Depositor EDS
% Data completeness (in resolution range)	99.0 (20.00-2.50) 98.8 (24.81-2.37)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.36Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.269 , 0.317 0.268 , 0.317	Depositor DCC
R_{free} test set	1018 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	55.6	Xtriage
Anisotropy	0.418	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 73.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 23901 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2823	wwPDB-VP
Average B, all atoms (Å ²)	120.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	1	0.60	0/2840	0.94	5/3837 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	104	PHE	C-N-CD	-16.95	83.31	120.60
1	1	104	PHE	C-N-CA	10.22	164.91	122.00
1	1	333	ASP	CB-CG-OD2	-5.55	113.30	118.30
1	1	277	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	1	314	ASN	N-CA-C	5.01	124.52	111.00

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	1	2792	0	2809	221	0
2	1	31	0	0	3	0
All	All	2823	0	2809	221	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 39.

All (221) 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)
1:1:49:ARG:HA	1:1:52:ARG:HD2	1.43	1.00
1:1:21:LEU:HD13	1:1:43:VAL:HG23	1.52	0.90
1:1:17:LYS:HE3	1:1:21:LEU:HD21	1.50	0.89
1:1:297:VAL:HG12	1:1:298:ARG:H	1.40	0.87
1:1:96:LEU:O	1:1:100:THR:HG22	1.77	0.84
1:1:235:GLN:HA	1:1:238:ASN:HB2	1.56	0.84
1:1:88:GLU:O	1:1:92:LYS:HB2	1.81	0.81
1:1:183:ARG:HB2	1:1:305:GLN:HG2	1.65	0.78
1:1:348:ALA:O	1:1:350:ARG:N	2.17	0.77
1:1:253:ILE:HD11	1:1:281:LEU:HD12	1.66	0.76
1:1:18:GLU:OE1	1:1:19:THR:HG23	1.87	0.74
1:1:245:ARG:HH11	1:1:245:ARG:HB3	1.53	0.74
1:1:210:ASP:OD1	1:1:210:ASP:N	2.16	0.73
1:1:64:LEU:HD12	1:1:64:LEU:O	1.87	0.73
1:1:17:LYS:HA	1:1:20:ARG:HD2	1.69	0.72
1:1:316:VAL:HG23	1:1:328:PRO:HB3	1.71	0.72
1:1:5:LEU:HD12	1:1:5:LEU:O	1.89	0.72
1:1:88:GLU:O	1:1:92:LYS:HD3	1.90	0.72
1:1:218:LYS:HB2	1:1:221:GLU:CG	2.21	0.71
1:1:257:CYS:SG	1:1:269:LEU:HD23	2.29	0.71
1:1:54:VAL:HA	1:1:57:PHE:CD2	2.26	0.70
1:1:18:GLU:HB3	1:1:47:ALA:HA	1.73	0.70
1:1:70:LEU:O	1:1:73:GLU:O	2.08	0.70
1:1:274:LEU:O	1:1:274:LEU:HD22	1.92	0.69
1:1:61:GLU:HG2	1:1:64:LEU:HD23	1.75	0.69
1:1:5:LEU:C	1:1:5:LEU:HD12	2.13	0.69
1:1:228:ARG:HH21	1:1:240:THR:HA	1.57	0.69
1:1:76:ALA:HB1	1:1:79:ARG:HB2	1.75	0.69
1:1:227:MET:SD	1:1:245:ARG:NH1	2.66	0.68
1:1:14:ILE:N	1:1:15:PRO:HD2	2.09	0.68
1:1:321:THR:CG2	1:1:323:LEU:H	2.07	0.68
1:1:291:LYS:NZ	1:1:299:PRO:HG3	2.08	0.68
1:1:107:ALA:O	1:1:170:ASN:HA	1.94	0.68
1:1:54:VAL:HG13	1:1:57:PHE:CZ	2.30	0.67
1:1:284:LYS:O	1:1:288:GLU:HG2	1.95	0.67
1:1:28:LEU:HD12	1:1:28:LEU:N	2.11	0.66
1:1:208:GLU:HG2	1:1:208:GLU:O	1.96	0.66
1:1:61:GLU:HG2	1:1:64:LEU:CD2	2.27	0.65
1:1:218:LYS:HB2	1:1:221:GLU:HG2	1.78	0.65
1:1:105:PRO:O	1:1:107:ALA:N	2.25	0.64
1:1:61:GLU:O	1:1:64:LEU:HB3	1.97	0.64
1:1:6:GLU:O	1:1:11:ILE:HD12	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:5:LEU:HD21	1:1:96:LEU:CD2	2.28	0.63
1:1:49:ARG:HG2	1:1:49:ARG:HH11	1.63	0.63
1:1:129:GLU:OE1	1:1:158:GLY:HA2	1.99	0.63
1:1:21:LEU:HD22	1:1:43:VAL:HG21	1.81	0.62
1:1:84:PRO:O	1:1:88:GLU:HG2	2.00	0.62
1:1:280:GLU:OE1	1:1:283:ARG:NH2	2.32	0.61
1:1:245:ARG:HH11	1:1:245:ARG:CB	2.13	0.61
1:1:91:LYS:O	1:1:95:GLU:HG2	2.00	0.61
1:1:30:ASP:OD1	1:1:37:PRO:HB3	2.01	0.61
1:1:22:LYS:O	1:1:26:ARG:HG3	2.01	0.61
1:1:348:ALA:C	1:1:350:ARG:H	2.04	0.61
1:1:11:ILE:HD13	1:1:11:ILE:H	1.66	0.60
1:1:54:VAL:HG13	1:1:57:PHE:CE2	2.36	0.60
1:1:83:LYS:N	1:1:84:PRO:HD2	2.17	0.59
1:1:46:GLU:CG	1:1:49:ARG:HH21	2.16	0.59
1:1:204:GLU:OE2	1:1:205:VAL:N	2.36	0.59
1:1:18:GLU:CD	1:1:19:THR:HG23	2.21	0.59
1:1:21:LEU:HD22	1:1:43:VAL:CG2	2.33	0.59
1:1:18:GLU:CB	1:1:47:ALA:HA	2.33	0.59
1:1:321:THR:CG2	1:1:323:LEU:HB2	2.33	0.59
1:1:300:ILE:HD13	1:1:300:ILE:H	1.68	0.59
1:1:57:PHE:C	1:1:57:PHE:CD1	2.76	0.58
1:1:11:ILE:CD1	1:1:11:ILE:H	2.17	0.58
1:1:57:PHE:HA	1:1:60:LEU:HB2	1.86	0.57
1:1:44:SER:O	1:1:47:ALA:HB3	2.03	0.57
1:1:183:ARG:CB	1:1:305:GLN:HG2	2.33	0.57
1:1:228:ARG:HB3	1:1:241:ASP:OD1	2.04	0.57
1:1:59:SER:O	1:1:62:SER:HB2	2.05	0.57
1:1:321:THR:HG23	1:1:323:LEU:H	1.68	0.56
1:1:17:LYS:HE3	1:1:21:LEU:CD2	2.30	0.56
1:1:154:GLY:HA2	1:1:160:ASP:OD2	2.04	0.56
1:1:49:ARG:O	1:1:52:ARG:HB2	2.05	0.56
1:1:51:ARG:O	1:1:55:ASP:HB2	2.05	0.56
1:1:70:LEU:HD11	1:1:74:LEU:O	2.06	0.56
1:1:210:ASP:O	1:1:212:GLU:N	2.36	0.55
1:1:103:ASN:O	1:1:103:ASN:CG	2.45	0.55
1:1:73:GLU:OE1	1:1:75:PRO:O	2.24	0.55
1:1:155:PRO:CD	1:1:160:ASP:OD2	2.55	0.55
1:1:14:ILE:N	1:1:15:PRO:CD	2.69	0.54
1:1:211:GLU:HA	1:1:214:GLU:OE1	2.07	0.54
1:1:25:GLU:OE2	1:1:40:ALA:HB3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:249:LEU:HB2	1:1:250:PRO:HD3	1.90	0.54
1:1:252:GLY:O	1:1:254:THR:HG22	2.08	0.54
1:1:70:LEU:HA	1:1:73:GLU:O	2.09	0.53
1:1:57:PHE:O	1:1:61:GLU:HB2	2.09	0.53
1:1:228:ARG:O	1:1:228:ARG:HG2	2.09	0.53
1:1:299:PRO:HB2	1:1:300:ILE:HD13	1.91	0.53
1:1:46:GLU:HG3	1:1:49:ARG:HH21	1.73	0.52
1:1:300:ILE:O	1:1:300:ILE:HG12	2.09	0.52
1:1:62:SER:O	1:1:66:GLY:N	2.43	0.52
1:1:63:ASP:C	1:1:65:GLN:H	2.12	0.52
1:1:111:ALA:HB2	1:1:172:TYR:HA	1.90	0.52
1:1:291:LYS:HZ3	1:1:299:PRO:HG3	1.73	0.52
1:1:113:LEU:HA	1:1:204:GLU:O	2.10	0.52
1:1:262:SER:HB2	1:1:264:ILE:CD1	2.40	0.52
1:1:5:LEU:C	1:1:7:GLY:H	2.12	0.52
1:1:5:LEU:C	1:1:7:GLY:N	2.63	0.52
1:1:110:ASN:HD22	1:1:110:ASN:N	2.08	0.52
1:1:6:GLU:OE1	1:1:53:THR:CG2	2.58	0.52
1:1:76:ALA:HB1	1:1:79:ARG:CB	2.39	0.52
1:1:31:PRO:HA	1:1:37:PRO:HG2	1.91	0.52
1:1:155:PRO:HD3	1:1:160:ASP:OD2	2.10	0.52
1:1:297:VAL:HG12	1:1:298:ARG:N	2.19	0.51
1:1:73:GLU:CD	1:1:75:PRO:O	2.48	0.51
1:1:169:GLU:HG2	1:1:170:ASN:ND2	2.25	0.51
1:1:34:TRP:O	1:1:38:GLU:HG2	2.10	0.51
1:1:95:GLU:O	1:1:99:GLN:N	2.39	0.51
1:1:213:VAL:HG12	1:1:213:VAL:O	2.10	0.51
1:1:335:ASP:HA	2:1:1029:HOH:O	2.10	0.51
1:1:318:ASP:HB3	1:1:321:THR:HG22	1.92	0.51
1:1:321:THR:HG22	1:1:323:LEU:H	1.75	0.51
1:1:348:ALA:C	1:1:350:ARG:N	2.63	0.51
1:1:228:ARG:O	1:1:229:ALA:C	2.49	0.51
1:1:12:PHE:C	1:1:15:PRO:HD2	2.31	0.50
1:1:208:GLU:CG	1:1:208:GLU:O	2.59	0.50
1:1:51:ARG:HG2	1:1:51:ARG:HH11	1.77	0.50
1:1:253:ILE:HD12	1:1:278:LEU:HD23	1.93	0.50
1:1:174:LEU:O	1:1:177:PRO:HD2	2.10	0.50
1:1:210:ASP:C	1:1:212:GLU:H	2.15	0.50
1:1:50:LEU:O	1:1:53:THR:HB	2.11	0.50
1:1:28:LEU:CD1	1:1:28:LEU:N	2.75	0.49
1:1:282:GLU:HA	1:1:282:GLU:OE1	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:323:LEU:HD13	1:1:339:LEU:HD23	1.94	0.49
1:1:263:GLN:NE2	1:1:267:LYS:HE3	2.27	0.49
1:1:40:ALA:HA	1:1:43:VAL:HG22	1.95	0.49
1:1:73:GLU:OE2	1:1:76:ALA:HB2	2.12	0.49
1:1:48:ALA:HB1	1:1:52:ARG:NH2	2.28	0.49
1:1:211:GLU:HA	1:1:214:GLU:HB2	1.94	0.49
1:1:127:TRP:CE2	1:1:184:LEU:HB2	2.48	0.49
1:1:5:LEU:HD21	1:1:96:LEU:HD23	1.95	0.48
1:1:218:LYS:O	1:1:222:LEU:HD13	2.13	0.48
1:1:300:ILE:HD13	1:1:300:ILE:N	2.27	0.48
1:1:27:ARG:HG2	1:1:29:GLU:H	1.79	0.48
1:1:6:GLU:OE2	1:1:11:ILE:HG21	2.14	0.48
1:1:97:TYR:O	1:1:100:THR:HG23	2.14	0.48
1:1:70:LEU:CD1	1:1:74:LEU:O	2.62	0.48
1:1:63:ASP:C	1:1:65:GLN:N	2.66	0.48
1:1:83:LYS:N	1:1:84:PRO:CD	2.76	0.48
1:1:76:ALA:HB1	1:1:79:ARG:CG	2.44	0.47
1:1:34:TRP:O	1:1:37:PRO:HD2	2.14	0.47
1:1:274:LEU:HD22	1:1:274:LEU:C	2.36	0.47
1:1:28:LEU:H	1:1:28:LEU:HD12	1.80	0.46
1:1:36:ASP:N	1:1:37:PRO:CD	2.78	0.46
1:1:95:GLU:HA	1:1:95:GLU:OE1	2.13	0.46
1:1:33:LEU:HD12	1:1:33:LEU:N	2.30	0.46
1:1:306:ILE:HG13	1:1:307:ARG:N	2.30	0.46
1:1:54:VAL:HA	1:1:57:PHE:CE2	2.51	0.46
1:1:101:LEU:HD21	1:1:345:GLU:HG2	1.98	0.46
1:1:13:ASP:N	1:1:15:PRO:HD2	2.31	0.46
1:1:222:LEU:CD1	1:1:222:LEU:N	2.79	0.46
1:1:123:GLU:HB3	1:1:199:SER:OG	2.16	0.46
1:1:40:ALA:HA	1:1:43:VAL:CG2	2.46	0.46
1:1:218:LYS:HB2	1:1:221:GLU:HG3	1.98	0.46
1:1:69:GLU:O	1:1:73:GLU:HG3	2.16	0.46
1:1:105:PRO:C	1:1:107:ALA:H	2.17	0.45
1:1:21:LEU:HD13	1:1:43:VAL:C	2.36	0.45
1:1:53:THR:HA	1:1:56:THR:HG22	1.98	0.45
1:1:193:SER:C	1:1:195:ARG:H	2.19	0.45
1:1:46:GLU:HG2	1:1:49:ARG:HH21	1.79	0.45
1:1:56:THR:O	1:1:60:LEU:HB2	2.16	0.45
1:1:185:VAL:HB	1:1:310:VAL:HB	1.99	0.45
1:1:264:ILE:H	1:1:264:ILE:HD13	1.81	0.45
1:1:66:GLY:C	1:1:68:LEU:H	2.19	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:137:ARG:O	1:1:141:ARG:HG2	2.16	0.45
1:1:51:ARG:HH22	1:1:52:ARG:HE	1.64	0.45
1:1:1:LEU:C	1:1:3:GLN:N	2.70	0.45
1:1:327:ASP:OD1	1:1:327:ASP:N	2.48	0.45
1:1:57:PHE:C	1:1:57:PHE:HD1	2.18	0.44
1:1:289:GLU:O	1:1:292:ALA:N	2.41	0.44
1:1:221:GLU:C	1:1:222:LEU:HD12	2.38	0.44
1:1:36:ASP:H	1:1:37:PRO:CD	2.30	0.44
1:1:53:THR:CA	1:1:56:THR:HG22	2.47	0.44
1:1:218:LYS:O	1:1:221:GLU:HB2	2.18	0.44
1:1:289:GLU:C	1:1:291:LYS:N	2.70	0.44
1:1:287:GLU:C	1:1:289:GLU:N	2.72	0.43
1:1:191:ASP:C	1:1:191:ASP:OD1	2.56	0.43
1:1:21:LEU:CD1	1:1:43:VAL:HG23	2.36	0.43
1:1:11:ILE:CD1	1:1:11:ILE:N	2.79	0.43
1:1:172:TYR:CG	1:1:207:PRO:HB3	2.54	0.43
1:1:289:GLU:C	1:1:291:LYS:H	2.22	0.43
1:1:49:ARG:HG2	1:1:49:ARG:NH1	2.33	0.43
1:1:221:GLU:OE1	1:1:221:GLU:HA	2.18	0.43
1:1:220:GLU:HG3	2:1:1023:HOH:O	2.19	0.43
1:1:218:LYS:O	1:1:221:GLU:N	2.36	0.43
1:1:241:ASP:O	1:1:242:SER:HB2	2.18	0.43
1:1:103:ASN:O	1:1:103:ASN:ND2	2.52	0.43
1:1:341:TRP:HA	1:1:341:TRP:CE3	2.54	0.43
1:1:291:LYS:HZ1	1:1:299:PRO:HG3	1.82	0.43
1:1:127:TRP:HA	1:1:130:MET:HE3	2.01	0.43
1:1:18:GLU:HB2	1:1:47:ALA:HB1	2.00	0.42
1:1:34:TRP:C	1:1:37:PRO:HD2	2.39	0.42
1:1:110:ASN:N	1:1:110:ASN:ND2	2.67	0.42
1:1:28:LEU:CD1	1:1:28:LEU:H	2.31	0.42
1:1:244:VAL:HG21	1:1:267:LYS:HG2	2.01	0.42
1:1:93:LEU:O	1:1:94:ASP:C	2.57	0.42
1:1:84:PRO:O	1:1:88:GLU:CG	2.65	0.42
1:1:175:LEU:HD23	1:1:175:LEU:HA	1.81	0.42
1:1:245:ARG:HH11	1:1:245:ARG:CG	2.33	0.41
1:1:262:SER:HB2	1:1:264:ILE:HD11	2.01	0.41
1:1:95:GLU:O	1:1:96:LEU:C	2.58	0.41
1:1:126:ASP:O	1:1:130:MET:HG3	2.19	0.41
1:1:248:HIS:CE1	1:1:251:THR:HG23	2.55	0.41
1:1:94:ASP:O	1:1:95:GLU:C	2.58	0.41
1:1:210:ASP:O	1:1:211:GLU:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:69:GLU:O	1:1:73:GLU:CG	2.69	0.41
1:1:68:LEU:O	1:1:72:GLU:HB2	2.20	0.41
1:1:289:GLU:O	1:1:291:LYS:N	2.53	0.41
1:1:73:GLU:HG3	1:1:73:GLU:O	2.21	0.41
1:1:195:ARG:NH2	2:1:1015:HOH:O	2.54	0.41
1:1:310:VAL:CG1	1:1:315:TYR:CZ	3.03	0.41
1:1:281:LEU:O	1:1:281:LEU:HD23	2.20	0.41
1:1:70:LEU:HD12	1:1:74:LEU:HA	2.02	0.41
1:1:13:ASP:C	1:1:15:PRO:HD2	2.41	0.41
1:1:287:GLU:C	1:1:289:GLU:H	2.24	0.41
1:1:53:THR:C	1:1:56:THR:HG22	2.42	0.40
1:1:321:THR:HG23	1:1:323:LEU:HB2	2.02	0.40
1:1:172:TYR:O	1:1:176:SER:HB3	2.21	0.40
1:1:228:ARG:NH2	1:1:240:THR:HA	2.29	0.40
1:1:193:SER:O	1:1:195:ARG:N	2.48	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	1	349/365 (96%)	290 (83%)	43 (12%)	16 (5%)	3 3

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	65	GLN
1	1	105	PRO
1	1	106	HIS
1	1	211	GLU
1	1	229	ALA
1	1	10	GLY

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Mol	Chain	Res	Type
1	1	34	TRP
1	1	230	SER
1	1	299	PRO
1	1	349	GLY
1	1	104	PHE
1	1	232	PRO
1	1	242	SER
1	1	209	VAL
1	1	295	GLY
1	1	215	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	1	297/309 (96%)	248 (84%)	49 (16%)	3 5

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	5	LEU
1	1	11	ILE
1	1	23	GLU
1	1	24	LEU
1	1	45	GLN
1	1	50	LEU
1	1	57	PHE
1	1	61	GLU
1	1	62	SER
1	1	64	LEU
1	1	65	GLN
1	1	69	GLU
1	1	70	LEU
1	1	73	GLU
1	1	78	GLU
1	1	94	ASP

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Mol	Chain	Res	Type
1	1	100	THR
1	1	103	ASN
1	1	104	PHE
1	1	105	PRO
1	1	108	GLU
1	1	132	LEU
1	1	142	GLN
1	1	147	GLU
1	1	160	ASP
1	1	169	GLU
1	1	184	LEU
1	1	195	ARG
1	1	204	GLU
1	1	210	ASP
1	1	215	VAL
1	1	216	VAL
1	1	222	LEU
1	1	228	ARG
1	1	230	SER
1	1	244	VAL
1	1	245	ARG
1	1	254	THR
1	1	258	GLN
1	1	260	THR
1	1	264	ILE
1	1	274	LEU
1	1	300	ILE
1	1	305	GLN
1	1	310	VAL
1	1	321	THR
1	1	323	LEU
1	1	324	MET
1	1	350	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	65	GLN
1	1	103	ASN
1	1	110	ASN
1	1	142	GLN
1	1	170	ASN

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Mol	Chain	Res	Type
1	1	258	GLN
1	1	263	GLN
1	1	314	ASN
1	1	326	HIS

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 carbohydrates 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	1	351/365 (96%)	2.37	105 (29%) 1 0	41, 90, 239, 276	0

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1	236	GLY	24.1
1	1	82	LEU	22.9
1	1	43	VAL	20.5
1	1	26	ARG	16.5
1	1	85	GLU	16.3
1	1	68	LEU	14.5
1	1	78	GLU	14.3
1	1	35	ASN	14.0
1	1	229	ALA	14.0
1	1	29	GLU	13.9
1	1	76	ALA	13.6
1	1	75	PRO	13.5
1	1	23	GLU	13.4
1	1	34	TRP	13.2
1	1	71	MET	13.0
1	1	42	LYS	12.6
1	1	28	LEU	12.5
1	1	239	THR	11.8
1	1	67	LEU	11.7
1	1	84	PRO	11.6
1	1	30	ASP	11.5
1	1	44	SER	11.0
1	1	240	THR	10.8
1	1	233	GLY	10.7
1	1	14	ILE	10.7
1	1	237	VAL	10.3
1	1	31	PRO	10.1

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Mol	Chain	Res	Type	RSRZ
1	1	232	PRO	10.1
1	1	74	LEU	9.8
1	1	39	ALA	9.7
1	1	19	THR	9.5
1	1	235	GLN	9.1
1	1	20	ARG	8.9
1	1	297	VAL	8.8
1	1	33	LEU	8.8
1	1	72	GLU	8.1
1	1	17	LYS	8.1
1	1	12	PHE	7.8
1	1	27	ARG	7.7
1	1	36	ASP	7.3
1	1	293	LEU	7.2
1	1	81	ALA	7.0
1	1	38	GLU	7.0
1	1	230	SER	6.8
1	1	234	GLY	6.7
1	1	45	GLN	6.6
1	1	238	ASN	6.4
1	1	296	GLU	6.4
1	1	22	LYS	6.3
1	1	80	GLU	6.3
1	1	79	ARG	6.3
1	1	86	LEU	5.9
1	1	294	ARG	5.9
1	1	24	LEU	5.8
1	1	40	ALA	5.8
1	1	298	ARG	5.7
1	1	46	GLU	5.6
1	1	11	ILE	5.4
1	1	32	SER	5.4
1	1	66	GLY	5.4
1	1	77	GLU	5.1
1	1	41	ARG	5.0
1	1	1	LEU	4.8
1	1	301	GLU	4.7
1	1	231	GLY	4.4
1	1	192	ALA	4.4
1	1	55	ASP	4.3
1	1	295	GLY	4.2
1	1	37	PRO	4.1

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Mol	Chain	Res	Type	RSRZ
1	1	299	PRO	4.1
1	1	13	ASP	4.0
1	1	241	ASP	4.0
1	1	111	ALA	3.9
1	1	83	LYS	3.7
1	1	18	GLU	3.6
1	1	291	LYS	3.4
1	1	112	ILE	3.4
1	1	224	ILE	3.3
1	1	3	GLN	3.3
1	1	89	ALA	3.3
1	1	135	TYR	3.1
1	1	15	PRO	3.0
1	1	300	ILE	3.0
1	1	6	GLU	3.0
1	1	257	CYS	2.9
1	1	65	GLN	2.7
1	1	164	ILE	2.7
1	1	134	MET	2.6
1	1	287	GLU	2.6
1	1	70	LEU	2.5
1	1	246	VAL	2.5
1	1	163	GLN	2.5
1	1	274	LEU	2.5
1	1	206	ILE	2.4
1	1	58	ARG	2.4
1	1	52	ARG	2.3
1	1	349	GLY	2.3
1	1	292	ALA	2.3
1	1	113	LEU	2.2
1	1	131	LEU	2.2
1	1	256	THR	2.2
1	1	25	GLU	2.1
1	1	172	TYR	2.1
1	1	73	GLU	2.0
1	1	114	THR	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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.