



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 27, 2026 – 05:14 PM EDT

PDB ID : 5Y83 / pdb_00005y83
Title : Crystal structure of YidC from *Thermotoga maritima*
Authors : Huang, Y.; Xin, Y.
Deposited on : 2017-08-18
Resolution : 3.84 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

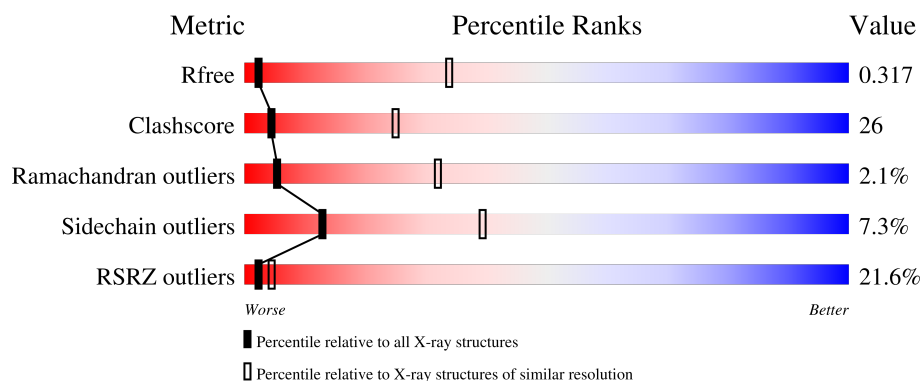
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.84 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	1169 (4.00-3.68)
Clashscore	190562	1211 (4.00-3.68)
Ramachandran outliers	187476	1156 (4.00-3.68)
Sidechain outliers	187428	1149 (4.00-3.68)
RSRZ outliers	180081	1168 (4.00-3.68)

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	451	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2679 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 Membrane protein insertase YidC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	342	Total	C	N	O	S	0	0	0
			2679	1779	418	477	5			

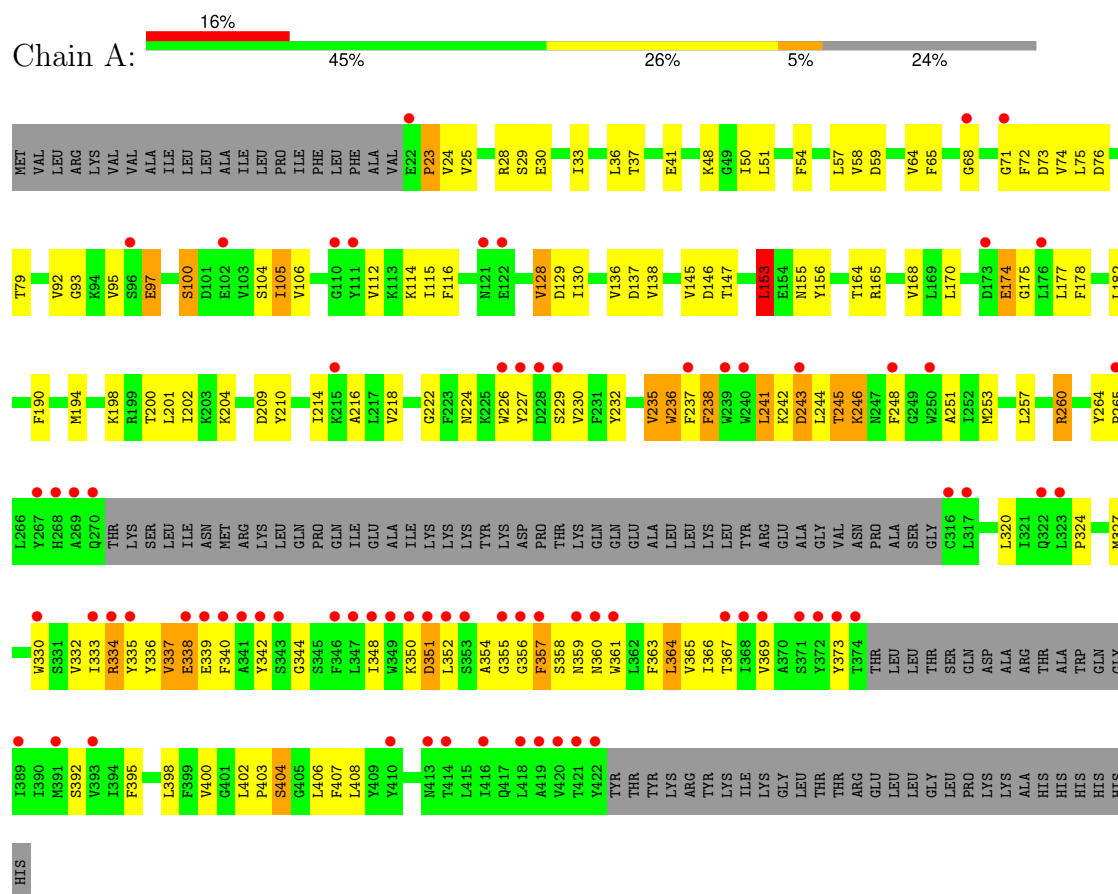
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	VAL	ILE	engineered mutation	UNP Q9X1H2
A	25	VAL	LYS	engineered mutation	UNP Q9X1H2
A	446	HIS	-	expression tag	UNP Q9X1H2
A	447	HIS	-	expression tag	UNP Q9X1H2
A	448	HIS	-	expression tag	UNP Q9X1H2
A	449	HIS	-	expression tag	UNP Q9X1H2
A	450	HIS	-	expression tag	UNP Q9X1H2
A	451	HIS	-	expression tag	UNP Q9X1H2

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: Membrane protein insertase YidC



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	75.75Å 103.60Å 129.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.76 – 3.84 42.76 – 3.84	Depositor EDS
% Data completeness (in resolution range)	75.2 (42.76-3.84) 75.4 (42.76-3.84)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.20 (at 3.88Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.264 , 0.312 0.269 , 0.317	Depositor DCC
R_{free} test set	406 reflections (3.97%)	wwPDB-VP
Wilson B-factor (Å ²)	38.2	Xtriage
Anisotropy	0.176	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 55.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.76	EDS
Total number of atoms	2679	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.58% 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	0.36	0/2746	0.85	5/3733 (0.1%)

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

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	245	THR	N-CA-C	-9.62	95.88	110.30
1	A	23	PRO	N-CA-CB	8.07	111.72	103.25
1	A	28	ARG	CB-CG-CD	-5.77	98.03	111.30
1	A	230	VAL	CB-CA-C	-5.58	105.21	111.80
1	A	236	TRP	N-CA-C	-5.22	105.23	111.03

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	174	GLU	Peptide
1	A	68	GLY	Peptide

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	2679	0	2587	139	0
All	All	2679	0	2587	139	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 26.

All (139) 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:330:TRP:CZ3	1:A:403:PRO:HG2	1.17	1.67
1:A:330:TRP:CZ3	1:A:403:PRO:CG	1.83	1.59
1:A:330:TRP:CH2	1:A:403:PRO:CD	1.87	1.54
1:A:330:TRP:CH2	1:A:403:PRO:CG	1.93	1.51
1:A:330:TRP:CH2	1:A:403:PRO:HG2	1.52	1.41
1:A:155:ASN:O	1:A:156:TYR:CD1	1.78	1.36
1:A:330:TRP:CH2	1:A:403:PRO:HD2	1.64	1.22
1:A:155:ASN:OD1	1:A:175:GLY:HA3	1.36	1.21
1:A:330:TRP:CE3	1:A:406:LEU:HD21	1.82	1.15
1:A:330:TRP:CZ3	1:A:403:PRO:CD	2.22	1.13
1:A:330:TRP:HZ3	1:A:403:PRO:CG	1.39	1.08
1:A:337:VAL:HG12	1:A:340:PHE:HB2	1.16	1.07
1:A:330:TRP:CE3	1:A:406:LEU:CD2	2.38	1.07
1:A:330:TRP:CZ3	1:A:403:PRO:HD2	1.88	1.06
1:A:337:VAL:CG1	1:A:340:PHE:HB2	1.86	1.05
1:A:155:ASN:OD1	1:A:175:GLY:CA	2.07	1.02
1:A:330:TRP:HE3	1:A:406:LEU:HD21	1.19	1.02
1:A:330:TRP:HZ3	1:A:403:PRO:CB	1.72	1.01
1:A:337:VAL:HG12	1:A:340:PHE:CB	1.99	0.92
1:A:363:PHE:HA	1:A:366:ILE:HB	1.53	0.91
1:A:330:TRP:CH2	1:A:403:PRO:HD3	2.05	0.90
1:A:155:ASN:O	1:A:156:TYR:CG	2.25	0.89
1:A:330:TRP:HH2	1:A:403:PRO:CG	1.59	0.89
1:A:330:TRP:HE3	1:A:406:LEU:CD2	1.84	0.87
1:A:218:VAL:HG13	1:A:224:ASN:HD21	1.40	0.84
1:A:330:TRP:HH2	1:A:403:PRO:CD	1.61	0.80
1:A:168:VAL:HG22	1:A:194:MET:HG3	1.65	0.79
1:A:333:ILE:O	1:A:337:VAL:HB	1.82	0.78
1:A:330:TRP:CE3	1:A:406:LEU:HD23	2.21	0.76
1:A:334:ARG:HB2	1:A:337:VAL:O	1.86	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:ASN:OD1	1:A:175:GLY:N	2.21	0.74
1:A:95:VAL:HG12	1:A:97:GLU:H	1.52	0.73
1:A:330:TRP:HZ3	1:A:403:PRO:HB2	1.53	0.72
1:A:155:ASN:C	1:A:156:TYR:CD1	2.68	0.72
1:A:41:GLU:HB2	1:A:57:LEU:HD11	1.72	0.71
1:A:72:PHE:O	1:A:114:LYS:NZ	2.25	0.69
1:A:354:ALA:HB1	1:A:355:GLY:C	2.17	0.69
1:A:330:TRP:CZ3	1:A:403:PRO:CB	2.58	0.69
1:A:245:THR:O	1:A:246:LYS:O	2.13	0.66
1:A:354:ALA:HB3	1:A:404:SER:H	1.60	0.66
1:A:146:ASP:OD1	1:A:147:THR:N	2.29	0.65
1:A:330:TRP:O	1:A:333:ILE:HG22	1.96	0.65
1:A:354:ALA:HB3	1:A:404:SER:N	2.11	0.65
1:A:361:TRP:HA	1:A:364:LEU:HG	1.78	0.65
1:A:253:MET:HE3	1:A:408:LEU:HD11	1.79	0.64
1:A:74:VAL:HG11	1:A:112:VAL:HG11	1.80	0.63
1:A:210:TYR:CZ	1:A:214:ILE:HG13	2.33	0.62
1:A:155:ASN:O	1:A:156:TYR:CE1	2.48	0.62
1:A:218:VAL:HG13	1:A:224:ASN:ND2	2.12	0.62
1:A:260:ARG:O	1:A:264:TYR:HB3	1.99	0.62
1:A:242:LYS:NZ	1:A:248:PHE:O	2.32	0.62
1:A:333:ILE:HD11	1:A:340:PHE:CE2	2.35	0.62
1:A:358:SER:HA	1:A:361:TRP:HB2	1.82	0.61
1:A:334:ARG:HA	1:A:335:TYR:C	2.26	0.61
1:A:364:LEU:HD22	1:A:395:PHE:HB2	1.83	0.60
1:A:232:TYR:O	1:A:236:TRP:HB2	2.02	0.59
1:A:115:ILE:HB	1:A:129:ASP:HB2	1.85	0.59
1:A:198:LYS:O	1:A:202:ILE:HG12	2.03	0.59
1:A:337:VAL:HG12	1:A:337:VAL:O	2.02	0.58
1:A:204:LYS:NZ	1:A:339:GLU:OE1	2.35	0.58
1:A:29:SER:OG	1:A:30:GLU:N	2.36	0.57
1:A:241:LEU:HD21	1:A:251:ALA:O	2.05	0.56
1:A:54:PHE:HB3	1:A:65:PHE:HB3	1.85	0.56
1:A:350:LYS:HE3	1:A:359:ASN:HB2	1.86	0.56
1:A:106:VAL:HG13	1:A:115:ILE:HG12	1.88	0.56
1:A:354:ALA:HB1	1:A:355:GLY:O	2.05	0.56
1:A:330:TRP:HZ3	1:A:403:PRO:HG2	0.98	0.56
1:A:64:VAL:HG12	1:A:164:THR:HB	1.88	0.55
1:A:36:LEU:HD23	1:A:41:GLU:HG3	1.89	0.55
1:A:340:PHE:CE2	1:A:352:LEU:HB3	2.41	0.54
1:A:260:ARG:HA	1:A:260:ARG:NH2	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:GLY:HA3	1:A:100:SER:OG	2.08	0.54
1:A:334:ARG:CA	1:A:335:TYR:CB	2.87	0.53
1:A:330:TRP:CZ3	1:A:403:PRO:HB2	2.38	0.53
1:A:242:LYS:HZ3	1:A:251:ALA:HB3	1.74	0.52
1:A:334:ARG:CD	1:A:338:GLU:HA	2.40	0.52
1:A:330:TRP:HH2	1:A:403:PRO:HD3	1.51	0.52
1:A:232:TYR:HD1	1:A:235:VAL:HB	1.75	0.52
1:A:365:VAL:O	1:A:369:VAL:HG23	2.10	0.52
1:A:356:GLY:HA3	1:A:400:VAL:HA	1.91	0.52
1:A:334:ARG:N	1:A:335:TYR:CB	2.73	0.52
1:A:264:TYR:CD1	1:A:265:PRO:HD3	2.46	0.51
1:A:75:LEU:HB2	1:A:137:ASP:HB2	1.92	0.51
1:A:33:ILE:HG21	1:A:105:ILE:HD11	1.93	0.51
1:A:178:PHE:HE1	1:A:182:LEU:HD23	1.75	0.50
1:A:334:ARG:HA	1:A:335:TYR:O	2.13	0.49
1:A:50:ILE:HA	1:A:71:GLY:O	2.12	0.49
1:A:54:PHE:CD2	1:A:194:MET:HE3	2.48	0.49
1:A:237:PHE:O	1:A:241:LEU:HB3	2.12	0.49
1:A:128:VAL:HG13	1:A:190:PHE:HB2	1.95	0.49
1:A:153:LEU:HD22	1:A:216:ALA:HB1	1.95	0.49
1:A:156:TYR:OH	1:A:209:ASP:OD2	2.26	0.48
1:A:232:TYR:CD1	1:A:235:VAL:HB	2.48	0.48
1:A:361:TRP:O	1:A:364:LEU:HB2	2.13	0.48
1:A:73:ASP:O	1:A:138:VAL:HA	2.14	0.48
1:A:360:ASN:HB3	1:A:407:PHE:CG	2.49	0.47
1:A:351:ASP:O	1:A:352:LEU:HB2	2.13	0.47
1:A:334:ARG:O	1:A:334:ARG:HG2	2.15	0.47
1:A:165:ARG:NH1	1:A:222:GLY:O	2.37	0.47
1:A:198:LYS:HE2	1:A:336:TYR:O	2.13	0.47
1:A:95:VAL:C	1:A:97:GLU:H	2.24	0.46
1:A:360:ASN:O	1:A:364:LEU:HD23	2.16	0.46
1:A:24:VAL:HG13	1:A:37:THR:HG22	1.98	0.46
1:A:367:THR:HG1	1:A:392:SER:HG	1.64	0.45
1:A:51:LEU:HD21	1:A:194:MET:HE1	1.98	0.45
1:A:332:VAL:C	1:A:335:TYR:CB	2.90	0.45
1:A:226:TRP:O	1:A:227:TYR:HD1	2.00	0.45
1:A:92:VAL:O	1:A:100:SER:OG	2.32	0.45
1:A:170:LEU:HD21	1:A:182:LEU:HD11	1.98	0.45
1:A:145:VAL:HG13	1:A:146:ASP:H	1.82	0.44
1:A:25:VAL:HG13	1:A:97:GLU:CD	2.42	0.44
1:A:360:ASN:HB3	1:A:407:PHE:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:ILE:HD13	1:A:138:VAL:HG21	2.00	0.44
1:A:333:ILE:O	1:A:334:ARG:HB2	2.18	0.44
1:A:54:PHE:CG	1:A:194:MET:HE3	2.53	0.43
1:A:342:TYR:C	1:A:344:GLY:H	2.26	0.43
1:A:242:LYS:HD3	1:A:242:LYS:HA	1.73	0.43
1:A:320:LEU:O	1:A:324:PRO:HD2	2.18	0.43
1:A:238:PHE:O	1:A:242:LYS:HB2	2.19	0.43
1:A:48:LYS:HB2	1:A:50:ILE:HG23	2.00	0.42
1:A:330:TRP:CZ2	1:A:403:PRO:HD2	2.40	0.42
1:A:58:VAL:HG13	1:A:59:ASP:H	1.83	0.42
1:A:79:THR:O	1:A:79:THR:OG1	2.34	0.42
1:A:336:TYR:C	1:A:337:VAL:HG23	2.45	0.42
1:A:357:PHE:HD1	1:A:357:PHE:HA	1.70	0.42
1:A:59:ASP:OD1	1:A:59:ASP:N	2.53	0.42
1:A:104:SER:HA	1:A:116:PHE:O	2.20	0.41
1:A:198:LYS:HE3	1:A:200:THR:OG1	2.20	0.41
1:A:330:TRP:CZ3	1:A:406:LEU:HD23	2.56	0.41
1:A:334:ARG:HD2	1:A:338:GLU:HA	2.02	0.41
1:A:153:LEU:H	1:A:153:LEU:HG	1.61	0.41
1:A:340:PHE:CZ	1:A:352:LEU:HB3	2.55	0.41
1:A:226:TRP:CD1	1:A:226:TRP:N	2.88	0.41
1:A:243:ASP:HA	1:A:244:LEU:HA	1.44	0.41
1:A:333:ILE:HD11	1:A:340:PHE:HE2	1.83	0.41
1:A:198:LYS:HB3	1:A:201:LEU:HD12	2.04	0.40
1:A:174:GLU:O	1:A:177:LEU:HB2	2.21	0.40
1:A:257:LEU:HD23	1:A:257:LEU:HA	1.86	0.40
1:A:402:LEU:HD23	1:A:402:LEU:HA	1.96	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	336/451 (74%)	304 (90%)	25 (7%)	7 (2%)	5	32

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	23	PRO
1	A	246	LYS
1	A	334	ARG
1	A	337	VAL
1	A	153	LEU
1	A	348	ILE
1	A	373	TYR

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	273/405 (67%)	253 (93%)	20 (7%)	13	39

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	76	ASP
1	A	97	GLU
1	A	100	SER
1	A	105	ILE
1	A	128	VAL
1	A	136	VAL
1	A	153	LEU
1	A	229	SER
1	A	235	VAL
1	A	238	PHE
1	A	241	LEU
1	A	243	ASP
1	A	260	ARG
1	A	327	MET

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Mol	Chain	Res	Type
1	A	338	GLU
1	A	351	ASP
1	A	357	PHE
1	A	364	LEU
1	A	398	LEU
1	A	404	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	108	ASN
1	A	219	ASN

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	342/451 (75%)	1.12	74 (21%) 2 4	8, 60, 167, 225	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	413	ASN	8.3
1	A	268	HIS	8.1
1	A	227	TYR	5.9
1	A	374	THR	5.0
1	A	359	ASN	4.9
1	A	111	TYR	4.9
1	A	373	TYR	4.5
1	A	340	PHE	4.5
1	A	351	ASP	4.4
1	A	267	TYR	4.3
1	A	421	THR	4.1
1	A	335	TYR	4.1
1	A	334	ARG	3.7
1	A	422	TYR	3.7
1	A	173	ASP	3.6
1	A	360	ASN	3.5
1	A	237	PHE	3.4
1	A	316	CYS	3.3
1	A	215	LYS	3.3
1	A	71	GLY	3.2
1	A	356	GLY	3.2
1	A	248	PHE	3.1
1	A	339	GLU	3.1
1	A	369	VAL	3.1
1	A	343	SER	3.1
1	A	346	PHE	3.0
1	A	341	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	347	LEU	3.0
1	A	110	GLY	3.0
1	A	372	TYR	3.0
1	A	243	ASP	2.9
1	A	352	LEU	2.8
1	A	226	TRP	2.8
1	A	229	SER	2.8
1	A	353	SER	2.7
1	A	418	LEU	2.7
1	A	357	PHE	2.7
1	A	96	SER	2.7
1	A	348	ILE	2.7
1	A	333	ILE	2.6
1	A	389	ILE	2.6
1	A	410	TYR	2.6
1	A	368	ILE	2.6
1	A	270	GLN	2.6
1	A	416	ILE	2.5
1	A	239	TRP	2.5
1	A	322	GLN	2.5
1	A	323	LEU	2.5
1	A	68	GLY	2.5
1	A	176	LEU	2.5
1	A	355	GLY	2.4
1	A	269	ALA	2.4
1	A	102	GLU	2.4
1	A	349	TRP	2.4
1	A	317	LEU	2.4
1	A	361	TRP	2.4
1	A	391	MET	2.3
1	A	420	VAL	2.3
1	A	121	ASN	2.3
1	A	367	THR	2.2
1	A	240	TRP	2.2
1	A	414	THR	2.2
1	A	330	TRP	2.2
1	A	350	LYS	2.2
1	A	228	ASP	2.1
1	A	419	ALA	2.1
1	A	250	TRP	2.1
1	A	22	GLU	2.1
1	A	122	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	371	SER	2.1
1	A	342	TYR	2.1
1	A	393	VAL	2.1
1	A	338	GLU	2.0
1	A	265	PRO	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.