



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:43 PM UTC

PDB ID : 3MCM / pdb_00003mcm
Title : Crystal Structure of the 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase dihydropteroate synthase bifunctional enzyme from Francisella tularensis
Authors : Pemble IV, C.W.; Mehta, P.K.; Mehra, S.; Li, Z.; Lee, R.E.; White, S.W.
Deposited on : 2010-03-29
Resolution : 2.20 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

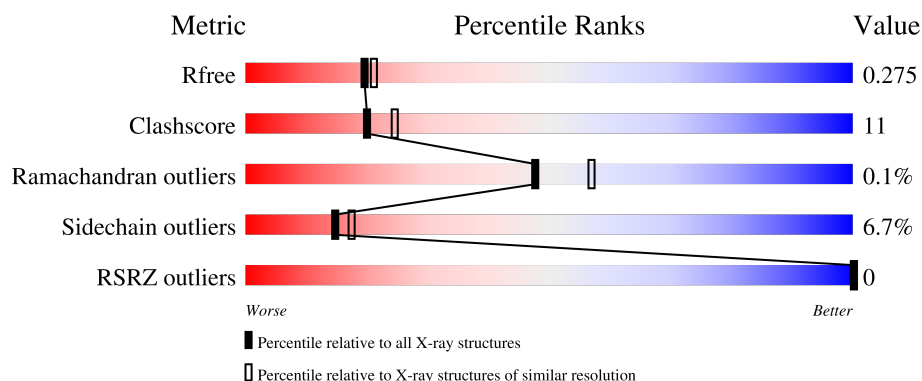
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	442	
1	B	442	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6176 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 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase/dihydropteroate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	368	Total	C	N	O	S	0	1	0
			2979	1907	517	549	6			
1	B	377	Total	C	N	O	S	0	2	0
			3064	1963	530	565	6			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP Q2A2W3
A	-18	GLY	-	expression tag	UNP Q2A2W3
A	-17	SER	-	expression tag	UNP Q2A2W3
A	-16	SER	-	expression tag	UNP Q2A2W3
A	-15	HIS	-	expression tag	UNP Q2A2W3
A	-14	HIS	-	expression tag	UNP Q2A2W3
A	-13	HIS	-	expression tag	UNP Q2A2W3
A	-12	HIS	-	expression tag	UNP Q2A2W3
A	-11	HIS	-	expression tag	UNP Q2A2W3
A	-10	HIS	-	expression tag	UNP Q2A2W3
A	-9	SER	-	expression tag	UNP Q2A2W3
A	-8	SER	-	expression tag	UNP Q2A2W3
A	-7	GLY	-	expression tag	UNP Q2A2W3
A	-6	LEU	-	expression tag	UNP Q2A2W3
A	-5	VAL	-	expression tag	UNP Q2A2W3
A	-4	PRO	-	expression tag	UNP Q2A2W3
A	-3	ARG	-	expression tag	UNP Q2A2W3
A	-2	GLY	-	expression tag	UNP Q2A2W3
A	-1	SER	-	expression tag	UNP Q2A2W3
A	0	HIS	-	expression tag	UNP Q2A2W3
A	1	MET	-	expression tag	UNP Q2A2W3
A	2	VAL	-	expression tag	UNP Q2A2W3
B	-19	MET	-	expression tag	UNP Q2A2W3
B	-18	GLY	-	expression tag	UNP Q2A2W3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-17	SER	-	expression tag	UNP Q2A2W3
B	-16	SER	-	expression tag	UNP Q2A2W3
B	-15	HIS	-	expression tag	UNP Q2A2W3
B	-14	HIS	-	expression tag	UNP Q2A2W3
B	-13	HIS	-	expression tag	UNP Q2A2W3
B	-12	HIS	-	expression tag	UNP Q2A2W3
B	-11	HIS	-	expression tag	UNP Q2A2W3
B	-10	HIS	-	expression tag	UNP Q2A2W3
B	-9	SER	-	expression tag	UNP Q2A2W3
B	-8	SER	-	expression tag	UNP Q2A2W3
B	-7	GLY	-	expression tag	UNP Q2A2W3
B	-6	LEU	-	expression tag	UNP Q2A2W3
B	-5	VAL	-	expression tag	UNP Q2A2W3
B	-4	PRO	-	expression tag	UNP Q2A2W3
B	-3	ARG	-	expression tag	UNP Q2A2W3
B	-2	GLY	-	expression tag	UNP Q2A2W3
B	-1	SER	-	expression tag	UNP Q2A2W3
B	0	HIS	-	expression tag	UNP Q2A2W3
B	1	MET	-	expression tag	UNP Q2A2W3
B	2	VAL	-	expression tag	UNP Q2A2W3

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	63	Total O 63 63	0	0
3	B	69	Total O 69 69	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	42.82Å 57.78Å 105.13Å 91.13° 99.39° 111.64°	Depositor
Resolution (Å)	38.44 – 2.20 38.44 – 2.20	Depositor EDS
% Data completeness (in resolution range)	94.2 (38.44-2.20) 94.3 (38.44-2.20)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.21 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.5_2	Depositor
R, R_{free}	0.215 , 0.278 0.214 , 0.275	Depositor DCC
R_{free} test set	2227 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	33.9	Xtriage
Anisotropy	0.062	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.085 for h,-h-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6176	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.85% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	0.53	0/3017	0.84	1/4055 (0.0%)
1	B	0.51	0/3108	0.85	3/4177 (0.1%)
All	All	0.52	0/6125	0.84	4/8232 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	272	ILE	CB-CA-C	-6.23	104.05	111.65
1	B	356	ASP	N-CA-C	-5.98	106.32	113.97
1	B	143	HIS	CA-C-N	5.38	125.20	119.28
1	B	143	HIS	C-N-CA	5.38	125.20	119.28

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	2979	0	3119	74	0
1	B	3064	0	3209	67	0
2	A	1	0	0	0	0
3	A	63	0	0	1	0
3	B	69	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6176	0	6328	141	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 11.

All (141) 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:330:LYS:HG3	1:B:374:LEU:HD11	1.56	0.88
1:A:284:ILE:HD11	1:A:333:LEU:HD21	1.54	0.87
1:A:366:ILE:HD11	1:A:412:LEU:HB3	1.57	0.86
1:B:143:HIS:CE1	1:B:145:LYS:HB2	2.22	0.75
1:A:165:LYS:N	1:A:165:LYS:HD3	2.05	0.72
1:A:1:MET:HE3	1:A:67:SER:OG	1.93	0.69
1:A:257:ARG:HB2	1:A:280:GLU:HB2	1.75	0.68
1:A:340:GLN:NE2	1:A:373:GLU:HB3	2.09	0.67
1:A:372:LEU:O	1:A:373:GLU:HB2	1.96	0.66
1:A:257:ARG:HD2	1:A:280:GLU:HG3	1.78	0.64
1:B:110:LEU:HD12	1:B:111:ILE:N	2.13	0.64
1:B:182:GLN:HE21	1:B:217:LYS:HE3	1.62	0.63
1:B:330:LYS:O	1:B:334:LEU:HG	1.99	0.63
1:A:338:ILE:HD11	1:A:343:ILE:HG13	1.81	0.63
1:A:340:GLN:HE22	1:A:373:GLU:HB3	1.63	0.62
1:A:194:ARG:N	1:A:194:ARG:HD3	2.14	0.62
1:A:204:SER:O	1:A:422:ILE:HG21	1.99	0.62
1:B:58:ARG:NH1	1:B:247:ILE:HG22	2.15	0.61
1:B:279:VAL:HG12	3:B:468:HOH:O	1.99	0.61
1:B:240:LYS:HE3	1:B:269:HIS:HD2	1.66	0.60
1:B:300:ILE:HG23	1:B:329:LYS:HE3	1.83	0.60
1:B:240:LYS:CE	1:B:269:HIS:HD2	2.15	0.60
1:A:275:MET:HB2	1:A:297:LYS:HB2	1.82	0.60
1:B:208:ILE:HG12	1:B:251:LEU:HB2	1.83	0.59
1:A:8:ILE:HG12	1:A:102:LEU:CD2	2.32	0.59
1:B:301:ILE:HG13	1:B:346:ASP:HB3	1.85	0.59
1:A:381:SER:HB2	1:A:419:VAL:HA	1.85	0.58
1:B:233:ASN:OD1	1:B:269:HIS:HE1	1.86	0.58
1:B:328:GLN:O	1:B:332:ILE:HD12	2.03	0.58
1:B:377:LEU:C	1:B:377:LEU:HD12	2.29	0.58
1:B:359:ARG:O	1:B:363:GLU:HG3	2.03	0.57
1:B:112:LEU:HD23	1:B:117:LEU:HD11	1.86	0.57
1:B:284:ILE:HD11	1:B:333:LEU:HD21	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:GLN:OE1	1:A:65:LYS:HD3	2.06	0.56
1:B:117:LEU:C	1:B:117:LEU:HD12	2.30	0.56
1:A:58:ARG:HD3	1:A:247:ILE:HA	1.88	0.55
1:A:367:GLU:O	1:A:371:ARG:HG2	2.07	0.55
1:A:341:GLN:O	1:A:375:LYS:NZ	2.33	0.55
1:A:8:ILE:HG12	1:A:102:LEU:HD22	1.89	0.54
1:A:208:ILE:HG12	1:A:251:LEU:HB2	1.88	0.54
1:A:112:LEU:O	1:A:118:THR:HA	2.07	0.54
1:A:302:HIS:CD2	1:A:322:VAL:HG13	2.44	0.53
1:A:256:THR:HG21	1:A:261:VAL:HG22	1.89	0.53
1:A:134:LEU:C	1:A:134:LEU:HD23	2.35	0.52
1:A:279:VAL:CG1	1:A:301:ILE:HD12	2.39	0.52
1:B:194[B]:ARG:NH2	3:B:467:HOH:O	2.42	0.52
1:B:266:LEU:O	1:B:270:HIS:HB3	2.10	0.52
1:A:81:ASP:O	1:A:85:LYS:HG3	2.10	0.52
1:A:21:LEU:HB3	1:A:86:ILE:HD12	1.92	0.51
1:A:403:ARG:O	1:A:407:ARG:HG2	2.11	0.51
1:B:35:ILE:HD11	1:B:67:SER:HB2	1.93	0.51
1:B:389:LEU:HD21	1:B:397:THR:HG22	1.93	0.51
1:A:302:HIS:HA	1:A:325:TYR:CE1	2.45	0.51
1:A:211:ILE:HD12	1:A:252:VAL:HG13	1.93	0.51
1:A:171:THR:HG23	1:A:414:ILE:O	2.10	0.51
1:A:190:ASP:OD1	1:A:190:ASP:C	2.53	0.51
1:A:409:LEU:HB3	1:A:414:ILE:HG13	1.92	0.51
1:A:347:ILE:HG21	1:A:349:PHE:CE2	2.46	0.51
1:B:381:SER:OG	1:B:420:HIS:HD2	1.93	0.50
1:A:80:LYS:O	1:A:84:LEU:HG	2.12	0.50
1:B:112:LEU:O	1:B:118:THR:HA	2.12	0.50
1:B:58:ARG:HH11	1:B:247:ILE:HG22	1.77	0.49
1:B:182:GLN:NE2	1:B:217:LYS:HG3	2.28	0.49
1:B:257:ARG:HD3	1:B:280:GLU:CG	2.42	0.49
1:B:384:PRO:HG2	1:B:391:LYS:HG3	1.94	0.49
1:B:172:ILE:HG12	1:B:416:ILE:HG12	1.93	0.49
1:B:199:ASP:O	1:B:203:GLN:HG2	2.12	0.49
1:A:215:SER:OG	1:A:216:THR:N	2.42	0.48
1:A:330:LYS:O	1:A:334:LEU:HG	2.14	0.48
1:B:257:ARG:HB2	1:B:280:GLU:CG	2.43	0.48
1:A:399:ASP:O	1:A:402:THR:HG22	2.13	0.48
1:A:35:ILE:HD11	1:A:67:SER:HB2	1.95	0.48
1:A:279:VAL:HG12	1:A:301:ILE:HD12	1.94	0.48
1:B:381:SER:HB2	1:B:419:VAL:HA	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:LEU:HD22	1:A:272:ILE:HD11	1.94	0.48
1:A:240:LYS:HA	1:A:243:LEU:HD13	1.96	0.47
1:A:164:LEU:C	1:A:165:LYS:HD3	2.39	0.47
1:A:409:LEU:O	1:A:414:ILE:HG12	2.14	0.47
1:A:194:ARG:HD3	1:A:194:ARG:H	1.80	0.47
1:B:129:PHE:HA	1:B:161:ILE:CD1	2.45	0.47
1:B:153:ILE:N	1:B:153:ILE:HD12	2.29	0.47
1:B:377:LEU:HD12	1:B:378:VAL:N	2.29	0.47
1:A:248:TYR:CE2	1:A:250:PRO:HA	2.50	0.47
1:A:338:ILE:HD11	1:A:343:ILE:CG1	2.45	0.47
1:B:150:ASP:HB3	1:B:153:ILE:HD13	1.96	0.47
1:A:368:ILE:O	1:A:372:LEU:HG	2.14	0.46
1:B:58:ARG:HD2	3:B:482:HOH:O	2.15	0.46
1:A:71:LYS:O	1:A:72:PRO:C	2.56	0.46
1:A:40:LEU:HD21	1:A:168:LEU:HD13	1.98	0.46
1:A:412:LEU:HD23	1:A:412:LEU:N	2.31	0.45
1:B:173:ARG:N	1:B:173:ARG:HD3	2.32	0.45
1:B:112:LEU:CD2	1:B:117:LEU:HD11	2.47	0.45
1:A:191:ASP:OD2	1:A:191:ASP:N	2.50	0.45
1:A:294:TYR:O	1:A:296:LYS:HE2	2.17	0.45
1:B:329:LYS:NZ	3:B:476:HOH:O	2.49	0.44
1:A:339:ALA:HB1	1:A:341:GLN:NE2	2.32	0.44
1:A:284:ILE:HG23	1:A:285:GLU:N	2.31	0.44
1:A:390:THR:O	1:A:393:SER:OG	2.35	0.44
1:B:158:LEU:HD23	1:B:158:LEU:HA	1.71	0.44
1:B:240:LYS:NZ	1:B:269:HIS:HD2	2.16	0.44
1:A:181:ASN:C	1:A:183:SER:H	2.25	0.44
1:B:257:ARG:HB2	1:B:280:GLU:HB2	2.00	0.44
1:A:21:LEU:HD23	1:A:21:LEU:HA	1.85	0.44
1:B:3:GLN:CD	1:B:65:LYS:HD3	2.43	0.43
1:B:191:ASP:OD2	1:B:191:ASP:N	2.50	0.43
1:B:119:ILE:HA	1:B:120:PRO:C	2.42	0.43
1:A:327:GLU:O	1:A:331:GLN:HG2	2.18	0.43
1:B:172:ILE:CD1	1:B:208:ILE:HD11	2.49	0.43
1:A:368:ILE:HG22	1:A:372:LEU:CD1	2.49	0.43
1:B:357:THR:HA	1:B:360:TYR:HB3	2.01	0.43
1:B:110:LEU:HD12	1:B:111:ILE:H	1.81	0.43
1:B:347:ILE:HD13	1:B:361:LEU:HB3	2.00	0.43
1:B:384:PRO:HB3	1:B:389:LEU:O	2.18	0.42
1:B:213:ALA:HB1	1:B:231:LYS:HD2	2.01	0.42
1:B:257:ARG:HD3	1:B:280:GLU:HG3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:11:ASN:C	1:B:57:ILE:HD11	2.44	0.42
1:B:291:ILE:O	1:B:295:ASN:N	2.52	0.42
1:B:288:ALA:HB1	1:B:336:HIS:HB2	2.00	0.42
1:A:168:LEU:HB2	3:A:475:HOH:O	2.19	0.42
1:A:257:ARG:CB	1:A:280:GLU:HB2	2.46	0.42
1:A:258:LYS:CB	1:A:261:VAL:HG13	2.50	0.42
1:A:377:LEU:C	1:A:377:LEU:HD23	2.45	0.42
1:A:257:ARG:HB2	1:A:280:GLU:CB	2.48	0.42
1:A:327:GLU:O	1:A:330:LYS:HB3	2.20	0.41
1:B:84:LEU:C	1:B:84:LEU:HD23	2.45	0.41
1:A:168:LEU:HD12	1:A:168:LEU:HA	1.83	0.41
1:A:282:ASN:O	1:A:283:ASN:HB2	2.21	0.41
1:B:381:SER:CB	1:B:420:HIS:HD2	2.33	0.41
1:A:203:GLN:NE2	1:A:247:ILE:HD13	2.35	0.41
1:B:117:LEU:HD12	1:B:117:LEU:O	2.20	0.41
1:A:399:ASP:HA	1:A:402:THR:HG22	2.02	0.41
1:B:405:LEU:O	1:B:409:LEU:HG	2.19	0.41
1:B:365:ILE:HG21	1:B:414:ILE:HD11	2.02	0.41
1:A:36:ARG:HD2	1:A:137:LEU:HD23	2.02	0.41
1:B:300:ILE:HG23	1:B:329:LYS:CE	2.48	0.41
1:B:44:LYS:O	1:B:45:ALA:HB2	2.21	0.40
1:A:174:MET:HA	1:A:208:ILE:O	2.21	0.40
1:B:143:HIS:HA	1:B:144:PRO:HD2	1.91	0.40
1:A:209:ILE:HD12	1:A:211:ILE:HD11	2.04	0.40
1:B:58:ARG:HD3	1:B:247:ILE:HA	2.04	0.40
1:B:195:LYS:HD3	1:B:238:TYR:CE1	2.56	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	353/442 (80%)	337 (96%)	15 (4%)	1 (0%)	36	42
1	B	365/442 (83%)	353 (97%)	12 (3%)	0	100	100
All	All	718/884 (81%)	690 (96%)	27 (4%)	1 (0%)	48	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	349	PHE

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	335/396 (85%)	305 (91%)	30 (9%)	9	9
1	B	344/396 (87%)	329 (96%)	15 (4%)	25	34
All	All	679/792 (86%)	634 (93%)	45 (7%)	15	18

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	5	ILE
1	A	19	ILE
1	A	71	LYS
1	A	98	ARG
1	A	100	ILE
1	A	117	LEU
1	A	118	THR
1	A	168	LEU
1	A	172	ILE
1	A	185	SER
1	A	190	ASP
1	A	194	ARG
1	A	223	ILE
1	A	243	LEU

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Mol	Chain	Res	Type
1	A	258	LYS
1	A	261	VAL
1	A	268	LYS
1	A	280	GLU
1	A	303	ASN
1	A	320	ASP
1	A	327	GLU
1	A	328	GLN
1	A	338	ILE
1	A	365	ILE
1	A	371	ARG
1	A	386	VAL
1	A	387	LEU
1	A	393	SER
1	A	412	LEU
1	B	2	VAL
1	B	11	ASN
1	B	36	ARG
1	B	84	LEU
1	B	118	THR
1	B	168	LEU
1	B	172	ILE
1	B	181	ASN
1	B	190	ASP
1	B	247	ILE
1	B	268	LYS
1	B	282	ASN
1	B	359	ARG
1	B	371	ARG
1	B	377	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	GLN
1	A	30	GLN
1	A	182	GLN
1	A	203	GLN
1	A	295	ASN
1	A	302	HIS
1	A	303	ASN
1	A	341	GLN

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Mol	Chain	Res	Type
1	A	342	ASN
1	B	11	ASN
1	B	30	GLN
1	B	182	GLN
1	B	242	GLN
1	B	269	HIS
1	B	282	ASN
1	B	295	ASN
1	B	302	HIS
1	B	342	ASN
1	B	364	ASN
1	B	420	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 ⓘ

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	368/442 (83%)	-1.23	0 100 100	19, 39, 72, 85	1 (0%)
1	B	377/442 (85%)	-1.27	0 100 100	18, 37, 67, 82	2 (0%)
All	All	745/884 (84%)	-1.25	0 100 100	18, 38, 70, 85	3 (0%)

There are no RSRZ outliers to report.

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MG	A	423	1/1	0.98	0.05	58,58,58,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.