



# Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 06:24 pm BST

PDB ID : 2GFW  
Title : Structure of wild type E. coli FabF (KASII)  
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Deposited on : 2006-03-23  
Resolution : 2.40 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](mailto: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.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

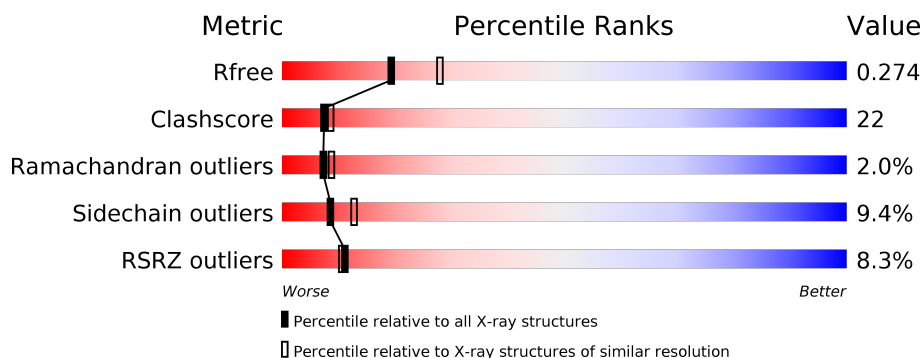
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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))
$R_{free}$	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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  $\geq 3$ , 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	427	<div> <div>8%</div> <div>59%</div> <div>32%</div> <div>.</div> <div>.</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3101 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 3-oxoacyl-[acyl-carrier-protein] synthase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	411	Total	C	N	O	S	0	0	0
			3004	1875	527	585	17			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	MET	-	EXPRESSION TAG	UNP P0AAI5
A	-13	ARG	-	EXPRESSION TAG	UNP P0AAI5
A	-12	GLY	-	EXPRESSION TAG	UNP P0AAI5
A	-11	SER	-	EXPRESSION TAG	UNP P0AAI5
A	-10	HIS	-	EXPRESSION TAG	UNP P0AAI5
A	-9	HIS	-	EXPRESSION TAG	UNP P0AAI5
A	-8	HIS	-	EXPRESSION TAG	UNP P0AAI5
A	-7	HIS	-	EXPRESSION TAG	UNP P0AAI5
A	-6	HIS	-	EXPRESSION TAG	UNP P0AAI5
A	-5	HIS	-	EXPRESSION TAG	UNP P0AAI5
A	-4	GLY	-	EXPRESSION TAG	UNP P0AAI5
A	-3	SER	-	EXPRESSION TAG	UNP P0AAI5
A	-2	ALA	-	EXPRESSION TAG	UNP P0AAI5
A	-1	CYS	-	EXPRESSION TAG	UNP P0AAI5
A	0	VAL	-	EXPRESSION TAG	UNP P0AAI5

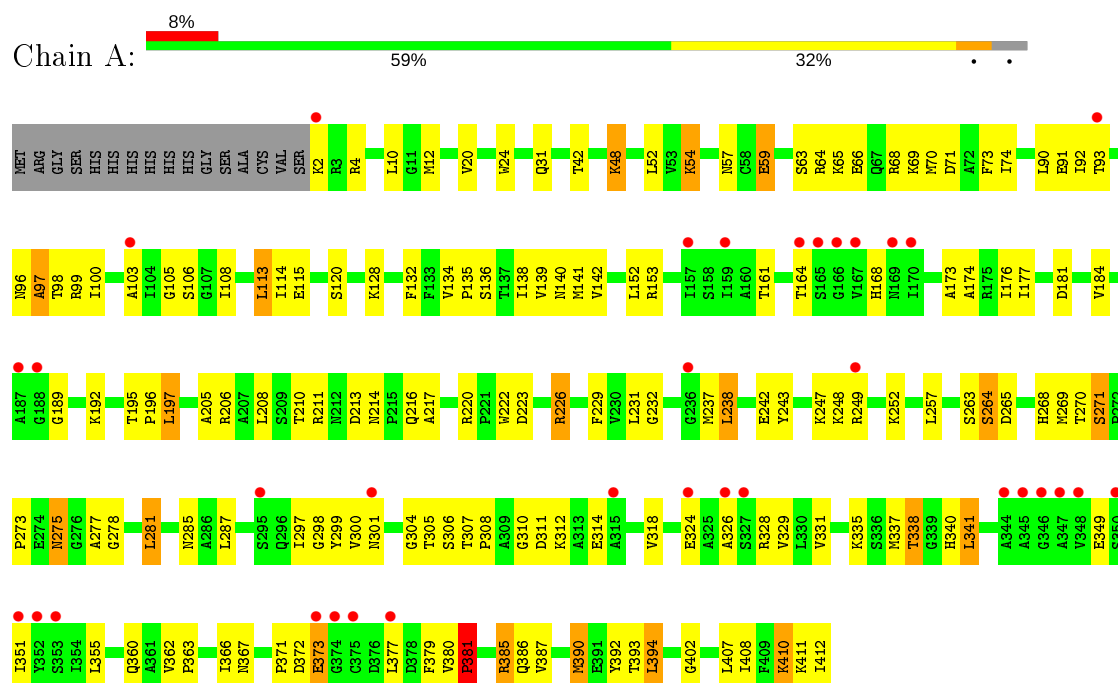
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	97	Total	O	0	0
			97	97		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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: 3-oxoacyl-[acyl-carrier-protein] synthase 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.37Å 75.37Å 145.70Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	65.94 – 2.40 31.81 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.3 (65.94-2.40) 99.5 (31.81-2.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.31 (at 2.39Å)	Xtriage
Refinement program	BUSTER-TNT 1.1.0	Depositor
R, $R_{free}$	0.202 , 0.268 0.204 , 0.274	Depositor DCC
$R_{free}$ test set	989 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	60.0	Xtriage
Anisotropy	0.301	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 61.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3101	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.92% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.63	0/3056	0.82	2/4133 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	381	PRO	N-CA-C	7.58	131.82	112.10
1	A	226	ARG	CB-CA-C	-5.33	99.73	110.40

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	3004	0	2970	133	0
2	A	97	0	0	15	2
All	All	3101	0	2970	133	2

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 22.

All (133) 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:268:HIS:HD2	1:A:271:SER:H	1.10	0.95
1:A:128:LYS:HE2	1:A:128:LYS:HA	1.48	0.92
1:A:91:GLU:H	1:A:249:ARG:NH1	1.69	0.90
1:A:100:ILE:HG22	1:A:152:LEU:HD22	1.55	0.88
1:A:91:GLU:HB2	1:A:249:ARG:HH22	1.39	0.87
1:A:243:TYR:CZ	1:A:247:LYS:HE3	2.09	0.87
1:A:298:GLY:HA3	1:A:390:MET:HG3	1.58	0.85
1:A:91:GLU:H	1:A:249:ARG:HH12	1.23	0.84
1:A:91:GLU:HB2	1:A:249:ARG:NH2	1.92	0.84
1:A:100:ILE:CG2	1:A:152:LEU:HD22	2.08	0.83
1:A:326:ALA:HB3	2:A:502:HOH:O	1.84	0.78
1:A:220:ARG:HD3	1:A:223:ASP:OD2	1.84	0.77
1:A:90:LEU:HD21	1:A:100:ILE:HD13	1.69	0.74
1:A:392:TYR:CE1	1:A:410:LYS:HG3	2.22	0.74
1:A:281:LEU:HD22	1:A:285:ASN:HD21	1.51	0.74
1:A:120:SER:HB3	1:A:128:LYS:HB3	1.70	0.73
1:A:238:LEU:HD23	1:A:238:LEU:N	2.03	0.73
1:A:210:THR:HB	2:A:473:HOH:O	1.88	0.72
1:A:257:LEU:HD21	1:A:407:LEU:HD22	1.71	0.72
1:A:138:ILE:HD12	1:A:140:ASN:OD1	1.89	0.71
1:A:242:GLU:HG2	2:A:504:HOH:O	1.91	0.70
1:A:66:GLU:OE1	1:A:69:LYS:HD2	1.92	0.70
1:A:71:ASP:HA	1:A:113:LEU:HD22	1.74	0.69
1:A:243:TYR:CE1	1:A:247:LYS:HE3	2.27	0.69
1:A:229:PHE:HE1	1:A:231:LEU:HD13	1.58	0.69
1:A:220:ARG:NH1	1:A:223:ASP:OD2	2.25	0.68
1:A:265:ASP:OD1	1:A:278:GLY:HA3	1.93	0.68
1:A:385:ARG:NH1	2:A:480:HOH:O	2.25	0.68
1:A:331:VAL:O	1:A:379:PHE:HA	1.93	0.68
1:A:211:ARG:NH1	2:A:477:HOH:O	2.20	0.67
1:A:237:MET:C	1:A:238:LEU:HD23	2.16	0.67
1:A:195:THR:HB	1:A:196:PRO:HD2	1.77	0.66
1:A:226:ARG:NH1	1:A:311:ASP:HB2	2.11	0.65
1:A:297:ILE:O	1:A:329:VAL:HG23	1.97	0.64
1:A:308:PRO:O	1:A:312:LYS:HG3	1.97	0.64
1:A:128:LYS:HE2	1:A:128:LYS:CA	2.23	0.63
1:A:301:ASN:ND2	2:A:464:HOH:O	2.24	0.62
1:A:177:ILE:HG12	2:A:507:HOH:O	1.98	0.62
1:A:71:ASP:CA	1:A:113:LEU:HD22	2.29	0.62
1:A:91:GLU:N	1:A:249:ARG:HH12	1.96	0.61
1:A:268:HIS:CD2	1:A:270:THR:H	2.18	0.61
1:A:161:THR:OG1	1:A:168:HIS:HD2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:268:HIS:CD2	1:A:271:SER:H	2.03	0.60
1:A:281:LEU:HD22	1:A:285:ASN:ND2	2.15	0.60
1:A:97:ALA:HB1	1:A:153:ARG:HG3	1.82	0.60
1:A:93:THR:H	1:A:96:ASN:HB2	1.67	0.59
1:A:42:THR:O	1:A:48:LYS:HD3	2.03	0.57
1:A:115:GLU:HG2	1:A:197:LEU:HD22	1.87	0.57
1:A:73:PHE:CE1	1:A:74:ILE:HG13	2.39	0.57
1:A:337:MET:HG3	1:A:366:ILE:HG12	1.86	0.57
1:A:10:LEU:HD22	1:A:351:ILE:HG12	1.87	0.56
1:A:90:LEU:HD21	1:A:100:ILE:CD1	2.34	0.56
1:A:177:ILE:CD1	2:A:507:HOH:O	2.53	0.56
1:A:68:ARG:HG2	1:A:68:ARG:O	2.06	0.56
1:A:93:THR:H	1:A:96:ASN:CB	2.20	0.55
1:A:220:ARG:HG3	1:A:220:ARG:O	2.07	0.55
1:A:59:GLU:HA	1:A:59:GLU:OE1	2.07	0.54
1:A:206:ARG:NH1	2:A:495:HOH:O	2.26	0.54
1:A:2:LYS:O	1:A:2:LYS:HG3	2.07	0.54
1:A:298:GLY:HA3	1:A:390:MET:CG	2.35	0.54
1:A:134:VAL:HB	1:A:135:PRO:HD3	1.90	0.53
1:A:138:ILE:HG13	1:A:141:MET:HG2	1.91	0.53
1:A:277:ALA:HA	2:A:501:HOH:O	2.07	0.52
1:A:299:TYR:HB3	1:A:393:THR:HG22	1.91	0.52
1:A:4:ARG:NH2	1:A:243:TYR:CE2	2.77	0.52
1:A:360:GLN:O	1:A:387:VAL:HG22	2.09	0.52
1:A:335:LYS:HA	1:A:338:THR:HG22	1.92	0.52
1:A:226:ARG:HH22	1:A:312:LYS:HE2	1.74	0.52
1:A:91:GLU:O	1:A:96:ASN:ND2	2.42	0.52
1:A:90:LEU:HD12	1:A:249:ARG:HH11	1.75	0.51
1:A:210:THR:O	1:A:210:THR:HG22	2.09	0.51
1:A:12:MET:HE3	1:A:20:VAL:HA	1.93	0.51
1:A:385:ARG:HG3	1:A:386:GLN:N	2.25	0.51
1:A:314:GLU:O	1:A:318:VAL:HG23	2.11	0.51
1:A:222:TRP:CD1	1:A:311:ASP:HB3	2.46	0.50
1:A:273:PRO:HB2	1:A:275:ASN:HB3	1.92	0.50
1:A:238:LEU:CD2	1:A:238:LEU:N	2.74	0.50
1:A:222:TRP:CE2	1:A:379:PHE:CE1	3.00	0.50
1:A:307:THR:OG1	1:A:310:GLY:HA3	2.12	0.50
1:A:4:ARG:N	2:A:504:HOH:O	2.45	0.50
1:A:184:VAL:CA	2:A:507:HOH:O	2.60	0.49
1:A:226:ARG:HH11	1:A:311:ASP:HB2	1.75	0.49
1:A:69:LYS:HE2	1:A:132:PHE:CE1	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:GLY:O	1:A:189:GLY:HA2	2.13	0.48
1:A:115:GLU:OE2	1:A:197:LEU:HB2	2.13	0.48
1:A:57:ASN:OD1	1:A:59:GLU:HB2	2.14	0.47
1:A:134:VAL:HB	1:A:135:PRO:CD	2.44	0.47
1:A:205:ALA:O	1:A:206:ARG:HB2	2.14	0.47
1:A:74:ILE:HA	1:A:142:VAL:HG22	1.96	0.47
1:A:195:THR:HB	1:A:196:PRO:CD	2.45	0.47
1:A:287:LEU:HD21	1:A:297:ILE:HD12	1.96	0.47
1:A:287:LEU:HD21	1:A:297:ILE:CD1	2.45	0.47
1:A:120:SER:HB3	1:A:128:LYS:CB	2.43	0.47
1:A:184:VAL:HA	2:A:507:HOH:O	2.14	0.47
1:A:264:SER:HA	1:A:402:GLY:O	2.15	0.47
1:A:411:LYS:HG2	1:A:412:ILE:HG13	1.97	0.47
1:A:232:GLY:HA3	1:A:341:LEU:HD22	1.96	0.46
1:A:108:ILE:O	1:A:108:ILE:HG22	2.16	0.46
1:A:90:LEU:HD23	1:A:92:ILE:CD1	2.46	0.46
1:A:135:PRO:O	1:A:141:MET:HG3	2.15	0.46
1:A:394:LEU:HD12	1:A:408:ILE:HG13	1.98	0.45
1:A:362:VAL:HA	1:A:363:PRO:HD3	1.81	0.45
1:A:164:THR:O	1:A:164:THR:HG22	2.17	0.45
1:A:392:TYR:CE1	1:A:410:LYS:NZ	2.85	0.45
1:A:217:ALA:HA	1:A:367:ASN:ND2	2.32	0.45
1:A:134:VAL:N	1:A:135:PRO:HD2	2.33	0.44
1:A:176:ILE:HG23	1:A:181:ASP:HB2	2.00	0.44
1:A:100:ILE:HG12	1:A:184:VAL:HB	1.99	0.44
1:A:380:VAL:N	1:A:381:PRO:CD	2.80	0.44
1:A:269:MET:CB	2:A:458:HOH:O	2.65	0.44
1:A:355:LEU:HD23	1:A:355:LEU:HA	1.77	0.44
1:A:305:THR:HG22	1:A:335:LYS:HE2	1.99	0.44
1:A:52:LEU:O	1:A:54:LYS:HE2	2.17	0.43
1:A:263:SER:HB2	1:A:281:LEU:HD13	1.99	0.43
1:A:300:VAL:HG13	1:A:394:LEU:HD23	2.01	0.43
1:A:223:ASP:O	1:A:226:ARG:HG3	2.18	0.42
1:A:301:ASN:ND2	1:A:349:GLU:HB3	2.34	0.42
1:A:100:ILE:HG21	1:A:152:LEU:HD22	1.94	0.42
1:A:63:SER:O	1:A:65:LYS:N	2.53	0.41
1:A:68:ARG:HH11	1:A:68:ARG:HG3	1.85	0.41
1:A:103:ALA:HB3	1:A:173:ALA:HB2	2.01	0.41
1:A:275:ASN:C	1:A:275:ASN:HD22	2.22	0.41
1:A:174:ALA:HB2	1:A:257:LEU:HD13	2.01	0.41
1:A:24:TRP:CZ3	1:A:363:PRO:HG3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:THR:OG1	1:A:96:ASN:HB2	2.21	0.41
1:A:387:VAL:HG21	1:A:390:MET:HE2	2.02	0.41
1:A:97:ALA:O	1:A:99:ARG:N	2.54	0.41
1:A:232:GLY:C	1:A:341:LEU:HD22	2.42	0.40
1:A:106:SER:HB3	1:A:139:VAL:HG22	2.04	0.40
1:A:248:LYS:HE3	1:A:248:LYS:HB2	1.75	0.40
1:A:113:LEU:HD23	1:A:136:SER:HB2	2.03	0.40
1:A:31:GLN:O	1:A:337:MET:HB3	2.21	0.40
1:A:373:GLU:N	2:A:503:HOH:O	2.55	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:485:HOH:O	2:A:485:HOH:O[5_555]	0.96	1.24
2:A:474:HOH:O	2:A:474:HOH:O[5_555]	1.39	0.81

## 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	409/427 (96%)	376 (92%)	25 (6%)	8 (2%)	 

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	371	PRO
1	A	373	GLU
1	A	98	THR
1	A	304	GLY
1	A	97	ALA
1	A	306	SER

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Mol	Chain	Res	Type
1	A	64	ARG
1	A	381	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	307/320 (96%)	278 (91%)	29 (9%)	8 13

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	LYS
1	A	54	LYS
1	A	59	GLU
1	A	70	MET
1	A	113	LEU
1	A	114	ILE
1	A	192	LYS
1	A	197	LEU
1	A	208	LEU
1	A	213	ASP
1	A	214	ASN
1	A	216	GLN
1	A	238	LEU
1	A	252	LYS
1	A	264	SER
1	A	271	SER
1	A	275	ASN
1	A	281	LEU
1	A	324	GLU
1	A	328	ARG
1	A	338	THR
1	A	340	HIS
1	A	341	LEU
1	A	372	ASP

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Mol	Chain	Res	Type
1	A	377	LEU
1	A	385	ARG
1	A	390	MET
1	A	394	LEU
1	A	410	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	123	ASN
1	A	168	HIS
1	A	214	ASN
1	A	216	GLN
1	A	268	HIS
1	A	275	ASN
1	A	301	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 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 ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	411/427 (96%)	0.23	34 (8%) 11 10	39, 60, 96, 128	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	326	ALA	4.0
1	A	347	ALA	3.8
1	A	170	ILE	3.8
1	A	167	VAL	3.7
1	A	373	GLU	3.2
1	A	169	ASN	3.2
1	A	345	ALA	3.1
1	A	188	GLY	3.0
1	A	236	GLY	2.9
1	A	374	GLY	2.9
1	A	159	ILE	2.9
1	A	249	ARG	2.9
1	A	348	VAL	2.9
1	A	375	CYS	2.8
1	A	346	GLY	2.8
1	A	353	SER	2.8
1	A	295	SER	2.5
1	A	166	GLY	2.5
1	A	315	ALA	2.4
1	A	2	LYS	2.4
1	A	157	ILE	2.3
1	A	165	SER	2.3
1	A	324	GLU	2.3
1	A	351	ILE	2.3
1	A	187	ALA	2.3
1	A	350	SER	2.3
1	A	352	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	301	ASN	2.2
1	A	327	SER	2.2
1	A	93	THR	2.2
1	A	377	LEU	2.2
1	A	103	ALA	2.1
1	A	344	ALA	2.1
1	A	164	THR	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 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.