



# Full wwPDB X-ray Structure Validation Report ⓘ

May 27, 2020 – 12:04 am BST

PDB ID : 4HQ6  
Title : BC domain in the presence of citrate  
Authors : Heo, Y.S.  
Deposited on : 2012-10-25  
Resolution : 2.70 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.

---

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

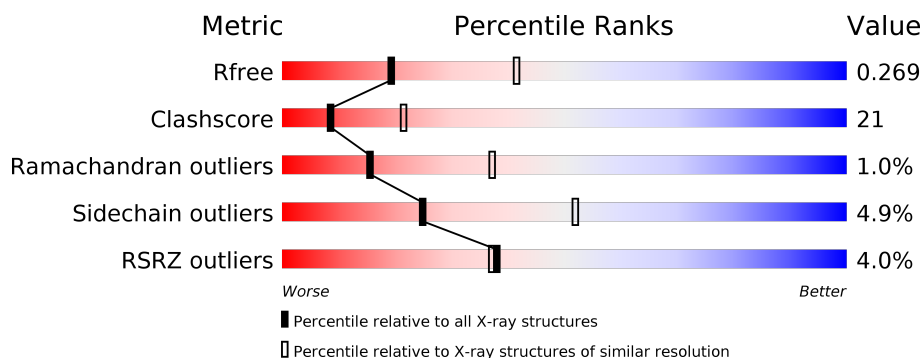
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	573	<div> <div>3%</div> <div>55%</div> <div>28%</div> <div>•</div> <div>14%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3915 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 Acetyl-CoA carboxylase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	494	Total	C	N	O	S	0	0	0
			3871	2468	671	714	18			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	211	MET	-	EXPRESSION TAG	UNP O00763
A	212	ARG	-	EXPRESSION TAG	UNP O00763
A	213	GLY	-	EXPRESSION TAG	UNP O00763
A	214	SER	-	EXPRESSION TAG	UNP O00763
A	215	GLY	-	EXPRESSION TAG	UNP O00763
A	216	SER	-	EXPRESSION TAG	UNP O00763
A	236	ILE	LEU	ENGINEERED MUTATION	UNP O00763
A	776	LEU	VAL	ENGINEERED MUTATION	UNP O00763
A	777	GLU	-	EXPRESSION TAG	UNP O00763
A	778	HIS	-	EXPRESSION TAG	UNP O00763
A	779	HIS	-	EXPRESSION TAG	UNP O00763
A	780	HIS	-	EXPRESSION TAG	UNP O00763
A	781	HIS	-	EXPRESSION TAG	UNP O00763
A	782	HIS	-	EXPRESSION TAG	UNP O00763
A	783	HIS	-	EXPRESSION TAG	UNP O00763

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	44	Total	O	0	0
			44	44		

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.

- [illegible]

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.59 Å 75.59 Å 188.78 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.98 – 2.70 32.71 – 2.70	Depositor EDS
% Data completeness (in resolution range)	86.4 (19.98-2.70) 86.2 (32.71-2.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.53 (at 2.68 Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.221 , 0.273 0.219 , 0.269	Depositor DCC
$R_{free}$ test set	760 reflections (4.60%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	50.5	Xtriage
Anisotropy	0.569	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 46.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.039 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	3915	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% 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	0.41	0/3961	0.60	0/5376

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	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	623	TYR	Sidechain

### 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	3871	0	3826	159	0
2	A	44	0	0	5	0
All	All	3915	0	3826	159	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 21.

All (159) 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:464:ILE:O	1:A:465:ARG:HD3	1.78	0.84
1:A:739:ASN:O	1:A:743:THR:HG23	1.78	0.83
1:A:753:THR:O	1:A:756:LEU:HD13	1.82	0.79
1:A:478:ARG:HA	1:A:481:GLN:HE21	1.48	0.79
1:A:709:ASN:ND2	1:A:712:GLU:H	1.82	0.78
1:A:267:ASN:ND2	1:A:268:ASN:H	1.83	0.76
1:A:254:PHE:HA	1:A:615:ARG:HH12	1.50	0.76
1:A:267:ASN:HD22	1:A:268:ASN:H	1.29	0.76
1:A:525:ARG:HB3	2:A:827:HOH:O	1.88	0.72
1:A:391:VAL:HG13	1:A:422:ILE:HD13	1.69	0.71
1:A:436:ASP:OD1	1:A:438:ASP:HB2	1.91	0.70
1:A:538:ILE:HD11	1:A:751:ILE:HA	1.73	0.70
1:A:296:VAL:HG21	1:A:342:ILE:HD13	1.74	0.69
1:A:655:SER:O	1:A:733:THR:HG21	1.93	0.69
1:A:254:PHE:HA	1:A:615:ARG:NH1	2.10	0.66
1:A:708:GLU:CD	1:A:708:GLU:H	1.99	0.66
1:A:621:LEU:HD21	1:A:627:PRO:HG3	1.78	0.65
1:A:385:LYS:HG2	1:A:490:PHE:CZ	2.32	0.65
1:A:273:VAL:HG21	1:A:669:VAL:HG11	1.78	0.65
1:A:435:LYS:HE3	1:A:439:GLU:OE2	1.96	0.65
1:A:552:ILE:HG22	1:A:556:LYS:HD2	1.77	0.65
1:A:276:MET:HE2	1:A:314:ALA:HA	1.79	0.63
1:A:267:ASN:HD22	1:A:268:ASN:N	1.96	0.62
1:A:378:ALA:N	1:A:421:ARG:NH1	2.47	0.62
1:A:364:LEU:HD22	1:A:369:VAL:HG11	1.81	0.62
1:A:280:ARG:HB3	1:A:290:GLU:HG2	1.81	0.61
1:A:318:VAL:HG21	1:A:338:ILE:HD13	1.82	0.61
1:A:709:ASN:HD22	1:A:709:ASN:C	2.03	0.61
1:A:325:ASN:HA	1:A:328:ASN:OD1	2.01	0.60
1:A:435:LYS:HG2	1:A:439:GLU:OE2	2.01	0.59
1:A:276:MET:HE1	1:A:314:ALA:HB2	1.84	0.59
1:A:403:SER:OG	1:A:432:GLY:O	2.18	0.59
1:A:473:PHE:HB3	1:A:474:PRO:HD3	1.85	0.58
1:A:378:ALA:N	1:A:421:ARG:HH11	2.02	0.58
1:A:276:MET:HE3	1:A:295:PHE:HB3	1.86	0.57
1:A:594:MET:CE	1:A:681:TRP:HE1	2.18	0.57
1:A:289:ASN:ND2	1:A:291:ARG:H	2.03	0.57
1:A:291:ARG:HD2	2:A:808:HOH:O	2.05	0.57

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:351:TRP:HA	1:A:584:ARG:HD2	1.86	0.57
1:A:419:GLY:O	1:A:420:LYS:HB3	2.03	0.57
1:A:452:MET:SD	1:A:494:LEU:HD13	2.45	0.57
1:A:523:ILE:HD12	1:A:523:ILE:N	2.20	0.57
1:A:655:SER:HB2	1:A:684:PHE:CZ	2.40	0.57
1:A:584:ARG:HG3	1:A:584:ARG:HH11	1.70	0.56
1:A:276:MET:CE	1:A:314:ALA:HA	2.35	0.56
1:A:462:LYS:HE2	1:A:483:GLU:HG2	1.88	0.56
1:A:756:LEU:HD12	1:A:756:LEU:H	1.70	0.55
1:A:262:LYS:HG3	1:A:344:VAL:HG12	1.88	0.55
1:A:534:ALA:HB2	1:A:591:CYS:HB3	1.87	0.55
1:A:737:LEU:O	1:A:741:LEU:HG	2.05	0.55
1:A:756:LEU:HD12	1:A:756:LEU:N	2.21	0.55
1:A:530:ILE:HG22	1:A:531:VAL:HG23	1.88	0.55
1:A:727:ARG:HB3	1:A:729:ASP:OD1	2.07	0.54
1:A:364:LEU:HD22	1:A:369:VAL:CG1	2.38	0.53
1:A:305:LYS:HA	1:A:305:LYS:HE3	1.90	0.53
1:A:594:MET:HE1	1:A:681:TRP:HE1	1.74	0.53
1:A:561:VAL:O	1:A:562:SER:HB3	2.09	0.53
1:A:504:GLN:HG2	1:A:592:THR:HG21	1.92	0.53
1:A:709:ASN:HD21	1:A:712:GLU:H	1.54	0.53
1:A:724:LEU:HD22	1:A:730:PHE:CG	2.44	0.52
1:A:594:MET:HE1	1:A:704:PHE:HB3	1.91	0.52
1:A:436:ASP:HB2	2:A:803:HOH:O	2.10	0.51
1:A:276:MET:HE1	1:A:314:ALA:CB	2.40	0.51
1:A:296:VAL:HG11	1:A:342:ILE:HD11	1.91	0.51
1:A:385:LYS:HD2	1:A:389:THR:OG1	2.10	0.51
1:A:594:MET:HE1	1:A:704:PHE:CB	2.39	0.51
1:A:534:ALA:HB3	1:A:648:VAL:HB	1.93	0.51
1:A:325:ASN:N	1:A:325:ASN:HD22	2.07	0.50
1:A:377:GLU:C	1:A:421:ARG:HH11	2.14	0.50
1:A:594:MET:HE1	1:A:681:TRP:NE1	2.26	0.50
1:A:594:MET:CE	1:A:704:PHE:HB3	2.42	0.50
1:A:450:PRO:HB3	2:A:812:HOH:O	2.11	0.50
1:A:569:LEU:O	1:A:576:PHE:HA	2.12	0.49
1:A:289:ASN:HD22	1:A:290:GLU:N	2.09	0.49
1:A:340:LYS:O	1:A:343:PRO:HB3	2.12	0.49
1:A:572:GLN:CD	1:A:572:GLN:H	2.15	0.49
1:A:301:PRO:HD3	1:A:320:VAL:O	2.13	0.49
1:A:584:ARG:HH12	1:A:586:GLN:HG2	1.77	0.49
1:A:247:PRO:O	1:A:251:VAL:HG23	2.14	0.48

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:LYS:HG2	1:A:344:VAL:HA	1.95	0.48
1:A:708:GLU:OE1	1:A:712:GLU:HG3	2.14	0.48
1:A:296:VAL:HA	1:A:316:HIS:O	2.14	0.48
1:A:299:VAL:HG12	1:A:304:LEU:HB2	1.95	0.47
1:A:676:SER:HB3	1:A:719:VAL:HG12	1.95	0.47
1:A:397:VAL:HG22	1:A:550:CYS:HB3	1.96	0.47
1:A:669:VAL:HG13	1:A:669:VAL:O	2.14	0.47
1:A:465:ARG:HG3	1:A:476:LEU:HD22	1.96	0.47
1:A:589:HIS:ND1	1:A:590:PRO:HD3	2.30	0.47
1:A:710:ARG:O	1:A:714:ILE:HG13	2.15	0.47
1:A:728:GLY:O	1:A:731:ARG:HG2	2.14	0.47
1:A:286:MET:HE2	1:A:286:MET:HA	1.96	0.47
1:A:457:GLU:HB2	1:A:487:SER:HB2	1.97	0.47
1:A:287:PHE:C	1:A:289:ASN:N	2.67	0.46
1:A:325:ASN:N	1:A:325:ASN:ND2	2.64	0.46
1:A:495:ALA:HB1	1:A:569:LEU:HD21	1.98	0.46
1:A:647:HIS:CD2	1:A:710:ARG:HA	2.51	0.46
1:A:454:LYS:HG2	1:A:464:ILE:HG23	1.97	0.46
1:A:457:GLU:HB2	1:A:487:SER:CB	2.45	0.46
1:A:465:ARG:CG	1:A:476:LEU:HD22	2.45	0.46
1:A:457:GLU:HB2	1:A:487:SER:OG	2.16	0.45
1:A:656:GLU:OE1	1:A:656:GLU:HA	2.17	0.45
1:A:380:TRP:HA	1:A:380:TRP:CE3	2.52	0.45
1:A:300:THR:HG22	1:A:320:VAL:HG23	1.99	0.44
1:A:523:ILE:CD1	1:A:523:ILE:N	2.80	0.44
1:A:439:GLU:O	1:A:442:GLU:HB2	2.17	0.44
1:A:357:ASN:O	1:A:361:PRO:HD2	2.17	0.44
1:A:589:HIS:N	1:A:590:PRO:CD	2.80	0.44
1:A:614:HIS:HD2	2:A:830:HOH:O	2.00	0.44
1:A:267:ASN:ND2	1:A:268:ASN:N	2.59	0.44
1:A:286:MET:HA	1:A:286:MET:CE	2.48	0.44
1:A:523:ILE:H	1:A:523:ILE:CD1	2.31	0.44
1:A:268:ASN:HA	1:A:272:ALA:HB2	2.00	0.44
1:A:496:GLN:O	1:A:497:HIS:C	2.56	0.44
1:A:336:VAL:HG21	1:A:363:LEU:CB	2.48	0.43
1:A:545:GLU:O	1:A:548:GLU:HB2	2.18	0.43
1:A:668:THR:O	1:A:685:SER:HA	2.18	0.43
1:A:264:LEU:HB3	1:A:347:VAL:HG22	1.99	0.43
1:A:357:ASN:HD21	1:A:359:LYS:HE3	1.82	0.43
1:A:268:ASN:HB2	1:A:310:TYR:CE2	2.53	0.43
1:A:499:ARG:HD3	1:A:751:ILE:O	2.17	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:756:LEU:H	1:A:756:LEU:CD1	2.31	0.43
1:A:683:TYR:HE1	1:A:702:HIS:HB2	1.84	0.43
1:A:377:GLU:HB2	1:A:421:ARG:NH1	2.34	0.43
1:A:655:SER:N	1:A:684:PHE:HZ	2.16	0.43
1:A:751:ILE:HG23	1:A:752:ASP:N	2.34	0.43
1:A:520:ASP:HB3	1:A:533:GLU:HB2	2.00	0.42
1:A:410:GLU:H	1:A:410:GLU:HG3	1.62	0.42
1:A:318:VAL:HA	1:A:319:PRO:HD3	1.83	0.42
1:A:262:LYS:CG	1:A:344:VAL:HA	2.49	0.42
1:A:409:VAL:HG11	1:A:423:SER:O	2.19	0.42
1:A:584:ARG:NH1	1:A:584:ARG:HG3	2.34	0.42
1:A:318:VAL:O	1:A:318:VAL:HG23	2.20	0.42
1:A:361:PRO:HB3	1:A:371:PHE:CD2	2.55	0.42
1:A:303:ASP:OD1	1:A:668:THR:HG21	2.20	0.42
1:A:725:SER:HA	1:A:730:PHE:O	2.20	0.42
1:A:630:VAL:HG12	1:A:630:VAL:O	2.19	0.42
1:A:561:VAL:O	1:A:562:SER:CB	2.68	0.41
1:A:523:ILE:H	1:A:523:ILE:HD12	1.86	0.41
1:A:709:ASN:C	1:A:709:ASN:ND2	2.73	0.41
1:A:276:MET:HE3	1:A:295:PHE:CB	2.49	0.41
1:A:496:GLN:O	1:A:497:HIS:O	2.39	0.41
1:A:587:VAL:HG13	1:A:588:GLU:HG3	2.01	0.41
1:A:496:GLN:HE21	1:A:496:GLN:HB2	1.62	0.41
1:A:736:TYR:CE2	1:A:737:LEU:HG	2.56	0.41
1:A:332:VAL:O	1:A:336:VAL:HG23	2.21	0.41
1:A:336:VAL:HG21	1:A:363:LEU:HB3	2.03	0.41
1:A:446:ARG:HH11	1:A:446:ARG:HG2	1.85	0.41
1:A:299:VAL:O	1:A:319:PRO:HA	2.21	0.41
1:A:683:TYR:CE1	1:A:702:HIS:HB2	2.56	0.41
1:A:289:ASN:C	1:A:289:ASN:HD22	2.24	0.41
1:A:418:GLN:HG2	1:A:418:GLN:O	2.20	0.41
1:A:551:ALA:HB1	1:A:566:VAL:HG21	2.03	0.41
1:A:275:CYS:HB2	1:A:348:TRP:CH2	2.57	0.40
1:A:402:TRP:HB2	1:A:491:LEU:O	2.20	0.40
1:A:402:TRP:CH2	1:A:404:GLY:HA3	2.57	0.40
1:A:709:ASN:HD22	1:A:712:GLU:H	1.64	0.40
1:A:726:ILE:O	1:A:727:ARG:C	2.58	0.40
1:A:257:ASP:O	1:A:258:ARG:HB2	2.20	0.40
1:A:426:GLU:O	1:A:426:GLU:HG2	2.21	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	486/573 (85%)	448 (92%)	33 (7%)	5 (1%)	15	37

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	497	HIS
1	A	562	SER
1	A	573	ASP
1	A	574	GLY
1	A	420	LYS

### 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	412/477 (86%)	392 (95%)	20 (5%)	25	52

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

Mol	Chain	Res	Type
1	A	267	ASN
1	A	281	ARG
1	A	289	ASN
1	A	305	LYS
1	A	325	ASN
1	A	343	PRO

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	410	GLU
1	A	445	GLU
1	A	465	ARG
1	A	497	HIS
1	A	528	GLN
1	A	572	GLN
1	A	573	ASP
1	A	615	ARG
1	A	708	GLU
1	A	709	ASN
1	A	711	GLU
1	A	724	LEU
1	A	729	ASP
1	A	749	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	267	ASN
1	A	289	ASN
1	A	325	ASN
1	A	353	HIS
1	A	367	ASN
1	A	481	GLN
1	A	496	GLN
1	A	524	GLN
1	A	528	GLN
1	A	699	GLN
1	A	709	ASN
1	A	716	ASN
1	A	739	ASN
1	A	747	GLN
1	A	748	ASN
1	A	749	ASN

### 5.3.3 RNA ⓘ

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, 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	494/573 (86%)	0.24	20 (4%) 38 37	31, 53, 79, 103	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	240	ARG	3.3
1	A	730	PHE	3.2
1	A	420	LYS	3.1
1	A	563	ALA	3.0
1	A	564	GLY	2.9
1	A	686	VAL	2.8
1	A	590	PRO	2.8
1	A	239	HIS	2.6
1	A	667	GLY	2.5
1	A	731	ARG	2.5
1	A	411	TRP	2.4
1	A	527	HIS	2.3
1	A	587	VAL	2.3
1	A	526	ARG	2.3
1	A	699	GLN	2.2
1	A	656	GLU	2.1
1	A	304	LEU	2.1
1	A	589	HIS	2.1
1	A	525	ARG	2.0
1	A	342	ILE	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.