



# Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 08:19 am BST

PDB ID : 3JRW  
Title : Phosphorylated BC domain of ACC2  
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Deposited on : 2009-09-09  
Resolution : 2.60 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  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
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

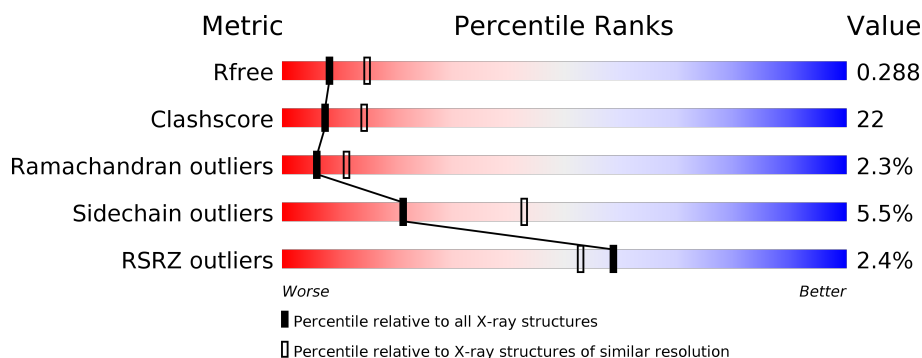
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	587	<div> <div>2%</div> <div> <div></div> <div>51%</div> <div>32%</div> <div>•</div> <div>15%</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3960 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
			Total	C	N	O	P	S			
1	A	499	3907	2487	676	724	1	19	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	205	MET	-	EXPRESSION TAG	UNP O00763
A	206	ARG	-	EXPRESSION TAG	UNP O00763
A	207	GLY	-	EXPRESSION TAG	UNP O00763
A	208	SER	-	EXPRESSION TAG	UNP O00763
A	209	GLY	-	EXPRESSION TAG	UNP O00763
A	210	SER	-	EXPRESSION TAG	UNP O00763
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	776	LEU	-	EXPRESSION TAG	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
A	784	LEU	-	EXPRESSION TAG	UNP O00763
A	785	GLU	-	EXPRESSION TAG	UNP O00763
A	786	HIS	-	EXPRESSION TAG	UNP O00763
A	787	HIS	-	EXPRESSION TAG	UNP O00763
A	788	HIS	-	EXPRESSION TAG	UNP O00763
A	789	HIS	-	EXPRESSION TAG	UNP O00763
A	790	HIS	-	EXPRESSION TAG	UNP O00763

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Chain	Residue	Modelled	Actual	Comment	Reference
A	791	HIS	-	EXPRESSION TAG	UNP O00763

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	53	Total	O	0	0
			53	53		

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 ( $\text{RSRZ} > 2$ ). 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.

Chain A:

Sequence logo for Chain A showing amino acid conservation across 100 positions. The y-axis represents information content in bits (0.00 to 2.00). The x-axis shows positions 1 to 100. A color scale at the top indicates conservation levels: 29% (red), 51% (green), 32% (yellow), and 15% (grey). Amino acids are listed below the logo, with some highlighted in orange or red to indicate high conservation. Specific residues like L613, L724, and T731 are highlighted in red.

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.74Å 75.74Å 189.47Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.85 – 2.60 19.85 – 2.39	Depositor EDS
% Data completeness (in resolution range)	90.9 (19.85-2.60) 83.4 (19.85-2.39)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.36 (at 2.38Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.234 , 0.294 0.230 , 0.288	Depositor DCC
$R_{free}$ test set	898 reflections (4.18%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	45.4	Xtriage
Anisotropy	0.601	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 40.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.044 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	3960	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% 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](#)

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

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	0.42	0/3985	0.63	0/5404

There are no bond length outliers.

There are no bond angle outliers.

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	3907	0	3857	171	0
2	A	53	0	0	8	0
All	All	3960	0	3857	171	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 22.

All (171) 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:267:ASN:ND2	1:A:268:ASN:H	1.64	0.94
1:A:267:ASN:HD22	1:A:268:ASN:N	1.67	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:LYS:O	1:A:305:LYS:HE3	1.73	0.88
1:A:267:ASN:HD22	1:A:268:ASN:H	0.91	0.87
1:A:708:GLU:CD	1:A:708:GLU:H	1.81	0.84
1:A:454:LYS:HG2	1:A:464:ILE:HD12	1.60	0.84
1:A:251:VAL:HG21	1:A:259:VAL:HG22	1.64	0.79
1:A:273:VAL:HG21	1:A:669:VAL:HG11	1.67	0.77
1:A:240:ARG:HG2	1:A:241:ASP:H	1.51	0.76
1:A:221:MET:HG3	1:A:223:GLY:H	1.50	0.76
1:A:325:ASN:HA	1:A:328:ASN:OD1	1.87	0.75
1:A:436:ASP:OD1	1:A:438:ASP:HB2	1.88	0.73
1:A:454:LYS:HG2	1:A:464:ILE:CD1	2.18	0.72
1:A:325:ASN:HD22	1:A:326:ASN:H	1.38	0.71
1:A:385:LYS:HG2	1:A:490:PHE:CZ	2.26	0.70
1:A:289:ASN:ND2	1:A:291:ARG:H	1.89	0.69
1:A:508:ASP:HB3	1:A:613:LEU:HD13	1.75	0.68
1:A:301:PRO:HD3	1:A:320:VAL:O	1.95	0.67
1:A:378:ALA:N	1:A:421:ARG:NH1	2.43	0.67
1:A:499:ARG:O	1:A:569:LEU:HD12	1.95	0.65
1:A:621:LEU:HD21	1:A:627:PRO:HG3	1.76	0.65
1:A:296:VAL:HA	1:A:316:HIS:O	1.98	0.63
1:A:325:ASN:HD22	1:A:326:ASN:N	1.96	0.63
1:A:677:SER:HA	2:A:17:HOH:O	1.99	0.63
1:A:462:LYS:NZ	1:A:483:GLU:HG3	2.14	0.62
1:A:269:GLY:O	1:A:273:VAL:HG23	1.99	0.62
1:A:594:MET:HE1	1:A:681:TRP:HE1	1.64	0.62
1:A:385:LYS:HD2	1:A:389:THR:OG1	2.00	0.61
1:A:221:MET:CE	1:A:224:LEU:HD13	2.31	0.61
1:A:375:PRO:HB2	1:A:377:GLU:OE1	2.00	0.61
1:A:753:THR:O	1:A:756:LEU:HD13	1.99	0.61
1:A:318:VAL:HG21	1:A:338:ILE:HD13	1.81	0.61
1:A:473:PHE:HB3	1:A:474:PRO:HD3	1.83	0.61
1:A:710:ARG:O	1:A:714:ILE:HG13	2.01	0.61
1:A:462:LYS:HB3	1:A:484:ILE:HD11	1.83	0.60
1:A:336:VAL:HG21	1:A:363:LEU:HB3	1.83	0.60
1:A:520:ASP:HB3	1:A:533:GLU:HB2	1.83	0.60
1:A:709:ASN:HD22	1:A:709:ASN:C	2.04	0.60
1:A:743:THR:O	1:A:747:GLN:HG2	2.00	0.60
1:A:286:MET:HE2	1:A:286:MET:HA	1.83	0.60
1:A:325:ASN:ND2	1:A:326:ASN:N	2.48	0.60
1:A:220:SER:HB2	1:A:274:LYS:HD3	1.83	0.59
1:A:709:ASN:ND2	1:A:712:GLU:H	2.00	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:436:ASP:HB2	2:A:12:HOH:O	2.05	0.57
1:A:594:MET:HE1	1:A:681:TRP:NE1	2.20	0.56
1:A:464:ILE:O	1:A:465:ARG:HD3	2.06	0.56
1:A:594:MET:CE	1:A:681:TRP:HE1	2.19	0.56
1:A:325:ASN:ND2	1:A:326:ASN:H	2.04	0.55
1:A:221:MET:HE3	1:A:224:LEU:HD13	1.88	0.55
1:A:544:PHE:HA	1:A:547:MET:HE2	1.88	0.54
1:A:318:VAL:HG21	1:A:338:ILE:HG21	1.88	0.54
1:A:544:PHE:HA	1:A:547:MET:CE	2.37	0.54
1:A:220:SER:HB2	1:A:274:LYS:CD	2.37	0.54
1:A:371:PHE:HB3	2:A:26:HOH:O	2.06	0.54
1:A:280:ARG:HB3	1:A:290:GLU:HG3	1.88	0.53
1:A:380:TRP:HA	1:A:380:TRP:CE3	2.43	0.53
1:A:221:MET:HB3	1:A:681:TRP:CE2	2.44	0.53
1:A:377:GLU:HB2	1:A:421:ARG:NH1	2.24	0.53
1:A:244:VAL:HB	1:A:249:GLU:HG2	1.91	0.52
1:A:262:LYS:CG	1:A:344:VAL:HG12	2.39	0.52
1:A:262:LYS:HG2	1:A:344:VAL:HG12	1.90	0.52
1:A:525:ARG:HD3	1:A:530:ILE:HG13	1.89	0.52
1:A:477:PHE:O	1:A:481:GLN:HG3	2.09	0.52
1:A:398:PRO:HB2	1:A:576:PHE:O	2.10	0.52
1:A:306:ALA:O	1:A:307:ASN:HB2	2.11	0.51
1:A:725:SER:HA	1:A:730:PHE:O	2.11	0.51
1:A:739:ASN:O	1:A:743:THR:HG23	2.11	0.50
1:A:223:GLY:O	1:A:224:LEU:HB3	2.11	0.50
1:A:411:TRP:CZ2	1:A:557:THR:HG23	2.47	0.50
1:A:273:VAL:O	1:A:277:ARG:HG3	2.11	0.50
1:A:708:GLU:CD	1:A:708:GLU:N	2.59	0.50
1:A:220:SER:OG	1:A:277:ARG:HD3	2.12	0.50
1:A:683:TYR:CE1	1:A:702:HIS:HB2	2.46	0.50
1:A:299:VAL:HG12	1:A:304:LEU:HB2	1.94	0.49
1:A:328:ASN:O	1:A:330:ALA:N	2.45	0.49
1:A:538:ILE:HD11	1:A:751:ILE:HA	1.93	0.49
1:A:509:GLN:HG3	2:A:3:HOH:O	2.11	0.49
1:A:589:HIS:ND1	1:A:590:PRO:HD3	2.27	0.49
1:A:402:TRP:HB2	1:A:491:LEU:O	2.12	0.49
1:A:635:PHE:O	1:A:638:PRO:HD3	2.11	0.49
1:A:240:ARG:HG2	1:A:241:ASP:N	2.23	0.49
1:A:464:ILE:O	1:A:465:ARG:CD	2.61	0.49
1:A:377:GLU:H	1:A:377:GLU:CD	2.16	0.49
1:A:561:VAL:O	1:A:562:SER:HB3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:351:TRP:HA	1:A:584:ARG:HD2	1.94	0.48
1:A:495:ALA:CB	1:A:569:LEU:HD21	2.43	0.48
1:A:221:MET:HE1	1:A:224:LEU:HD13	1.95	0.48
1:A:289:ASN:HD22	1:A:289:ASN:C	2.17	0.48
1:A:325:ASN:HD22	1:A:325:ASN:N	2.10	0.48
1:A:435:LYS:HG2	1:A:439:GLU:CD	2.34	0.48
1:A:649:ILE:HG12	1:A:713:ALA:HB1	1.96	0.48
1:A:560:TYR:OH	1:A:583:PRO:HA	2.13	0.48
1:A:434:VAL:HG23	1:A:434:VAL:O	2.14	0.47
1:A:523:ILE:HD13	2:A:4:HOH:O	2.13	0.47
1:A:251:VAL:CG2	1:A:259:VAL:HG22	2.39	0.47
1:A:222:SEP:O3P	1:A:277:ARG:NH2	2.46	0.47
1:A:452:MET:SD	1:A:494:LEU:HD13	2.54	0.47
1:A:296:VAL:HG22	1:A:316:HIS:HB2	1.95	0.47
1:A:462:LYS:HZ3	1:A:483:GLU:HG3	1.80	0.47
1:A:411:TRP:CE3	1:A:411:TRP:HA	2.50	0.47
1:A:724:LEU:HD22	1:A:730:PHE:CG	2.50	0.47
1:A:289:ASN:ND2	1:A:289:ASN:C	2.68	0.46
1:A:709:ASN:C	1:A:709:ASN:ND2	2.68	0.46
1:A:545:GLU:O	1:A:548:GLU:HB2	2.15	0.46
1:A:384:ASP:HB2	2:A:19:HOH:O	2.16	0.46
1:A:305:LYS:HE3	1:A:305:LYS:C	2.35	0.46
1:A:625:GLU:HG3	1:A:633:ILE:HG12	1.98	0.46
1:A:636:GLU:HG2	1:A:637:THR:HG23	1.98	0.46
1:A:300:THR:HG22	1:A:320:VAL:HG23	1.98	0.46
1:A:519:ARG:NH2	2:A:1:HOH:O	2.49	0.46
1:A:680:VAL:HG22	1:A:705:SER:HB2	1.98	0.46
1:A:380:TRP:HE3	1:A:380:TRP:HA	1.80	0.45
1:A:507:ALA:HB1	2:A:16:HOH:O	2.16	0.45
1:A:565:THR:HB	1:A:582:ASN:HB2	1.97	0.45
1:A:617:LYS:HB3	1:A:617:LYS:HE3	1.81	0.45
1:A:655:SER:HB2	1:A:684:PHE:CZ	2.51	0.45
1:A:648:VAL:HG12	1:A:649:ILE:N	2.31	0.45
1:A:340:LYS:HD2	1:A:367:ASN:ND2	2.32	0.44
1:A:361:PRO:HB3	1:A:371:PHE:CD2	2.52	0.44
1:A:324:PRO:HB2	1:A:326:ASN:OD1	2.17	0.44
1:A:280:ARG:NH2	1:A:291:ARG:NH1	2.65	0.44
1:A:286:MET:HE1	1:A:628:TRP:CH2	2.52	0.44
1:A:500:HIS:O	1:A:501:LEU:HD23	2.18	0.44
1:A:372:LEU:N	1:A:372:LEU:HD12	2.33	0.44
1:A:378:ALA:N	1:A:421:ARG:HH11	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:541:LEU:O	1:A:545:GLU:HG3	2.18	0.43
1:A:572:GLN:HA	1:A:751:ILE:HD11	2.00	0.43
1:A:246:SER:O	1:A:247:PRO:C	2.55	0.43
1:A:724:LEU:O	1:A:727:ARG:HB2	2.18	0.43
1:A:305:LYS:HE3	1:A:305:LYS:CA	2.49	0.43
1:A:455:ALA:HB1	1:A:487:SER:OG	2.19	0.43
1:A:728:GLY:C	1:A:730:PHE:H	2.22	0.43
1:A:523:ILE:HD12	1:A:523:ILE:N	2.33	0.43
1:A:302:GLU:N	1:A:302:GLU:CD	2.72	0.42
1:A:722:LYS:O	1:A:725:SER:OG	2.28	0.42
1:A:422:ILE:CG2	1:A:557:THR:HG22	2.49	0.42
1:A:289:ASN:HD22	1:A:290:GLU:N	2.17	0.42
1:A:340:LYS:O	1:A:343:PRO:HB3	2.19	0.42
1:A:504:GLN:HG2	1:A:592:THR:HG21	2.00	0.42
1:A:747:GLN:HA	1:A:747:GLN:HE21	1.82	0.42
1:A:584:ARG:HH12	1:A:586:GLN:HG2	1.85	0.42
1:A:478:ARG:HA	1:A:481:GLN:HE21	1.84	0.42
1:A:755:TRP:HA	1:A:758:TYR:CE1	2.55	0.42
1:A:267:ASN:ND2	1:A:268:ASN:N	2.43	0.42
1:A:523:ILE:HG13	1:A:756:LEU:HD21	2.02	0.41
1:A:524:GLN:HA	1:A:528:GLN:O	2.20	0.41
1:A:581:LEU:HD23	1:A:581:LEU:C	2.41	0.41
1:A:465:ARG:NH2	1:A:479:GLN:HG2	2.35	0.41
1:A:495:ALA:HB1	1:A:569:LEU:HD21	2.01	0.41
1:A:294:ARG:H	1:A:294:ARG:HG2	1.64	0.41
1:A:422:ILE:HB	1:A:557:THR:CG2	2.50	0.41
1:A:244:VAL:HG21	1:A:250:PHE:HB2	2.02	0.41
1:A:641:PRO:HA	1:A:642:PRO:HD2	1.87	0.41
1:A:247:PRO:HG2	1:A:261:GLU:HB3	2.02	0.41
1:A:220:SER:HG	1:A:277:ARG:HD3	1.85	0.41
1:A:589:HIS:CG	1:A:590:PRO:HD3	2.56	0.41
1:A:630:VAL:HG12	1:A:630:VAL:O	2.21	0.41
1:A:366:LYS:HE2	1:A:366:LYS:HB3	1.91	0.41
1:A:410:GLU:H	1:A:410:GLU:CD	2.24	0.41
1:A:377:GLU:HB2	1:A:421:ARG:CZ	2.51	0.41
1:A:572:GLN:HA	1:A:751:ILE:CG1	2.51	0.41
1:A:572:GLN:HA	1:A:751:ILE:HG12	2.03	0.41
1:A:600:LEU:HA	1:A:600:LEU:HD23	1.85	0.41
1:A:502:GLU:O	1:A:518:GLY:HA3	2.22	0.40
1:A:561:VAL:O	1:A:562:SER:CB	2.69	0.40
1:A:571:SER:HB3	1:A:575:SER:OG	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:680:VAL:HA	1:A:704:PHE:O	2.22	0.40
1:A:441:LEU:HD21	1:A:473:PHE:HB3	2.04	0.40
1:A:648:VAL:CG1	1:A:649:ILE:N	2.85	0.40
1:A:378:ALA:N	1:A:421:ARG:HH12	2.18	0.40
1:A:453:ILE:CG2	1:A:480:VAL:HG21	2.52	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	488/587 (83%)	438 (90%)	39 (8%)	11 (2%)	<b>6</b> <b>11</b>

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	497	HIS
1	A	329	TYR
1	A	562	SER
1	A	676	SER
1	A	420	LYS
1	A	574	GLY
1	A	755	TRP
1	A	613	LEU
1	A	733	THR
1	A	729	ASP
1	A	328	ASN

### 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	415/489 (85%)	392 (94%)	23 (6%)	21	43

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	224	LEU
1	A	257	ASP
1	A	267	ASN
1	A	281	ARG
1	A	289	ASN
1	A	305	LYS
1	A	325	ASN
1	A	380	TRP
1	A	410	GLU
1	A	442	GLU
1	A	465	ARG
1	A	479	GLN
1	A	521	CYS
1	A	572	GLN
1	A	601	PRO
1	A	613	LEU
1	A	708	GLU
1	A	709	ASN
1	A	711	GLU
1	A	724	LEU
1	A	732	THR
1	A	749	ASN
1	A	752	ASP

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

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Mol	Chain	Res	Type
1	A	325	ASN
1	A	327	ASN
1	A	367	ASN
1	A	481	GLN
1	A	524	GLN
1	A	528	GLN
1	A	679	ASN
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 ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
1	SEP	A	222	1	8,9,10	2.71	3 (37%)	8,12,14	2.08	2 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SEP	A	222	1	-	5/5/8/10	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	222	SEP	P-OG	4.76	1.75	1.60
1	A	222	SEP	P-O2P	4.55	1.72	1.54
1	A	222	SEP	P-O1P	3.42	1.61	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	222	SEP	OG-CB-CA	3.87	111.91	108.14
1	A	222	SEP	P-OG-CB	-3.34	109.08	118.30

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	222	SEP	N-CA-CB-OG
1	A	222	SEP	CA-CB-OG-P
1	A	222	SEP	CB-OG-P-O2P
1	A	222	SEP	CB-OG-P-O3P
1	A	222	SEP	CB-OG-P-O1P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	222	SEP	1	0

## 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 [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, 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	498/587 (84%)	-0.34	12 (2%) 59 53	33, 61, 87, 120	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	242	PHE	3.5
1	A	527	HIS	3.1
1	A	241	ASP	3.0
1	A	240	ARG	3.0
1	A	420	LYS	3.0
1	A	496	GLN	2.8
1	A	239	HIS	2.4
1	A	526	ARG	2.3
1	A	666	SER	2.2
1	A	731	ARG	2.1
1	A	678	LYS	2.1
1	A	667	GLY	2.0

### 6.2 Non-standard residues in protein, DNA, RNA chains [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	SEP	A	222	10/11	0.96	0.11	62,64,67,67	0

### 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.