



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 15, 2025 – 12:36 PM EDT

PDB ID : 9EAV / pdb\_00009eav  
Title : Structure of Citrobacter BubCD(D104A/Y370F)-BubB-BubA(155-229)  
Authors : Ye, Q.; Corbett, K.D.  
Deposited on : 2024-11-11  
Resolution : 1.93 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0rc1  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.45.1

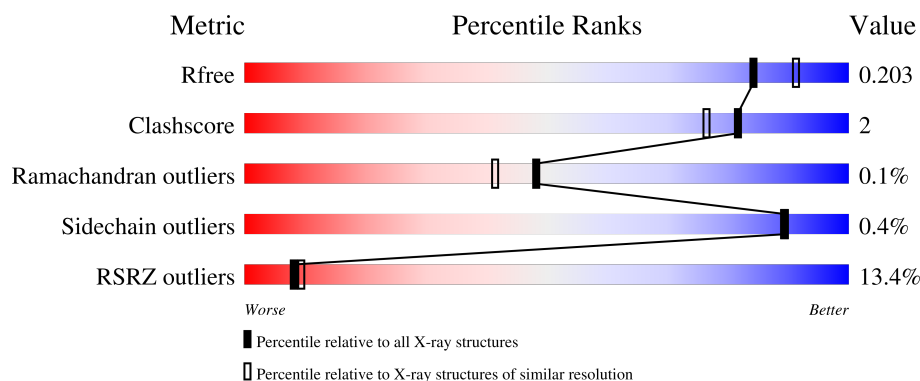
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.93 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))
$R_{free}$	164625	1306 (1.94-1.94)
Clashscore	180529	1400 (1.94-1.94)
Ramachandran outliers	177936	1387 (1.94-1.94)
Sidechain outliers	177891	1387 (1.94-1.94)
RSRZ outliers	164620	1306 (1.94-1.94)

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  $\geq 3$ , 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	458	<div> <div>7%</div> <div> <div></div> <div>91%</div> <div>7%</div> <div></div> </div> </div>
1	B	458	<div> <div>2%</div> <div> <div></div> <div>93%</div> <div>5%</div> <div></div> </div> </div>
2	C	78	<div> <div>%</div> <div> <div></div> <div>87%</div> <div>8%</div> <div></div> </div> </div>
3	D	136	<div> <div>84%</div> <div> <div></div> <div>90%</div> <div></div> <div>6%</div> </div> </div>
3	E	136	<div> <div>4%</div> <div> <div></div> <div>87%</div> <div>7%</div> <div>6%</div> </div> </div>

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 10351 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 Citrobacter BubCD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	450	Total	C	N	O	S	0	0	0
			3506	2215	599	675	17			
1	B	448	Total	C	N	O	S	0	0	0
			3491	2205	597	672	17			

- Molecule 2 is a protein called Citrobacter BubA.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	75	Total	C	N	O	0	0	0
			603	385	107	111			

- Molecule 3 is a protein called Citrobacter BubB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	128	Total	C	N	O	S	0	0	0
			1040	660	181	193	6			
3	E	128	Total	C	N	O	S	0	0	0
			1040	660	181	193	6			

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Na	0	0
			1	1		
4	B	1	Total	Na	0	0
			1	1		

- Molecule 5 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: C<sub>10</sub>H<sub>14</sub>N<sub>5</sub>O<sub>7</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

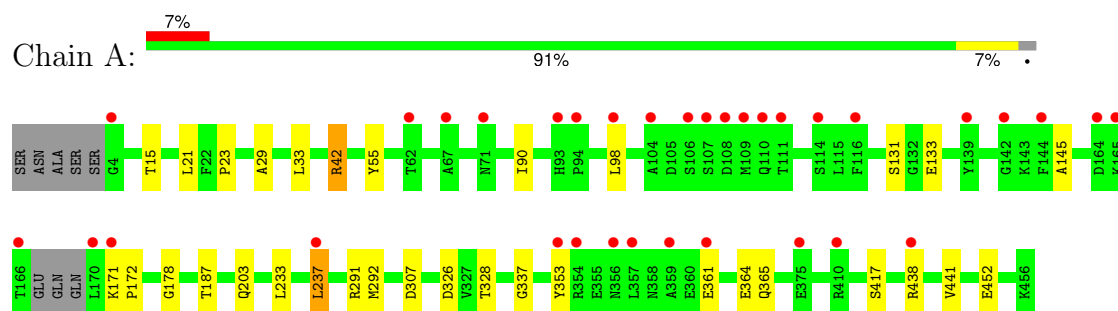
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	172	Total	O	0	0
			172	172		
6	B	360	Total	O	0	0
			360	360		
6	C	33	Total	O	0	0
			33	33		
6	D	2	Total	O	0	0
			2	2		
6	E	79	Total	O	0	0
			79	79		

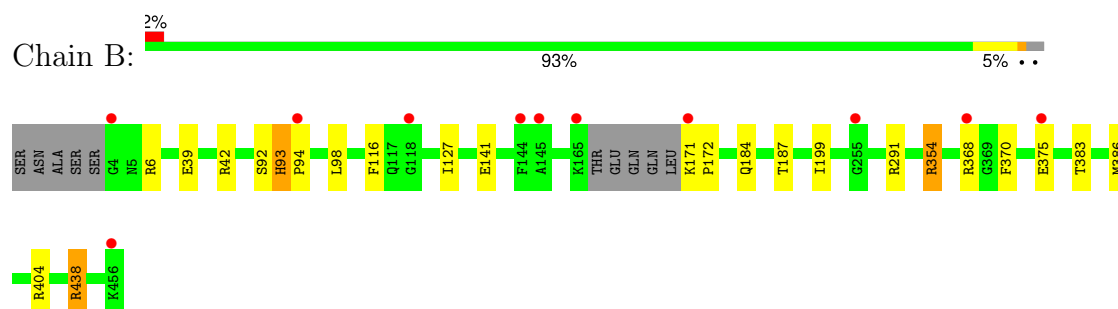
### 3 Residue-property plots

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.

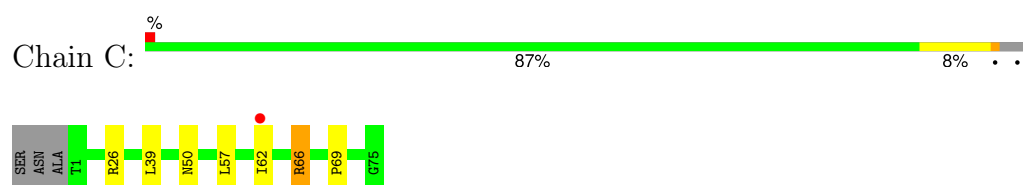
#### • Molecule 1: Citrobacter BubCD



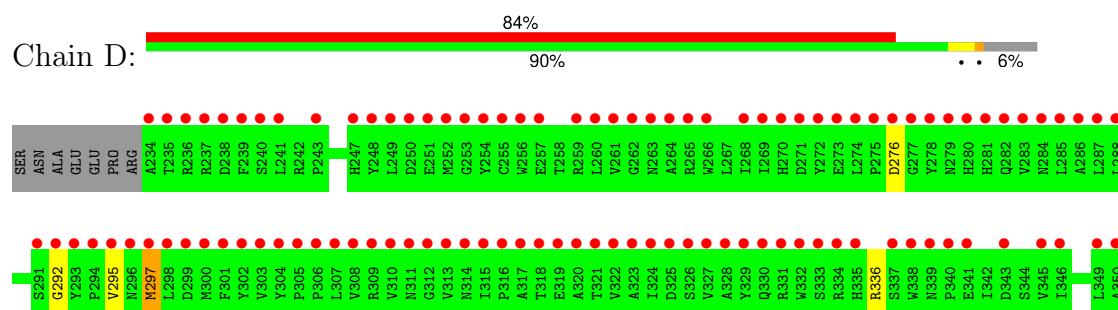
#### • Molecule 1: Citrobacter BubCD

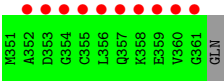


#### • Molecule 2: Citrobacter BubA

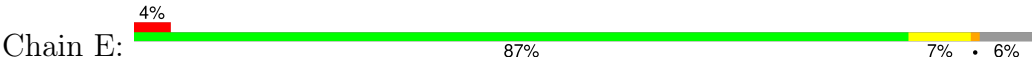


#### • Molecule 3: Citrobacter BubB





● Molecule 3: Citrobacter BubB



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	136.84Å 136.84Å 172.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.21 – 1.93 34.21 – 1.93	Depositor EDS
% Data completeness (in resolution range)	100.0 (34.21-1.93) 99.9 (34.21-1.93)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.89 (at 1.94Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, $R_{free}$	0.183 , 0.204 0.183 , 0.203	Depositor DCC
$R_{free}$ test set	6237 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	40.6	Xtriage
Anisotropy	0.006	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 46.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	10351	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.13% 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

### 5.1 Standard geometry

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

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	0.61	1/3569 (0.0%)	0.66	0/4829
1	B	0.74	2/3554 (0.1%)	0.76	2/4808 (0.0%)
2	C	0.54	0/615	0.60	1/834 (0.1%)
3	D	0.75	1/1069 (0.1%)	0.75	0/1460
3	E	0.75	1/1069 (0.1%)	0.75	0/1460
All	All	0.69	5/9876 (0.1%)	0.71	3/13391 (0.0%)

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
1	B	0	3
2	C	0	1
3	D	0	1
3	E	0	1
All	All	0	7

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	438	ARG	CB-CG	5.76	1.69	1.52
3	D	297	MET	SD-CE	-5.69	1.65	1.79
3	E	297	MET	SD-CE	-5.64	1.65	1.79
1	B	404	ARG	CD-NE	-5.49	1.38	1.46
1	A	145	ALA	CA-C	5.20	1.54	1.52

All (3) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	66	ARG	CG-CD-NE	-6.67	97.33	112.00
1	B	6	ARG	CA-CB-CG	5.57	125.23	114.10
1	B	6	ARG	CG-CD-NE	5.13	123.29	112.00

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	42	ARG	Sidechain
1	B	291	ARG	Sidechain
1	B	354	ARG	Sidechain
1	B	368	ARG	Sidechain
2	C	66	ARG	Sidechain
3	D	336	ARG	Sidechain
3	E	336	ARG	Sidechain

## 5.2 Too-close contacts

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	3506	0	3480	23	1
1	B	3491	0	3462	17	0
2	C	603	0	620	5	0
3	D	1040	0	991	4	1
3	E	1040	0	991	5	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	B	23	0	12	0	0
6	A	172	0	0	2	1
6	B	360	0	0	5	0
6	C	33	0	0	2	0
6	D	2	0	0	0	0
6	E	79	0	0	0	1
All	All	10351	0	9556	47	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 2.

All (47) 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:39:GLU:OE1	6:B:601:HOH:O	1.71	1.08
1:A:292:MET:HG3	3:D:295:VAL:HG11	1.60	0.82
1:B:184:GLN:HG3	6:B:621:HOH:O	1.87	0.74
1:A:337:GLY:O	6:A:701:HOH:O	2.06	0.72
1:B:93:HIS:O	1:B:94:PRO:C	2.36	0.67
1:B:354:ARG:HD2	6:B:740:HOH:O	1.95	0.67
2:C:50:ASN:HB2	6:C:102:HOH:O	1.95	0.67
1:A:15:THR:OG1	6:A:702:HOH:O	2.13	0.66
1:B:438:ARG:NH2	6:B:603:HOH:O	2.30	0.65
1:B:199:ILE:HD13	1:B:386:MET:HG3	1.82	0.62
1:A:33:LEU:HB2	1:A:90:ILE:HD11	1.82	0.61
1:A:292:MET:HE2	3:D:295:VAL:HB	1.86	0.58
3:E:234:ALA:HB2	3:E:255:CYS:SG	2.45	0.57
1:B:93:HIS:O	1:B:127:ILE:HG21	2.06	0.56
3:E:336:ARG:HD2	3:E:351:MET:SD	2.46	0.55
1:A:361:GLU:O	1:A:365:GLN:HG2	2.06	0.55
1:A:42:ARG:NH2	1:A:187:THR:OG1	2.40	0.55
1:A:131:SER:OG	1:A:133:GLU:OE1	2.20	0.54
1:B:93:HIS:HA	1:B:127:ILE:CG2	2.37	0.54
3:E:336:ARG:NH2	3:E:343:ASP:OD1	2.36	0.54
1:B:42:ARG:NH2	1:B:187:THR:OG1	2.41	0.53
1:B:370:PHE:HB3	6:B:609:HOH:O	2.08	0.53
1:A:328:THR:HG21	2:C:69:PRO:HG2	1.90	0.52
1:A:438:ARG:HH21	1:A:441:VAL:HG21	1.76	0.50
2:C:26:ARG:HD2	6:C:112:HOH:O	2.09	0.50
1:A:23:PRO:HG3	1:A:55:TYR:OH	2.12	0.50
1:A:452:GLU:OE2	3:D:292:GLY:N	2.39	0.48
1:B:98:LEU:C	1:B:98:LEU:HD12	2.40	0.47
2:C:39:LEU:HD11	2:C:62:ILE:HD11	1.97	0.46
1:B:93:HIS:O	1:B:127:ILE:CG2	2.64	0.46
1:A:21:LEU:HA	1:A:29:ALA:HB3	1.97	0.46
1:A:233:LEU:O	1:A:237:LEU:HD13	2.16	0.45
1:B:93:HIS:CG	1:B:94:PRO:N	2.84	0.44
1:A:328:THR:HG21	2:C:69:PRO:CG	2.47	0.43
1:A:171:LYS:HG3	1:A:172:PRO:HD2	1.99	0.43
1:A:172:PRO:HB3	1:A:178:GLY:HA3	2.00	0.43
1:A:98:LEU:C	1:A:98:LEU:HD12	2.44	0.42
1:B:93:HIS:HA	1:B:127:ILE:HG23	2.01	0.42
1:A:353:TYR:CD2	3:D:297:MET:HE2	2.55	0.42
1:B:171:LYS:HG3	1:B:172:PRO:HD2	2.02	0.41
1:A:23:PRO:HG3	1:A:55:TYR:CZ	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:116:PHE:CE1	1:B:141:GLU:HA	2.56	0.41
3:E:273:GLU:OE2	3:E:282:GLN:OE1	2.37	0.41
3:E:239:PHE:CZ	3:E:265:ARG:HB3	2.55	0.41
1:A:203:GLN:OE1	1:B:383:THR:HG22	2.20	0.41
1:A:291:ARG:NH1	1:A:307:ASP:OD1	2.47	0.41
1:A:326:ASP:OD1	1:A:417:SER:OG	2.33	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)
6:A:839:HOH:O	6:E:432:HOH:O[4_545]	1.68	0.52
1:A:364:GLU:OE2	3:D:276:ASP:N[8_555]	2.18	0.02

## 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	446/458 (97%)	435 (98%)	11 (2%)	0	100	100
1	B	444/458 (97%)	430 (97%)	13 (3%)	1 (0%)	44	37
2	C	73/78 (94%)	72 (99%)	1 (1%)	0	100	100
3	D	126/136 (93%)	121 (96%)	5 (4%)	0	100	100
3	E	126/136 (93%)	121 (96%)	5 (4%)	0	100	100
All	All	1215/1266 (96%)	1179 (97%)	35 (3%)	1 (0%)	48	41

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	93	HIS

### 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	378/387 (98%)	377 (100%)	1 (0%)	91	91
1	B	376/387 (97%)	374 (100%)	2 (0%)	86	86
2	C	67/69 (97%)	66 (98%)	1 (2%)	60	52
3	D	112/119 (94%)	112 (100%)	0	100	100
3	E	112/119 (94%)	112 (100%)	0	100	100
All	All	1045/1081 (97%)	1041 (100%)	4 (0%)	89	89

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	237	LEU
1	B	92	SER
1	B	375	GLU
2	C	57	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	117	GLN
1	B	159	HIS
2	C	32	ASN
3	D	282	GLN
3	E	282	GLN

### 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

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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$
5	AMP	B	501	-	21,25,25	1.22	3 (14%)	23,38,38	1.75	4 (17%)

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
5	AMP	B	501	-	-	0/6/26/26	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	501	AMP	O4'-C1'	-2.84	1.37	1.40
5	B	501	AMP	P-O1P	2.57	1.58	1.50
5	B	501	AMP	P-O3P	-2.19	1.46	1.54

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	501	AMP	N3-C2-N1	-5.35	121.41	128.67
5	B	501	AMP	O3P-P-O2P	3.20	119.80	107.80
5	B	501	AMP	C1'-N9-C4	-2.64	122.00	126.64
5	B	501	AMP	C4'-O4'-C1'	-2.12	107.98	109.92

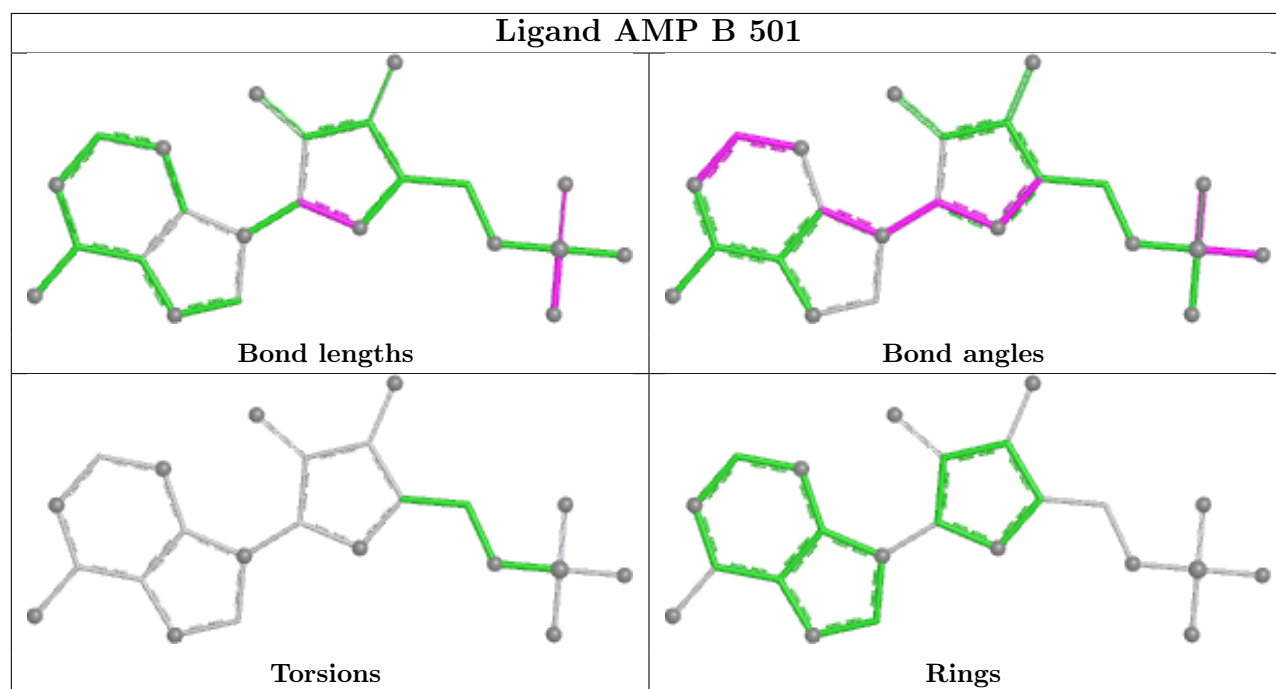
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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	450/458 (98%)	0.41	34 (7%) 21 23	30, 52, 89, 135	0
1	B	448/458 (97%)	-0.11	11 (2%) 58 64	29, 40, 63, 103	0
2	C	75/78 (96%)	0.56	1 (1%) 74 78	46, 58, 88, 107	0
3	D	128/136 (94%)	4.27	114 (89%) 0 0	24, 38, 58, 66	128 (100%)
3	E	128/136 (94%)	0.06	5 (3%) 44 48	30, 43, 61, 97	0
All	All	1229/1266 (97%)	0.60	165 (13%) 8 9	24, 45, 82, 135	128 (10%)

All (165) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	310	VAL	11.6
3	D	313	VAL	11.5
3	D	311	ASN	9.3
3	E	234	ALA	8.9
3	D	357	GLN	8.9
3	D	328	ALA	8.4
3	D	308	VAL	8.3
3	D	303	VAL	7.6
3	D	320	ALA	7.5
3	D	333	SER	7.4
3	D	332	TRP	7.3
3	D	352	ALA	7.2
3	D	285	LEU	7.1
3	D	286	ALA	7.0
3	D	276	ASP	6.8
3	D	312	GLY	6.8
3	D	235	THR	6.7
3	D	331	ARG	6.6
3	D	322	VAL	6.6
3	D	281	HIS	6.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
3	D	301	PHE	6.6
3	D	302	TYR	6.5
3	D	309	ARG	6.4
3	D	305	PRO	6.3
3	D	234	ALA	6.2
3	D	360	VAL	6.2
3	D	334	ARG	6.1
3	D	356	LEU	5.9
3	D	274	LEU	5.8
3	D	329	TYR	5.7
3	D	282	GLN	5.7
3	D	275	PRO	5.7
3	D	304	TYR	5.7
3	D	317	ALA	5.7
3	D	278	TYR	5.6
3	D	330	GLN	5.6
3	D	327	VAL	5.5
3	D	306	PRO	5.5
3	D	315	ILE	5.4
3	D	300	MET	5.3
3	D	355	CYS	5.3
1	A	104	ALA	5.0
3	D	273	GLU	4.9
3	D	272	TYR	4.9
3	D	255	CYS	4.9
3	D	340	PRO	4.9
1	A	170	LEU	4.8
3	D	295	VAL	4.8
3	D	358	LYS	4.7
3	D	279	ASN	4.7
3	D	299	ASP	4.7
3	D	292	GLY	4.6
3	D	359	GLU	4.6
1	A	109	MET	4.5
1	A	144	PHE	4.5
3	D	294	PRO	4.5
3	D	321	THR	4.5
3	D	261	VAL	4.4
3	D	326	SER	4.4
3	D	354	GLY	4.4
3	E	235	THR	4.4
3	D	254	TYR	4.3

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Mol	Chain	Res	Type	RSRZ
3	D	280	HIS	4.3
3	D	341	GLU	4.3
3	D	323	ALA	4.3
3	D	266	TRP	4.2
1	B	165	LYS	4.1
3	D	324	ILE	4.1
3	D	353	ASP	4.1
1	B	255	GLY	4.1
3	D	318	THR	4.1
3	D	339	ASN	4.0
3	D	260	LEU	3.9
3	D	262	GLY	3.9
3	D	297	MET	3.9
3	D	319	GLU	3.8
3	D	239	PHE	3.8
1	A	354	ARG	3.8
3	D	307	LEU	3.7
1	A	166	THR	3.6
1	A	237	LEU	3.6
3	D	243	PRO	3.5
1	A	357	LEU	3.5
3	D	314	ASN	3.5
3	D	349	LEU	3.5
1	A	4	GLY	3.5
3	D	335	HIS	3.4
3	D	283	VAL	3.4
3	D	241	LEU	3.4
1	B	4	GLY	3.4
3	D	247	HIS	3.3
3	D	291	SER	3.3
3	D	277	GLY	3.3
3	D	249	LEU	3.3
3	D	248	TYR	3.3
1	A	111	THR	3.3
1	A	108	ASP	3.2
3	E	360	VAL	3.2
3	D	236	ARG	3.2
3	D	269	ILE	3.2
3	D	264	ALA	3.2
3	D	251	GLU	3.2
1	B	144	PHE	3.1
3	D	268	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	94	PRO	3.1
3	D	252	MET	3.1
3	D	298	LEU	3.1
3	D	346	ILE	3.0
3	D	263	ASN	2.9
1	A	106	SER	2.8
1	A	94	PRO	2.8
3	D	270	HIS	2.8
1	A	165	LYS	2.8
3	D	288	LEU	2.8
3	D	338	TRP	2.8
1	B	368	ARG	2.7
3	D	237	ARG	2.7
1	A	353	TYR	2.7
3	D	253	GLY	2.7
3	D	316	PRO	2.7
3	D	361	GLY	2.7
1	A	375	GLU	2.6
3	D	271	ASP	2.6
3	D	296	ASN	2.6
3	D	337	SER	2.6
3	D	284	ASN	2.6
3	D	250	ASP	2.6
1	B	118	GLY	2.5
1	B	145	ALA	2.5
1	A	171	LYS	2.5
1	B	171	LYS	2.5
1	A	361	GLU	2.5
3	D	350	ALA	2.5
3	D	345	VAL	2.5
1	A	93	HIS	2.4
3	D	325	ASP	2.4
1	A	98	LEU	2.4
3	D	256	TRP	2.4
3	E	361	GLY	2.4
3	D	287	LEU	2.3
2	C	62	ILE	2.3
3	D	257	GLU	2.3
1	A	116	PHE	2.3
1	A	356	ASN	2.3
3	D	293	TYR	2.3
3	D	265	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	438	ARG	2.3
1	A	142	GLY	2.2
1	A	71	ASN	2.2
1	A	110	GLN	2.2
3	D	343	ASP	2.2
1	B	375	GLU	2.2
3	D	259	ARG	2.2
1	A	67	ALA	2.1
3	D	238	ASP	2.1
1	A	410	ARG	2.1
1	A	62	THR	2.1
1	A	139	TYR	2.1
3	E	236	ARG	2.1
1	A	164	ASP	2.0
1	B	456	LYS	2.0
1	A	114	SER	2.0
3	D	240	SER	2.0
1	A	359	ALA	2.0
1	A	107	SER	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](#)

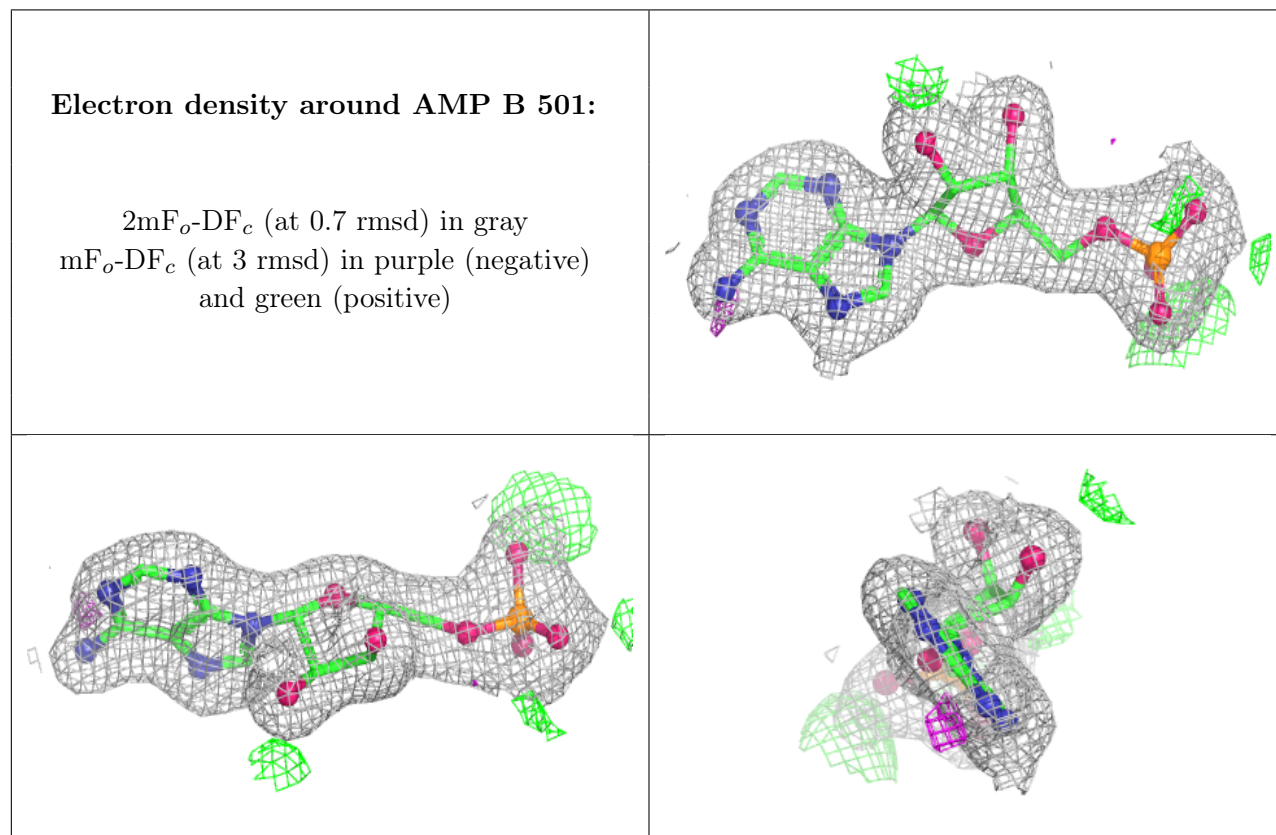
There are no oligosaccharides in this entry.

## 6.4 Ligands [i](#)

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( $\text{\AA}^2$ )	Q<0.9
4	NA	A	601	1/1	0.93	0.07	61,61,61,61	0
5	AMP	B	501	23/23	0.95	0.07	32,37,42,45	0
4	NA	B	502	1/1	0.98	0.07	42,42,42,42	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.