



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 4, 2023 – 04:15 PM EDT

PDB ID : 3U1B  
Title : Crystal structure of the S238R mutant of mycrocine immunity protein (MccF) with AMP  
Authors : Nocek, B.; Gu, M.; Zhou, M.; Anderson, W.F.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases (CSGID)  
Deposited on : 2011-09-29  
Resolution : 1.60 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.

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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
buster-report : 1.1.7 (2018)  
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) : 2.35

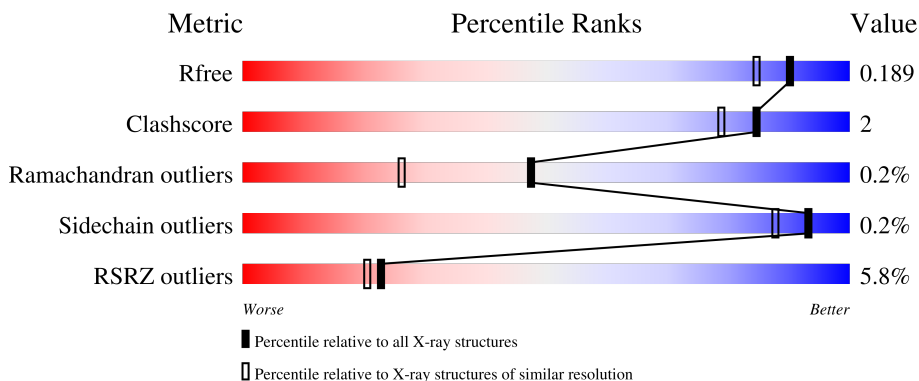
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.60 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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 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	336	 3% 95% 5%
1	B	336	 8% 93% 6%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5891 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.

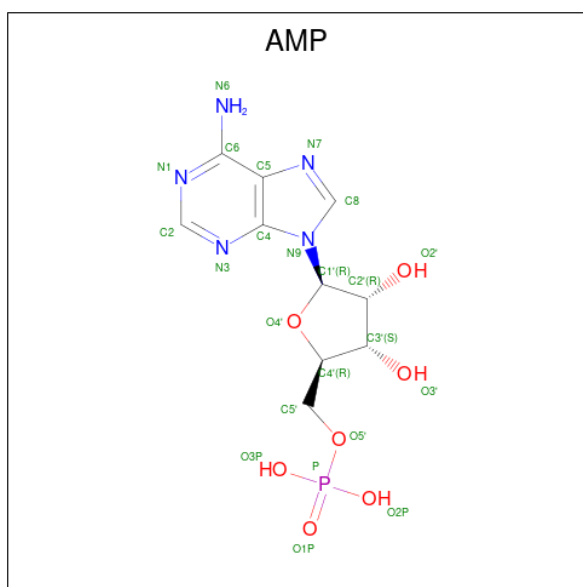
- Molecule 1 is a protein called Microcin immunity protein MccF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	336	2686	1729	439	504	14	0	4	0
1	B	333	2650	1707	435	494	14	0	1	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q81RT8
A	-1	ASN	-	expression tag	UNP Q81RT8
A	0	ALA	-	expression tag	UNP Q81RT8
A	238	ARG	SER	engineered mutation	UNP Q81RT8
B	-2	SER	-	expression tag	UNP Q81RT8
B	-1	ASN	-	expression tag	UNP Q81RT8
B	0	ALA	-	expression tag	UNP Q81RT8
B	238	ARG	SER	engineered mutation	UNP Q81RT8

- Molecule 2 is ADENOSINE MONOPHOSPHATE (three-letter code: 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
2	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	255	Total	O	0	0
			255	255		
3	B	254	Total	O	0	0
			254	254		

### 3 Residue-property plots [i](#)

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.

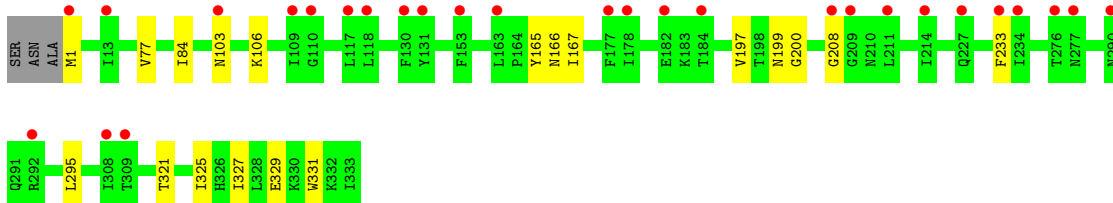
- Molecule 1: Microcin immunity protein MccF

Chain A: 



- Molecule 1: Microcin immunity protein MccF

Chain B: 



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	118.55Å 118.55Å 56.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.69 – 1.60 33.69 – 1.60	Depositor EDS
% Data completeness (in resolution range)	98.8 (33.69-1.60) 98.8 (33.69-1.60)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.21 (at 1.60Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, $R_{free}$	0.164 , 0.190 0.166 , 0.189	Depositor DCC
$R_{free}$ test set	5099 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.8	Xtrriage
Anisotropy	0.331	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 49.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.022 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	5891	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% 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: AMP

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	0.68	0/2767	0.74	1/3756 (0.0%)
1	B	0.70	0/2722	0.73	0/3696
All	All	0.69	0/5489	0.73	1/7452 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	310	MET	CG-SD-CE	-5.05	92.11	100.20

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	2686	0	2648	9	0
1	B	2650	0	2611	15	0
2	A	23	0	12	1	0
2	B	23	0	12	0	0
3	A	255	0	0	1	0
3	B	254	0	0	3	0
All	All	5891	0	5283	24	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 2.

All (24) 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:28:LYS:NZ	1:A:182:GLU:OE2	2.20	0.71
1:A:299:PHE:CE1	1:A:325:ILE:HD12	2.33	0.63
1:B:200:GLY:H	1:B:321:THR:HG23	1.63	0.62
1:B:199:ASN:HB3	1:B:321:THR:HG22	1.81	0.62
1:B:199:ASN:CB	1:B:321:THR:HG22	2.30	0.61
1:B:165:TYR:CD2	1:B:331:TRP:CH2	2.89	0.61
1:A:168:LYS:HE3	3:A:351:HOH:O	2.01	0.60
1:B:103:ASN:ND2	3:B:421:HOH:O	2.34	0.59
1:B:167:ILE:HD12	1:B:325:ILE:HG22	1.86	0.58
1:A:151:LYS:CD	1:A:155:GLU:CD	2.76	0.53
1:B:167:ILE:HD12	1:B:325:ILE:CG2	2.39	0.52
1:B:167:ILE:HD11	1:B:327:ILE:HD11	1.91	0.52
1:A:22:VAL:HB	1:A:84:ILE:HG21	1.96	0.48
1:B:321:THR:HG21	3:B:563:HOH:O	2.14	0.47
1:A:208:GLY:HA3	1:A:233:PHE:O	2.16	0.45
1:B:166:ASN:OD1	3:B:579:HOH:O	2.21	0.44
1:B:208:GLY:HA3	1:B:233:PHE:O	2.18	0.43
1:A:112[A]:SER:OG	2:A:401:AMP:O3P	2.33	0.43
1:A:151:LYS:CD	1:A:151:LYS:C	2.87	0.43
1:B:1:MET:CE	1:B:329:GLU:OE1	2.67	0.43
1:B:77:VAL:O	1:B:106:LYS:HE3	2.20	0.42
1:A:169:GLN:HG2	1:A:194:TRP:CE3	2.55	0.42
1:B:200:GLY:H	1:B:321:THR:CG2	2.31	0.42
1:B:197:VAL:HB	1:B:295:LEU:HG	2.03	0.41

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	338/336 (101%)	328 (97%)	10 (3%)	0	100	100
1	B	332/336 (99%)	322 (97%)	9 (3%)	1 (0%)	41	21
All	All	670/672 (100%)	650 (97%)	19 (3%)	1 (0%)	47	29

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	84	ILE

### 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	296/296 (100%)	295 (100%)	1 (0%)	92	87
1	B	291/296 (98%)	291 (100%)	0	100	100
All	All	587/592 (99%)	586 (100%)	1 (0%)	93	88

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	102	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	HIS
1	B	215	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 [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

2 ligands are 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
2	AMP	B	401	-	22,25,25	0.94	0	25,38,38	1.77	5 (20%)
2	AMP	A	401	-	22,25,25	0.89	0	25,38,38	1.65	6 (24%)

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
2	AMP	B	401	-	-	2/6/26/26	0/3/3/3
2	AMP	A	401	-	-	1/6/26/26	0/3/3/3

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	AMP	N3-C2-N1	-4.74	121.27	128.68
2	A	401	AMP	N3-C2-N1	-4.67	121.38	128.68
2	A	401	AMP	O3P-P-O5'	-3.73	96.81	106.73
2	B	401	AMP	C1'-N9-C4	-3.15	121.11	126.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	AMP	C2-N1-C6	2.99	123.86	118.75
2	B	401	AMP	C4-C5-N7	-2.97	106.31	109.40
2	B	401	AMP	O3P-P-O5'	-2.96	98.86	106.73
2	A	401	AMP	C2-N1-C6	2.64	123.27	118.75
2	A	401	AMP	C1'-N9-C4	-2.20	122.78	126.64
2	A	401	AMP	N6-C6-N1	2.13	123.00	118.57
2	A	401	AMP	O2P-P-O1P	2.01	118.54	110.68

There are no chirality outliers.

All (3) torsion outliers are listed below:

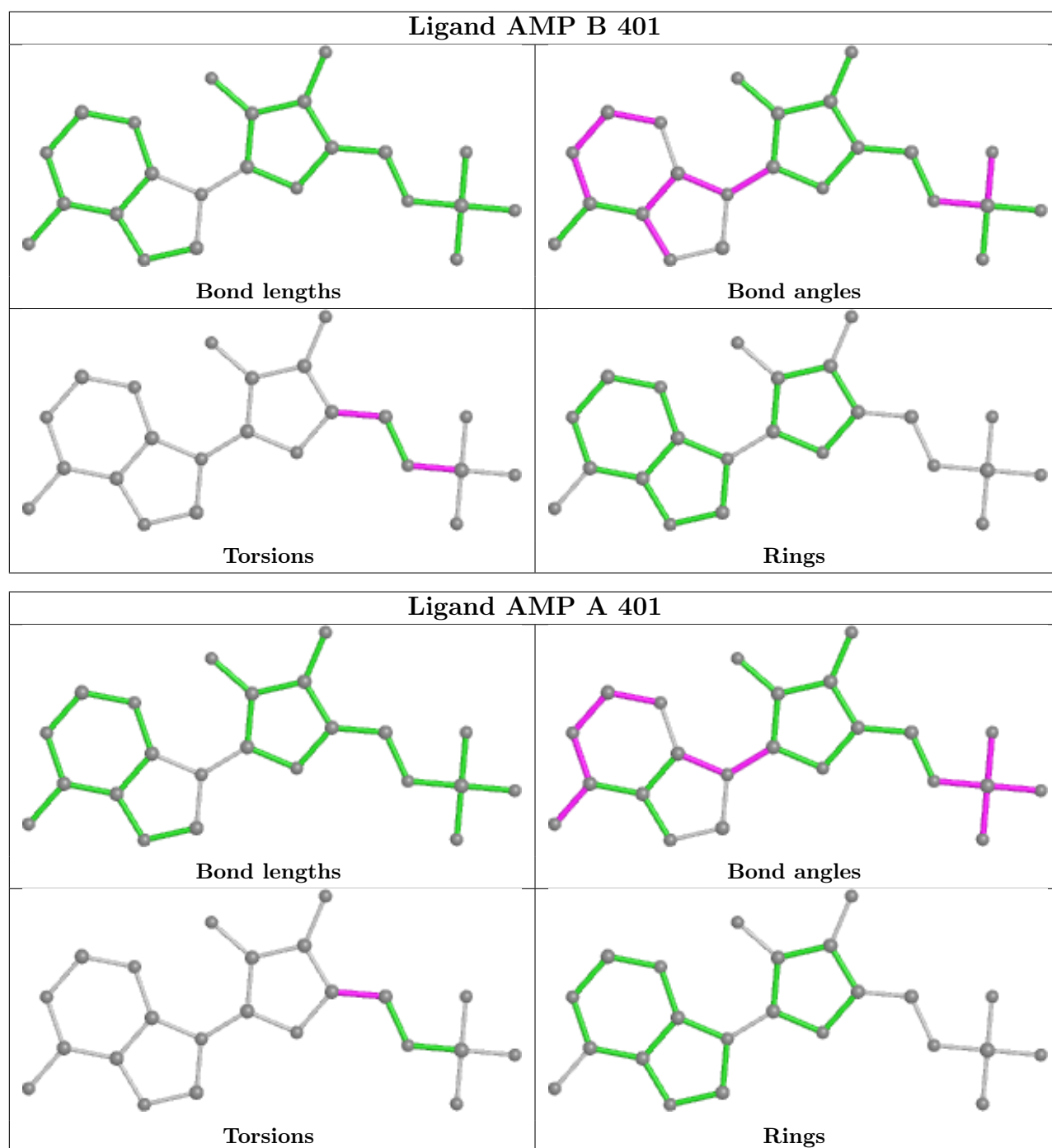
Mol	Chain	Res	Type	Atoms
2	B	401	AMP	O4'-C4'-C5'-O5'
2	B	401	AMP	C5'-O5'-P-O2P
2	A	401	AMP	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	AMP	1	0

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	336/336 (100%)	0.04	11 (3%) 46 43	19, 30, 47, 61	0
1	B	333/336 (99%)	0.28	28 (8%) 11 9	20, 30, 52, 74	0
All	All	669/672 (99%)	0.16	39 (5%) 23 20	19, 30, 48, 74	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	184	THR	3.7
1	B	178	ILE	3.4
1	B	131	TYR	3.4
1	B	109	ILE	3.3
1	B	292	ARG	3.2
1	A	117	LEU	3.2
1	B	153	PHE	3.2
1	B	211	LEU	2.9
1	B	234	ILE	2.9
1	B	233	PHE	2.8
1	B	177	PHE	2.8
1	B	209	GLY	2.8
1	A	184	THR	2.7
1	B	182	GLU	2.7
1	B	290	ASN	2.7
1	B	118	LEU	2.7
1	B	276	THR	2.7
1	B	214	ILE	2.6
1	B	1	MET	2.6
1	A	178	ILE	2.6
1	B	130	PHE	2.6
1	A	333	ILE	2.5
1	B	103	ASN	2.5
1	B	117	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	227	GLN	2.5
1	A	109	ILE	2.4
1	B	208	GLY	2.4
1	A	118	LEU	2.4
1	A	24	TYR	2.4
1	A	53	TYR	2.3
1	B	309	THR	2.3
1	A	131	TYR	2.3
1	A	182	GLU	2.2
1	B	277	ASN	2.1
1	B	110	GLY	2.1
1	B	163	LEU	2.1
1	B	13	ILE	2.1
1	B	308	ILE	2.1
1	A	52	ARG	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 monosaccharides in this entry.

## 6.4 Ligands [i](#)

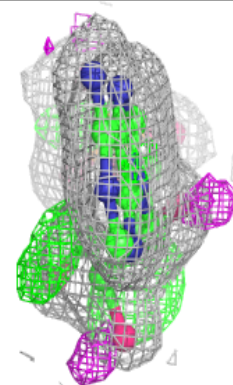
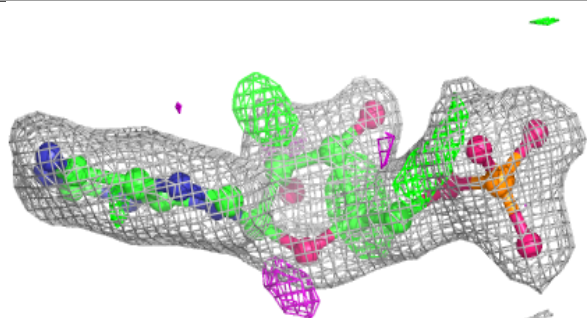
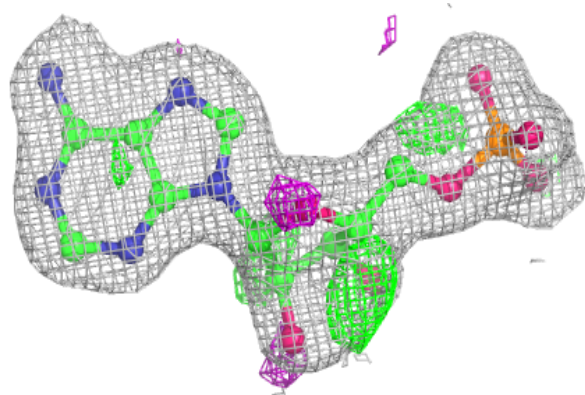
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q < 0.9
2	AMP	A	401	23/23	0.94	0.10	29,33,44,46	0
2	AMP	B	401	23/23	0.94	0.10	28,31,41,51	0

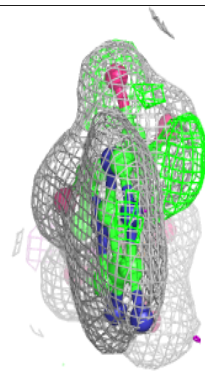
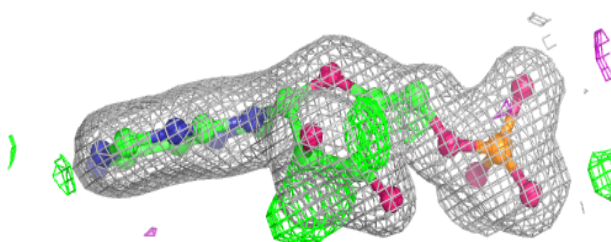
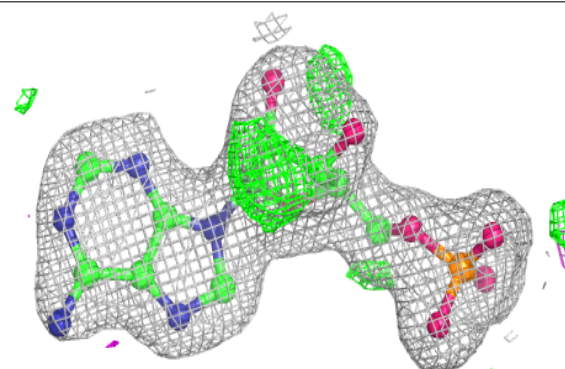
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around AMP A 401:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around AMP B 401:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.