



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 1, 2022 – 06:10 pm BST

PDB ID : 7PB3  
Title : Structural and Functional analysis of the Proline Racemase (ProR) from the Gram-positive bacterium *Acetoanaerobium sticklandii*  
Authors : Najmudin, S.; Pan, X.-S.; McAuley, K.E.; Fisher, L.M.; Sanderson, M.R.  
Deposited on : 2021-07-30  
Resolution : 2.84 Å (reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.29  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.29

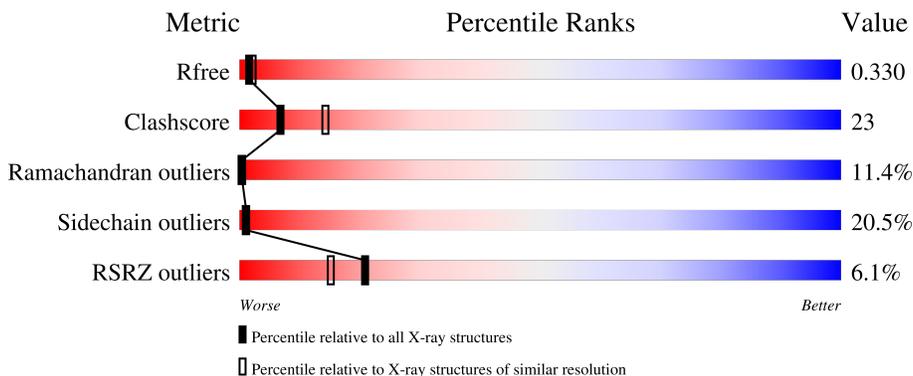
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.84 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	1031 (2.86-2.82)
Clashscore	141614	1078 (2.86-2.82)
Ramachandran outliers	138981	1050 (2.86-2.82)
Sidechain outliers	138945	1051 (2.86-2.82)
RSRZ outliers	127900	1019 (2.86-2.82)

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	AAA	343	
1	BBB	343	

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 10400 atoms, of which 5214 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.

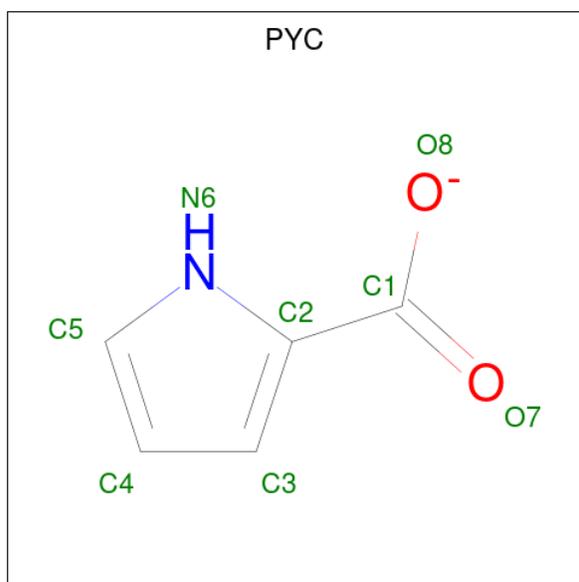
- Molecule 1 is a protein called Proline racemase A (AsProR).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	AAA	335	5188	1649	2603	421	500	15	71	0	0
1	BBB	335	5188	1649	2603	421	500	15	71	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	336	LEU	-	expression tag	UNP E3PTZ4
AAA	337	GLU	-	expression tag	UNP E3PTZ4
AAA	338	HIS	-	expression tag	UNP E3PTZ4
AAA	339	HIS	-	expression tag	UNP E3PTZ4
AAA	340	HIS	-	expression tag	UNP E3PTZ4
AAA	341	HIS	-	expression tag	UNP E3PTZ4
AAA	342	HIS	-	expression tag	UNP E3PTZ4
AAA	343	HIS	-	expression tag	UNP E3PTZ4
BBB	336	LEU	-	expression tag	UNP E3PTZ4
BBB	337	GLU	-	expression tag	UNP E3PTZ4
BBB	338	HIS	-	expression tag	UNP E3PTZ4
BBB	339	HIS	-	expression tag	UNP E3PTZ4
BBB	340	HIS	-	expression tag	UNP E3PTZ4
BBB	341	HIS	-	expression tag	UNP E3PTZ4
BBB	342	HIS	-	expression tag	UNP E3PTZ4
BBB	343	HIS	-	expression tag	UNP E3PTZ4

- Molecule 2 is PYRROLE-2-CARBOXYLATE (three-letter code: PYC) (formula: C<sub>5</sub>H<sub>4</sub>NO<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
2	AAA	1	Total	C	H	N	O	0	0
			12	5	4	1	2		
2	BBB	1	Total	C	H	N	O	0	0
			12	5	4	1	2		



D327	F328	L329	K330	Y331	Y335	LEU	GLU	HIS						
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## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.04Å 109.04Å 105.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	77.22 – 2.84 77.10 – 2.84	Depositor EDS
% Data completeness (in resolution range)	61.4 (77.22-2.84) 61.4 (77.10-2.84)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.31 (at 2.86Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.251 , 0.330 0.253 , 0.330	Depositor DCC
$R_{free}$ test set	542 reflections (5.69%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	117.6	Xtrriage
Anisotropy	0.048	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.018 for -h,-l,-k 0.016 for l,-k,h	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	10400	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	134.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.57% 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: PYC

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	AAA	0.66	0/2634	0.81	1/3556 (0.0%)
1	BBB	0.67	0/2634	0.82	0/3556
All	All	0.67	0/5268	0.82	1/7112 (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	AAA	0	1
1	BBB	0	3
All	All	0	4

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	AAA	61	ASP	CB-CA-C	5.20	120.81	110.40

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AAA	158	VAL	Peptide
1	BBB	232	GLU	Peptide
1	BBB	273	LEU	Peptide
1	BBB	47	TYR	Peptide

## 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	AAA	2585	2603	2593	117	0
1	BBB	2585	2603	2593	125	0
2	AAA	8	4	4	2	0
2	BBB	8	4	4	1	0
All	All	5186	5214	5194	242	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 23.

The worst 5 of 242 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:BBB:174:SER:O	1:BBB:175:PHE:O	1.87	0.92
1:AAA:199:LEU:HD22	1:AAA:203:ILE:HD11	1.57	0.86
1:BBB:290:LYS:HB3	1:BBB:310:THR:OG1	1.81	0.81
1:AAA:72:ASN:HD22	1:AAA:75:ALA:HB2	1.47	0.77
1:BBB:207:ILE:O	1:BBB:207:ILE:HG22	1.84	0.77

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	AAA	333/343 (97%)	237 (71%)	57 (17%)	39 (12%)	0 0
1	BBB	333/343 (97%)	242 (73%)	54 (16%)	37 (11%)	0 0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	666/686 (97%)	479 (72%)	111 (17%)	76 (11%)	<b>0</b> <b>0</b>

5 of 76 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	32	GLU
1	AAA	62	MET
1	AAA	75	ALA
1	AAA	123	ALA
1	AAA	134	ASN

### 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	AAA	285/293 (97%)	222 (78%)	63 (22%)	<b>1</b> <b>0</b>
1	BBB	285/293 (97%)	231 (81%)	54 (19%)	<b>1</b> <b>1</b>
All	All	570/586 (97%)	453 (80%)	117 (20%)	<b>1</b> <b>1</b>

5 of 117 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	302	PHE
1	BBB	288	MET
1	BBB	79	ILE
1	BBB	281	TYR
1	BBB	218	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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	PYC	BBB	401	-	8,8,8	1.89	2 (25%)	8,10,10	1.37	0
2	PYC	AAA	401	-	8,8,8	1.88	2 (25%)	8,10,10	1.31	0

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	PYC	BBB	401	-	-	0/2/4/4	0/1/1/1
2	PYC	AAA	401	-	-	1/2/4/4	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	BBB	401	PYC	C2-C1	-4.37	1.44	1.50
2	AAA	401	PYC	C2-C1	-4.07	1.45	1.50
2	AAA	401	PYC	O8-C1	-3.24	1.20	1.30
2	BBB	401	PYC	O8-C1	-2.87	1.21	1.30

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

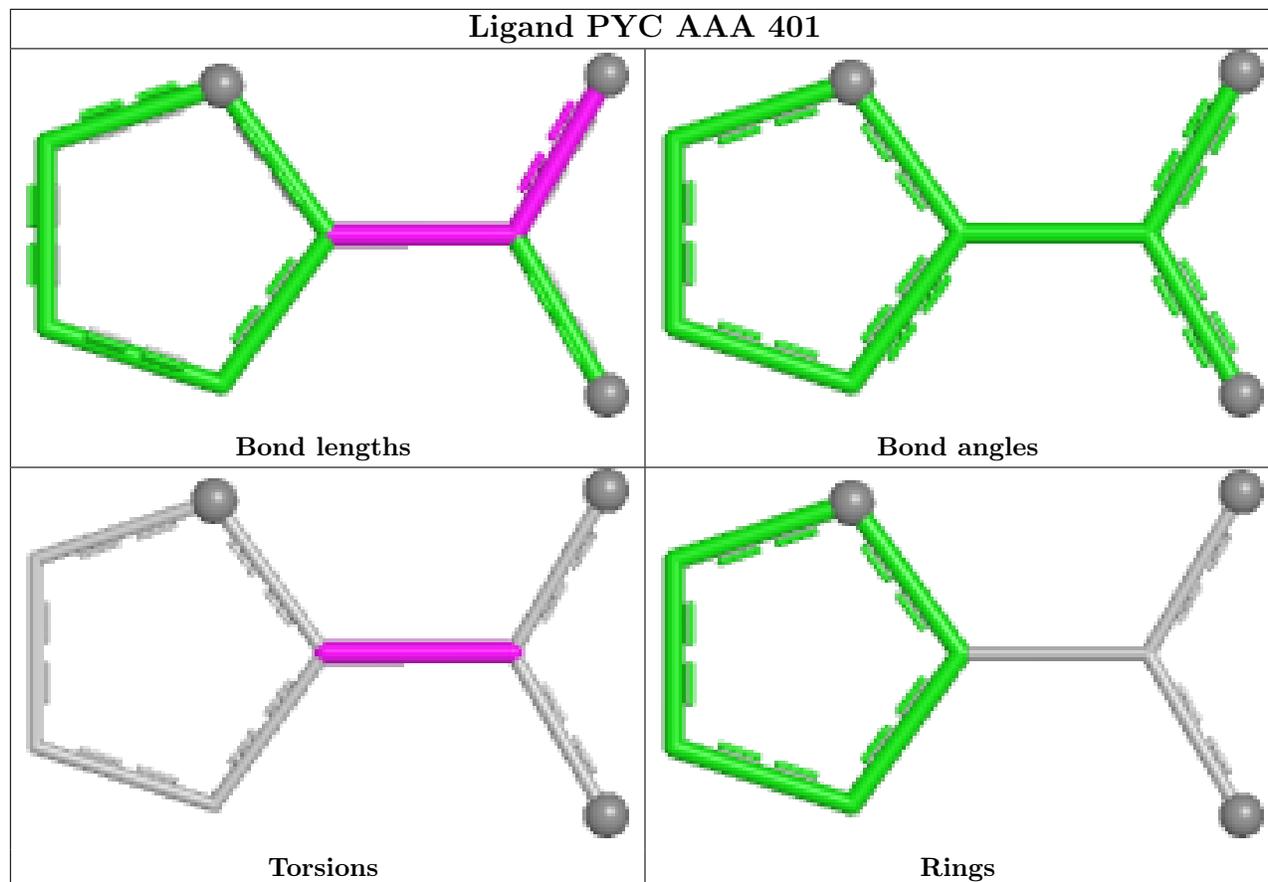
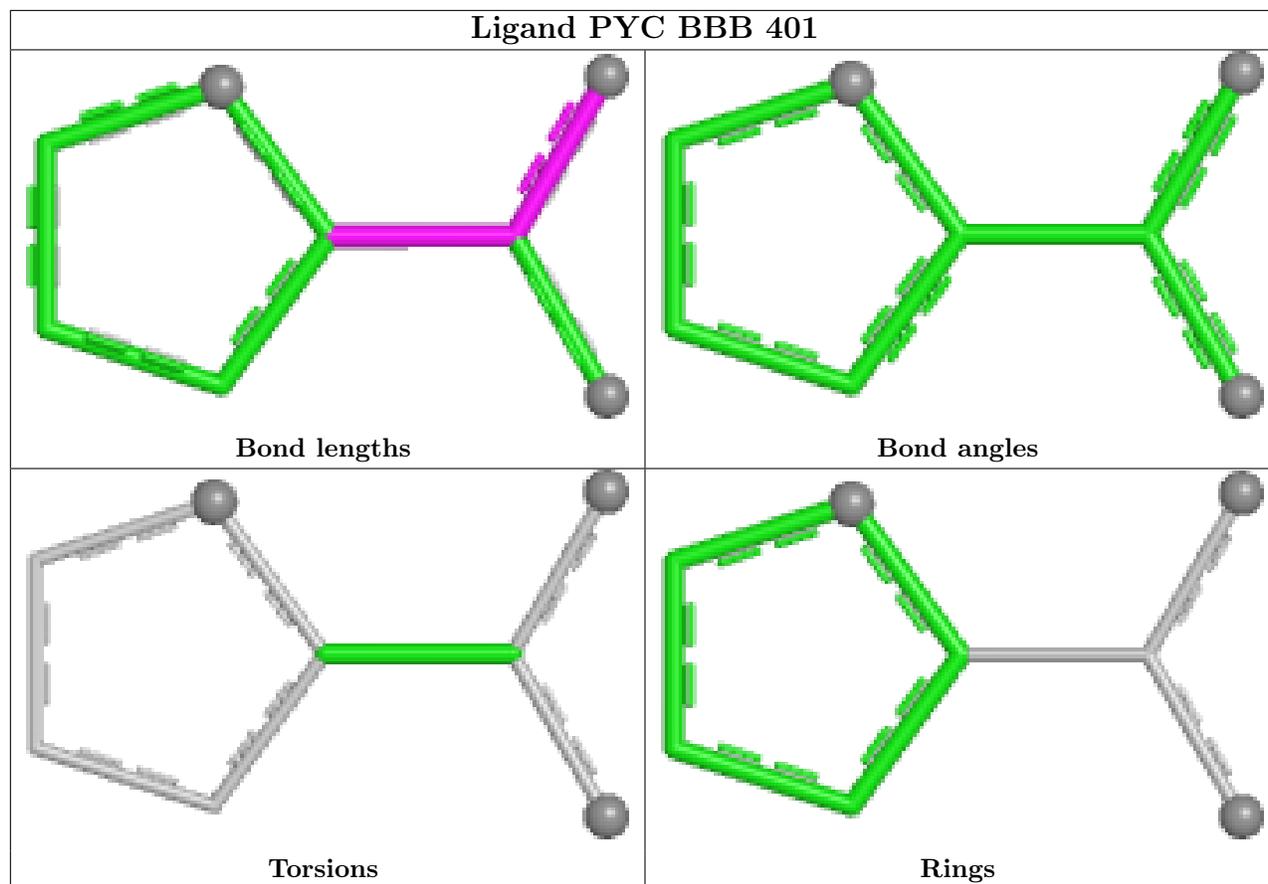
Mol	Chain	Res	Type	Atoms
2	AAA	401	PYC	O7-C1-C2-N6

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	BBB	401	PYC	1	0
2	AAA	401	PYC	2	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 [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	AAA	335/343 (97%)	0.19	17 (5%) 28 21	82, 122, 171, 199	0
1	BBB	335/343 (97%)	0.36	24 (7%) 15 10	85, 139, 207, 227	0
All	All	670/686 (97%)	0.28	41 (6%) 21 15	82, 129, 200, 227	0

The worst 5 of 41 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	172	GLY	5.8
1	BBB	311	GLY	4.7
1	BBB	187	LYS	4.2
1	BBB	220	HIS	4.1
1	AAA	264	LEU	4.0

### 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](#)

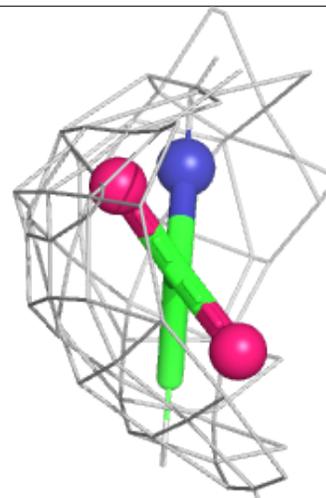
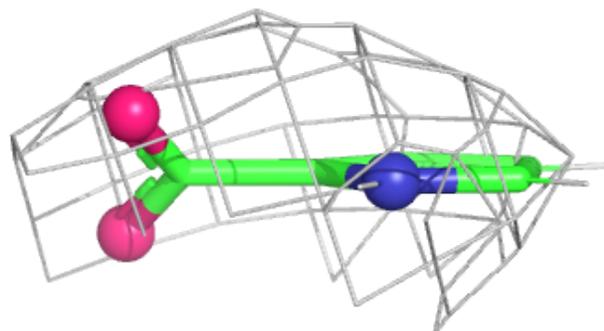
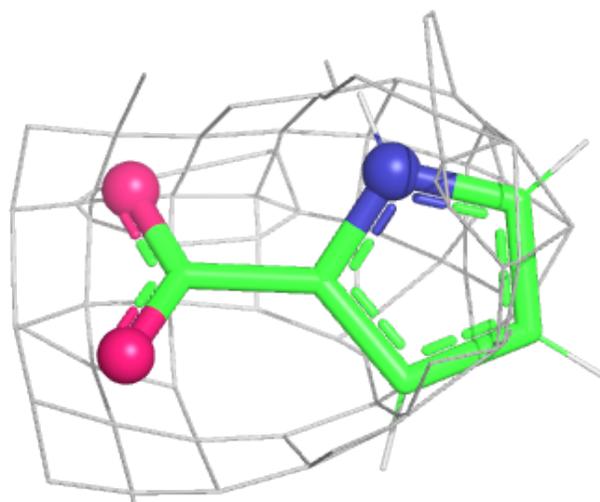
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q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

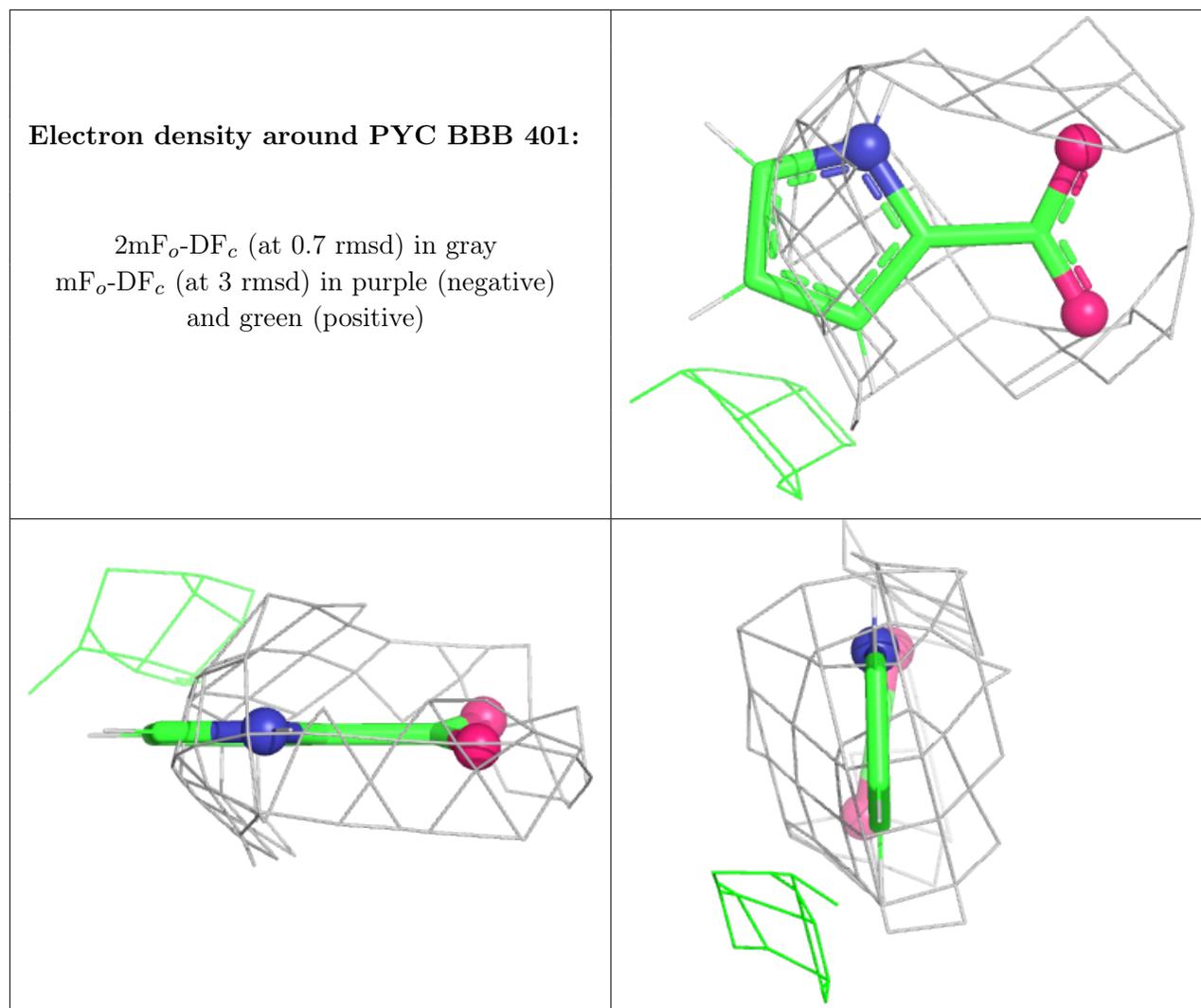
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PYC	AAA	401	8/8	0.96	0.21	116,123,126,127	0
2	PYC	BBB	401	8/8	0.96	0.19	154,156,158,159	0

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 PYC AAA 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.