



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 15, 2026 – 10:29 AM UTC

PDB ID : 8A3F / pdb_00008a3f
Title : Proline Racemase (ProR) from the Gram-positive bacterium *Acetoanaerobium sticklandii* from isotropic tetragonal data at 3.15 Å
Authors : Najmudin, S.; Pan, X.-S.; McAuley, K.E.; Fisher, L.M.; Sanderson, M.R.
Deposited on : 2022-06-08
Resolution : 3.15 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

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>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

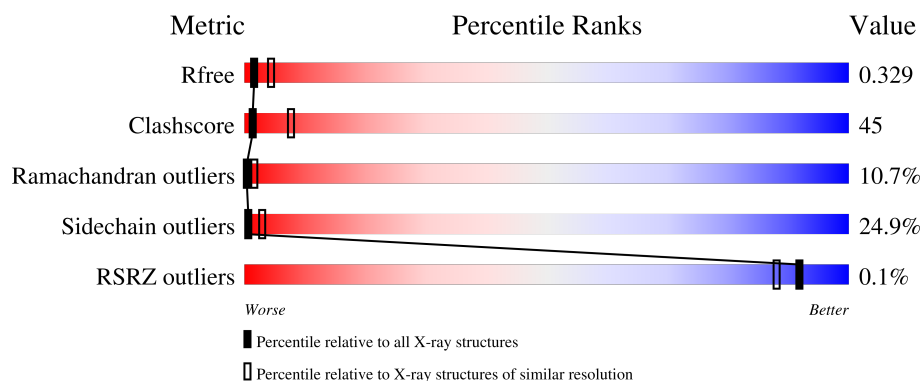
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.15 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}	180053	2361 (3.20-3.12)
Clashscore	190562	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)

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 ≥ 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	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PYC	BBB	401	-	-	X	-

2 Entry composition

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.

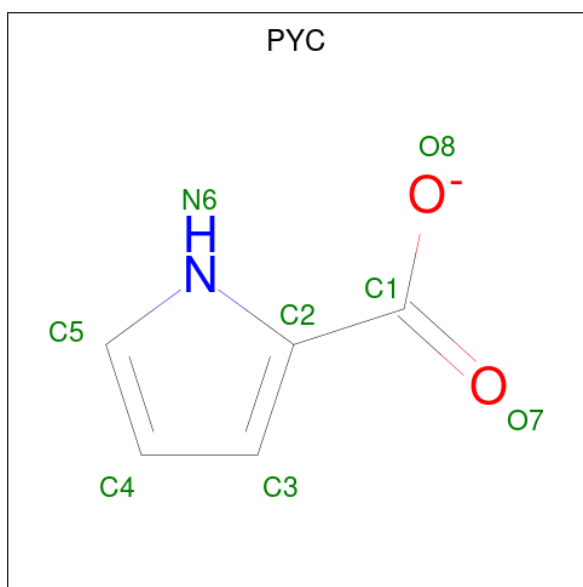
- Molecule 1 is a protein called Proline racemase A (AsProR).

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

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 (CCD ID: PYC) (formula: $C_5H_4NO_2$) (labeled as "Ligand of Interest" by depositor).



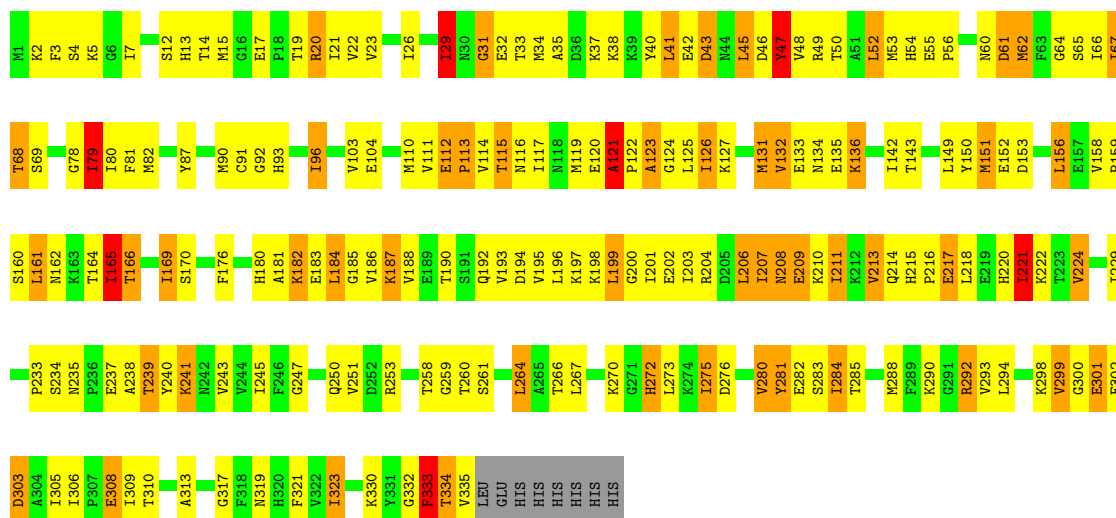
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
2	AAA	1	12	5	4	1	2	0	0
2	BBB	1	Total	C	H	N	O	0	0
			12	5	4	1	2		

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.

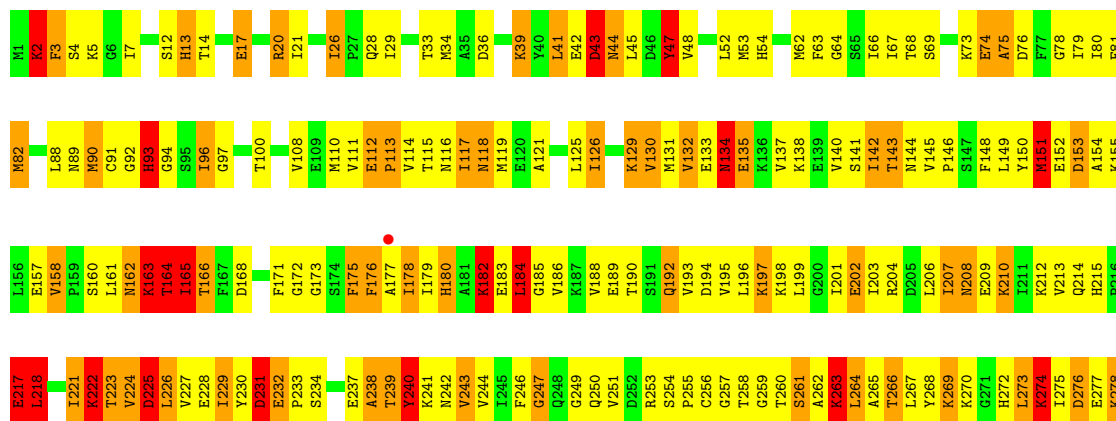
• Molecule 1: Proline racemase A (AsProR)

Chain AAA: 



• Molecule 1: Proline racemase A (AsProR)

Chain BBB: 



F279	V280	Y281	E282	S283	I284	T285		M288	F289	K290	G291	R292	V293	L294		T297	K298	V299	G300	E301	F302	D303	A304	I305	I306	P307		T310		A313		F321	V322	I323	D324	P325	F326	D327	P328	L329	K330	Y331	G332	F333	I334	V335	LEU	GLU	HIS	HIS	HIS	HIS	HIS	HIS
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4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	109.72Å 109.72Å 104.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	77.71 – 3.15 77.59 – 3.15	Depositor EDS
% Data completeness (in resolution range)	100.0 (77.71-3.15) 100.0 (77.59-3.15)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 3.13Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.266 , 0.330 0.265 , 0.329	Depositor DCC
R_{free} test set	690 reflections (5.95%)	wwPDB-VP
Wilson B-factor (Å ²)	101.1	Xtriage
Anisotropy	0.465	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 104.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.048 for -h,-l,-k 0.029 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10400	wwPDB-VP
Average B, all atoms (Å ²)	135.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.20% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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	1.02	0/2634	1.43	3/3556 (0.1%)
1	BBB	1.04	0/2634	1.57	6/3556 (0.2%)
All	All	1.03	0/5268	1.50	9/7112 (0.1%)

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	8
1	BBB	0	9
All	All	0	17

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BBB	164	THR	CB-CA-C	-28.73	53.25	110.42
1	BBB	164	THR	N-CA-C	12.89	138.25	110.80
1	BBB	164	THR	N-CA-CB	-11.00	91.90	110.49
1	BBB	48	VAL	N-CA-C	-5.63	105.01	110.42
1	AAA	96	ILE	CA-C-N	5.47	126.17	119.99

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AAA	121	ALA	Peptide

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Mol	Chain	Res	Type	Group
1	AAA	208	ASN	Peptide
1	AAA	29	ILE	Peptide
1	AAA	47	TYR	Peptide
1	AAA	60	ASN	Peptide

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	AAA	2585	2603	2593	181	1
1	BBB	2585	2603	2592	288	2
2	AAA	8	4	4	2	0
2	BBB	8	4	4	4	0
All	All	5186	5214	5193	469	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 45.

The worst 5 of 469 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:155:LYS:HE3	1:BBB:164:THR:HG22	1.28	1.15
1:BBB:273:LEU:HD21	1:BBB:277:GLU:HB3	1.43	1.00
1:AAA:5:LYS:HB2	1:AAA:323:ILE:HD11	1.41	0.99
1:BBB:229:ILE:O	1:BBB:242:ASN:HB2	1.63	0.97
1:BBB:178:ILE:HG12	1:BBB:230:TYR:HE1	1.33	0.94

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)
1:AAA:69:SER:HB2	1:BBB:69:SER:HG[7_555]	1.29	0.31
1:BBB:13:HIS:HE2	1:BBB:327:ASP:OD1[8_555]	1.56	0.04

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%)	242 (73%)	63 (19%)	28 (8%)	0	3
1	BBB	333/343 (97%)	235 (71%)	55 (16%)	43 (13%)	0	1
All	All	666/686 (97%)	477 (72%)	118 (18%)	71 (11%)	0	1

5 of 71 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	42	GLU
1	AAA	62	MET
1	AAA	112	GLU
1	AAA	121	ALA
1	AAA	221	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	AAA	285/293 (97%)	223 (78%)	62 (22%)	1	5
1	BBB	285/293 (97%)	205 (72%)	80 (28%)	0	2
All	All	570/586 (97%)	428 (75%)	142 (25%)	0	3

5 of 142 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	BBB	237	GLU

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Mol	Chain	Res	Type
1	BBB	254	SER
1	BBB	288	MET
1	AAA	281	TYR
1	AAA	280	VAL

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 oligosaccharides 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	AAA	401	-	8,8,8	1.38	1 (12%)	10,10,10	0.82	0
2	PYC	BBB	401	-	8,8,8	1.50	1 (12%)	10,10,10	0.83	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	AAA	401	-	-	0/4/4/4	0/1/1/1
2	PYC	BBB	401	-	-	0/4/4/4	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	BBB	401	PYC	O8-C1	-3.31	1.21	1.30
2	AAA	401	PYC	O8-C1	-3.18	1.21	1.30

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

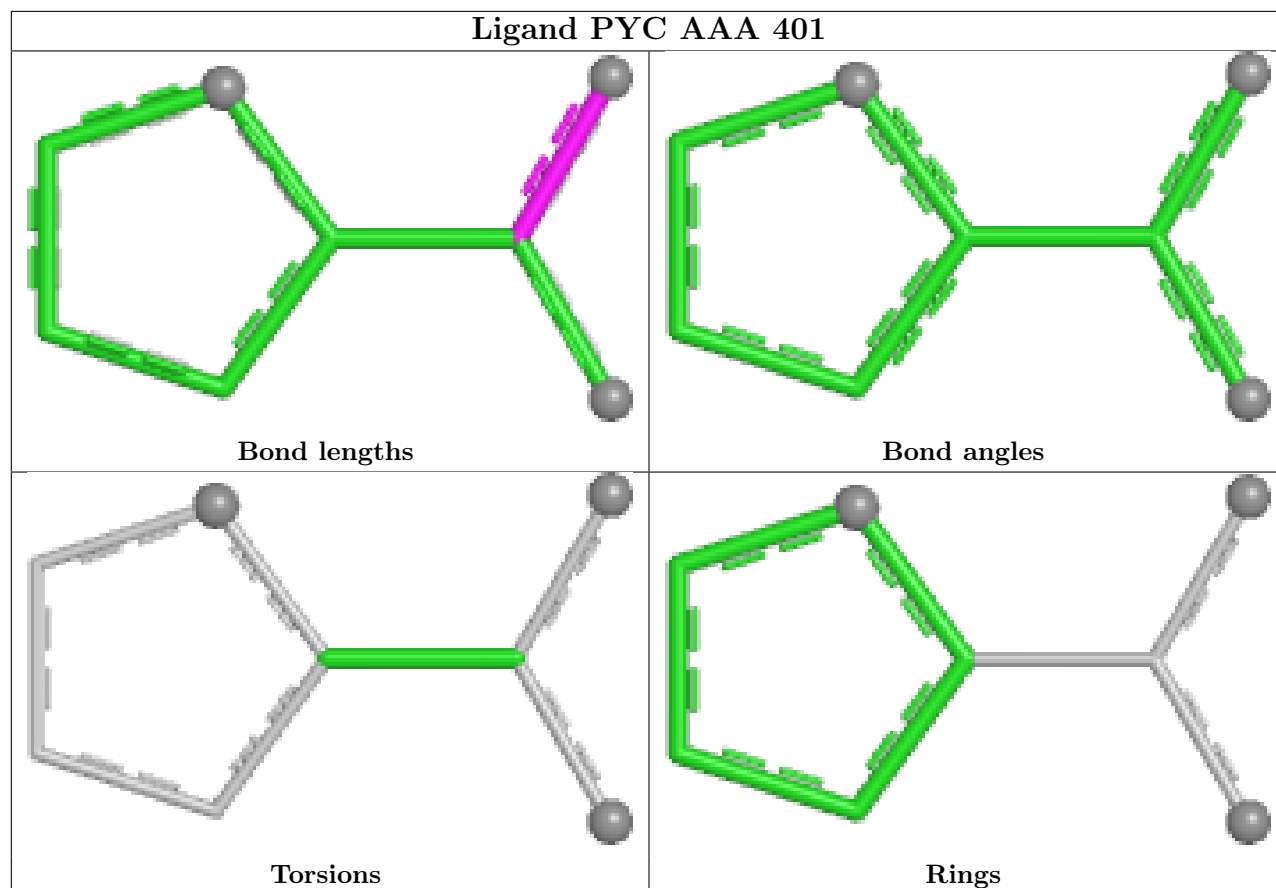
There are no ring outliers.

2 monomers are involved in 6 short contacts:

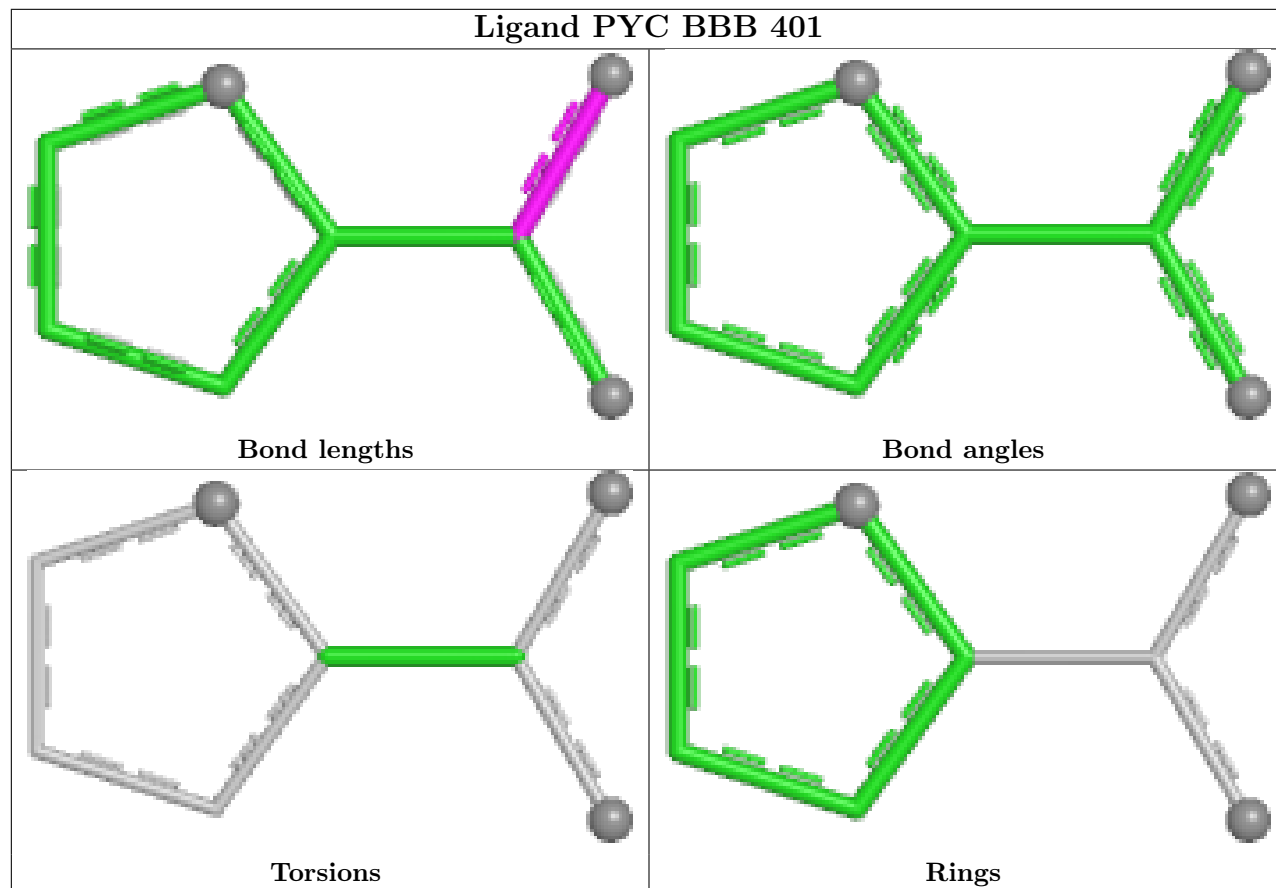
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AAA	401	PYC	2	0
2	BBB	401	PYC	4	0

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.

Ligand PYC AAA 401



Ligand PYC BBB 401



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, 95th 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 ²)	Q < 0.9
1	AAA	335/343 (97%)	-0.47	0	100 100	66, 117, 168, 207	0
1	BBB	335/343 (97%)	-0.40	1 (0%)	90 81	70, 138, 239, 281	0
All	All	670/686 (97%)	-0.44	1 (0%)	92 88	66, 125, 220, 281	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	177	ALA	2.1

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, 95th 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.

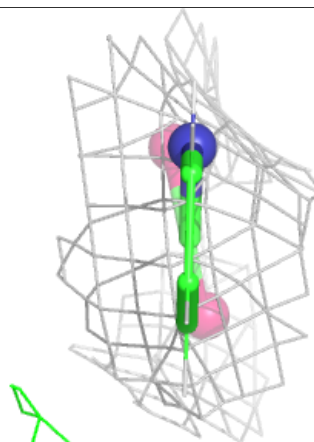
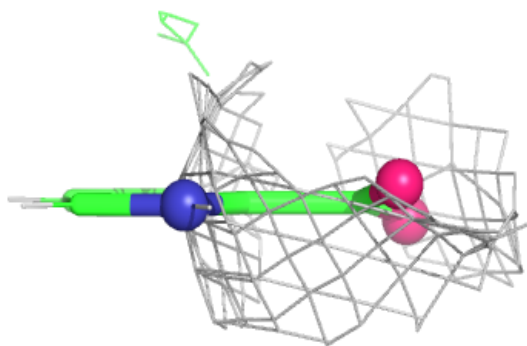
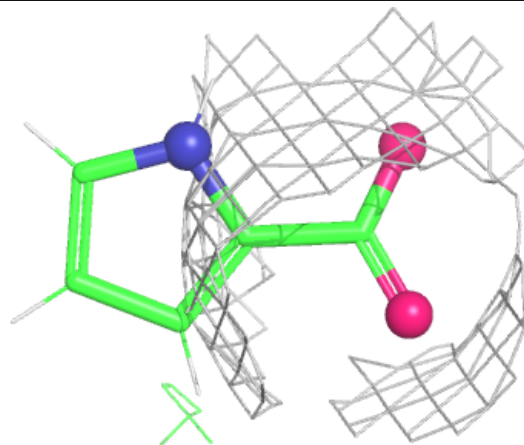
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q < 0.9
2	PYC	BBB	401	8/8	0.89	0.10	129,145,148,148	0
2	PYC	AAA	401	8/8	0.91	0.08	114,119,120,120	0

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.

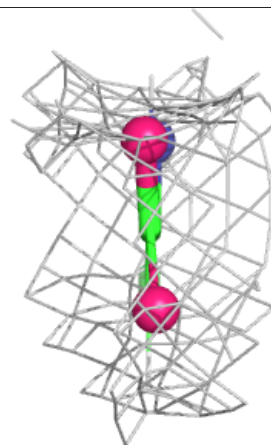
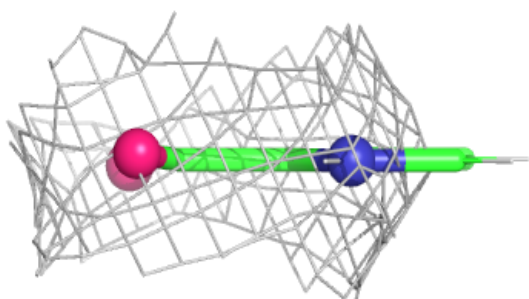
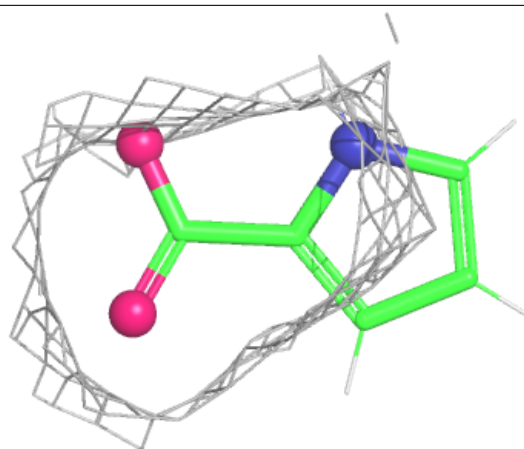
Electron density around PYC BBB 401:

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



Electron density around 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.