

# Full wwPDB X-ray Structure Validation Report (i)

Nov 7, 2023 – 03:14 PM JST

PDB ID : 6JVW

Title: Crystal structure of maleylpyruvate hydrolase from Sphingobium sp. SYK-6

in complex with manganese (II) ion and pyruvate

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Deposited on : 2019-04-17

Resolution : 2.25 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
A user guide is available at

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) 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 (1)) 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 : 2.36

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

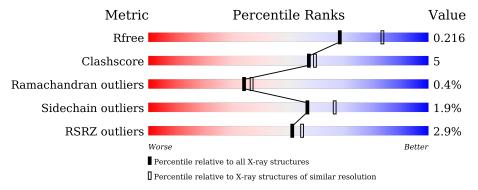
Validation Pipeline (wwPDB-VP) : 2.36

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
$R_{free}$	130704	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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 <=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	Α.	204	2%			
1	А	304	75%	10%	•	14%
1	В	304	77%	9%	•	13%



## 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4178 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 maleylpyruvate hydrolase.

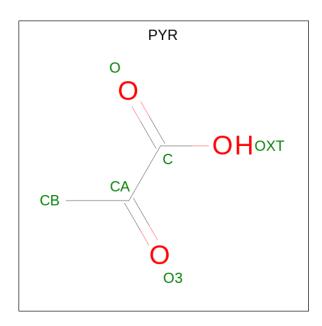
$\mathbf{Mol}$	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	260	Total 1982	C 1261	N 346	O 364	S 11	0	1	0
1	В	264	Total 2053	C 1304	N 364	O 374	S 11	0	5	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	297	LEU	-	expression tag	UNP G2IPX5
A	298	GLU	-	expression tag	UNP G2IPX5
A	299	HIS	-	expression tag	UNP G2IPX5
A	300	HIS	-	expression tag	UNP G2IPX5
A	301	HIS	-	expression tag	UNP G2IPX5
A	302	HIS	-	expression tag	UNP G2IPX5
A	303	HIS	-	expression tag	UNP G2IPX5
A	304	HIS	-	expression tag	UNP G2IPX5
В	297	LEU	-	expression tag	UNP G2IPX5
В	298	GLU	-	expression tag	UNP G2IPX5
В	299	HIS	-	expression tag	UNP G2IPX5
В	300	HIS	-	expression tag	UNP G2IPX5
В	301	HIS	-	expression tag	UNP G2IPX5
В	302	HIS	-	expression tag	UNP G2IPX5
В	303	HIS	-	expression tag	UNP G2IPX5
В	304	HIS	-	expression tag	UNP G2IPX5

• Molecule 2 is PYRUVIC ACID (three-letter code: PYR) (formula:  $C_3H_4O_3$ ) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 6 3 3	0	0
2	В	1	Total C O 6 3 3	0	0

• Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mn 1 1	0	0
3	В	1	Total Mn 1 1	0	0

• Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	В	1	Total 6	C 3	O 3	0	0

#### • Molecule 5 is water.

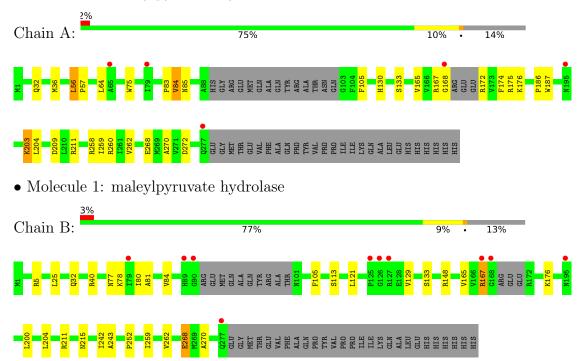
$\mathbf{Mol}$	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
5	A	51	Total O 51 51	0	0
5	В	72	Total O 72 72	0	0



# 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: maleylpyruvate hydrolase





## 4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 1 21 1	Depositor	
Cell constants	68.41Å 74.18Å 68.73Å 90.00° 119.07° 90.00°	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$ Resolution (Å)	31.58 - 2.25	Depositor	
resolution (A)	31.56  -  2.25	EDS	
% Data completeness	97.2 (31.58-2.25)	Depositor	
(in resolution range)	97.3 (31.56-2.25)	EDS	
$R_{merge}$	0.06	Depositor	
$R_{sym}$	(Not available)	Depositor	
$< I/\sigma(I) > 1$	3.57 (at 2.24Å)	Xtriage	
Refinement program	REFMAC 5.8.0238	Depositor	
D D	0.153 , 0.203	Depositor	
$R, R_{free}$	0.167 , $0.216$	DCC	
$R_{free}$ test set	1481 reflections (5.32%)	wwPDB-VP	
Wilson B-factor (Å <sup>2</sup> )	28.6	Xtriage	
Anisotropy	0.079	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	$0.42 \; ,  40.4$	EDS	
L-test for twinning <sup>2</sup>	$< L > = 0.48, < L^2> = 0.31$	Xtriage	
	0.000 for -h-l,k,h		
	0.000  for  l,k,-h-l		
Estimated twinning fraction	0.013  for h,-k,-h-l	Xtriage	
	0.009  for -h-l,-k,l		
	0.025 for l,-k,h		
$F_o, F_c$ correlation	0.96	EDS	
Total number of atoms	4178	wwPDB-VP	
Average B, all atoms $(\mathring{A}^2)$	34.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 47.37 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.0018e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

## 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: MN, PYR, GOL

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		
IVIOI	Chain	RMSZ $ \# Z  > 5$		RMSZ	# Z  > 5	
1	A	0.68	0/2023	0.89	0/2759	
1	В	0.70	0/2096	0.92	2/2856 (0.1%)	
All	All	0.69	0/4119	0.91	2/5615 (0.0%)	

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	В	148	ARG	NE-CZ-NH2	5.45	123.03	120.30
1	В	5	ARG	NE-CZ-NH2	-5.44	117.58	120.30

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	1982	0	2003	22	0
1	В	2053	0	2067	18	0
2	A	6	0	0	1	0
2	В	6	0	0	0	0
3	A	1	0	0	0	0
3	В	1	0	0	0	0
4	В	6	0	8	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	51	0	0	2	0
5	В	72	0	0	0	0
All	All	4178	0	4078	40	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 5.

All (40) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash	
		$\operatorname{distance}\left(\mathrm{\AA}\right)$	overlap (Å)	
1:A:84:VAL:HG23	1:A:85:ASN:H	1.16	1.06	
1:A:84:VAL:HG23	1:A:85:ASN:N	1.94	0.80	
1:B:167:ARG:HH11	1:B:167:ARG:HG3	1.50	0.75	
1:B:165:VAL:HB	1:B:176:LYS:HE3	1.72	0.70	
1:A:165:VAL:HB	1:A:176:LYS:HE3	1.73	0.69	
1:A:84:VAL:CG2	1:A:85:ASN:H	1.95	0.66	
1:B:32:GLN:HE22	1:B:40:ARG:NH1	1.93	0.66	
1:B:167:ARG:HH11	1:B:167:ARG:CG	2.08	0.65	
5:A:533:HOH:O	4:B:402:GOL:H11	1.97	0.64	
1:A:260:ARG:HD2	5:A:549:HOH:O	2.02	0.59	
1:A:83:PRO:O	1:A:84:VAL:HG22	2.06	0.56	
1:A:32:GLN:NE2	1:A:36:MET:H	2.05	0.54	
1:B:262:VAL:HG22	1:B:268:GLU:HB2	1.92	0.52	
1:A:105:PHE:CE1	1:A:176:LYS:HD3	2.46	0.50	
1:B:167:ARG:CG	1:B:167:ARG:NH1	2.72	0.50	
1:B:78:LYS:HA	4:B:402:GOL:H2	1.94	0.50	
1:B:105:PHE:CE2	1:B:176:LYS:HD3	2.47	0.50 0.49 0.49	
1:A:186:PRO:HG2	1:A:187:TRP:CD2	2.47		
1:A:84:VAL:CG2	1:A:85:ASN:N	2.61		
1:A:133:SER:HB3	1:A:204:LEU:HD12	1.94	0.49	
1:A:262:VAL:HG22	1:A:268:GLU:HB2	1.95	0.48	
1:A:172:ARG:HB2	1:A:175[B]:ARG:HG2	1.95	0.48	
1:B:259:ILE:O	1:B:270:ALA:HA	2.13	0.47	
1:B:200:LEU:O	1:B:215:ASN:HA	2.13	0.47	
1:A:203:LYS:HB2	1:A:203:LYS:HE2	1.63	0.47	
1:B:32:GLN:HE22	1:B:40:ARG:HH12	1.63	0.47	
1:A:258:ARG:NH1	1:A:272:ASP:OD1	2.48	0.46	
1:A:75:TRP:CZ2	1:B:77:ASN:HB2	2.51	0.46	
1:A:167:ARG:HD3	1:A:168:GLY:H	1.81	0.45	
1:A:56:LEU:N	1:A:57:PRO:CD	2.81	0.44	
1:A:176:LYS:NZ	2:A:401:PYR:O3	2.51	0.43	

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Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance} \; ({ m \AA})$	overlap (Å)
1:B:121:LEU:HD22	1:B:129:VAL:HG21	2.00	0.43
1:B:81:ALA:HA	1:B:243:ALA:HB3	2.00	0.43
1:A:259:ILE:O	1:A:270:ALA:HA	2.19	0.43
1:A:209:ASP:OD2	1:A:211:ARG:HD3	2.20	0.42
1:B:211:ARG:NH1	1:B:252:PRO:O	2.44	0.42
1:B:133:SER:HB3	1:B:204:LEU:HB2	2.01	0.42
1:A:64:LEU:HD23	1:A:64:LEU:HA	1.91	0.41
1:B:32:GLN:NE2	1:B:40:ARG:HH12	2.17	0.41
1:B:80:ILE:O	1:B:242:ILE:HA	2.21	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	Analysed Favoured Allower		Outliers	Percent	iles
1	A	255/304~(84%)	245 (96%)	9 (4%)	1 (0%)	34 3	7
1	В	263/304 (86%)	257 (98%)	5 (2%)	1 (0%)	34 3	7
All	All	518/608 (85%)	502 (97%)	14 (3%)	2 (0%)	34 3	7

#### All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	84	VAL
1	В	84	VAL

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	210/247 (85%)	206 (98%)	4 (2%)	57 66		
1	В	217/247 (88%)	213 (98%)	4 (2%)	59 68		
All	All	427/494 (86%)	419 (98%)	8 (2%)	57 66		

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	LEU
1	A	130	HIS
1	A	174	PHE
1	A	203	LYS
1	В	25	LEU
1	В	113	SER
1	В	167	ARG
1	В	268	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	ASN
1	A	66	GLN
1	В	37	ASN
1	В	131	HIS

#### 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)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	Tuno	Chain	Res	Link	Bond lengths			Bond angles		
MIOI	Type		rtes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
2	PYR	A	401	3	5,5,5	2.69	1 (20%)	3,6,6	1.89	1 (33%)
4	GOL	В	402	-	5,5,5	0.22	0	5,5,5	0.53	0
2	PYR	В	401	3	5,5,5	3.07	2 (40%)	3,6,6	0.73	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	PYR	A	401	3	-	0/4/4/4	-
4	GOL	В	402	-	-	4/4/4/4	-
2	PYR	В	401	3	-	0/4/4/4	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	$Ideal(\AA)$
2	В	401	PYR	CA-C	-6.06	1.32	1.54
2	A	401	PYR	CA-C	-5.86	1.33	1.54
2	В	401	PYR	OXT-C	-2.92	1.22	1.30

All (1) bond angle outliers are listed below:

$\mathbf{Mol}$	Chain	Res	Type	${f Atoms}$	$\mathbf{Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}(^{o})$
2	A	401	PYR	OXT-C-CA	3.19	122.70	113.97

There are no chirality outliers.

All (4) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
4	В	402	GOL	O1-C1-C2-C3
4	В	402	GOL	C1-C2-C3-O3
4	В	402	GOL	O2-C2-C3-O3
4	В	402	GOL	O1-C1-C2-O2

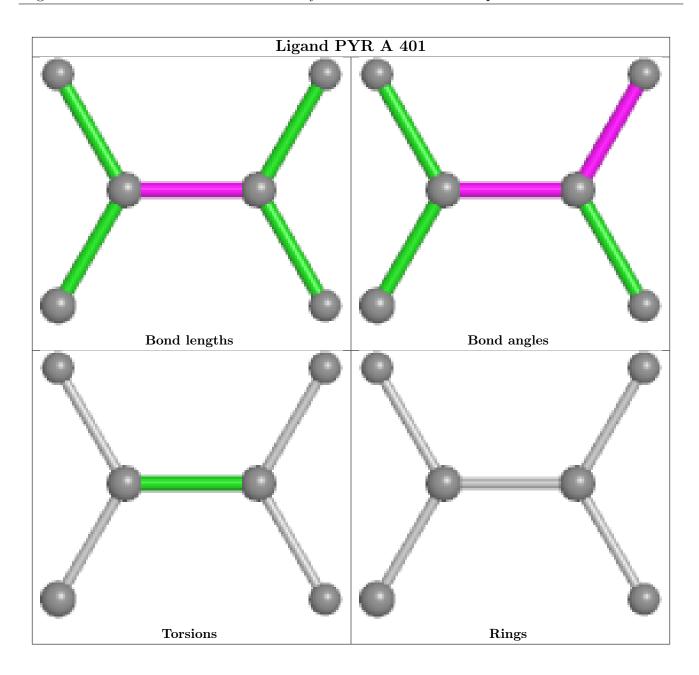
There are no ring outliers.

2 monomers are involved in 3 short contacts:

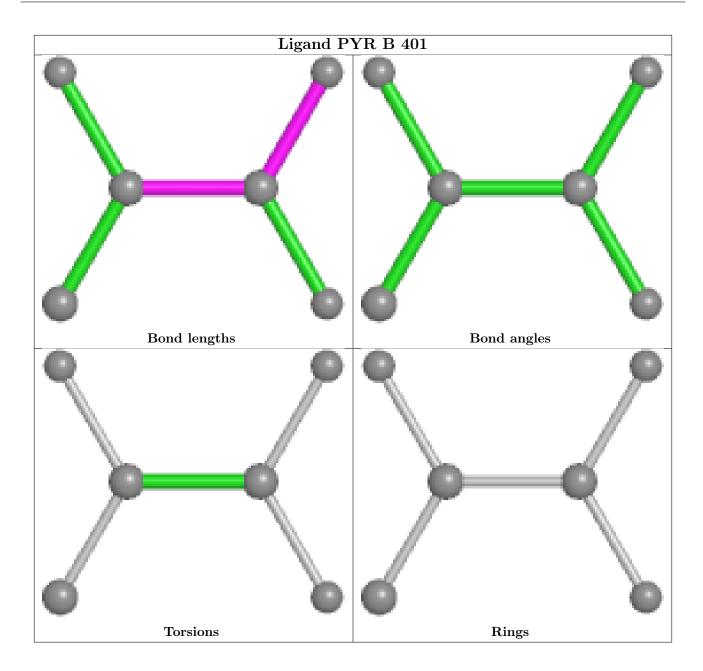
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	PYR	1	0
4	В	402	GOL	2	0

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 then 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,  $95^{th}$  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	$\langle { m RSRZ} \rangle$	$\# \mathrm{RSRZ}{>}2$	$OWAB(Å^2)$	Q<0.9
1	A	260/304~(85%)	-0.15	5 (1%) 66 69	19, 33, 56, 90	0
1	В	264/304~(86%)	-0.12	10 (3%) 40 43	18, 30, 56, 98	0
All	All	524/608 (86%)	-0.13	15 (2%) 51 55	18, 31, 56, 98	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	90	GLY	17.8
1	В	89	HIS	5.1
1	A	277	GLN	4.5
1	A	168	GLY	4.2
1	В	168	GLY	4.2
1	В	195	ASN	3.5
1	В	277	GLN	3.0
1	A	195	ASN	3.0
1	В	126	GLY	2.5
1	A	79	ILE	2.4
1	В	125	PRO	2.3
1	В	79	ILE	2.2
1	В	167	ARG	2.1
1	В	127	ARG	2.0
1	A	65	ALA	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.

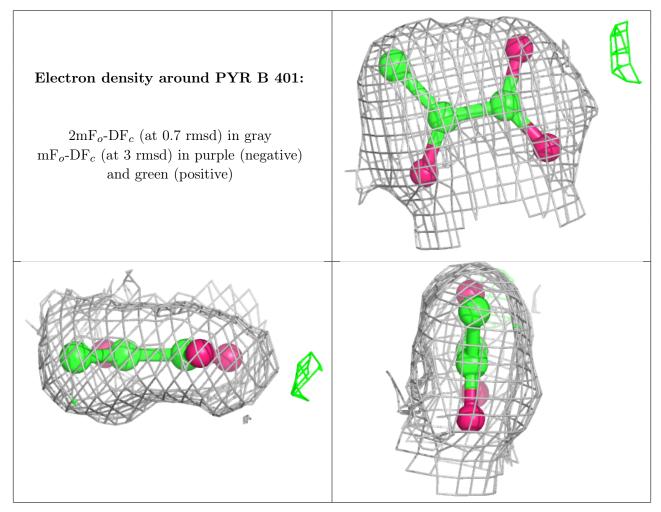


#### 6.4 Ligands (i)

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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathring{\mathbf{A}}^2)$	Q<0.9
2	PYR	В	401	6/6	0.95	0.10	41,43,45,46	0
4	GOL	В	402	6/6	0.95	0.28	30,32,35,37	0
2	PYR	A	401	6/6	0.96	0.11	46,53,54,58	0
3	MN	В	403	1/1	1.00	0.07	29,29,29,29	0
3	MN	A	402	1/1	1.00	0.05	34,34,34,34	0

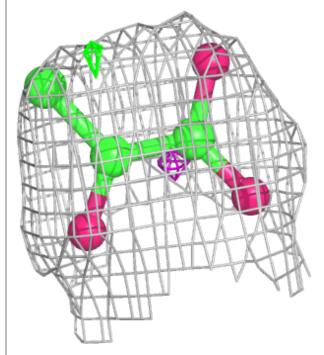
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

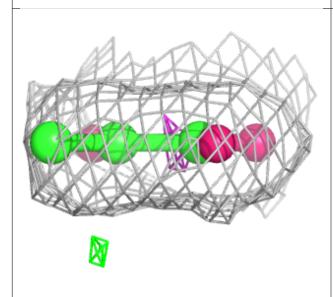


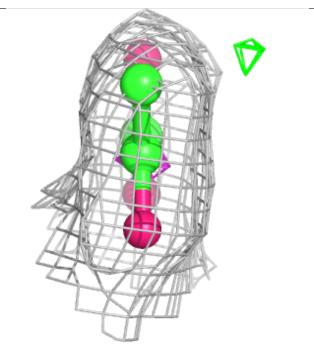


# Electron density around PYR A 401:

 $2 {
m mF}_o {
m -DF}_c$  (at 0.7 rmsd) in gray  ${
m mF}_o {
m -DF}_c$  (at 3 rmsd) in purple (negative) and green (positive)



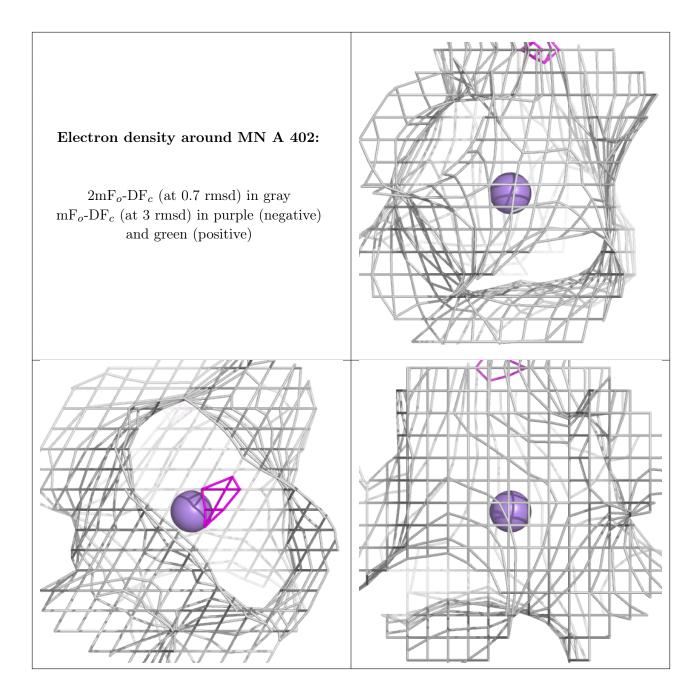






# Electron density around MN B 403: $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray ${\rm mF}_o\text{-}{\rm DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)





## 6.5 Other polymers (i)

There are no such residues in this entry.

