

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

May 19, 2022 – 03:05 pm BST

PDB ID 7Z5P

> Title : Bilirubin oxidase from Bacillus pumilus

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2.99 Å(reported) Resolution

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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity 4.02b-467Xtriage (Phenix) 1.13

EDS 2.28.1buster-report 1.1.7 (2018)

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

> Refmac 5.8.0267

CCP4 7.1.010 (Gargrove) Engh & Huber (2001)

Ideal geometry (proteins) Ideal geometry (DNA, RNA) Parkinson et al. (1996)

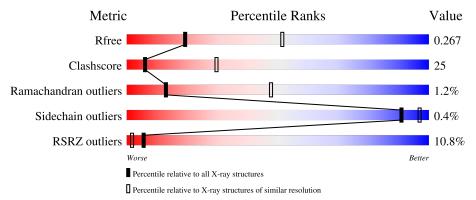
Validation Pipeline (wwPDB-VP) 2.28.1

## 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 2.99 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	A	515	63%	34%			
1	В	515	64%	33%			

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	CU	A	604	_	-	X	-



# 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 8243 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 Copper oxidase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	505	Total 4120	C 2643	N 709	O 755	S 13	3	0	0
1	В	505	Total 4115	C 2640	N 709	O 753	S 13	1	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	510	HIS	-	expression tag	UNP A8FAG9
A	511	HIS	-	expression tag	UNP A8FAG9
A	512	HIS	-	expression tag	UNP A8FAG9
A	513	HIS	-	expression tag	UNP A8FAG9
A	514	HIS	-	expression tag	UNP A8FAG9
A	515	HIS	-	expression tag	UNP A8FAG9
В	510	HIS	_	expression tag	UNP A8FAG9
В	511	HIS	-	expression tag	UNP A8FAG9
В	512	HIS	_	expression tag	UNP A8FAG9
В	513	HIS	-	expression tag	UNP A8FAG9
В	514	HIS	-	expression tag	UNP A8FAG9
В	515	HIS	-	expression tag	UNP A8FAG9

• Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu) (labeled as "Ligand of Interest" by depositor).

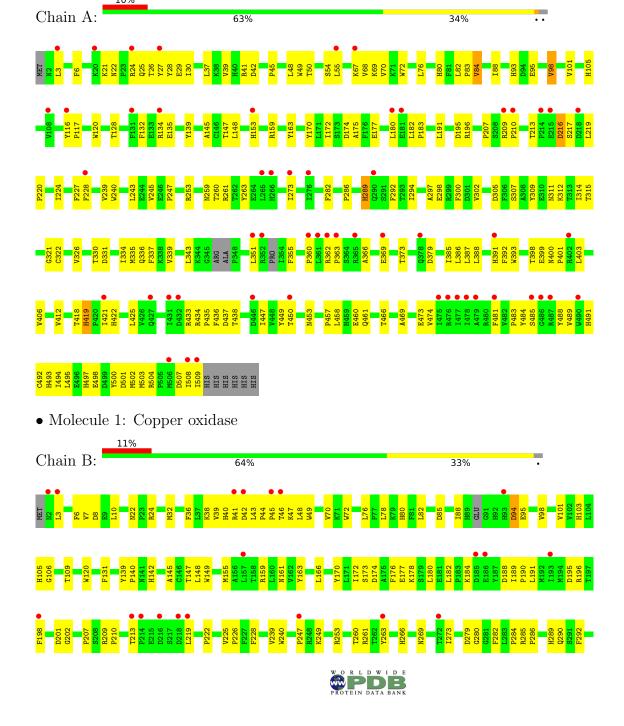
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total Cu 4 4	0	0
2	В	4	Total Cu 4 4	0	0

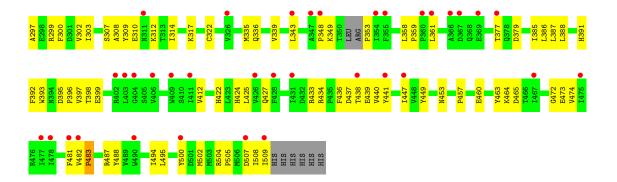


# 3 Residue-property plots (i)

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: Copper oxidase







# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	198.96Å 63.51Å 115.96Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $124.57^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	59.22 - 2.99	Depositor
Resolution (A)	59.22 - 2.99	EDS
% Data completeness	98.1 (59.22-2.99)	Depositor
(in resolution range)	98.4 (59.22-2.99)	EDS
$R_{merge}$	0.19	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.60 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.18.2-3874	Depositor
D.D.	0.254 , $0.267$	Depositor
$R, R_{free}$	0.254 , $0.267$	DCC
$R_{free}$ test set	2405  reflections  (10.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	78.0	Xtriage
Anisotropy	0.790	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning <sup>2</sup>	$< L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	0.008  for -h-2*l,-k,l	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	8243	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.96% of the height of the origin peak. No significant pseudotranslation is detected.

<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: CU

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	0.45	0/4249	0.73	0/5793	
1	В	0.45	0/4245	0.67	0/5789	
All	All	0.45	0/8494	0.70	0/11582	

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 maintenain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	В	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	В	94	ASP	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	A	4120	0	3992	211	0
1	В	4115	0	3986	189	0
2	A	4	0	0	2	0
2	В	4	0	0	0	0
All	All	8243	0	7978	400	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 25.

The worst 5 of 400 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:A:387:LEU:HD11	1:A:392:PHE:CE1	1.68	1.26
1:A:393:TRP:HE1	1:A:503:MET:HE2	1.15	1.07
1:A:117:PRO:HG2	1:A:503:MET:HE1	1.36	1.06
1:A:393:TRP:HE1	1:A:503:MET:CE	1.72	1.02
1:A:401:PRO:HD2	1:A:507:ASP:O	1.64	0.96

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	Pe	Percentiles	
1	A	499/515~(97%)	446 (89%)	46 (9%)	7 (1%)		11	43
1	В	499/515~(97%)	454 (91%)	40 (8%)	5 (1%)		15	53
All	All	998/1030 (97%)	900 (90%)	86 (9%)	12 (1%)		13	48

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	93	HIS

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Mol	Chain	Res	Type
1	A	289	HIS
1	A	360	PRO
1	В	95	GLU
1	В	94	ASP

#### 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	453/462 (98%)	451 (100%)	2 (0%)	91	97	
1	В	452/462 (98%)	450 (100%)	2 (0%)	91	97	
All	All	905/924 (98%)	901 (100%)	4 (0%)	91	97	

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

Mol	Chain	Res	Type
1	A	216	ASP
1	A	322	CYS
1	В	322	CYS
1	В	507	ASP

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

Mol	Chain	Res	Type
1	A	105	HIS
1	A	419	HIS
1	В	2	ASN
1	В	40	HIS
1	В	105	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 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

### 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	<RSRZ $>$	# RSRZ > 2		$OWAB(Å^2)$	Q<0.9
1	A	505/515~(98%)	0.71	54 (10%) 6	2	62, 85, 136, 190	5 (0%)
1	В	505/515 (98%)	0.71	55 (10%) 5	2	49, 86, 134, 207	2 (0%)
All	All	1010/1030 (98%)	0.71	109 (10%)	5 2	49, 85, 135, 207	7 (0%)

The worst 5 of 109 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	362	ARG	8.8
1	A	369	GLU	8.1
1	В	438	THR	7.1
1	В	403	LEU	7.0
1	В	93	HIS	6.9

### 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.

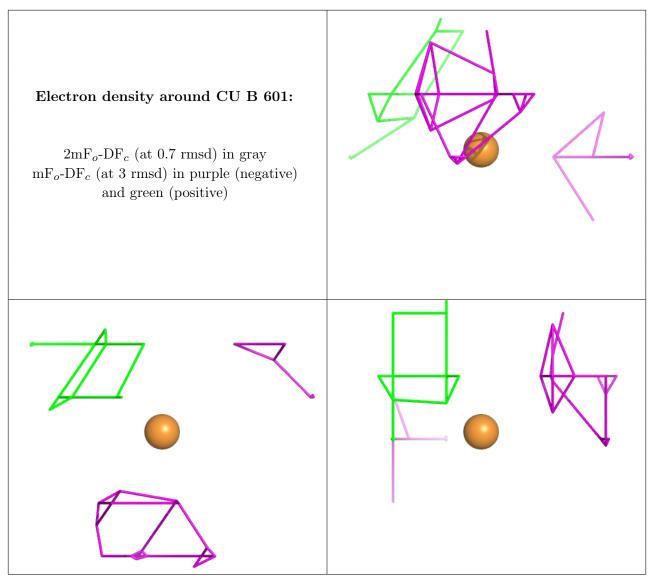
#### 6.4 Ligands (i)

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.

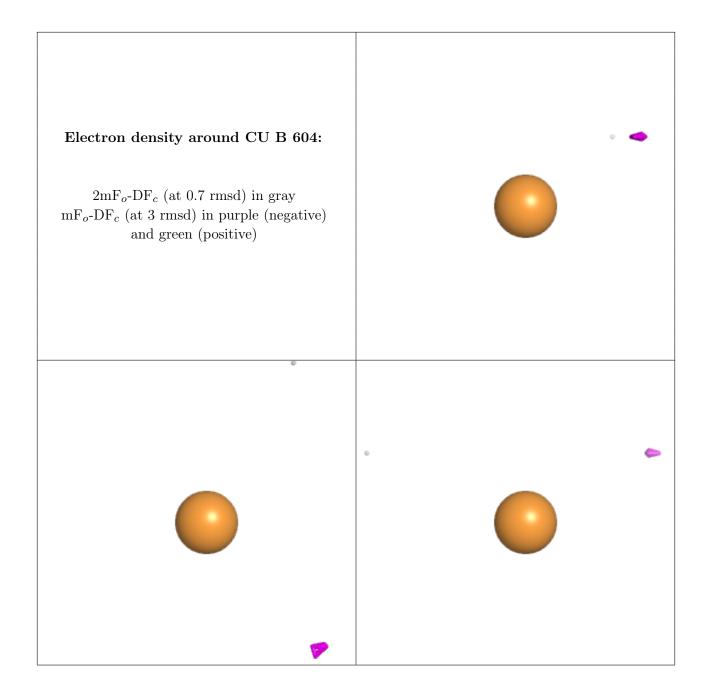


Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	CU	В	601	1/1	0.73	0.18	114,114,114,114	0
2	CU	В	604	1/1	0.81	0.08	107,107,107,107	0
2	CU	В	603	1/1	0.87	0.28	96,96,96,96	0
2	CU	В	602	1/1	0.88	0.27	96,96,96,96	0
2	CU	A	601	1/1	0.89	0.07	96,96,96,96	0
2	CU	A	602	1/1	0.91	0.22	96,96,96,96	0
2	CU	A	603	1/1	0.94	0.17	96,96,96,96	0
2	CU	A	604	1/1	0.95	0.06	104,104,104,104	0

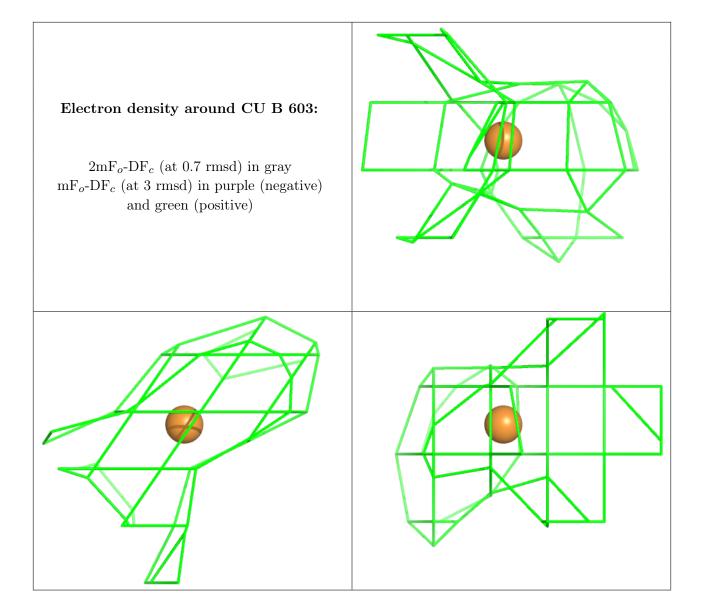
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



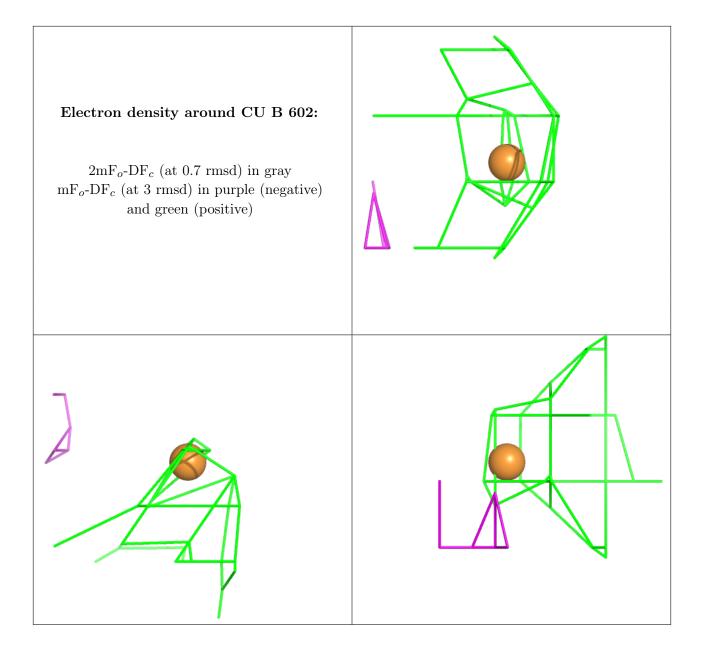




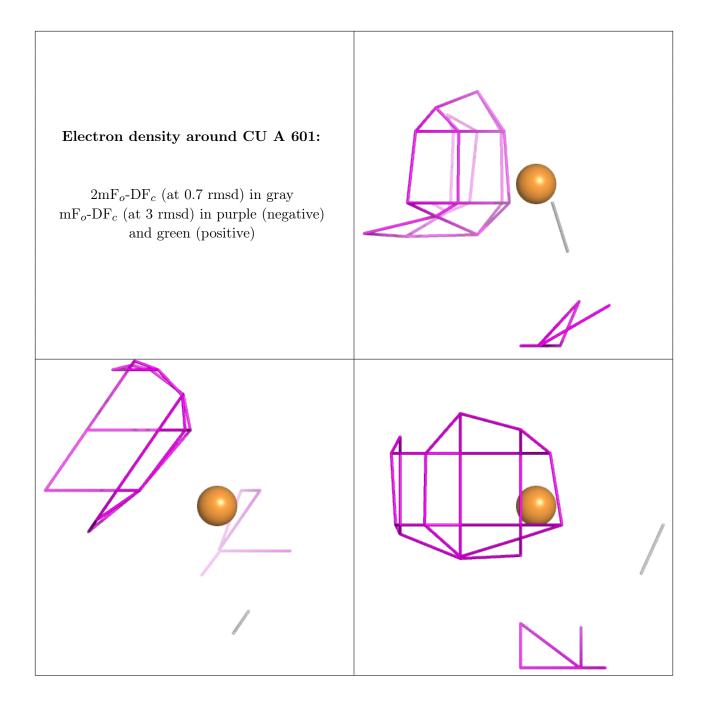




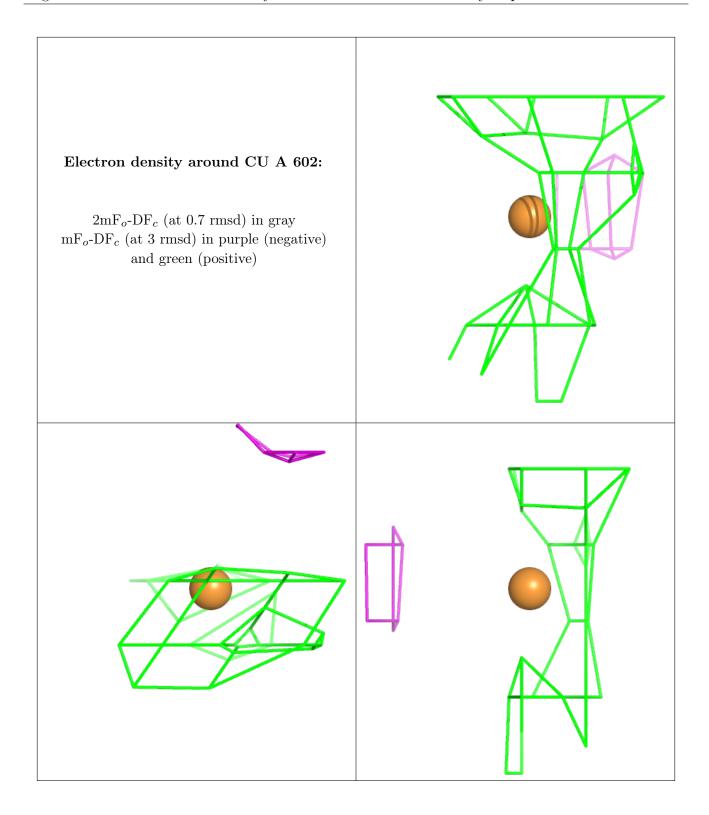




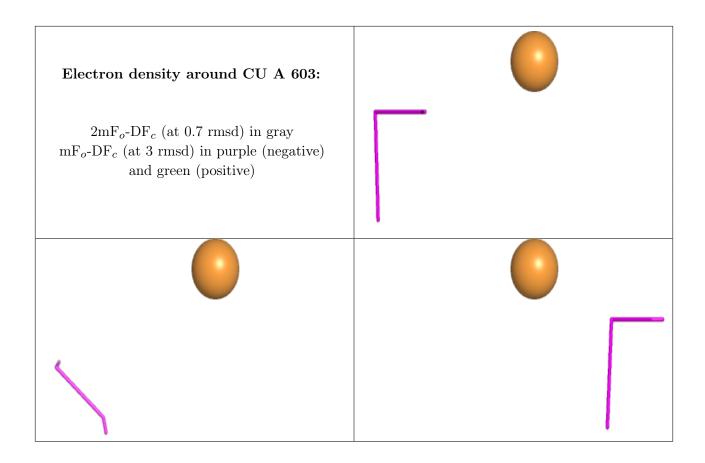




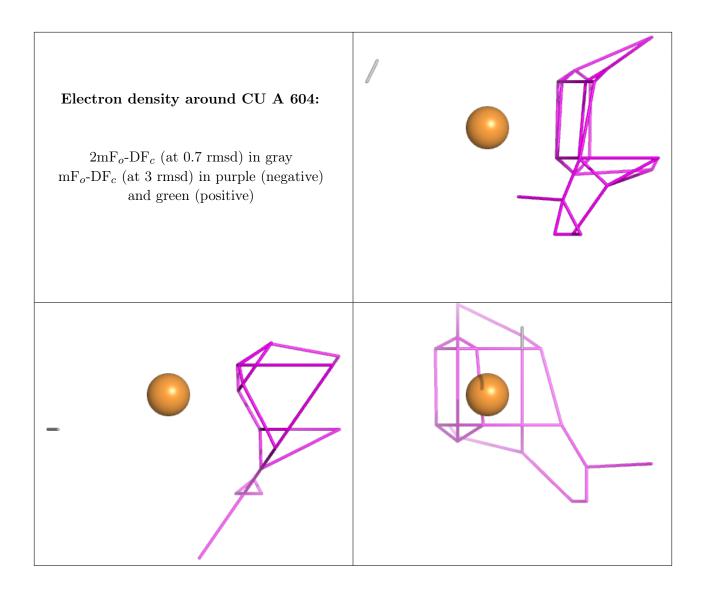












## 6.5 Other polymers (i)

There are no such residues in this entry.

