



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 23, 2024 – 04:05 PM EST

PDB ID : 8ENZ  
Title : Crystal structure of alpha-COPI-WD40 domain K15A mutant.  
Authors : Dey, D.; Hasan, S.S.  
Deposited on : 2022-09-30  
Resolution : 1.65 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

<https://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 : 2.36  
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) : 2.36

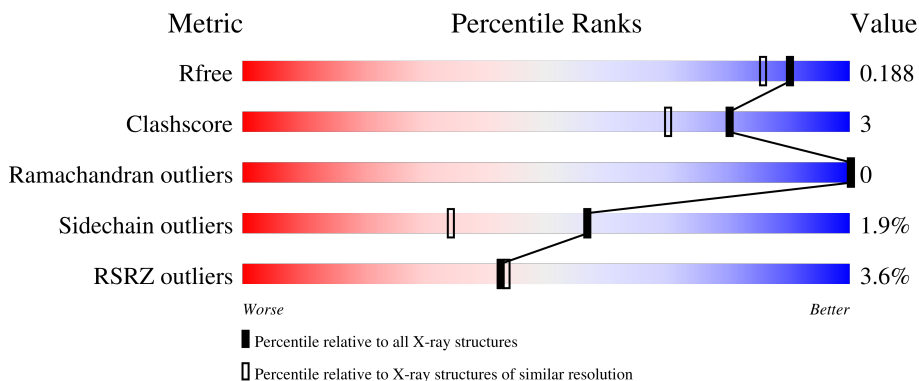
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.65 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	1827 (1.66-1.66)
Clashscore	141614	1931 (1.66-1.66)
Ramachandran outliers	138981	1891 (1.66-1.66)
Sidechain outliers	138945	1891 (1.66-1.66)
RSRZ outliers	127900	1791 (1.66-1.66)

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	337	 3% 84% 6% 10%
1	B	337	 4% 83% 8% 8%
1	C	337	 3% 84% 6% 10%

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 15450 atoms, of which 7234 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 Putative coatomer subunit alpha.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	303	4854	1577	2385	445	430	17	0	0	0
1	B	310	4976	1612	2451	457	438	18	0	1	0
1	C	304	4876	1583	2398	447	431	17	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	ALA	LYS	engineered mutation	UNP Q96WV5
A	181	LYS	LEU	conflict	UNP Q96WV5
A	185	LYS	LEU	conflict	UNP Q96WV5
A	192	LYS	ILE	conflict	UNP Q96WV5
A	196	LYS	LEU	conflict	UNP Q96WV5
A	197	LYS	PHE	conflict	UNP Q96WV5
A	328	SER	-	expression tag	UNP Q96WV5
A	329	ALA	-	expression tag	UNP Q96WV5
A	330	TRP	-	expression tag	UNP Q96WV5
A	331	SER	-	expression tag	UNP Q96WV5
A	332	HIS	-	expression tag	UNP Q96WV5
A	333	PRO	-	expression tag	UNP Q96WV5
A	334	GLN	-	expression tag	UNP Q96WV5
A	335	PHE	-	expression tag	UNP Q96WV5
A	336	GLU	-	expression tag	UNP Q96WV5
A	337	LYS	-	expression tag	UNP Q96WV5
B	15	ALA	LYS	engineered mutation	UNP Q96WV5
B	181	LYS	LEU	conflict	UNP Q96WV5
B	185	LYS	LEU	conflict	UNP Q96WV5
B	192	LYS	ILE	conflict	UNP Q96WV5
B	196	LYS	LEU	conflict	UNP Q96WV5
B	197	LYS	PHE	conflict	UNP Q96WV5
B	328	SER	-	expression tag	UNP Q96WV5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	329	ALA	-	expression tag	UNP Q96WV5
B	330	TRP	-	expression tag	UNP Q96WV5
B	331	SER	-	expression tag	UNP Q96WV5
B	332	HIS	-	expression tag	UNP Q96WV5
B	333	PRO	-	expression tag	UNP Q96WV5
B	334	GLN	-	expression tag	UNP Q96WV5
B	335	PHE	-	expression tag	UNP Q96WV5
B	336	GLU	-	expression tag	UNP Q96WV5
B	337	LYS	-	expression tag	UNP Q96WV5
C	15	ALA	LYS	engineered mutation	UNP Q96WV5
C	181	LYS	LEU	conflict	UNP Q96WV5
C	185	LYS	LEU	conflict	UNP Q96WV5
C	192	LYS	ILE	conflict	UNP Q96WV5
C	196	LYS	LEU	conflict	UNP Q96WV5
C	197	LYS	PHE	conflict	UNP Q96WV5
C	328	SER	-	expression tag	UNP Q96WV5
C	329	ALA	-	expression tag	UNP Q96WV5
C	330	TRP	-	expression tag	UNP Q96WV5
C	331	SER	-	expression tag	UNP Q96WV5
C	332	HIS	-	expression tag	UNP Q96WV5
C	333	PRO	-	expression tag	UNP Q96WV5
C	334	GLN	-	expression tag	UNP Q96WV5
C	335	PHE	-	expression tag	UNP Q96WV5
C	336	GLU	-	expression tag	UNP Q96WV5
C	337	LYS	-	expression tag	UNP Q96WV5

- Molecule 2 is ACETYL GROUP (three-letter code: ACE) (formula: C<sub>2</sub>H<sub>4</sub>O) (labeled as "Ligand of Interest" by depositor).



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

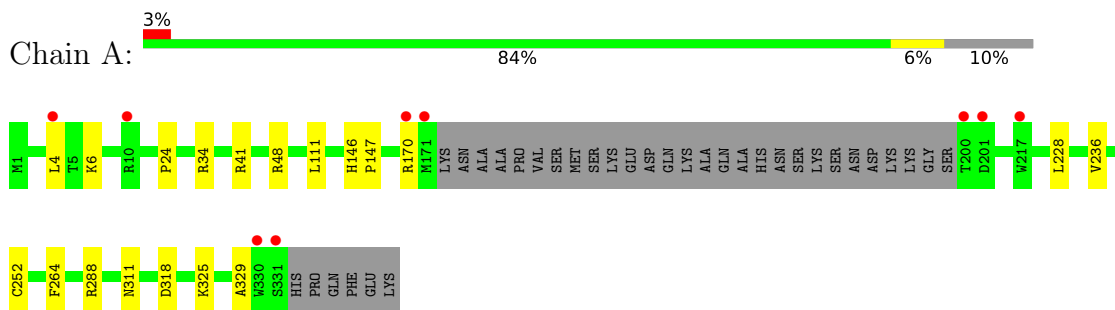
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	262	Total O 262 262	0	0
3	B	257	Total O 257 257	0	0
3	C	216	Total O 216 216	0	0

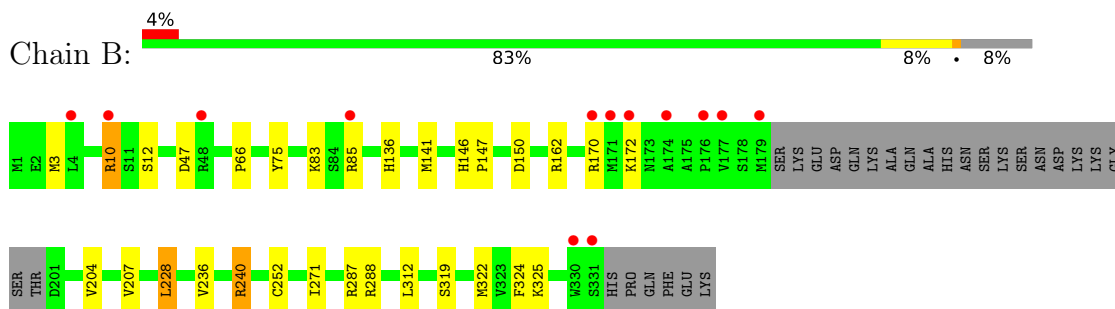
### 3 Residue-property plots [i](#)

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.

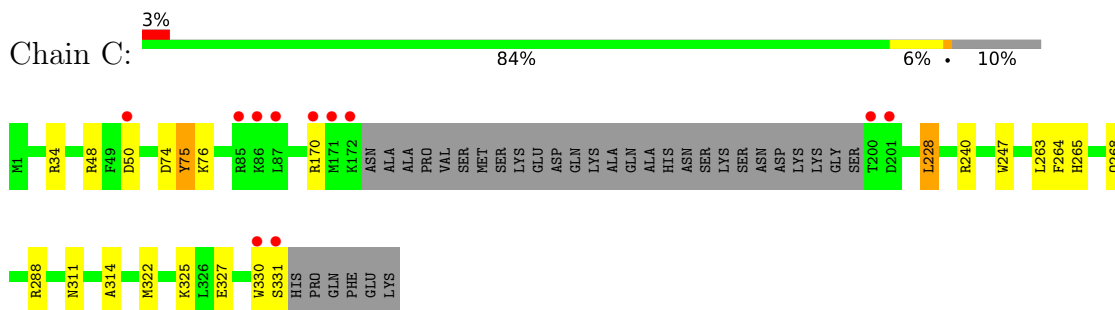
- Molecule 1: Putative coatomer subunit alpha



- Molecule 1: Putative coatomer subunit alpha



- Molecule 1: Putative coatomer subunit alpha



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	37.49Å 172.26Å 71.48Å 90.00° 99.91° 90.00°	Depositor
Resolution (Å)	28.71 – 1.65 28.84 – 1.65	Depositor EDS
% Data completeness (in resolution range)	96.6 (28.71-1.65) 98.5 (28.84-1.65)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.45 (at 1.65Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.163 , 0.193 0.158 , 0.188	Depositor DCC
$R_{free}$ test set	5243 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.9	Xtrriage
Anisotropy	0.245	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.47 , 51.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	15450	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 24.48 % 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 3.8027e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: ACE

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	0.69	0/2544	0.83	2/3457 (0.1%)
1	B	0.69	1/2604 (0.0%)	0.85	2/3537 (0.1%)
1	C	0.71	1/2553 (0.0%)	0.81	1/3468 (0.0%)
All	All	0.70	2/7701 (0.0%)	0.83	5/10462 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	141	MET	CG-SD	5.20	1.94	1.81
1	C	311	ASN	CB-CG	5.14	1.62	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	318	ASP	CB-CG-OD1	5.90	123.61	118.30
1	B	141	MET	CG-SD-CE	5.71	109.34	100.20
1	A	111	LEU	CA-CB-CG	5.48	127.90	115.30
1	B	228	LEU	CB-CG-CD2	-5.21	102.14	111.00
1	C	228	LEU	CB-CG-CD1	-5.05	102.41	111.00

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	2469	2385	2385	9	1
1	B	2525	2451	2450	15	1
1	C	2478	2398	2398	15	0
2	A	3	0	3	0	0
2	B	3	0	3	0	0
2	C	3	0	3	0	0
3	A	262	0	0	0	0
3	B	257	0	0	1	0
3	C	216	0	0	1	1
All	All	8216	7234	7242	39	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 3.

The worst 5 of 39 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:B:287:ARG:NH1	3:B:501:HOH:O	2.11	0.84
1:A:4:LEU:HD12	1:A:6:LYS:HE3	1.70	0.74
1:B:228:LEU:HD21	1:B:271:ILE:HG23	1.77	0.66
1:B:162[B]:ARG:HD3	1:B:207:VAL:HG22	1.77	0.65
1:A:6:LYS:NZ	1:A:325:LYS:HD2	2.14	0.63

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)
3:C:592:HOH:O	3:C:686:HOH:O[1_655]	2.02	0.18
1:A:329:ALA:O	1:B:240:ARG:HE[1_455]	1.55	0.05

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	299/337 (89%)	287 (96%)	12 (4%)	0	100	100
1	B	307/337 (91%)	292 (95%)	15 (5%)	0	100	100
1	C	300/337 (89%)	286 (95%)	14 (5%)	0	100	100
All	All	906/1011 (90%)	865 (96%)	41 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	268/297 (90%)	266 (99%)	2 (1%)	84	73
1	B	274/297 (92%)	266 (97%)	8 (3%)	42	16
1	C	269/297 (91%)	264 (98%)	5 (2%)	57	34
All	All	811/891 (91%)	796 (98%)	15 (2%)	57	36

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	240	ARG
1	C	288	ARG
1	B	288	ARG
1	C	331	SER
1	C	75	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	128	ASN

### 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](#)

3 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	ACE	C	401	1	1,2,2	0.41	0	1,1,1	0.05	0
2	ACE	A	401	1	1,2,2	0.55	0	1,1,1	0.01	0
2	ACE	B	401	1	1,2,2	0.93	0	1,1,1	0.41	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

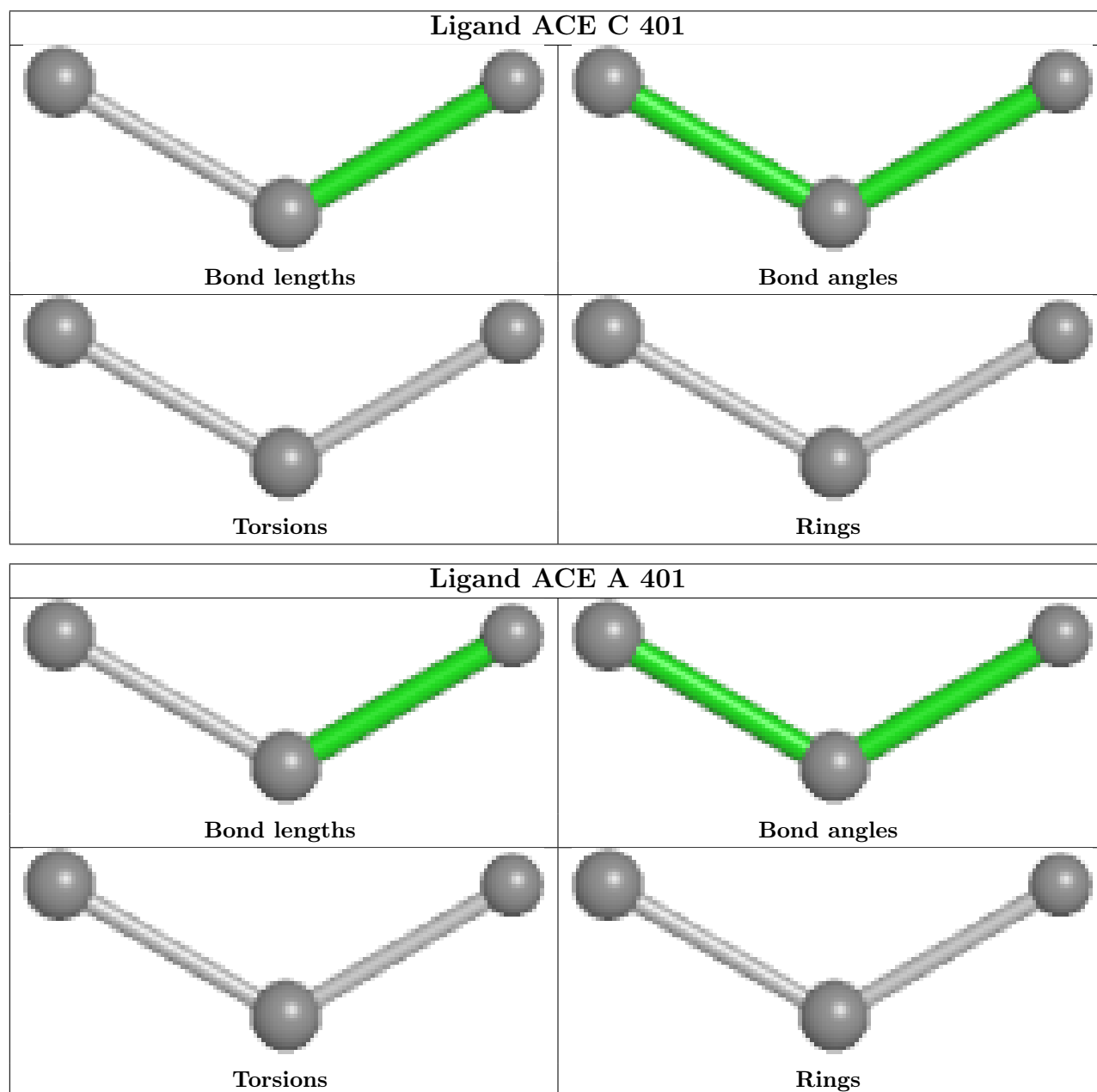
There are no torsion outliers.

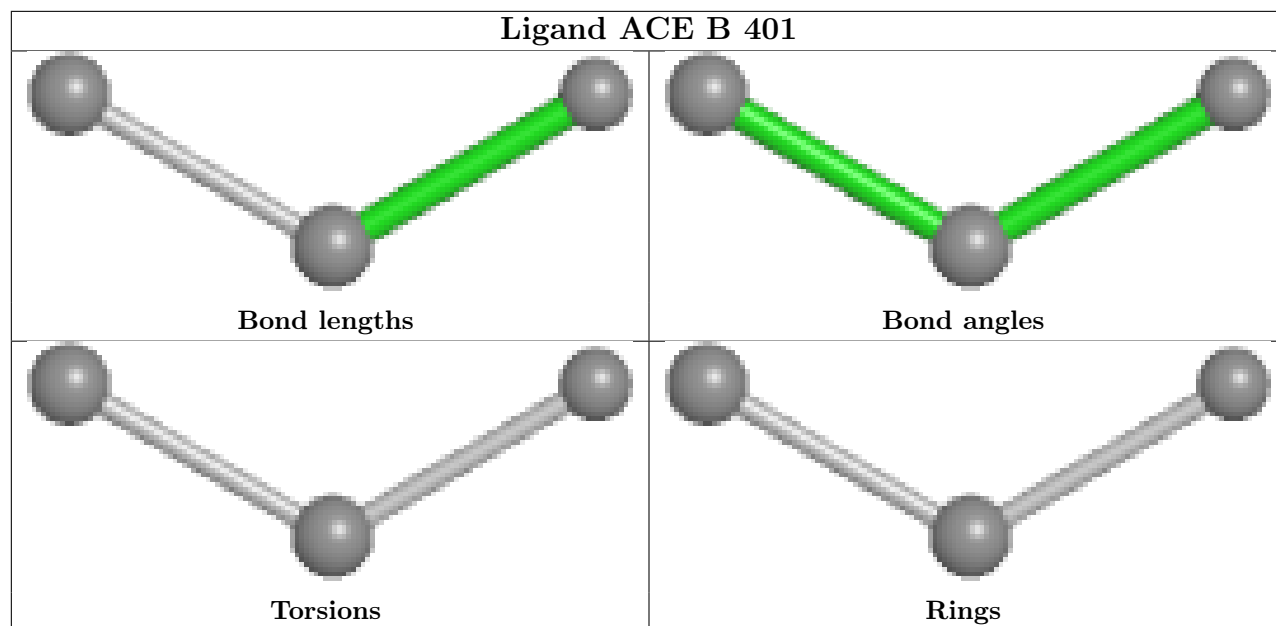
There are no ring outliers.

No monomer is involved in short contacts.

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	A	303/337 (89%)	-0.14	9 (2%) 50 51	12, 19, 34, 54	0
1	B	310/337 (91%)	-0.03	13 (4%) 36 35	13, 20, 38, 51	0
1	C	304/337 (90%)	0.01	11 (3%) 42 43	13, 22, 38, 62	0
All	All	917/1011 (90%)	-0.05	33 (3%) 42 43	12, 20, 37, 62	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	330	TRP	6.9
1	C	171	MET	5.6
1	A	200	THR	5.1
1	B	177	VAL	5.0
1	B	171	MET	5.0

### 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](#)

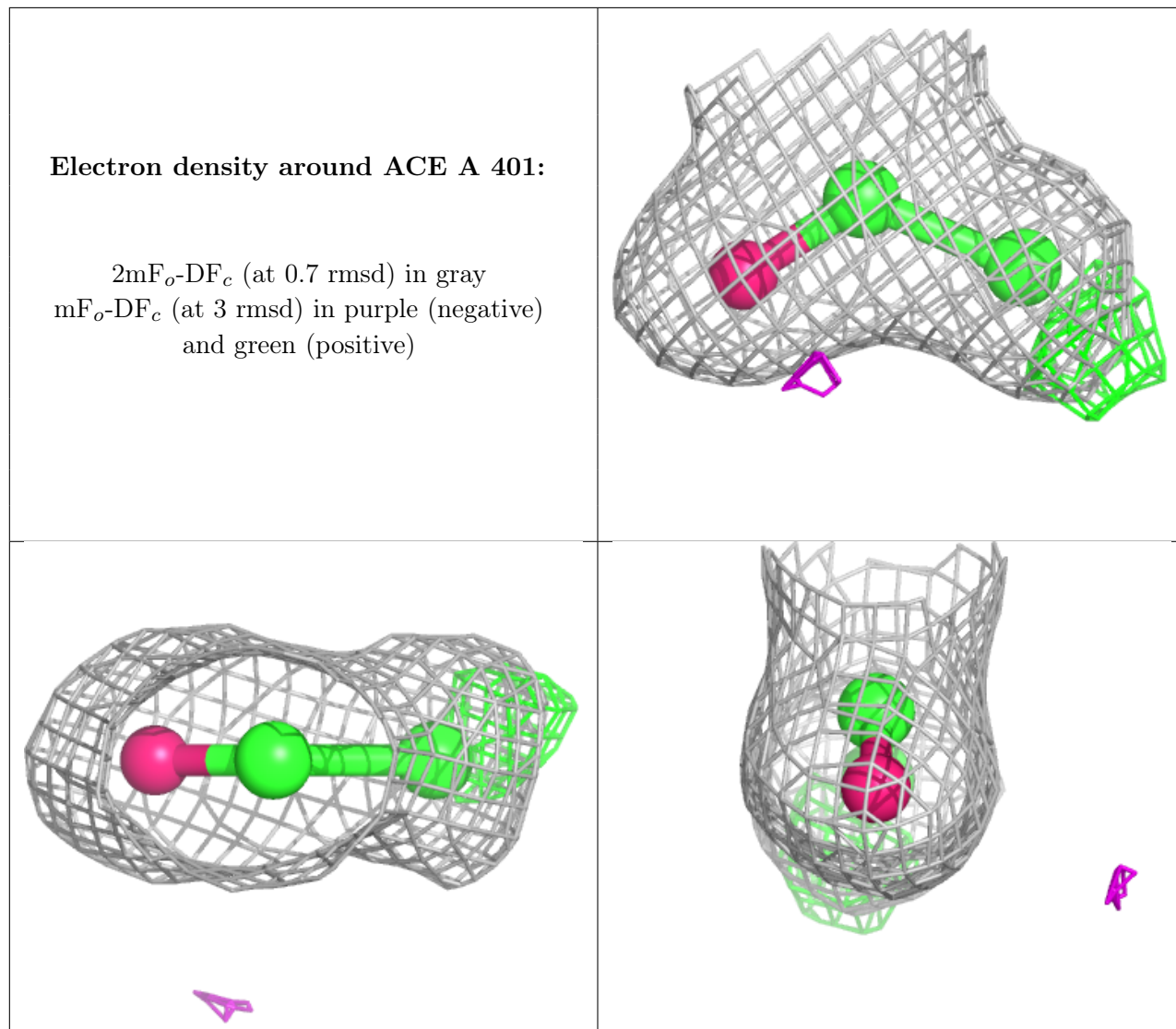
There are no monosaccharides in this entry.

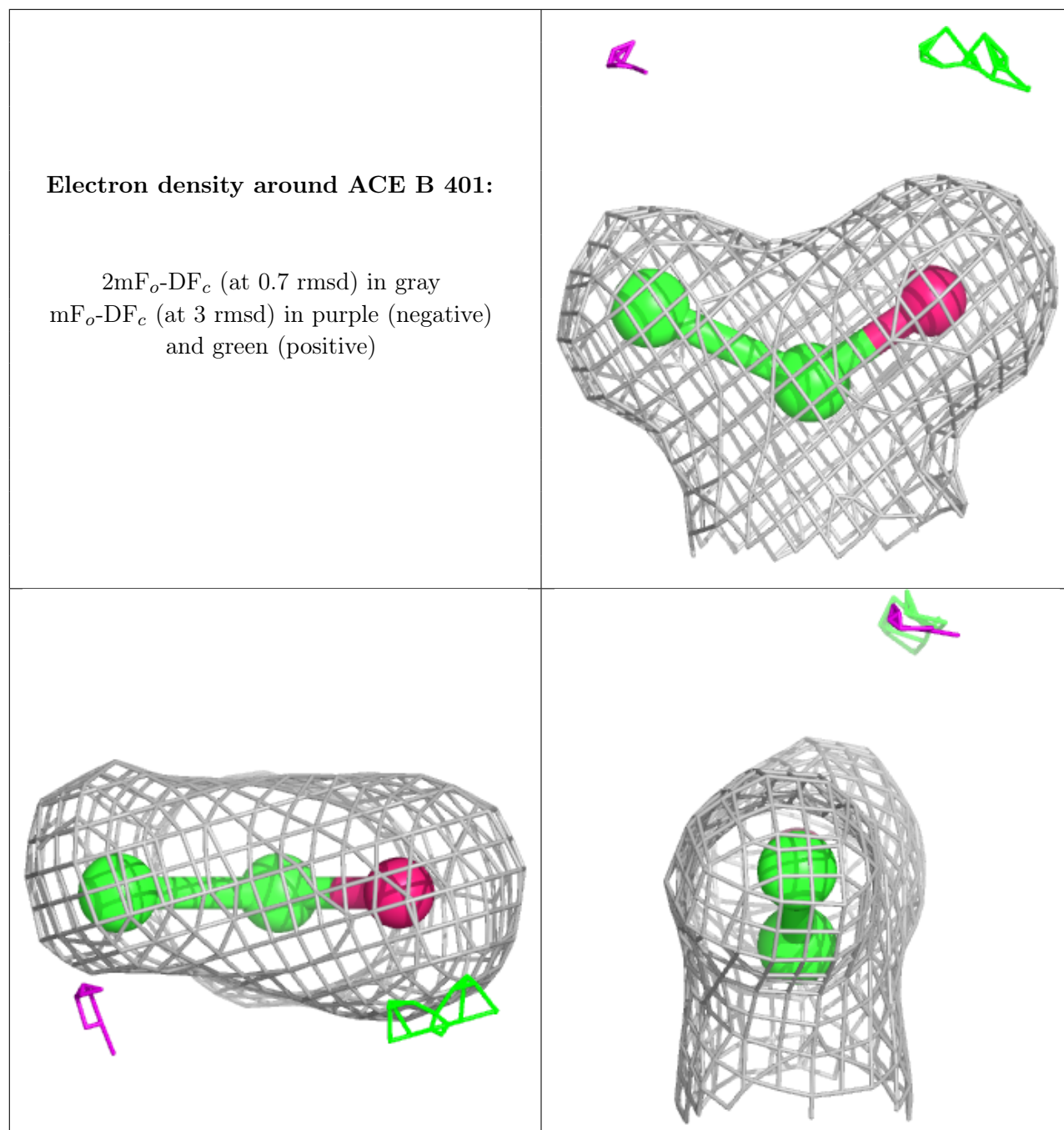
### 6.4 Ligands [i](#)

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.

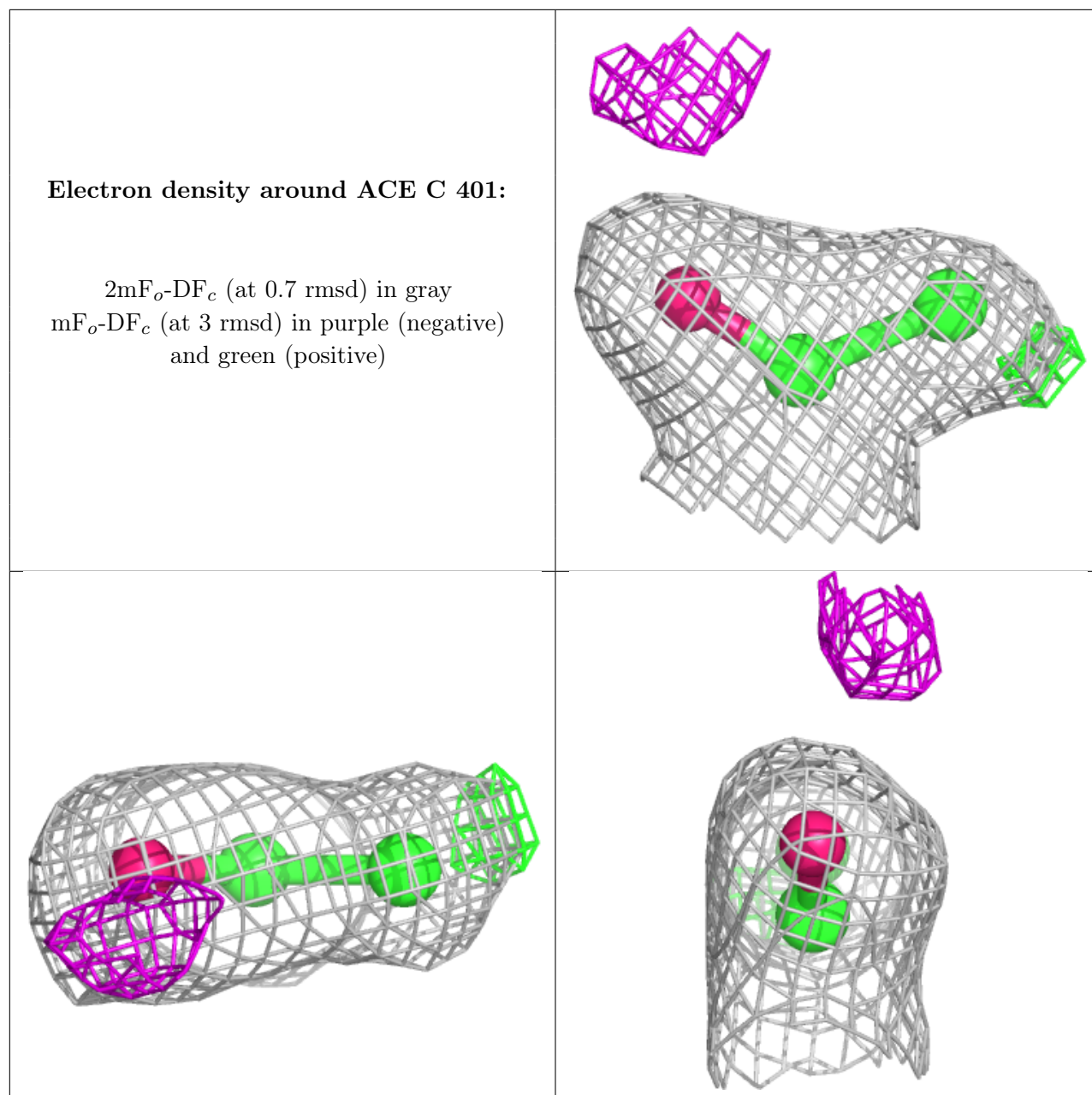
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ACE	A	401	3/3	0.95	0.08	25,25,26,26	0
2	ACE	B	401	3/3	0.97	0.06	24,24,24,26	0
2	ACE	C	401	3/3	0.98	0.06	21,21,23,24	0

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.