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P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report (i)

Jan 23, 2023 – 12:09 PM JST

PDB ID	:	7YJS
Title	:	Crystal structure of MCR-1-S treated by sodium aurothiosulfate
Authors	:	Zhang, Q.; Sun, H.; Wang, M.
Deposited on	:	2022-07-20
Resolution	:	2.50 Å(reported)

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

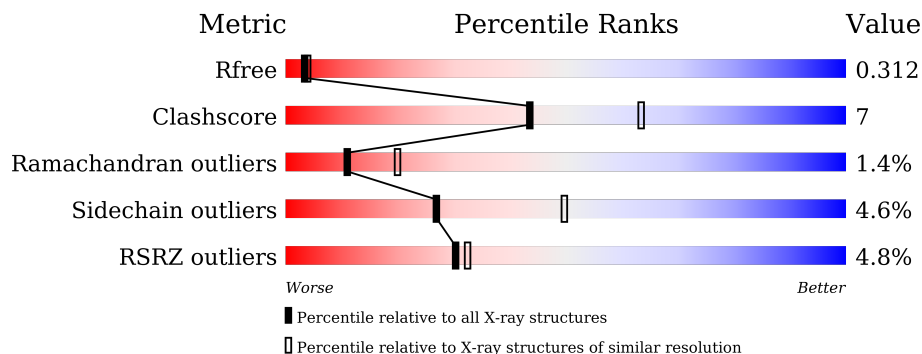|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.3
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

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 2.50 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	Percentile Ranks	Value
Rfree		0.312
Clashscore		7
Ramachandran outliers		1.4%
Sidechain outliers		4.6%
RSRZ outliers		4.8%

Worse   *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	336	.% 80% 15% · ·
1	B	336	8% 73% 21% · ·

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2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 5090 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 Probable phosphatidylethanolamine transferase Mcr-1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	323	Total 2536	C 1593	N 426	O 500	P 1	S 16	0	2	0
1	B	323	Total 2529	C 1589	N 426	O 497	P 1	S 16	1	3	0

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	206	HIS	-	expression tag	UNP A0A0R6L508
A	207	MET	-	expression tag	UNP A0A0R6L508
A	208	LEU	-	expression tag	UNP A0A0R6L508
A	209	GLU	-	expression tag	UNP A0A0R6L508
A	210	GLY	-	expression tag	UNP A0A0R6L508
A	211	GLY	-	expression tag	UNP A0A0R6L508
A	212	SER	-	expression tag	UNP A0A0R6L508
A	213	GLY	-	expression tag	UNP A0A0R6L508
A	214	GLY	-	expression tag	UNP A0A0R6L508
A	215	SER	-	expression tag	UNP A0A0R6L508
A	216	GLY	-	expression tag	UNP A0A0R6L508
A	217	GLY	-	expression tag	UNP A0A0R6L508
A	218	SER	-	expression tag	UNP A0A0R6L508
B	206	HIS	-	expression tag	UNP A0A0R6L508
B	207	MET	-	expression tag	UNP A0A0R6L508
B	208	LEU	-	expression tag	UNP A0A0R6L508
B	209	GLU	-	expression tag	UNP A0A0R6L508
B	210	GLY	-	expression tag	UNP A0A0R6L508
B	211	GLY	-	expression tag	UNP A0A0R6L508
B	212	SER	-	expression tag	UNP A0A0R6L508
B	213	GLY	-	expression tag	UNP A0A0R6L508
B	214	GLY	-	expression tag	UNP A0A0R6L508
B	215	SER	-	expression tag	UNP A0A0R6L508
B	216	GLY	-	expression tag	UNP A0A0R6L508
B	217	GLY	-	expression tag	UNP A0A0R6L508

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Chain	Residue	Modelled	Actual	Comment	Reference
B	218	SER	-	expression tag	UNP A0A0R6L508

- Molecule 2 is GOLD ION (three-letter code: AU) (formula: Au) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Au 1	0	0
2	B	1	Total 1	Au 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	19	Total 19	O 19	0	0
3	B	4	Total 4	O 4	0	0

# 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: Probable phosphatidylethanolamine transferase Mcr-1
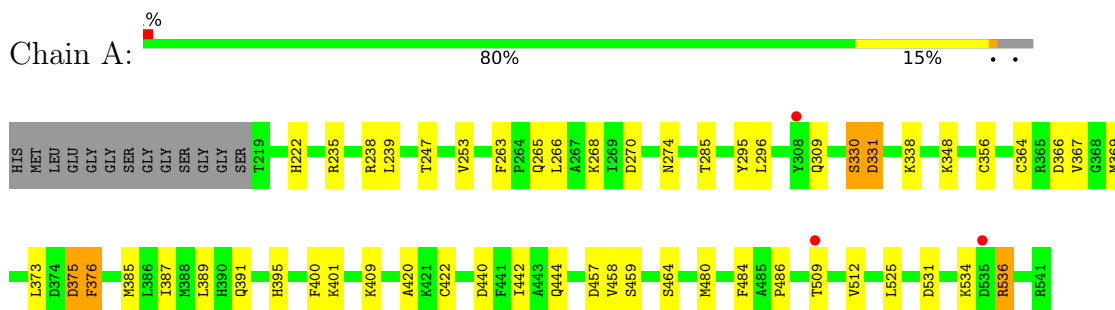
• Molecule 1: Probable phosphatidylethanolamine transferase Mcr-1
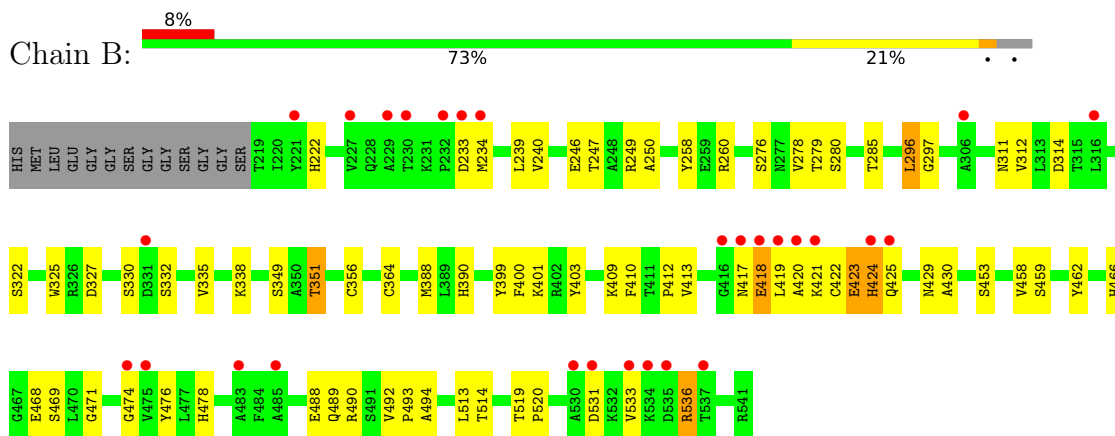
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	47.10Å 84.74Å 81.82Å 90.00° 98.48° 90.00°	Depositor
Resolution (Å)	58.52 – 2.50 80.93 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (58.52-2.50) 99.8 (80.93-2.50)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.71 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.223 , 0.310 0.225 , 0.312	Depositor DCC
R_{free} test set	1130 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å^2)	23.1	Xtriage
Anisotropy	0.186	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 44.1	EDS
L-test for twinning[2]	$< |L| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	5090	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.76% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]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.

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: AU, TPO

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	0.48	0/2587	0.68	0/3512
1	B	0.38	0/2584	0.58	0/3509
All	All	0.44	0/5171	0.63	0/7021

There are no bond length outliers.

There are no bond angle outliers.

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	2536	0	2420	26	0
1	B	2529	0	2415	40	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	19	0	0	1	0
3	B	4	0	0	0	0
All	All	5090	0	4835	66	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 7.

The worst 5 of 66 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:314:ASP:OD2	1:B:338:LYS:NZ	2.20	0.72
1:A:531:ASP:HA	1:A:534:LYS:HG3	1.72	0.71
1:B:418:GLU:HB2	1:B:421:LYS:HB2	1.76	0.66
1:B:312:VAL:HB	1:B:519:THR:HG23	1.83	0.61
1:B:520:PRO:HG3	1:B:536:ARG:HG2	1.84	0.59

There are no symmetry-related clashes.

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	322/336 (96%)	300 (93%)	19 (6%)	3 (1%)	17	31
1	B	323/336 (96%)	297 (92%)	20 (6%)	6 (2%)	8	13
All	All	645/672 (96%)	597 (93%)	39 (6%)	9 (1%)	11	20

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	420	ALA
1	B	424	HIS
1	A	330	SER
1	A	376	PHE
1	B	419	LEU

5.3.2 Protein sidechains ⓘ

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.

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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	275/281 (98%)	263 (96%)	12 (4%)	28	52
1	B	273/281 (97%)	260 (95%)	13 (5%)	25	48
All	All	548/562 (98%)	523 (95%)	25 (5%)	27	50

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	276	SER
1	B	351	THR
1	B	536	ARG
1	B	322	SER
1	B	388	MET

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

Mol	Chain	Res	Type
1	B	343	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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	#$|Z| > 2$
1	TPO	B	285	1,2	8,10,11	1.65	1 (12%)	10,14,16	1.41	1 (10%)
1	TPO	A	285	1,2	8,10,11	1.03	0	10,14,16	1.33	1 (10%)

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
1	TPO	B	285	1,2	-	2/9/11/13	-
1	TPO	A	285	1,2	-	1/9/11/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	285	TPO	P-O1P	3.35	1.61	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	285	TPO	P-OG1-CB	-3.60	112.32	123.21
1	B	285	TPO	P-OG1-CB	-3.45	112.79	123.21

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	285	TPO	CB-OG1-P-O2P
1	A	285	TPO	O-C-CA-CB
1	B	285	TPO	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5   Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6   Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	A	322/336 (95%)	0.18	3 (0%)	84	86	9, 18, 35, 53	0
1	B	322/336 (95%)	0.75	28 (8%)	10	10	18, 35, 59, 87	1 (0%)
All	All	644/672 (95%)	0.47	31 (4%)	30	32	9, 27, 55, 87	1 (0%)

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	418	GLU	4.6
1	B	421	LYS	3.5
1	B	420	ALA	3.5
1	B	232	PRO	3.2
1	A	308	TYR	3.1

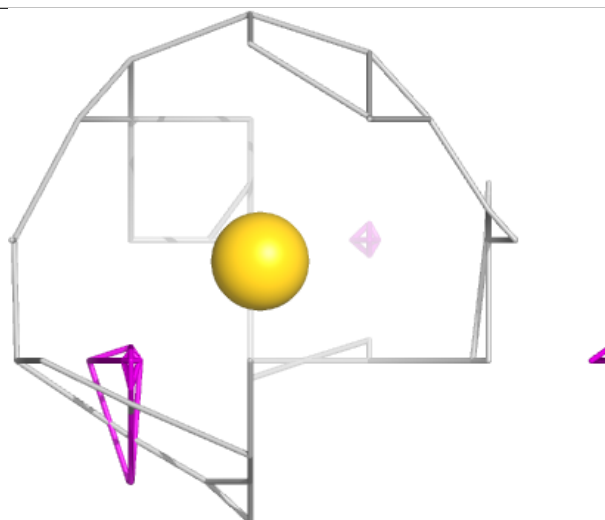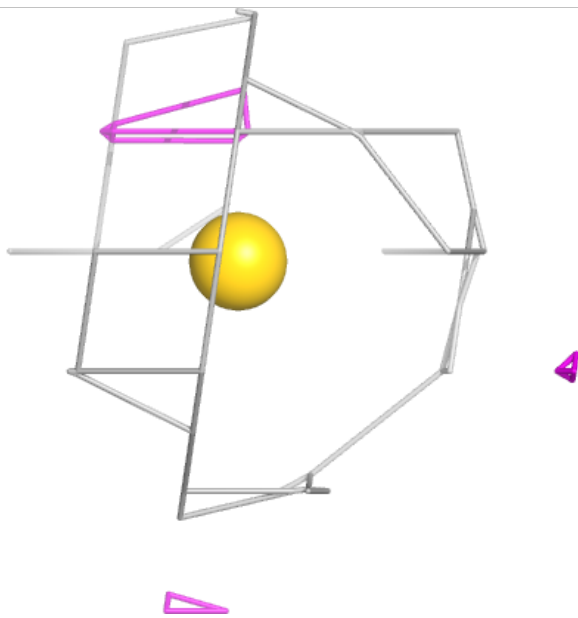## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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
1	TPO	B	285	11/12	0.81	0.24	29,41,46,58	0
1	TPO	A	285	11/12	0.92	0.18	14,19,29,41	0

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.
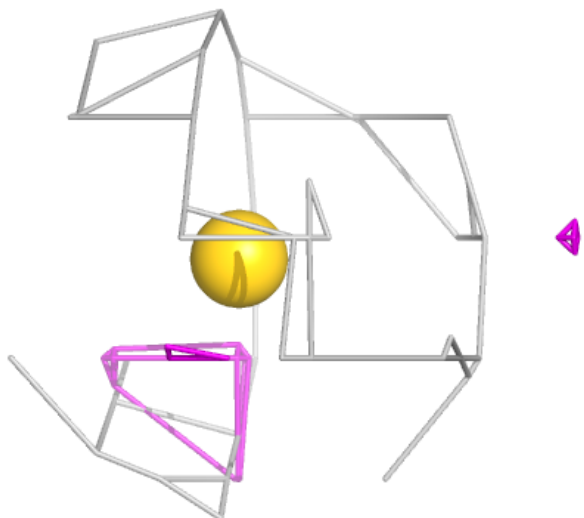
6.4   Ligands (i)

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, 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.
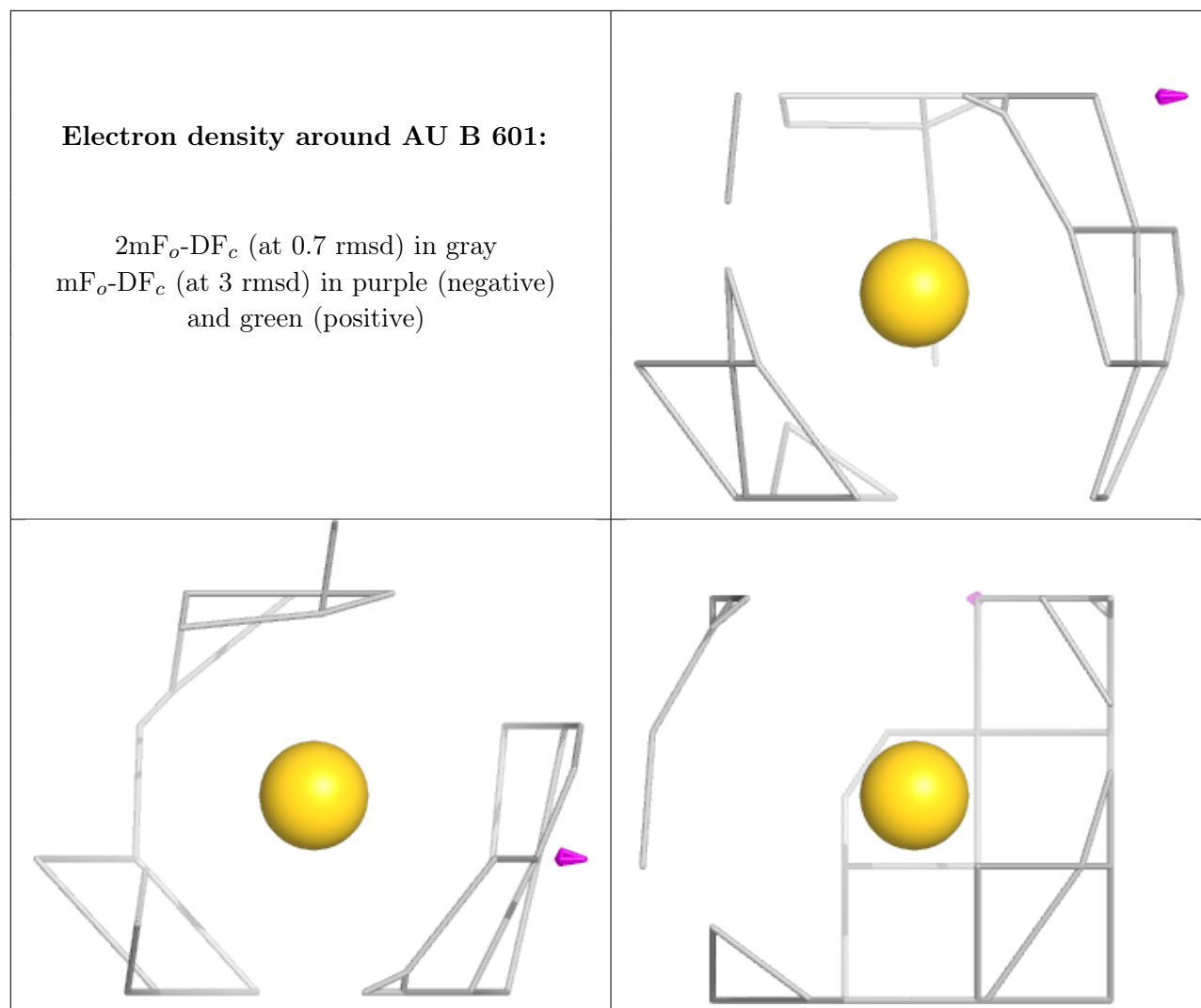
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($Å^2$)	Q<0.9
2	AU	A	601	1/1	0.97	0.05	15,15,15,15	1
2	AU	B	601	1/1	0.98	0.04	34,34,34,34	1

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 AU A 601:

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

Electron density around AU B 601:

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

6.5 Other polymers ⓘ

There are no such residues in this entry.