



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 14, 2022 – 04:10 am BST

PDB ID : 7B5A  
Title : X-ray crystal structure of Sporosarcina pasteurii urease inhibited by Ag(PET3)2NO3 determined at 1.97 Angstroms  
Authors : Mazzei, L.; Cianci, M.; Ciurli, S.  
Deposited on : 2020-12-03  
Resolution : 1.97 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](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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.27
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

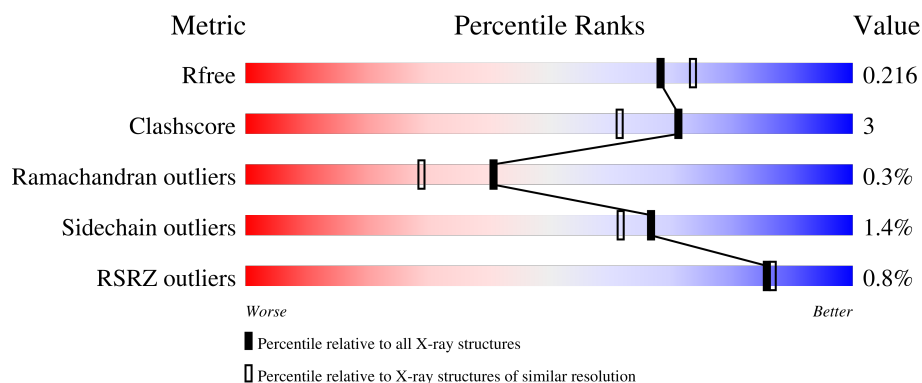
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


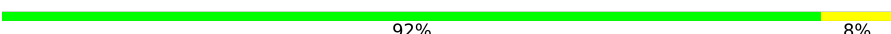

The reported resolution of this entry is 1.97 Å.

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	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (2.00-1.96)

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	AAA	100	 90% 10%
2	BBB	122	 92% 8%
3	CCC	570	 90% 10% .

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
4	EDO	AAA	204	-	X	-	-
4	EDO	CCC	605	-	-	X	-

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 6792 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 Urease subunit gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	100	Total	C	N	O	S	0	6	0
			822	517	138	160	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	20	ALA	LEU	variant	UNP P41022
AAA	22	LYS	ARG	variant	UNP P41022

- Molecule 2 is a protein called Urease subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	BBB	122	Total	C	N	O	S	0	2	0
			967	597	173	196	1			

- Molecule 3 is a protein called Urease subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	CCC	570	Total	C	N	O	S	0	15	0
			4423	2777	760	860	26			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CCC	35	TYR	-	insertion	UNP P41020
CCC	?	-	VAL	deletion	UNP P41020

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	AAA	1	Total	C	O	0	0
			4	2	2		
4	AAA	1	Total	C	O	0	0
			4	2	2		
4	AAA	1	Total	C	O	0	0
			4	2	2		
4	AAA	1	Total	C	O	0	0
			4	2	2		
4	CCC	1	Total	C	O	0	0
			4	2	2		
4	CCC	1	Total	C	O	0	0
			4	2	2		
4	CCC	1	Total	C	O	0	0
			4	2	2		
4	CCC	1	Total	C	O	0	0
			4	2	2		
4	CCC	1	Total	C	O	0	0
			4	2	2		
4	CCC	1	Total	C	O	0	0
			4	2	2		
4	CCC	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	AAA	1	Total	O	S	0	0
			5	4	1		
5	AAA	1	Total	O	S	0	0
			5	4	1		
5	BBB	1	Total	O	S	0	0
			5	4	1		
5	BBB	1	Total	O	S	0	0
			5	4	1		
5	BBB	1	Total	O	S	0	0
			5	4	1		
5	CCC	1	Total	O	S	0	0
			5	4	1		
5	CCC	1	Total	O	S	0	0
			5	4	1		
5	CCC	1	Total	O	S	0	0
			5	4	1		
5	CCC	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	CCC	2	Total	Ni	0	0
			2	2		

- Molecule 7 is OXYGEN ATOM (three-letter code: O) (formula: O).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	CCC	1	Total O 1 1	0	0

- Molecule 8 is SILVER ION (three-letter code: AG) (formula: Ag) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	CCC	2	Total Ag 2 2	0	0

- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	AAA	63	Total O 63 63	0	0
9	BBB	93	Total O 93 93	0	0
9	CCC	317	Total O 317 317	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: Urease subunit gamma

Chain AAA:  90% 10%

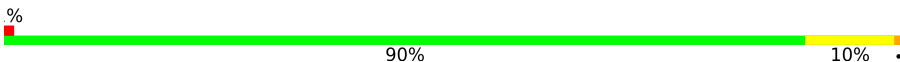


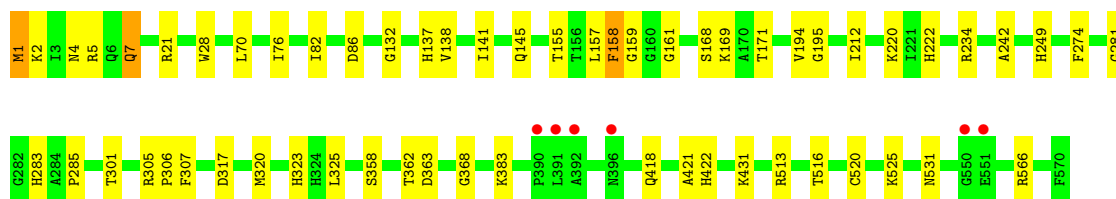
- Molecule 2: Urease subunit beta

Chain BBB:  92% 8%



- Molecule 3: Urease subunit alpha

Chain CCC:  90% 10% .





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	131.49Å 131.49Å 189.52Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	97.80 – 1.97 97.61 – 1.97	Depositor EDS
% Data completeness (in resolution range)	100.0 (97.80-1.97) 100.0 (97.61-1.97)	Depositor EDS
$R_{merge}$	0.20	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.60 (at 1.97Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.167 , 0.209 0.178 , 0.216	Depositor DCC
$R_{free}$ test set	3343 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.5	Xtriage
Anisotropy	0.727	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	6792	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% of the height of the origin peak. No significant pseudotranslation is detected.*

<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: CXM, NI, O, SO4, KCX, AG, EDO

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	0.81	0/828	0.88	0/1113
2	BBB	0.78	0/979	0.92	0/1316
3	CCC	0.81	0/4513	0.91	3/6111 (0.0%)
All	All	0.80	0/6320	0.91	3/8540 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	CCC	520	CYS	CB-CA-C	-6.65	97.09	110.40
3	CCC	234	ARG	CG-CD-NE	-5.32	100.63	111.80
3	CCC	21	ARG	NE-CZ-NH1	5.21	122.91	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	AAA	822	0	837	4	1
2	BBB	967	0	946	6	1
3	CCC	4423	0	4406	36	0
4	AAA	16	0	24	0	0
4	CCC	36	0	54	6	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	AAA	10	0	0	1	0
5	BBB	15	0	0	1	0
5	CCC	25	0	0	0	0
6	CCC	2	0	0	0	0
7	CCC	1	0	0	0	0
8	CCC	2	0	0	0	0
9	AAA	63	0	0	0	0
9	BBB	93	0	0	1	0
9	CCC	317	0	0	1	0
All	All	6792	0	6267	43	1

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.

All (43) 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)
3:CCC:513:ARG:HD3	4:CCC:605:EDO:C1	2.03	0.89
3:CCC:141:ILE:H	3:CCC:145:GLN:HE22	1.40	0.70
3:CCC:513:ARG:HD3	4:CCC:605:EDO:H11	1.72	0.68
3:CCC:513:ARG:HB3	4:CCC:605:EDO:H11	1.78	0.64
3:CCC:513:ARG:HD3	4:CCC:605:EDO:O1	1.98	0.63
2:BBB:17:GLY:O	3:CCC:5[A]:ARG:HG2	2.03	0.57
2:BBB:19:ILE:HG12	3:CCC:5[A]:ARG:HD2	1.86	0.56
3:CCC:513:ARG:NH1	4:CCC:605:EDO:O1	2.36	0.55
3:CCC:70:LEU:HD11	3:CCC:86:ASP:HB3	1.89	0.54
3:CCC:320:MET:HA	3:CCC:325:LEU:HB2	1.92	0.52
3:CCC:301:THR:CG2	3:CCC:363:ASP:HB2	2.41	0.51
3:CCC:307:PHE:O	3:CCC:383:LYS:HE3	2.11	0.51
1:AAA:30:LEU:HD13	1:AAA:38:ILE:HD12	1.94	0.50
3:CCC:421:ALA:O	3:CCC:431[B]:LYS:HE3	2.11	0.49
3:CCC:4:ASN:OD1	3:CCC:7:GLN:NE2	2.46	0.49
3:CCC:212:ILE:HG21	3:CCC:242:ALA:HB1	1.94	0.49
3:CCC:161:GLY:HA2	3:CCC:168:SER:OG	2.13	0.49
2:BBB:13:ARG:HD3	9:BBB:381:HOH:O	2.13	0.48
3:CCC:358:SER:HA	3:CCC:531:ASN:HB3	1.95	0.48
3:CCC:137:HIS:CE1	3:CCC:274:PHE:CD2	3.03	0.47
3:CCC:422:HIS:CE1	3:CCC:516:THR:O	2.68	0.47
1:AAA:73:VAL:N	1:AAA:74:PRO:CD	2.78	0.46
2:BBB:13:ARG:HG3	3:CCC:28:TRP:CZ3	2.51	0.46
3:CCC:358:SER:OG	3:CCC:525:LYS:HE3	2.16	0.46

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AAA:205:SO4:O2	3:CCC:566:ARG:NH1	2.46	0.46
3:CCC:132:GLY:HA3	3:CCC:155:THR:OG1	2.17	0.45
3:CCC:169:LYS:HE3	9:CCC:987:HOH:O	2.17	0.45
3:CCC:249:HIS:CE1	3:CCC:281:GLY:HA3	2.51	0.45
1:AAA:81[A]:GLN:HG2	1:AAA:94:THR:OG1	2.18	0.44
3:CCC:157:LEU:O	3:CCC:194:VAL:HA	2.18	0.44
3:CCC:158:PHE:CE2	3:CCC:418[A]:GLN:CG	3.00	0.44
3:CCC:513:ARG:CD	4:CCC:605:EDO:H11	2.46	0.44
3:CCC:171:THR:HG22	3:CCC:222:HIS:CG	2.53	0.43
2:BBB:31:ARG:N	5:BBB:201:SO4:O3	2.48	0.43
3:CCC:220:KCX:CX	3:CCC:222:HIS:HD2	2.31	0.43
1:AAA:9:GLU:O	1:AAA:12[A]:GLN:HB2	2.19	0.43
3:CCC:362:THR:O	3:CCC:368:GLY:HA3	2.19	0.42
2:BBB:103:THR:HG23	2:BBB:113:ILE:HD11	2.02	0.41
3:CCC:138:VAL:O	3:CCC:159:GLY:HA3	2.20	0.41
3:CCC:158:PHE:CE1	3:CCC:195:GLY:HA3	2.56	0.41
3:CCC:76:ILE:O	3:CCC:82:ILE:HA	2.21	0.41
3:CCC:1:MET:HG3	3:CCC:2:LYS:N	2.36	0.40
3:CCC:305:ARG:HA	3:CCC:306:PRO:HA	1.83	0.40

All (1) 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:59:GLU:OE2	2:BBB:81:GLU:OE2[8_676]	2.17	0.03

## 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	104/100 (104%)	104 (100%)	0	0	<b>100</b> <b>100</b>

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	BBB	122/122 (100%)	116 (95%)	5 (4%)	1 (1%)	19	9
3	CCC	582/570 (102%)	559 (96%)	22 (4%)	1 (0%)	47	38
All	All	808/792 (102%)	779 (96%)	27 (3%)	2 (0%)	41	38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	BBB	99	ILE
3	CCC	283	HIS

### 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.

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	89/83 (107%)	88 (99%)	1 (1%)	73	70
2	BBB	103/101 (102%)	99 (96%)	4 (4%)	32	19
3	CCC	472/458 (103%)	466 (99%)	6 (1%)	69	64
All	All	664/642 (103%)	653 (98%)	11 (2%)	67	53

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	100	SER
2	BBB	33[A]	SER
2	BBB	33[B]	SER
2	BBB	54[A]	GLU
2	BBB	54[B]	GLU
3	CCC	1	MET
3	CCC	7	GLN
3	CCC	158	PHE
3	CCC	285	PRO
3	CCC	317	ASP
3	CCC	323	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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	$\# Z  > 2$
3	KCX	CCC	220	6,3	7,11,12	0.55	0	4,12,14	0.30	0
1	CXM	AAA	1	1	6,10,11	0.53	0	5,11,13	1.12	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
3	KCX	CCC	220	6,3	-	0/7/10/12	-
1	CXM	AAA	1	1	-	0/7/10/12	-

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	CCC	220	KCX	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 28 ligands modelled in this entry, 5 are monoatomic - leaving 23 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
5	SO4	CCC	618	8	4,4,4	0.40	0	6,6,6	0.27	0
4	EDO	AAA	204	-	3,3,3	1.79	1 (33%)	2,2,2	1.86	1 (50%)
4	EDO	AAA	203	-	3,3,3	0.78	0	2,2,2	0.35	0
5	SO4	CCC	617	-	4,4,4	0.28	0	6,6,6	0.10	0
4	EDO	AAA	201	-	3,3,3	1.13	0	2,2,2	0.55	0
4	EDO	CCC	612	-	3,3,3	0.35	0	2,2,2	0.53	0
5	SO4	AAA	206	-	4,4,4	0.44	0	6,6,6	0.23	0
4	EDO	CCC	614	-	3,3,3	0.66	0	2,2,2	0.17	0
5	SO4	CCC	619	-	4,4,4	0.28	0	6,6,6	0.12	0
4	EDO	AAA	202	-	3,3,3	0.49	0	2,2,2	0.28	0
5	SO4	AAA	205	-	4,4,4	0.32	0	6,6,6	0.26	0
4	EDO	CCC	605	-	3,3,3	0.74	0	2,2,2	0.41	0
4	EDO	CCC	608	-	3,3,3	0.81	0	2,2,2	0.23	0
4	EDO	CCC	607	-	3,3,3	0.33	0	2,2,2	0.50	0
4	EDO	CCC	604	-	3,3,3	0.36	0	2,2,2	0.88	0
4	EDO	CCC	611	-	3,3,3	0.69	0	2,2,2	0.49	0
4	EDO	CCC	613	-	3,3,3	0.30	0	2,2,2	0.85	0
5	SO4	BBB	202	-	4,4,4	0.32	0	6,6,6	0.11	0
5	SO4	BBB	203	-	4,4,4	0.26	0	6,6,6	0.11	0
4	EDO	CCC	603	-	3,3,3	1.10	0	2,2,2	0.99	0
5	SO4	BBB	201	-	4,4,4	0.31	0	6,6,6	0.11	0
5	SO4	CCC	616	-	4,4,4	0.25	0	6,6,6	0.15	0
5	SO4	CCC	615	-	4,4,4	0.26	0	6,6,6	0.24	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
4	EDO	CCC	612	-	-	0/1/1/1	-
4	EDO	CCC	611	-	-	1/1/1/1	-
4	EDO	AAA	204	-	-	1/1/1/1	-
4	EDO	CCC	614	-	-	1/1/1/1	-
4	EDO	CCC	613	-	-	0/1/1/1	-
4	EDO	AAA	203	-	-	0/1/1/1	-
4	EDO	AAA	202	-	-	0/1/1/1	-
4	EDO	CCC	605	-	-	1/1/1/1	-
4	EDO	CCC	608	-	-	0/1/1/1	-
4	EDO	CCC	603	-	-	1/1/1/1	-
4	EDO	AAA	201	-	-	0/1/1/1	-
4	EDO	CCC	607	-	-	0/1/1/1	-
4	EDO	CCC	604	-	-	1/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	AAA	204	EDO	O1-C1	2.11	1.53	1.42

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	AAA	204	EDO	O2-C2-C1	2.63	130.84	111.91

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	AAA	204	EDO	O1-C1-C2-O2
4	CCC	611	EDO	O1-C1-C2-O2
4	CCC	605	EDO	O1-C1-C2-O2
4	CCC	603	EDO	O1-C1-C2-O2
4	CCC	614	EDO	O1-C1-C2-O2
4	CCC	604	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	AAA	205	SO4	1	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	CCC	605	EDO	6	0
5	BBB	201	SO4	1	0

## 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	AAA	99/100 (99%)	-0.41	0 100 100	32, 36, 45, 65	0
2	BBB	122/122 (100%)	-0.57	0 100 100	35, 40, 61, 78	0
3	CCC	569/570 (99%)	-0.45	6 (1%) 80 82	31, 37, 53, 93	0
All	All	790/792 (99%)	-0.46	6 (0%) 86 87	31, 38, 54, 93	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	CCC	392	ALA	3.0
3	CCC	550	GLY	2.8
3	CCC	396	ASN	2.2
3	CCC	551	GLU	2.1
3	CCC	390	PRO	2.1
3	CCC	391	LEU	2.1

### 6.2 Non-standard residues in protein, DNA, RNA chains [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(Å <sup>2</sup> )	Q<0.9
1	CXM	AAA	1	11/12	0.95	0.10	31,39,42,45	0
3	KCX	CCC	220	12/13	0.98	0.06	28,35,38,39	0

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands ⓘ

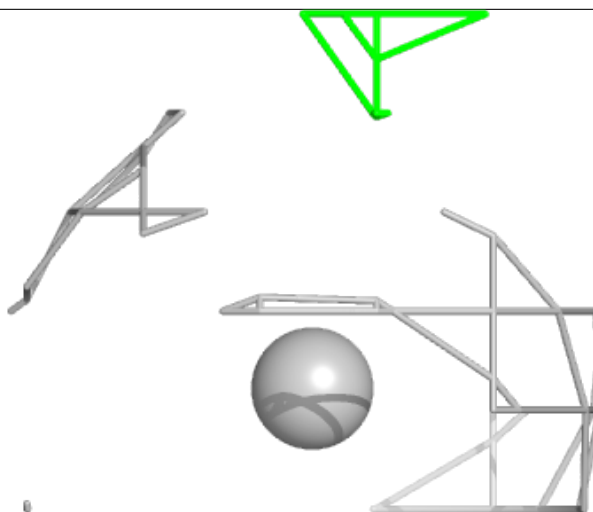
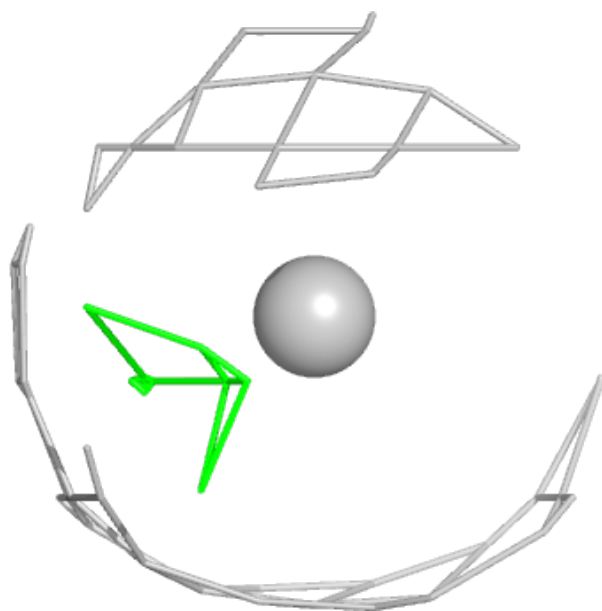
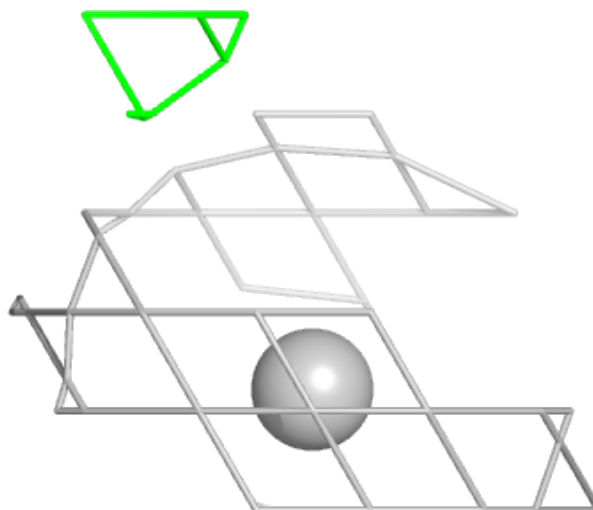
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

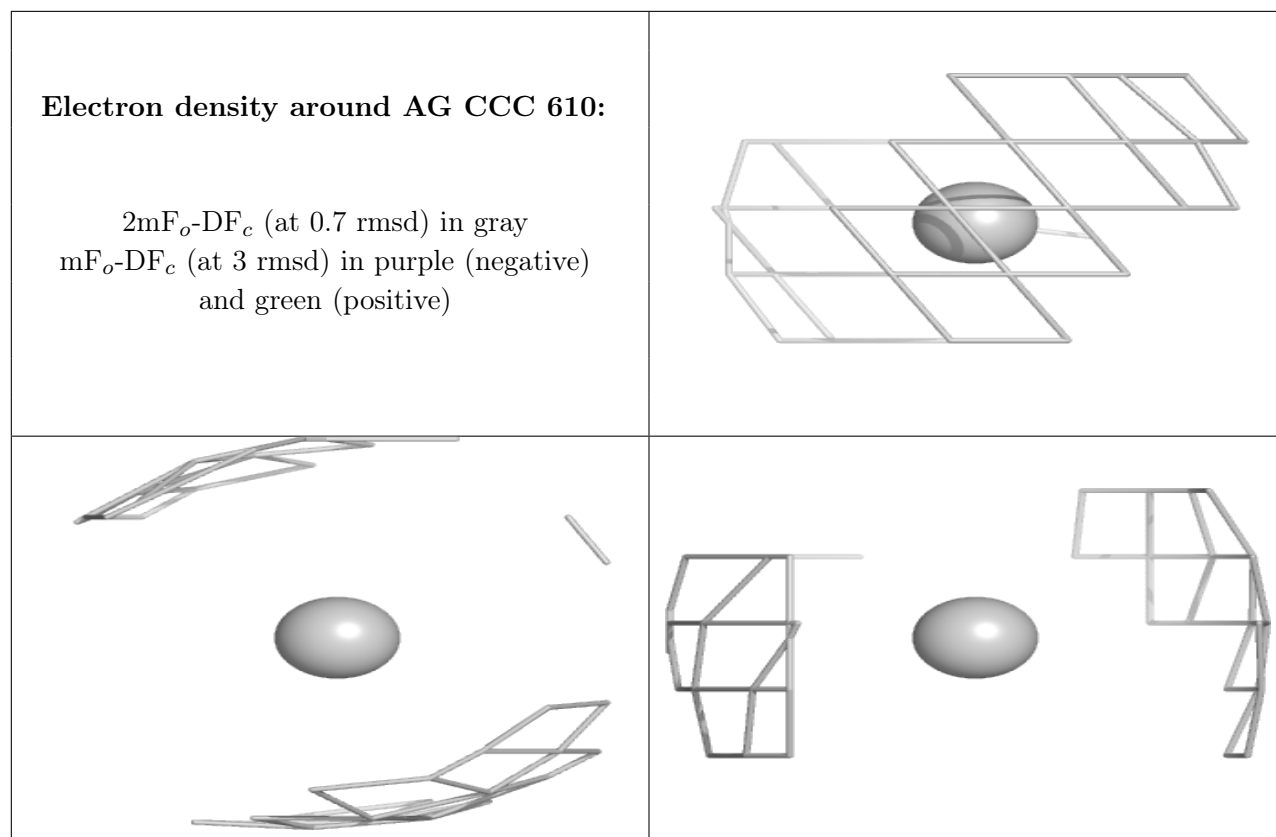
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	SO4	CCC	619	5/5	0.61	0.25	51,54,65,66	5
4	EDO	CCC	614	4/4	0.77	0.17	70,74,75,75	0
5	SO4	AAA	205	5/5	0.81	0.18	67,110,114,148	0
4	EDO	CCC	605	4/4	0.83	0.22	54,66,68,69	0
4	EDO	AAA	204	4/4	0.86	0.13	36,53,57,57	0
5	SO4	BBB	203	5/5	0.89	0.30	100,104,115,121	0
5	SO4	BBB	202	5/5	0.89	0.13	82,95,110,111	0
4	EDO	CCC	611	4/4	0.90	0.13	51,55,56,63	0
4	EDO	CCC	604	4/4	0.90	0.23	58,65,66,67	0
4	EDO	AAA	203	4/4	0.90	0.15	53,57,60,65	0
5	SO4	BBB	201	5/5	0.91	0.19	108,111,118,140	0
5	SO4	CCC	615	5/5	0.91	0.13	68,73,79,91	0
4	EDO	CCC	603	4/4	0.91	0.13	63,71,74,75	0
4	EDO	CCC	613	4/4	0.92	0.17	52,61,62,64	0
5	SO4	CCC	617	5/5	0.92	0.11	82,82,85,95	5
4	EDO	CCC	608	4/4	0.92	0.15	48,50,53,53	0
5	SO4	AAA	206	5/5	0.94	0.13	83,90,91,95	5
5	SO4	CCC	616	5/5	0.94	0.22	68,79,103,104	0
4	EDO	CCC	612	4/4	0.95	0.19	51,55,56,61	0
4	EDO	CCC	607	4/4	0.96	0.09	37,43,44,45	0
4	EDO	AAA	201	4/4	0.97	0.08	45,45,45,45	0
4	EDO	AAA	202	4/4	0.97	0.13	43,47,47,48	0
7	O	CCC	606	1/1	0.97	0.08	34,34,34,34	0
6	NI	CCC	601	1/1	0.99	0.08	37,37,37,37	0
6	NI	CCC	602	1/1	0.99	0.09	39,39,39,39	0
5	SO4	CCC	618	5/5	0.99	0.06	40,42,42,45	0
8	AG	CCC	609	1/1	1.00	0.07	43,43,43,43	0
8	AG	CCC	610	1/1	1.00	0.07	43,43,43,43	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 AG CCC 609:**

$2mF_o-DF_c$  (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.