



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 3, 2024 – 07:29 AM EST

PDB ID : 6CZ9  
Title : The arsenate respiratory reductase (Arr) complex from *Shewanella* sp. ANA-3 bound to arsenite  
Authors : Glasser, N.R.; Newman, D.K.  
Deposited on : 2018-04-08  
Resolution : 1.80 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

<http://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

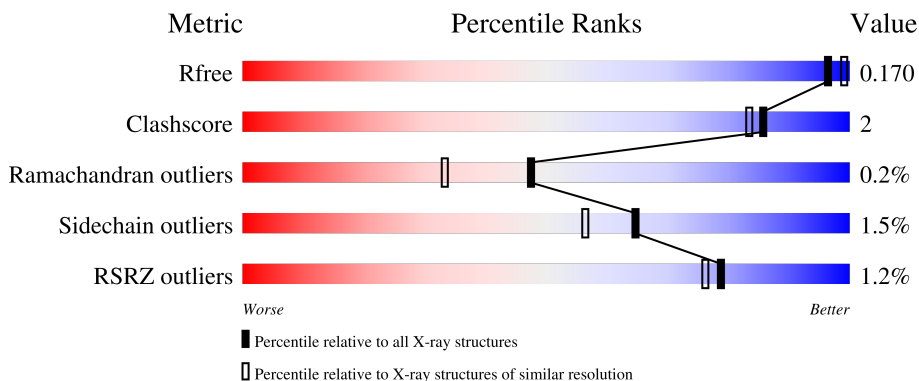
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	814	 94% 6%
1	C	814	 94% 5%
2	B	234	 93% 7%
2	D	234	 92% 8%

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:

<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
6	AST	C	905	-	-	X	-
7	FMT	A	907	-	-	X	-

## 2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 34836 atoms, of which 15897 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 ArrA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	814	12544	4070	6163	1105	1179	27	0	4	0
1	C	807	12546	4063	6176	1103	1176	28	0	5	0

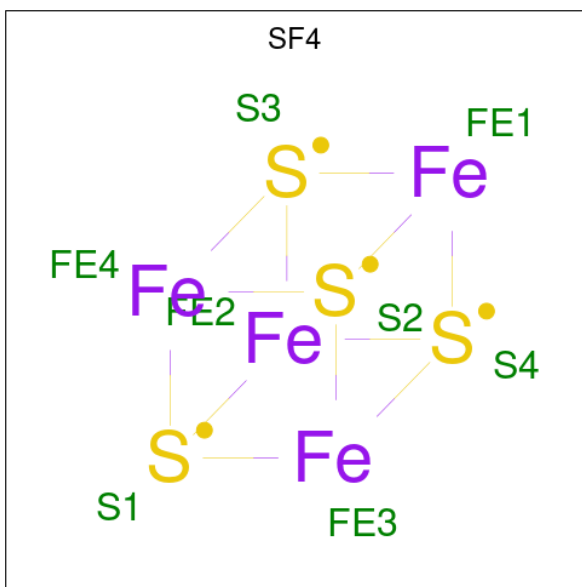
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	41	GLY	-	expression tag	UNP Q7WTU0
C	41	GLY	-	expression tag	UNP Q7WTU0

- Molecule 2 is a protein called 4Fe-4S ferredoxin, iron-sulfur binding domain protein.

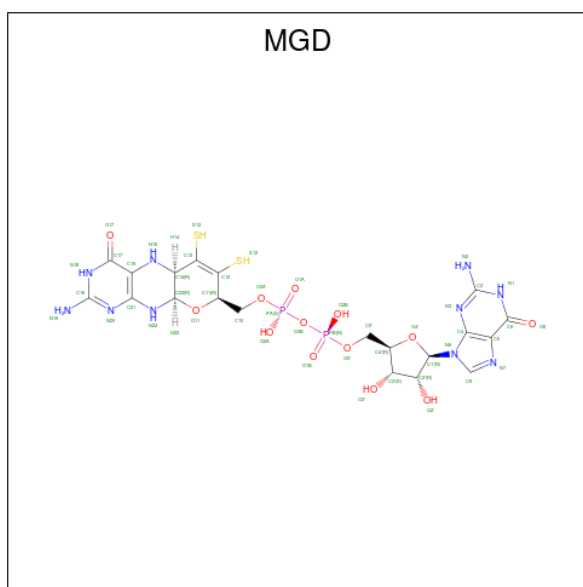
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	B	234	3516	1106	1724	321	342	23	0	4	0
2	D	234	3472	1098	1695	317	339	23	0	5	0

- Molecule 3 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe<sub>4</sub>S<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Fe	S	0	0
			8	4	4		
3	B	1	Total	Fe	S	0	0
			8	4	4		
3	B	1	Total	Fe	S	0	0
			8	4	4		
3	B	1	Total	Fe	S	0	0
			8	4	4		
3	B	1	Total	Fe	S	0	0
			8	4	4		
3	C	1	Total	Fe	S	0	0
			8	4	4		
3	D	1	Total	Fe	S	0	0
			8	4	4		
3	D	1	Total	Fe	S	0	0
			8	4	4		
3	D	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 4 is 2-AMINO-5,6-DIMERCAPTO-7-METHYL-3,7,8A,9-TETRAHYDRO-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-4-ONE GUANOSINE DINUCLEOTIDE (three-letter code: MGD) (formula: C<sub>20</sub>H<sub>26</sub>N<sub>10</sub>O<sub>13</sub>P<sub>2</sub>S<sub>2</sub>).

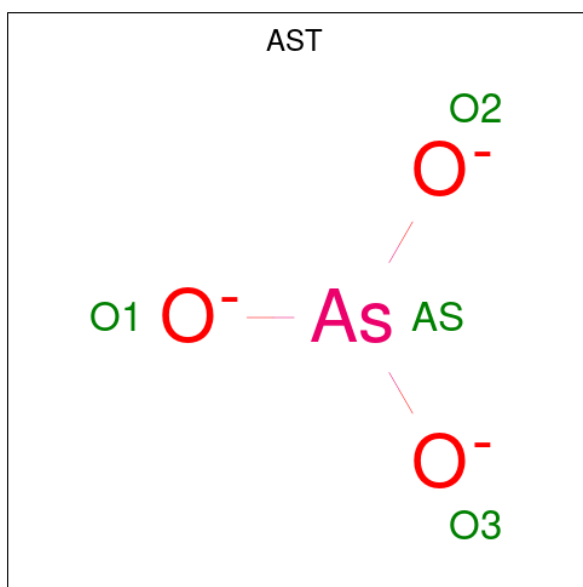


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	
			Total	C	H	N	O	P			S
4	A	1	Total	C	H	N	O	P	S	0	0
			68	20	21	10	13	2	2		
4	A	1	Total	C	H	N	O	P	S	0	0
			69	20	22	10	13	2	2		
4	C	1	Total	C	H	N	O	P	S	0	0
			68	20	21	10	13	2	2		
4	C	1	Total	C	H	N	O	P	S	0	0
			68	20	21	10	13	2	2		

- Molecule 5 is MOLYBDENUM ATOM (three-letter code: MO) (formula: Mo).

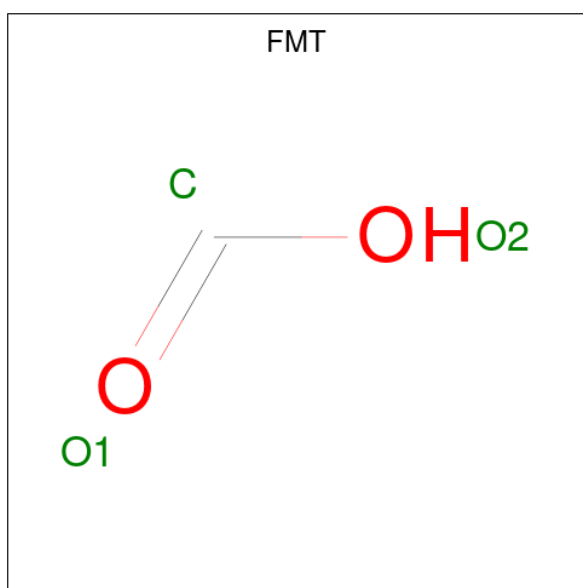
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mo	0	0
			1	1		
5	C	1	Total	Mo	0	0
			1	1		

- Molecule 6 is ARSENITE (three-letter code: AST) (formula: AsO<sub>3</sub>).



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

- Molecule 7 is FORMIC ACID (three-letter code: FMT) (formula:  $\text{CH}_2\text{O}_2$ ).



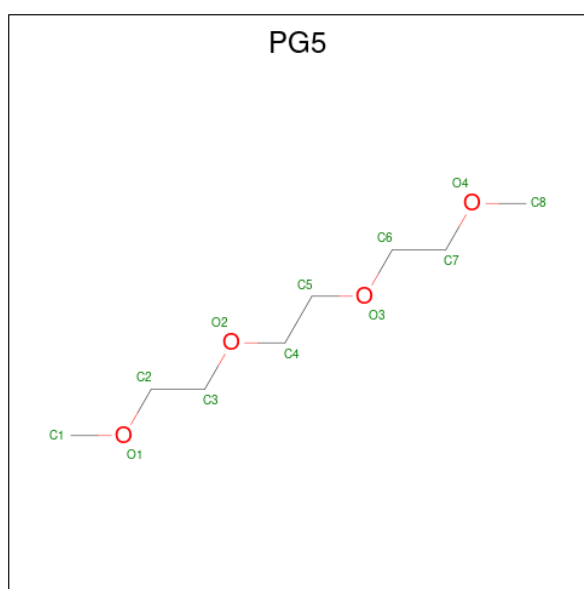
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	H	O	0	0
			4	1	1	2		
7	A	1	Total	C	H	O	0	0
			4	1	1	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	H	O	0	0
			4	1	1	2		
7	A	1	Total	C	H	O	0	0
			4	1	1	2		
7	B	1	Total	C	H	O	0	0
			4	1	1	2		
7	C	1	Total	C	H	O	0	0
			4	1	1	2		
7	C	1	Total	C	H	O	0	0
			4	1	1	2		
7	C	1	Total	C	H	O	0	0
			4	1	1	2		

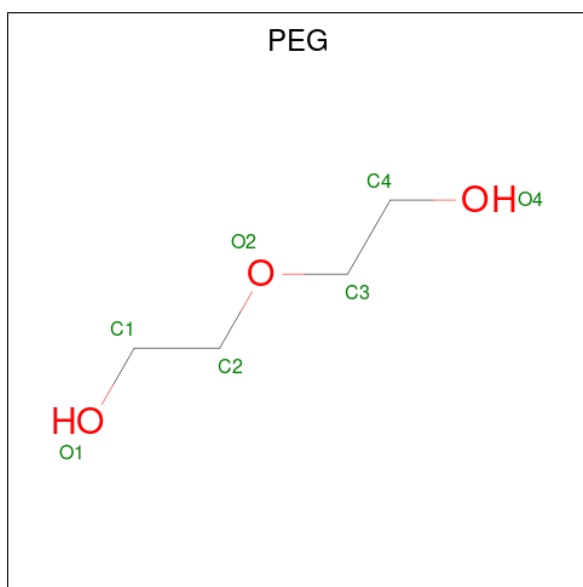
- Molecule 8 is 1-METHOXY-2-[2-(2-METHOXY-ETHOXY)]-ETHANE (three-letter code: PG5) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	H	O	0	0
			30	8	18	4		
8	C	1	Total	C	H	O	0	0
			30	8	18	4		

- Molecule 9 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
9	D	1	17	4	10	3	0	0

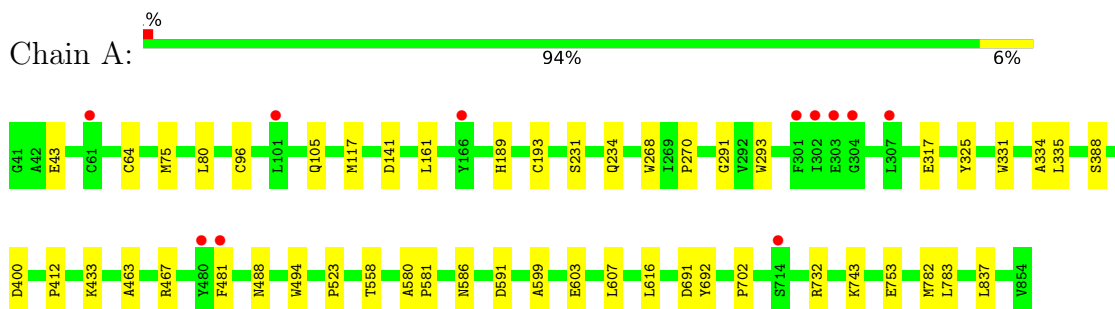
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	770	Total	O	0	0
			770	770		
10	B	303	Total	O	0	0
			303	303		
10	C	938	Total	O	0	0
			938	938		
10	D	275	Total	O	0	0
			275	275		

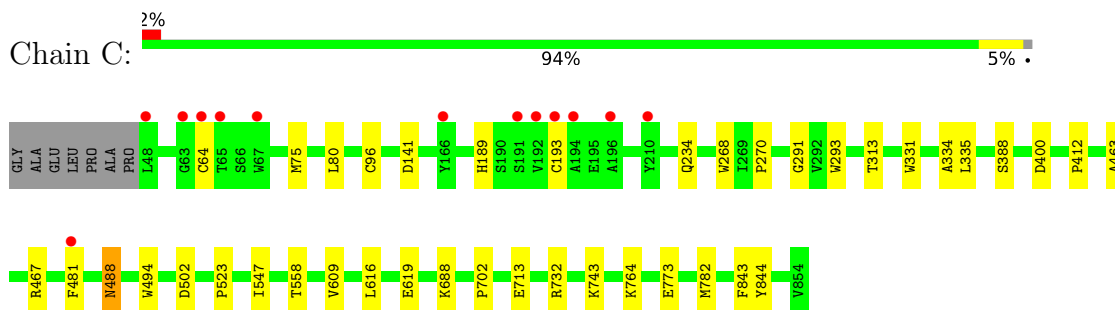
### 3 Residue-property plots [i](#)

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.

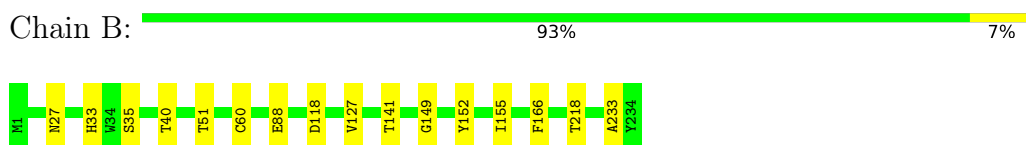
- Molecule 1: ArrA



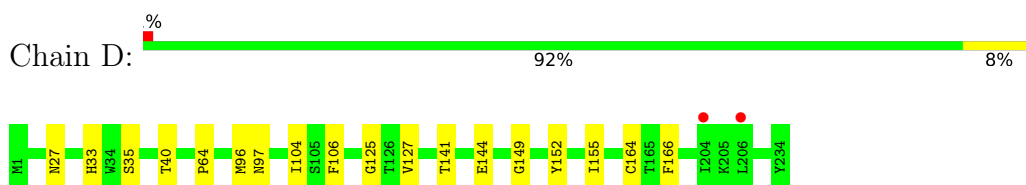
- Molecule 1: ArrA



- Molecule 2: 4Fe-4S ferredoxin, iron-sulfur binding domain protein



- Molecule 2: 4Fe-4S ferredoxin, iron-sulfur binding domain protein



## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	232.51Å 86.31Å 147.37Å 90.00° 127.72° 90.00°	Depositor
Resolution (Å)	39.37 – 1.80 38.88 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.0 (39.37-1.80) 97.9 (38.88-1.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.86 (at 1.81Å)	Xtrriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, $R_{free}$	0.142 , 0.169 0.143 , 0.170	Depositor DCC
$R_{free}$ test set	2594 reflections (1.24%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.8	Xtrriage
Anisotropy	0.392	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 55.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.009 for -h-2*1,-k,l	Xtrriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	34836	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% 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: PEG, MO, AST, MGD, SF4, PG5, FMT

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	0.30	0/6567	0.51	0/8911
1	C	0.31	0/6557	0.53	0/8887
2	B	0.30	0/1843	0.55	0/2505
2	D	0.30	0/1831	0.55	0/2493
All	All	0.31	0/16798	0.53	0/22796

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	6381	6163	6181	28	0
1	C	6370	6176	6197	23	0
2	B	1792	1724	1732	9	0
2	D	1777	1695	1703	10	0
3	A	8	0	0	0	0
3	B	32	0	0	1	0
3	C	8	0	0	0	0
3	D	32	0	0	2	0
4	A	94	43	43	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	94	42	42	1	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
6	A	4	0	0	1	0
6	C	4	0	0	2	0
7	A	12	4	4	2	0
7	B	3	1	1	0	0
7	C	9	3	3	1	0
8	A	12	18	18	1	0
8	C	12	18	18	0	0
9	D	7	10	10	0	0
10	A	770	0	0	9	1
10	B	303	0	0	3	2
10	C	938	0	0	8	1
10	D	275	0	0	2	1
All	All	18939	15897	15952	72	3

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 2.

The worst 5 of 72 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:C:713:GLU:OE1	10:C:1001:HOH:O	1.88	0.92
1:C:313:THR:OG1	10:C:1002:HOH:O	1.94	0.86
1:A:43:GLU:OE2	10:A:1001:HOH:O	1.99	0.80
1:A:193:CYS:SG	6:A:905:AST:AS	3.01	0.79
1:A:325:TYR:OH	10:A:1002:HOH:O	2.02	0.77

All (3) 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)
10:A:1418:HOH:O	10:B:492:HOH:O[4_546]	1.97	0.23
10:C:1013:HOH:O	10:C:1669:HOH:O[4_555]	2.16	0.04
10:B:656:HOH:O	10:D:561:HOH:O[4_556]	2.19	0.01

## 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	A	816/814 (100%)	786 (96%)	29 (4%)	1 (0%)	51	36
1	C	810/814 (100%)	782 (96%)	27 (3%)	1 (0%)	51	36
2	B	236/234 (101%)	230 (98%)	5 (2%)	1 (0%)	34	21
2	D	237/234 (101%)	232 (98%)	3 (1%)	2 (1%)	19	7
All	All	2099/2096 (100%)	2030 (97%)	64 (3%)	5 (0%)	47	33

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	334	ALA
1	C	334	ALA
2	B	127	VAL
2	D	127	VAL
2	D	125	GLY

### 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	660/672 (98%)	650 (98%)	10 (2%)	65	56
1	C	663/672 (99%)	654 (99%)	9 (1%)	67	59
2	B	201/201 (100%)	198 (98%)	3 (2%)	65	56
2	D	197/201 (98%)	193 (98%)	4 (2%)	55	44
All	All	1721/1746 (99%)	1695 (98%)	26 (2%)	65	56

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	141	ASP
1	C	400	ASP
2	D	164	CYS
1	C	234	GLN
1	C	481	PHE

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

### 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 29 ligands modelled in this entry, 2 are monoatomic - leaving 27 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	$\# Z  > 2$
3	SF4	D	303	2	0,12,12	-	-	-		
3	SF4	B	301	2	0,12,12	-	-	-		
7	FMT	C	906	-	2,2,2	0.75	0	1,1,1	0.44	0
9	PEG	D	305	-	6,6,6	0.45	0	5,5,5	1.15	0
7	FMT	C	908	-	2,2,2	0.69	0	1,1,1	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
7	FMT	A	906	-	2,2,2	0.81	0	1,1,1	0.51	0
8	PG5	A	910	-	11,11,11	0.52	0	10,10,10	0.21	0
7	FMT	A	907	-	2,2,2	0.72	0	1,1,1	0.48	0
3	SF4	B	302	2	0,12,12	-	-	-	-	-
3	SF4	A	901	1	0,12,12	-	-	-	-	-
7	FMT	A	909	-	2,2,2	0.77	0	1,1,1	0.54	0
6	AST	A	905	-	0,3,3	-	-	0,3,3	-	-
3	SF4	B	303	2	0,12,12	-	-	-	-	-
3	SF4	D	304	2	0,12,12	-	-	-	-	-
7	FMT	B	305	-	2,2,2	0.77	0	1,1,1	0.46	0
4	MGD	A	903	5	41,52,52	5.18	27 (65%)	40,81,81	2.68	12 (30%)
3	SF4	B	304	2	0,12,12	-	-	-	-	-
4	MGD	C	903	5	41,52,52	5.04	28 (68%)	40,81,81	2.43	11 (27%)
4	MGD	A	902	5	41,52,52	5.03	28 (68%)	40,81,81	2.74	13 (32%)
7	FMT	C	907	-	2,2,2	0.87	0	1,1,1	0.41	0
4	MGD	C	902	5	41,52,52	4.81	29 (70%)	40,81,81	2.89	14 (35%)
3	SF4	C	901	1	0,12,12	-	-	-	-	-
6	AST	C	905	-	0,3,3	-	-	0,3,3	-	-
8	PG5	C	909	-	11,11,11	0.50	0	10,10,10	0.44	0
7	FMT	A	908	-	2,2,2	0.64	0	1,1,1	0.31	0
3	SF4	D	302	2	0,12,12	-	-	-	-	-
3	SF4	D	301	2	0,12,12	-	-	-	-	-

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	SF4	B	304	2	-	-	0/6/5/5
4	MGD	C	903	5	-	2/18/66/66	0/6/6/6
3	SF4	D	303	2	-	-	0/6/5/5
4	MGD	A	902	5	-	4/18/66/66	0/6/6/6
4	MGD	C	902	5	-	3/18/66/66	0/6/6/6
8	PG5	A	910	-	-	3/9/9/9	-
3	SF4	B	301	2	-	-	0/6/5/5
3	SF4	C	901	1	-	-	0/6/5/5
9	PEG	D	305	-	-	2/4/4/4	-
3	SF4	B	303	2	-	-	0/6/5/5
8	PG5	C	909	-	-	6/9/9/9	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SF4	A	901	1	-	-	0/6/5/5
3	SF4	B	302	2	-	-	0/6/5/5
3	SF4	D	304	2	-	-	0/6/5/5
3	SF4	D	302	2	-	-	0/6/5/5
3	SF4	D	301	2	-	-	0/6/5/5
4	MGD	A	903	5	-	1/18/66/66	0/6/6/6

The worst 5 of 112 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	903	MGD	C16-C21	13.01	1.60	1.38
4	A	902	MGD	C16-C21	12.97	1.60	1.38
4	C	903	MGD	C16-C21	12.78	1.60	1.38
4	A	903	MGD	O11-C11	12.53	1.60	1.43
4	C	903	MGD	O11-C11	12.51	1.60	1.43

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	902	MGD	O11-C23-N22	-14.16	94.02	108.57
4	A	902	MGD	O11-C23-N22	-13.47	94.72	108.57
4	A	903	MGD	O11-C23-C14	12.01	116.97	108.96
4	C	903	MGD	O11-C23-C14	9.83	115.52	108.96
4	C	903	MGD	O11-C23-N22	6.86	115.62	108.57

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	902	MGD	PB-O3B-PA-O3A
4	C	902	MGD	PB-O3B-PA-O3A
8	A	910	PG5	O3-C6-C7-O4
8	C	909	PG5	O2-C4-C5-O3
9	D	305	PEG	O1-C1-C2-O2

There are no ring outliers.

10 monomers are involved in 13 short contacts:

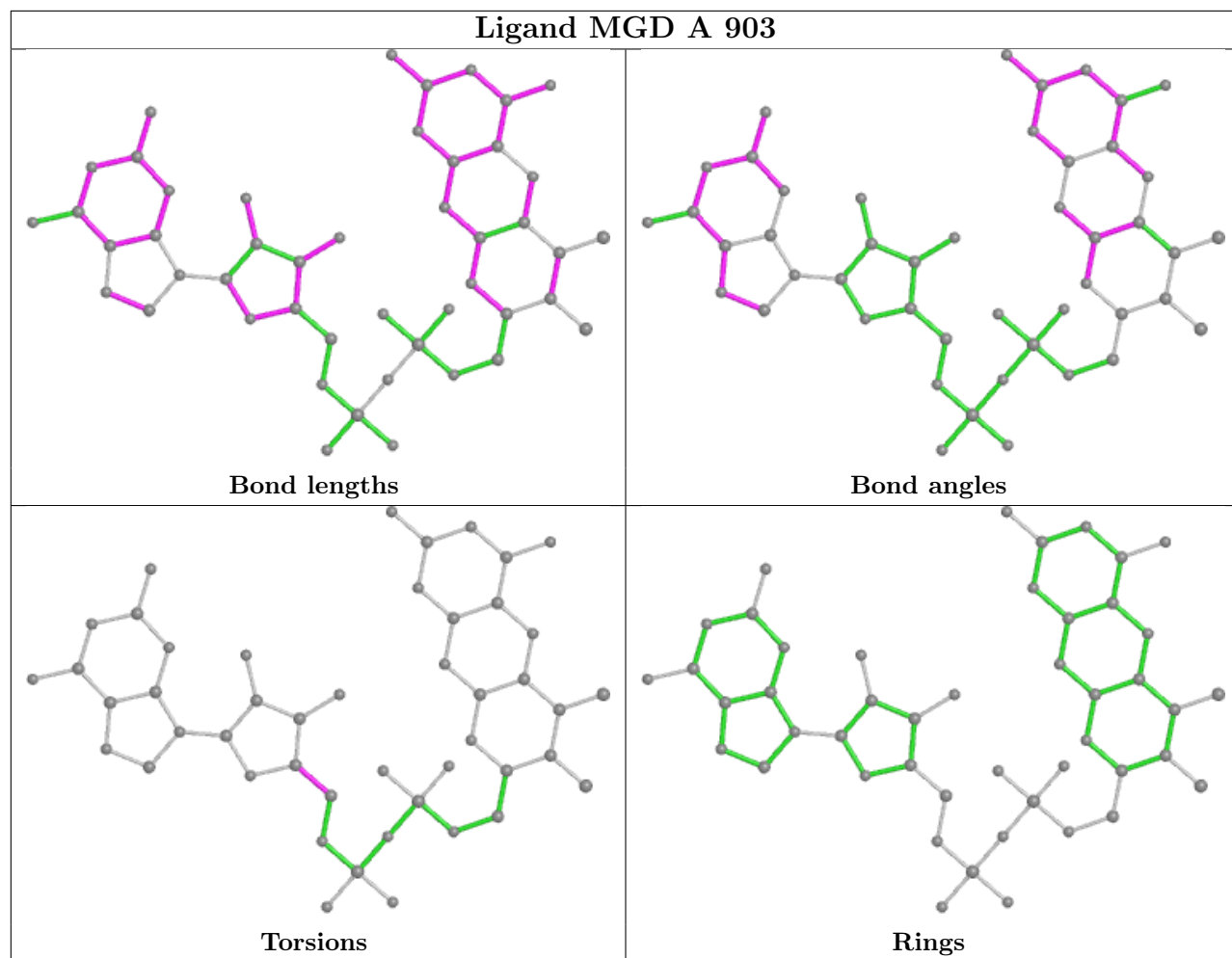
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	303	SF4	1	0
8	A	910	PG5	1	0

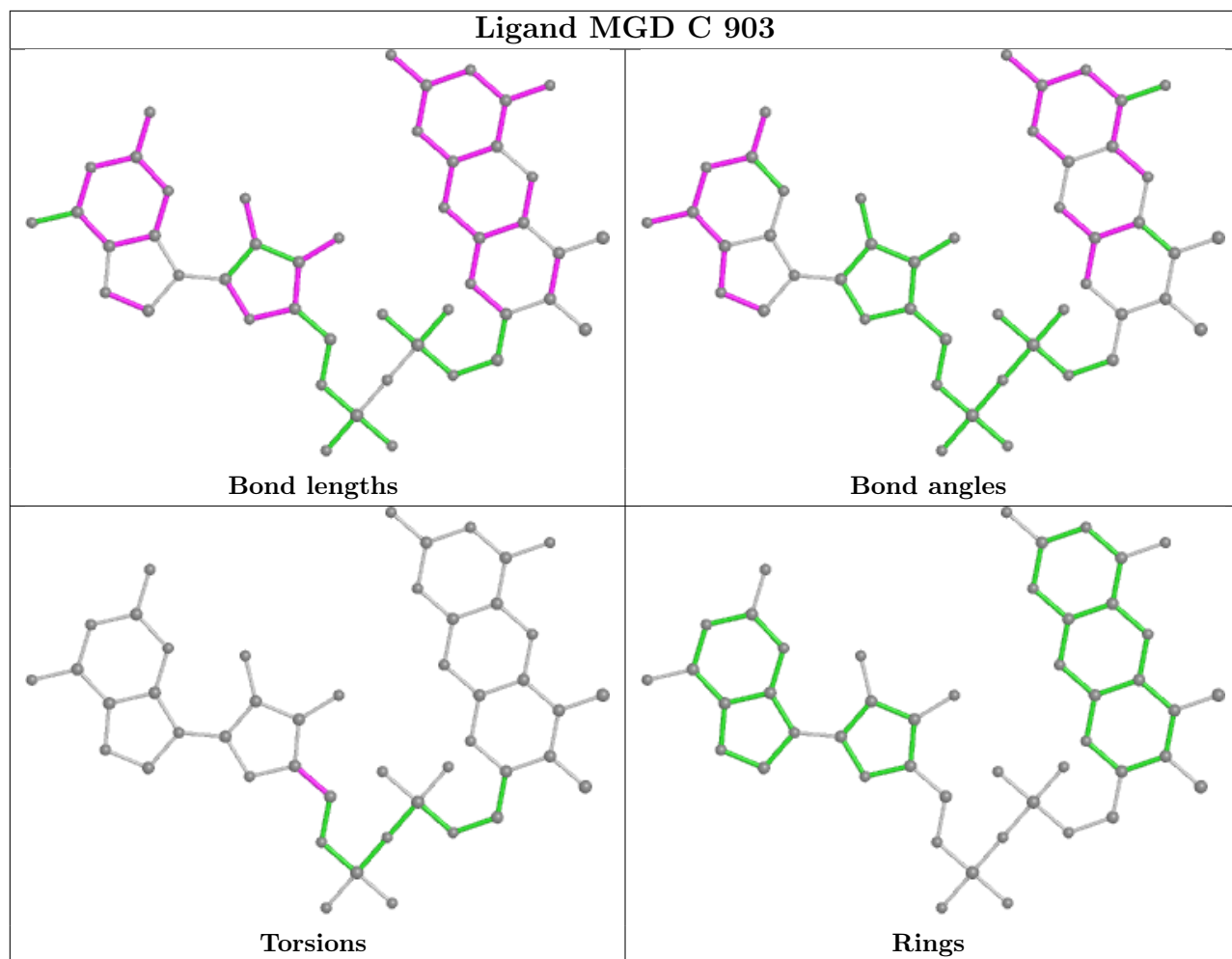
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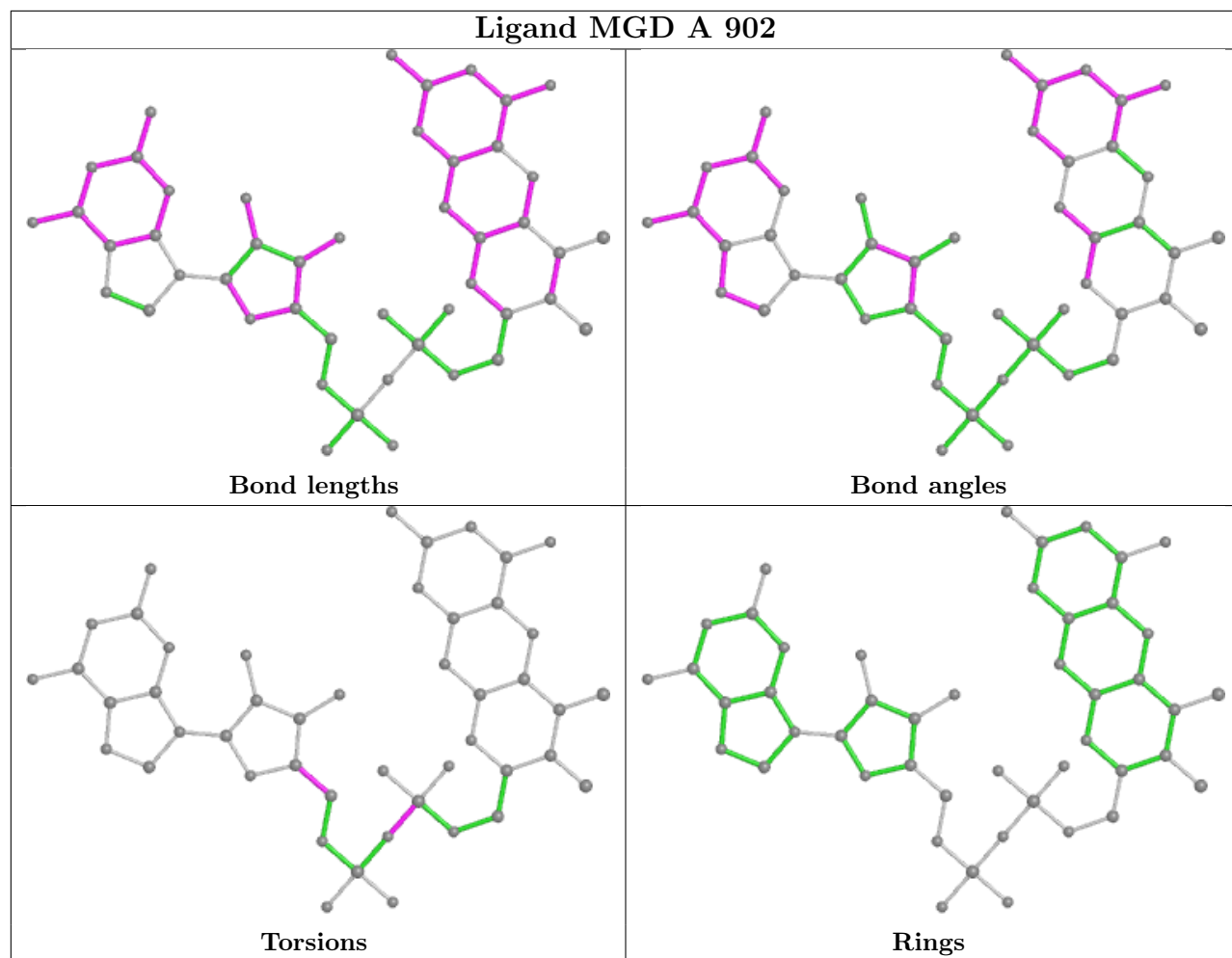
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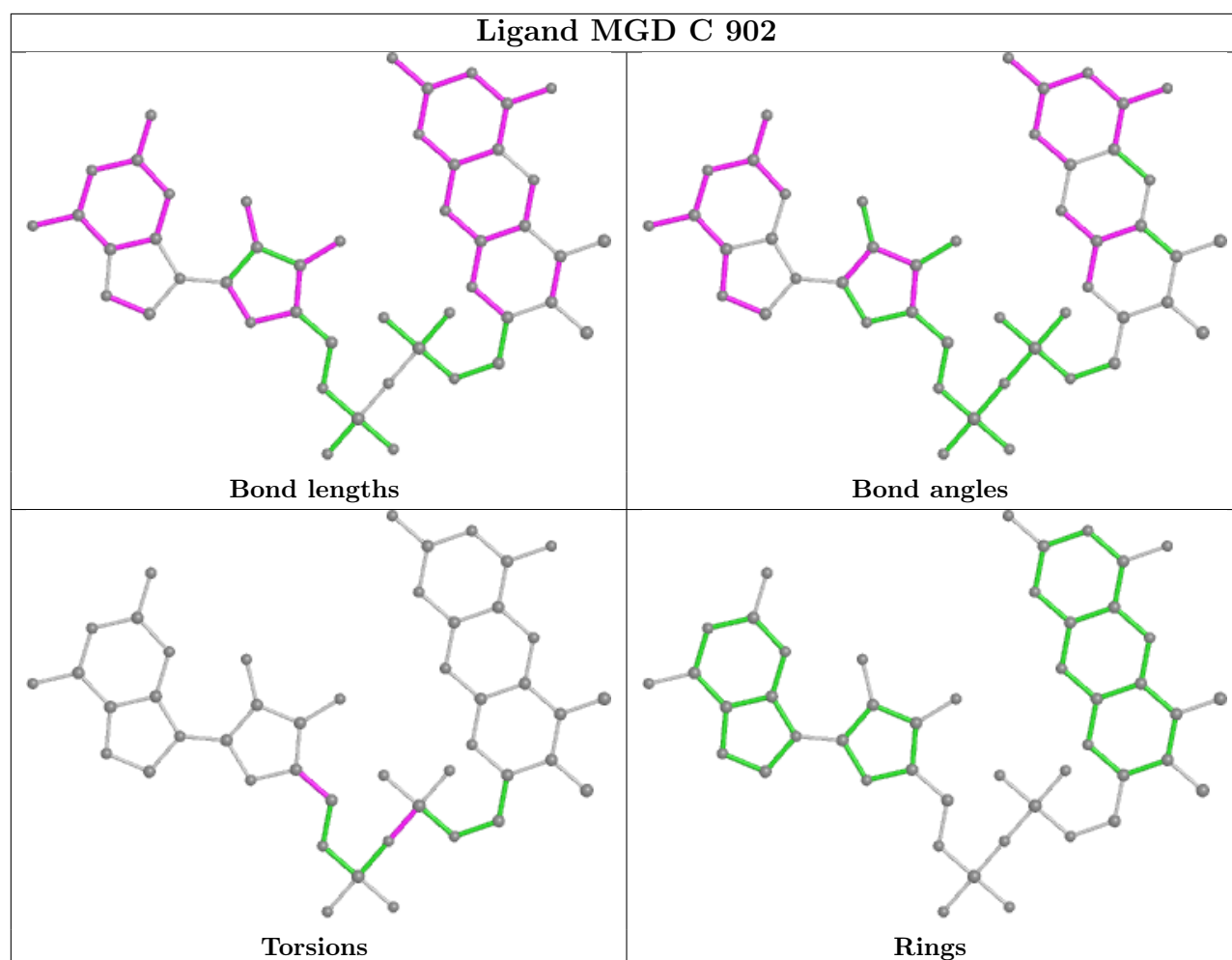
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	907	FMT	2	0
3	B	302	SF4	1	0
6	A	905	AST	1	0
4	A	902	MGD	2	0
7	C	907	FMT	1	0
4	C	902	MGD	1	0
6	C	905	AST	2	0
3	D	302	SF4	1	0

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 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	814/814 (100%)	-0.18	11 (1%) 75 72	20, 33, 54, 80	0
1	C	807/814 (99%)	-0.34	13 (1%) 72 68	19, 26, 42, 72	0
2	B	234/234 (100%)	-0.60	0 100 100	20, 27, 45, 69	0
2	D	234/234 (100%)	-0.44	2 (0%) 84 82	21, 27, 45, 70	0
All	All	2089/2096 (99%)	-0.32	26 (1%) 79 76	19, 29, 49, 80	0

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	48	LEU	5.1
1	A	481	PHE	3.8
1	A	302	ILE	3.5
1	A	307	LEU	3.4
1	C	194	ALA	2.8

### 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.

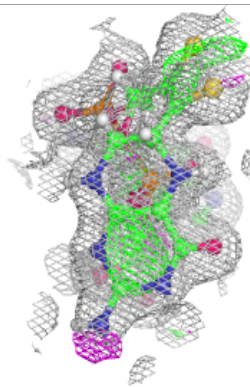
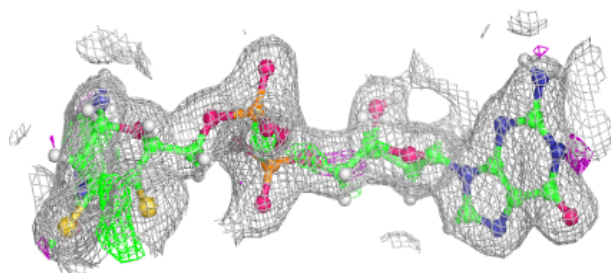
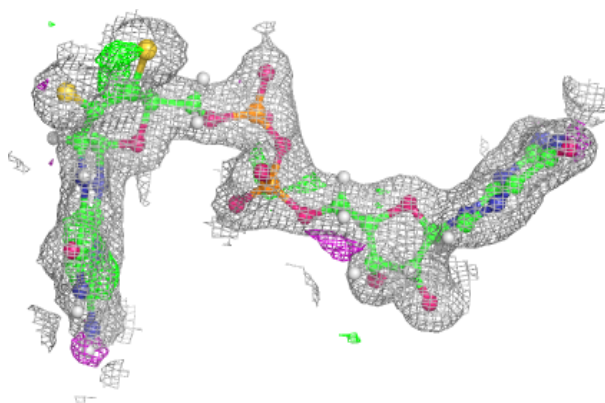
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
6	AST	C	905	4/4	0.70	0.33	19,26,31,66	4
8	PG5	A	910	12/12	0.82	0.26	50,68,85,86	0
9	PEG	D	305	7/7	0.82	0.17	42,62,83,98	0
8	PG5	C	909	12/12	0.84	0.16	45,63,73,95	0
7	FMT	A	909	3/3	0.93	0.13	39,41,64,77	0
7	FMT	A	906	3/3	0.94	0.14	34,41,50,50	0
7	FMT	A	908	3/3	0.95	0.07	28,34,50,60	0
4	MGD	A	902	47/47	0.96	0.16	20,26,33,35	0
4	MGD	C	902	47/47	0.97	0.16	18,22,27,29	0
6	AST	A	905	4/4	0.97	0.21	20,25,25,35	4
4	MGD	A	903	47/47	0.97	0.17	24,26,32,34	0
7	FMT	B	305	3/3	0.98	0.11	41,50,54,65	0
7	FMT	C	906	3/3	0.98	0.09	27,31,33,35	0
7	FMT	C	907	3/3	0.98	0.33	8,9,49,51	0
7	FMT	C	908	3/3	0.98	0.15	31,37,37,44	0
4	MGD	C	903	47/47	0.98	0.17	17,21,25,29	0
3	SF4	D	301	8/8	0.98	0.06	23,24,25,25	0
3	SF4	B	301	8/8	0.98	0.06	23,23,24,25	0
3	SF4	D	304	8/8	0.99	0.05	24,25,25,25	0
3	SF4	B	302	8/8	0.99	0.06	20,21,21,21	0
3	SF4	B	303	8/8	0.99	0.05	22,23,23,24	0
3	SF4	B	304	8/8	0.99	0.04	26,27,28,28	0
3	SF4	C	901	8/8	0.99	0.08	19,20,20,20	0
3	SF4	A	901	8/8	0.99	0.10	20,21,21,21	0
3	SF4	D	302	8/8	0.99	0.06	21,22,22,22	0
3	SF4	D	303	8/8	0.99	0.05	24,25,25,26	0
7	FMT	A	907	3/3	0.99	0.28	13,15,20,89	0
5	MO	C	904	1/1	1.00	0.10	23,23,23,23	0
5	MO	A	904	1/1	1.00	0.09	28,28,28,28	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.

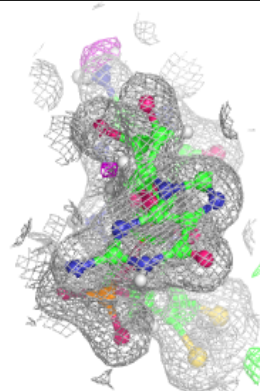
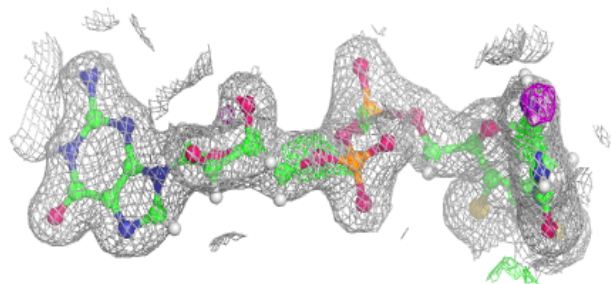
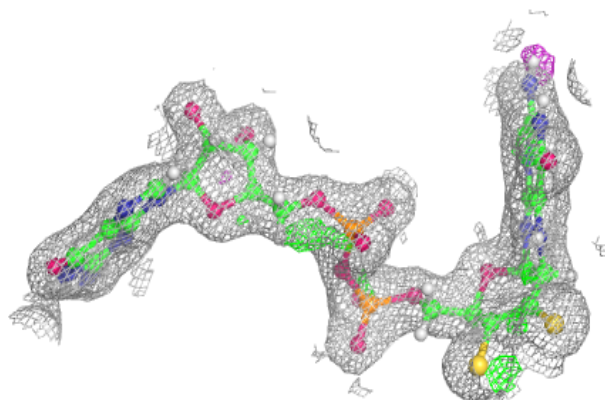


**Electron density around MGD A 902:**

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

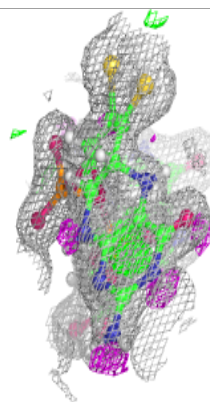
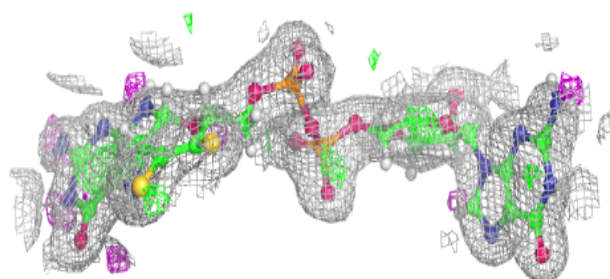
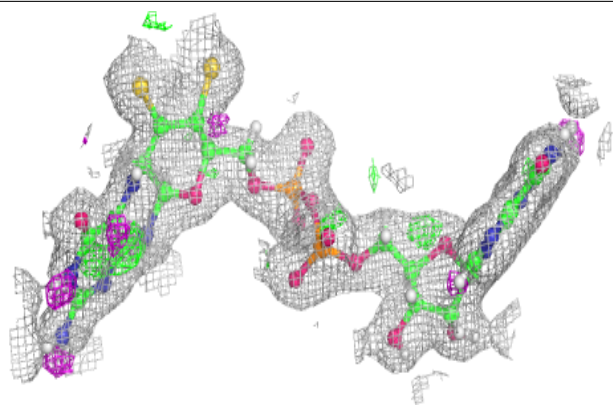
**Electron density around MGD C 902:**

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

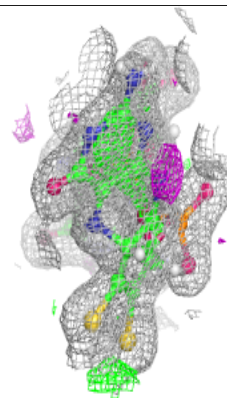
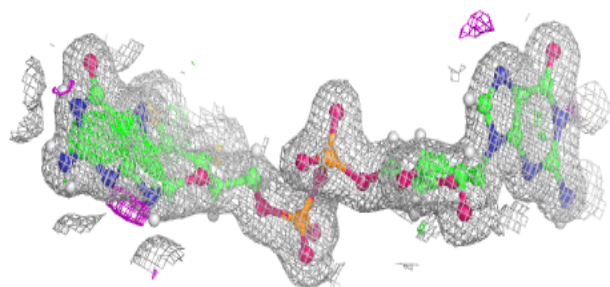
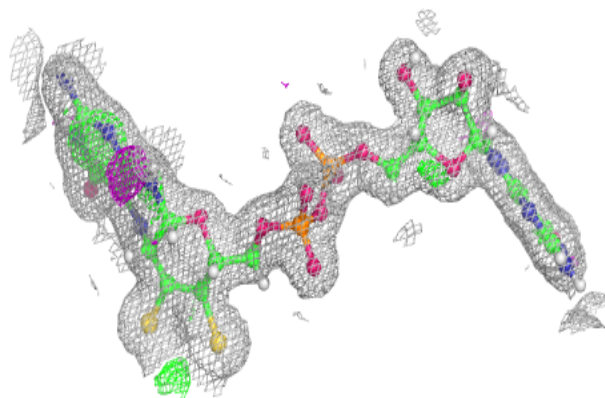


**Electron density around MGD A 903:**

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

**Electron density around MGD C 903:**

$2mF_o-DF_c$  (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.