Full wwPDB X-ray Structure Validation Report (i)

Jul 3, 2024 – 11:01 AM EDT

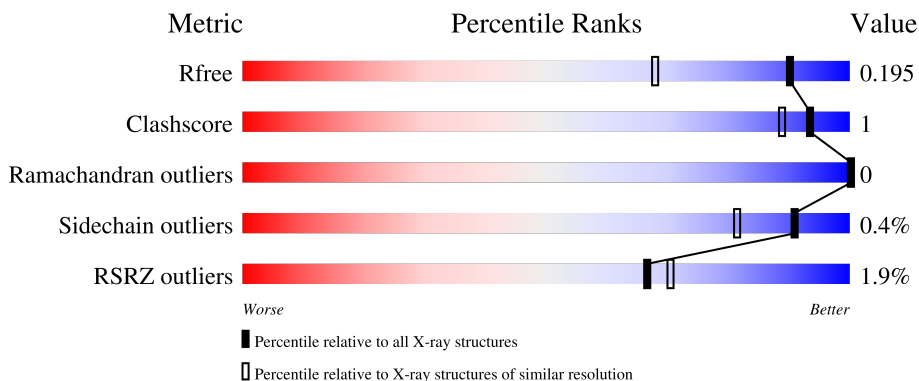|		
PDB ID	:	8VMT
Title	:	Homing endonuclease I-PpoI-DNA complex:reaction at pH7.0 (K+ MES) with 500 uM Mg2+ for 160s
Authors	:	Chang, C.; Gao, Y.
Deposited on	:	2024-01-13
Resolution	:	1.48 Å(reported)

1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
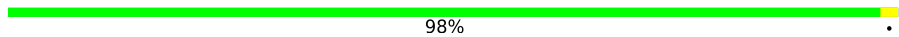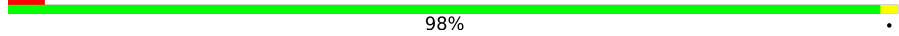*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.48 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		0.195
Clashscore		1
Ramachandran outliers		0
Sidechain outliers		0.4%
RSRZ outliers		1.9%

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	4690 (1.50-1.46)
Clashscore	141614	4955 (1.50-1.46)
Ramachandran outliers	138981	4846 (1.50-1.46)
Sidechain outliers	138945	4844 (1.50-1.46)
RSRZ outliers	127900	4614 (1.50-1.46)

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	C	21	76% 19% 5%
1	D	21	81% 19%
2	A	162	98% •
2	B	162	4% 98% •

2 Entry composition ⓘ

There are 7 unique types of molecules in this entry. The entry contains 3838 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 DNA chain called DNA (5'-D(*TP*TP*GP*AP*CP*TP*CP*TP*CP*TP* TP*AP*AP*GP*AP*GP*AP*GP*TP*CP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	21	Total	C	N	O	P	0	2	0
			471	226	86	137	22			
1	D	21	Total	C	N	O	P	0	2	0
			471	226	86	137	22			

- Molecule 2 is a protein called Intron-encoded endonuclease I-PpoI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	162	Total	C	N	O	S	0	0	0
			1245	786	232	219	8			
2	B	162	Total	C	N	O	S	0	1	0
			1249	789	232	220	8			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total	Na	0	0
			1	1		
4	D	1	Total	Na	0	0
			1	1		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

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GOL

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total 6	C 3	O 3	0	0
5	D	1	Total 6	C 3	O 3	0	0
5	A	1	Total 6	C 3	O 3	0	0
5	A	1	Total 6	C 3	O 3	0	0
5	B	1	Total 6	C 3	O 3	0	0

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total 2	Zn 2	0	0
6	B	2	Total 2	Zn 2	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	41	Total 41	O 41	0	0
7	D	46	Total 46	O 46	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	143	Total 143	O 143	0	1
7	B	134	Total 134	O 134	0	1

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.
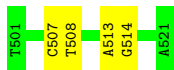
• Molecule 1: DNA (5'-D(*TP*TP*GP*AP*CP*TP*CP*TP*CP*TP*TP*AP*AP*GP*AP*GP *AP*GP*TP*CP*A)-3')

Chain C:

76%   19%   5%

• Molecule 1: DNA (5'-D(*TP*TP*GP*AP*CP*TP*CP*TP*CP*TP*TP*AP*AP*GP*AP*GP *AP*GP*TP*CP*A)-3')
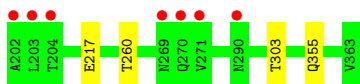
Chain D:

81%   19%

• Molecule 2: Intron-encoded endonuclease I-PpoI

Chain A:

98%

• Molecule 2: Intron-encoded endonuclease I-PpoI

Chain B:

4%

98%

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	113.58Å 113.58Å 87.99Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.18 – 1.48 49.18 – 1.48	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.18-1.48) 100.0 (49.18-1.48)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.13 (at 1.48Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.179 , 0.196 0.178 , 0.195	Depositor DCC
R_{free} test set	5399 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å^2)	17.2	Xtriage
Anisotropy	0.303	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 37.5	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.023 for -h,-k,l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	3838	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.54% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NA, ZN, GOL, MG

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	C	0.90	2/529 (0.4%)	1.02	1/812 (0.1%)
1	D	0.85	0/529	1.02	0/812
2	A	0.44	0/1286	0.67	0/1760
2	B	0.46	0/1293	0.66	0/1770
All	All	0.61	2/3637 (0.1%)	0.79	1/5154 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	414[B]	DG	OP3-P	6.58	1.69	1.61
1	C	414[A]	DG	OP3-P	6.58	1.69	1.61

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	411	DT	O4'-C1'-N1	-5.15	104.39	108.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	C	471	0	262	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	471	0	262	3	0
2	A	1245	0	1191	2	0
2	B	1249	0	1198	2	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	12	0	16	0	0
5	B	6	0	8	0	0
5	C	6	0	8	0	0
5	D	6	0	8	0	0
6	A	2	0	0	0	0
6	B	2	0	0	0	0
7	A	143	0	0	0	0
7	B	134	0	0	0	0
7	C	41	0	0	0	0
7	D	46	0	0	0	0
All	All	3838	0	2953	9	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 1.

All (9) 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:D:513[B]:DA:O3'	1:D:514[B]:DG:P	2.54	0.66
1:D:513[B]:DA:O3'	1:D:514[B]:DG:OP2	2.24	0.56
2:B:260:THR:HB	2:B:303[B]:THR:HG21	1.92	0.52
1:C:413[B]:DA:O3'	1:C:414[B]:DG:P	2.70	0.49
1:D:507:DC:H2'	1:D:508:DT:C6	2.51	0.46
1:C:413[B]:DA:O3'	1:C:414[B]:DG:OP1	2.35	0.45
2:A:4:THR:OG1	2:A:7:GLN:HG3	2.20	0.41
1:C:407:DC:H2'	1:C:408:DT:C6	2.57	0.40
2:A:108:PRO:HB2	2:B:355:GLN:O	2.21	0.40

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	
2	A	160/162 (99%)	160 (100%)	0	0	100	100
2	B	161/162 (99%)	160 (99%)	1 (1%)	0	100	100
All	All	321/324 (99%)	320 (100%)	1 (0%)	0	100	100

There are no Ramachandran outliers to report.

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	
2	A	133/133 (100%)	133 (100%)	0	100	100
2	B	134/133 (101%)	133 (99%)	1 (1%)	84	68
All	All	267/266 (100%)	266 (100%)	1 (0%)	91	81

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	217	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	69	ASN
2	B	290	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 13 ligands modelled in this entry, 8 are monoatomic - leaving 5 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	GOL	C	503	-	5,5,5	1.24	0	5,5,5	1.05	0
5	GOL	B	403	-	5,5,5	0.09	0	5,5,5	0.28	0
5	GOL	A	603	-	5,5,5	1.30	1 (20%)	5,5,5	1.12	0
5	GOL	D	603	-	5,5,5	1.08	0	5,5,5	1.27	1 (20%)
5	GOL	A	604	-	5,5,5	0.71	0	5,5,5	1.06	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
5	GOL	C	503	-	-	0/4/4/4	-
5	GOL	B	403	-	-	0/4/4/4	-
5	GOL	A	603	-	-	4/4/4/4	-
5	GOL	D	603	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	A	604	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	603	GOL	O2-C2	-2.01	1.37	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	D	603	GOL	C3-C2-C1	-2.04	103.78	111.70

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	603	GOL	O1-C1-C2-C3
5	A	604	GOL	C1-C2-C3-O3
5	A	603	GOL	O2-C2-C3-O3
5	A	603	GOL	O1-C1-C2-O2
5	A	604	GOL	O2-C2-C3-O3
5	A	603	GOL	C1-C2-C3-O3

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	C	1
1	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	413[B]:DA	O3'	414[B]:DG	P	2.70
1	D	513[B]:DA	O3'	514[B]:DG	P	2.54

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	C	21/21 (100%)	-0.24	0	100	100	16, 23, 28, 31	0
1	D	21/21 (100%)	-0.28	0	100	100	16, 23, 28, 31	0
2	A	162/162 (100%)	-0.04	0	100	100	13, 18, 29, 39	0
2	B	162/162 (100%)	0.16	7 (4%)	35	38	14, 18, 37, 50	0
All	All	366/366 (100%)	0.02	7 (1%)	66	70	13, 19, 32, 50	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	202	ALA	4.4
2	B	203	LEU	3.4
2	B	269	ASN	2.8
2	B	290	ASN	2.7
2	B	270	GLN	2.7
2	B	271	VAL	2.3
2	B	204	THR	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

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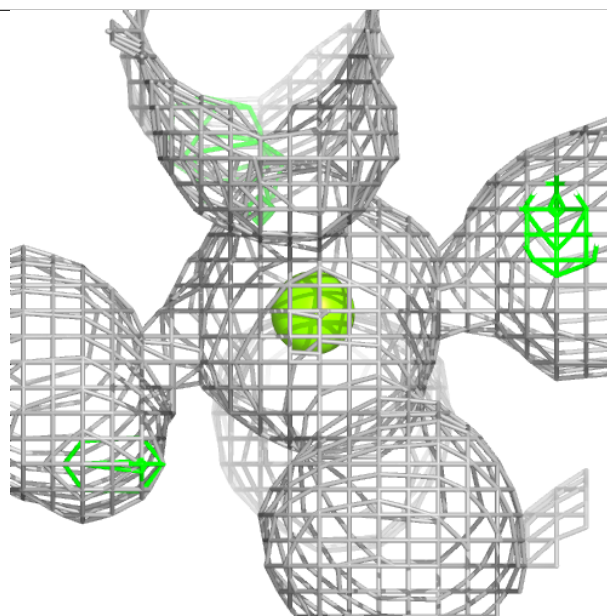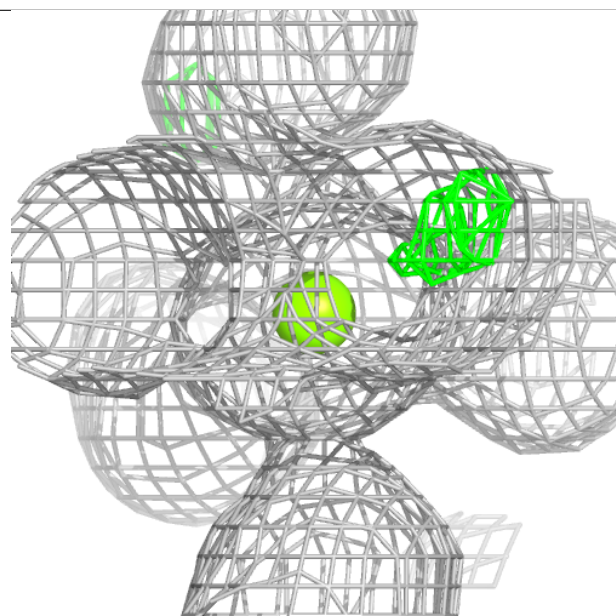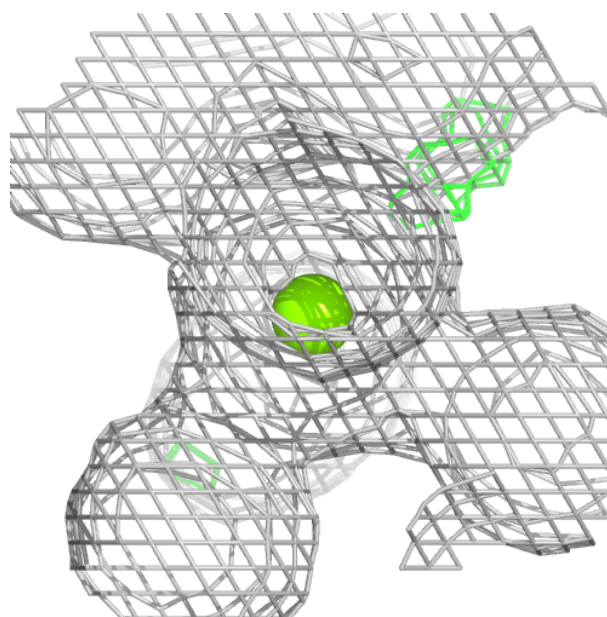PROTEIN DATA BANK

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, 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.
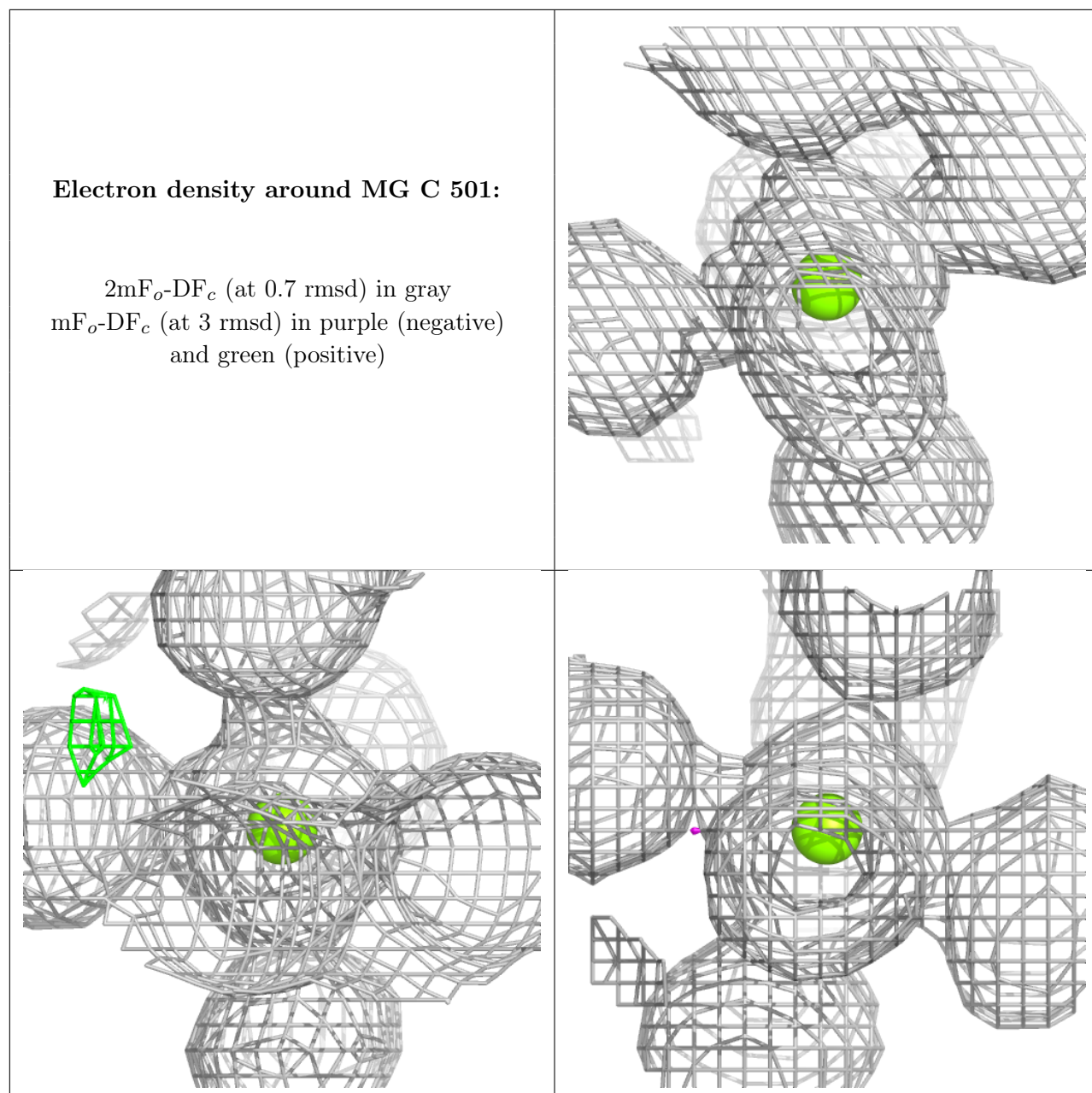
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	GOL	A	604	6/6	0.88	0.32	33,38,42,47	0
5	GOL	D	603	6/6	0.90	0.22	21,28,38,41	0
5	GOL	C	503	6/6	0.91	0.15	24,27,34,41	0
5	GOL	A	603	6/6	0.93	0.13	19,26,35,35	0
5	GOL	B	403	6/6	0.97	0.08	16,18,19,25	0
4	NA	D	602	1/1	0.99	0.08	15,15,15,15	1
3	MG	D	601	1/1	0.99	0.08	15,15,15,15	1
6	ZN	A	602	1/1	0.99	0.09	14,14,14,14	0
4	NA	C	502	1/1	1.00	0.07	15,15,15,15	1
6	ZN	A	601	1/1	1.00	0.08	16,16,16,16	0
3	MG	C	501	1/1	1.00	0.07	15,15,15,15	1
6	ZN	B	401	1/1	1.00	0.08	15,15,15,15	0
6	ZN	B	402	1/1	1.00	0.09	14,14,14,14	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 MG D 601:

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

Electron density around MG C 501:

$2mF_o\text{-}DF_c$ (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.