Full wwPDB X-ray Structure Validation Report (i)

Jan 18, 2023 – 06:02 PM EST

PDB ID	:	7TG9
Title	:	[T:Ag+/Hg2+:T--(pH11-pH7; 300s in metals)] Metal-mediated DNA base pair in tensegrity triangle grown at pH 11 and soaked in pH 7 with Ag+ and Hg2+ for 300s
Authors	:	Lu, B.; Vecchioni, S.; Seeman, N.C.; Sha, R.; Ohayon, Y.P.
Deposited on	:	2022-01-07
Resolution	:	4.69 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

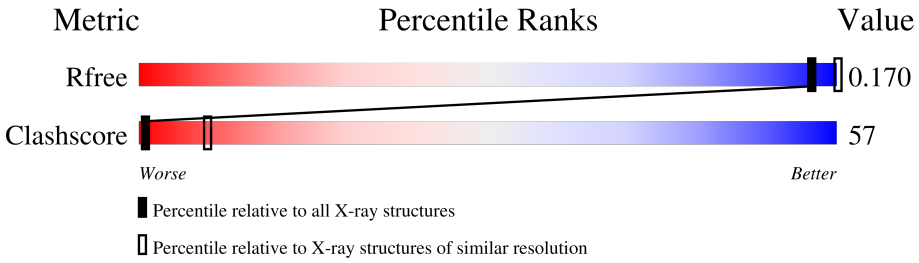
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.31.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.69 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	1085 (5.58-3.80)
Clashscore	141614	1159 (5.60-3.80)

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 >=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%

Mol	Chain	Length	Quality of chain
1	A	21	48% 52%
2	B	7	57% 43%
3	C	7	86% 14%
4	D	7	71% 29%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 860 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(*GP*AP*GP*CP*AP*GP*CP*CP*TP*GP*TP*TP*TP*GP*GP*AP*CP*AP*TP*CP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	A	21	429	205	80	124	20	0	0	0

- Molecule 2 is a DNA chain called DNA (5'-D(P*CP*CP*AP*TP*AP*CP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	B	7	140	67	26	40	7	0	0	0

- Molecule 3 is a DNA chain called DNA (5'-D(P*GP*GP*CP*TP*GP*CP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	C	7	144	68	25	44	7	0	0	0

- Molecule 4 is a DNA chain called DNA (5'-D(P*CP*TP*GP*AP*TP*GP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
4	D	7	145	69	24	45	7	0	0	0

- Molecule 5 is MERCURY (II) ION (three-letter code: HG) (formula: Hg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Hg		
5	B	2	2	2	0	0

3 Residue-property plots (i)

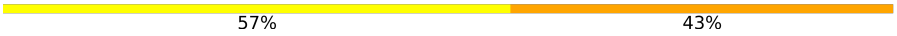
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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(*GP*AP*GP*CP*AP*GP*CP*CP*TP*GP*TP*TP*TP*GP*GP*AP*CP*AP*TP*CP*A)-3')

Chain A:

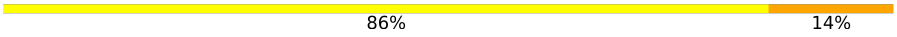
• Molecule 2: DNA (5'-D(P*CP*CP*AP*TP*AP*CP*A)-3')

Chain B:



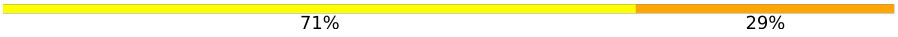
• Molecule 3: DNA (5'-D(P*GP*GP*CP*TP*GP*CP*T)-3')

Chain C:



• Molecule 4: DNA (5'-D(P*CP*TP*GP*AP*TP*GP*T)-3')

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α, β, γ	105.83Å 105.83Å 89.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.30 – 4.69 64.00 – 4.69	Depositor EDS
% Data completeness (in resolution range)	62.7 (32.30-4.69) 58.6 (64.00-4.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.02 (at 4.65Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.165 , 0.172 0.165 , 0.170	Depositor DCC
R_{free} test set	57 reflections (4.27%)	wwPDB-VP
Wilson B-factor (Å^2)	223.7	Xtriage
Anisotropy	1.267	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.14 , 999.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.064 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.83	EDS
Total number of atoms	860	wwPDB-VP
Average B, all atoms (Å^2)	264.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.77% of the height of the origin peak. No significant pseudotranslation is detected.*

[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: HG

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	1.54	9/481 (1.9%)	1.57	15/741 (2.0%)
2	B	1.73	3/156 (1.9%)	1.59	4/237 (1.7%)
3	C	1.06	0/160	1.26	3/245 (1.2%)
4	D	1.62	2/161 (1.2%)	1.44	0/245
All	All	1.52	14/958 (1.5%)	1.50	22/1468 (1.5%)

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1	DC	OP3-P	-10.52	1.48	1.61
1	A	11	DT	C1'-N1	8.36	1.60	1.49
1	A	12	DT	C5'-C4'	8.18	1.60	1.51
2	B	4	DT	C3'-O3'	7.67	1.53	1.44
4	D	4	DA	N9-C4	-6.82	1.33	1.37
1	A	12	DT	C1'-N1	6.77	1.58	1.49
1	A	15	DG	C3'-O3'	5.78	1.51	1.44
1	A	11	DT	N1-C2	5.31	1.42	1.38
2	B	2	DC	C3'-O3'	-5.30	1.37	1.44
2	B	3	DA	C3'-O3'	5.30	1.50	1.44
1	A	11	DT	C4'-O4'	5.26	1.50	1.45
1	A	13	DT	C4-C5	-5.15	1.40	1.45
1	A	20	DC	C3'-O3'	-5.12	1.37	1.44
1	A	10	DG	C3'-O3'	-5.03	1.37	1.44

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	4	DT	O4'-C1'-N1	9.95	114.97	108.00
1	A	11	DT	O4'-C1'-N1	8.40	113.88	108.00
1	A	12	DT	O5'-P-OP1	-7.86	98.63	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	7	DC	O4'-C1'-N1	7.64	113.35	108.00
1	A	13	DT	N3-C4-O4	6.89	124.03	119.90
1	A	12	DT	O4'-C1'-N1	6.47	112.53	108.00
1	A	12	DT	OP1-P-OP2	6.02	128.63	119.60
3	C	11	DT	N3-C4-O4	5.84	123.41	119.90
1	A	9	DT	N3-C4-O4	5.84	123.41	119.90
1	A	12	DT	C5-C4-O4	-5.73	120.89	124.90
1	A	20	DC	O4'-C4'-C3'	-5.70	102.22	104.50
1	A	11	DT	N3-C4-O4	5.60	123.26	119.90
1	A	19	DT	N3-C4-O4	5.55	123.23	119.90
1	A	12	DT	N3-C4-O4	5.48	123.19	119.90
2	B	4	DT	N3-C4-O4	5.39	123.13	119.90
2	B	7	DA	O4'-C1'-N9	5.36	111.75	108.00
2	B	4	DT	C5-C4-O4	-5.15	121.29	124.90
1	A	9	DT	C5-C4-O4	-5.11	121.32	124.90
3	C	11	DT	C5-C4-O4	-5.09	121.34	124.90
1	A	3	DG	O5'-P-OP2	-5.08	101.13	105.70
3	C	14	DT	C5-C4-O4	-5.06	121.36	124.90
1	A	4	DC	O4'-C4'-C3'	-5.05	102.48	104.50

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	429	0	238	43	0
2	B	140	0	79	6	0
3	C	144	0	80	11	0
4	D	145	0	81	12	0
5	B	2	0	0	0	0
All	All	860	0	478	69	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 57.

All (69) 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)
4:D:6:DG:H2"	4:D:7:DT:H5"	1.53	0.90
1:A:8:DC:H5"	1:A:8:DC:H6	1.53	0.72
1:A:3:DG:H2"	1:A:4:DC:O5'	1.91	0.71
1:A:2:DA:H1'	1:A:3:DG:OP2	1.91	0.70
3:C:8:DG:H3'	3:C:9:DG:H8	1.57	0.69
4:D:3:DG:H1'	4:D:4:DA:C8	2.31	0.66
3:C:8:DG:H3'	3:C:9:DG:C8	2.32	0.65
1:A:20:DC:H2"	1:A:21:DA:H8	1.64	0.62
1:A:11:DT:H2'	1:A:12:DT:H71	1.81	0.62
1:A:10:DG:H3'	1:A:11:DT:C6	2.34	0.62
2:B:1:DC:H2'	2:B:2:DC:C5	2.34	0.61
1:A:8:DC:H5"	1:A:8:DC:C6	2.37	0.57
1:A:5:DA:C4	1:A:6:DG:N7	2.73	0.57
1:A:2:DA:H2"	1:A:3:DG:C8	2.40	0.56
2:B:1:DC:C2	4:D:7:DT:N3	2.72	0.56
1:A:20:DC:C2'	1:A:21:DA:H8	2.17	0.56
4:D:4:DA:H2"	4:D:5:DT:H71	1.87	0.55
1:A:11:DT:H2"	1:A:12:DT:OP1	2.04	0.55
3:C:11:DT:H2'	3:C:12:DG:C8	2.43	0.53
1:A:1:DG:H2'	1:A:2:DA:C8	2.44	0.53
1:A:20:DC:H2"	1:A:21:DA:H5"	1.91	0.53
1:A:2:DA:H2"	1:A:3:DG:OP1	2.08	0.53
4:D:1:DC:H2"	4:D:2:DT:OP1	2.08	0.52
4:D:2:DT:H2"	4:D:3:DG:O5'	2.09	0.52
3:C:8:DG:H2'	3:C:8:DG:N3	2.25	0.52
1:A:15:DG:H2"	1:A:16:DA:O5'	2.12	0.50
1:A:9:DT:H2'	1:A:10:DG:C8	2.47	0.50
1:A:11:DT:C2'	1:A:12:DT:H71	2.41	0.50
1:A:20:DC:H2"	1:A:21:DA:C8	2.46	0.49
3:C:8:DG:C3'	3:C:9:DG:H8	2.22	0.49
1:A:2:DA:H2"	1:A:3:DG:H8	1.78	0.49
1:A:18:DA:H1'	1:A:19:DT:H5'	1.94	0.48
1:A:16:DA:H1'	1:A:17:DC:H5'	1.94	0.48
1:A:12:DT:C6	1:A:13:DT:H71	2.49	0.48
1:A:20:DC:C2'	1:A:21:DA:C8	2.97	0.47
1:A:10:DG:H3'	1:A:11:DT:H6	1.80	0.47
1:A:5:DA:C4	1:A:6:DG:C8	3.02	0.47
1:A:5:DA:C6	1:A:6:DG:C6	3.03	0.47
3:C:10:DC:H2'	3:C:10:DC:O2	2.14	0.46
3:C:10:DC:N3	3:C:11:DT:C4	2.84	0.46
4:D:3:DG:C4	4:D:4:DA:C5	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:DG:C2'	1:A:16:DA:C8	2.99	0.45
3:C:8:DG:N2	3:C:9:DG:H1'	2.31	0.45
4:D:6:DG:C2'	4:D:7:DT:H5"	2.37	0.45
1:A:2:DA:OP2	1:A:2:DA:H8	2.00	0.45
1:A:4:DC:H2'	1:A:5:DA:C8	2.53	0.44
1:A:7:DC:C2	1:A:8:DC:C5	3.06	0.44
3:C:12:DG:H1'	3:C:13:DC:H5'	2.00	0.44
1:A:2:DA:H1'	1:A:3:DG:P	2.58	0.43
1:A:12:DT:H2"	1:A:13:DT:C5'	2.48	0.43
2:B:4:DT:H2"	2:B:5:DA:OP2	2.16	0.43
4:D:4:DA:H2"	4:D:5:DT:OP2	2.18	0.43
1:A:3:DG:C6	1:A:4:DC:C4	3.06	0.43
1:A:12:DT:H2"	1:A:13:DT:O5'	2.19	0.43
3:C:9:DG:C2	3:C:10:DC:C6	3.07	0.43
1:A:1:DG:H3'	1:A:2:DA:H8	1.84	0.43
4:D:2:DT:H2'	4:D:3:DG:C8	2.54	0.43
1:A:12:DT:C5	1:A:13:DT:H73	2.54	0.42
1:A:3:DG:OP1	1:A:3:DG:H8	2.03	0.42
2:B:6:DC:H2"	2:B:7:DA:H2'	2.02	0.41
1:A:13:DT:H1'	1:A:14:DG:C5	2.56	0.41
2:B:1:DC:H1'	4:D:7:DT:C2	2.55	0.41
1:A:3:DG:C2	1:A:4:DC:C2	3.08	0.41
1:A:3:DG:C5	1:A:4:DC:C5	3.09	0.41
3:C:12:DG:C2	3:C:13:DC:C2	3.08	0.41
1:A:14:DG:H2"	1:A:15:DG:OP2	2.20	0.40
2:B:1:DC:H1'	4:D:7:DT:H2'	2.02	0.40
1:A:3:DG:C4	1:A:4:DC:C6	3.10	0.40
1:A:13:DT:O3'	1:A:14:DG:C8	2.74	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein molecules in this entry.

5.3.2 Protein sidechains (i)

There are no protein molecules in this entry.

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 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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

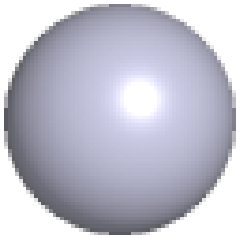
6.4 Ligands

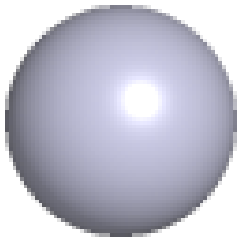
Unable to reproduce the depositors R factor - this section is therefore empty.

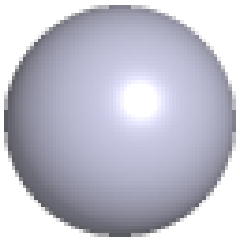
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around HG B 101:

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

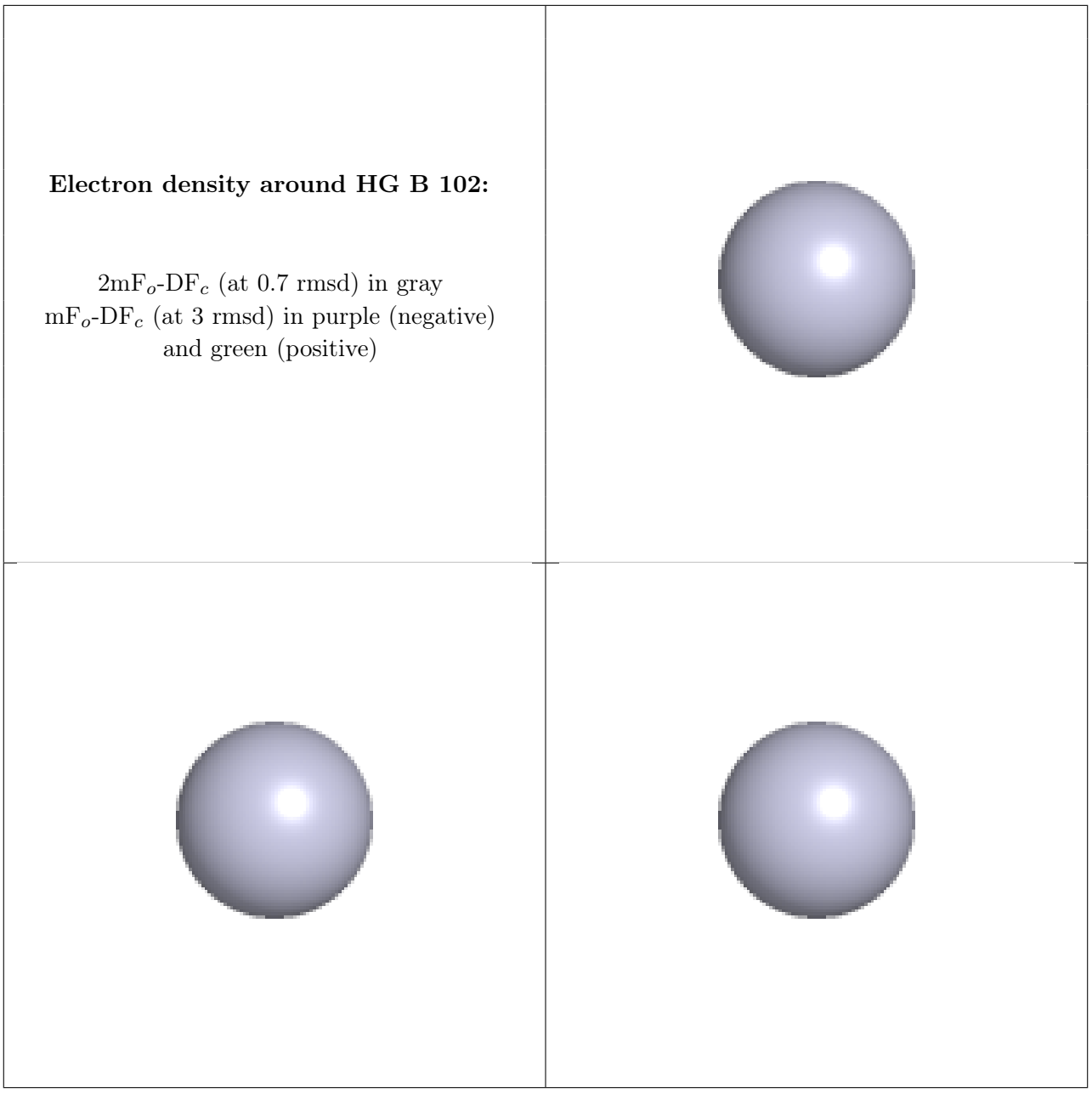






Electron density around HG B 102:

$2mF_o$-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)

Unable to reproduce the depositors R factor - this section is therefore empty.