



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 29, 2020 – 10:30 AM BST

PDB ID : 6UTU
Title : Crystal structure of minor pseudopilin ternary complex of XcpVWX from the Type 2 secretion system of *Pseudomonas aeruginosa* in the P3 space group
Authors : Zhang, Y.; Wang, S.; Jia, Z.
Deposited on : 2019-10-30
Resolution : 2.85 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

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
Xtriage (Phenix)	:	1.13
EDS	:	2.13
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)	:	2.13

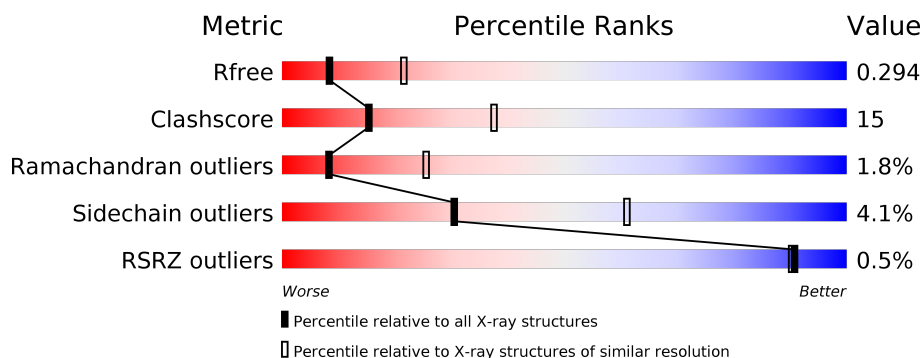
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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 on 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 $\leq 5\%$. 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	92	
1	D	92	
1	G	92	
2	B	194	
2	E	194	
2	H	194	

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Mol	Chain	Length	Quality of chain
3	C	273	<div><div></div><div>69%25%••</div></div>
3	F	273	<div><div></div><div>63%23%•13%</div></div>
3	I	273	<div><div></div><div>62%27%•10%</div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10560 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 Type II secretion system protein I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	63	Total	C	N	O	S	0	0	0
			444	286	79	78	1			
1	D	72	Total	C	N	O	S	0	0	0
			515	327	97	90	1			
1	G	58	Total	C	N	O	S	0	0	0
			418	267	76	74	1			

- Molecule 2 is a protein called Type II secretion system protein J.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	162	Total	C	N	O	S	0	0	0
			1275	798	245	229	3			
2	E	161	Total	C	N	O	S	0	0	0
			1250	785	240	222	3			
2	H	159	Total	C	N	O	S	0	0	0
			1244	778	241	223	2			

- Molecule 3 is a protein called Type II secretion system protein K.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	261	Total	C	N	O	S	0	0	0
			1871	1172	340	355	4			
3	F	238	Total	C	N	O	S	0	0	0
			1752	1102	317	329	4			
3	I	247	Total	C	N	O	S	0	0	0
			1780	1119	323	334	4			

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	I	3	Total 3	Ca 3	0	0
4	C	3	Total 3	Ca 3	0	0
4	F	3	Total 3	Ca 3	0	0

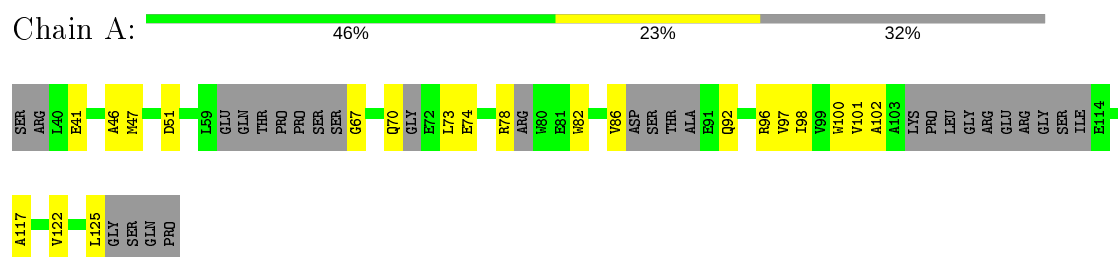
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total 2	O 2	0	0

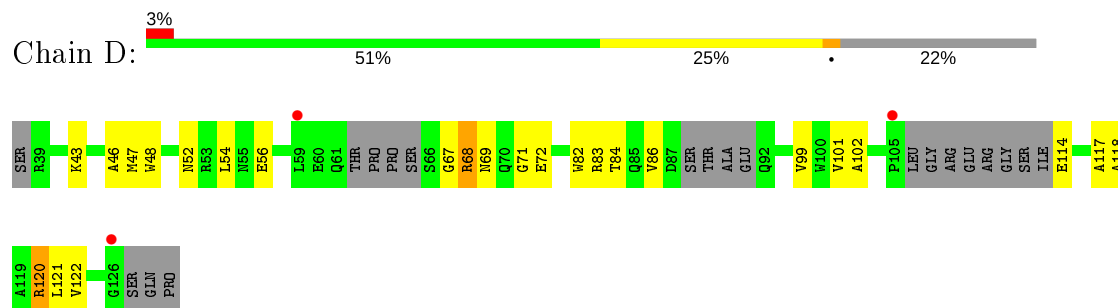
3 Residue-property plots

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.

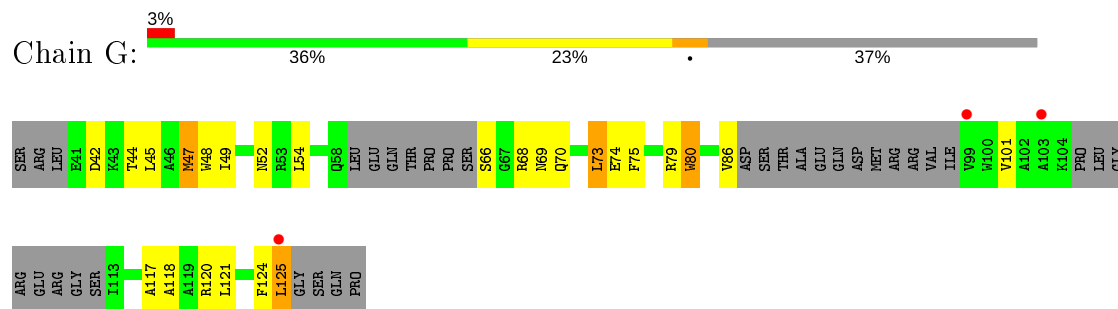
- Molecule 1: Type II secretion system protein I



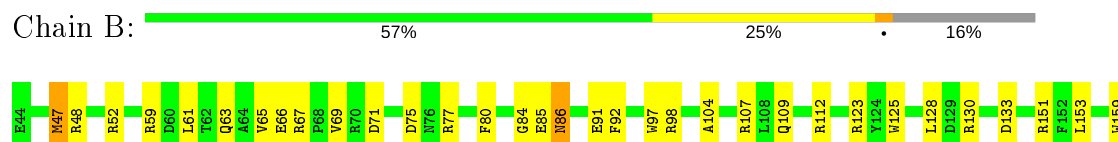
- Molecule 1: Type II secretion system protein I

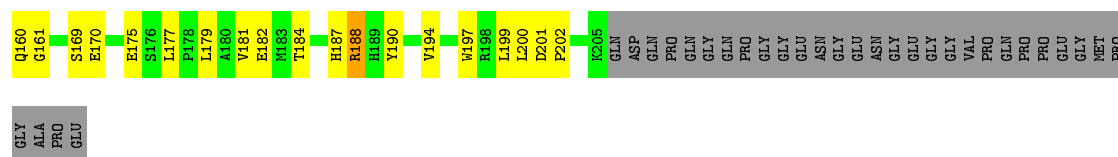


- Molecule 1: Type II secretion system protein I



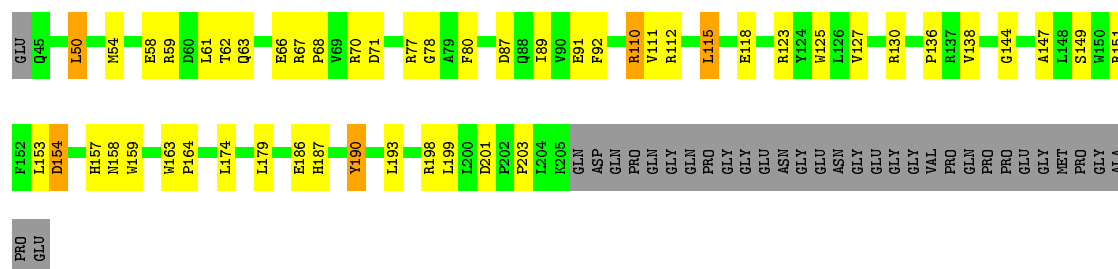
- Molecule 2: Type II secretion system protein J





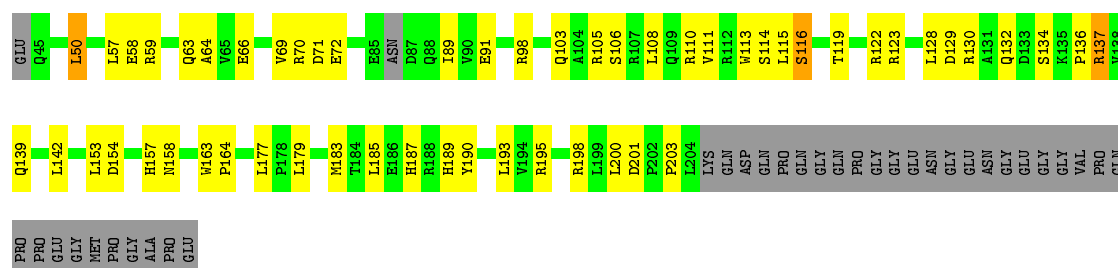
- Molecule 2: Type II secretion system protein J

Chain E: 57% 24% 17%



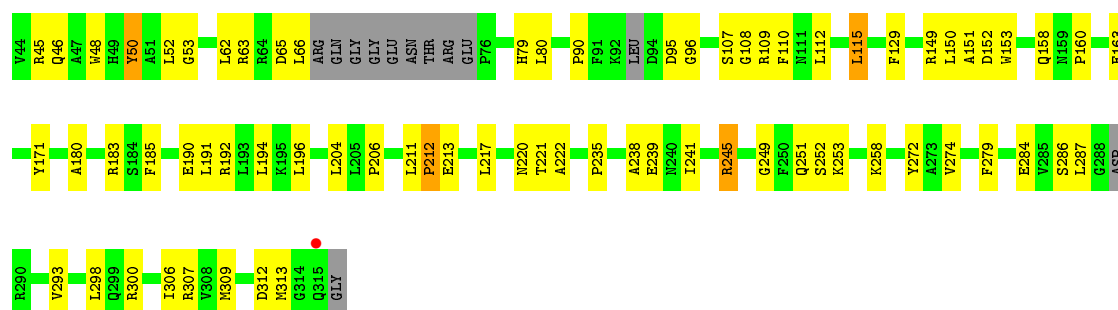
- Molecule 2: Type II secretion system protein J

Chain H: 54% 27% 18%



- Molecule 3: Type II secretion system protein K

Chain C: 69% 25%



- Molecule 3: Type II secretion system protein K

Chain F: 63% 23% 13%

4 Data and refinement statistics

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, α , β , γ	158.10 Å 158.10 Å 64.70 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.91 – 2.85 19.91 – 2.85	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.91-2.85) 100.0 (19.91-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.08 (at 2.83 Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.214 , 0.294 0.214 , 0.294	Depositor DCC
R_{free} test set	2108 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	79.0	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 45.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.068 for -h,-k,l 0.198 for h,-h-k,-l 0.073 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10560	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.49% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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:
CA

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	0.44	0/446	0.59	0/605
1	D	0.42	0/520	0.63	0/705
1	G	0.42	0/424	0.63	0/576
2	B	0.49	0/1303	0.64	0/1770
2	E	0.44	0/1278	0.69	0/1738
2	H	0.50	0/1270	0.68	1/1723 (0.1%)
3	C	0.48	0/1901	0.66	0/2590
3	F	0.43	0/1781	0.64	0/2425
3	I	0.45	0/1808	0.64	0/2466
All	All	0.46	0/10731	0.65	1/14598 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	H	57	LEU	CA-CB-CG	6.71	130.72	115.30

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	A	444	0	371	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	515	0	448	21	0
1	G	418	0	359	22	0
2	B	1275	0	1210	34	0
2	E	1250	0	1175	39	0
2	H	1244	0	1168	44	0
3	C	1871	0	1714	47	0
3	F	1752	0	1618	58	0
3	I	1780	0	1636	61	0
4	C	3	0	0	0	0
4	F	3	0	0	0	0
4	I	3	0	0	0	0
5	A	2	0	0	0	0
All	All	10560	0	9699	301	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 15.

The worst 5 of 301 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)
2:E:67:ARG:CD	3:F:183:ARG:HH12	1.82	0.93
3:F:59:GLU:HG2	3:F:306:ILE:HD12	1.51	0.92
2:E:123:ARG:HD3	2:E:138:VAL:HG12	1.54	0.86
3:F:276:THR:HG22	3:F:278:TYR:H	1.42	0.85
1:A:102:ALA:HB2	1:A:117:ALA:HA	1.60	0.81

There are no symmetry-related clashes.

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	51/92 (55%)	49 (96%)	1 (2%)	1 (2%)	7	23
1	D	64/92 (70%)	62 (97%)	2 (3%)	0	100	100
1	G	50/92 (54%)	46 (92%)	2 (4%)	2 (4%)	3	9
2	B	160/194 (82%)	151 (94%)	7 (4%)	2 (1%)	12	33
2	E	159/194 (82%)	146 (92%)	11 (7%)	2 (1%)	12	33
2	H	155/194 (80%)	139 (90%)	14 (9%)	2 (1%)	12	33
3	C	253/273 (93%)	229 (90%)	15 (6%)	9 (4%)	3	11
3	F	224/273 (82%)	206 (92%)	17 (8%)	1 (0%)	34	62
3	I	237/273 (87%)	210 (89%)	22 (9%)	5 (2%)	7	22
All	All	1353/1677 (81%)	1238 (92%)	91 (7%)	24 (2%)	8	25

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	85	GLU
2	B	86	ASN
3	C	96	GLY
3	C	212	PRO
3	F	270	VAL

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	A	31/76 (41%)	30 (97%)	1 (3%)	39	69
1	D	38/76 (50%)	36 (95%)	2 (5%)	22	50
1	G	32/76 (42%)	27 (84%)	5 (16%)	2	6
2	B	125/164 (76%)	120 (96%)	5 (4%)	31	62
2	E	119/164 (73%)	113 (95%)	6 (5%)	24	53
2	H	119/164 (73%)	116 (98%)	3 (2%)	47	76
3	C	170/225 (76%)	163 (96%)	7 (4%)	30	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	165/225 (73%)	159 (96%)	6 (4%)	35	66
3	I	162/225 (72%)	158 (98%)	4 (2%)	47	76
All	All	961/1395 (69%)	922 (96%)	39 (4%)	30	61

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	115	LEU
3	F	50	TYR
3	I	183	ARG
2	E	149	SER
2	E	154	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	158	GLN
3	F	182	ASN
3	I	220	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 9 ligands modelled in this entry, 9 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 [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, 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	63/92 (68%)	-0.05	0 100 100	59, 81, 95, 104	0
1	D	72/92 (78%)	-0.05	3 (4%) 36 31	66, 82, 102, 106	0
1	G	58/92 (63%)	0.22	3 (5%) 27 22	79, 93, 99, 102	0
2	B	162/194 (83%)	-0.32	0 100 100	40, 63, 83, 94	0
2	E	161/194 (82%)	-0.24	0 100 100	58, 73, 89, 103	0
2	H	159/194 (81%)	-0.31	0 100 100	45, 67, 90, 99	0
3	C	261/273 (95%)	-0.34	1 (0%) 92 92	45, 70, 87, 96	0
3	F	238/273 (87%)	-0.24	0 100 100	60, 80, 98, 104	0
3	I	247/273 (90%)	-0.22	0 100 100	49, 73, 92, 107	0
All	All	1421/1677 (84%)	-0.24	7 (0%) 91 90	40, 74, 95, 107	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	105	PRO	4.5
1	G	125	LEU	3.1
1	G	99	VAL	2.8
1	D	126	GLY	2.8
1	G	103	ALA	2.7

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](#)

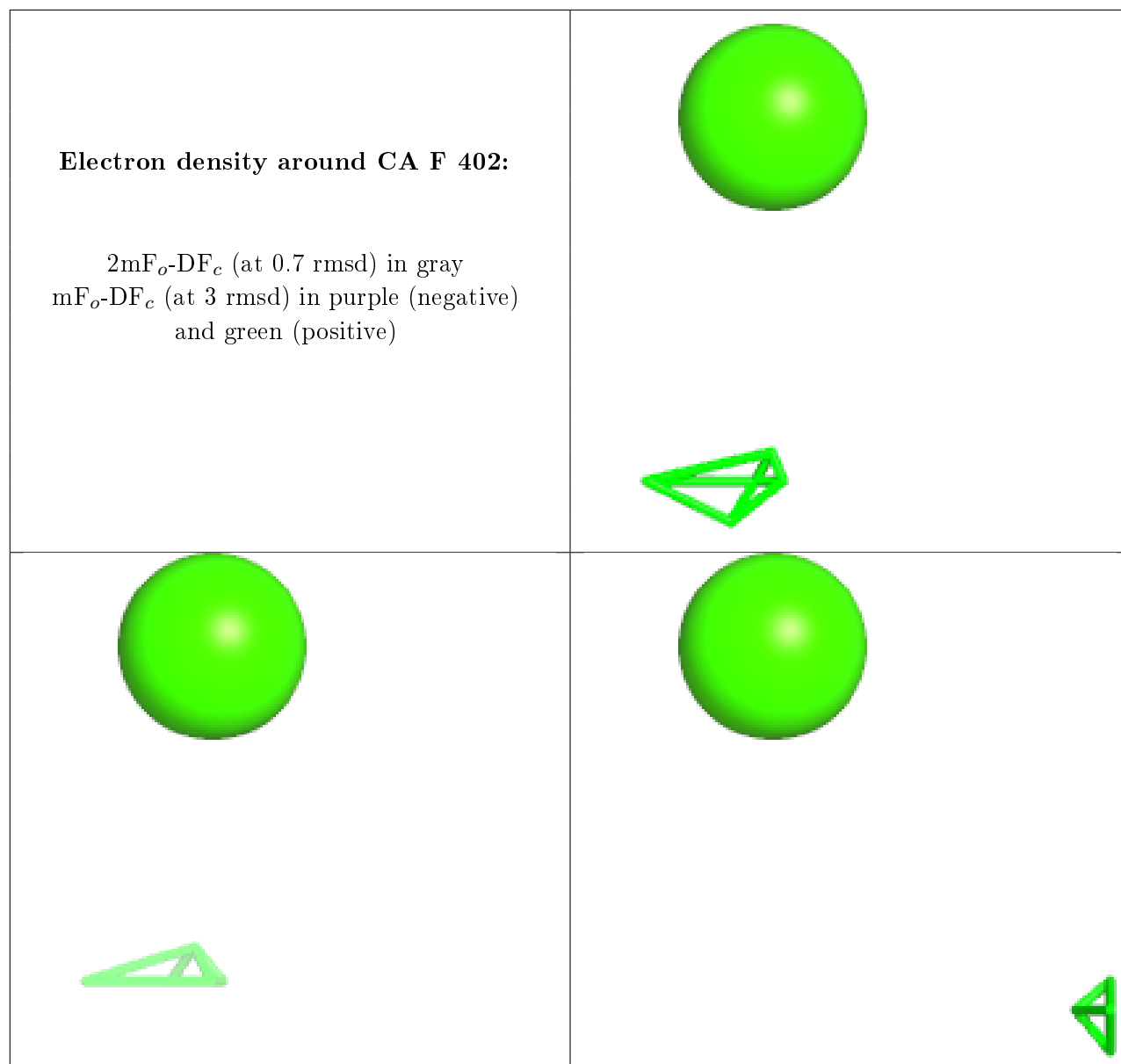
There are no monosaccharides in this entry.

6.4 Ligands

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.

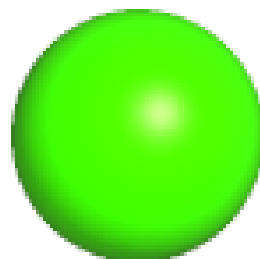
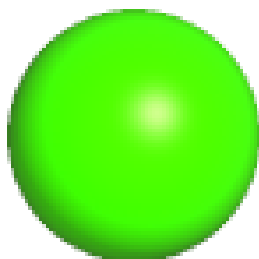
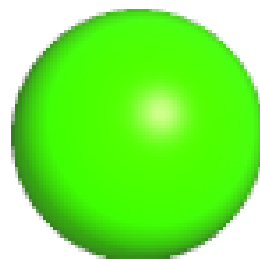
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	CA	F	402	1/1	0.85	0.17	77,77,77,77	0
4	CA	F	401	1/1	0.92	0.10	94,94,94,94	0
4	CA	C	403	1/1	0.92	0.14	68,68,68,68	0
4	CA	I	403	1/1	0.95	0.16	75,75,75,75	0
4	CA	C	401	1/1	0.95	0.12	80,80,80,80	0
4	CA	F	403	1/1	0.97	0.16	83,83,83,83	0
4	CA	I	401	1/1	0.98	0.11	88,88,88,88	0
4	CA	I	402	1/1	0.98	0.17	79,79,79,79	0
4	CA	C	402	1/1	0.99	0.14	73,73,73,73	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.



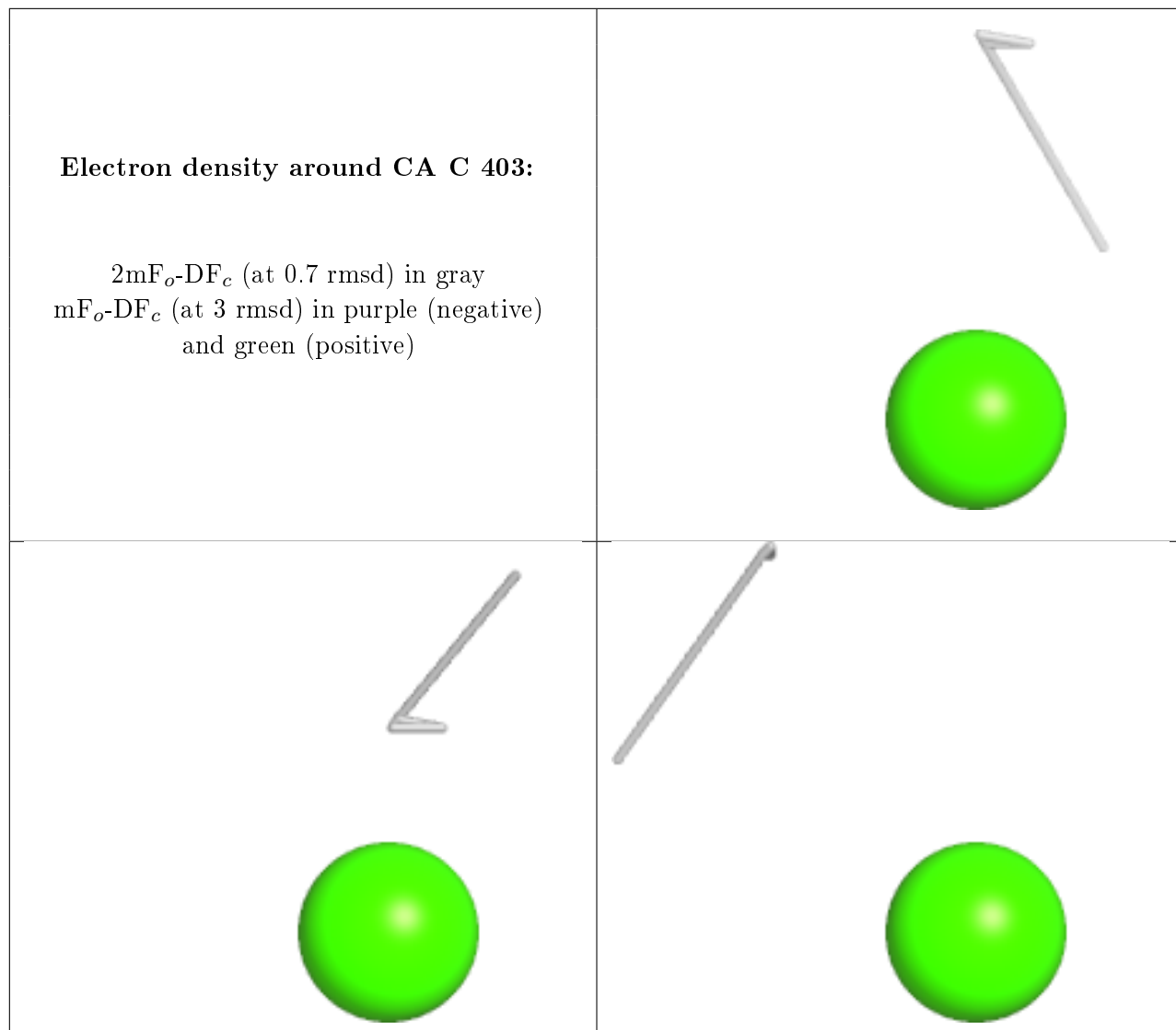
Electron density around CA F 401:

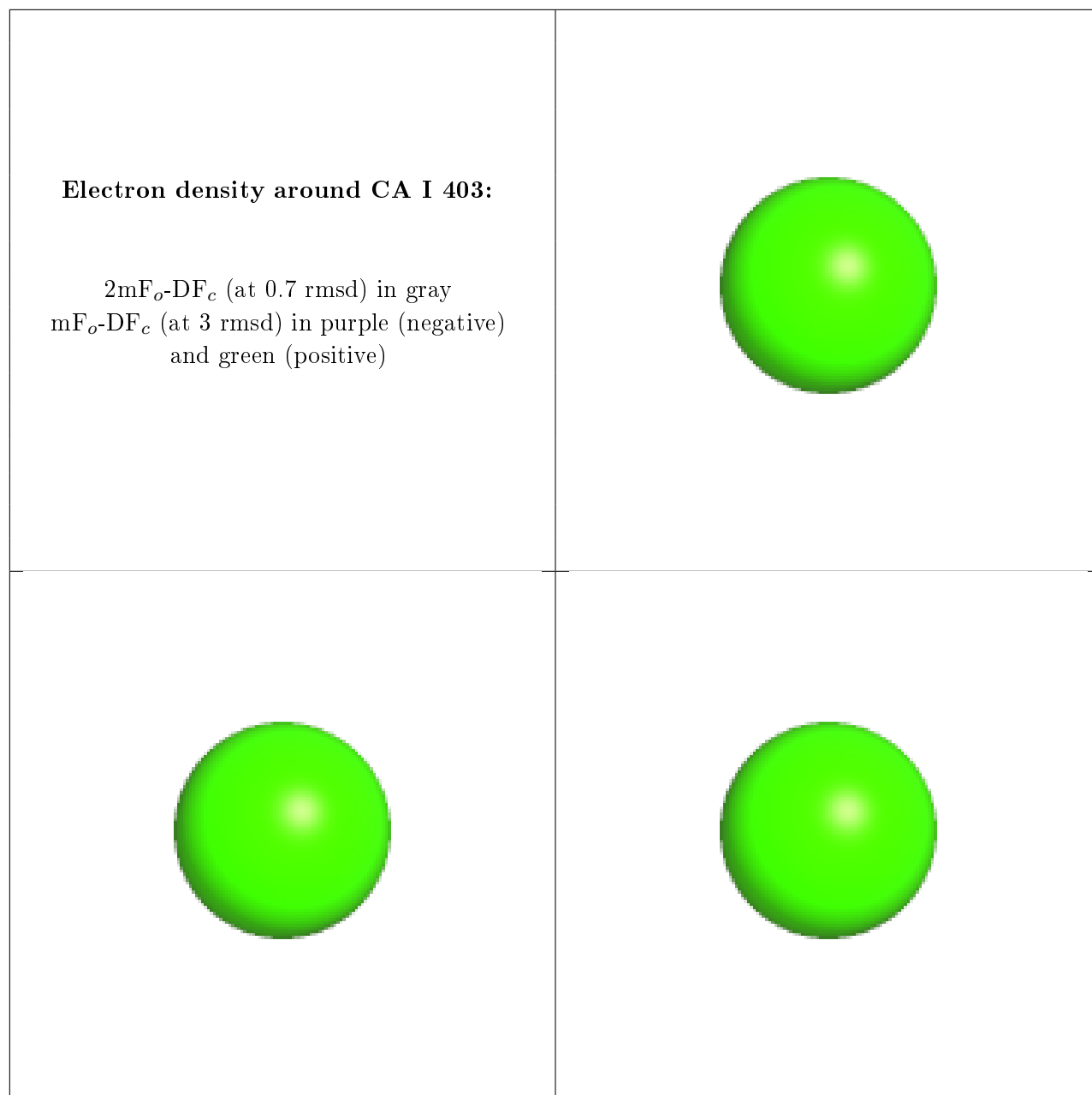
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

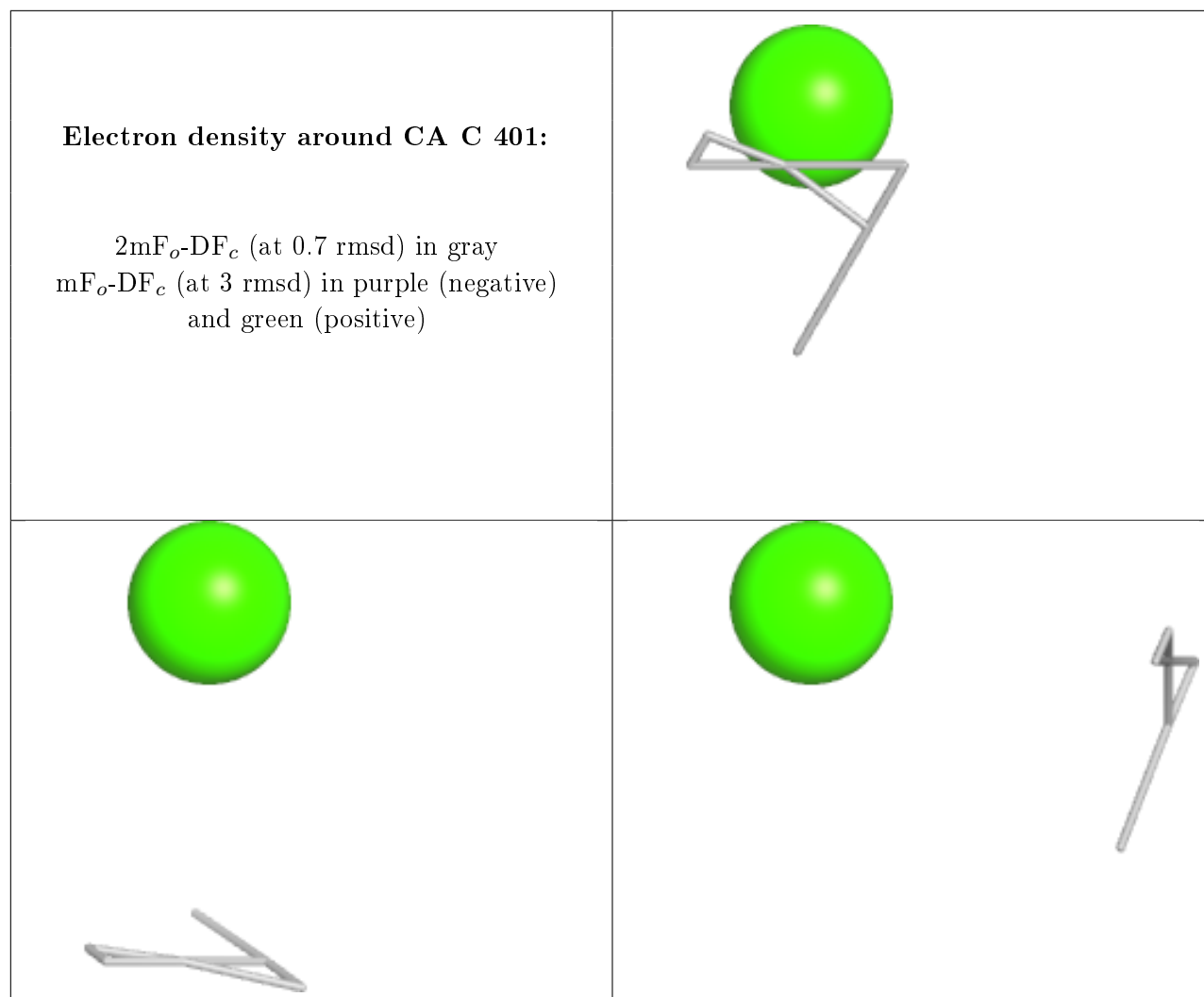


Electron density around CA C 403:

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

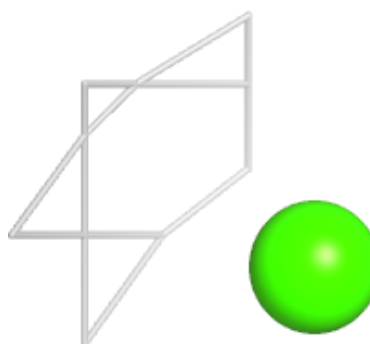
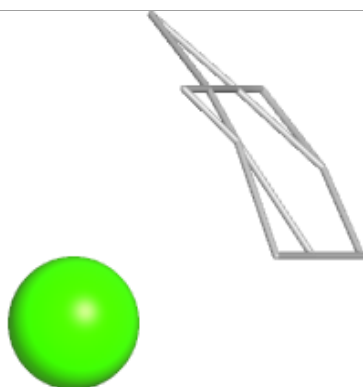
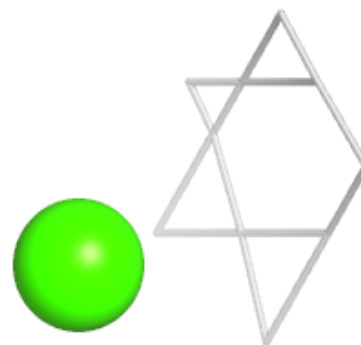




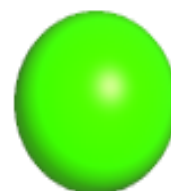
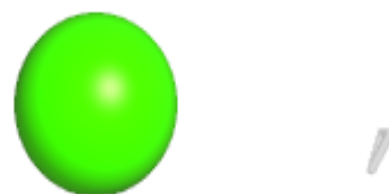


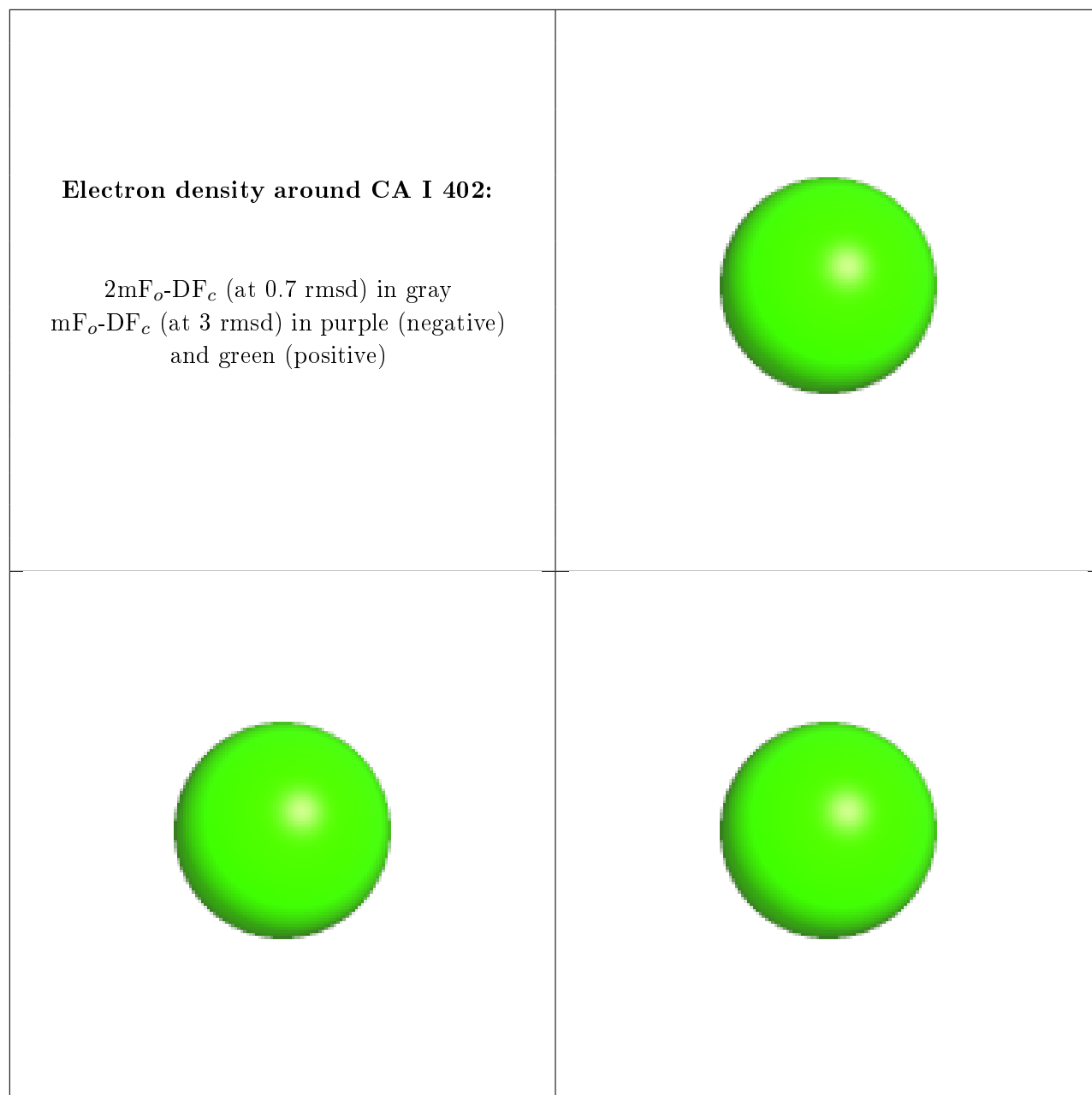
Electron density around CA F 403:

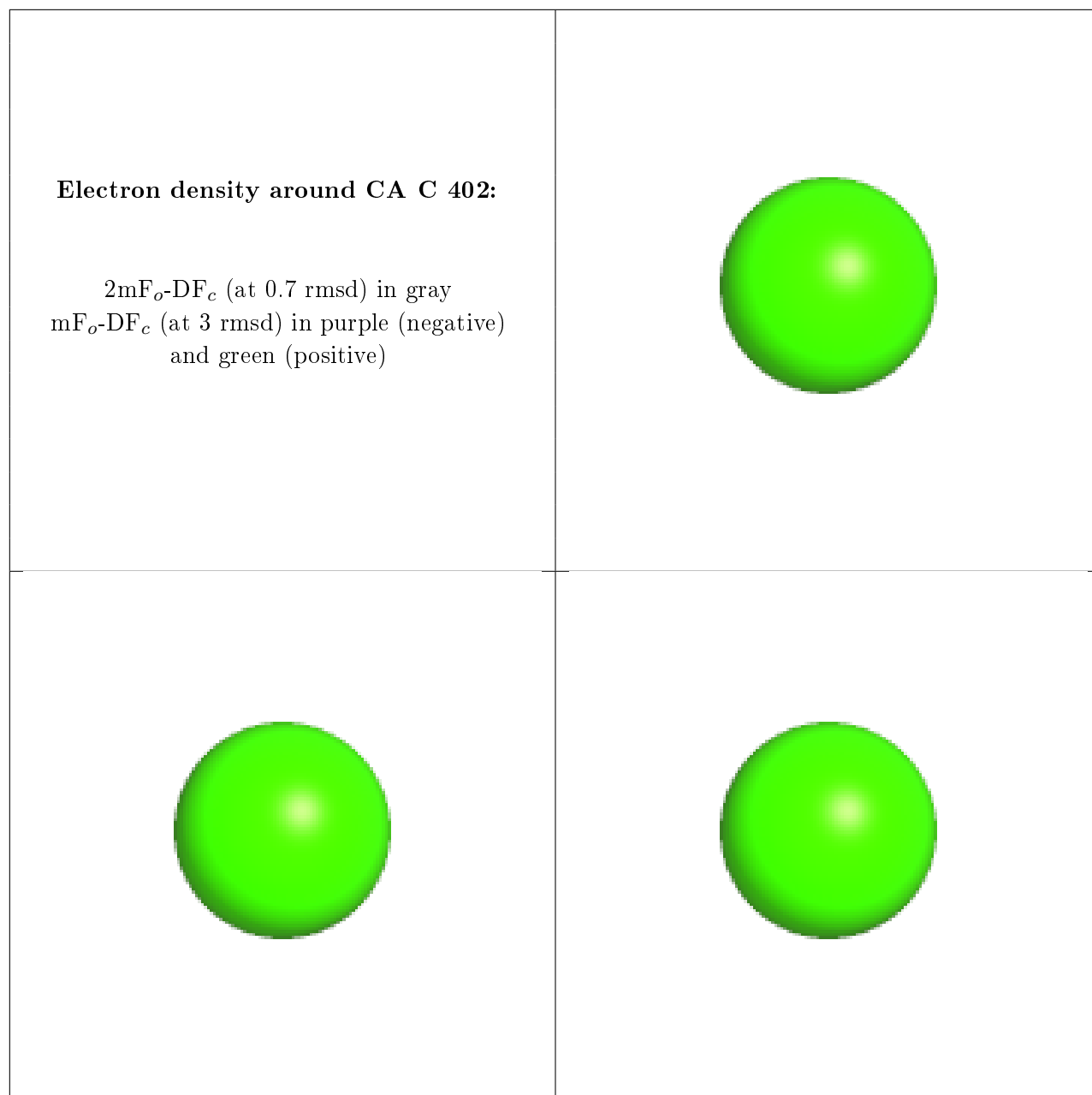
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around CA I 401:**

$2mF_o-DF_c$ (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.