



# Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 11:30 am BST

PDB ID : 6U39  
Title : 2.4 Angstrom crystal structure of the D129G Ca-CaM:CaV1.2 IQ domain complex  
Authors : Wang, K.; Van Petegem, F.  
Deposited on : 2019-08-21  
Resolution : 2.40 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.

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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  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

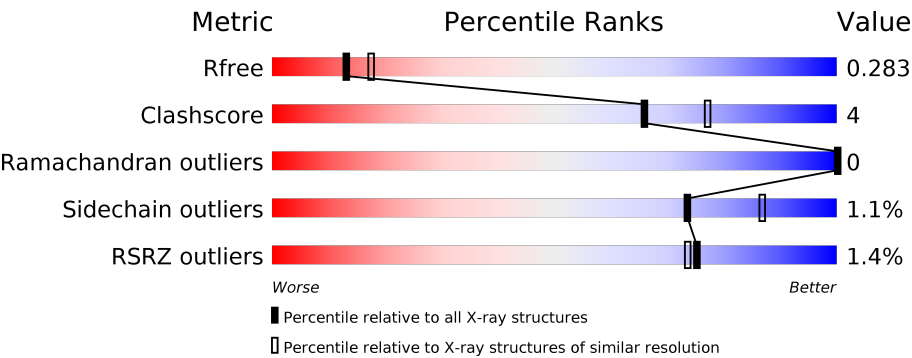
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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  $\geq 3$ , 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	148	<div><div>%</div><div><div></div><div>82%</div><div>7%</div><div>11%</div></div></div>
1	C	148	<div><div>%</div><div><div></div><div>84%</div><div>9%</div><div>7%</div></div></div>
1	E	148	<div><div></div><div><div></div><div>84%</div><div>9%</div><div>7%</div></div></div>
1	G	148	<div><div></div><div><div></div><div>90%</div><div></div><div>8%</div></div></div>
1	I	148	<div><div>2%</div><div><div></div><div>72%</div><div>16%</div><div>12%</div></div></div>
1	K	148	<div><div>2%</div><div><div></div><div>84%</div><div>11%</div><div>5%</div></div></div>

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Mol	Chain	Length	Quality of chain
1	M	148	
1	O	148	
1	Q	148	
1	S	148	
2	B	37	
2	D	37	
2	F	37	
2	H	37	
2	J	37	
2	L	37	
2	N	37	
2	P	37	
2	R	37	
2	T	37	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11377 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 Calmodulin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	132	Total	C	N	O	S	0	0	0
			922	573	152	189	8			
1	C	138	Total	C	N	O	S	0	0	0
			1015	629	163	215	8			
1	E	138	Total	C	N	O	S	0	0	0
			995	619	161	207	8			
1	G	136	Total	C	N	O	S	0	0	0
			971	601	162	200	8			
1	I	130	Total	C	N	O	S	0	0	0
			896	557	144	187	8			
1	K	141	Total	C	N	O	S	0	0	0
			1009	623	166	211	9			
1	M	135	Total	C	N	O	S	0	0	0
			941	587	151	195	8			
1	O	135	Total	C	N	O	S	0	0	0
			928	580	149	191	8			
1	Q	137	Total	C	N	O	S	0	0	0
			937	577	153	199	8			
1	S	138	Total	C	N	O	S	0	0	0
			945	588	153	195	9			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	129	GLY	ASP	engineered mutation	UNP P0DP23
C	129	GLY	ASP	engineered mutation	UNP P0DP23
E	129	GLY	ASP	engineered mutation	UNP P0DP23
G	129	GLY	ASP	engineered mutation	UNP P0DP23
I	129	GLY	ASP	engineered mutation	UNP P0DP23
K	129	GLY	ASP	engineered mutation	UNP P0DP23
M	129	GLY	ASP	engineered mutation	UNP P0DP23
O	129	GLY	ASP	engineered mutation	UNP P0DP23
Q	129	GLY	ASP	engineered mutation	UNP P0DP23

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Chain	Residue	Modelled	Actual	Comment	Reference
S	129	GLY	ASP	engineered mutation	UNP P0DP23

- Molecule 2 is a protein called Voltage-dependent L-type calcium channel subunit alpha-1C.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	23	Total	C	N	O	0	0	0
			165	112	24	29			
2	D	26	Total	C	N	O	0	0	0
			206	139	32	35			
2	F	23	Total	C	N	O	0	0	0
			175	118	27	30			
2	H	24	Total	C	N	O	0	0	0
			195	132	32	31			
2	J	26	Total	C	N	O	0	0	0
			189	129	27	33			
2	L	24	Total	C	N	O	0	0	0
			189	126	32	31			
2	N	24	Total	C	N	O	0	0	0
			169	114	25	30			
2	P	21	Total	C	N	O	0	0	0
			159	109	22	28			
2	R	25	Total	C	N	O	0	0	0
			181	124	27	30			
2	T	20	Total	C	N	O	0	0	0
			141	94	21	26			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1608	SER	-	expression tag	UNP Q13936
B	1609	ASN	-	expression tag	UNP Q13936
B	1610	ALA	-	expression tag	UNP Q13936
D	1608	SER	-	expression tag	UNP Q13936
D	1609	ASN	-	expression tag	UNP Q13936
D	1610	ALA	-	expression tag	UNP Q13936
F	1608	SER	-	expression tag	UNP Q13936
F	1609	ASN	-	expression tag	UNP Q13936
F	1610	ALA	-	expression tag	UNP Q13936
H	1608	SER	-	expression tag	UNP Q13936
H	1609	ASN	-	expression tag	UNP Q13936
H	1610	ALA	-	expression tag	UNP Q13936
J	1608	SER	-	expression tag	UNP Q13936

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Chain	Residue	Modelled	Actual	Comment	Reference
J	1609	ASN	-	expression tag	UNP Q13936
J	1610	ALA	-	expression tag	UNP Q13936
L	1608	SER	-	expression tag	UNP Q13936
L	1609	ASN	-	expression tag	UNP Q13936
L	1610	ALA	-	expression tag	UNP Q13936
N	1608	SER	-	expression tag	UNP Q13936
N	1609	ASN	-	expression tag	UNP Q13936
N	1610	ALA	-	expression tag	UNP Q13936
P	1608	SER	-	expression tag	UNP Q13936
P	1609	ASN	-	expression tag	UNP Q13936
P	1610	ALA	-	expression tag	UNP Q13936
R	1608	SER	-	expression tag	UNP Q13936
R	1609	ASN	-	expression tag	UNP Q13936
R	1610	ALA	-	expression tag	UNP Q13936
T	1608	SER	-	expression tag	UNP Q13936
T	1609	ASN	-	expression tag	UNP Q13936
T	1610	ALA	-	expression tag	UNP Q13936

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	3	Total 3 Ca 3	0	0
3	Q	3	Total 3 Ca 3	0	0
3	K	3	Total 3 Ca 3	0	0
3	E	3	Total 3 Ca 3	0	0
3	I	2	Total 2 Ca 2	0	0
3	C	3	Total 3 Ca 3	0	0
3	A	3	Total 3 Ca 3	0	0
3	O	3	Total 3 Ca 3	0	0
3	S	3	Total 3 Ca 3	0	0
3	M	3	Total 3 Ca 3	0	0

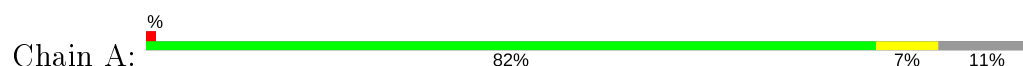
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	4	Total O 4 4	0	0
4	C	1	Total O 1 1	0	0
4	E	3	Total O 3 3	0	0
4	G	1	Total O 1 1	0	0
4	I	3	Total O 3 3	0	0
4	K	3	Total O 3 3	0	0
4	M	2	Total O 2 2	0	0
4	Q	1	Total O 1 1	0	0
4	S	2	Total O 2 2	0	0

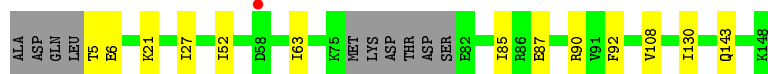
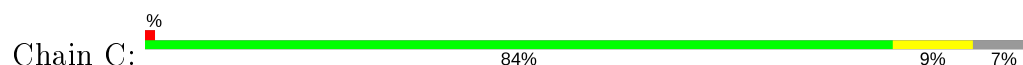
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

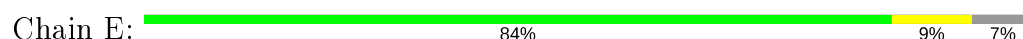
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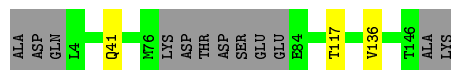
#### • Molecule 1: Calmodulin-1



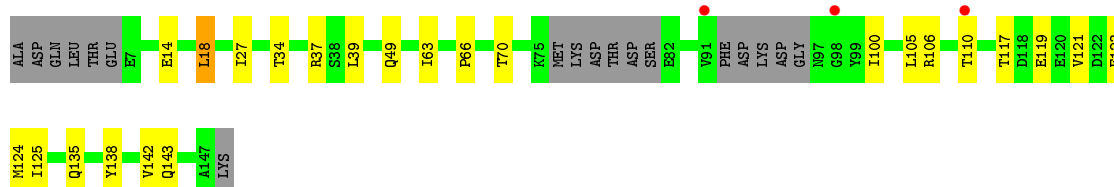
#### • Molecule 1: Calmodulin-1



#### • Molecule 1: Calmodulin-1




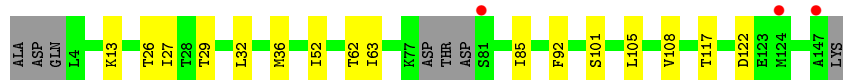
#### • Molecule 1: Calmodulin-1






- Molecule 1: Calmodulin-1

Chain K: 




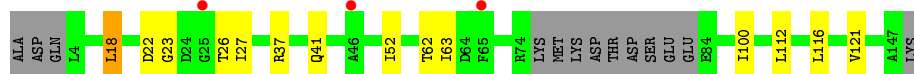
- Molecule 1: Calmodulin-1

Chain M: 




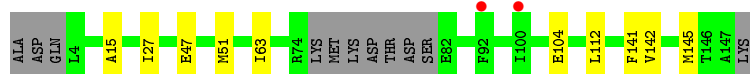
- Molecule 1: Calmodulin-1

Chain O: 




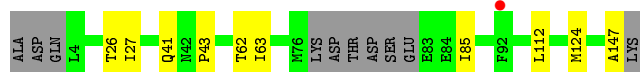
- Molecule 1: Calmodulin-1

Chain Q: 



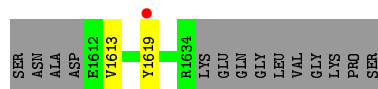
- Molecule 1: Calmodulin-1

Chain S: 



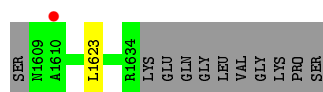
- Molecule 2: Voltage-dependent L-type calcium channel subunit alpha-1C

Chain B: 

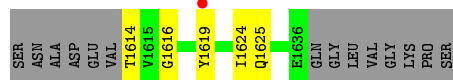


- Molecule 2: Voltage-dependent L-type calcium channel subunit alpha-1C

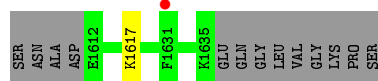
Chain D: 



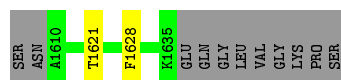
- Molecule 2: Voltage-dependent L-type calcium channel subunit alpha-1C



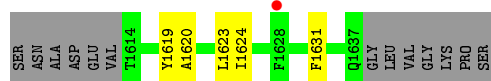
- Molecule 2: Voltage-dependent L-type calcium channel subunit alpha-1C



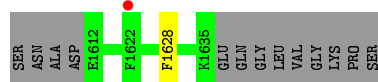
- Molecule 2: Voltage-dependent L-type calcium channel subunit alpha-1C



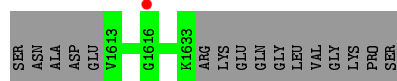
- Molecule 2: Voltage-dependent L-type calcium channel subunit alpha-1C



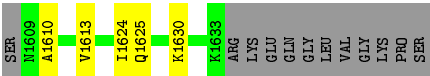
- Molecule 2: Voltage-dependent L-type calcium channel subunit alpha-1C



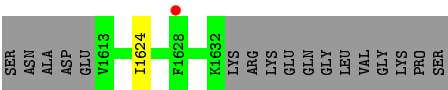
- Molecule 2: Voltage-dependent L-type calcium channel subunit alpha-1C



- Molecule 2: Voltage-dependent L-type calcium channel subunit alpha-1C



● Molecule 2: Voltage-dependent L-type calcium channel subunit alpha-1C



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 <sub>1</sub> 2 <sub>1</sub> 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	121.80 Å   161.66 Å   96.28 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	49.04 – 2.40 49.04 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.5 (49.04-2.40) 98.7 (49.04-2.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.77 (at 2.29 Å)	Xtriage
Refinement program	PHENIX 1.13 _2998	Depositor
R, $R_{free}$	0.232   ,   0.283 0.232   ,   0.283	Depositor DCC
$R_{free}$ test set	4193 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	67.9	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 60.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	11377	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% 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

### 5.1 Standard geometry

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	0.25	0/931	0.39	0/1259
1	C	0.25	0/1026	0.39	0/1386
1	E	0.24	0/1005	0.40	0/1362
1	G	0.24	0/981	0.38	0/1328
1	I	0.25	0/903	0.44	0/1223
1	K	0.24	0/1020	0.40	0/1381
1	M	0.27	0/952	0.41	0/1292
1	O	0.25	0/939	0.42	0/1278
1	Q	0.25	0/947	0.39	0/1286
1	S	0.24	0/956	0.39	0/1299
2	B	0.26	0/170	0.29	0/231
2	D	0.25	0/211	0.33	0/284
2	F	0.26	0/180	0.30	0/244
2	H	0.25	0/200	0.31	0/269
2	J	0.25	0/194	0.31	0/265
2	L	0.25	0/194	0.34	0/261
2	N	0.25	0/174	0.29	0/237
2	P	0.26	0/164	0.30	0/223
2	R	0.26	0/186	0.31	0/253
2	T	0.25	0/144	0.31	0/196
All	All	0.25	0/11477	0.39	0/15557

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 ⓘ

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	922	0	778	7	0
1	C	1015	0	905	8	0
1	E	995	0	871	11	0
1	G	971	0	854	4	0
1	I	896	0	762	16	0
1	K	1009	0	871	10	0
1	M	941	0	799	10	0
1	O	928	0	786	9	0
1	Q	937	0	761	7	0
1	S	945	0	783	7	0
2	B	165	0	115	2	0
2	D	206	0	187	1	0
2	F	175	0	138	5	0
2	H	195	0	178	2	0
2	J	189	0	152	1	0
2	L	189	0	154	6	0
2	N	169	0	115	0	0
2	P	159	0	123	0	0
2	R	181	0	148	4	0
2	T	141	0	107	1	0
3	A	3	0	0	0	0
3	C	3	0	0	0	0
3	E	3	0	0	0	0
3	G	3	0	0	0	0
3	I	2	0	0	0	0
3	K	3	0	0	0	0
3	M	3	0	0	0	0
3	O	3	0	0	0	0
3	Q	3	0	0	0	0
3	S	3	0	0	0	0
4	A	4	0	0	0	0
4	C	1	0	0	0	0
4	E	3	0	0	0	0
4	G	1	0	0	0	0
4	I	3	0	0	1	0
4	K	3	0	0	0	0
4	M	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	Q	1	0	0	0	0
4	S	2	0	0	0	0
All	All	11377	0	9587	84	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 4.

All (84) 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:87:GLU:OE1	1:C:90:ARG:NH2	2.20	0.75
1:I:27:ILE:HB	1:I:63:ILE:HB	1.69	0.75
1:G:41:GLN:HE22	2:H:1617:LYS:HE2	1.52	0.74
1:M:27:ILE:HB	1:M:63:ILE:HB	1.71	0.72
1:I:39:LEU:HD11	2:J:1621:THR:HG22	1.71	0.72
1:K:85:ILE:HD13	2:L:1623:LEU:HD23	1.76	0.68
1:K:29:THR:HG22	1:K:52:ILE:HG13	1.80	0.61
1:C:27:ILE:HB	1:C:63:ILE:HB	1.82	0.61
1:O:52:ILE:HA	1:O:63:ILE:HD11	1.84	0.60
1:S:27:ILE:HB	1:S:63:ILE:HB	1.83	0.59
1:Q:142:VAL:HG12	1:S:85:ILE:HG12	1.83	0.59
1:A:130:ILE:HD11	1:A:144:MET:HE1	1.84	0.59
1:O:27:ILE:HB	1:O:63:ILE:HB	1.84	0.58
2:L:1619:TYR:O	2:L:1623:LEU:HD13	2.03	0.58
1:S:112:LEU:HD12	2:T:1624:ILE:HD12	1.85	0.58
1:E:4:LEU:H	1:E:4:LEU:HD23	1.68	0.58
1:I:34:THR:HA	1:I:37:ARG:HE	1.69	0.57
1:I:106:ARG:O	1:I:110:THR:HG22	2.06	0.56
1:M:136:VAL:HG12	1:O:100:ILE:HB	1.88	0.55
1:M:52:ILE:HG23	1:M:63:ILE:HD11	1.89	0.54
1:M:55:VAL:HG23	1:M:63:ILE:HD12	1.90	0.54
1:A:121:VAL:HA	1:A:124:MET:HE3	1.90	0.54
1:M:39:LEU:HD21	1:M:112:LEU:HD11	1.91	0.53
1:I:117:THR:HG21	1:K:117:THR:OG1	2.09	0.53
1:E:117:THR:HG21	1:G:117:THR:OG1	2.09	0.52
1:E:112:LEU:HD12	2:F:1624:ILE:HD13	1.91	0.52
1:A:87:GLU:HG3	2:B:1613:VAL:HA	1.92	0.51
1:G:41:GLN:NE2	2:H:1617:LYS:HE2	2.23	0.51
1:Q:27:ILE:HB	1:Q:63:ILE:HB	1.92	0.51
1:C:5:THR:OG1	1:C:6:GLU:N	2.44	0.50
1:I:125:ILE:HG12	1:K:105:LEU:HD23	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:9:ILE:HG12	1:M:69:LEU:HD11	1.93	0.50
2:R:1610:ALA:O	2:R:1613:VAL:HG22	2.11	0.50
1:E:92:PHE:CZ	2:F:1624:ILE:HD11	2.47	0.50
1:M:41:GLN:O	1:M:43:PRO:HD3	2.13	0.48
1:K:32:LEU:O	1:K:36:MET:HG2	2.14	0.48
1:E:39:LEU:HD21	1:E:112:LEU:HD11	1.96	0.48
1:I:135:GLN:HG2	1:K:101:SER:HA	1.96	0.47
1:E:27:ILE:HB	1:E:63:ILE:HB	1.97	0.47
1:A:102:ALA:HB2	1:C:130:ILE:HG22	1.96	0.47
1:O:18:LEU:HD12	1:O:116:LEU:HG	1.97	0.47
1:E:116:LEU:HD11	2:F:1625:GLN:HG2	1.97	0.46
1:M:26:THR:HA	1:M:63:ILE:O	2.16	0.46
1:E:106:ARG:O	1:E:110:THR:HG23	2.16	0.46
1:A:142:VAL:HG22	1:C:85:ILE:HD13	1.98	0.46
1:I:49:GLN:NE2	4:I:601:HOH:O	2.49	0.46
1:O:112:LEU:O	1:O:116:LEU:HD12	2.16	0.45
1:S:41:GLN:O	1:S:43:PRO:HD3	2.16	0.45
1:I:138:TYR:O	1:I:142:VAL:HG13	2.17	0.45
1:C:92:PHE:CE1	1:C:108:VAL:HG21	2.51	0.45
1:I:124:MET:HG2	2:L:1631:PHE:CG	2.52	0.45
1:Q:112:LEU:HD12	2:R:1624:ILE:HD12	1.99	0.44
1:Q:141:PHE:O	1:Q:145:MET:HG2	2.18	0.44
1:S:124:MET:HE3	1:S:124:MET:HB2	1.77	0.44
1:I:14:GLU:O	1:I:18:LEU:HD23	2.18	0.44
1:I:100:ILE:HG22	1:I:105:LEU:HB2	1.99	0.44
1:K:85:ILE:HD13	2:L:1623:LEU:CD2	2.46	0.43
1:O:26:THR:HB	1:O:62:THR:OG1	2.18	0.43
1:C:143:GLN:HG3	1:E:4:LEU:HD21	1.99	0.43
2:R:1630:LYS:HZ1	1:S:147:ALA:HB3	1.84	0.43
1:I:66:PRO:O	1:I:70:THR:HG23	2.17	0.43
1:I:100:ILE:CG2	1:I:105:LEU:HB2	2.49	0.43
1:I:117:THR:O	1:I:121:VAL:HG13	2.19	0.42
1:A:84:GLU:HB3	2:B:1619:TYR:CD2	2.54	0.42
1:K:92:PHE:CD1	1:K:108:VAL:HG11	2.55	0.42
1:M:110:THR:HG23	1:O:121:VAL:HG11	2.01	0.42
1:A:145:MET:HG3	2:D:1623:LEU:HG	2.01	0.42
1:K:27:ILE:HB	1:K:63:ILE:HB	2.01	0.42
1:Q:47:GLU:O	1:Q:51:MET:HG3	2.20	0.42
2:L:1620:ALA:O	2:L:1624:ILE:HG13	2.20	0.41
1:O:37:ARG:HA	1:O:41:GLN:O	2.20	0.41
1:Q:104:GLU:H	1:Q:104:GLU:HG3	1.71	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:1619:TYR:CE2	2:L:1623:LEU:HD11	2.55	0.41
1:E:41:GLN:O	1:E:43:PRO:HD3	2.21	0.41
1:C:52:ILE:HA	1:C:63:ILE:HD11	2.03	0.41
1:K:26:THR:HB	1:K:62:THR:HB	2.03	0.41
1:S:26:THR:HB	1:S:62:THR:HB	2.03	0.41
2:F:1614:THR:HG23	2:F:1616:GLY:N	2.35	0.41
1:O:22:ASP:OD1	1:O:23:GLY:N	2.54	0.41
2:F:1614:THR:HG23	2:F:1616:GLY:H	1.85	0.40
1:I:119:GLU:O	1:I:123:GLU:HG3	2.21	0.40
1:M:38:SER:OG	1:M:111:ASN:HB3	2.21	0.40
1:E:100:ILE:HB	1:G:136:VAL:HG12	2.03	0.40
1:Q:15:ALA:HA	2:R:1625:GLN:HE22	1.86	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	
1	A	126/148 (85%)	124 (98%)	2 (2%)	0	100	100
1	C	134/148 (90%)	133 (99%)	1 (1%)	0	100	100
1	E	132/148 (89%)	127 (96%)	5 (4%)	0	100	100
1	G	132/148 (89%)	129 (98%)	3 (2%)	0	100	100
1	I	124/148 (84%)	118 (95%)	6 (5%)	0	100	100
1	K	137/148 (93%)	132 (96%)	5 (4%)	0	100	100
1	M	131/148 (88%)	127 (97%)	4 (3%)	0	100	100
1	O	131/148 (88%)	129 (98%)	2 (2%)	0	100	100
1	Q	133/148 (90%)	127 (96%)	6 (4%)	0	100	100
1	S	134/148 (90%)	130 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	21/37 (57%)	19 (90%)	2 (10%)	0	100	100
2	D	24/37 (65%)	24 (100%)	0	0	100	100
2	F	21/37 (57%)	20 (95%)	1 (5%)	0	100	100
2	H	22/37 (60%)	22 (100%)	0	0	100	100
2	J	24/37 (65%)	24 (100%)	0	0	100	100
2	L	22/37 (60%)	22 (100%)	0	0	100	100
2	N	22/37 (60%)	21 (96%)	1 (4%)	0	100	100
2	P	19/37 (51%)	18 (95%)	1 (5%)	0	100	100
2	R	23/37 (62%)	23 (100%)	0	0	100	100
2	T	18/37 (49%)	18 (100%)	0	0	100	100
All	All	1530/1850 (83%)	1487 (97%)	43 (3%)	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	
1	A	80/125 (64%)	78 (98%)	2 (2%)	47	67
1	C	99/125 (79%)	98 (99%)	1 (1%)	76	88
1	E	94/125 (75%)	94 (100%)	0	100	100
1	G	90/125 (72%)	90 (100%)	0	100	100
1	I	78/125 (62%)	76 (97%)	2 (3%)	46	66
1	K	93/125 (74%)	91 (98%)	2 (2%)	52	71
1	M	83/125 (66%)	83 (100%)	0	100	100
1	O	81/125 (65%)	80 (99%)	1 (1%)	71	85
1	Q	79/125 (63%)	79 (100%)	0	100	100
1	S	80/125 (64%)	80 (100%)	0	100	100
2	B	10/32 (31%)	10 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	18/32 (56%)	18 (100%)	0	100	100
2	F	13/32 (41%)	12 (92%)	1 (8%)	13	20
2	H	17/32 (53%)	17 (100%)	0	100	100
2	J	14/32 (44%)	13 (93%)	1 (7%)	14	23
2	L	14/32 (44%)	14 (100%)	0	100	100
2	N	10/32 (31%)	9 (90%)	1 (10%)	7	11
2	P	12/32 (38%)	12 (100%)	0	100	100
2	R	13/32 (41%)	13 (100%)	0	100	100
2	T	10/32 (31%)	10 (100%)	0	100	100
All	All	988/1570 (63%)	977 (99%)	11 (1%)	73	87

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

Mol	Chain	Res	Type
1	A	38	SER
1	A	86	ARG
1	C	21	LYS
2	F	1619	TYR
1	I	18	LEU
1	I	143	GLN
2	J	1628	PHE
1	K	13	LYS
1	K	122	ASP
2	N	1628	PHE
1	O	18	LEU

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

Mol	Chain	Res	Type
1	G	41	GLN
1	G	135	GLN
2	R	1625	GLN

### 5.3.3 RNA ⓘ

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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 29 ligands modelled in this entry, 29 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 [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 ⓘ

### 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, 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	132/148 (89%)	0.03	1 (0%) 86 84	52, 89, 132, 152	0
1	C	138/148 (93%)	0.11	1 (0%) 87 86	46, 74, 110, 131	0
1	E	138/148 (93%)	-0.03	0 100 100	50, 74, 96, 120	0
1	G	136/148 (91%)	-0.08	0 100 100	53, 79, 110, 130	0
1	I	130/148 (87%)	0.13	3 (2%) 60 58	52, 88, 129, 144	0
1	K	141/148 (95%)	-0.03	3 (2%) 63 61	53, 74, 106, 139	0
1	M	135/148 (91%)	0.02	0 100 100	64, 88, 111, 138	0
1	O	135/148 (91%)	0.08	3 (2%) 62 60	68, 93, 131, 146	0
1	Q	137/148 (92%)	-0.16	2 (1%) 73 72	60, 89, 125, 148	0
1	S	138/148 (93%)	-0.14	1 (0%) 87 86	62, 89, 124, 153	0
2	B	23/37 (62%)	-0.02	1 (4%) 35 33	73, 86, 108, 114	0
2	D	26/37 (70%)	0.27	1 (3%) 40 39	50, 73, 115, 117	0
2	F	23/37 (62%)	0.16	1 (4%) 35 33	70, 86, 113, 130	0
2	H	24/37 (64%)	0.05	1 (4%) 36 35	64, 79, 111, 122	0
2	J	26/37 (70%)	0.05	0 100 100	74, 95, 122, 128	0
2	L	24/37 (64%)	0.33	1 (4%) 36 35	62, 79, 105, 152	0
2	N	24/37 (64%)	0.25	1 (4%) 36 35	75, 95, 122, 132	0
2	P	21/37 (56%)	0.16	1 (4%) 30 29	78, 92, 109, 131	0
2	R	25/37 (67%)	-0.18	0 100 100	73, 89, 129, 142	0
2	T	20/37 (54%)	0.01	1 (5%) 28 27	77, 94, 113, 117	0
All	All	1596/1850 (86%)	0.01	22 (1%) 75 73	46, 85, 122, 153	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	O	46	ALA	3.6
1	O	65	PHE	3.6
1	A	57	ALA	3.5
2	D	1610	ALA	3.4
1	K	147	ALA	3.3
2	H	1631	PHE	3.3
1	I	91	VAL	2.9
1	Q	92	PHE	2.8
2	B	1619	TYR	2.7
1	K	124	MET	2.5
1	S	92	PHE	2.5
2	L	1628	PHE	2.5
2	P	1616	GLY	2.4
1	Q	100	ILE	2.4
1	I	110	THR	2.3
2	T	1628	PHE	2.3
1	I	98	GLY	2.2
1	O	25	GLY	2.2
2	F	1619	TYR	2.2
1	K	81	SER	2.2
1	C	58	ASP	2.1
2	N	1622	PHE	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 carbohydrates 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( $\text{\AA}^2$ )	Q<0.9
3	CA	A	501	1/1	0.83	0.14	132,132,132,132	0
3	CA	I	501	1/1	0.85	0.12	90,90,90,90	0

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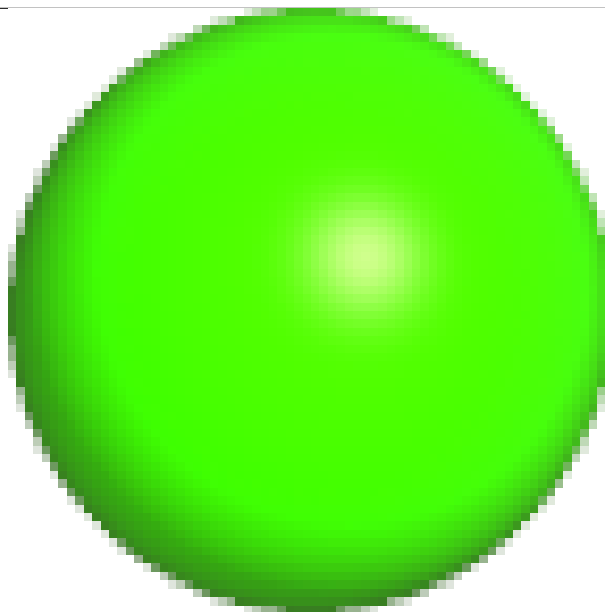
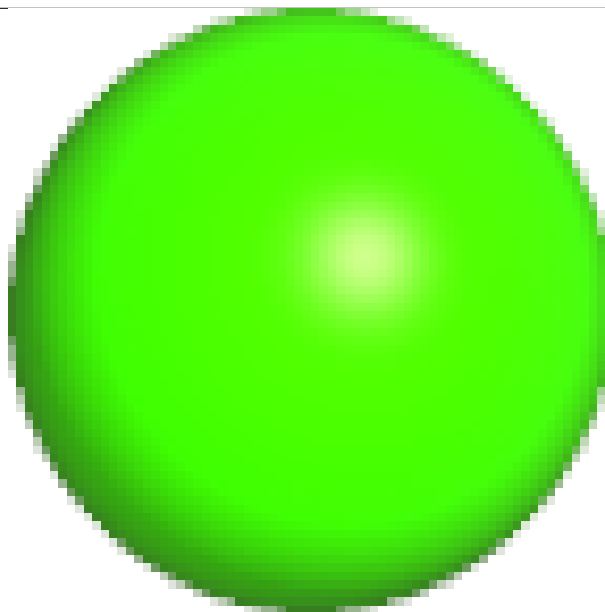
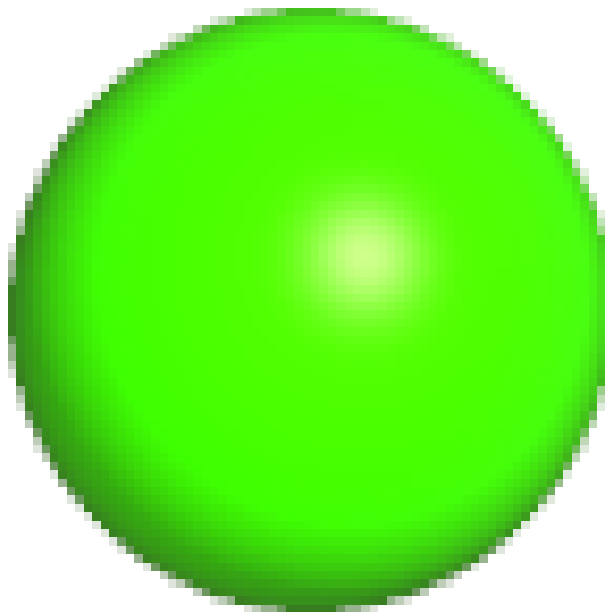
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	CA	S	503	1/1	0.89	0.06	91,91,91,91	0
3	CA	S	501	1/1	0.90	0.16	83,83,83,83	0
3	CA	E	503	1/1	0.93	0.17	77,77,77,77	0
3	CA	M	503	1/1	0.93	0.19	79,79,79,79	0
3	CA	C	502	1/1	0.93	0.10	80,80,80,80	0
3	CA	Q	501	1/1	0.94	0.09	85,85,85,85	0
3	CA	Q	503	1/1	0.94	0.10	110,110,110,110	0
3	CA	C	501	1/1	0.94	0.20	88,88,88,88	0
3	CA	M	501	1/1	0.94	0.11	99,99,99,99	0
3	CA	G	503	1/1	0.94	0.06	88,88,88,88	0
3	CA	O	501	1/1	0.95	0.09	117,117,117,117	0
3	CA	E	501	1/1	0.95	0.13	65,65,65,65	0
3	CA	C	503	1/1	0.96	0.17	59,59,59,59	0
3	CA	O	502	1/1	0.96	0.07	93,93,93,93	0
3	CA	A	502	1/1	0.97	0.10	114,114,114,114	0
3	CA	S	502	1/1	0.97	0.20	71,71,71,71	0
3	CA	K	501	1/1	0.97	0.20	67,67,67,67	0
3	CA	G	502	1/1	0.98	0.11	63,63,63,63	0
3	CA	M	502	1/1	0.98	0.14	80,80,80,80	0
3	CA	G	501	1/1	0.98	0.19	82,82,82,82	0
3	CA	I	502	1/1	0.98	0.15	63,63,63,63	0
3	CA	A	503	1/1	0.98	0.14	62,62,62,62	0
3	CA	Q	502	1/1	0.98	0.17	72,72,72,72	0
3	CA	O	503	1/1	0.98	0.14	77,77,77,77	0
3	CA	K	502	1/1	0.98	0.17	76,76,76,76	0
3	CA	K	503	1/1	0.99	0.16	59,59,59,59	0
3	CA	E	502	1/1	1.00	0.15	53,53,53,53	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 A 501:**

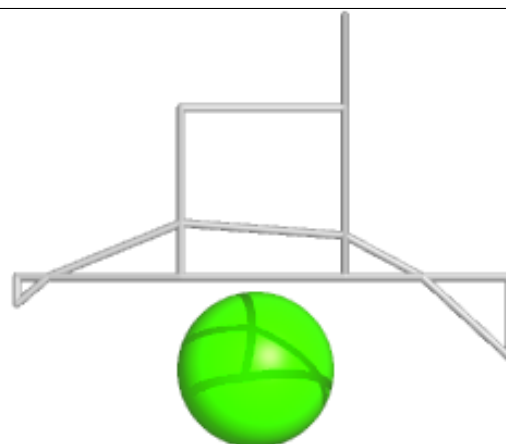
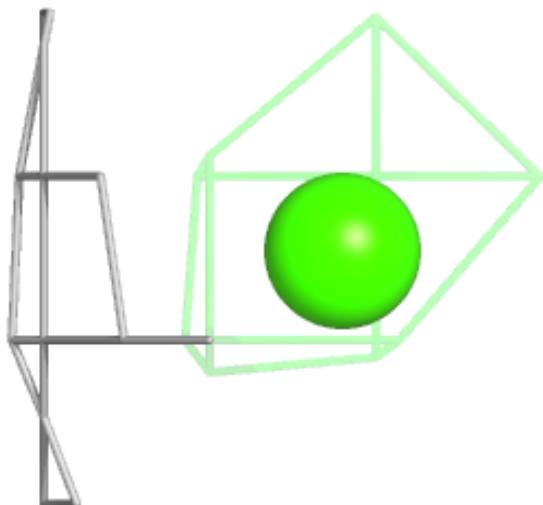
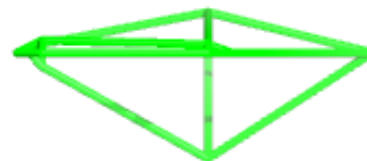
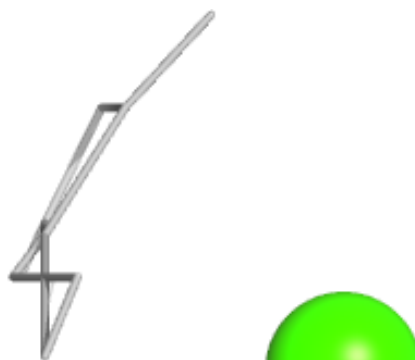
2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)





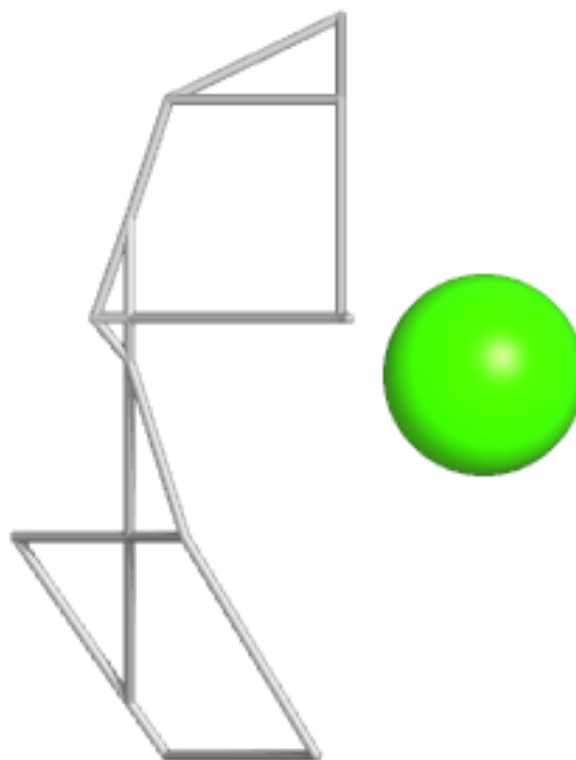
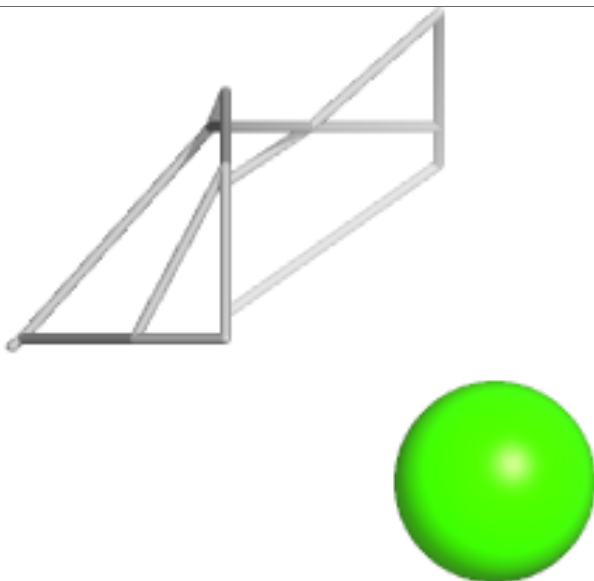
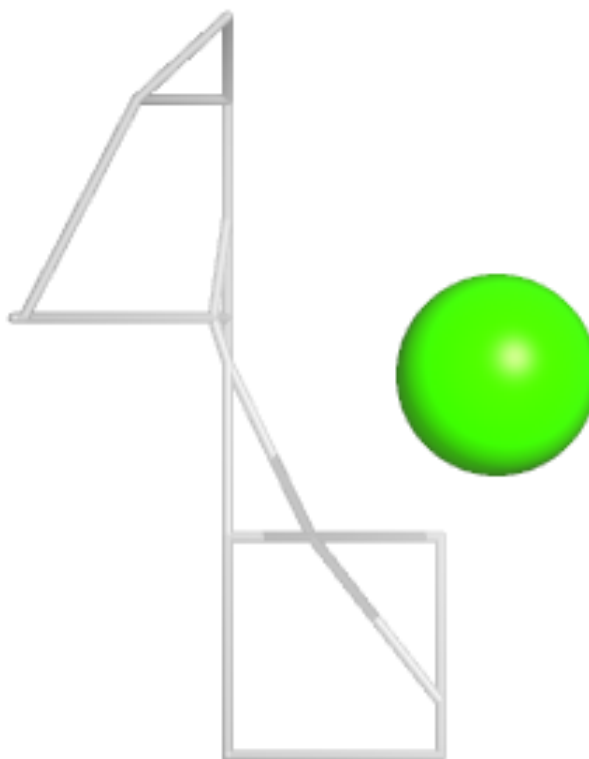
**Electron density around CA I 501:**

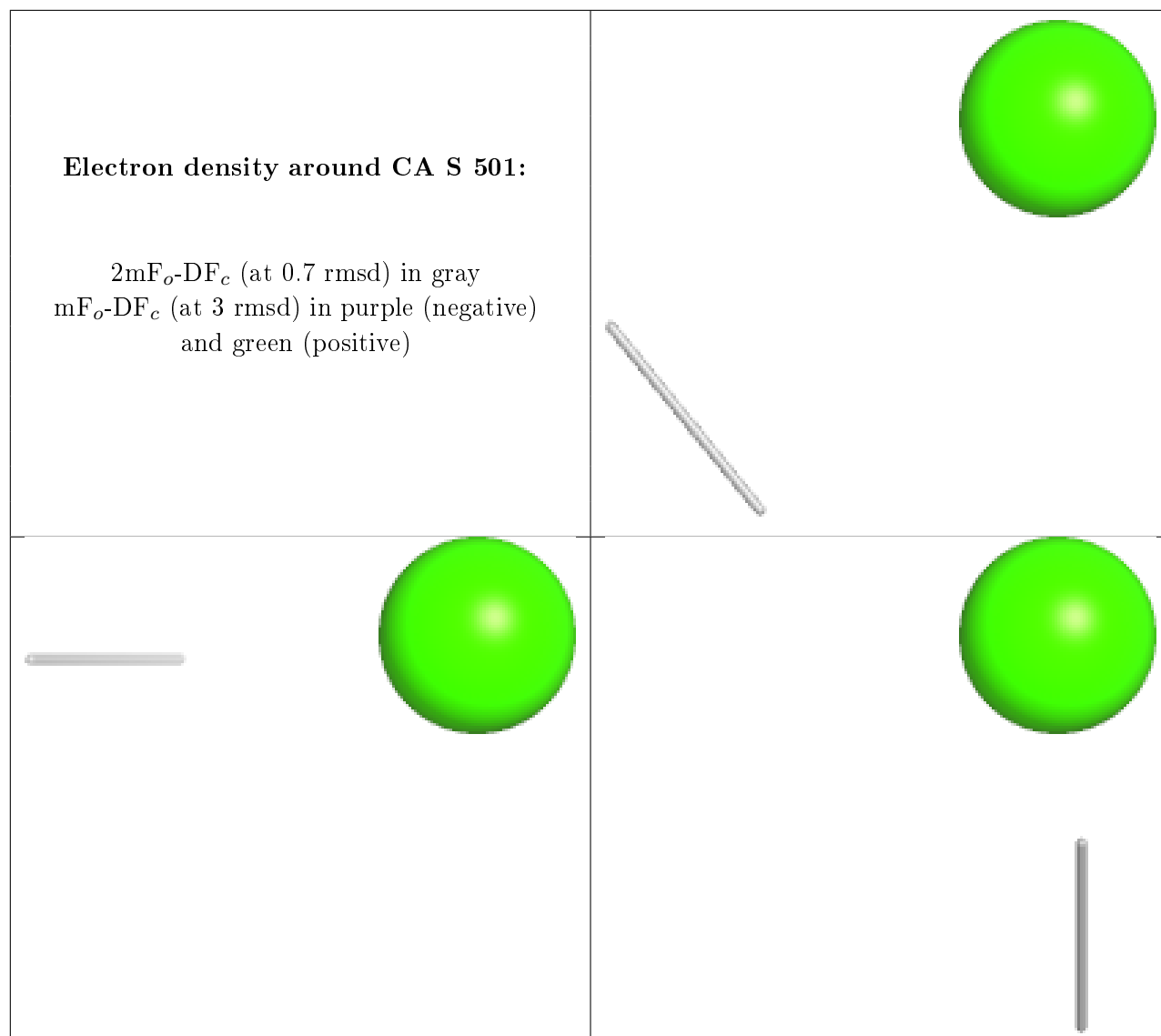
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

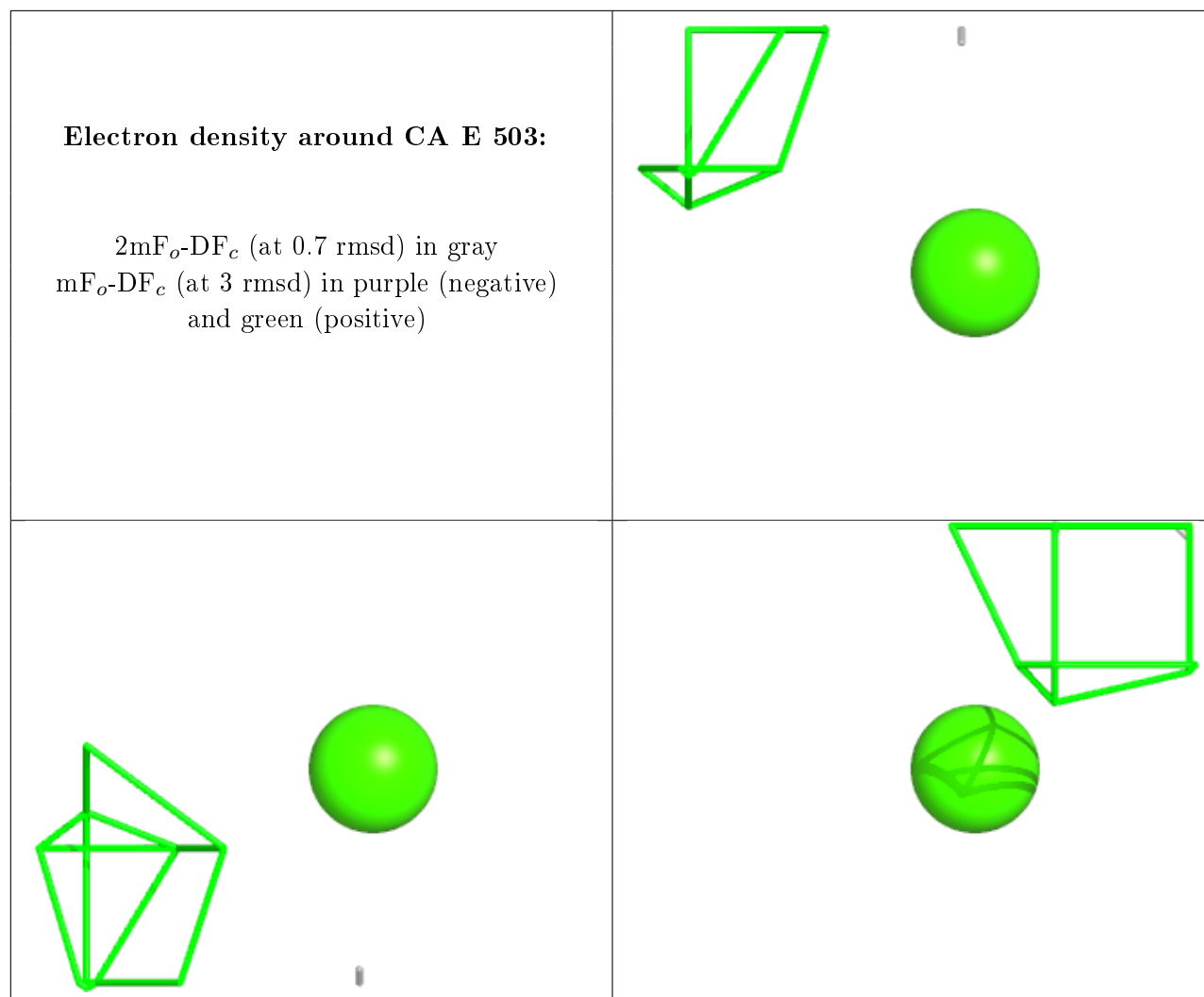


**Electron density around CA S 503:**

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

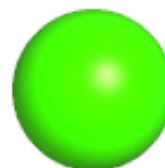
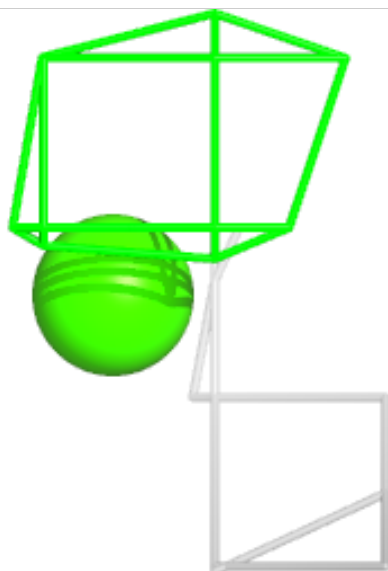
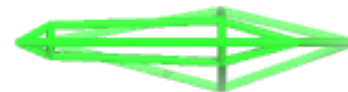






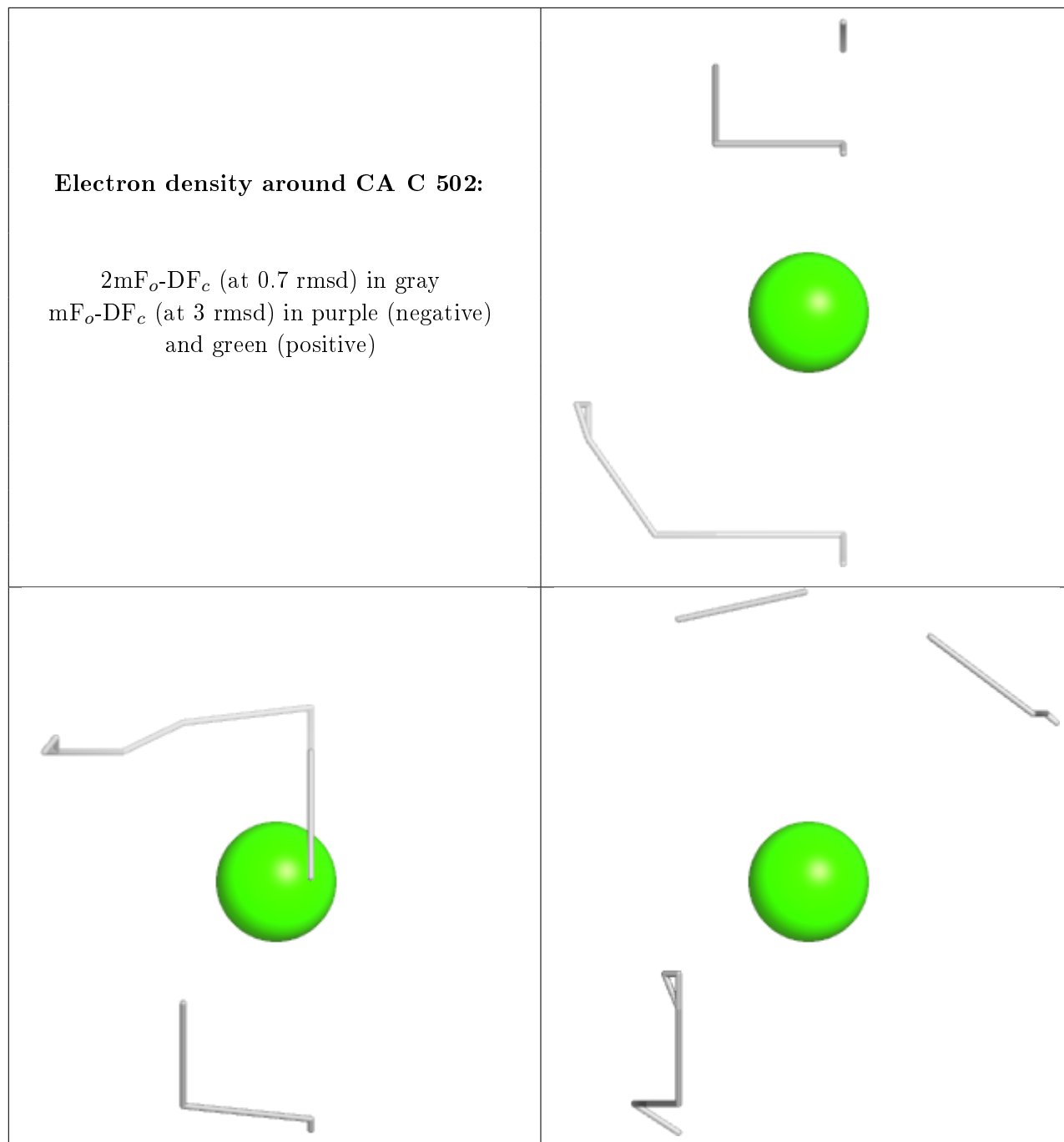
**Electron density around CA M 503:**

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



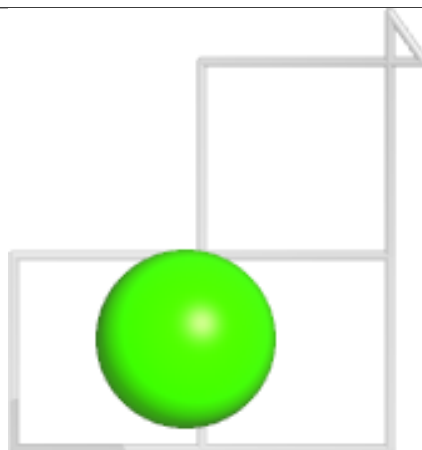
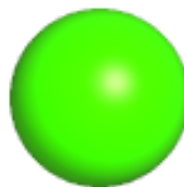
**Electron density around CA C 502:**

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



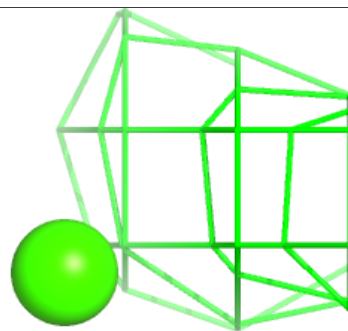
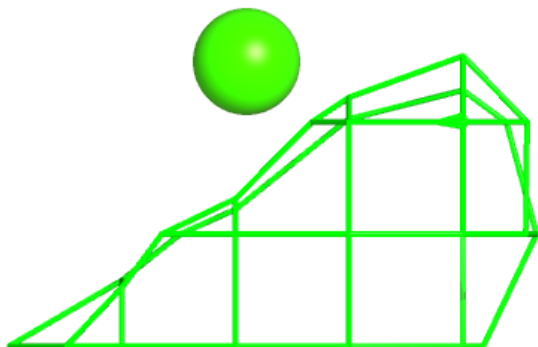
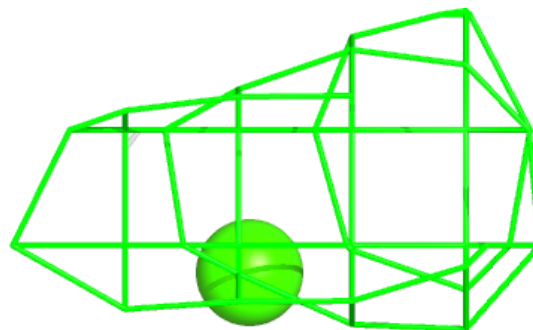
**Electron density around CA Q 501:**

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



**Electron density around CA Q 503:**

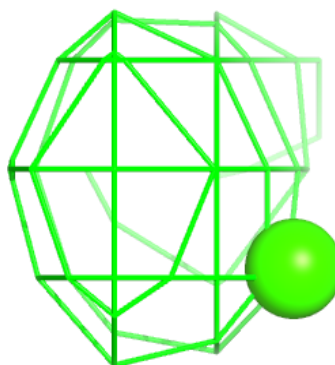
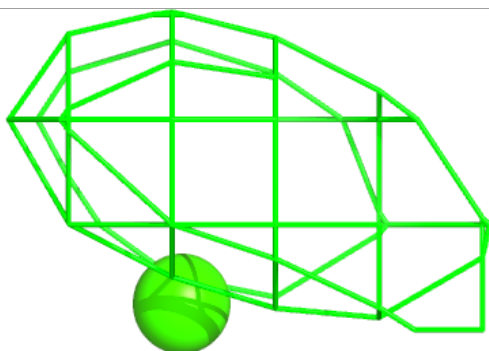
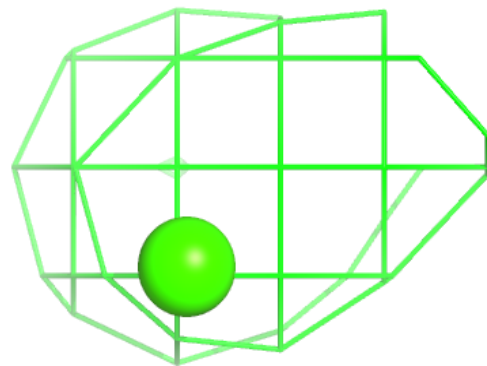
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





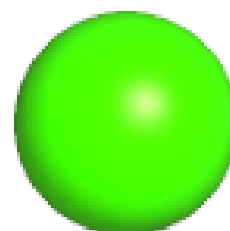
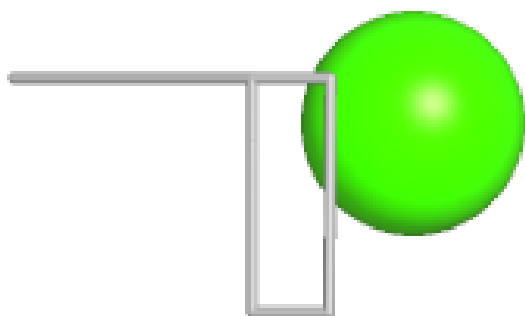
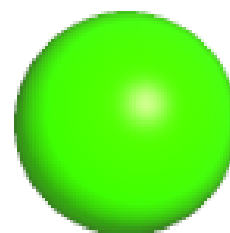
**Electron density around CA C 501:**

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



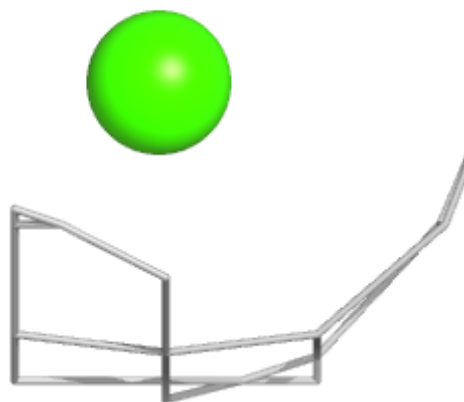
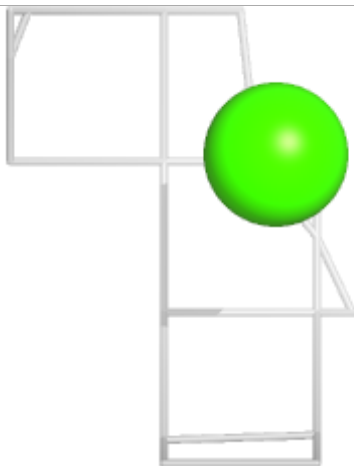
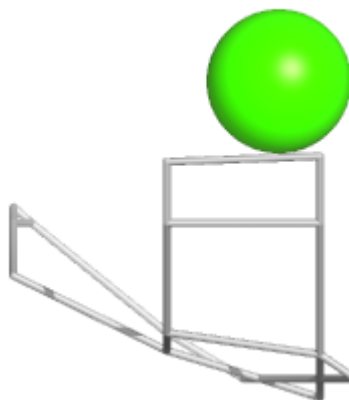
**Electron density around CA M 501:**

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



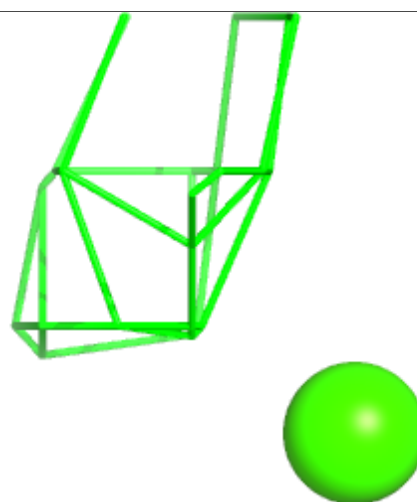
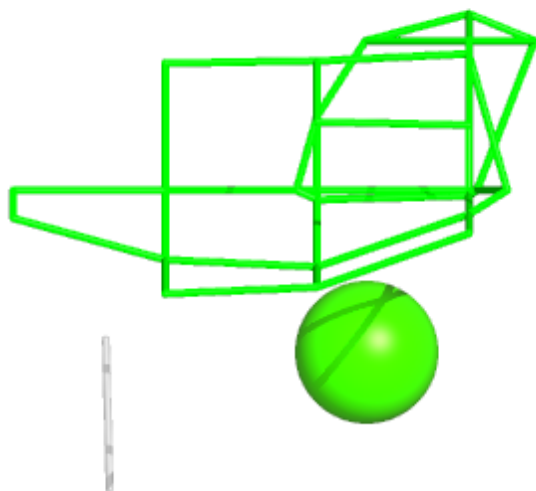
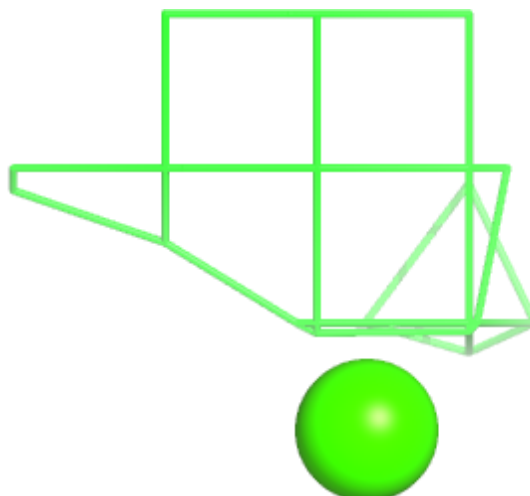
**Electron density around CA G 503:**

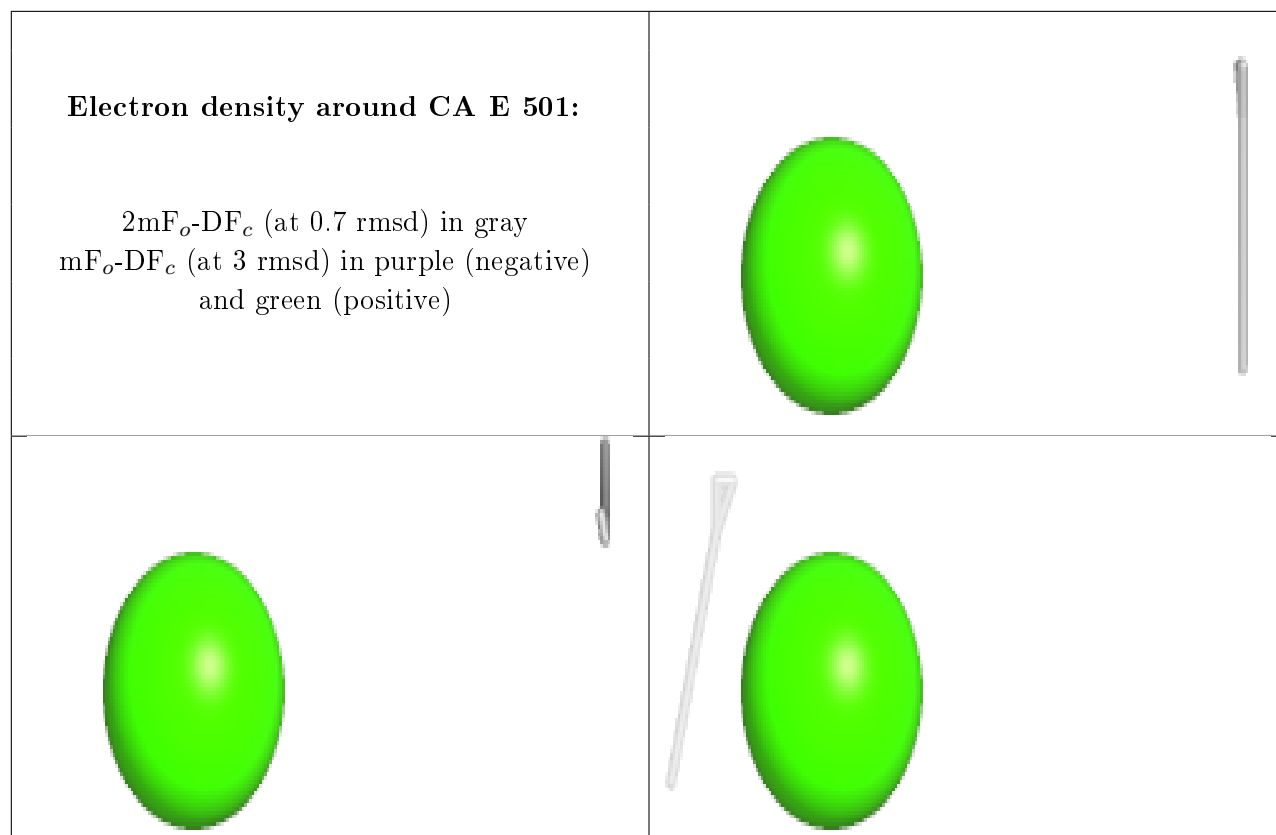
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around CA O 501:**

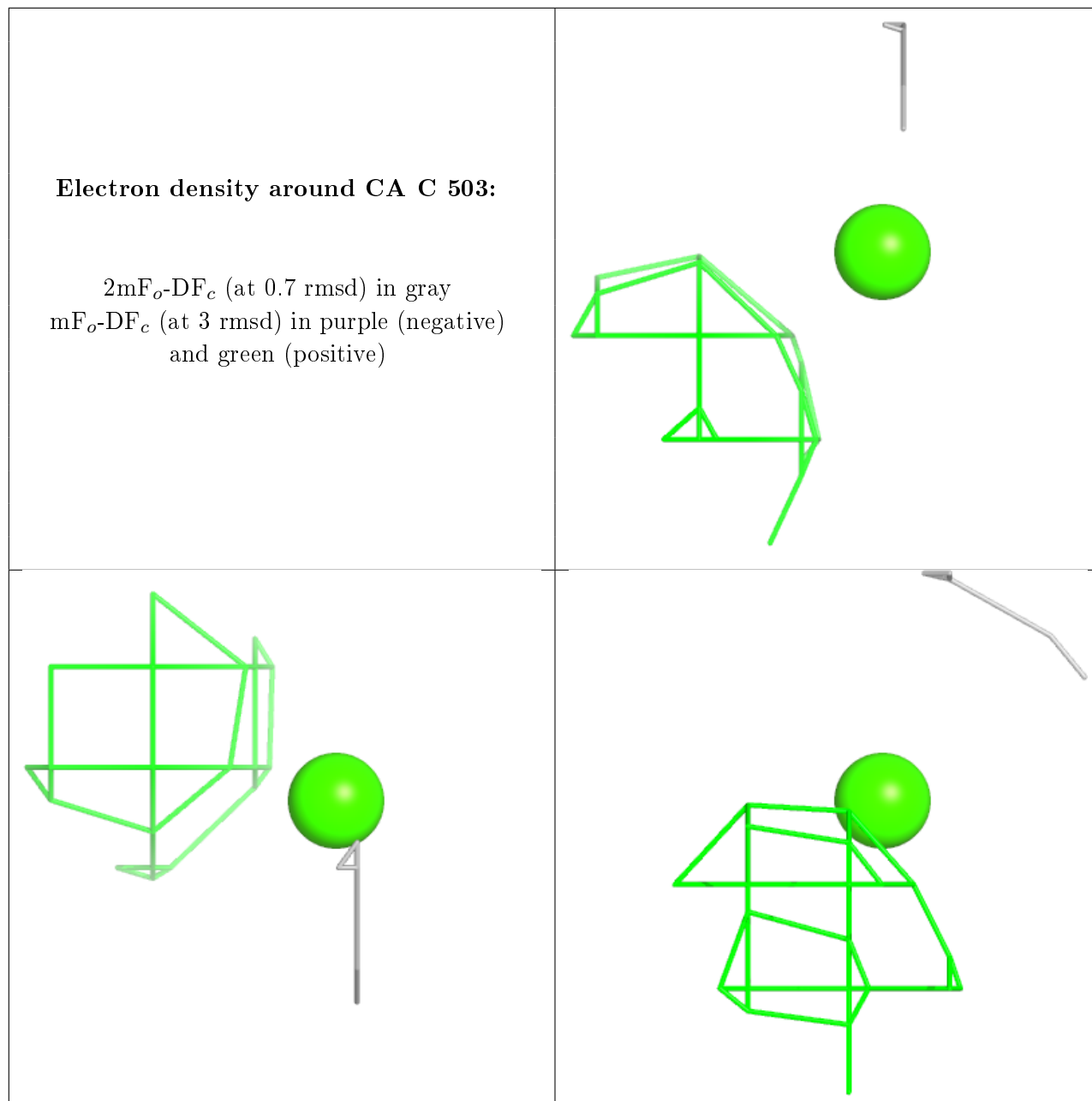
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





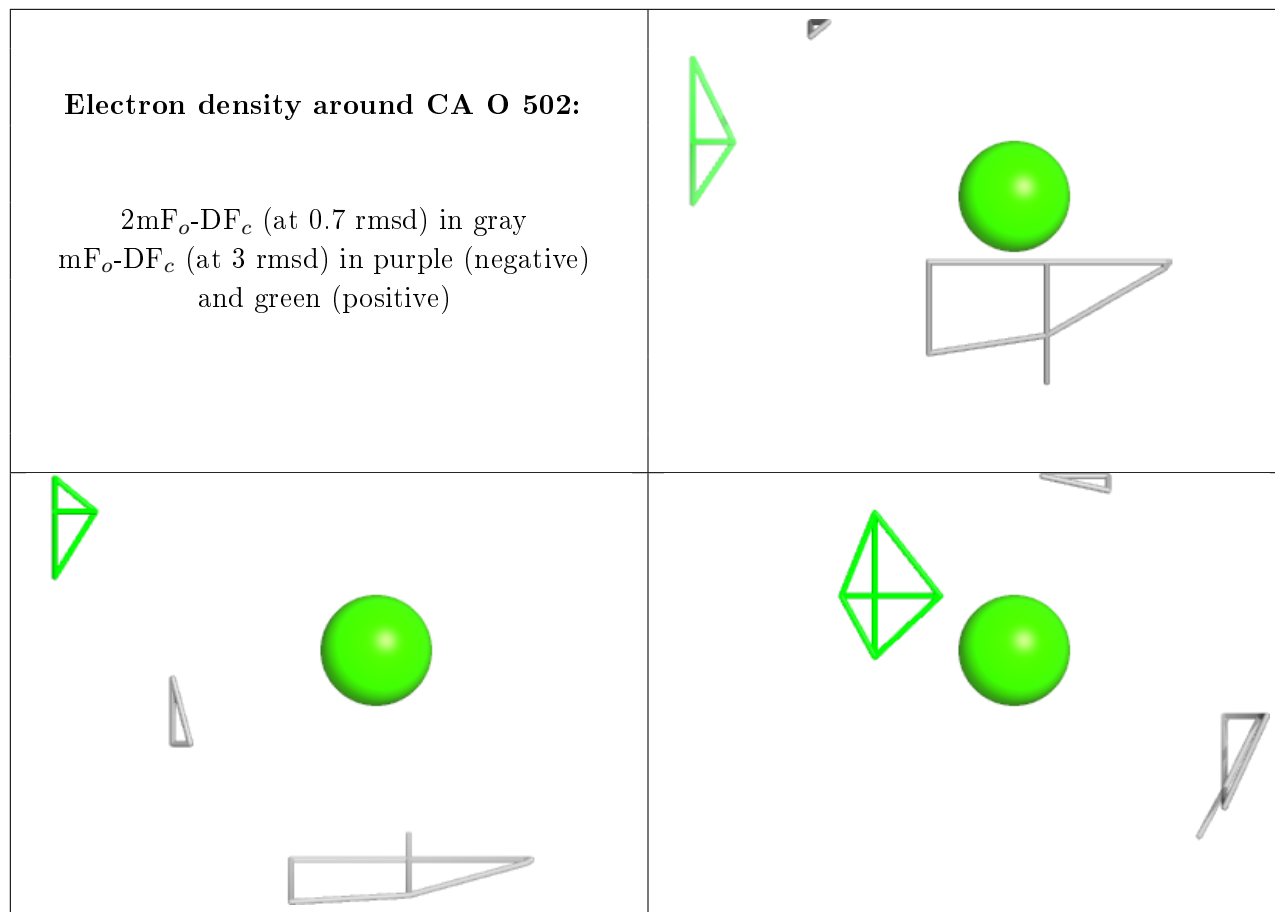
**Electron density around CA C 503:**

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



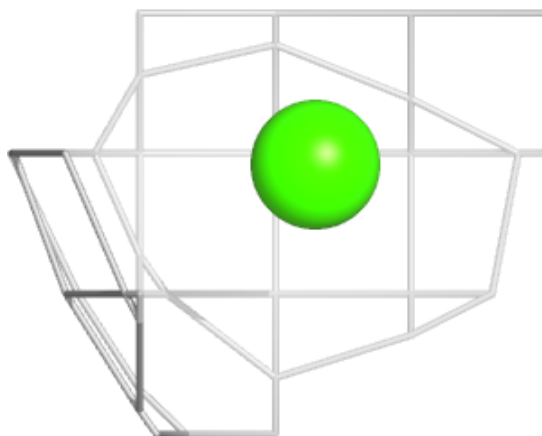
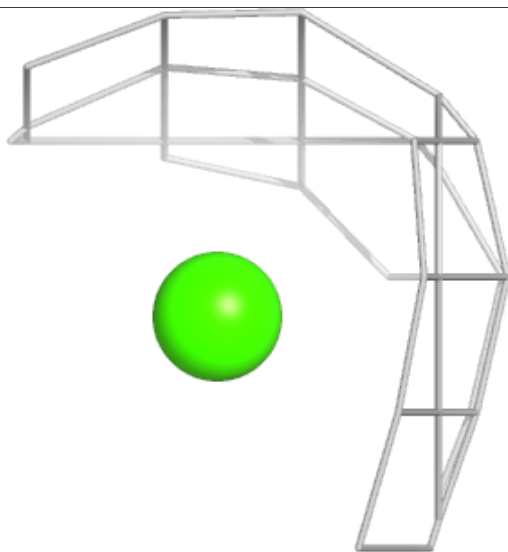
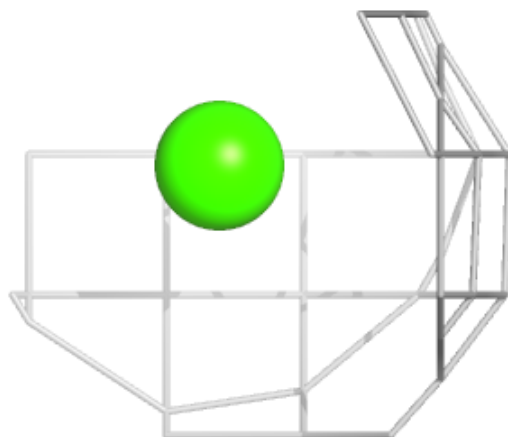
**Electron density around CA O 502:**

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

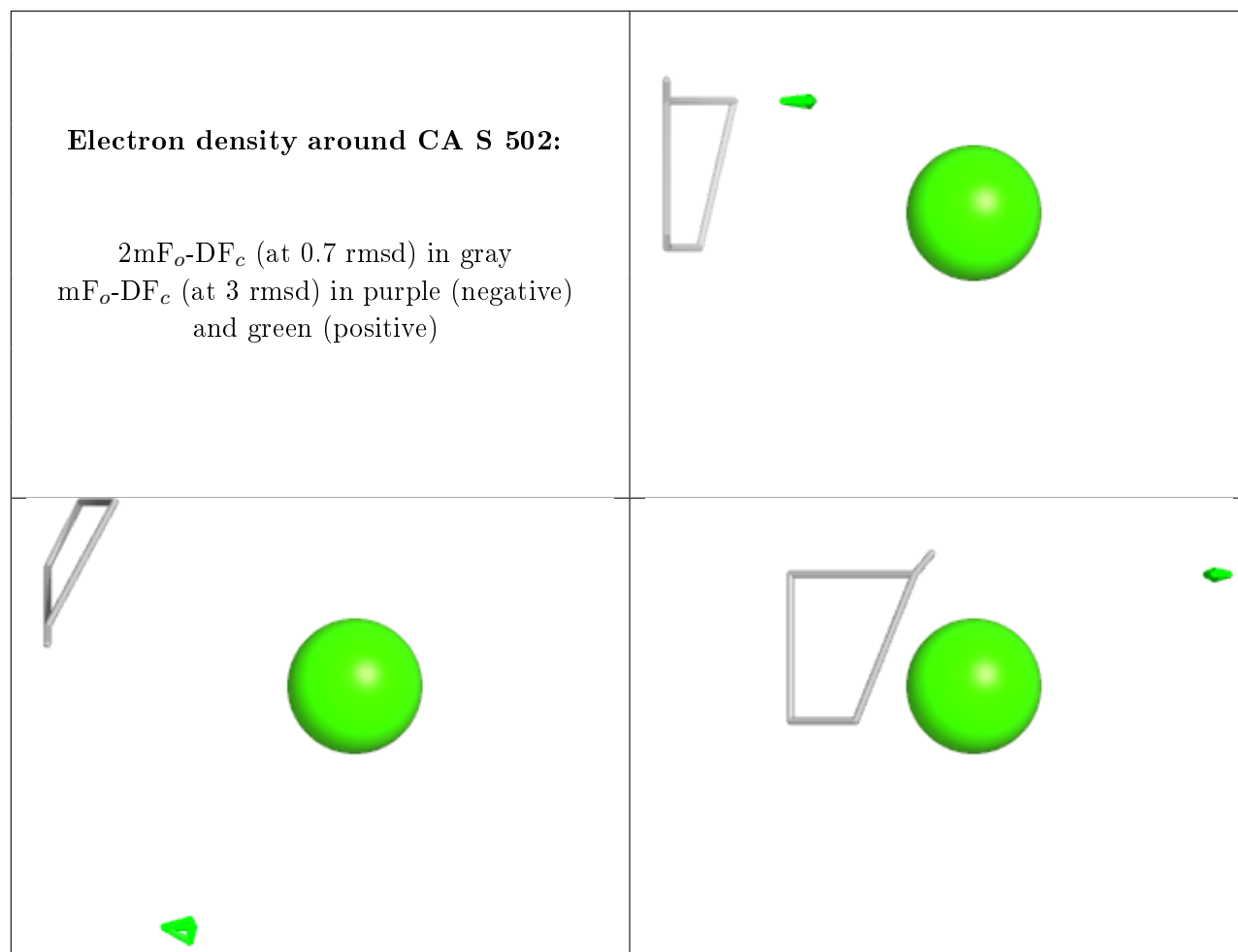


**Electron density around CA A 502:**

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

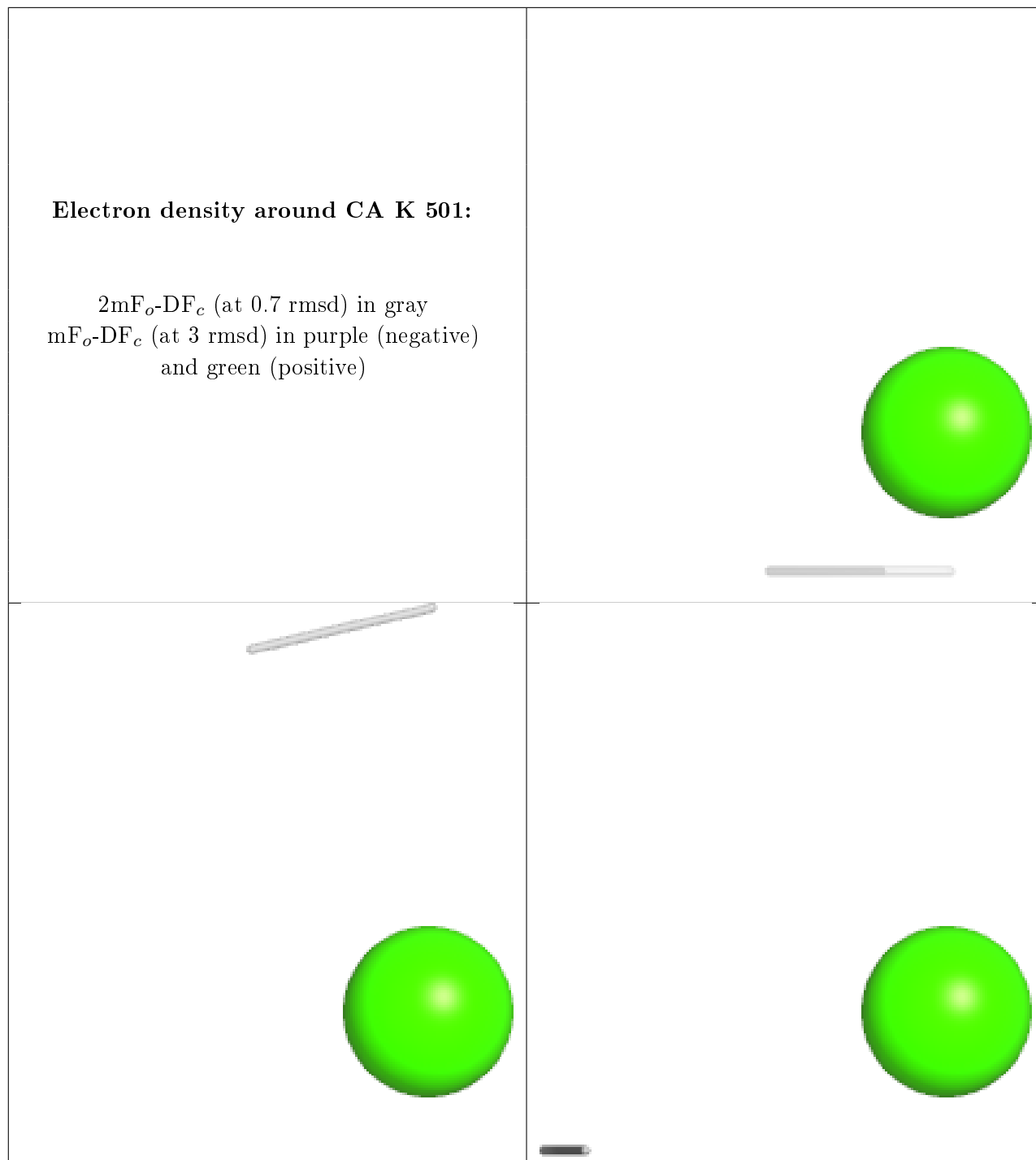


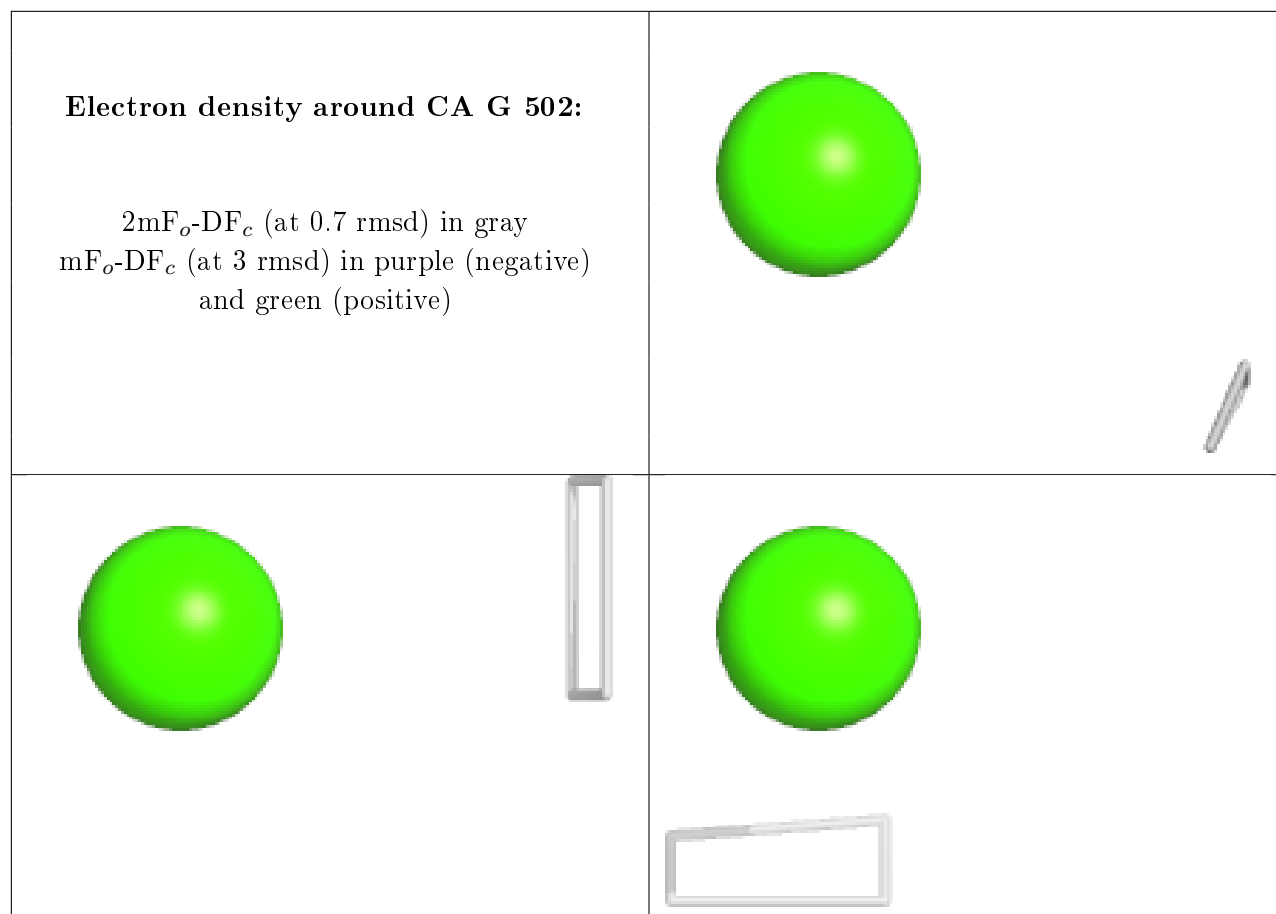




**Electron density around CA K 501:**

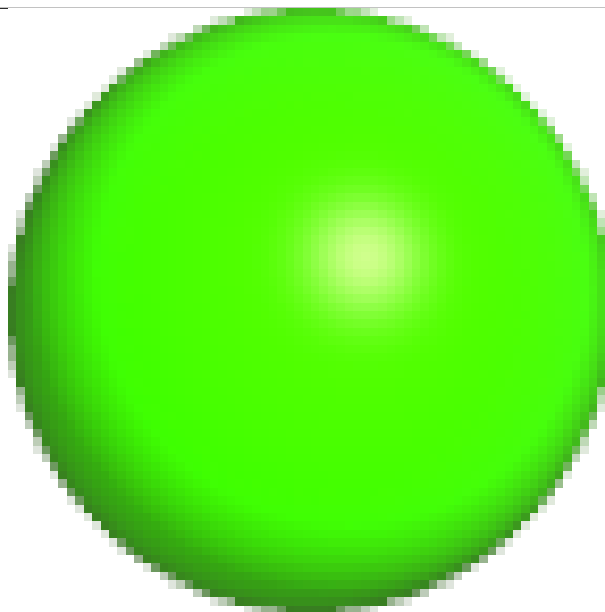
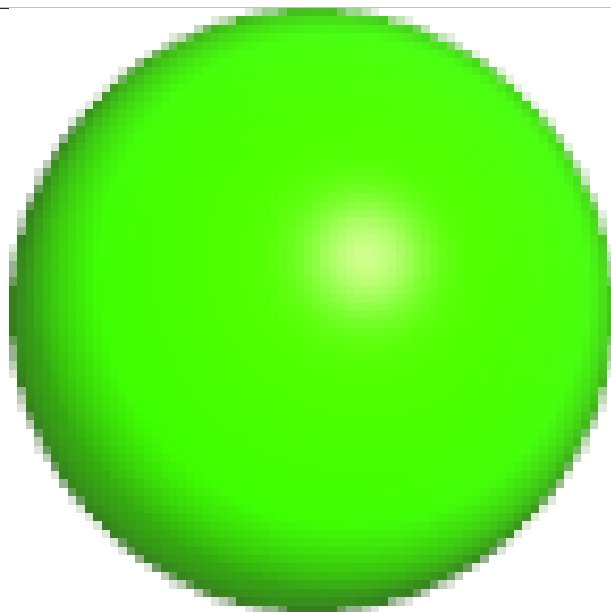
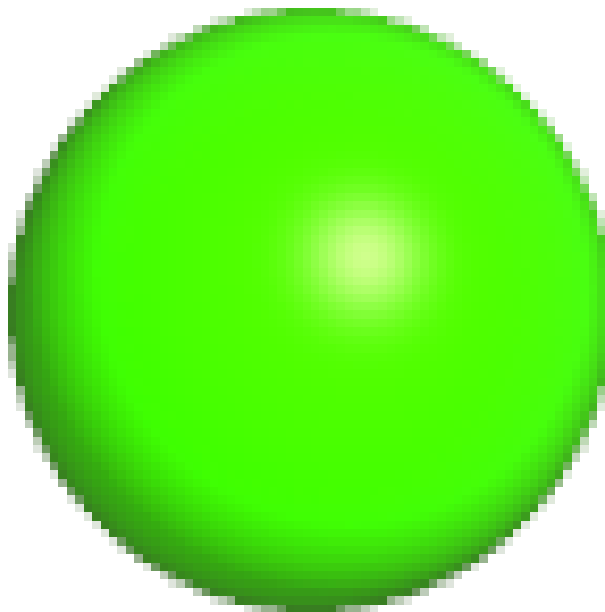
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





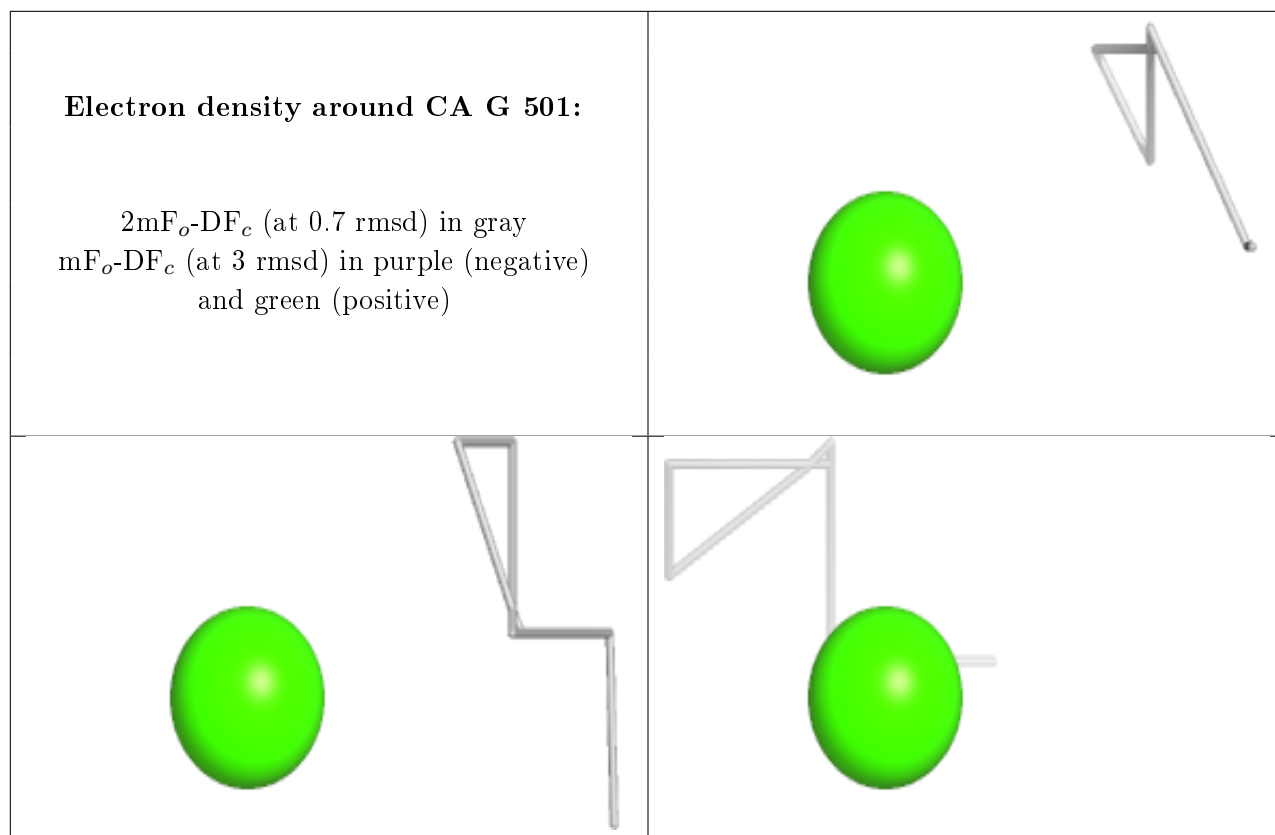
**Electron density around CA M 502:**

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

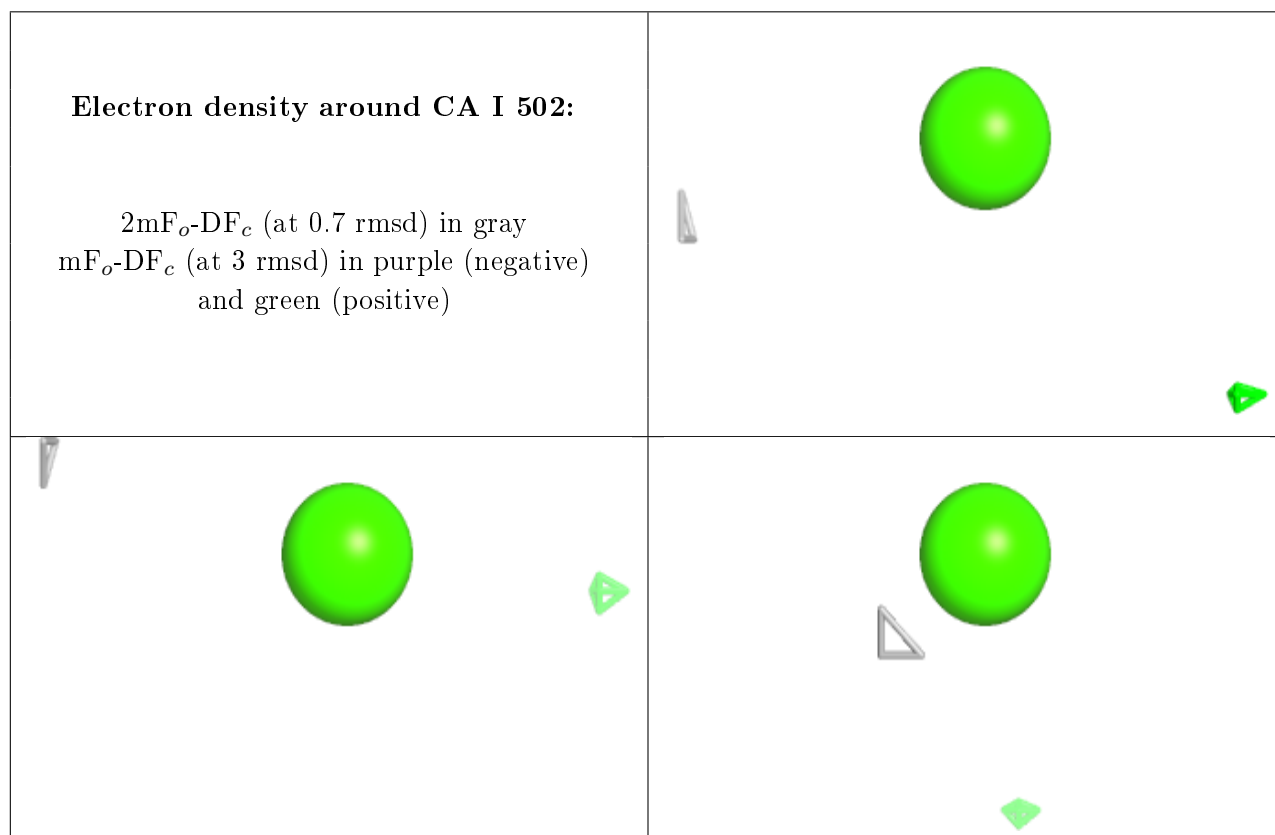


**Electron density around CA G 501:**

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

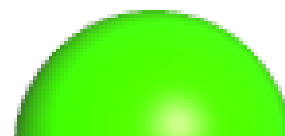
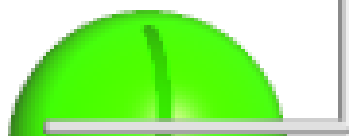
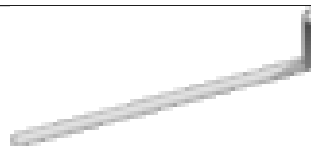
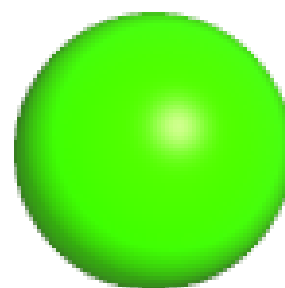
**Electron density around CA I 502:**

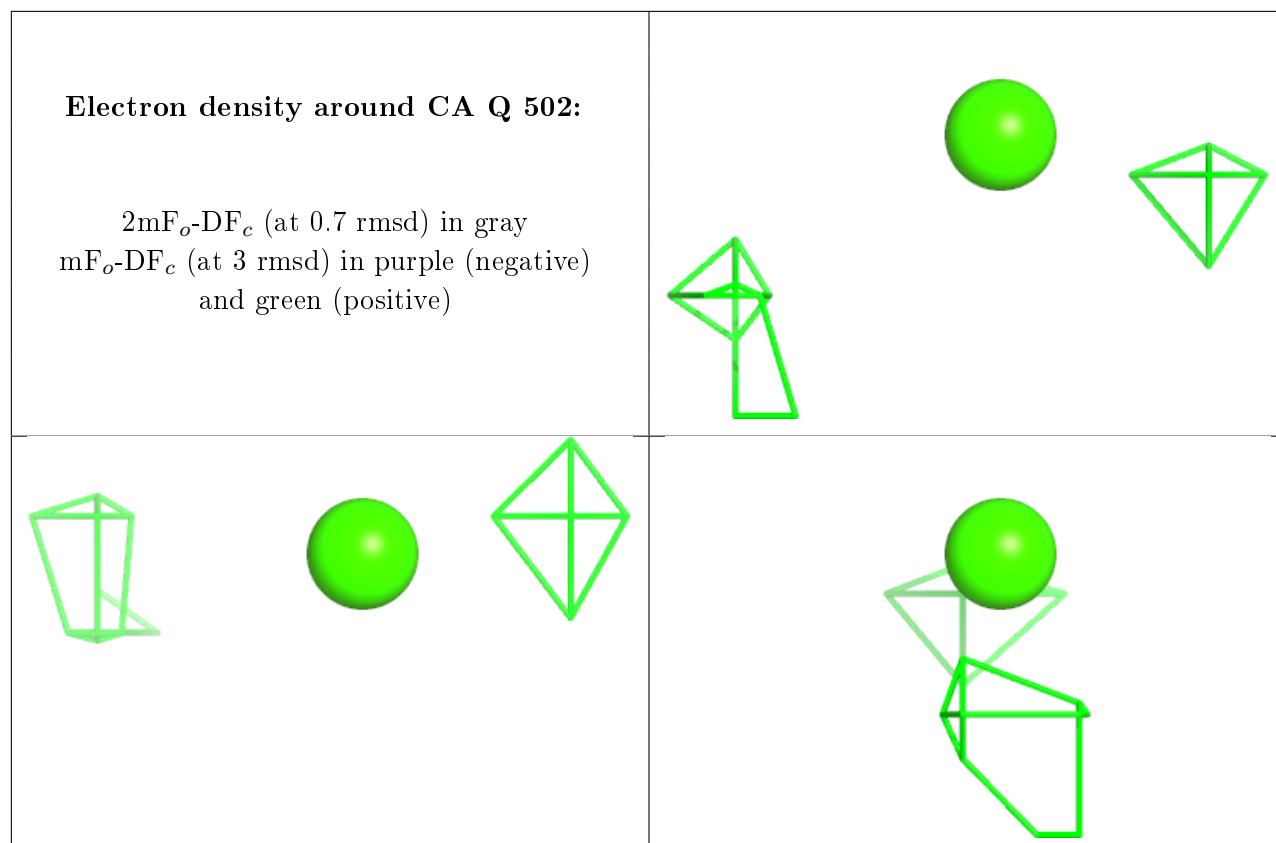
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around CA A 503:**

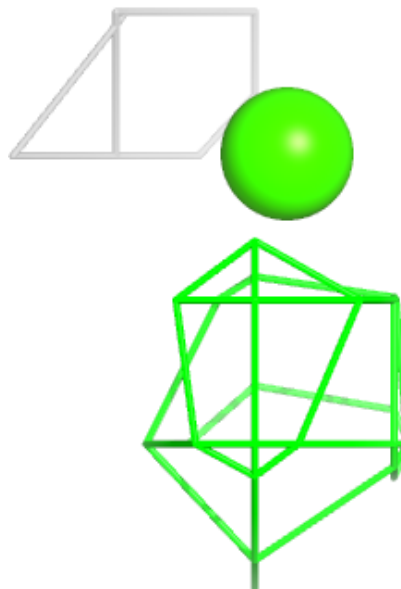
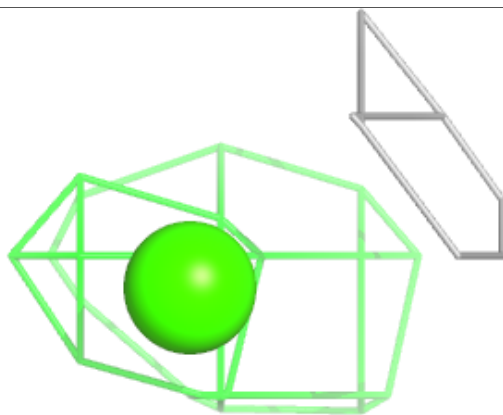
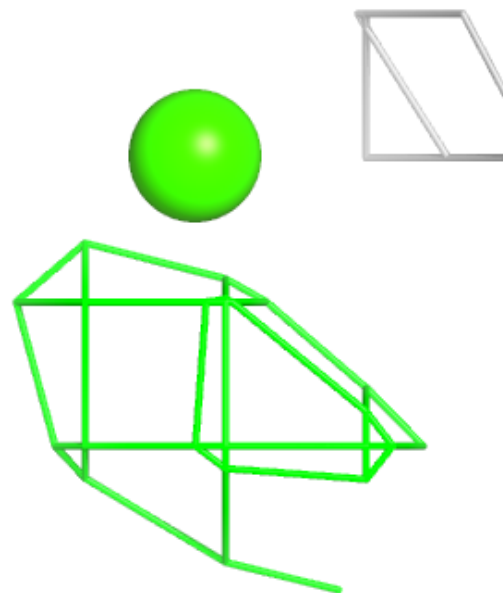
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around CA O 503:**

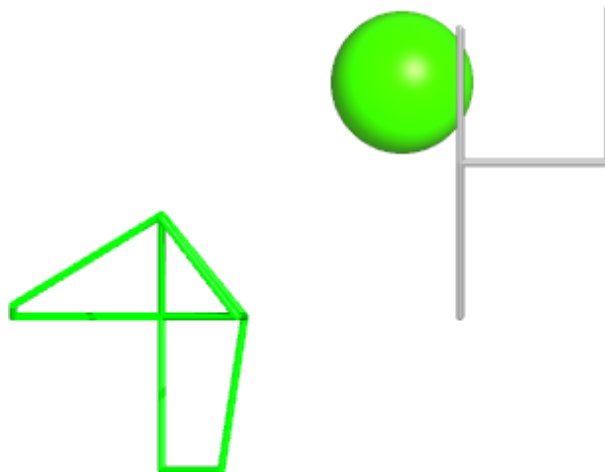
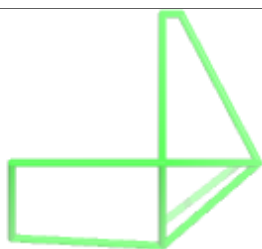
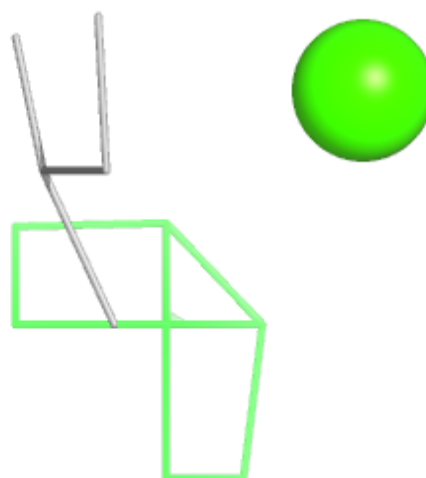
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





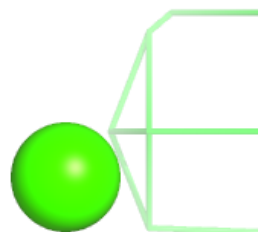
**Electron density around CA K 502:**

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



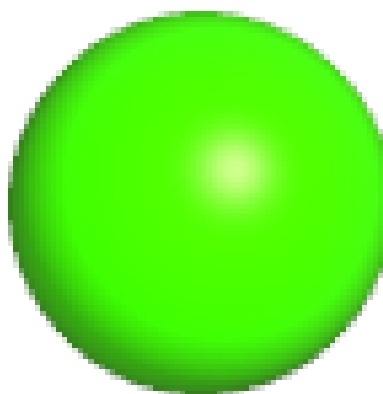
**Electron density around CA K 503:**

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



**Electron density around CA E 502:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers

There are no such residues in this entry.