



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 3, 2026 – 02:20 PM EDT

PDB ID : 9ZB8 / pdb_00009zb8
Title : Crystal Structure of Human GGPPS Bound to Selective Inhibitor CML-07-119
Authors : Ferens, F.G.; Tsantrizos, Y.S.; Lemieux, M.J.
Deposited on : 2025-11-20
Resolution : 2.64 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

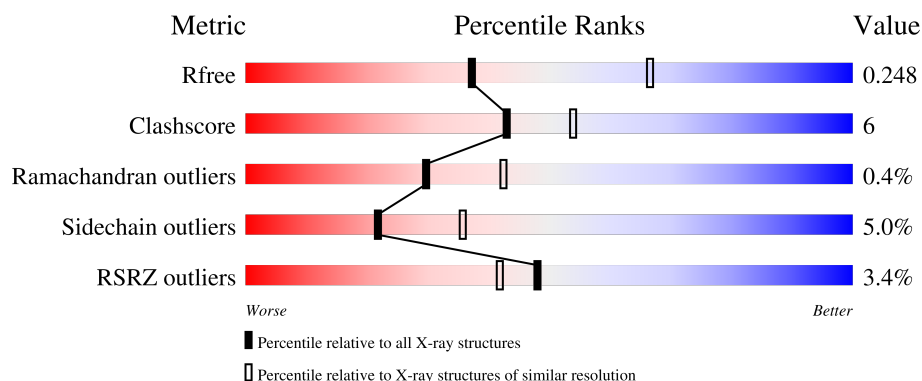
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.64 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}	180053	2053 (2.66-2.62)
Clashscore	190562	2097 (2.66-2.62)
Ramachandran outliers	187476	2066 (2.66-2.62)
Sidechain outliers	187428	2066 (2.66-2.62)
RSRZ outliers	180081	2052 (2.66-2.62)

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 $\leq 5\%$. 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	301	 2% 83% 13% . .
1	B	301	 % 79% 15% . .
1	C	301	 4% 78% 13% . . 5%
1	D	301	 % 81% 11% . .
1	E	301	 % 78% 14% . 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	301	3% 83% 10% 5%
1	G	301	3% 80% 17% • •
1	H	301	2% 83% 13% • • •
1	I	301	7% 82% 11% • 5%
1	J	301	79% 13% • • 5%
1	K	301	2% 78% 15% • • 5%
1	L	301	12% 69% 21% • • 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 57867 atoms, of which 28845 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 Geranylgeranyl pyrophosphate synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	297	Total	C	H	N	O	S	67	0	0
			4881	1565	2447	407	454	8			
1	B	293	Total	C	H	N	O	S	66	0	0
			4819	1547	2417	401	446	8			
1	C	286	Total	C	H	N	O	S	63	0	0
			4704	1507	2364	393	432	8			
1	D	288	Total	C	H	N	O	S	65	0	0
			4729	1517	2374	395	436	7			
1	E	287	Total	C	H	N	O	S	65	0	0
			4707	1511	2361	393	435	7			
1	F	286	Total	C	H	N	O	S	63	0	0
			4704	1507	2364	393	432	8			
1	G	297	Total	C	H	N	O	S	67	0	0
			4881	1565	2447	407	454	8			
1	H	297	Total	C	H	N	O	S	67	0	0
			4881	1565	2447	407	454	8			
1	I	286	Total	C	H	N	O	S	63	0	0
			4704	1507	2364	393	432	8			
1	J	287	Total	C	H	N	O	S	65	0	0
			4707	1511	2361	393	435	7			
1	K	286	Total	C	H	N	O	S	63	0	0
			4695	1508	2355	392	433	7			
1	L	286	Total	C	H	N	O	S	63	0	0
			4704	1507	2364	393	432	8			

There are 12 discrepancies between the modelled and reference sequences:

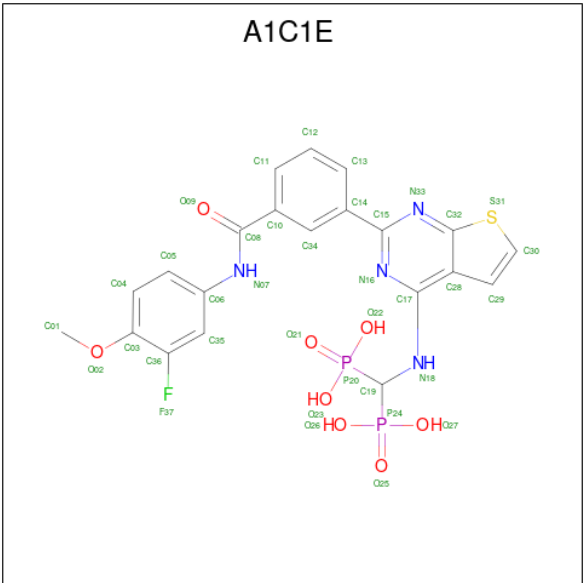
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP O95749
B	0	GLY	-	expression tag	UNP O95749
C	0	GLY	-	expression tag	UNP O95749
D	0	GLY	-	expression tag	UNP O95749
E	0	GLY	-	expression tag	UNP O95749

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	0	GLY	-	expression tag	UNP O95749
G	0	GLY	-	expression tag	UNP O95749
H	0	GLY	-	expression tag	UNP O95749
I	0	GLY	-	expression tag	UNP O95749
J	0	GLY	-	expression tag	UNP O95749
K	0	GLY	-	expression tag	UNP O95749
L	0	GLY	-	expression tag	UNP O95749

- Molecule 2 is {[2-3-[(3-fluoro-4-methoxyphenyl)carbamoyl]phenyl}thieno[2,3-d]pyrimidin-4-yl)amino]methylene}bis(phosphonic acid) (CCD ID: A1C1E) (formula: C₂₁H₁₉FN₄O₈P₂S) (labeled as "Ligand of Interest" by depositor).



Continued from previous page...

Mol	Chain	Residues	Atoms								ZeroOcc	AltConf
2	H	1	Total	C	F	H	N	O	P	S	0	0
			52	21	1	15	4	8	2	1		
2	I	1	Total	C	F	H	N	O	P	S	0	0
			52	21	1	15	4	8	2	1		
2	J	1	Total	C	F	H	N	O	P	S	0	0
			52	21	1	15	4	8	2	1		
2	K	1	Total	C	F	H	N	O	P	S	0	0
			52	21	1	15	4	8	2	1		
2	L	1	Total	C	F	H	N	O	P	S	0	0
			52	21	1	15	4	8	2	1		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Mg	0	0
			3	3		
3	B	3	Total	Mg	0	0
			3	3		
3	C	3	Total	Mg	0	0
			3	3		
3	D	3	Total	Mg	0	0
			3	3		
3	E	3	Total	Mg	0	0
			3	3		
3	F	3	Total	Mg	0	0
			3	3		
3	G	3	Total	Mg	0	0
			3	3		
3	H	3	Total	Mg	0	0
			3	3		
3	I	3	Total	Mg	0	0
			3	3		
3	J	3	Total	Mg	0	0
			3	3		
3	K	3	Total	Mg	0	0
			3	3		
3	L	3	Total	Mg	0	0
			3	3		

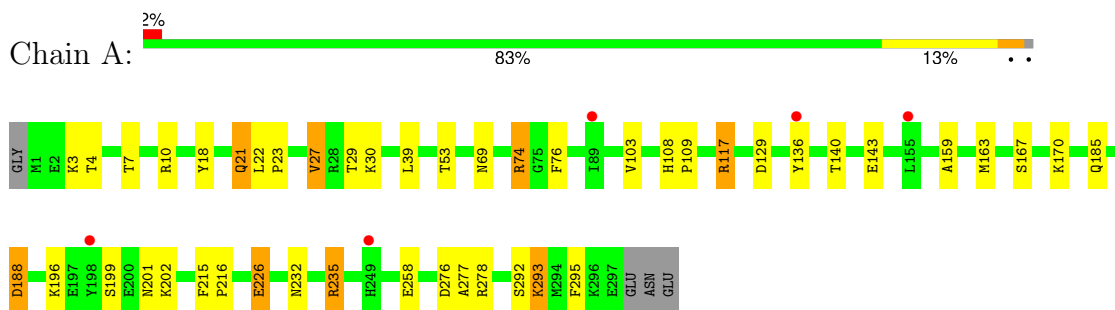
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	11	Total 11	O 11	0	0
4	B	8	Total 8	O 8	0	0
4	C	6	Total 6	O 6	0	0
4	D	11	Total 11	O 11	0	0
4	E	2	Total 2	O 2	0	0
4	F	4	Total 4	O 4	0	0
4	G	7	Total 7	O 7	0	0
4	H	12	Total 12	O 12	0	0
4	I	7	Total 7	O 7	0	0
4	J	8	Total 8	O 8	0	0
4	K	12	Total 12	O 12	0	0
4	L	3	Total 3	O 3	0	0

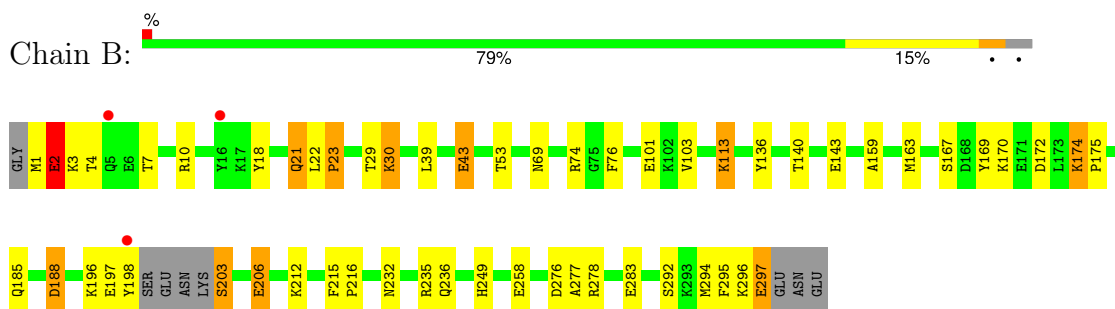
3 Residue-property plots [i](#)

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 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.

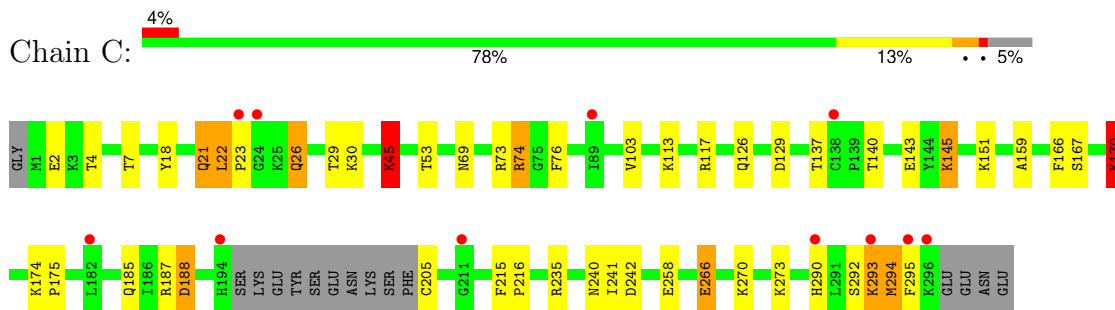
- Molecule 1: Geranylgeranyl pyrophosphate synthase



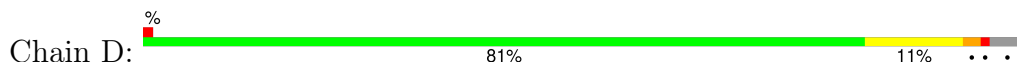
- Molecule 1: Geranylgeranyl pyrophosphate synthase



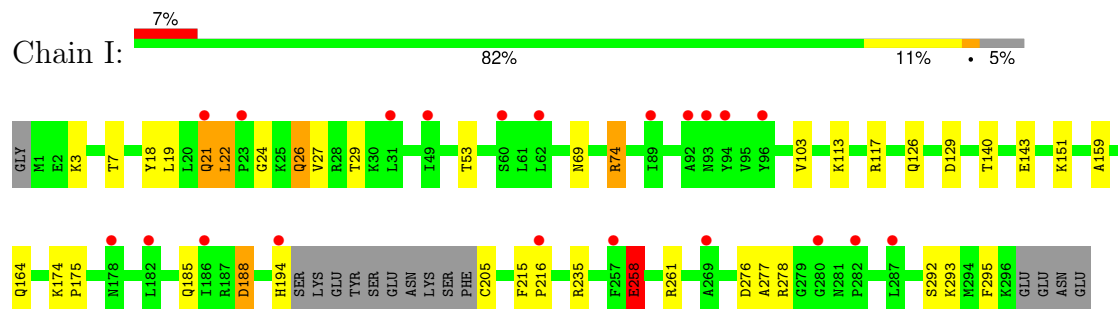
- Molecule 1: Geranylgeranyl pyrophosphate synthase



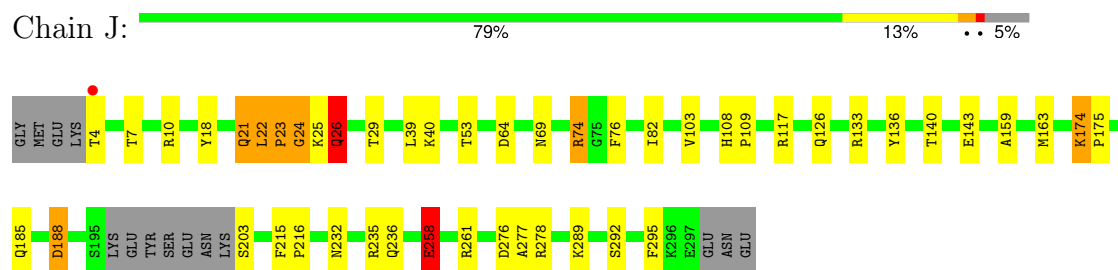
- Molecule 1: Geranylgeranyl pyrophosphate synthase



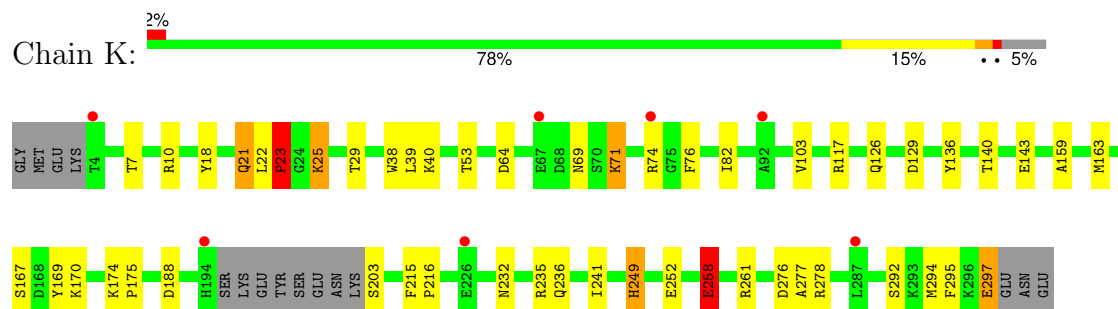
- Molecule 1: Geranylgeranyl pyrophosphate synthase



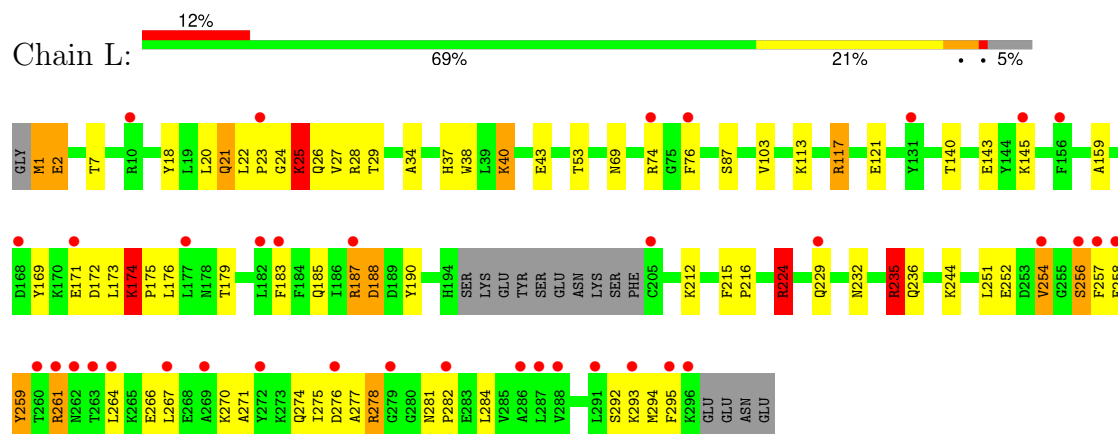
- Molecule 1: Geranylgeranyl pyrophosphate synthase



- Molecule 1: Geranylgeranyl pyrophosphate synthase



- Molecule 1: Geranylgeranyl pyrophosphate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	84.41Å 116.17Å 214.41Å 90.00° 99.27° 90.00°	Depositor
Resolution (Å)	106.03 – 2.64 106.03 – 2.64	Depositor EDS
% Data completeness (in resolution range)	45.4 (106.03-2.64) 45.4 (106.03-2.64)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.22 (at 2.65Å)	Xtriage
Refinement program	REFMAC 5.8.0430 (refmacat 0.4.105)	Depositor
R, R_{free}	0.209 , 0.247 0.209 , 0.248	Depositor DCC
R_{free} test set	2757 reflections (2.30%)	wwPDB-VP
Wilson B-factor (Å ²)	50.6	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 47.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.035 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	57867	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.33% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: MG, A1C1E

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	0.59	0/2487	1.12	8/3361 (0.2%)
1	B	0.59	0/2454	1.13	12/3316 (0.4%)
1	C	0.58	0/2390	1.15	12/3231 (0.4%)
1	D	0.60	0/2406	1.12	8/3253 (0.2%)
1	E	0.60	0/2397	1.09	6/3242 (0.2%)
1	F	0.56	0/2390	1.10	5/3231 (0.2%)
1	G	0.58	0/2487	1.10	5/3361 (0.1%)
1	H	0.59	0/2487	1.12	9/3361 (0.3%)
1	I	0.57	0/2390	1.07	8/3231 (0.2%)
1	J	0.60	0/2397	1.09	6/3242 (0.2%)
1	K	0.62	0/2391	1.10	9/3234 (0.3%)
1	L	0.62	0/2390	1.26	15/3231 (0.5%)
All	All	0.59	0/29066	1.12	103/39294 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	2
1	D	0	3
1	E	0	2
1	G	0	1
1	I	0	2
1	J	0	1
1	K	0	1
1	L	0	6
All	All	0	19

There are no bond length outliers.

The worst 5 of 103 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	25	LYS	CB-CA-C	-12.88	90.37	111.36
1	L	25	LYS	N-CA-CB	12.32	131.51	112.41
1	L	259	TYR	CA-CB-CG	10.22	132.30	113.90
1	A	29	THR	CA-CB-OG1	-8.67	96.60	109.60
1	C	266	GLU	CB-CG-CD	8.38	126.85	112.60

There are no chirality outliers.

5 of 19 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	74	ARG	Sidechain
1	C	235	ARG	Sidechain
1	C	74	ARG	Sidechain
1	D	117	ARG	Sidechain
1	D	235	ARG	Sidechain

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	2434	2447	2440	22	0
1	B	2402	2417	2409	30	0
1	C	2340	2364	2356	22	0
1	D	2355	2374	2363	26	0
1	E	2346	2361	2350	31	0
1	F	2340	2364	2356	19	0
1	G	2434	2447	2440	34	3
1	H	2434	2447	2440	26	0
1	I	2340	2364	2356	19	0
1	J	2346	2361	2350	27	0
1	K	2340	2355	2345	32	3
1	L	2340	2364	2356	84	0
2	A	37	15	0	0	0
2	B	37	15	0	0	0
2	C	37	15	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	37	15	0	0	0
2	E	37	15	0	0	0
2	F	37	15	0	0	0
2	G	37	15	0	0	0
2	H	37	15	0	0	0
2	I	37	15	0	1	0
2	J	37	15	0	1	0
2	K	37	15	0	0	0
2	L	37	15	0	1	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	D	3	0	0	0	0
3	E	3	0	0	0	0
3	F	3	0	0	0	0
3	G	3	0	0	0	0
3	H	3	0	0	0	0
3	I	3	0	0	0	0
3	J	3	0	0	0	0
3	K	3	0	0	0	0
3	L	3	0	0	0	0
4	A	11	0	0	0	0
4	B	8	0	0	0	0
4	C	6	0	0	1	0
4	D	11	0	0	0	0
4	E	2	0	0	0	0
4	F	4	0	0	2	0
4	G	7	0	0	5	0
4	H	12	0	0	1	0
4	I	7	0	0	3	0
4	J	8	0	0	2	0
4	K	12	0	0	4	0
4	L	3	0	0	1	0
All	All	29022	28845	28561	359	3

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 359 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:205:CYS:N	4:C:501:HOH:O	1.69	1.23
1:I:22:LEU:O	1:I:22:LEU:HD23	1.47	1.13
1:L:25:LYS:HA	1:L:28:ARG:NH2	1.65	1.09
1:L:169:TYR:OH	1:L:278:ARG:HB3	1.58	1.03
1:L:175:PRO:HB2	1:L:274:GLN:HE22	1.24	0.99

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:289:LYS:HE3	1:K:249:HIS:HD1[2_454]	1.33	0.27
1:G:33:GLN:O	1:K:297:GLU:OE2[2_454]	1.97	0.23
1:G:33:GLN:OE1	1:K:297:GLU:O[2_454]	2.16	0.04

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	295/301 (98%)	290 (98%)	4 (1%)	1 (0%)	36	50
1	B	289/301 (96%)	283 (98%)	4 (1%)	2 (1%)	18	27
1	C	282/301 (94%)	279 (99%)	3 (1%)	0	100	100
1	D	284/301 (94%)	281 (99%)	2 (1%)	1 (0%)	30	42
1	E	283/301 (94%)	277 (98%)	4 (1%)	2 (1%)	18	27
1	F	282/301 (94%)	278 (99%)	3 (1%)	1 (0%)	30	42
1	G	295/301 (98%)	289 (98%)	5 (2%)	1 (0%)	36	50
1	H	295/301 (98%)	290 (98%)	4 (1%)	1 (0%)	36	50
1	I	282/301 (94%)	277 (98%)	5 (2%)	0	100	100
1	J	283/301 (94%)	278 (98%)	3 (1%)	2 (1%)	18	27
1	K	282/301 (94%)	278 (99%)	3 (1%)	1 (0%)	30	42

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L	282/301 (94%)	276 (98%)	5 (2%)	1 (0%)	30	42
All	All	3434/3612 (95%)	3376 (98%)	45 (1%)	13 (0%)	30	42

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	2	GLU
1	E	24	GLY
1	J	24	GLY
1	D	23	PRO
1	F	23	PRO

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	269/272 (99%)	256 (95%)	13 (5%)	23	37
1	B	265/272 (97%)	252 (95%)	13 (5%)	22	37
1	C	258/272 (95%)	244 (95%)	14 (5%)	20	33
1	D	260/272 (96%)	249 (96%)	11 (4%)	26	44
1	E	259/272 (95%)	245 (95%)	14 (5%)	20	33
1	F	258/272 (95%)	247 (96%)	11 (4%)	26	42
1	G	269/272 (99%)	258 (96%)	11 (4%)	27	44
1	H	269/272 (99%)	256 (95%)	13 (5%)	23	37
1	I	258/272 (95%)	248 (96%)	10 (4%)	28	47
1	J	259/272 (95%)	249 (96%)	10 (4%)	28	47
1	K	258/272 (95%)	247 (96%)	11 (4%)	26	42
1	L	258/272 (95%)	233 (90%)	25 (10%)	8	11
All	All	3140/3264 (96%)	2984 (95%)	156 (5%)	22	36

5 of 156 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	74	ARG
1	L	229	GLN
1	J	276	ASP
1	K	297	GLU
1	L	266	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 95 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	185	GLN
1	I	90	ASN
1	G	249	HIS
1	H	185	GLN
1	J	26	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 48 ligands modelled in this entry, 36 are monoatomic - leaving 12 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
2	A1C1E	K	401	3	40,40,40	2.22	10 (25%)	53,60,60	5.13	25 (47%)
2	A1C1E	A	401	3	40,40,40	1.90	10 (25%)	53,60,60	4.54	22 (41%)
2	A1C1E	I	401	3	40,40,40	2.07	11 (27%)	53,60,60	3.78	24 (45%)
2	A1C1E	E	401	3	40,40,40	2.03	12 (30%)	53,60,60	4.86	25 (47%)
2	A1C1E	G	401	3	40,40,40	1.96	7 (17%)	53,60,60	4.38	17 (32%)
2	A1C1E	C	401	3	40,40,40	2.01	12 (30%)	53,60,60	4.59	26 (49%)
2	A1C1E	D	401	3	40,40,40	1.94	7 (17%)	53,60,60	4.90	23 (43%)
2	A1C1E	F	401	3	40,40,40	1.87	10 (25%)	53,60,60	3.48	19 (35%)
2	A1C1E	L	401	3	40,40,40	2.02	12 (30%)	53,60,60	3.28	20 (37%)
2	A1C1E	J	401	3	40,40,40	2.24	12 (30%)	53,60,60	5.13	16 (30%)
2	A1C1E	H	401	3	40,40,40	2.23	11 (27%)	53,60,60	4.64	17 (32%)
2	A1C1E	B	401	3	40,40,40	2.26	13 (32%)	53,60,60	3.92	16 (30%)

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
2	A1C1E	K	401	3	-	2/30/30/30	0/4/4/4
2	A1C1E	A	401	3	-	13/30/30/30	0/4/4/4
2	A1C1E	I	401	3	-	3/30/30/30	0/4/4/4
2	A1C1E	E	401	3	-	6/30/30/30	0/4/4/4
2	A1C1E	G	401	3	-	13/30/30/30	0/4/4/4
2	A1C1E	C	401	3	-	6/30/30/30	0/4/4/4
2	A1C1E	D	401	3	-	10/30/30/30	0/4/4/4
2	A1C1E	F	401	3	-	2/30/30/30	0/4/4/4
2	A1C1E	L	401	3	-	6/30/30/30	0/4/4/4
2	A1C1E	J	401	3	-	7/30/30/30	0/4/4/4
2	A1C1E	H	401	3	-	3/30/30/30	0/4/4/4
2	A1C1E	B	401	3	-	4/30/30/30	0/4/4/4

The worst 5 of 127 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	K	401	A1C1E	C17-N18	7.22	1.46	1.35
2	D	401	A1C1E	C17-N18	7.10	1.46	1.35

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	401	A1C1E	C17-N18	6.97	1.46	1.35
2	E	401	A1C1E	C17-N18	6.91	1.46	1.35
2	B	401	A1C1E	C17-N18	6.90	1.46	1.35

The worst 5 of 250 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	401	A1C1E	C32-S31-C30	27.57	98.80	90.62
2	D	401	A1C1E	C32-S31-C30	25.69	98.24	90.62
2	K	401	A1C1E	C32-S31-C30	25.13	98.07	90.62
2	A	401	A1C1E	C32-S31-C30	25.07	98.06	90.62
2	H	401	A1C1E	C32-S31-C30	22.77	97.38	90.62

There are no chirality outliers.

5 of 75 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	A1C1E	C28-C17-N18-C19
2	A	401	A1C1E	N16-C17-N18-C19
2	B	401	A1C1E	C36-C03-O02-C01
2	D	401	A1C1E	C36-C03-O02-C01
2	E	401	A1C1E	N18-C19-P24-O26

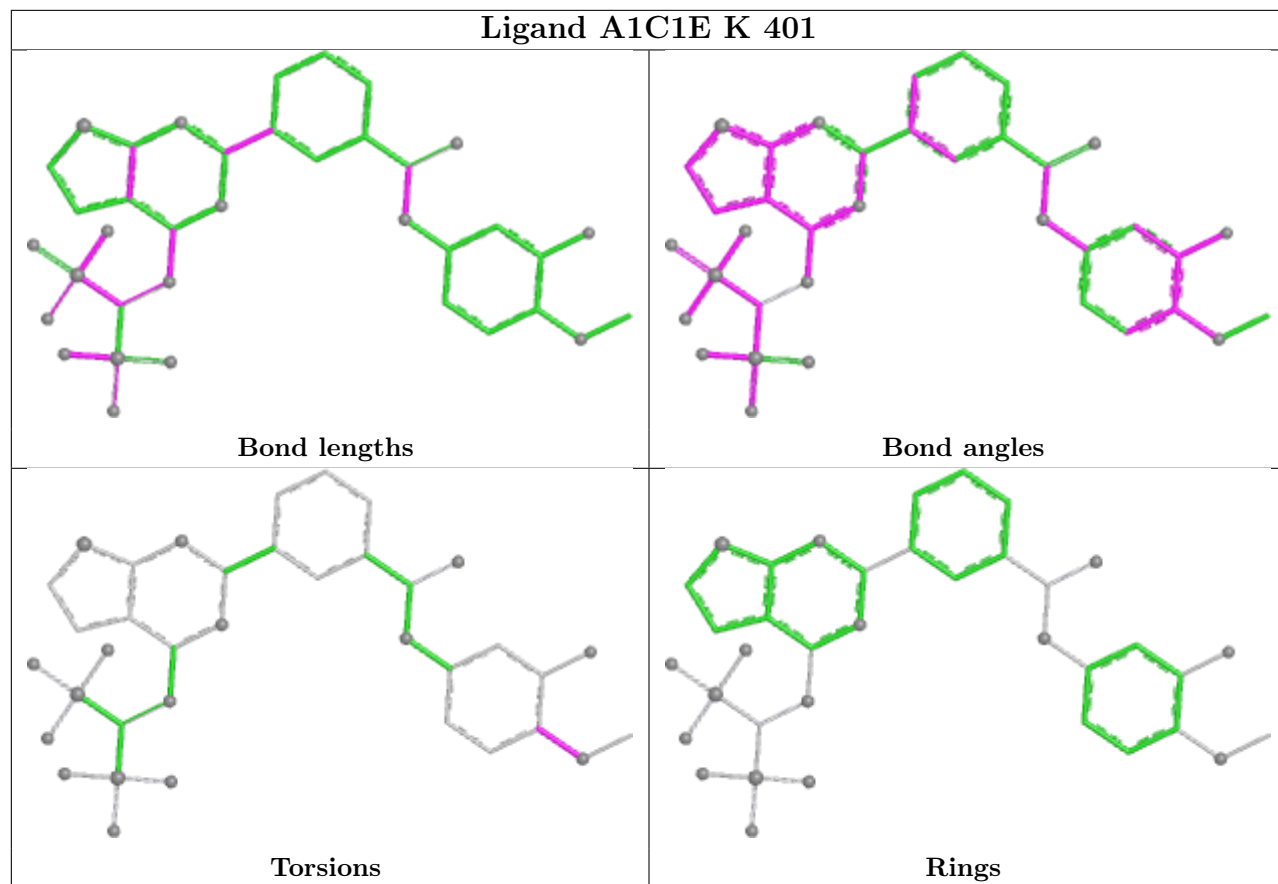
There are no ring outliers.

3 monomers are involved in 3 short contacts:

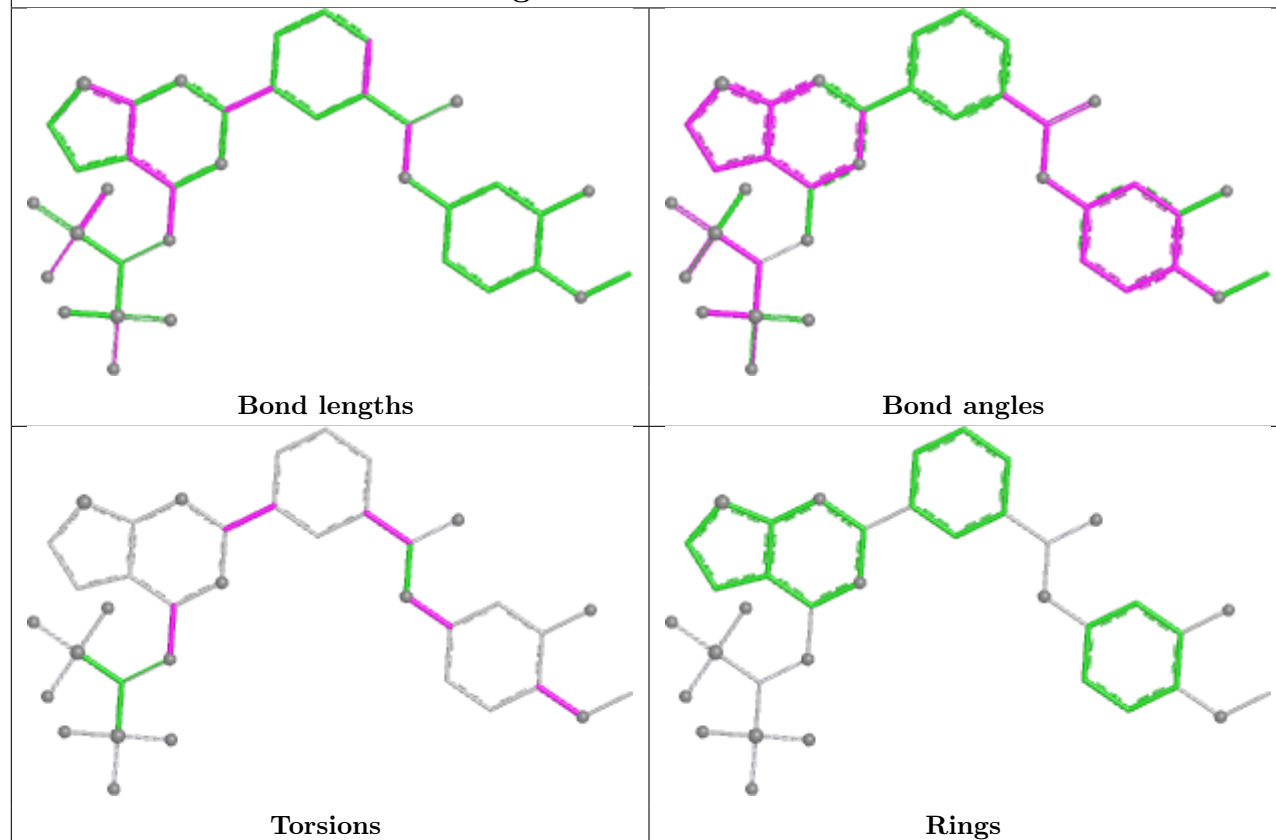
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	I	401	A1C1E	1	0
2	L	401	A1C1E	1	0
2	J	401	A1C1E	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient

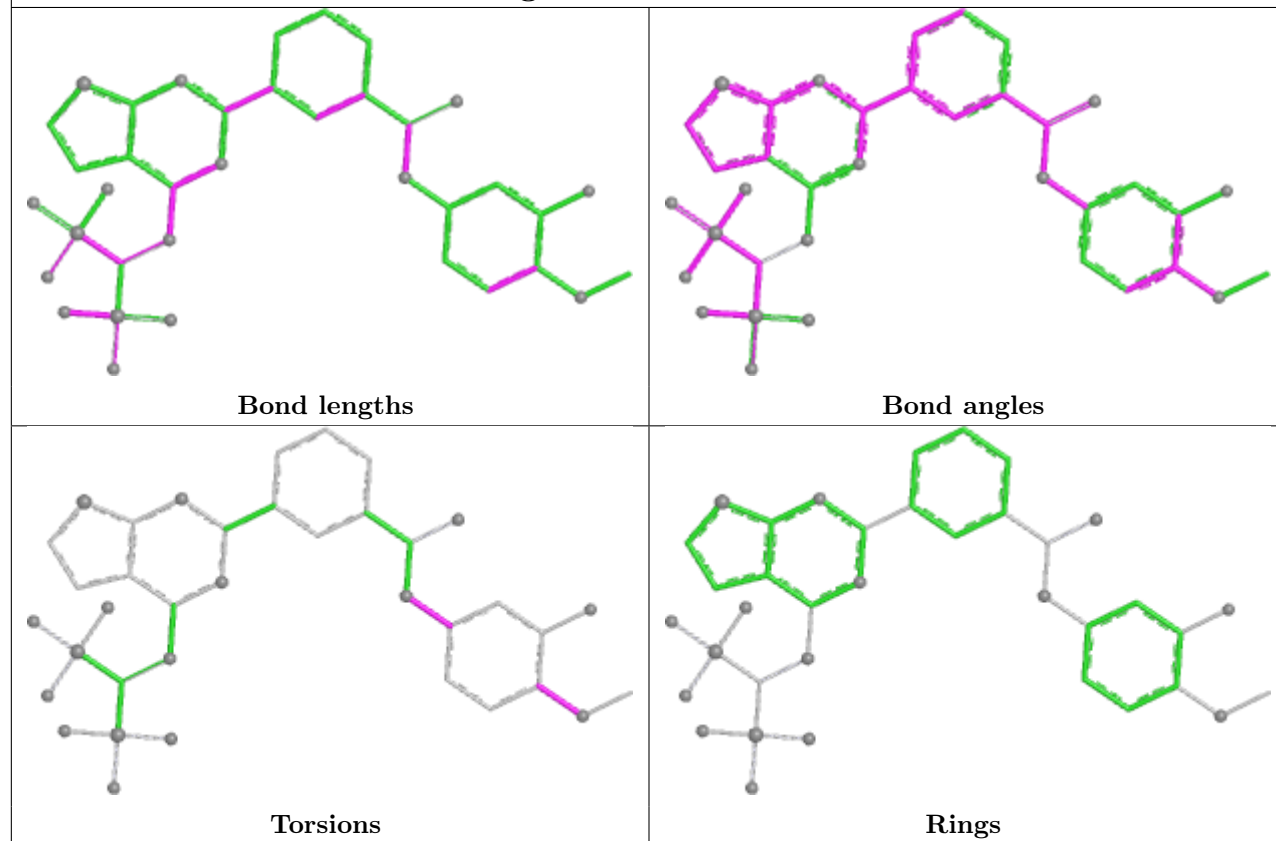
equivalents in the CSD to analyse the geometry.



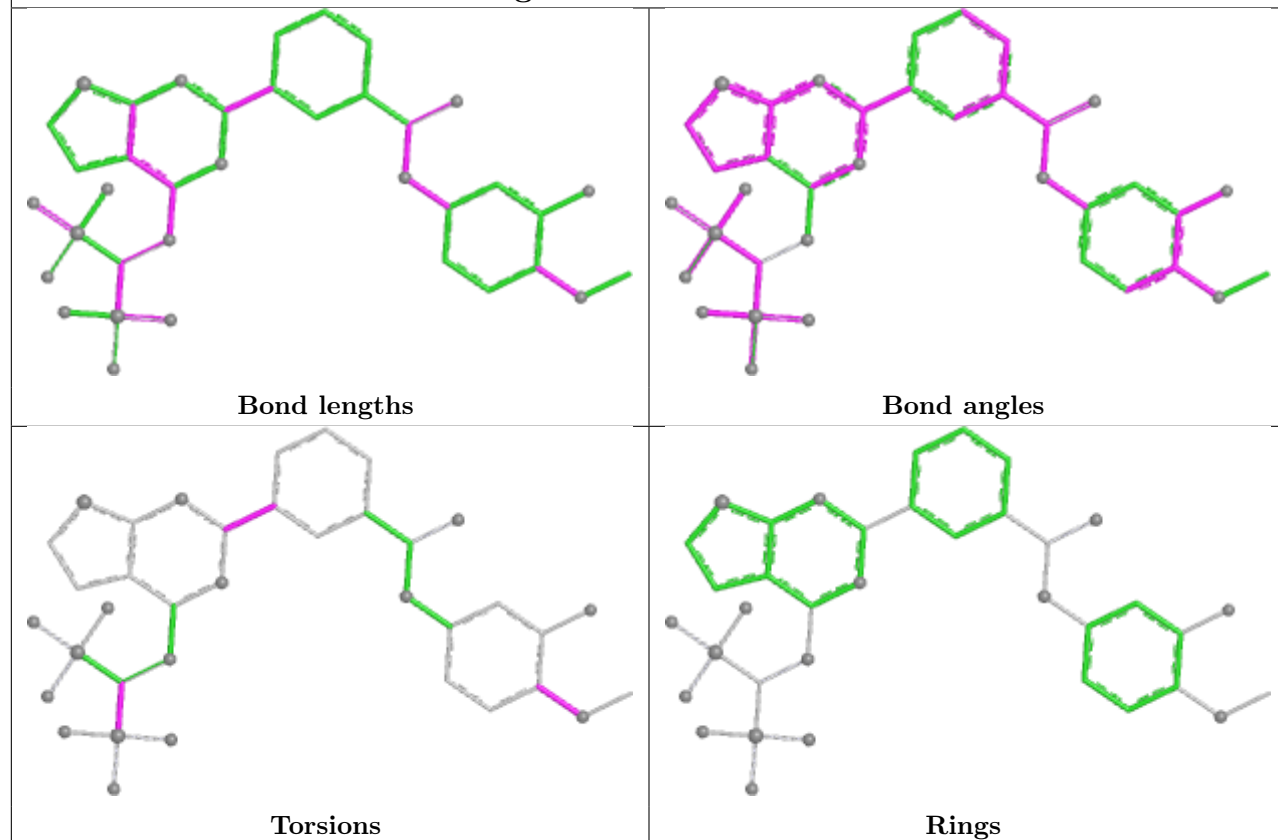
Ligand A1C1E A 401



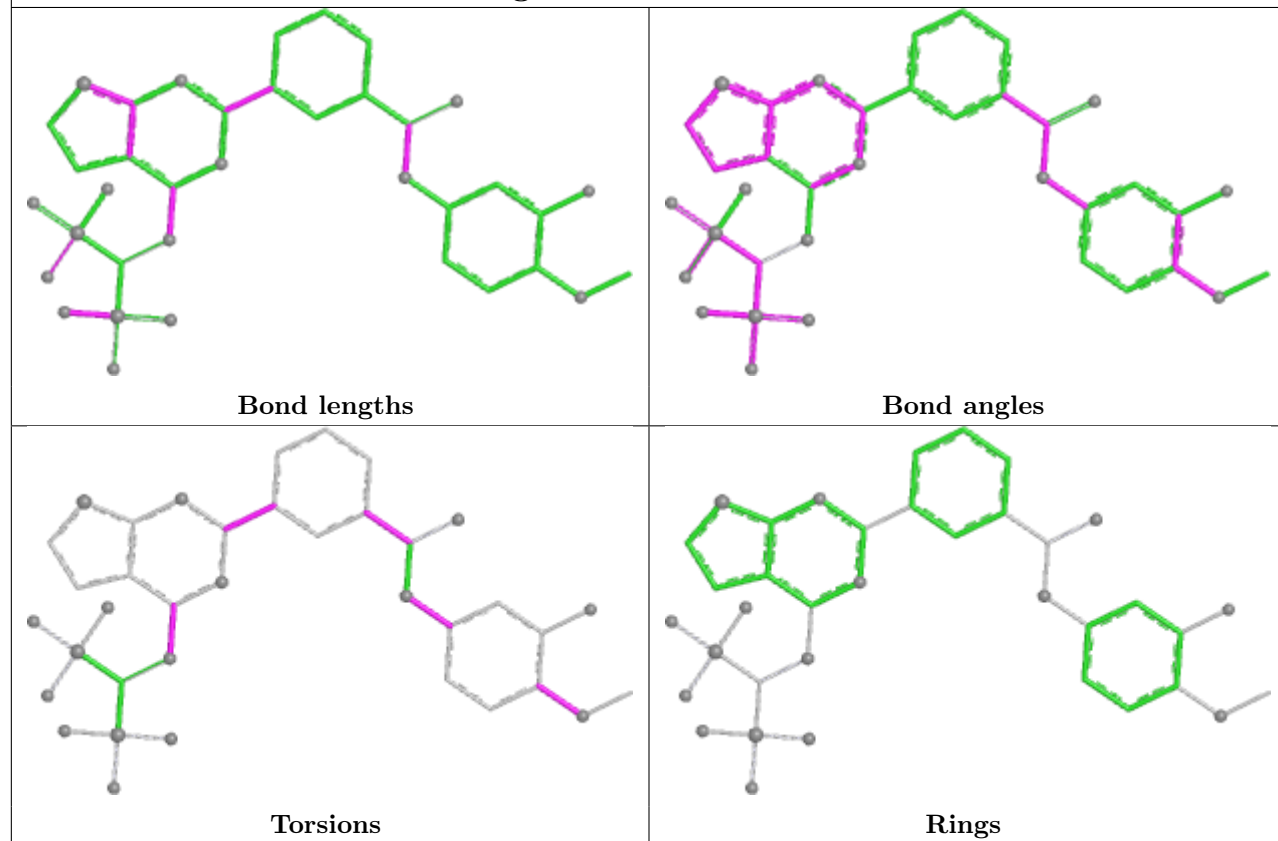
Ligand A1C1E I 401



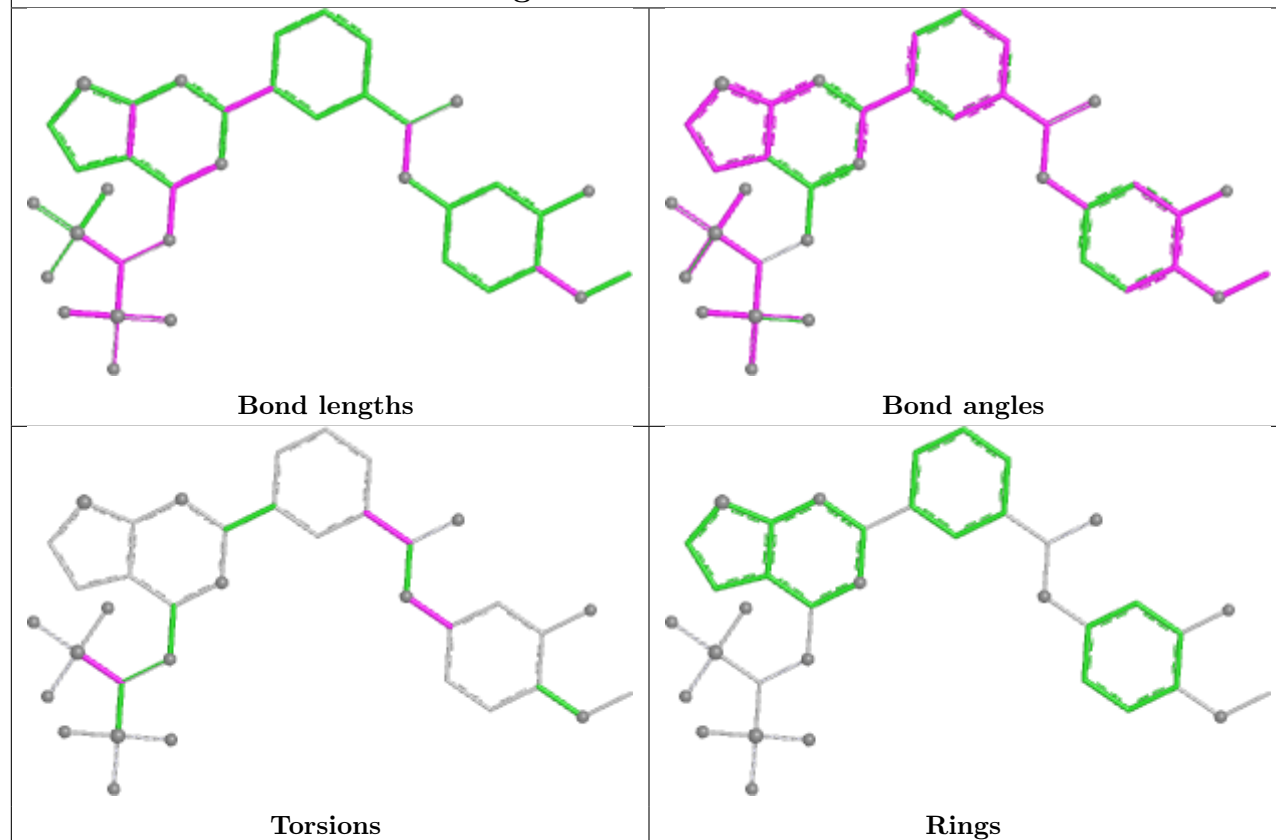
Ligand A1C1E E 401



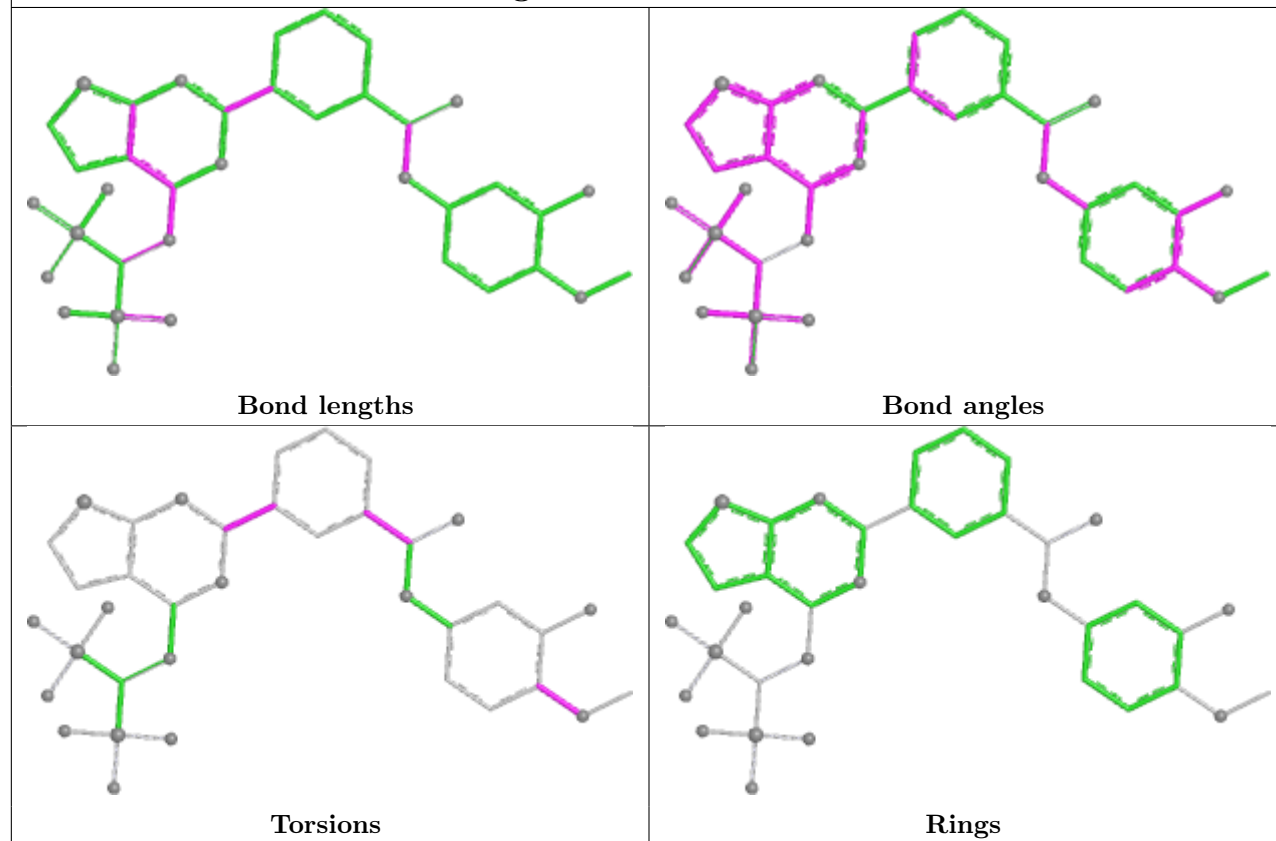
Ligand A1C1E G 401



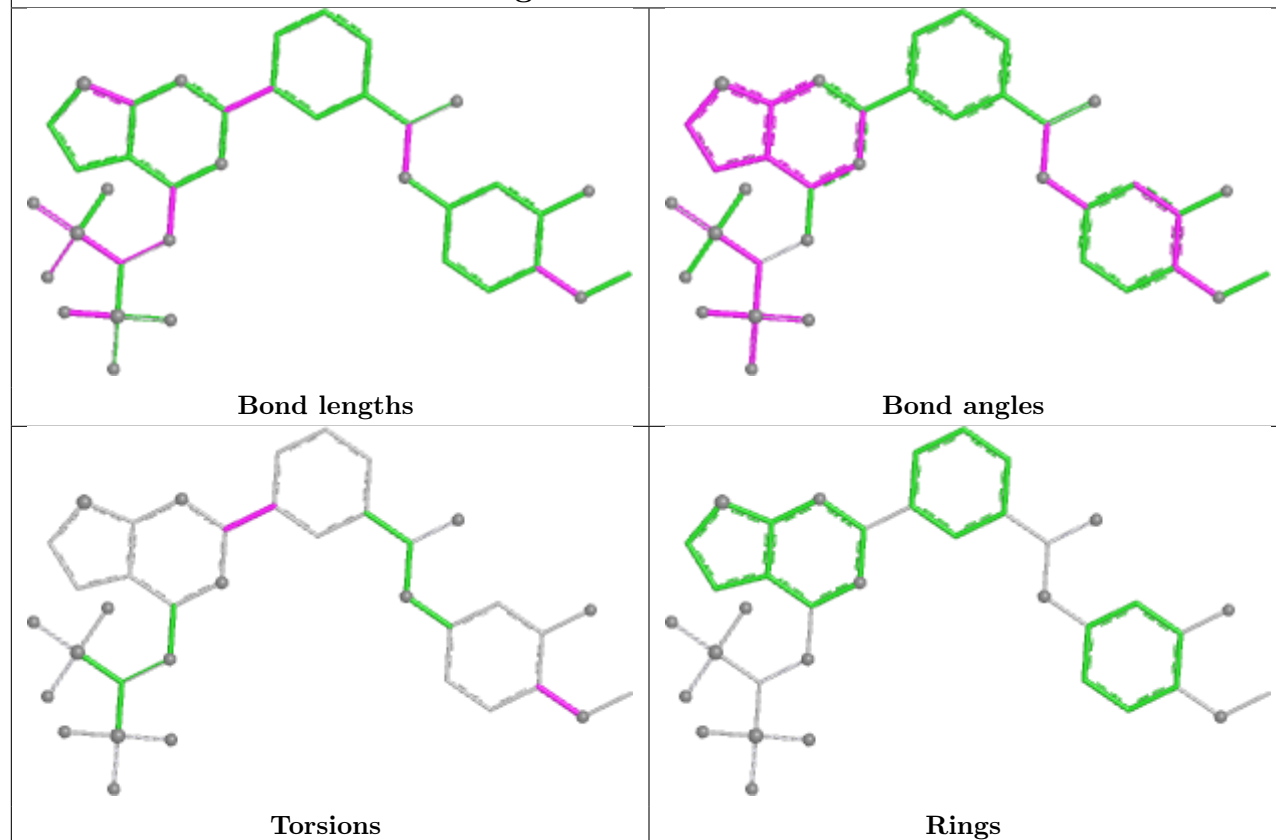
Ligand A1C1E C 401



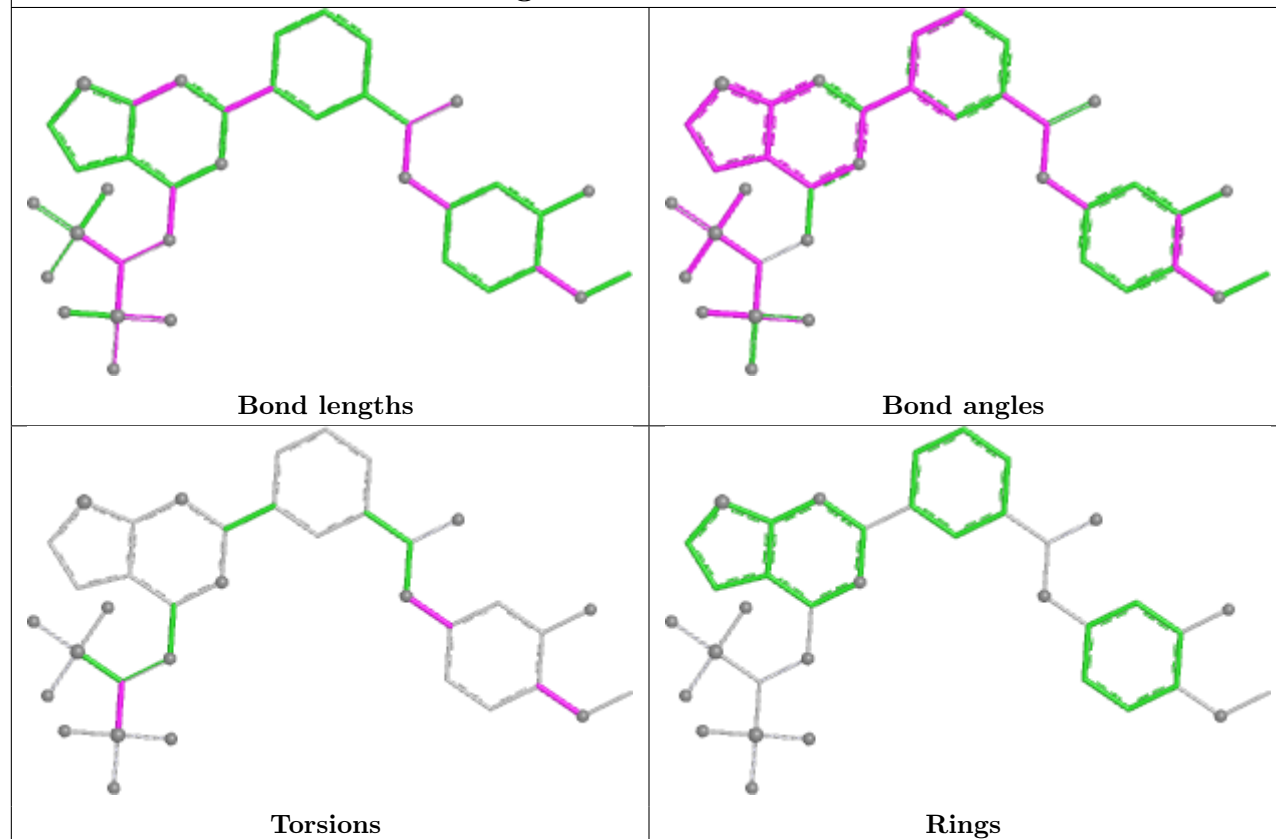
Ligand A1C1E D 401



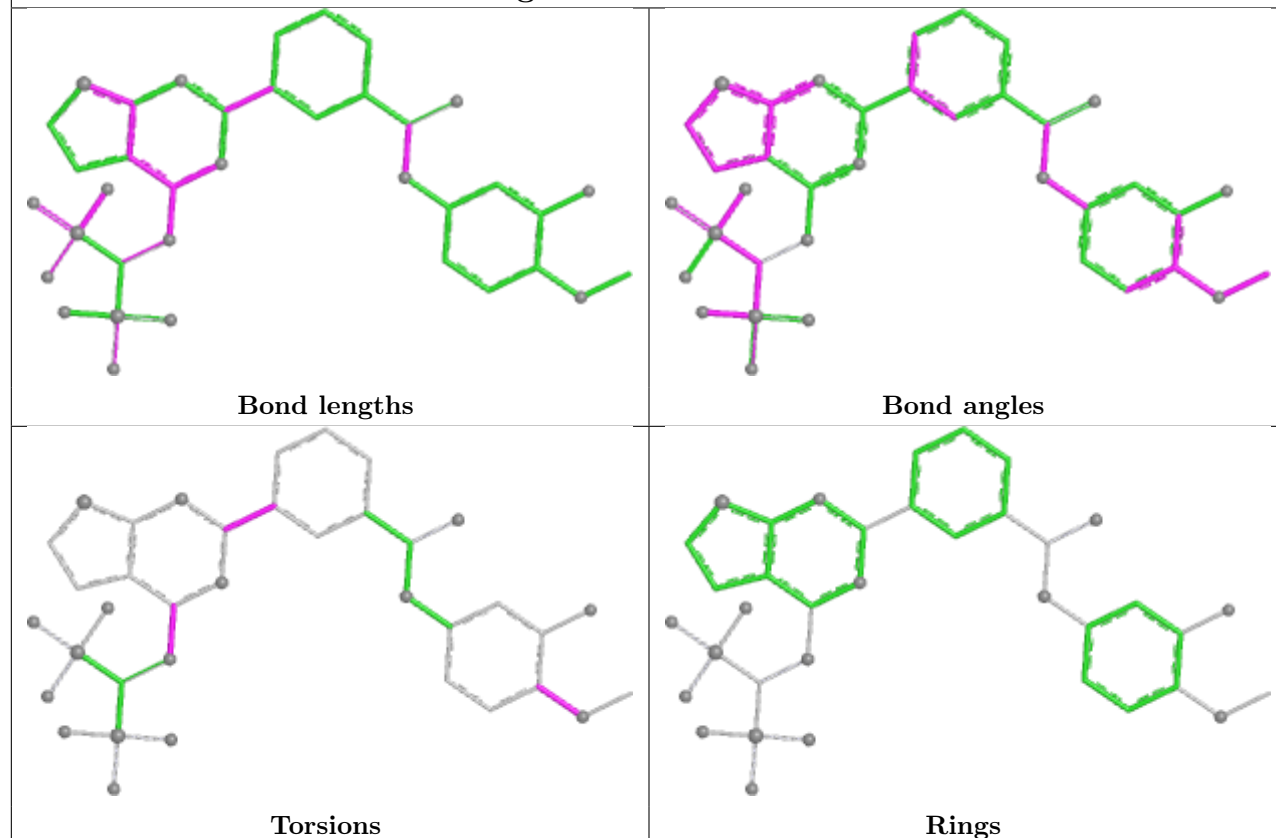
Ligand A1C1E F 401



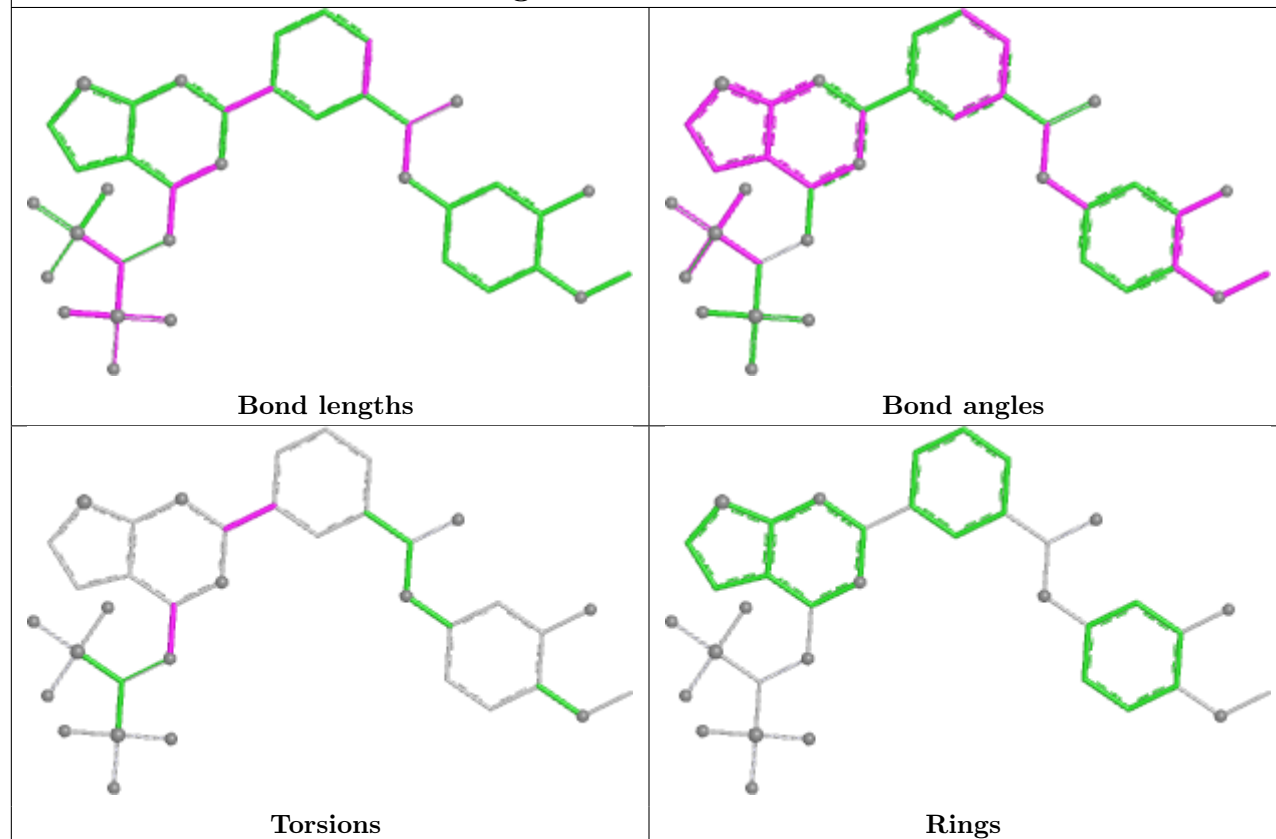
Ligand A1C1E L 401

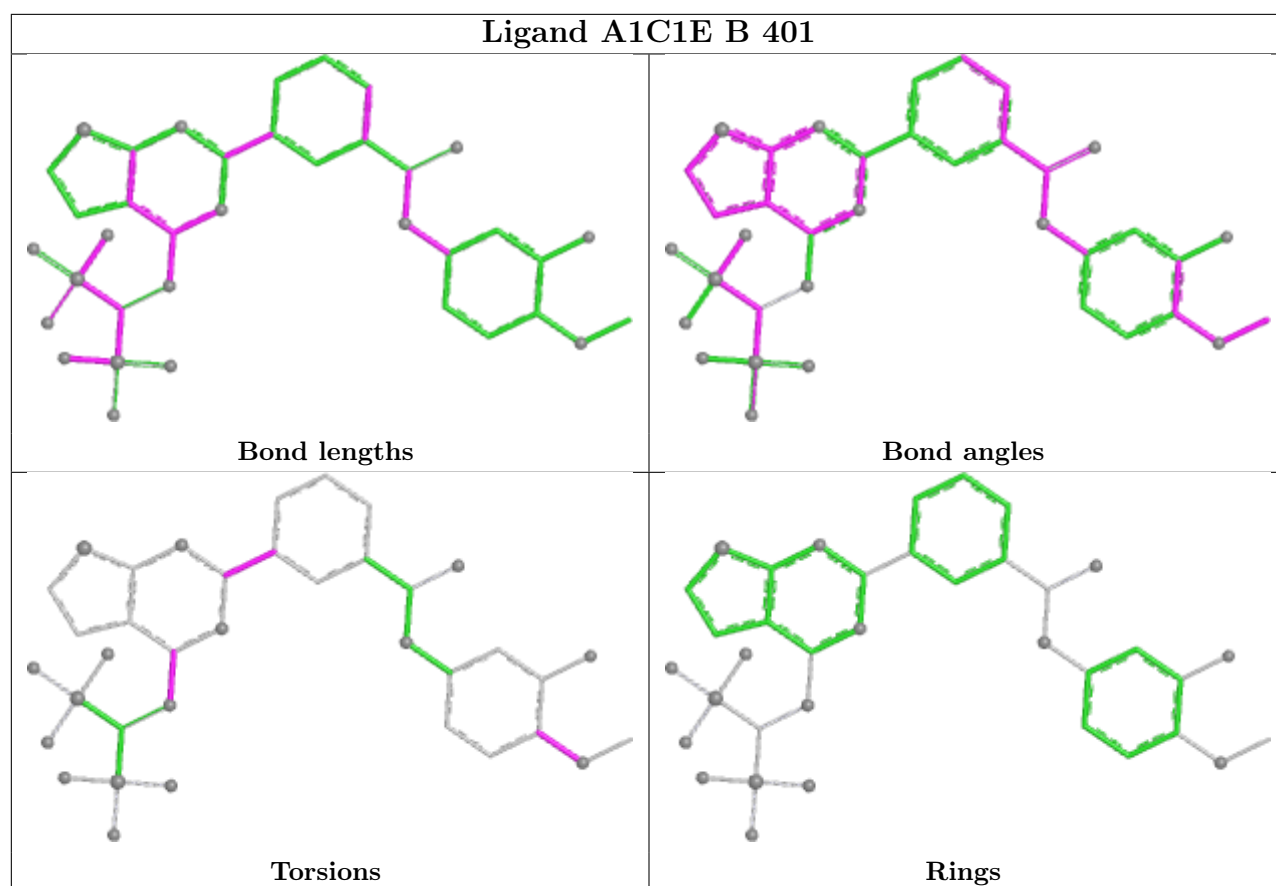


Ligand A1C1E J 401



Ligand A1C1E H 401





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	297/301 (98%)	0.09	5 (1%) 69 65	21, 42, 75, 147	0
1	B	293/301 (97%)	0.05	3 (1%) 79 76	20, 42, 72, 142	0
1	C	286/301 (95%)	0.40	11 (3%) 44 38	20, 61, 95, 124	0
1	D	288/301 (95%)	0.01	4 (1%) 73 70	18, 45, 83, 100	0
1	E	287/301 (95%)	0.03	4 (1%) 73 70	17, 40, 82, 98	0
1	F	286/301 (95%)	0.27	10 (3%) 47 41	19, 60, 90, 112	0
1	G	297/301 (98%)	0.36	9 (3%) 52 47	21, 51, 106, 124	0
1	H	297/301 (98%)	0.22	7 (2%) 59 55	20, 41, 80, 140	0
1	I	286/301 (95%)	0.67	21 (7%) 21 17	18, 75, 116, 135	0
1	J	287/301 (95%)	-0.04	1 (0%) 90 89	14, 38, 76, 91	0
1	K	286/301 (95%)	0.18	7 (2%) 59 55	14, 45, 92, 136	0
1	L	286/301 (95%)	0.76	37 (12%) 7 6	21, 72, 152, 173	0
All	All	3476/3612 (96%)	0.25	119 (3%) 48 42	14, 48, 102, 173	0

The worst 5 of 119 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	183	PHE	5.0
1	L	287	LEU	4.8
1	I	182	LEU	4.7
1	H	136	TYR	4.6
1	L	264	LEU	4.4

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 ⓘ

There are no oligosaccharides 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
3	MG	D	403	1/1	0.76	0.18	14,14,14,14	0
3	MG	E	404	1/1	0.82	0.11	17,17,17,17	0
3	MG	H	402	1/1	0.82	0.21	14,14,14,14	0
3	MG	G	404	1/1	0.83	0.14	11,11,11,11	0
3	MG	J	402	1/1	0.84	0.19	12,12,12,12	0
3	MG	K	402	1/1	0.84	0.13	18,18,18,18	0
3	MG	B	403	1/1	0.87	0.18	16,16,16,16	0
3	MG	G	403	1/1	0.87	0.15	13,13,13,13	0
3	MG	D	404	1/1	0.87	0.14	13,13,13,13	0
3	MG	C	402	1/1	0.88	0.09	14,14,14,14	0
3	MG	H	403	1/1	0.88	0.14	13,13,13,13	0
3	MG	B	402	1/1	0.88	0.16	20,20,20,20	0
3	MG	A	402	1/1	0.88	0.09	13,13,13,13	0
3	MG	L	403	1/1	0.88	0.10	13,13,13,13	0
3	MG	K	403	1/1	0.89	0.18	12,12,12,12	0
3	MG	F	402	1/1	0.89	0.14	14,14,14,14	0
3	MG	B	404	1/1	0.90	0.13	16,16,16,16	0
3	MG	L	404	1/1	0.90	0.12	21,21,21,21	0
3	MG	E	403	1/1	0.91	0.14	16,16,16,16	0
3	MG	I	403	1/1	0.91	0.10	13,13,13,13	0
3	MG	K	404	1/1	0.91	0.18	12,12,12,12	0
3	MG	I	404	1/1	0.91	0.15	19,19,19,19	0
3	MG	D	402	1/1	0.91	0.09	24,24,24,24	0
3	MG	L	402	1/1	0.92	0.09	13,13,13,13	0
3	MG	J	403	1/1	0.92	0.14	11,11,11,11	0
3	MG	A	403	1/1	0.92	0.13	11,11,11,11	0
3	MG	E	402	1/1	0.93	0.11	22,22,22,22	0
3	MG	C	403	1/1	0.93	0.06	14,14,14,14	0
2	A1C1E	C	401	37/37	0.93	0.10	34,49,56,58	0
3	MG	F	404	1/1	0.94	0.10	15,15,15,15	0
3	MG	H	404	1/1	0.94	0.12	19,19,19,19	0
2	A1C1E	I	401	37/37	0.94	0.11	40,62,74,76	0

Continued on next page...

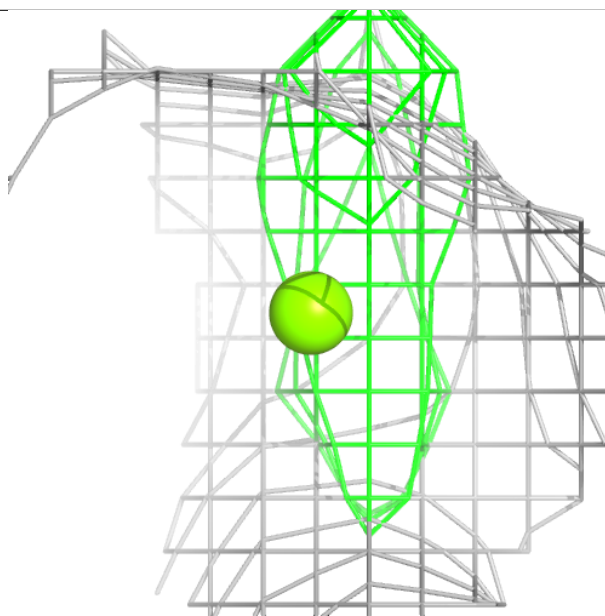
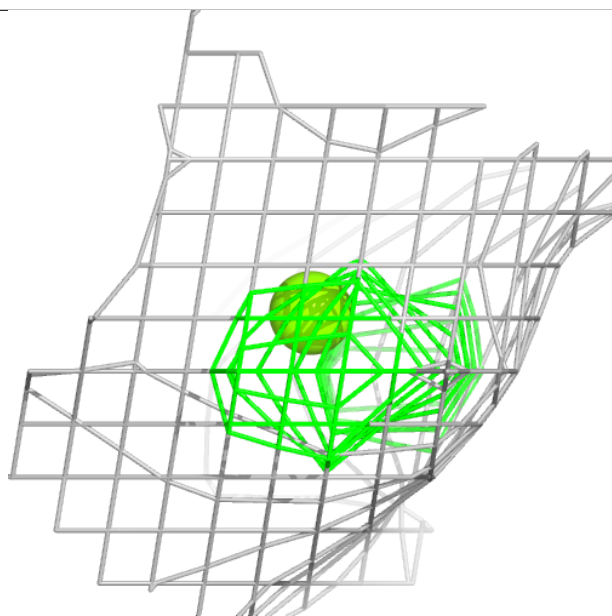
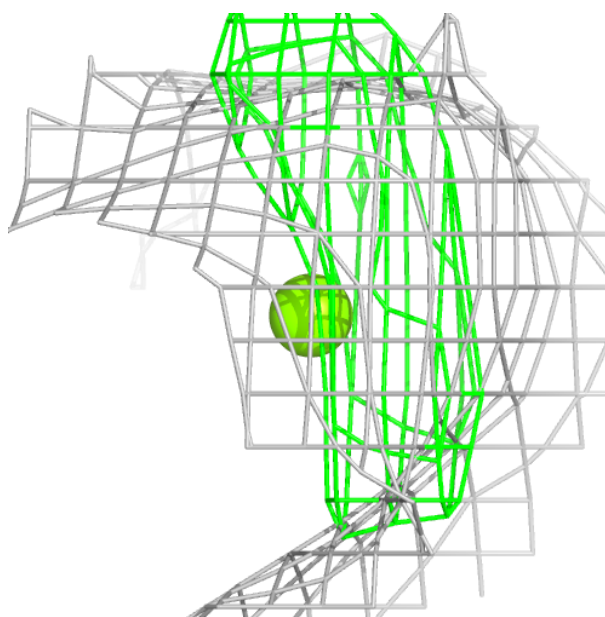
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	A1C1E	L	401	37/37	0.95	0.09	38,55,74,76	0
3	MG	F	403	1/1	0.95	0.10	18,18,18,18	0
2	A1C1E	F	401	37/37	0.96	0.08	32,47,62,63	0
2	A1C1E	G	401	37/37	0.96	0.07	29,45,62,64	0
2	A1C1E	B	401	37/37	0.96	0.07	27,33,39,41	0
2	A1C1E	E	401	37/37	0.96	0.08	26,38,67,69	0
3	MG	G	402	1/1	0.96	0.10	14,14,14,14	0
2	A1C1E	A	401	37/37	0.97	0.07	26,34,43,44	0
2	A1C1E	H	401	37/37	0.97	0.07	25,31,45,45	0
2	A1C1E	D	401	37/37	0.97	0.07	31,44,63,65	0
2	A1C1E	K	401	37/37	0.97	0.09	28,45,71,74	0
3	MG	C	404	1/1	0.97	0.08	19,19,19,19	0
3	MG	A	404	1/1	0.98	0.05	15,15,15,15	0
3	MG	J	404	1/1	0.98	0.07	16,16,16,16	0
2	A1C1E	J	401	37/37	0.98	0.07	21,32,61,64	0
3	MG	I	402	1/1	0.98	0.04	15,15,15,15	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.

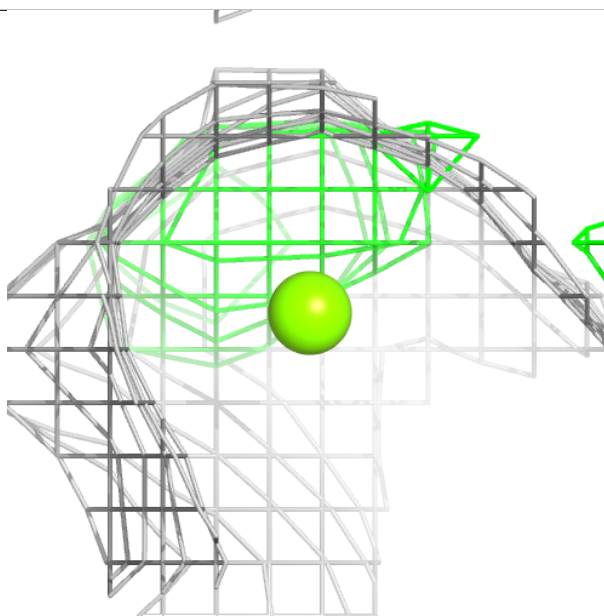
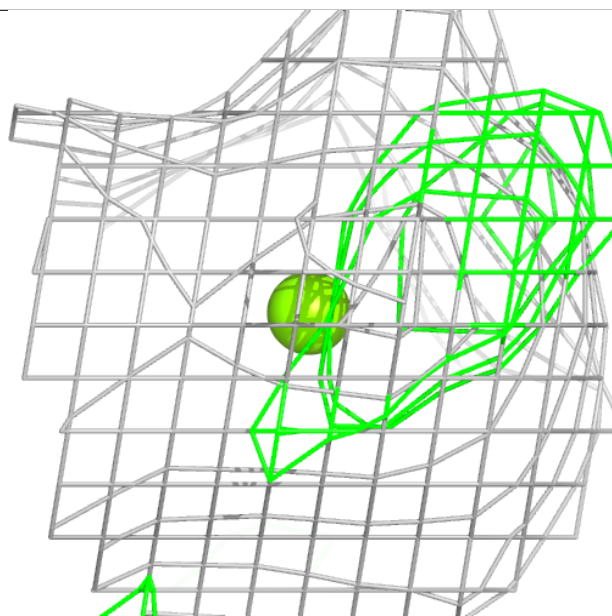
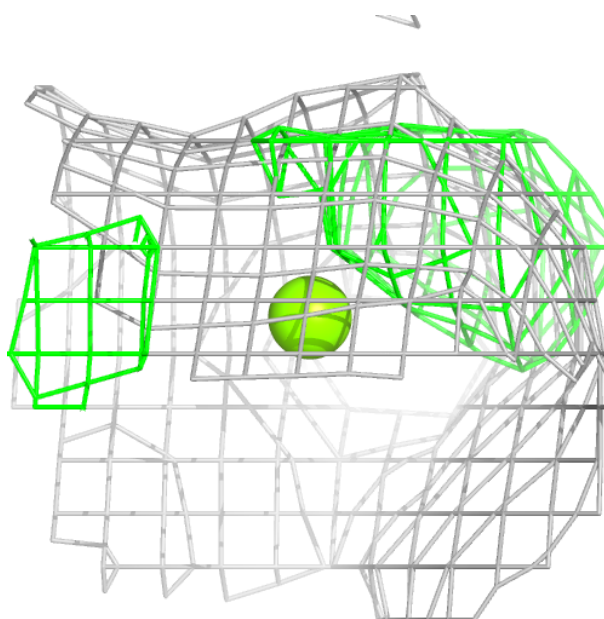
Electron density around MG D 403:

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



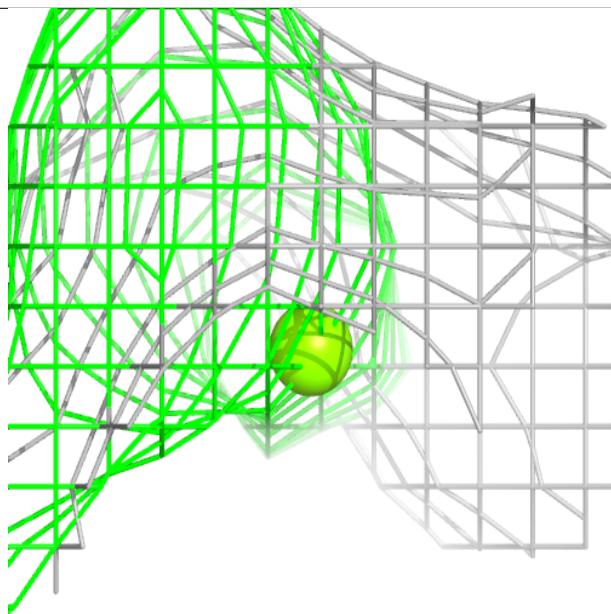
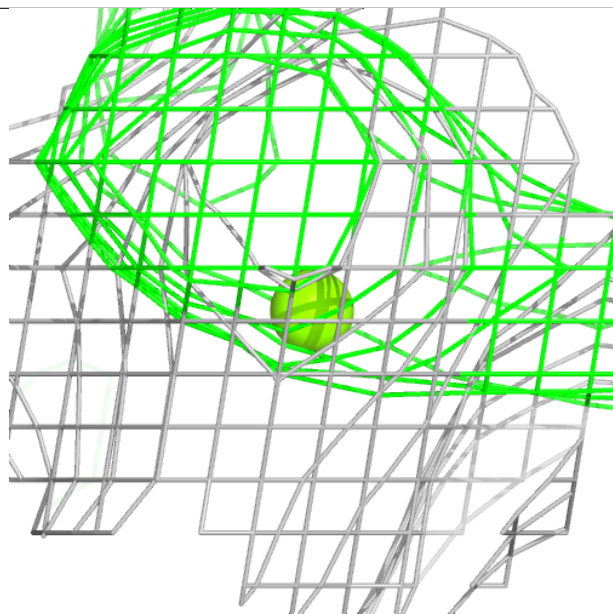
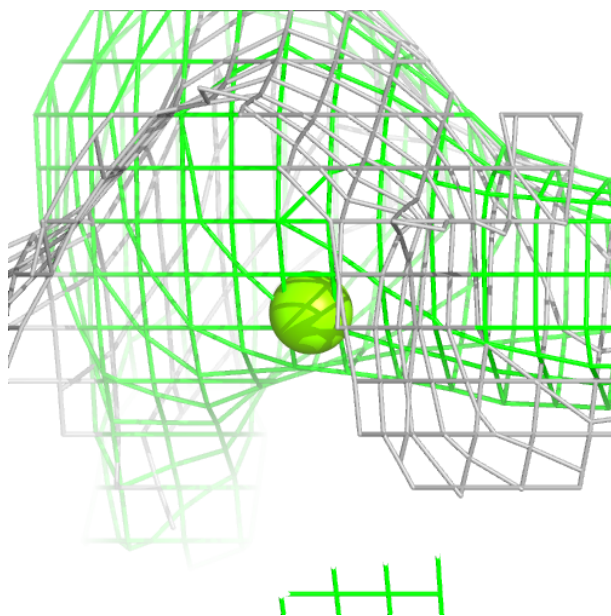
Electron density around MG E 404:

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



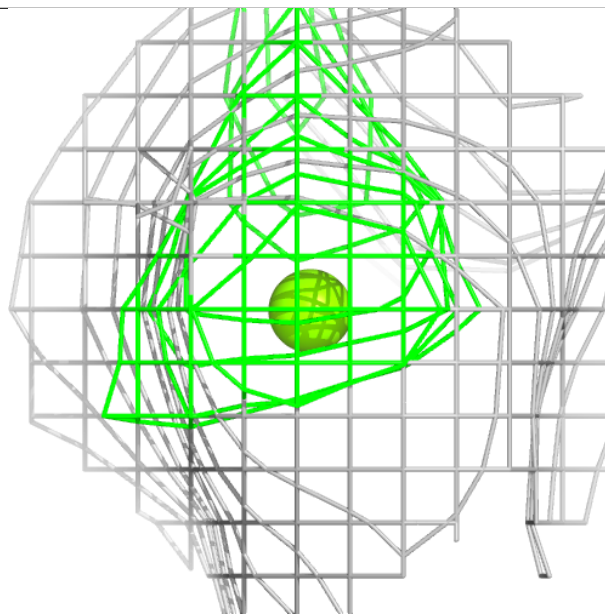
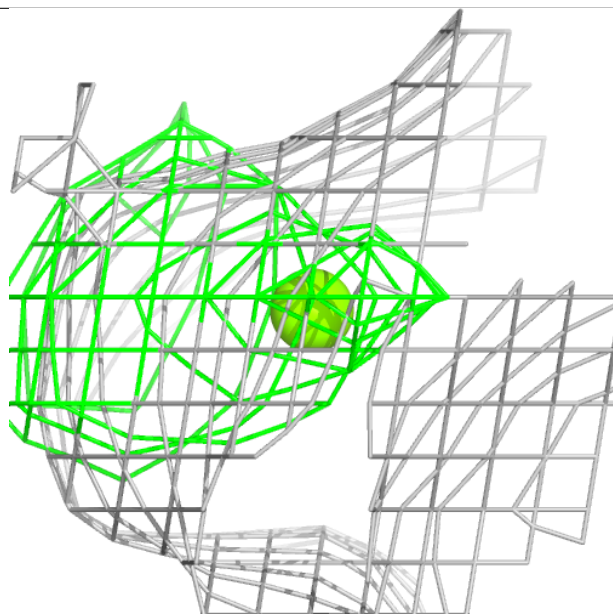
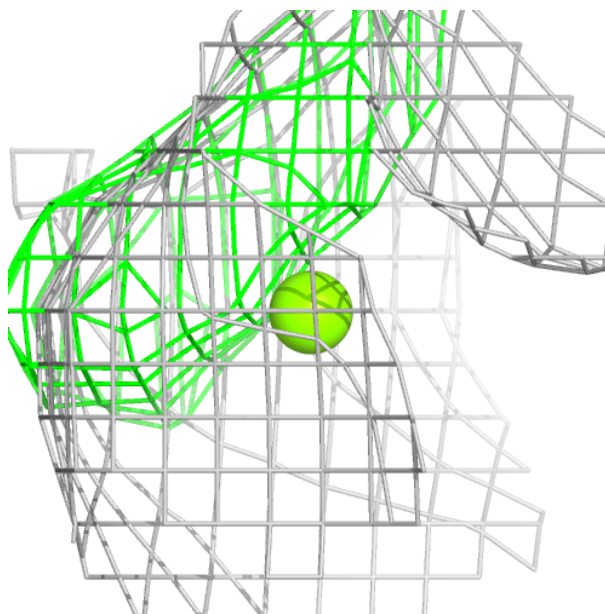
Electron density around MG H 402:

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



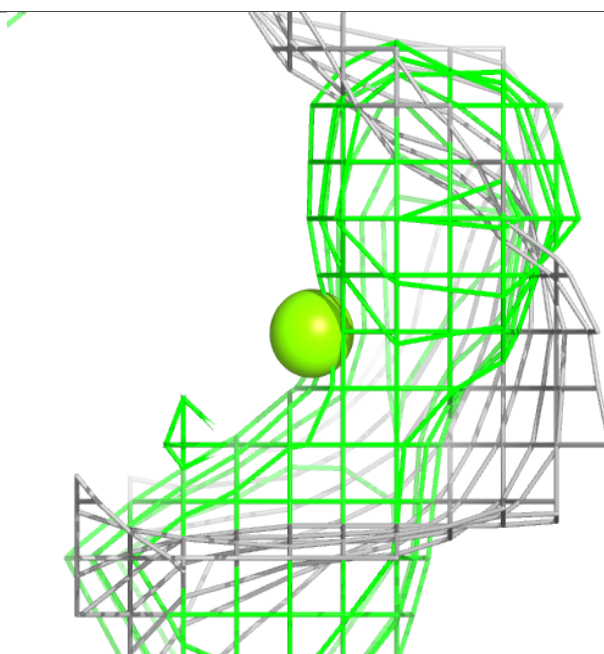
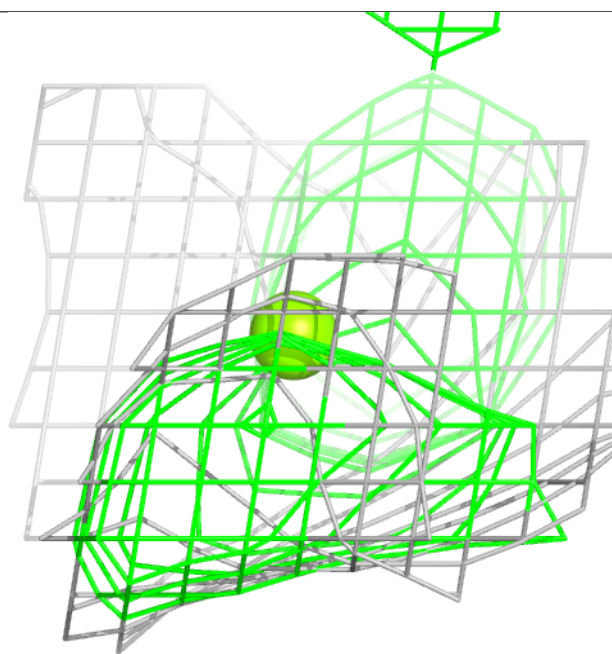
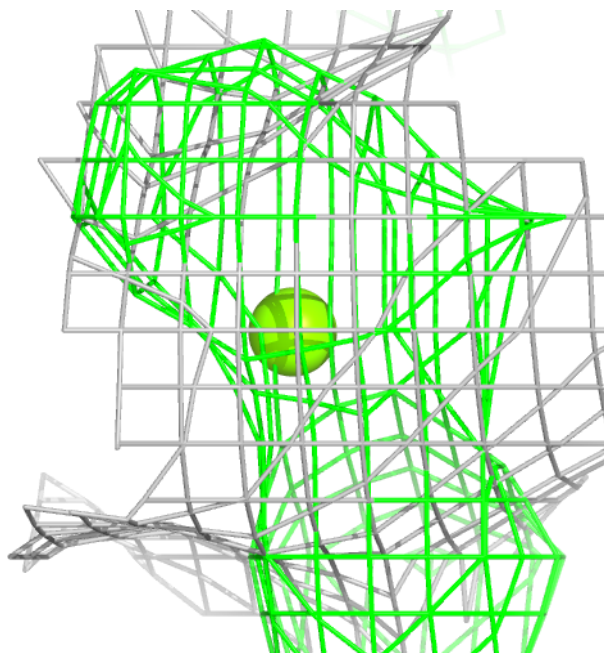
Electron density around MG G 404:

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



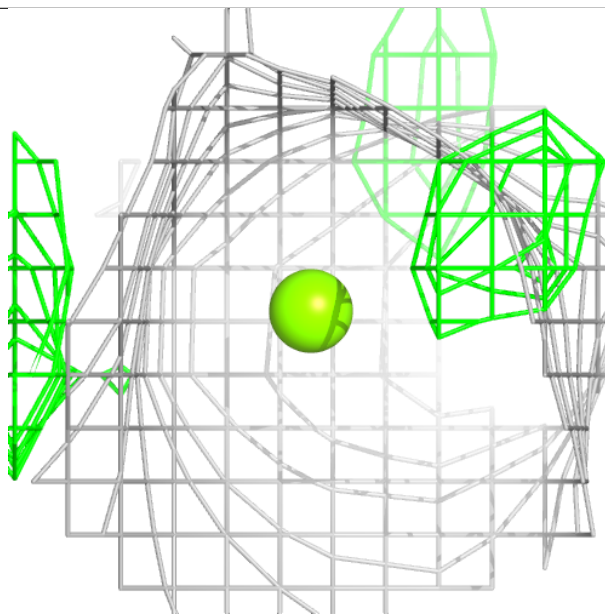
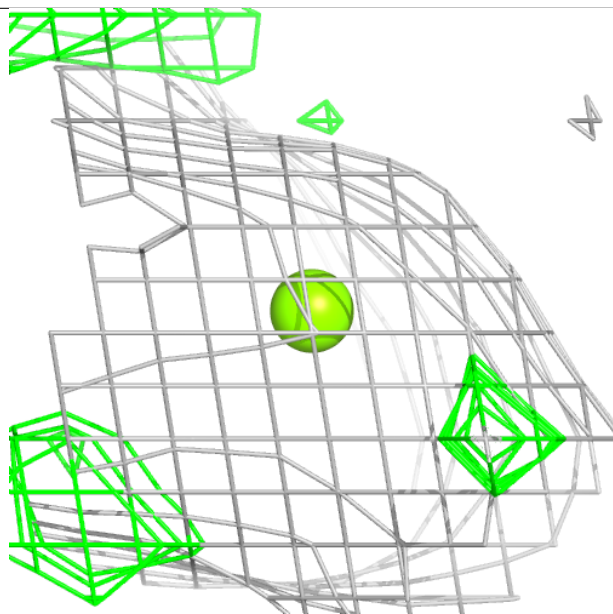
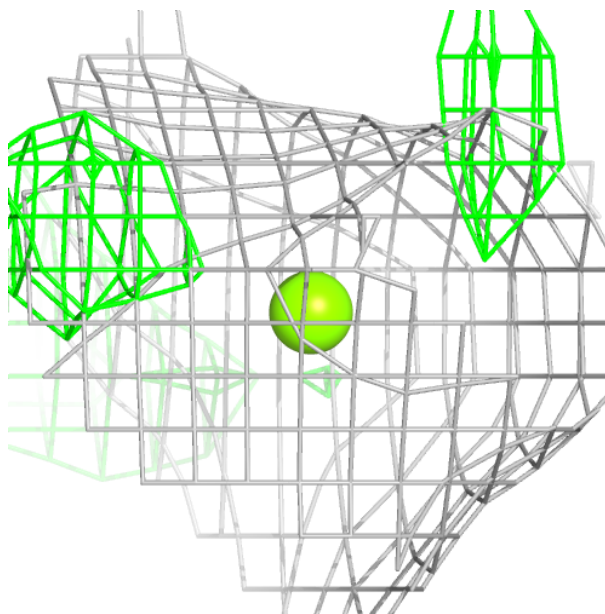
Electron density around MG J 402:

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



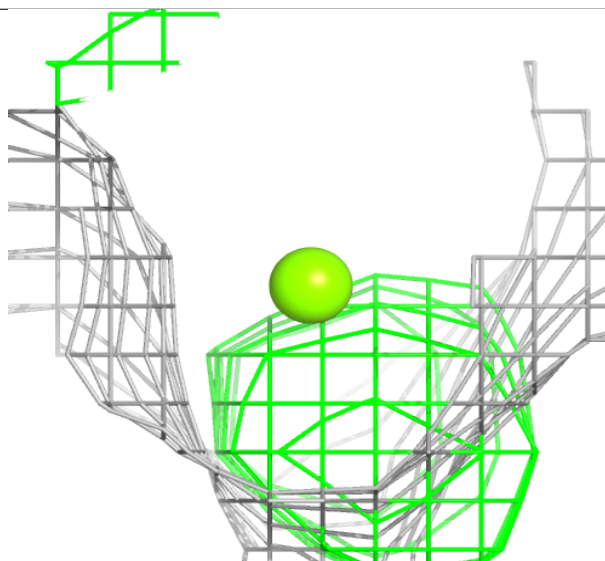
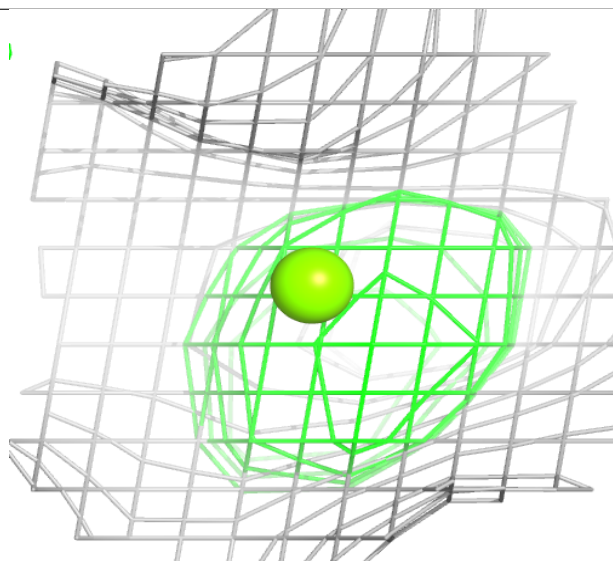
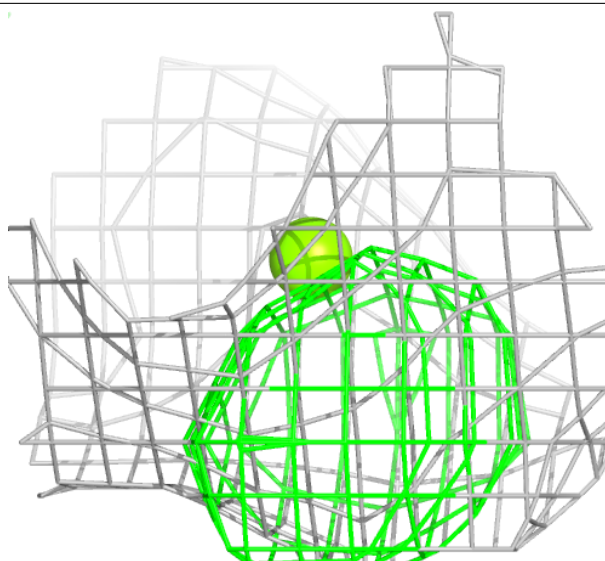
Electron density around MG K 402:

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



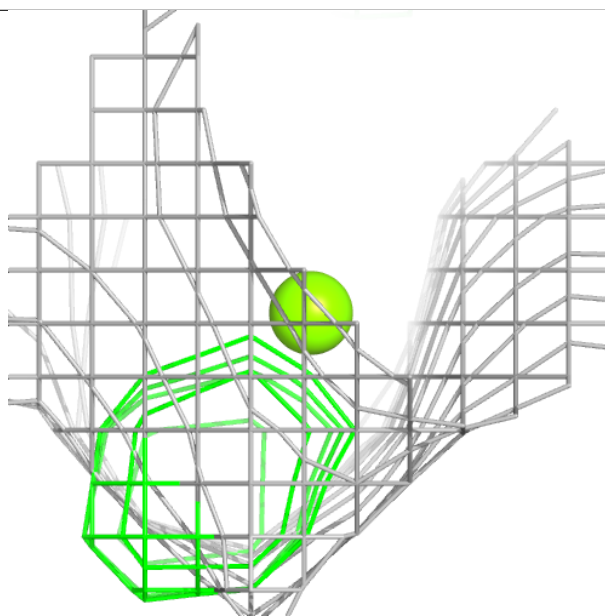
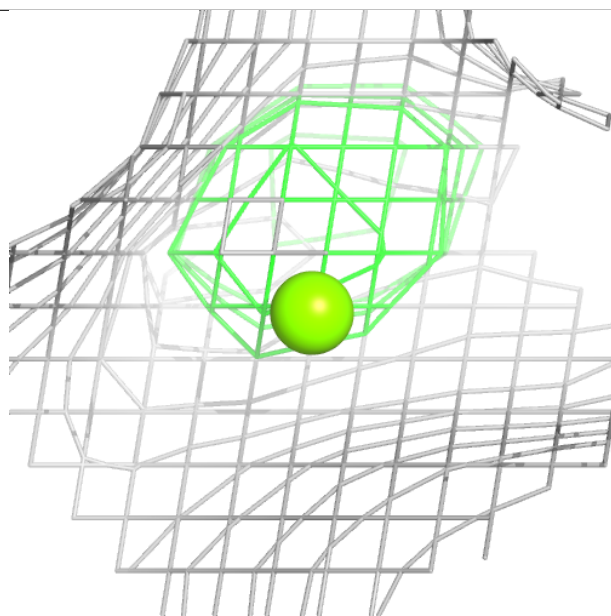
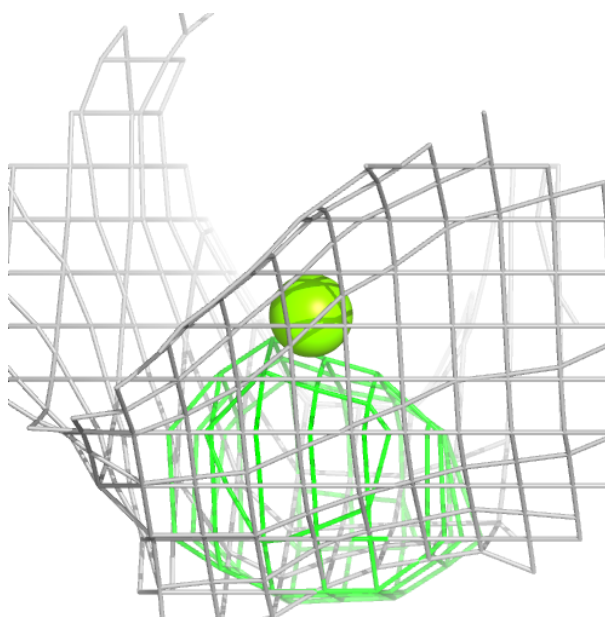
Electron density around MG B 403:

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



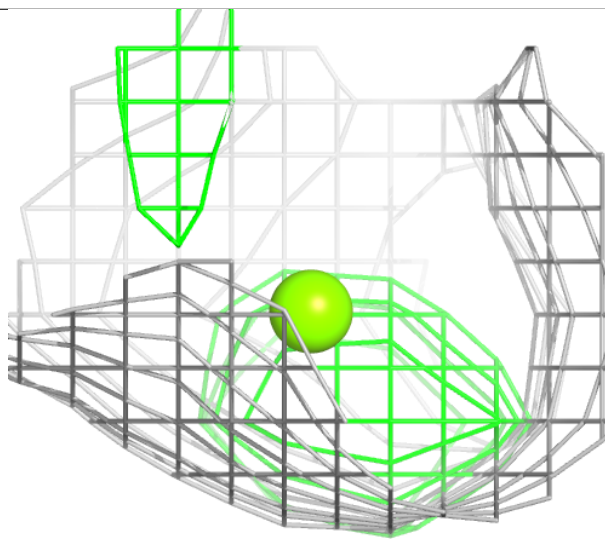
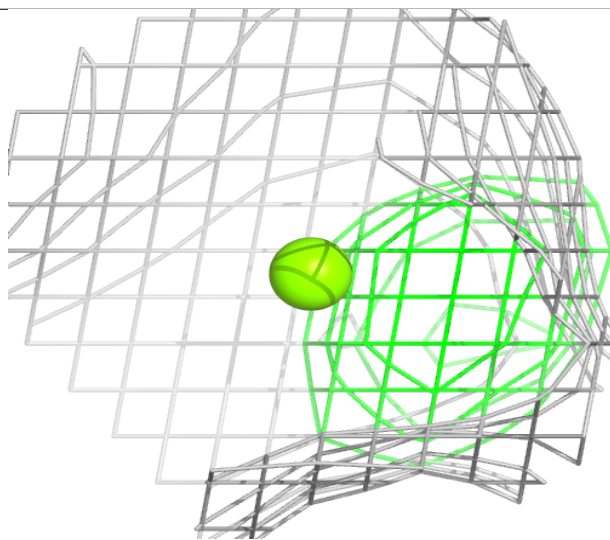
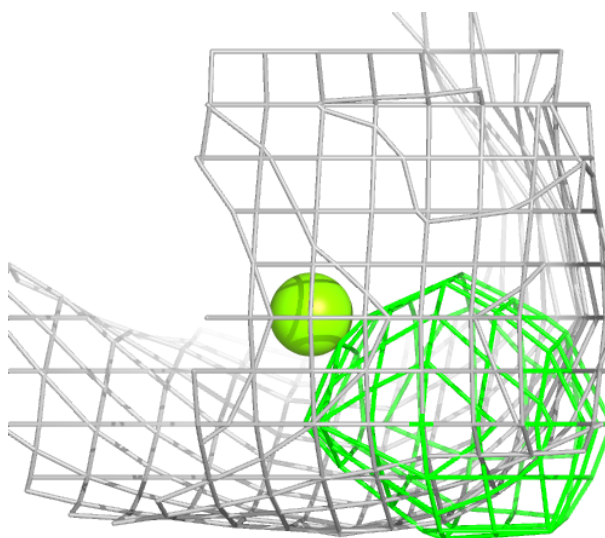
Electron density around MG G 403:

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



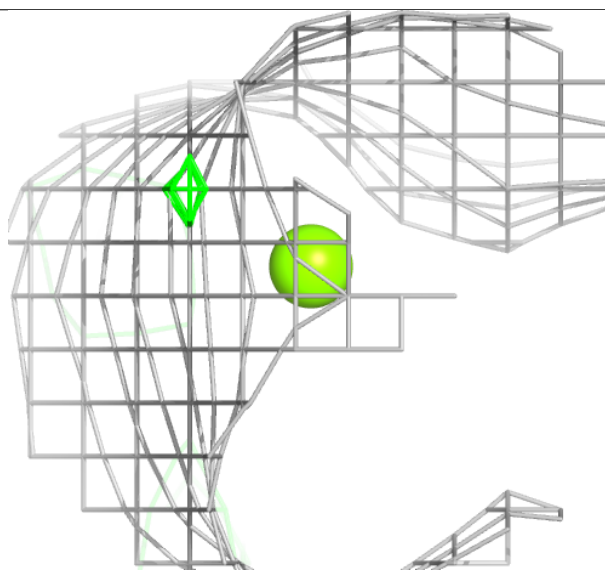
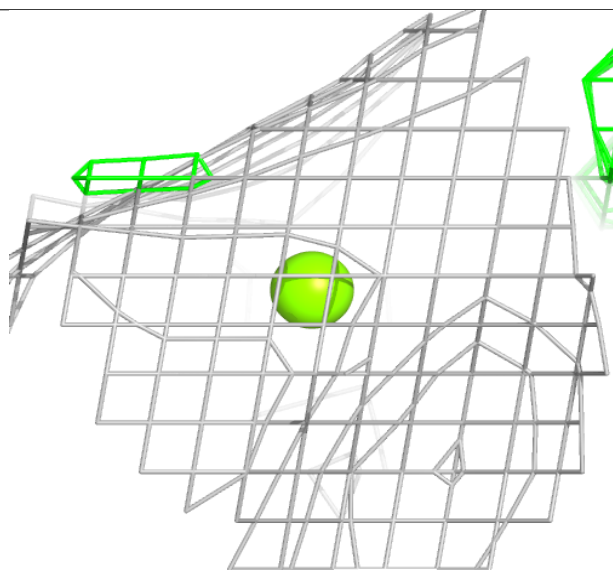
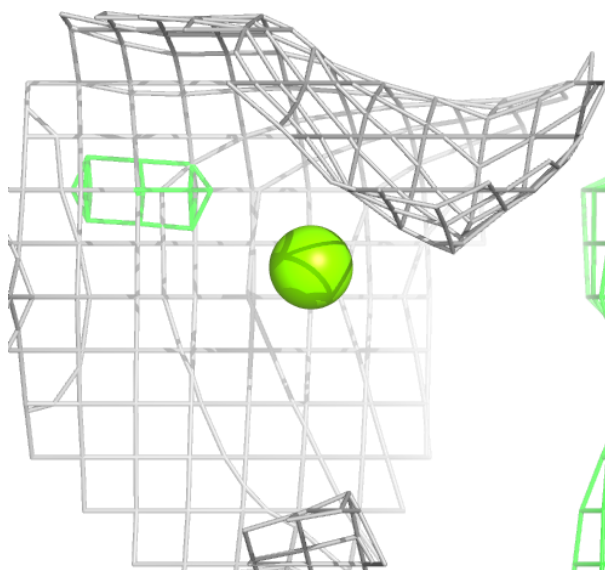
Electron density around MG D 404:

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



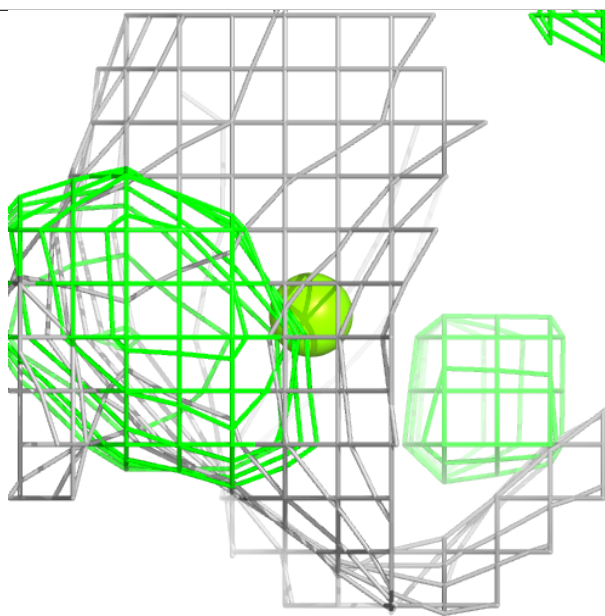
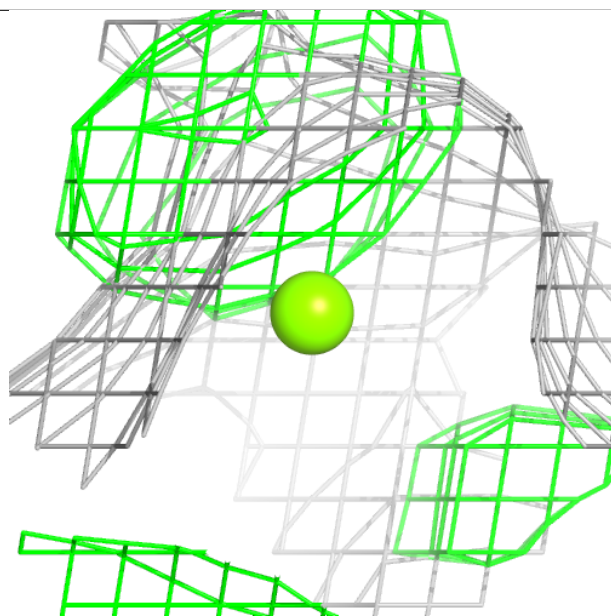
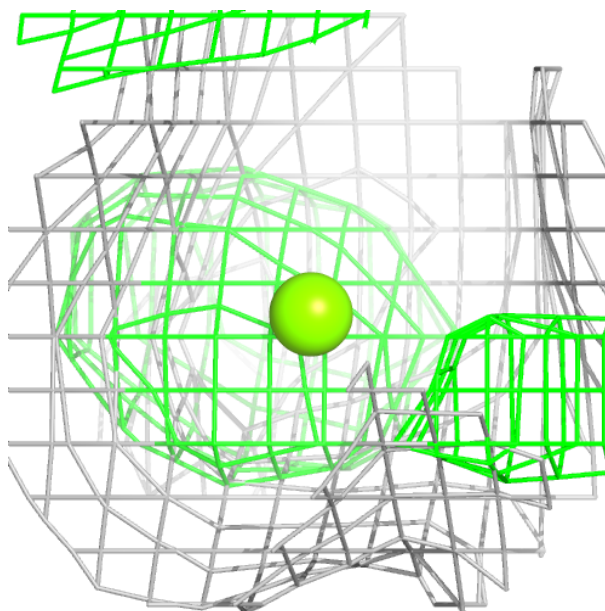
Electron density around MG C 402:

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



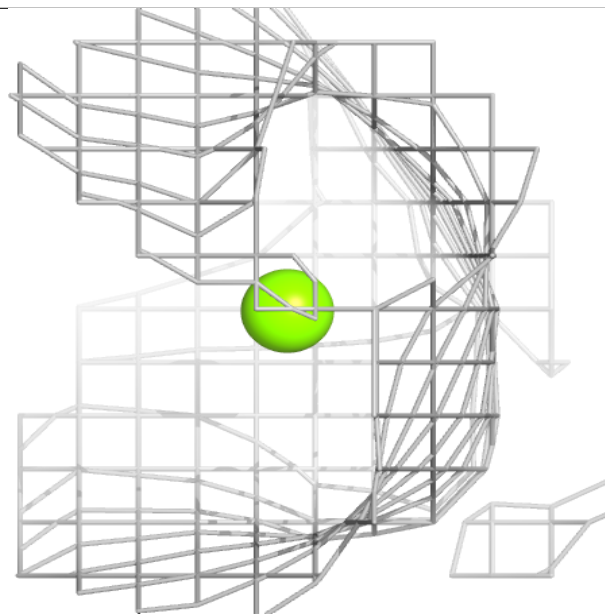
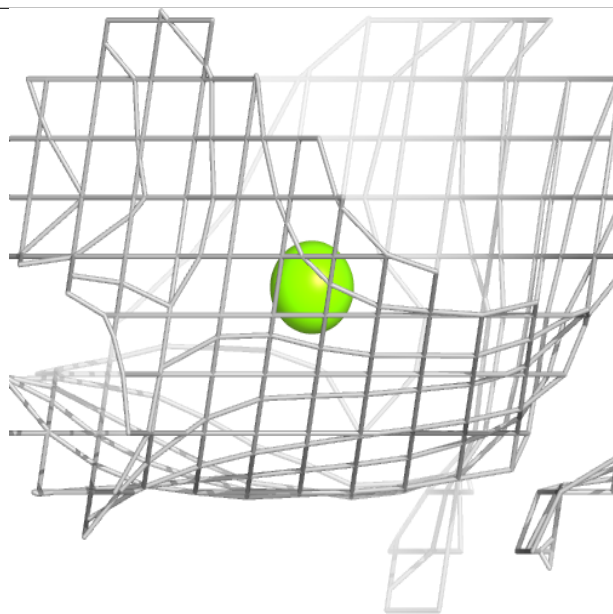
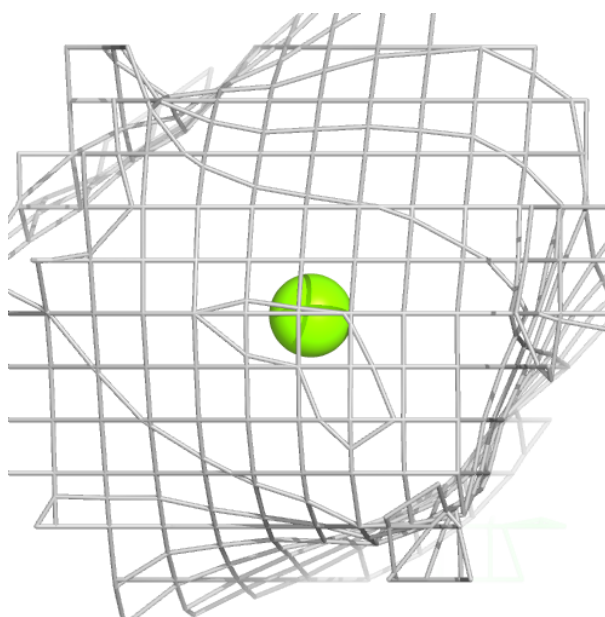
Electron density around MG H 403:

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



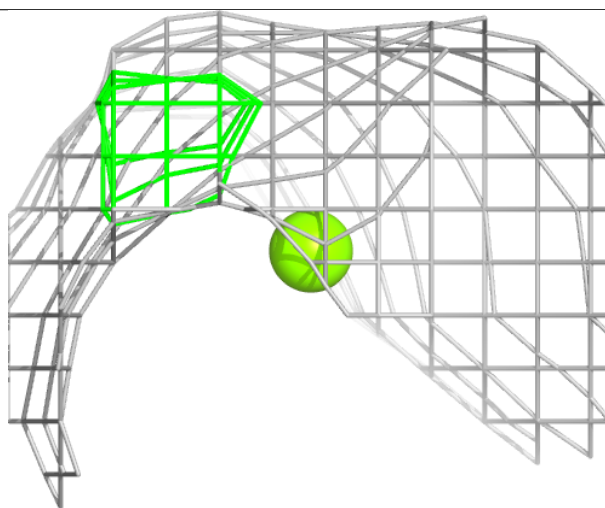
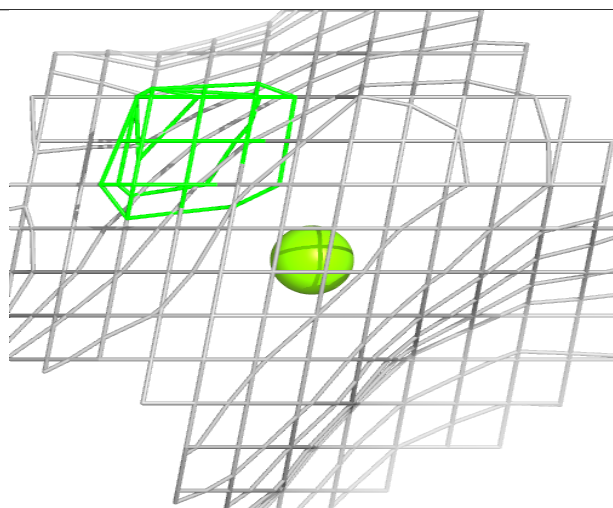
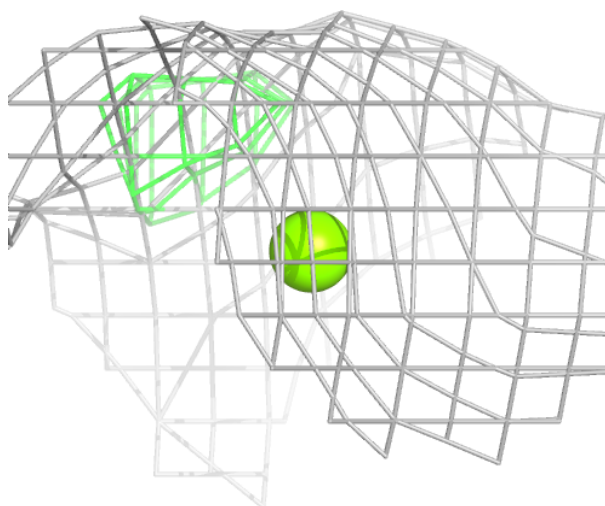
Electron density around MG B 402:

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



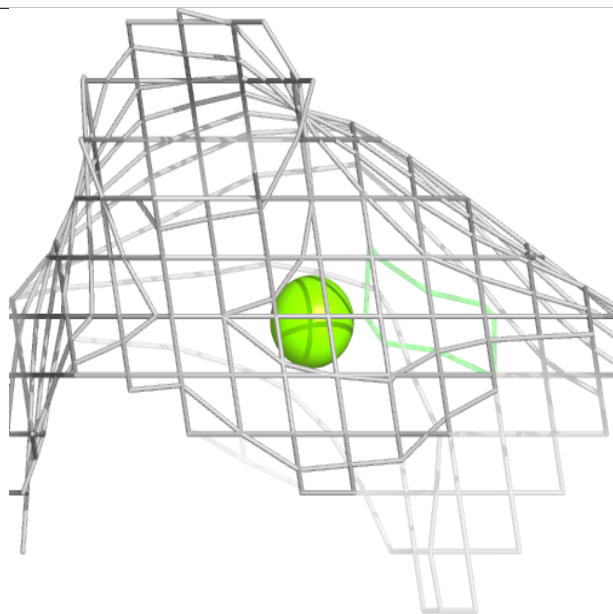
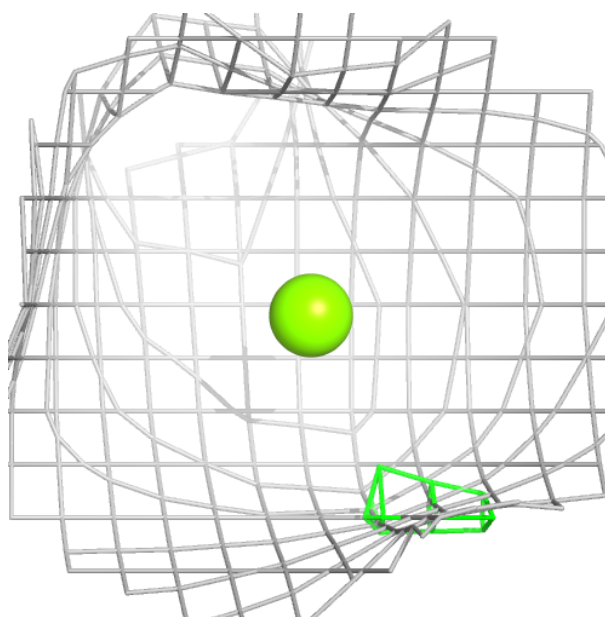
Electron density around MG A 402:

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



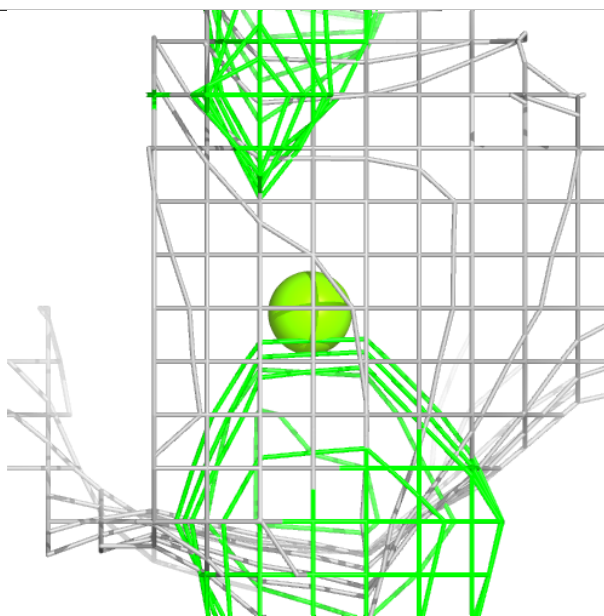
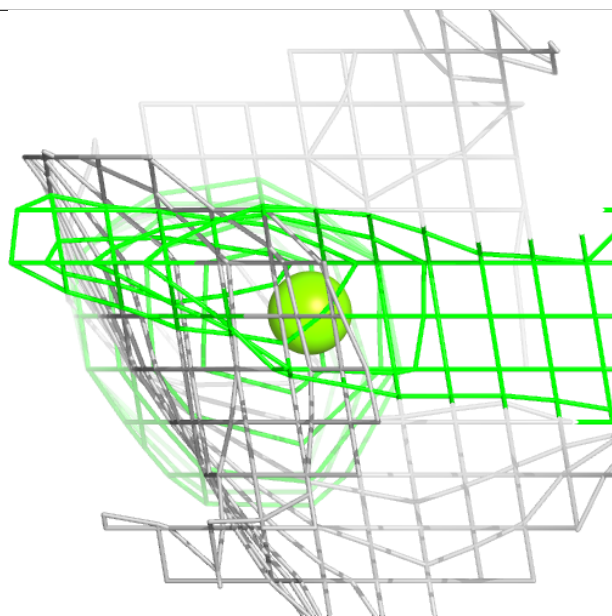
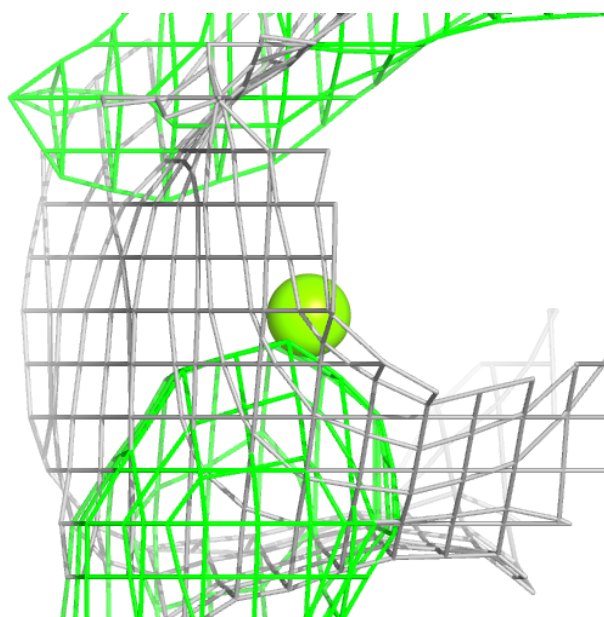
Electron density around MG L 403:

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



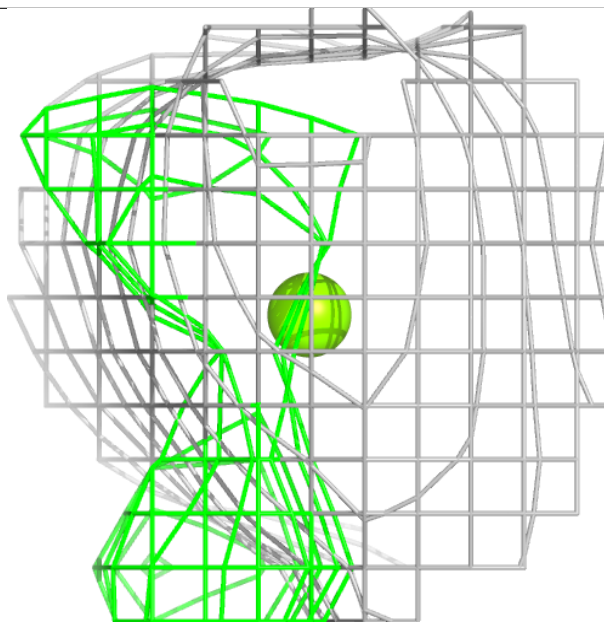
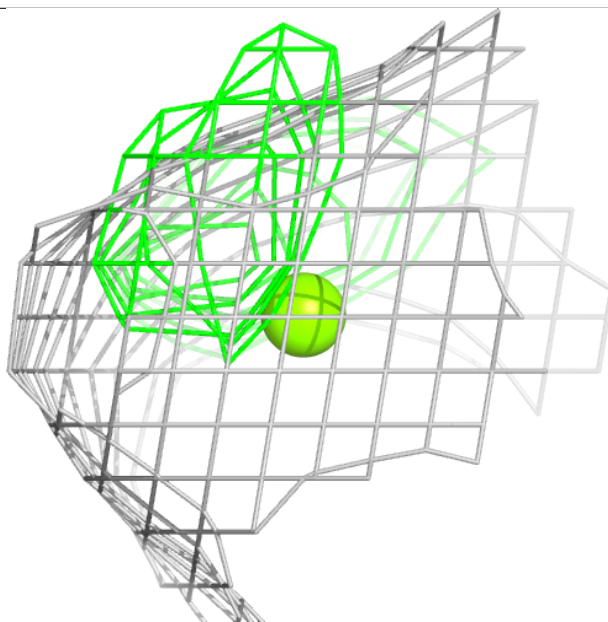
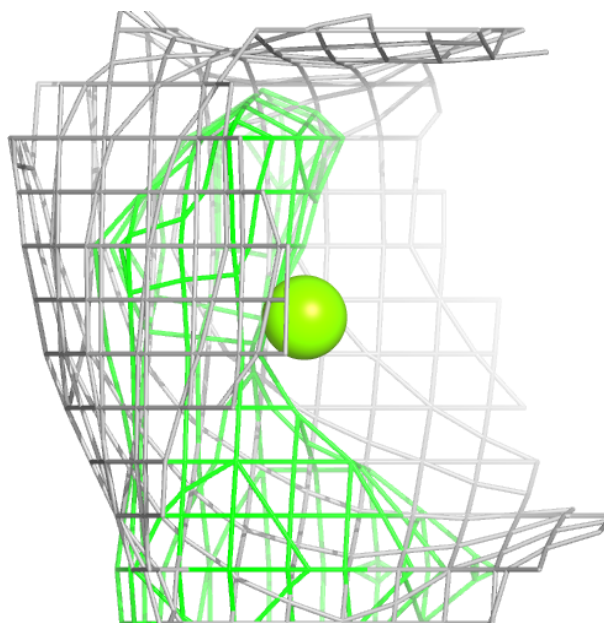
Electron density around MG K 403:

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



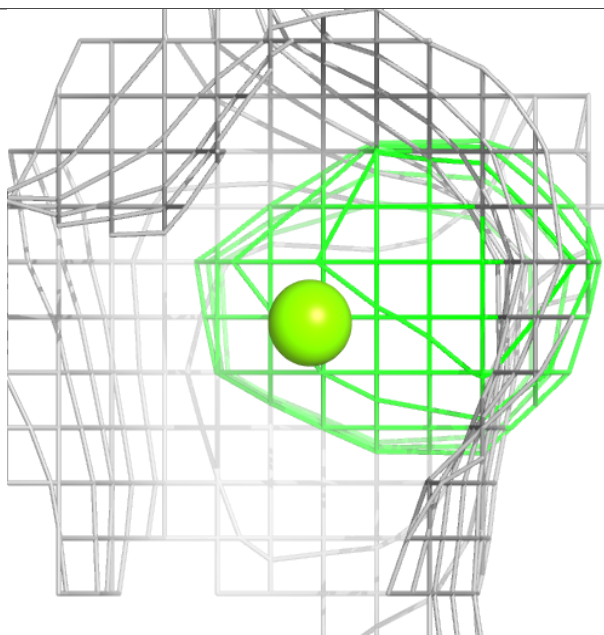
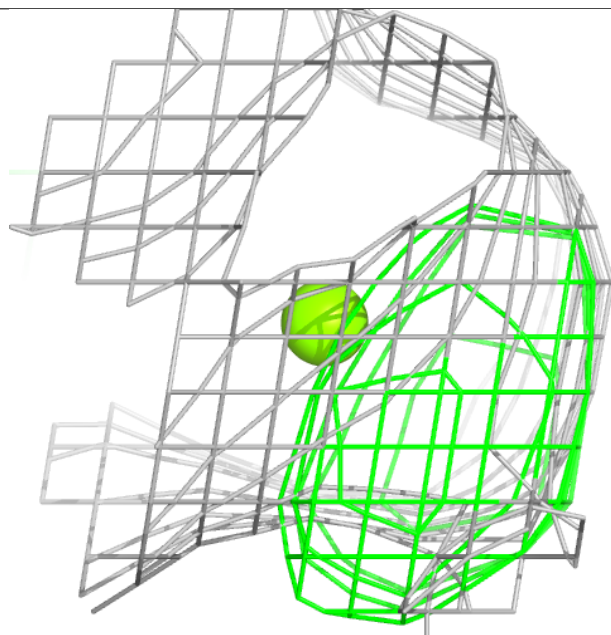
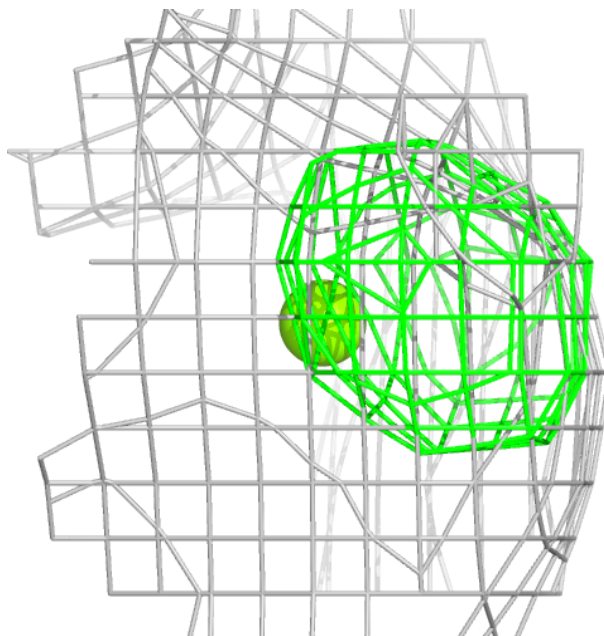
Electron density around MG F 402:

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



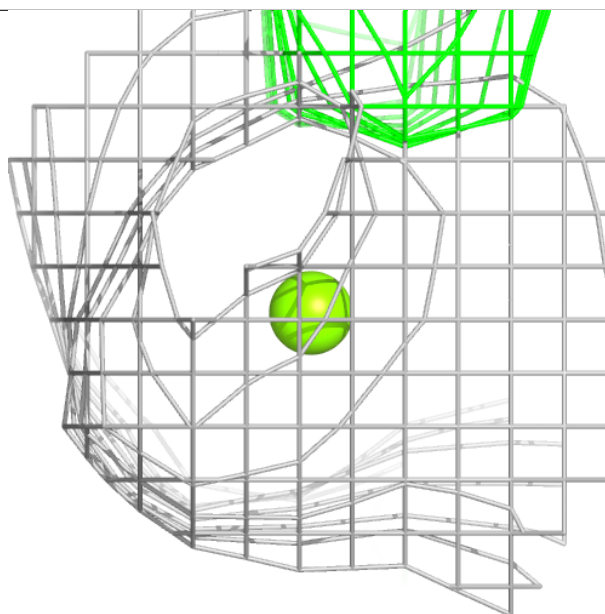
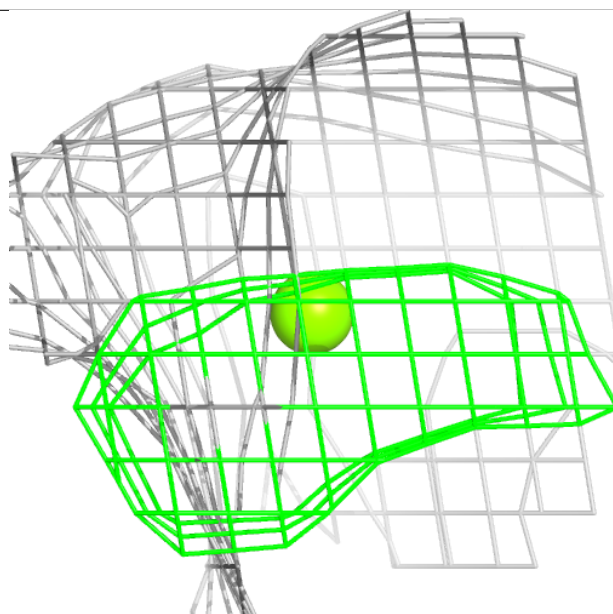
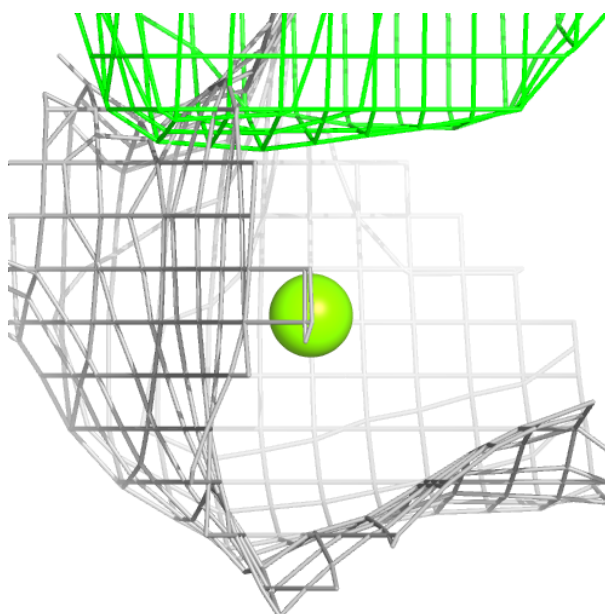
Electron density around MG B 404:

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



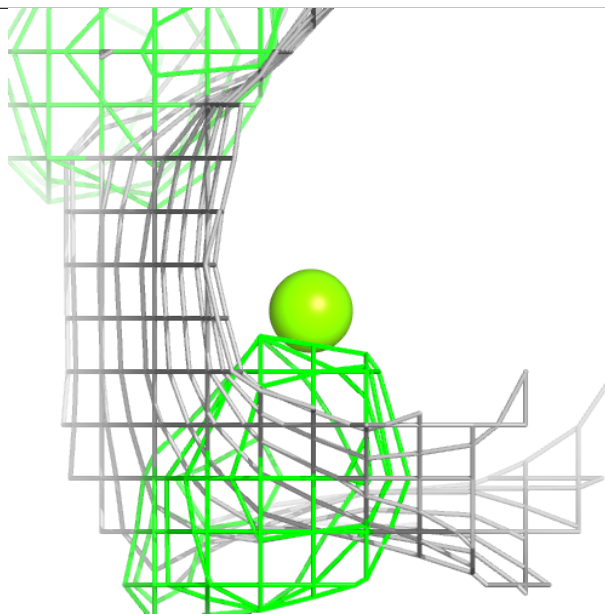
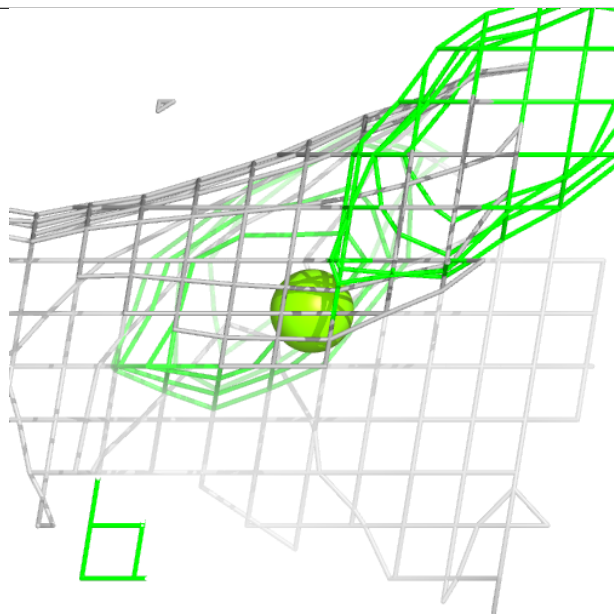
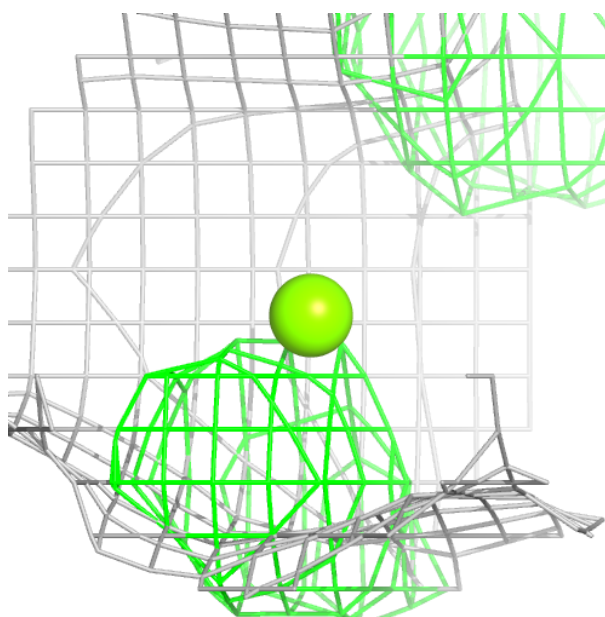
Electron density around MG L 404:

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



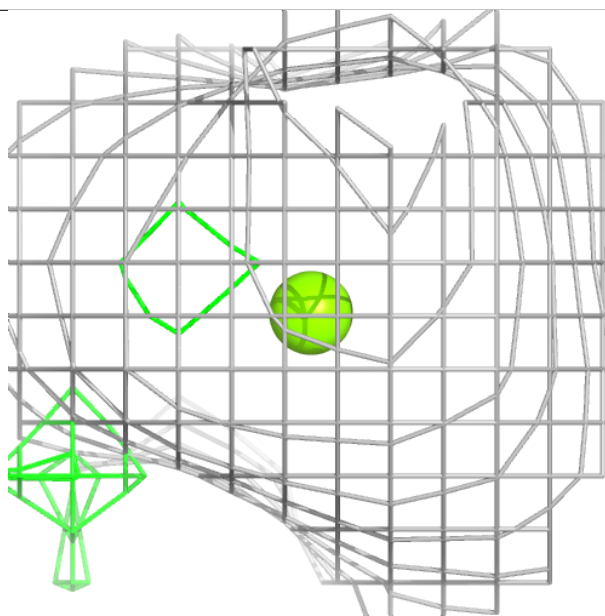
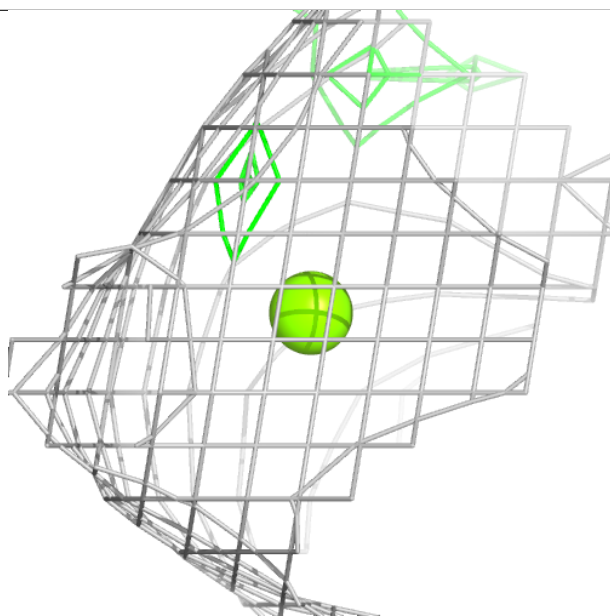
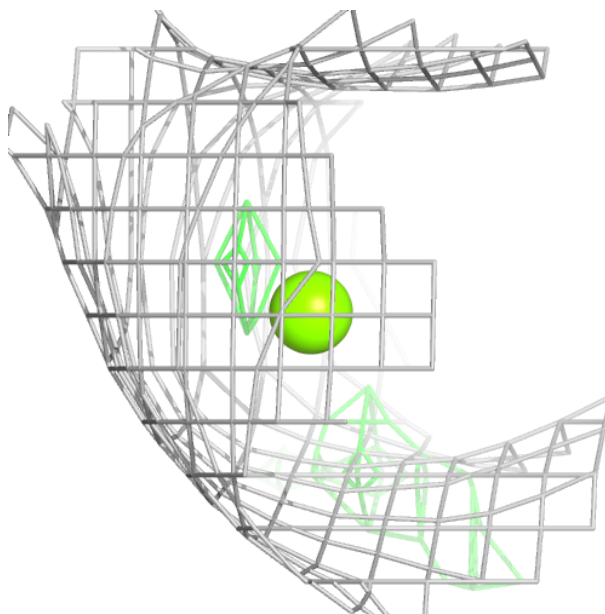
Electron density around MG E 403:

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



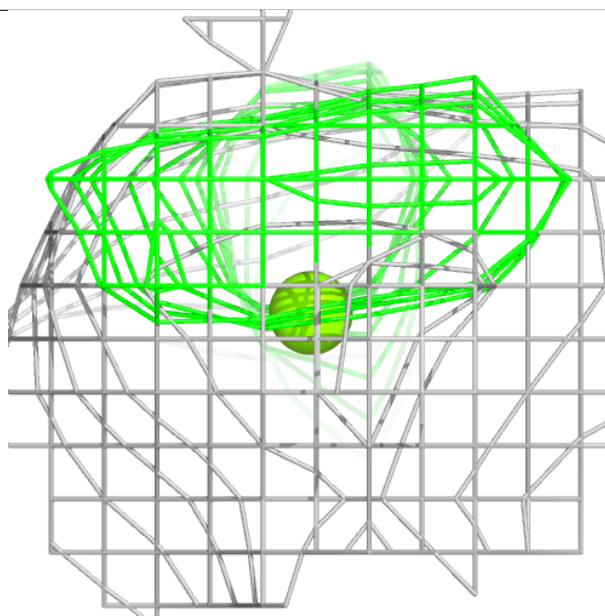
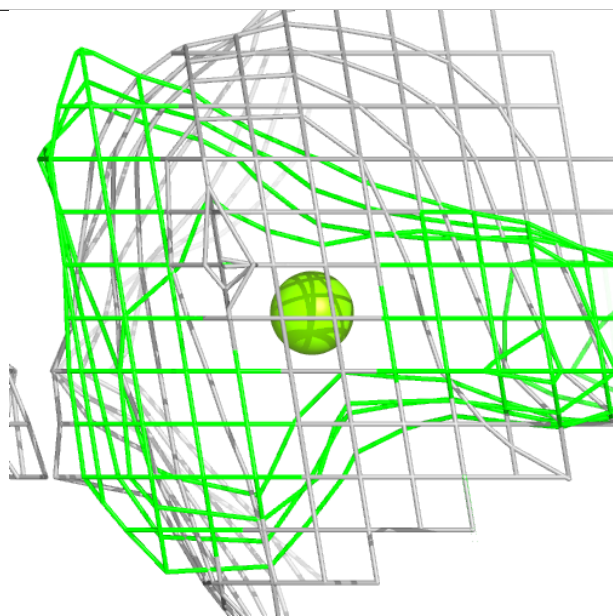
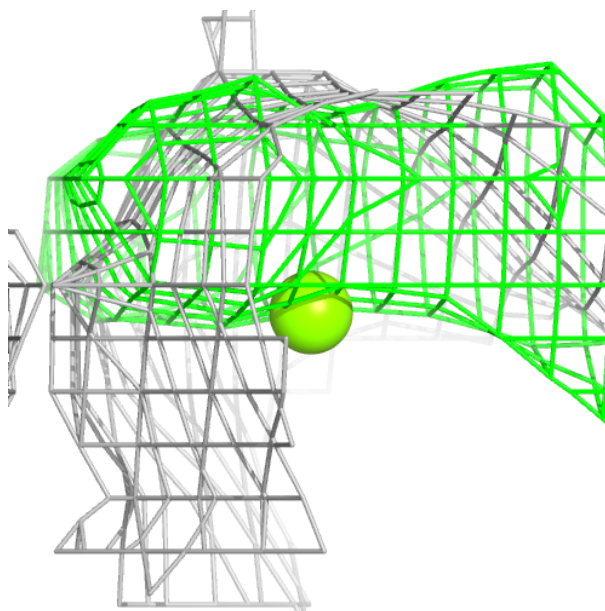
Electron density around MG I 403:

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



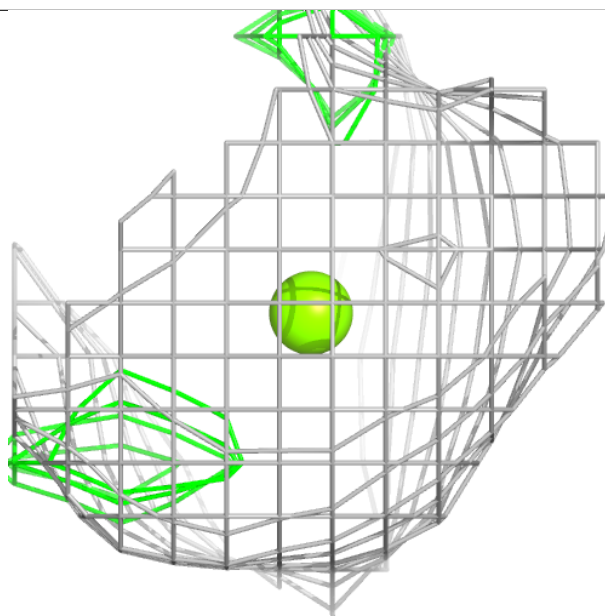
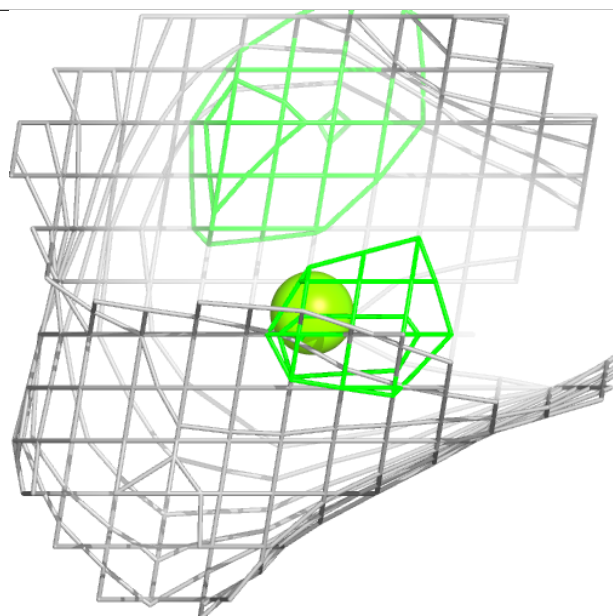
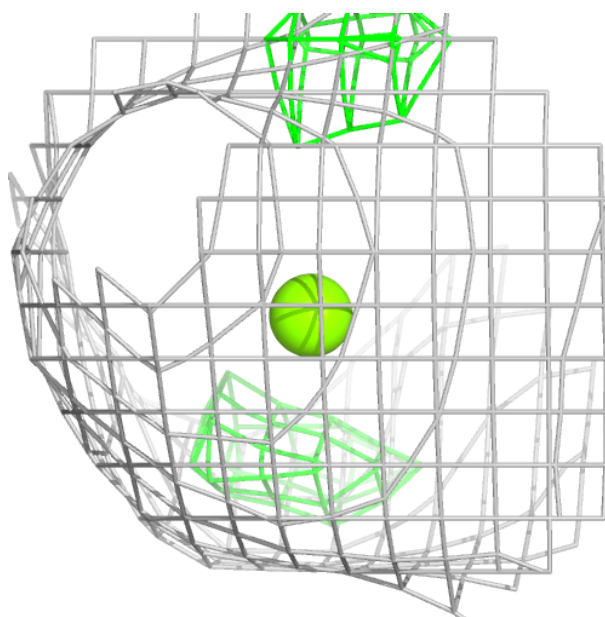
Electron density around MG K 404:

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



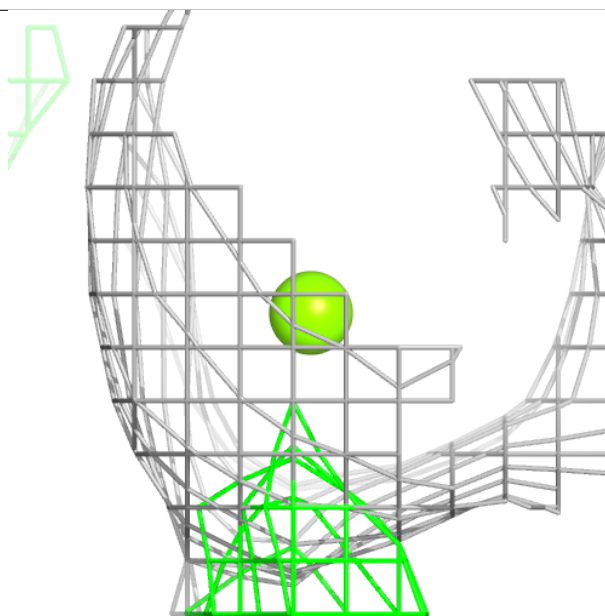
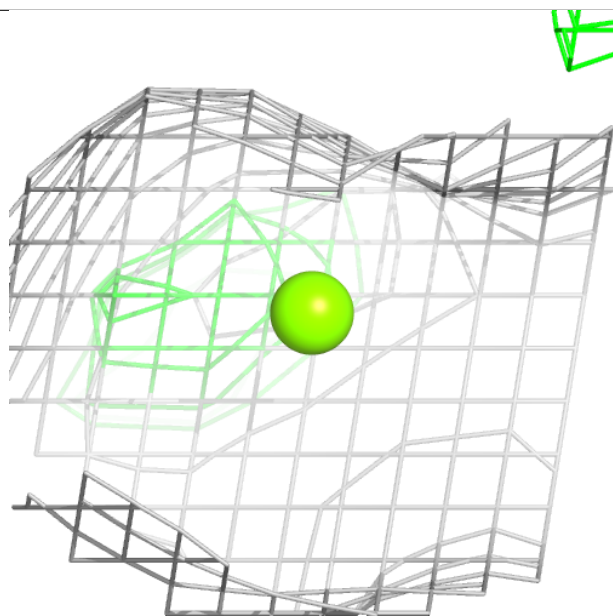
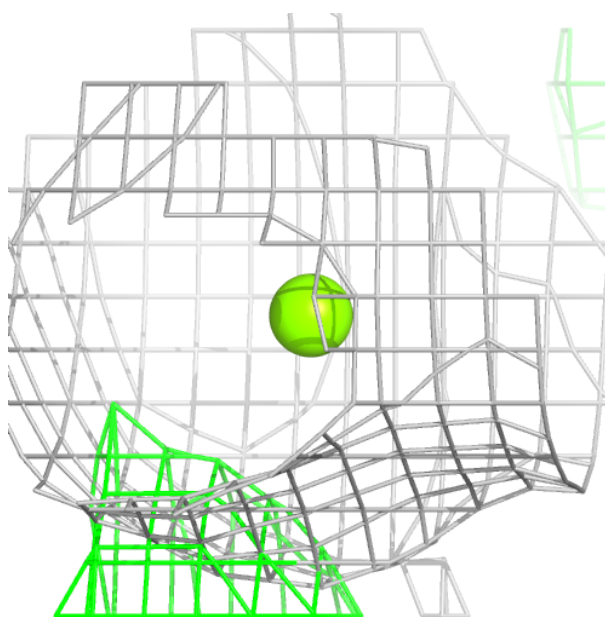
Electron density around MG I 404:

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



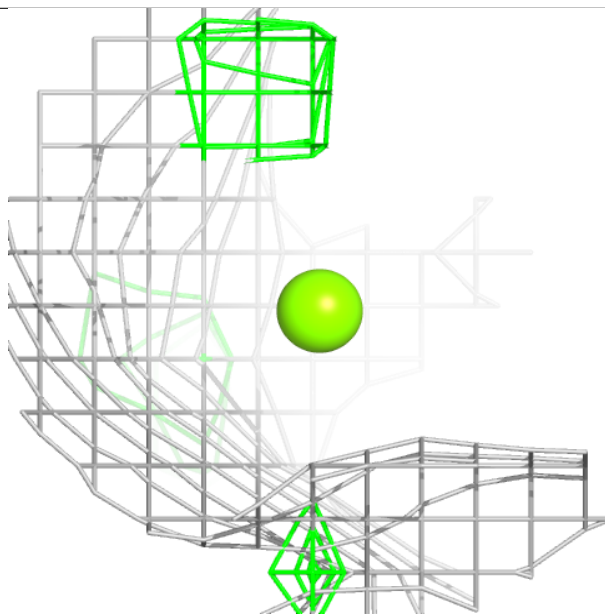
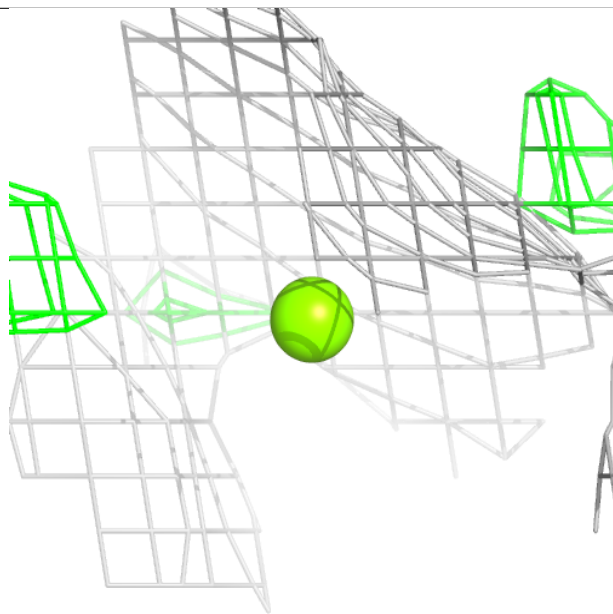
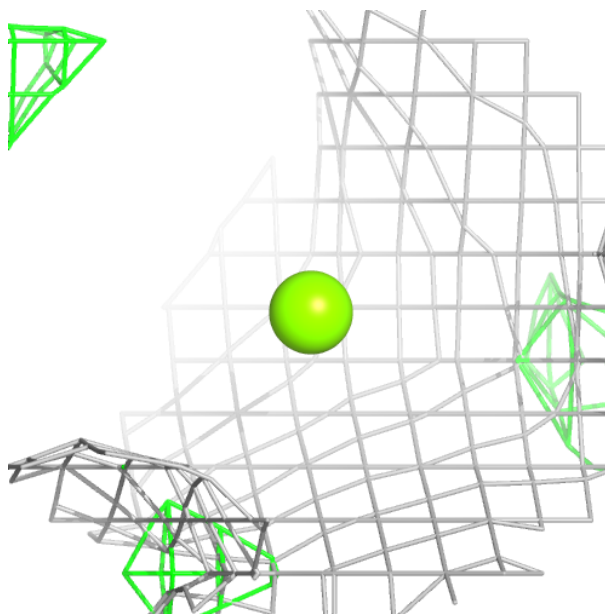
Electron density around MG D 402:

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



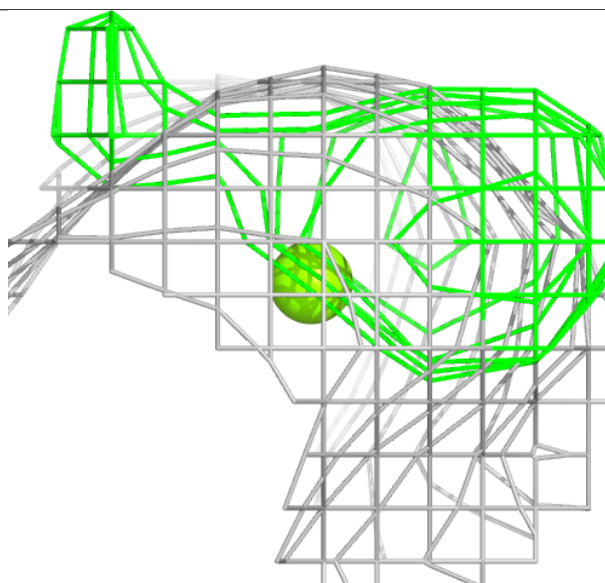
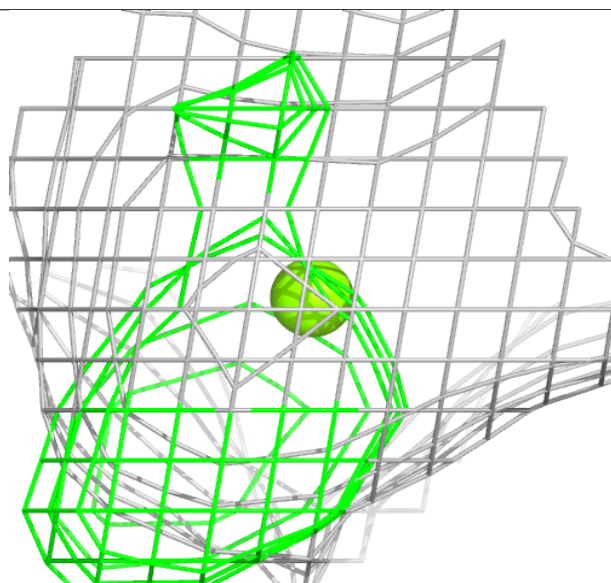
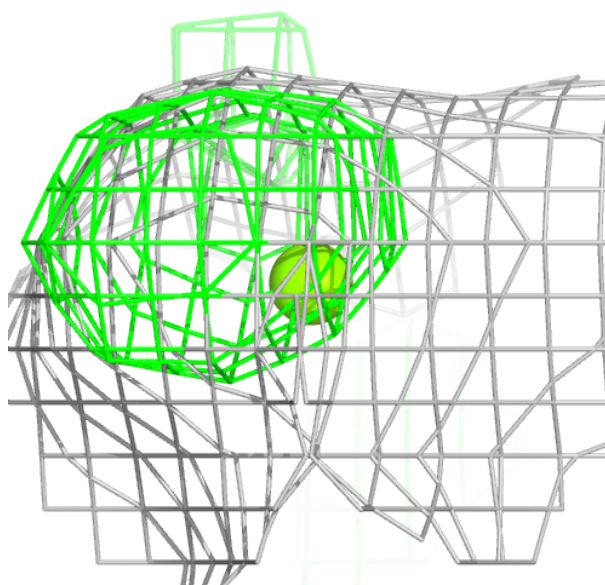
Electron density around MG L 402:

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



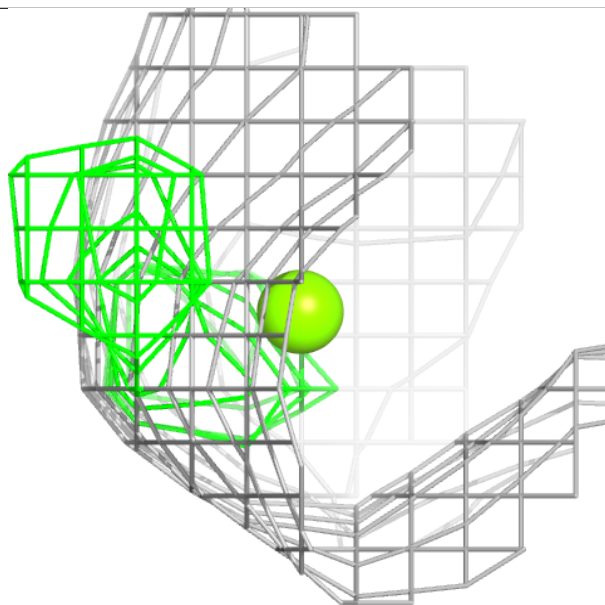
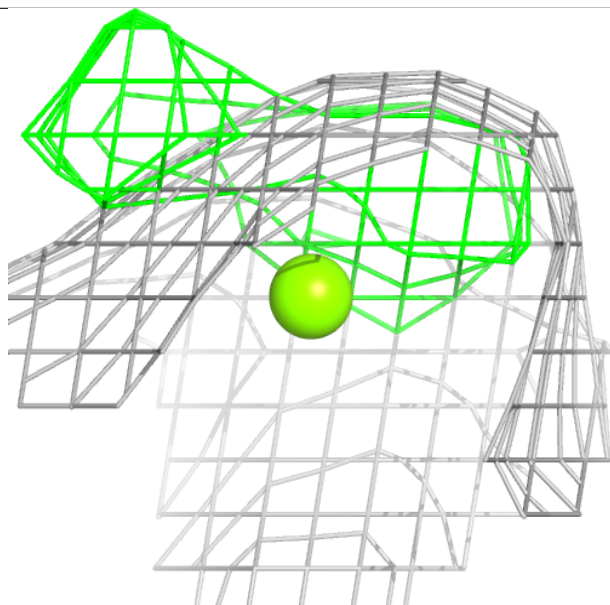
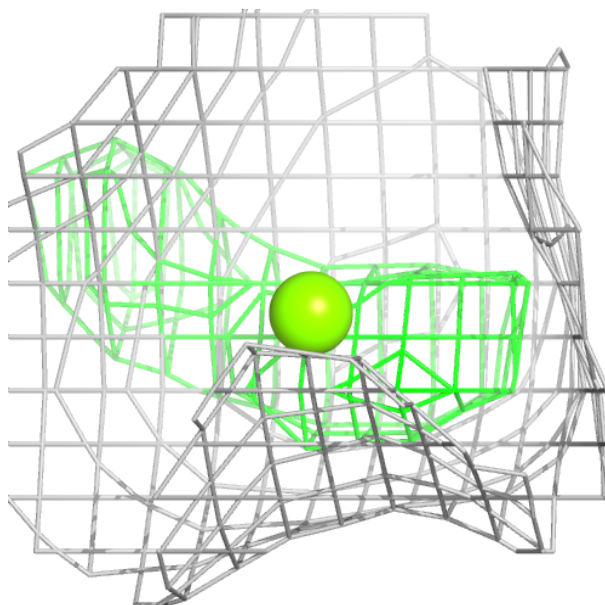
Electron density around MG J 403:

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



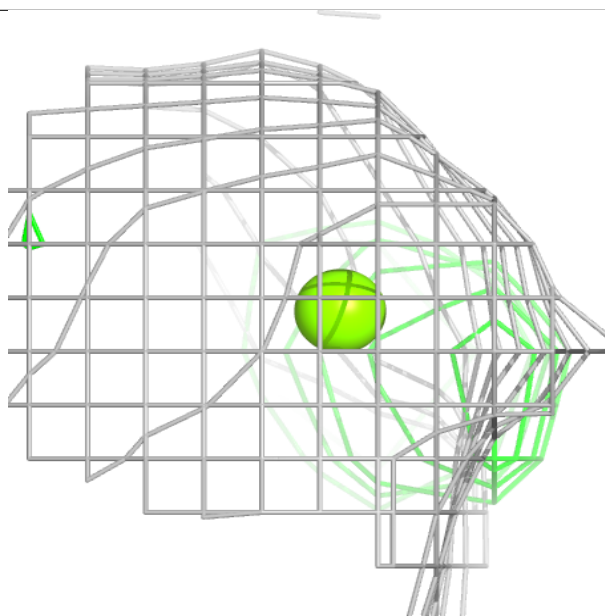
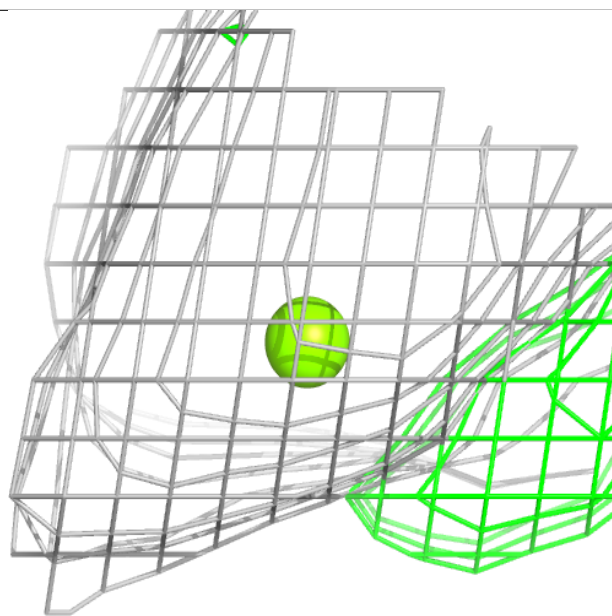
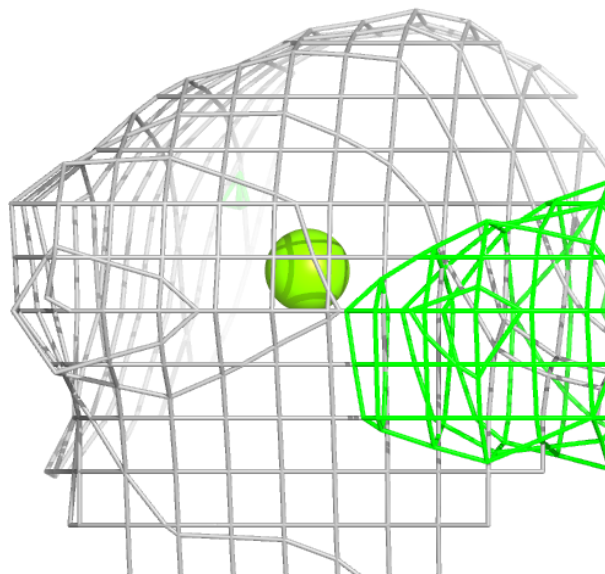
Electron density around MG A 403:

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



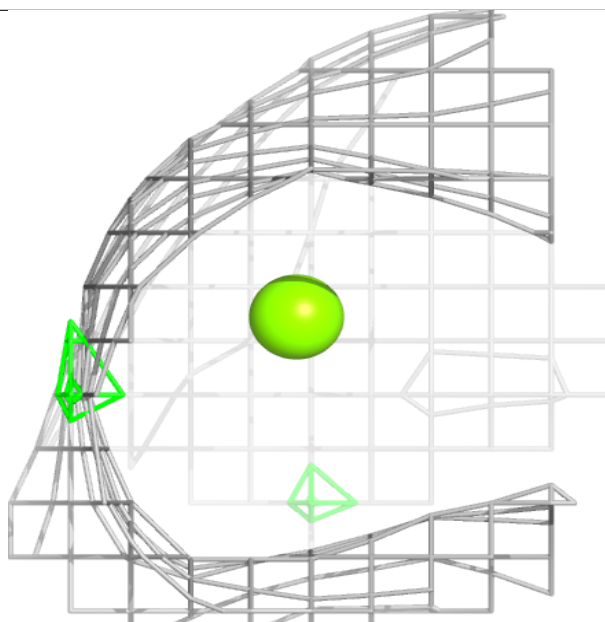
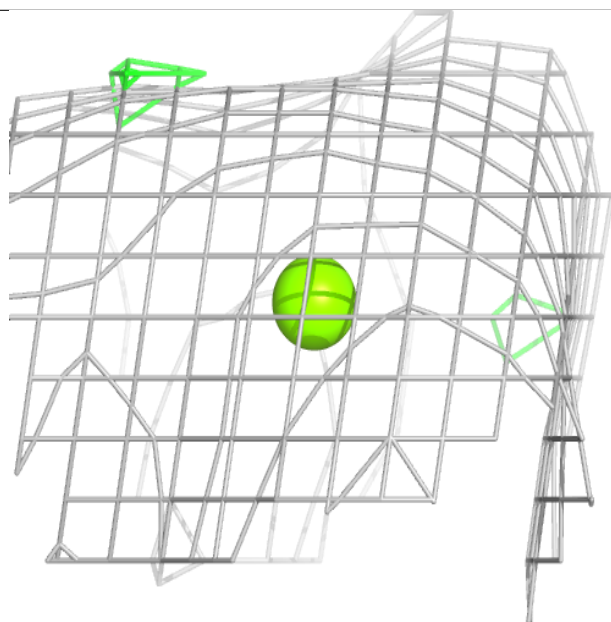
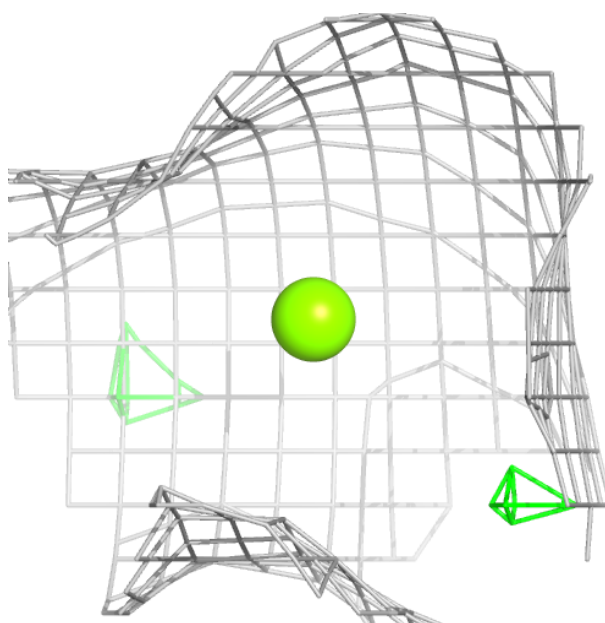
Electron density around MG E 402:

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



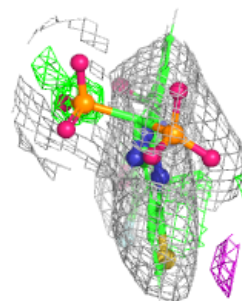
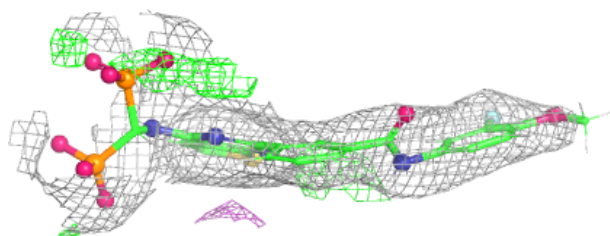
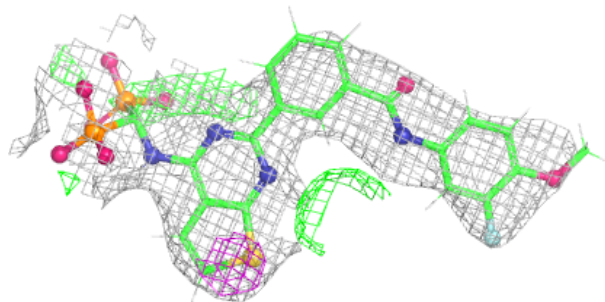
Electron density around MG C 403:

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



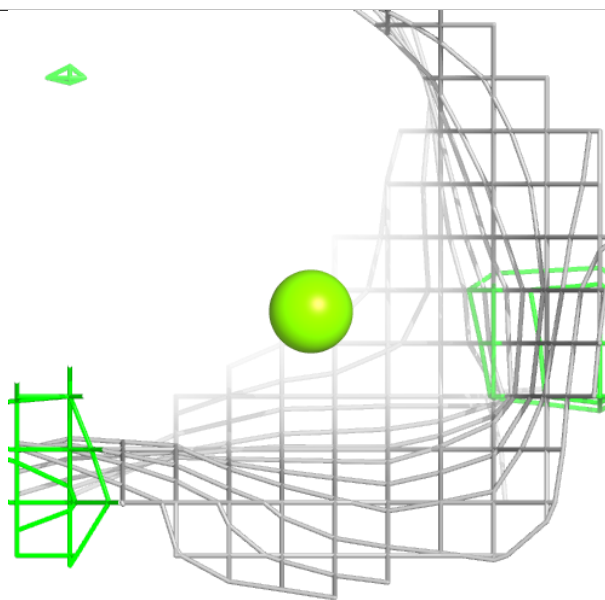
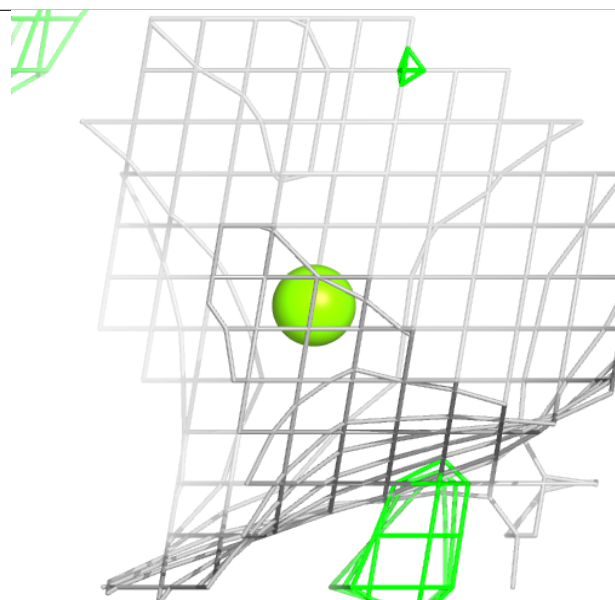
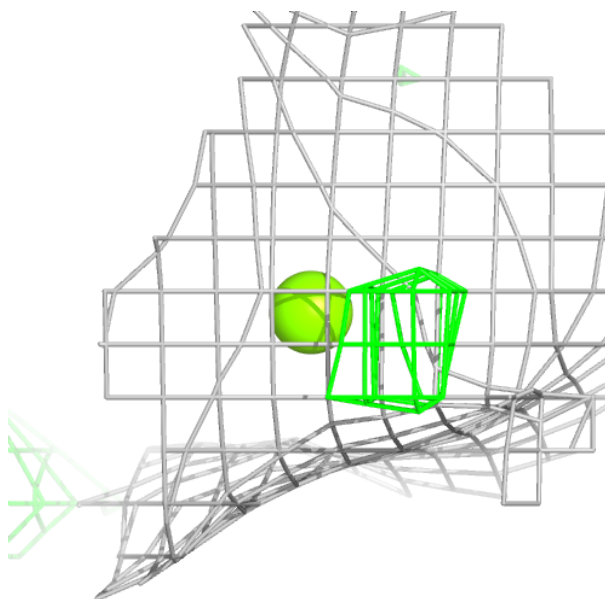
Electron density around A1C1E C 401:

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



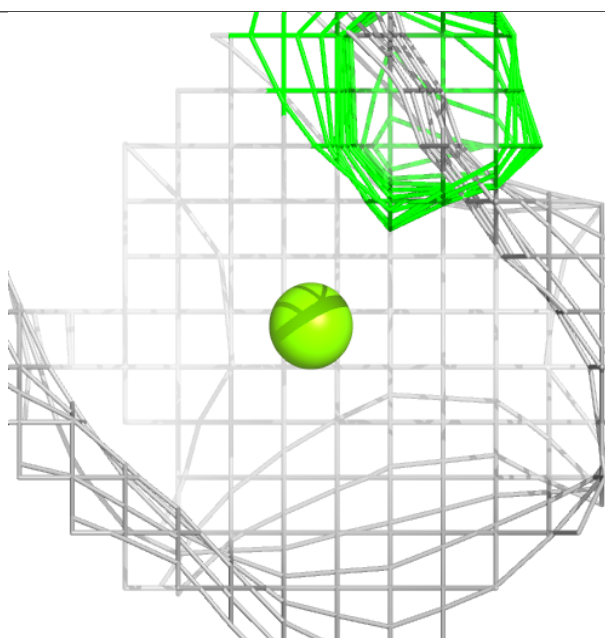
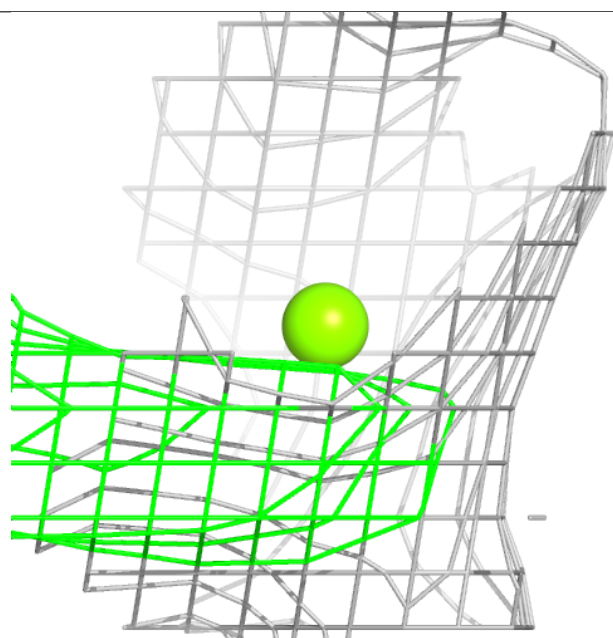
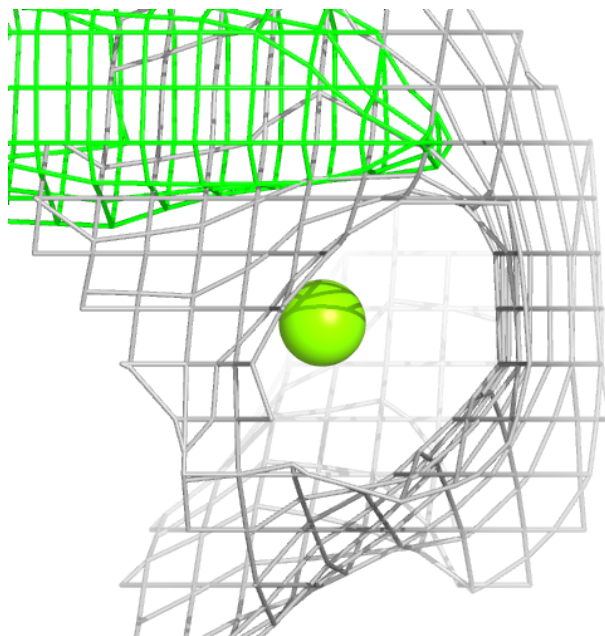
Electron density around MG F 404:

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



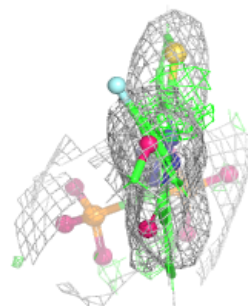
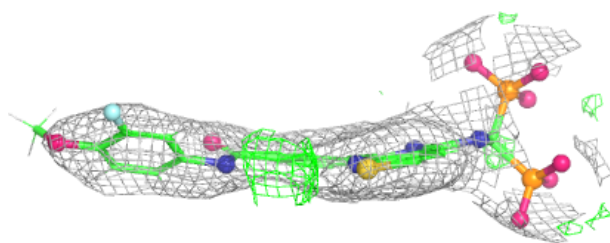
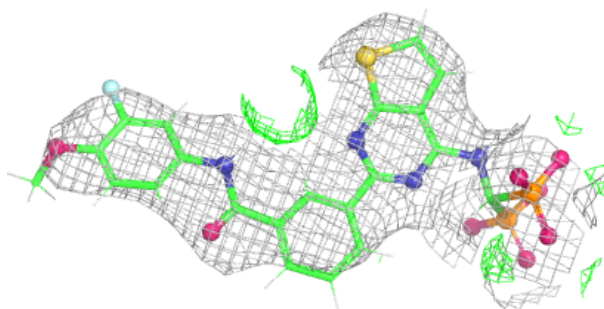
Electron density around MG H 404:

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

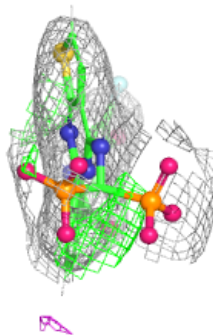
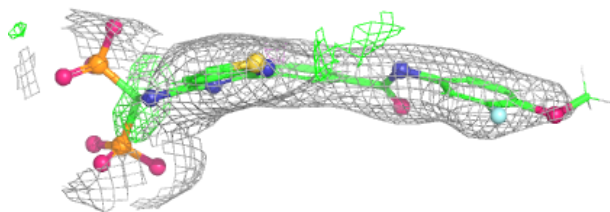
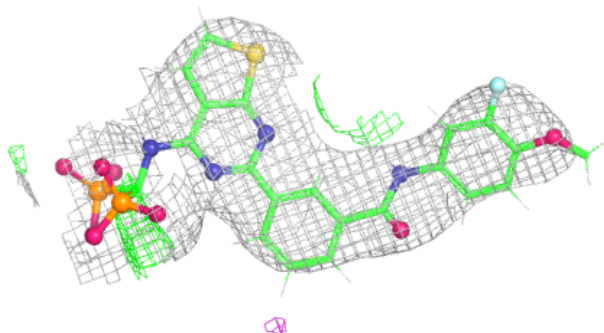


Electron density around A1C1E I 401:

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

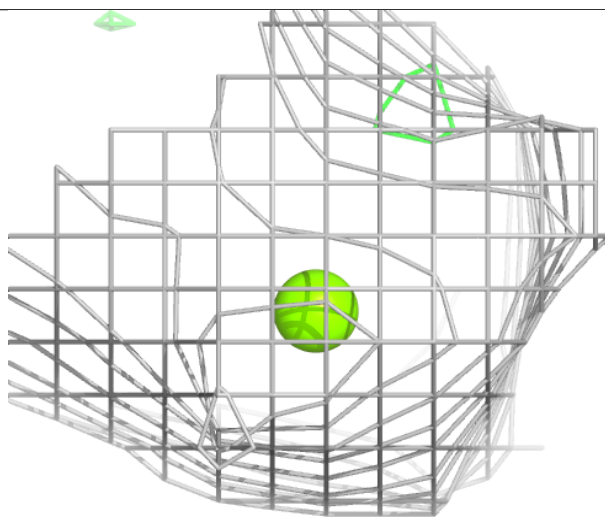
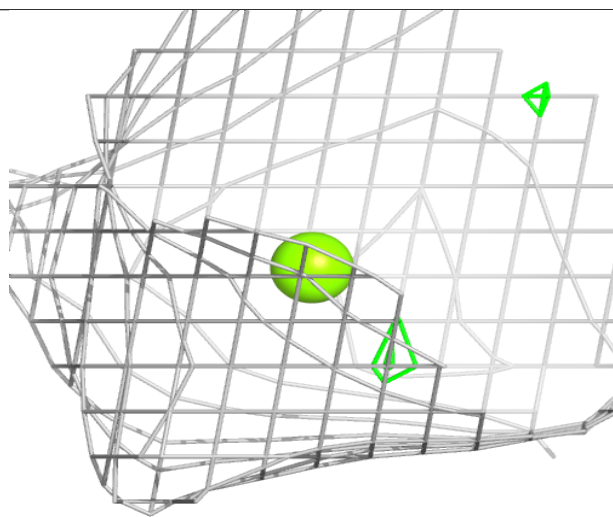
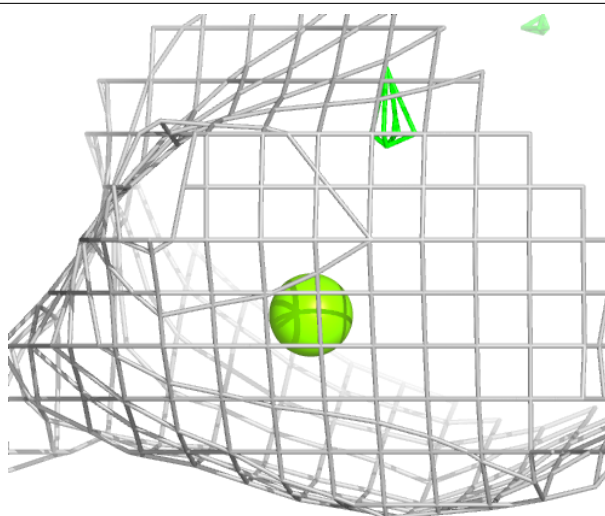
**Electron density around A1C1E L 401:**

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



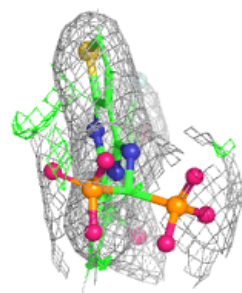
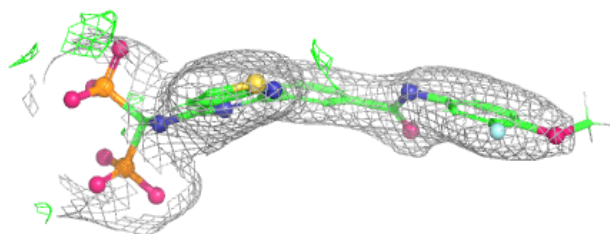
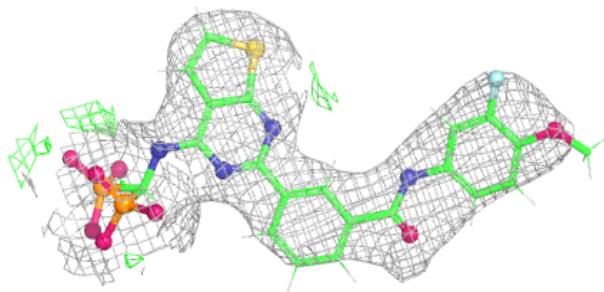
Electron density around MG F 403:

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

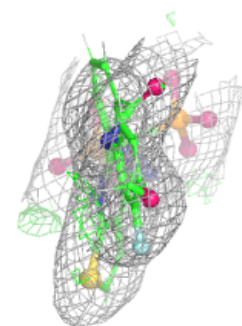
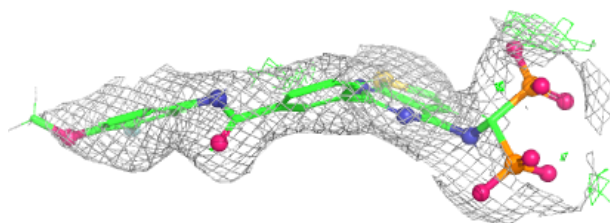
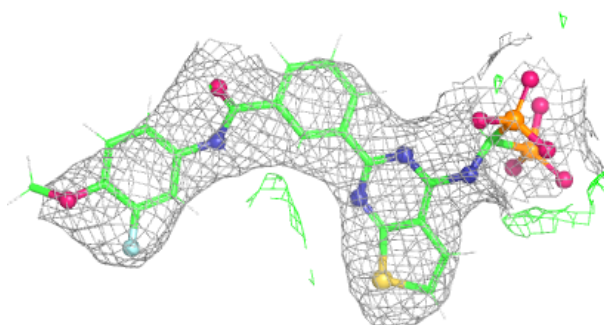


Electron density around A1C1E F 401:

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

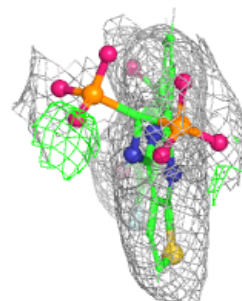
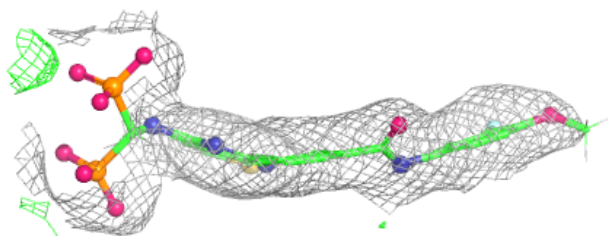
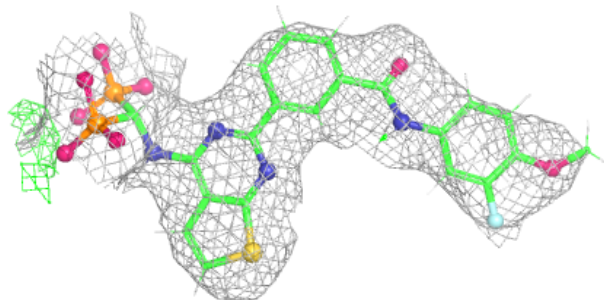
**Electron density around A1C1E G 401:**

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

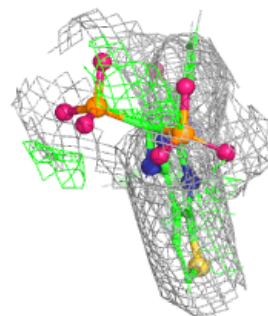
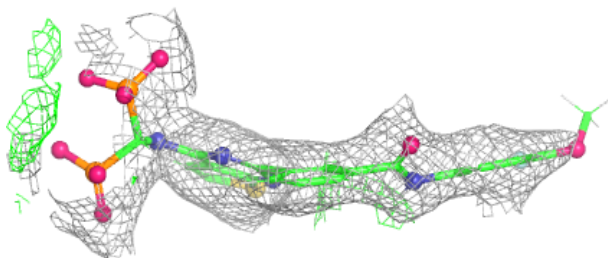
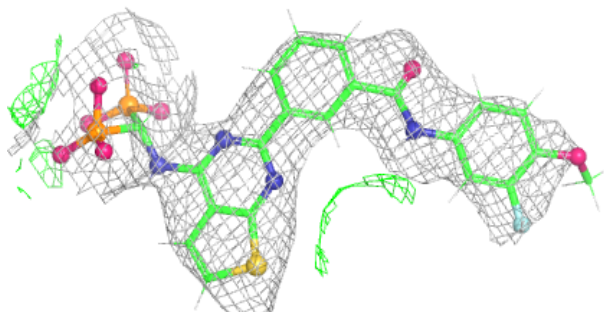


Electron density around A1C1E B 401:

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

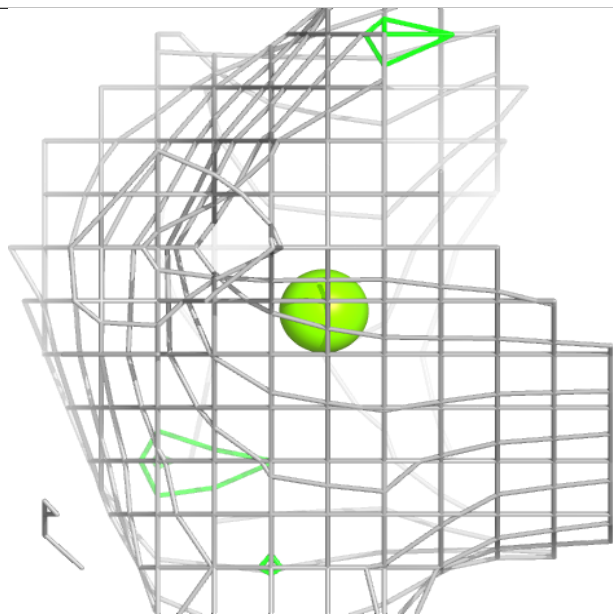
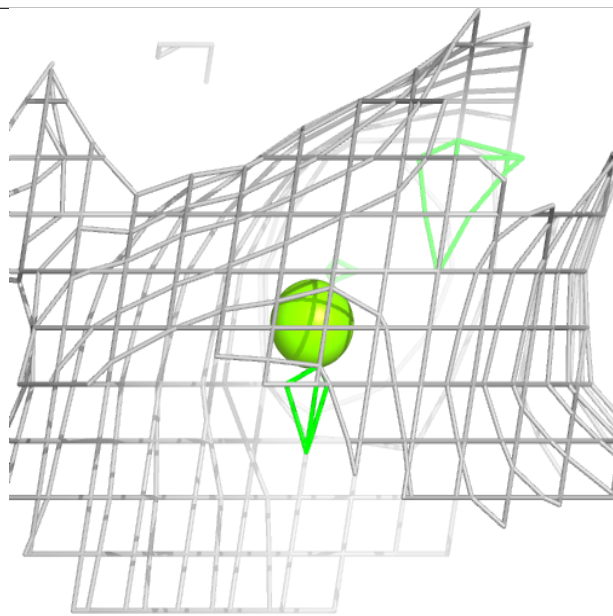
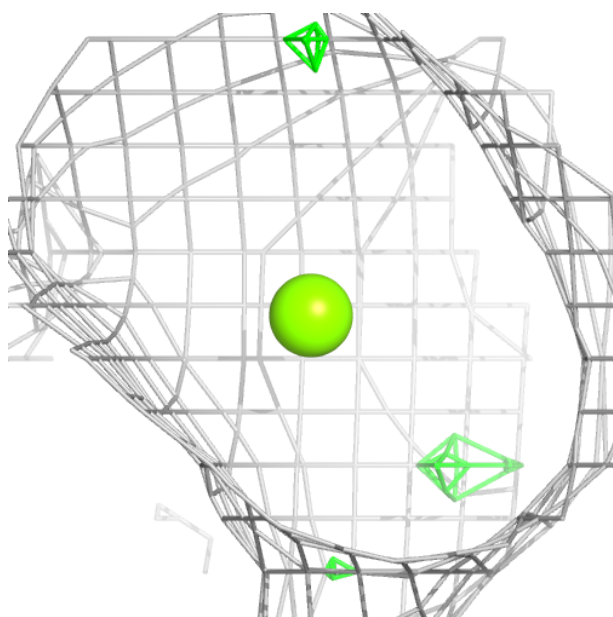
**Electron density around A1C1E E 401:**

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



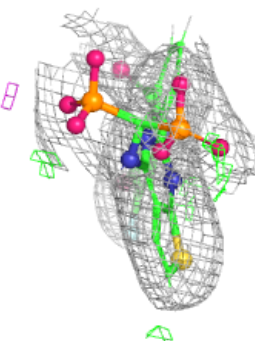
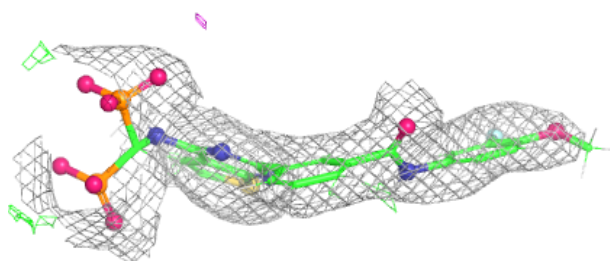
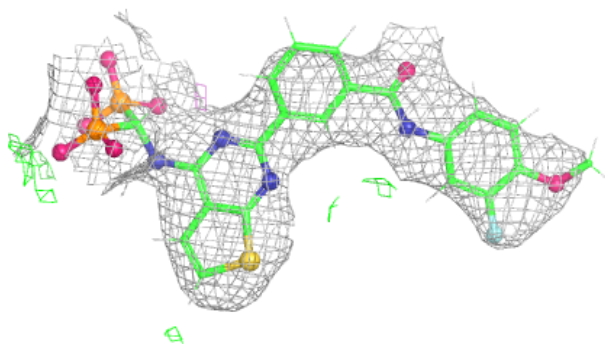
Electron density around MG G 402:

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

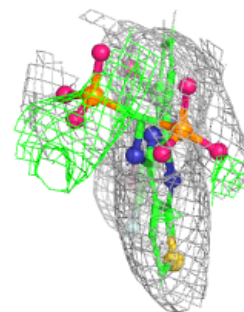
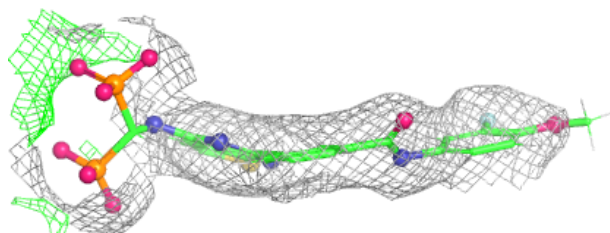
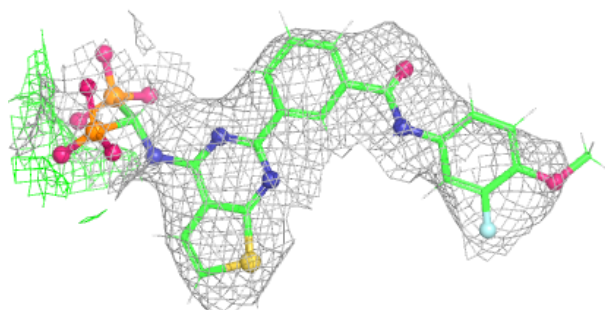


Electron density around A1C1E A 401:

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

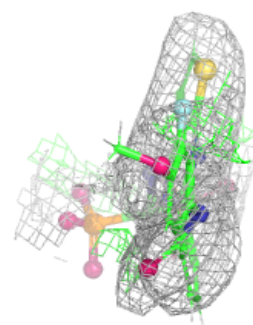
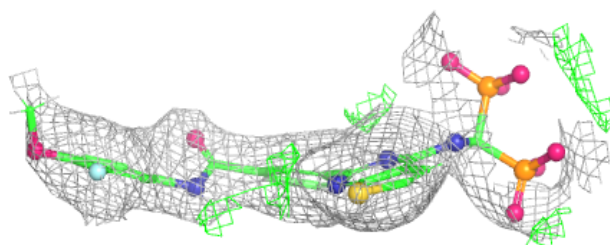
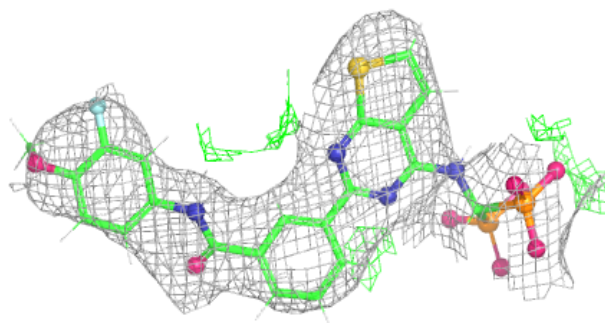
**Electron density around A1C1E H 401:**

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

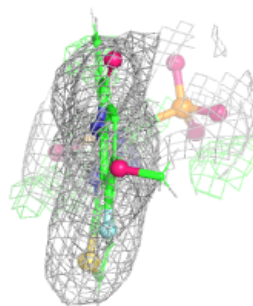
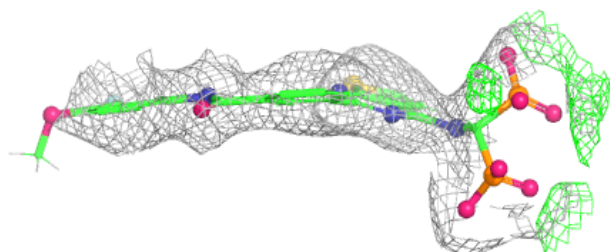
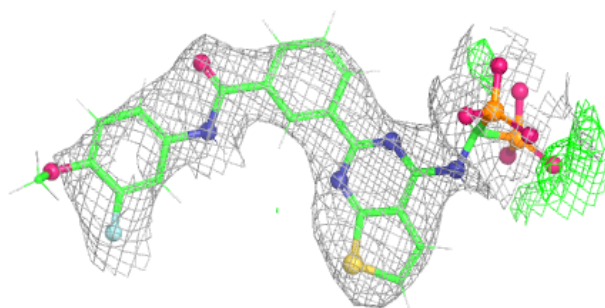


Electron density around A1C1E D 401:

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

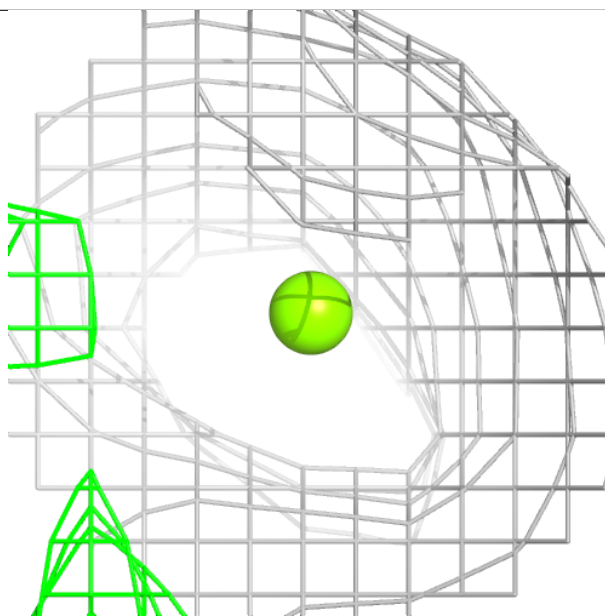
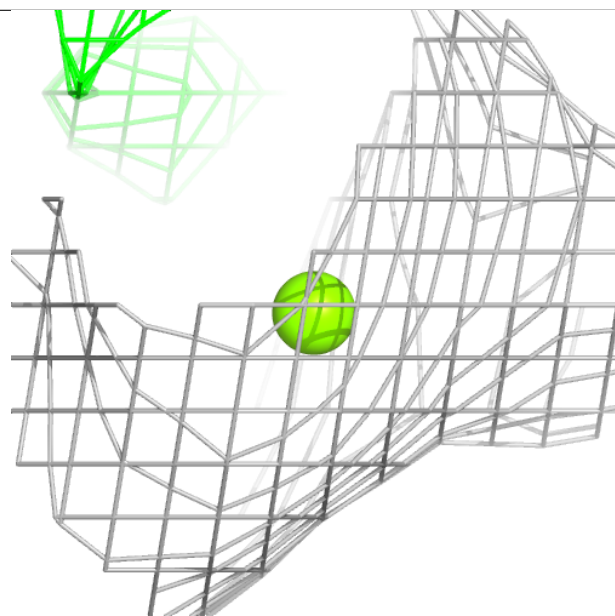
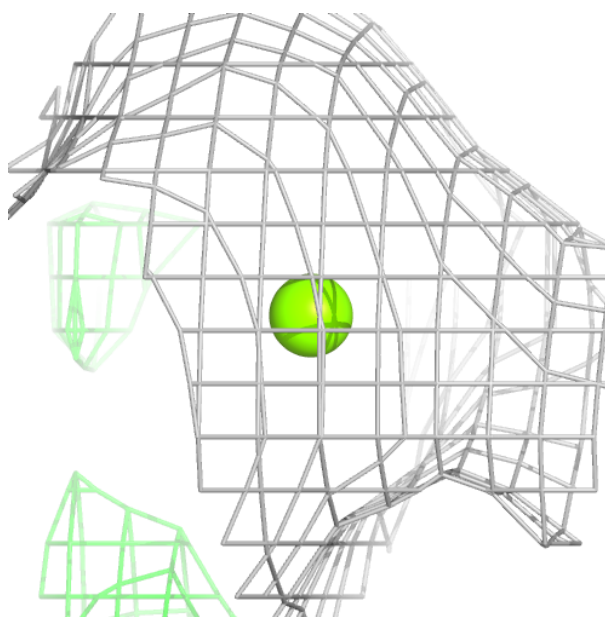
**Electron density around A1C1E K 401:**

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



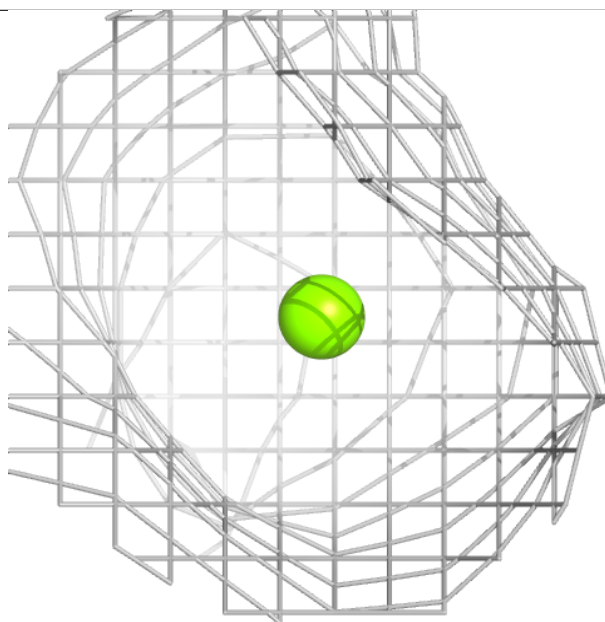
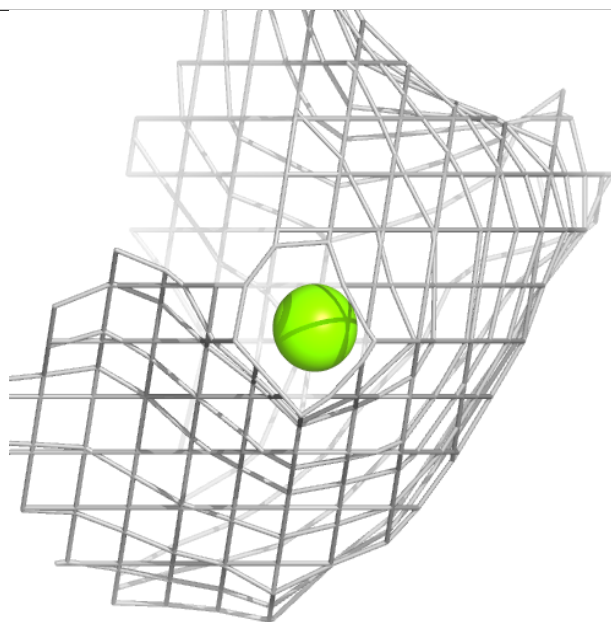
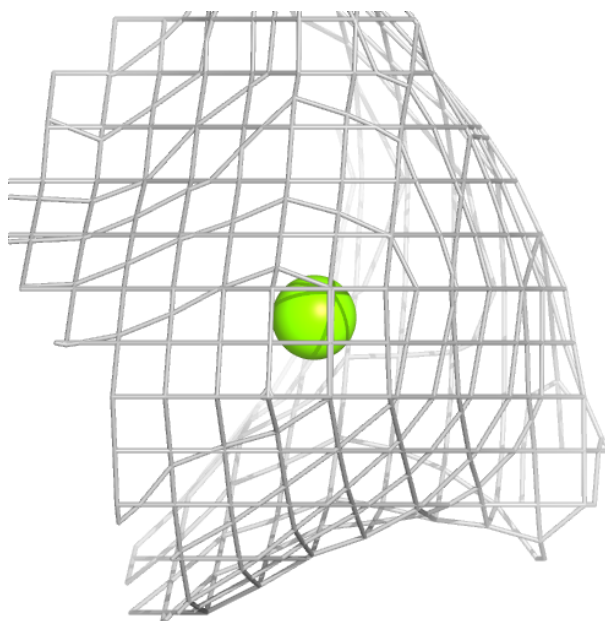
Electron density around MG C 404:

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



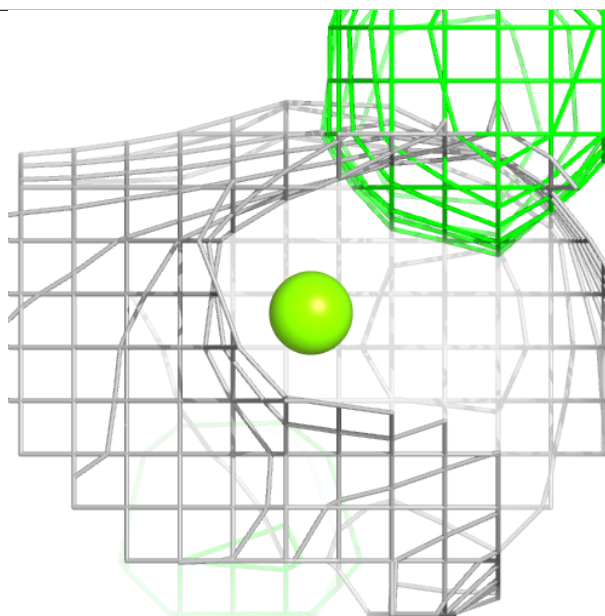
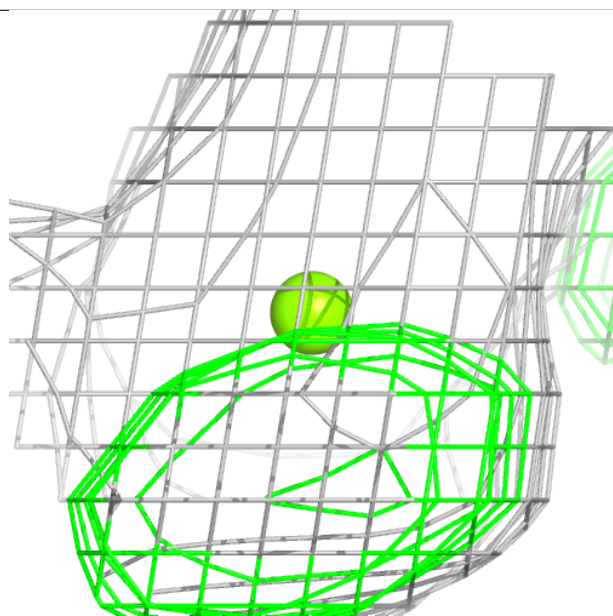
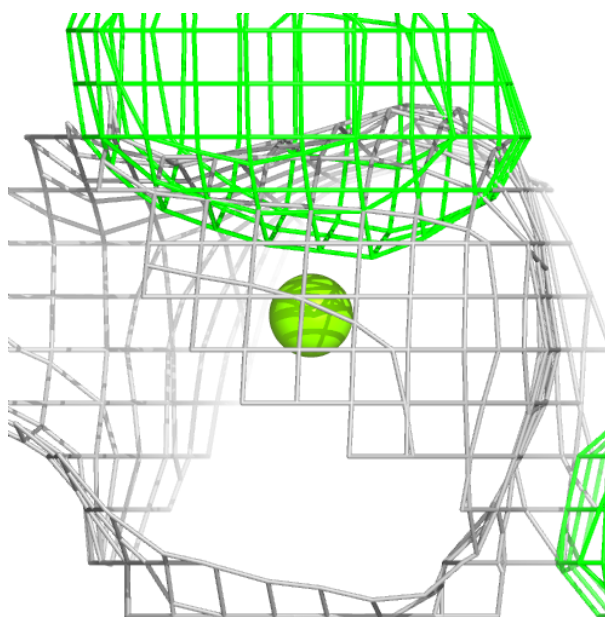
Electron density around MG A 404:

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



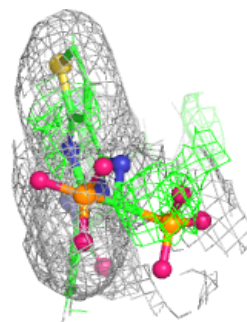
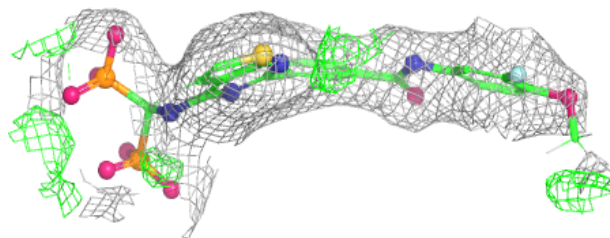
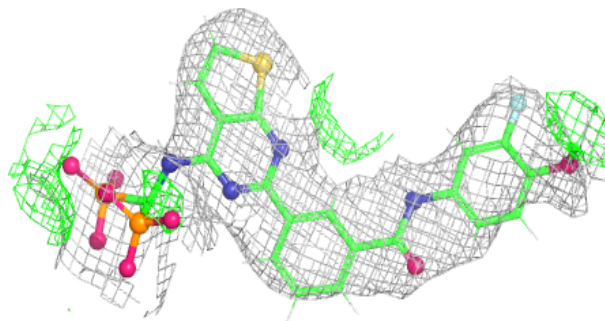
Electron density around MG J 404:

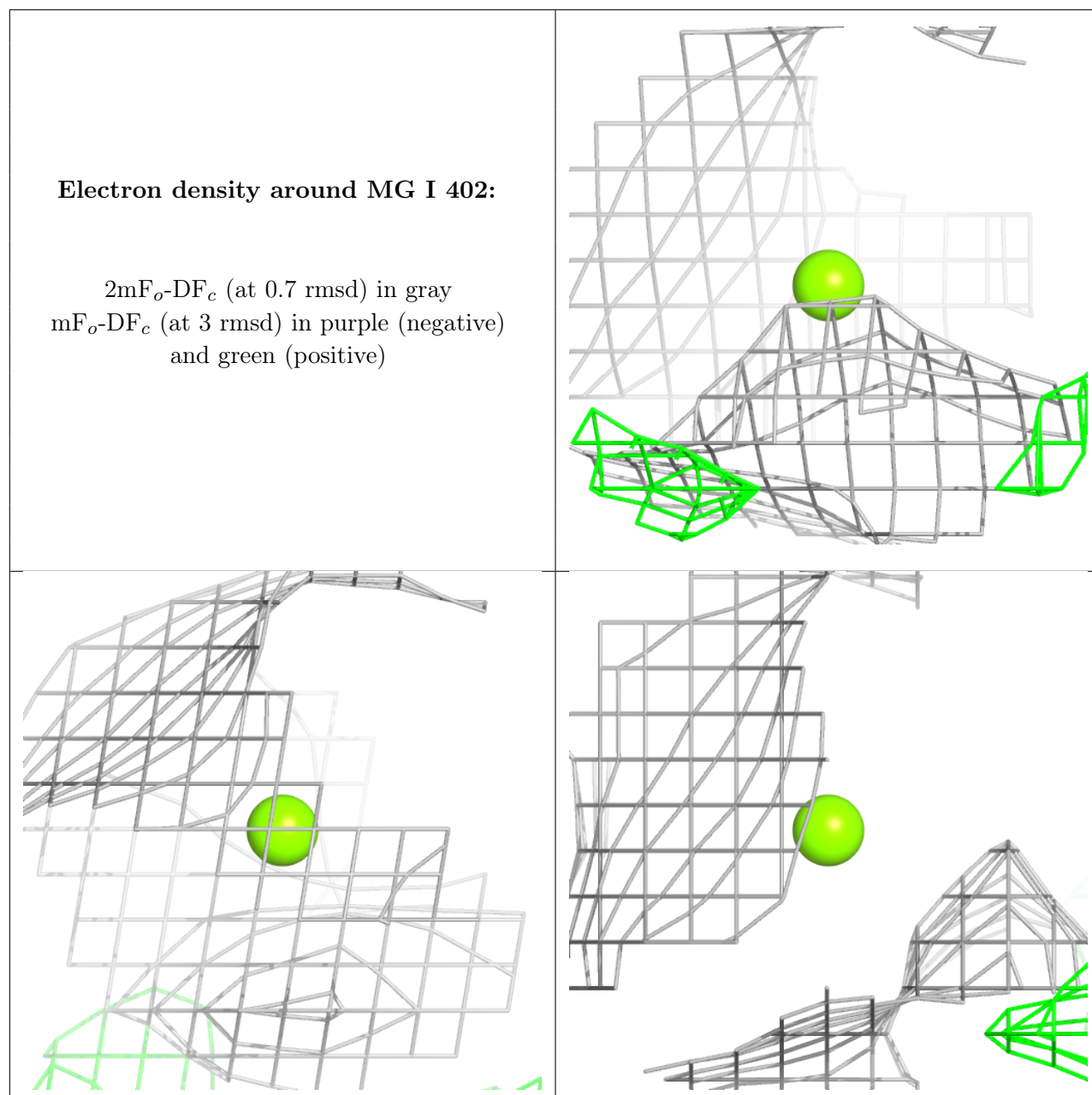
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around A1C1E J 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 ⓘ

There are no such residues in this entry.