



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 24, 2025 – 10:12 AM EST

PDB ID : 9YBQ / pdb_00009ybq
Title : Vibrio cholerae protein FrhA peptid-binding domain and adjacent split domain (S1127-F1439) in complex with peptide AGYTD X-ray crystallography structure
Authors : Wang, M.; Guo, S.; Kinrade, B.; Davies, P.
Deposited on : 2025-09-17
Resolution : 2.50 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
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.46

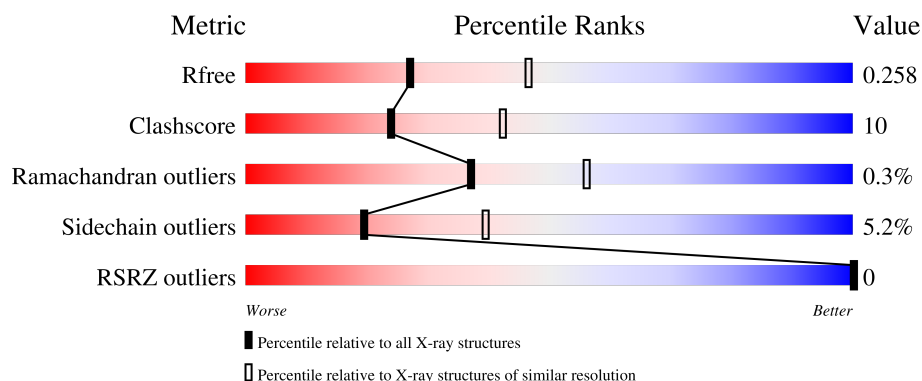
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	164625	5504 (2.50-2.50)
Clashscore	180529	6282 (2.50-2.50)
Ramachandran outliers	177936	6191 (2.50-2.50)
Sidechain outliers	177891	6193 (2.50-2.50)
RSRZ outliers	164620	5504 (2.50-2.50)

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	363	
1	B	363	
1	E	363	
1	G	363	
1	I	363	

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Mol	Chain	Length	Quality of chain
1	K	363	<div><div></div><div>65%19%15%</div></div>
2	M	5	<div><div></div><div>40%40%20%</div></div>
2	N	5	<div><div></div><div>40%40%20%</div></div>
2	O	5	<div><div></div><div>20%40%20%20%</div></div>
2	P	5	<div><div></div><div>80%20%</div></div>
2	Q	5	<div><div></div><div>60%20%20%</div></div>
2	R	5	<div><div></div><div>60%20%20%</div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 28638 atoms, of which 12980 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 Cadherin domain protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	314	Total	C	H	N	O	S	0	0	0
			4452	1425	2151	377	494	5			
1	B	315	Total	C	H	N	O	S	0	0	0
			4446	1427	2141	378	495	5			
1	E	316	Total	C	H	N	O	S	0	0	0
			4506	1436	2184	385	496	5			
1	G	312	Total	C	H	N	O	S	0	0	0
			4424	1415	2141	373	490	5			
1	I	305	Total	C	H	N	O	S	0	0	0
			4340	1383	2105	369	479	4			
1	K	309	Total	C	H	N	O	S	0	0	0
			4398	1406	2126	376	485	5			

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	initiating methionine	UNP A0A0H3AMP4
A	-19	ALA	-	expression tag	UNP A0A0H3AMP4
A	-18	SER	-	expression tag	UNP A0A0H3AMP4
A	-17	SER	-	expression tag	UNP A0A0H3AMP4
A	-16	HIS	-	expression tag	UNP A0A0H3AMP4
A	-15	HIS	-	expression tag	UNP A0A0H3AMP4
A	-14	HIS	-	expression tag	UNP A0A0H3AMP4
A	-13	HIS	-	expression tag	UNP A0A0H3AMP4
A	-12	HIS	-	expression tag	UNP A0A0H3AMP4
A	-11	HIS	-	expression tag	UNP A0A0H3AMP4
A	-10	SER	-	expression tag	UNP A0A0H3AMP4
A	-9	SER	-	expression tag	UNP A0A0H3AMP4
A	-8	GLY	-	expression tag	UNP A0A0H3AMP4
A	-7	LEU	-	expression tag	UNP A0A0H3AMP4
A	-6	VAL	-	expression tag	UNP A0A0H3AMP4
A	-5	PRO	-	expression tag	UNP A0A0H3AMP4
A	-4	ARG	-	expression tag	UNP A0A0H3AMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP A0A0H3AMP4
A	-2	SER	-	expression tag	UNP A0A0H3AMP4
A	-1	HIS	-	expression tag	UNP A0A0H3AMP4
A	0	MET	-	expression tag	UNP A0A0H3AMP4
A	36	ALA	VAL	conflict	UNP A0A0H3AMP4
B	-20	MET	-	initiating methionine	UNP A0A0H3AMP4
B	-19	ALA	-	expression tag	UNP A0A0H3AMP4
B	-18	SER	-	expression tag	UNP A0A0H3AMP4
B	-17	SER	-	expression tag	UNP A0A0H3AMP4
B	-16	HIS	-	expression tag	UNP A0A0H3AMP4
B	-15	HIS	-	expression tag	UNP A0A0H3AMP4
B	-14	HIS	-	expression tag	UNP A0A0H3AMP4
B	-13	HIS	-	expression tag	UNP A0A0H3AMP4
B	-12	HIS	-	expression tag	UNP A0A0H3AMP4
B	-11	HIS	-	expression tag	UNP A0A0H3AMP4
B	-10	SER	-	expression tag	UNP A0A0H3AMP4
B	-9	SER	-	expression tag	UNP A0A0H3AMP4
B	-8	GLY	-	expression tag	UNP A0A0H3AMP4
B	-7	LEU	-	expression tag	UNP A0A0H3AMP4
B	-6	VAL	-	expression tag	UNP A0A0H3AMP4
B	-5	PRO	-	expression tag	UNP A0A0H3AMP4
B	-4	ARG	-	expression tag	UNP A0A0H3AMP4
B	-3	GLY	-	expression tag	UNP A0A0H3AMP4
B	-2	SER	-	expression tag	UNP A0A0H3AMP4
B	-1	HIS	-	expression tag	UNP A0A0H3AMP4
B	0	MET	-	expression tag	UNP A0A0H3AMP4
B	36	ALA	VAL	conflict	UNP A0A0H3AMP4
E	-20	MET	-	initiating methionine	UNP A0A0H3AMP4
E	-19	ALA	-	expression tag	UNP A0A0H3AMP4
E	-18	SER	-	expression tag	UNP A0A0H3AMP4
E	-17	SER	-	expression tag	UNP A0A0H3AMP4
E	-16	HIS	-	expression tag	UNP A0A0H3AMP4
E	-15	HIS	-	expression tag	UNP A0A0H3AMP4
E	-14	HIS	-	expression tag	UNP A0A0H3AMP4
E	-13	HIS	-	expression tag	UNP A0A0H3AMP4
E	-12	HIS	-	expression tag	UNP A0A0H3AMP4
E	-11	HIS	-	expression tag	UNP A0A0H3AMP4
E	-10	SER	-	expression tag	UNP A0A0H3AMP4
E	-9	SER	-	expression tag	UNP A0A0H3AMP4
E	-8	GLY	-	expression tag	UNP A0A0H3AMP4
E	-7	LEU	-	expression tag	UNP A0A0H3AMP4
E	-6	VAL	-	expression tag	UNP A0A0H3AMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-5	PRO	-	expression tag	UNP A0A0H3AMP4
E	-4	ARG	-	expression tag	UNP A0A0H3AMP4
E	-3	GLY	-	expression tag	UNP A0A0H3AMP4
E	-2	SER	-	expression tag	UNP A0A0H3AMP4
E	-1	HIS	-	expression tag	UNP A0A0H3AMP4
E	0	MET	-	expression tag	UNP A0A0H3AMP4
E	36	ALA	VAL	conflict	UNP A0A0H3AMP4
G	-20	MET	-	initiating methionine	UNP A0A0H3AMP4
G	-19	ALA	-	expression tag	UNP A0A0H3AMP4
G	-18	SER	-	expression tag	UNP A0A0H3AMP4
G	-17	SER	-	expression tag	UNP A0A0H3AMP4
G	-16	HIS	-	expression tag	UNP A0A0H3AMP4
G	-15	HIS	-	expression tag	UNP A0A0H3AMP4
G	-14	HIS	-	expression tag	UNP A0A0H3AMP4
G	-13	HIS	-	expression tag	UNP A0A0H3AMP4
G	-12	HIS	-	expression tag	UNP A0A0H3AMP4
G	-11	HIS	-	expression tag	UNP A0A0H3AMP4
G	-10	SER	-	expression tag	UNP A0A0H3AMP4
G	-9	SER	-	expression tag	UNP A0A0H3AMP4
G	-8	GLY	-	expression tag	UNP A0A0H3AMP4
G	-7	LEU	-	expression tag	UNP A0A0H3AMP4
G	-6	VAL	-	expression tag	UNP A0A0H3AMP4
G	-5	PRO	-	expression tag	UNP A0A0H3AMP4
G	-4	ARG	-	expression tag	UNP A0A0H3AMP4
G	-3	GLY	-	expression tag	UNP A0A0H3AMP4
G	-2	SER	-	expression tag	UNP A0A0H3AMP4
G	-1	HIS	-	expression tag	UNP A0A0H3AMP4
G	0	MET	-	expression tag	UNP A0A0H3AMP4
G	36	ALA	VAL	conflict	UNP A0A0H3AMP4
I	-20	MET	-	initiating methionine	UNP A0A0H3AMP4
I	-19	ALA	-	expression tag	UNP A0A0H3AMP4
I	-18	SER	-	expression tag	UNP A0A0H3AMP4
I	-17	SER	-	expression tag	UNP A0A0H3AMP4
I	-16	HIS	-	expression tag	UNP A0A0H3AMP4
I	-15	HIS	-	expression tag	UNP A0A0H3AMP4
I	-14	HIS	-	expression tag	UNP A0A0H3AMP4
I	-13	HIS	-	expression tag	UNP A0A0H3AMP4
I	-12	HIS	-	expression tag	UNP A0A0H3AMP4
I	-11	HIS	-	expression tag	UNP A0A0H3AMP4
I	-10	SER	-	expression tag	UNP A0A0H3AMP4
I	-9	SER	-	expression tag	UNP A0A0H3AMP4
I	-8	GLY	-	expression tag	UNP A0A0H3AMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-7	LEU	-	expression tag	UNP A0A0H3AMP4
I	-6	VAL	-	expression tag	UNP A0A0H3AMP4
I	-5	PRO	-	expression tag	UNP A0A0H3AMP4
I	-4	ARG	-	expression tag	UNP A0A0H3AMP4
I	-3	GLY	-	expression tag	UNP A0A0H3AMP4
I	-2	SER	-	expression tag	UNP A0A0H3AMP4
I	-1	HIS	-	expression tag	UNP A0A0H3AMP4
I	0	MET	-	expression tag	UNP A0A0H3AMP4
I	36	ALA	VAL	conflict	UNP A0A0H3AMP4
K	-20	MET	-	initiating methionine	UNP A0A0H3AMP4
K	-19	ALA	-	expression tag	UNP A0A0H3AMP4
K	-18	SER	-	expression tag	UNP A0A0H3AMP4
K	-17	SER	-	expression tag	UNP A0A0H3AMP4
K	-16	HIS	-	expression tag	UNP A0A0H3AMP4
K	-15	HIS	-	expression tag	UNP A0A0H3AMP4
K	-14	HIS	-	expression tag	UNP A0A0H3AMP4
K	-13	HIS	-	expression tag	UNP A0A0H3AMP4
K	-12	HIS	-	expression tag	UNP A0A0H3AMP4
K	-11	HIS	-	expression tag	UNP A0A0H3AMP4
K	-10	SER	-	expression tag	UNP A0A0H3AMP4
K	-9	SER	-	expression tag	UNP A0A0H3AMP4
K	-8	GLY	-	expression tag	UNP A0A0H3AMP4
K	-7	LEU	-	expression tag	UNP A0A0H3AMP4
K	-6	VAL	-	expression tag	UNP A0A0H3AMP4
K	-5	PRO	-	expression tag	UNP A0A0H3AMP4
K	-4	ARG	-	expression tag	UNP A0A0H3AMP4
K	-3	GLY	-	expression tag	UNP A0A0H3AMP4
K	-2	SER	-	expression tag	UNP A0A0H3AMP4
K	-1	HIS	-	expression tag	UNP A0A0H3AMP4
K	0	MET	-	expression tag	UNP A0A0H3AMP4
K	36	ALA	VAL	conflict	UNP A0A0H3AMP4

- Molecule 2 is a protein called ALA-GLY-TYR-THR-ASP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	4	Total 54	C 19	H 22	N 4	O 9	0	0	0
2	N	4	Total 54	C 19	H 22	N 4	O 9	0	0	0
2	O	4	Total 54	C 19	H 22	N 4	O 9	0	0	0
2	P	4	Total 54	C 19	H 22	N 4	O 9	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	Q	4	Total	C	H	N	O	0	0	0
			54	19	22	4	9			
2	R	4	Total	C	H	N	O	0	0	0
			54	19	22	4	9			

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	6	Total	Ca	6	0
			6	6		
3	B	6	Total	Ca	6	0
			6	6		
3	E	6	Total	Ca	6	0
			6	6		
3	G	6	Total	Ca	6	0
			6	6		
3	I	6	Total	Ca	6	0
			6	6		
3	K	6	Total	Ca	6	0
			6	6		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	272	Total	O	0	0
			272	272		
4	B	288	Total	O	0	0
			288	288		
4	E	289	Total	O	0	0
			289	289		
4	G	281	Total	O	0	0
			281	281		
4	I	275	Total	O	0	0
			275	275		
4	K	285	Total	O	0	0
			285	285		
4	M	2	Total	O	0	0
			2	2		
4	N	5	Total	O	0	0
			5	5		
4	O	5	Total	O	0	0
			5	5		

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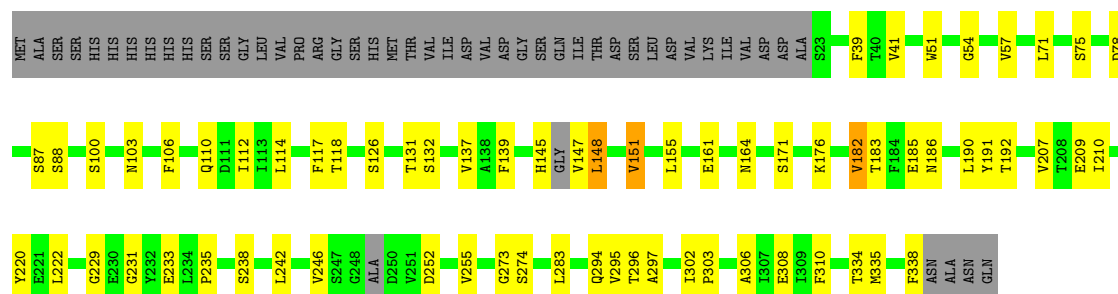
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	P	3	Total 3	O 3	0	0
4	Q	4	Total 4	O 4	0	0
4	R	3	Total 3	O 3	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

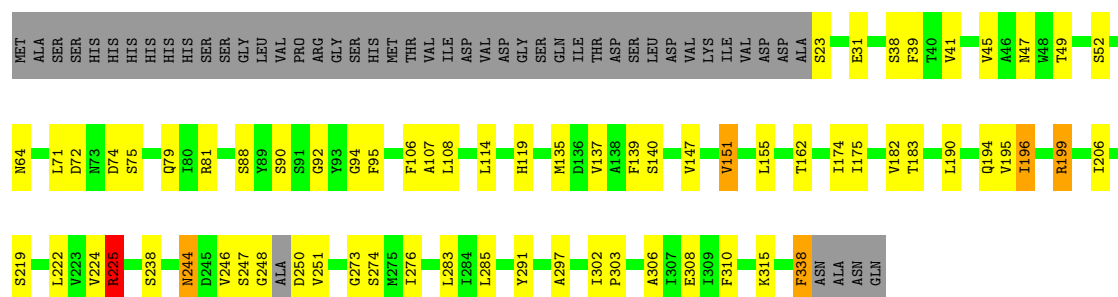
• Molecule 1: Cadherin domain protein

Chain A: 



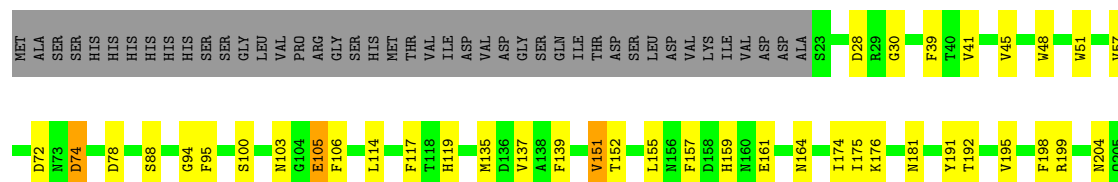
• Molecule 1: Cadherin domain protein

Chain B: 



• Molecule 1: Cadherin domain protein

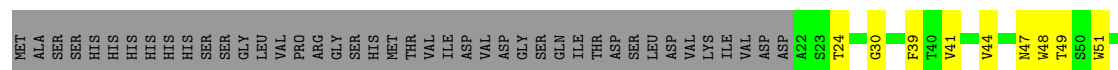
Chain E: 





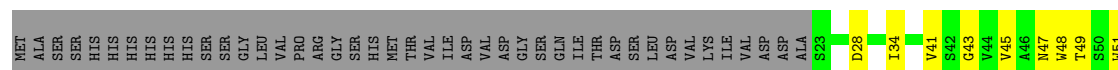
- Molecule 1: Cadherin domain protein

Chain G: 66% 20% 14%



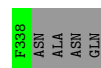
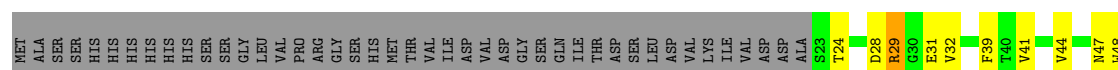
- Molecule 1: Cadherin domain protein

Chain I: 63% 21% 16%



- Molecule 1: Cadherin domain protein

Chain K: 65% 19% 15%



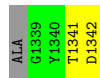
- Molecule 2: ALA-GLY-TYR-THR-ASP

Chain M:  40% 40% 20%

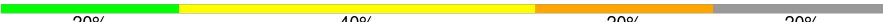


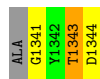
- Molecule 2: ALA-GLY-TYR-THR-ASP

Chain N:  40% 40% 20%




- Molecule 2: ALA-GLY-TYR-THR-ASP

Chain O:  20% 40% 20% 20%



- Molecule 2: ALA-GLY-TYR-THR-ASP

Chain P:  80% 20%



- Molecule 2: ALA-GLY-TYR-THR-ASP

Chain Q:  60% 20% 20%



- Molecule 2: ALA-GLY-TYR-THR-ASP

Chain R:  60% 20% 20%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	61.39Å 118.72Å 118.73Å 60.05° 76.45° 81.42°	Depositor
Resolution (Å)	59.18 – 2.50 59.18 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.3 (59.18-2.50) 98.4 (59.18-2.50)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.19 (at 2.20Å)	Xtriage
Refinement program	PHENIX (1.21.2_5419: ???)	Depositor
R, R_{free}	0.248 , 0.252 0.251 , 0.258	Depositor DCC
R_{free} test set	2036 reflections (1.45%)	wwPDB-VP
Wilson B-factor (Å ²)	20.5	Xtriage
Anisotropy	0.938	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.026 for -h,k-l,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	28638	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.01% 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:
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	0.85	0/2341	1.12	0/3200
1	B	0.96	0/2346	1.35	0/3208
1	E	0.74	0/2364	1.01	0/3232
1	G	0.76	0/2322	1.06	0/3174
1	I	0.78	0/2273	1.09	0/3106
1	K	0.79	0/2311	1.09	0/3156
2	M	0.89	0/32	1.33	0/41
2	N	0.73	0/32	1.07	0/41
2	O	1.01	0/32	1.21	0/41
2	P	0.62	0/32	0.70	0/41
2	Q	0.64	0/32	1.56	0/41
2	R	0.40	0/32	0.59	0/41
All	All	0.82	0/14149	1.12	0/19322

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	B	0	2
1	G	0	1
1	I	0	2
1	K	0	2
All	All	0	7

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	199	ARG	Sidechain
1	B	225	ARG	Sidechain
1	G	332	ARG	Sidechain
1	I	332	ARG	Sidechain
1	I	81	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	2301	2151	2151	43	0
1	B	2305	2141	2155	40	0
1	E	2322	2184	2183	42	0
1	G	2283	2141	2140	49	0
1	I	2235	2105	2102	48	0
1	K	2272	2126	2135	48	0
2	M	32	22	22	5	0
2	N	32	22	22	0	0
2	O	32	22	22	2	0
2	P	32	22	22	0	0
2	Q	32	22	22	2	0
2	R	32	22	22	1	0
3	A	6	0	0	0	0
3	B	6	0	0	0	0
3	E	6	0	0	0	0
3	G	6	0	0	0	0
3	I	6	0	0	0	0
3	K	6	0	0	0	0
4	A	272	0	0	5	0
4	B	288	0	0	8	0
4	E	289	0	0	5	0
4	G	281	0	0	12	0
4	I	275	0	0	14	0
4	K	285	0	0	14	0
4	M	2	0	0	0	0
4	N	5	0	0	0	0
4	O	5	0	0	1	0
4	P	3	0	0	0	0
4	Q	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	R	3	0	0	0	0
All	All	15658	12980	12998	266	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 10.

The worst 5 of 266 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:A:114:LEU:HD21	1:A:137:VAL:HG11	1.64	0.76
1:I:279:LEU:HD12	4:I:535:HOH:O	1.89	0.71
1:B:244:ASN:C	1:B:244:ASN:OD1	2.35	0.70
1:E:155:LEU:HD21	1:E:222:LEU:HD21	1.73	0.70
1:A:155:LEU:HD21	1:A:222:LEU:HD21	1.73	0.70

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	308/363 (85%)	293 (95%)	14 (4%)	1 (0%)	37	56
1	B	311/363 (86%)	297 (96%)	13 (4%)	1 (0%)	37	56
1	E	314/363 (86%)	299 (95%)	14 (4%)	1 (0%)	37	56
1	G	306/363 (84%)	288 (94%)	17 (6%)	1 (0%)	37	56
1	I	299/363 (82%)	287 (96%)	11 (4%)	1 (0%)	37	56
1	K	303/363 (84%)	293 (97%)	9 (3%)	1 (0%)	37	56
2	M	2/5 (40%)	2 (100%)	0	0	100	100
2	N	2/5 (40%)	2 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	O	2/5 (40%)	2 (100%)	0	0	100	100
2	P	2/5 (40%)	2 (100%)	0	0	100	100
2	Q	2/5 (40%)	2 (100%)	0	0	100	100
2	R	2/5 (40%)	2 (100%)	0	0	100	100
All	All	1853/2208 (84%)	1769 (96%)	78 (4%)	6 (0%)	37	56

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	88	SER
1	G	88	SER
1	E	88	SER
1	K	88	SER
1	A	88	SER

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	253/296 (86%)	241 (95%)	12 (5%)	22	44
1	B	253/296 (86%)	232 (92%)	21 (8%)	9	19
1	E	255/296 (86%)	245 (96%)	10 (4%)	27	52
1	G	251/296 (85%)	243 (97%)	8 (3%)	34	60
1	I	246/296 (83%)	236 (96%)	10 (4%)	26	50
1	K	250/296 (84%)	237 (95%)	13 (5%)	19	39
2	M	3/3 (100%)	1 (33%)	2 (67%)	0	0
2	N	3/3 (100%)	1 (33%)	2 (67%)	0	0
2	O	3/3 (100%)	1 (33%)	2 (67%)	0	0
2	P	3/3 (100%)	3 (100%)	0	100	100
2	Q	3/3 (100%)	3 (100%)	0	100	100
2	R	3/3 (100%)	3 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1526/1794 (85%)	1446 (95%)	80 (5%)	19	39

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	238	SER
1	K	218	ASN
1	I	301	SER
1	K	74	ASP
2	M	1344	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	215	ASN
1	I	160	ASN
1	I	73	ASN
1	K	53	ASN
1	B	84	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 36 ligands modelled in this entry, 36 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	314/363 (86%)	-1.49	0 100 100	7, 32, 81, 148	0
1	B	315/363 (86%)	-1.46	0 100 100	7, 32, 74, 206	0
1	E	316/363 (87%)	-1.44	0 100 100	7, 32, 84, 160	0
1	G	312/363 (85%)	-1.47	0 100 100	7, 32, 77, 148	0
1	I	305/363 (84%)	-1.48	0 100 100	7, 32, 74, 148	0
1	K	309/363 (85%)	-1.45	0 100 100	7, 32, 74, 148	0
2	M	4/5 (80%)	-0.84	0 100 100	34, 53, 56, 90	0
2	N	4/5 (80%)	-0.97	0 100 100	34, 53, 56, 90	0
2	O	4/5 (80%)	-0.90	0 100 100	34, 53, 56, 90	0
2	P	4/5 (80%)	-1.15	0 100 100	34, 53, 56, 90	0
2	Q	4/5 (80%)	-1.20	0 100 100	34, 53, 56, 90	0
2	R	4/5 (80%)	-1.04	0 100 100	34, 53, 56, 90	0
All	All	1895/2208 (85%)	-1.46	0 100 100	7, 32, 78, 206	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

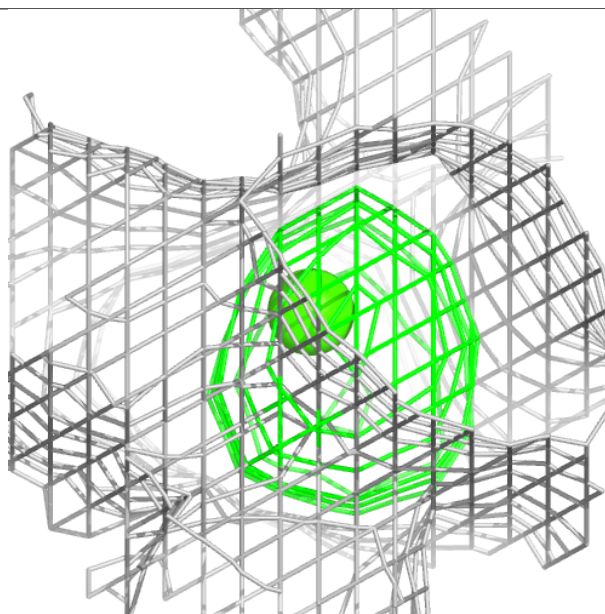
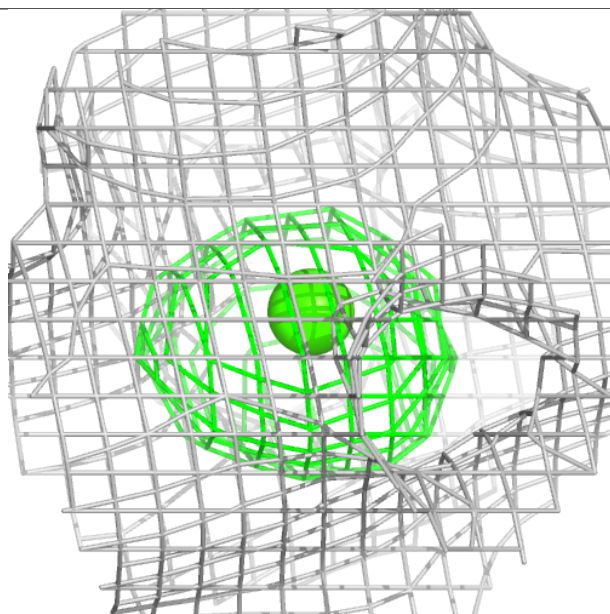
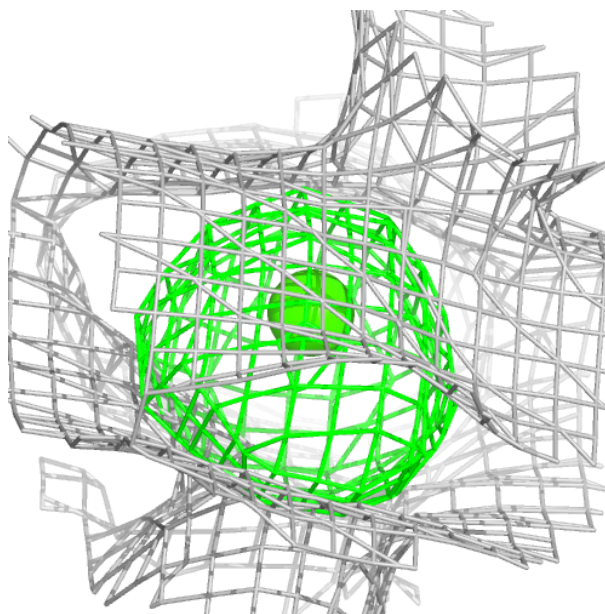
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	CA	A	401	1/1	-	-	31,31,31,31	1
3	CA	A	402	1/1	-	-	31,31,31,31	1
3	CA	A	403	1/1	-	-	29,29,29,29	1
3	CA	A	404	1/1	-	-	29,29,29,29	1
3	CA	A	405	1/1	-	-	23,23,23,23	1
3	CA	A	406	1/1	-	-	20,20,20,20	1
3	CA	B	401	1/1	-	-	31,31,31,31	1
3	CA	B	402	1/1	-	-	31,31,31,31	1
3	CA	B	403	1/1	-	-	29,29,29,29	1
3	CA	B	404	1/1	-	-	29,29,29,29	1
3	CA	B	405	1/1	-	-	23,23,23,23	1
3	CA	B	406	1/1	-	-	20,20,20,20	1
3	CA	E	401	1/1	-	-	31,31,31,31	1
3	CA	E	402	1/1	-	-	31,31,31,31	1
3	CA	E	403	1/1	-	-	29,29,29,29	1
3	CA	E	404	1/1	-	-	29,29,29,29	1
3	CA	E	405	1/1	-	-	23,23,23,23	1
3	CA	E	406	1/1	-	-	20,20,20,20	1
3	CA	G	401	1/1	-	-	31,31,31,31	1
3	CA	G	402	1/1	-	-	31,31,31,31	1
3	CA	G	403	1/1	-	-	29,29,29,29	1
3	CA	G	404	1/1	-	-	29,29,29,29	1
3	CA	G	405	1/1	-	-	23,23,23,23	1
3	CA	G	406	1/1	-	-	20,20,20,20	1
3	CA	I	401	1/1	-	-	31,31,31,31	1
3	CA	I	402	1/1	-	-	31,31,31,31	1
3	CA	I	403	1/1	-	-	29,29,29,29	1
3	CA	I	404	1/1	-	-	29,29,29,29	1
3	CA	I	405	1/1	-	-	23,23,23,23	1
3	CA	I	406	1/1	-	-	20,20,20,20	1
3	CA	K	401	1/1	-	-	31,31,31,31	1
3	CA	K	402	1/1	-	-	31,31,31,31	1
3	CA	K	403	1/1	-	-	29,29,29,29	1
3	CA	K	404	1/1	-	-	29,29,29,29	1
3	CA	K	405	1/1	-	-	23,23,23,23	1
3	CA	K	406	1/1	-	-	20,20,20,20	1

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.

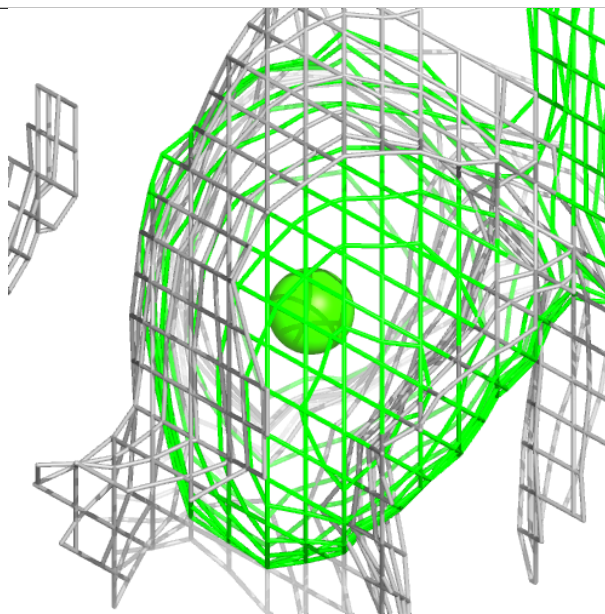
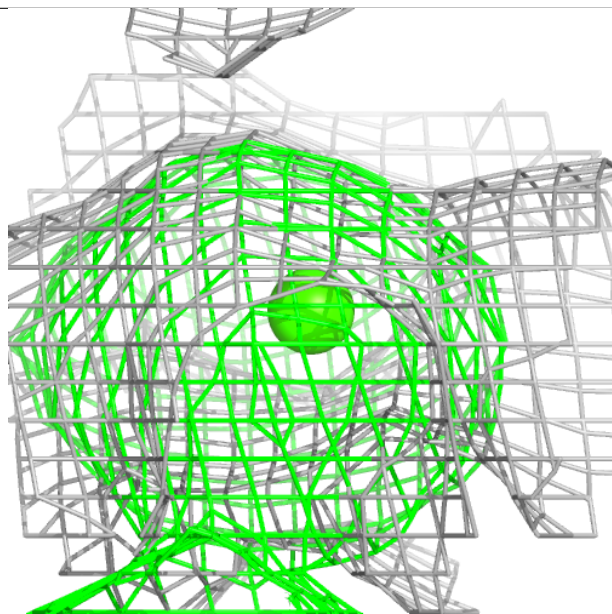
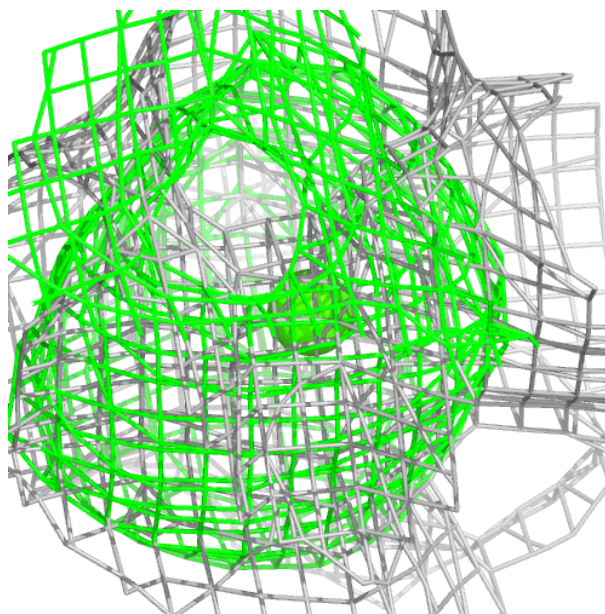
Electron density around CA A 401:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



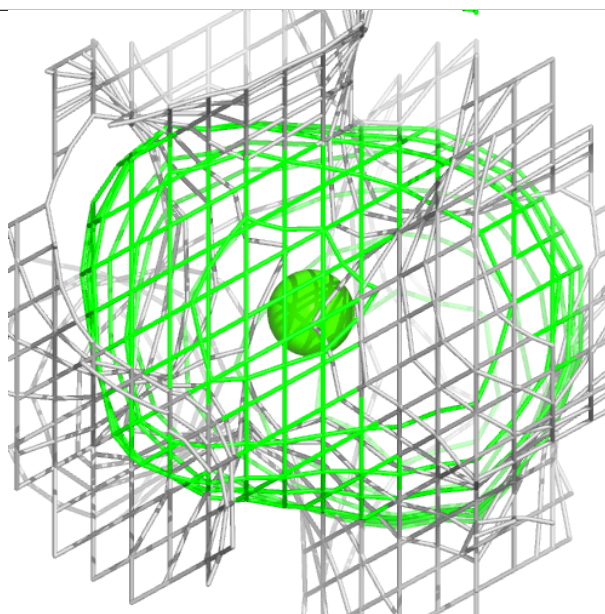
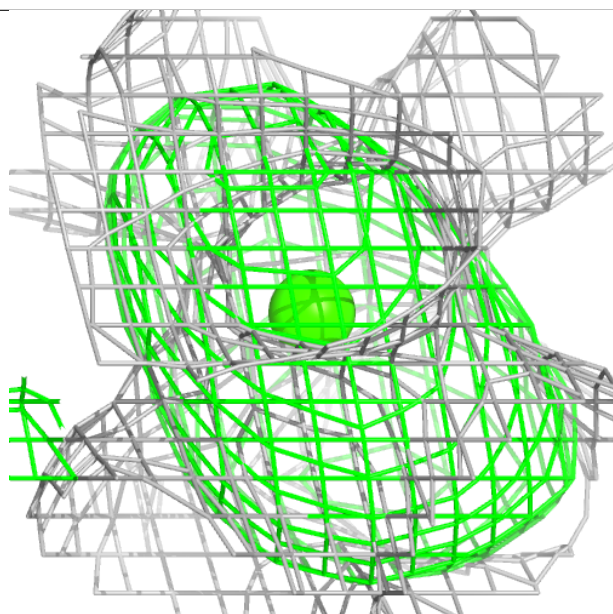
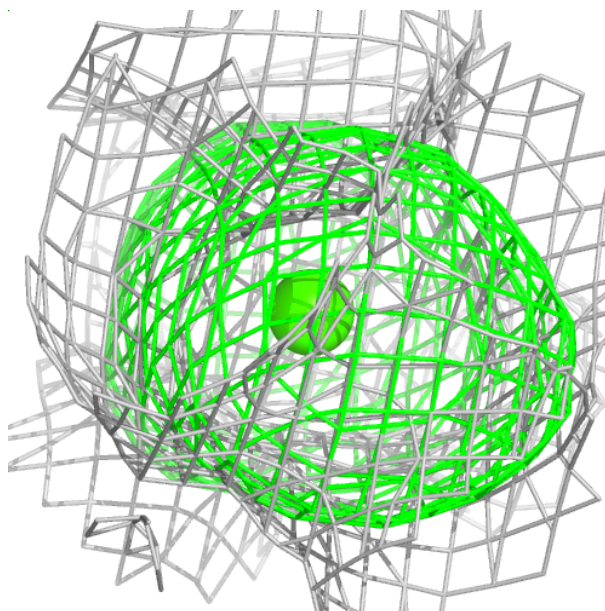
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and green (positive)



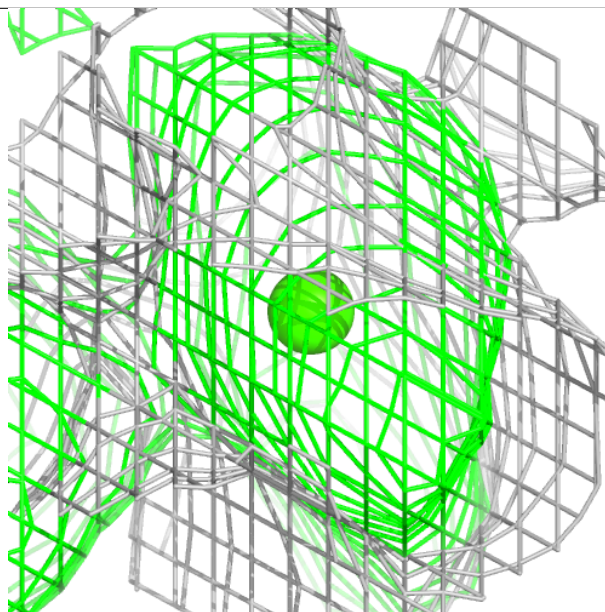
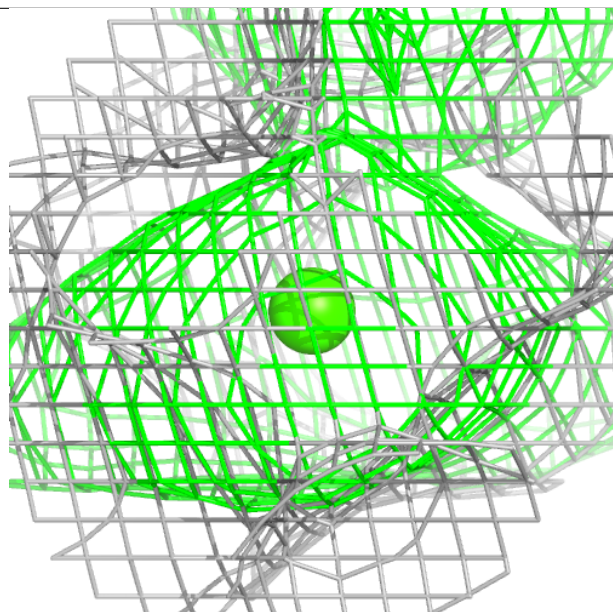
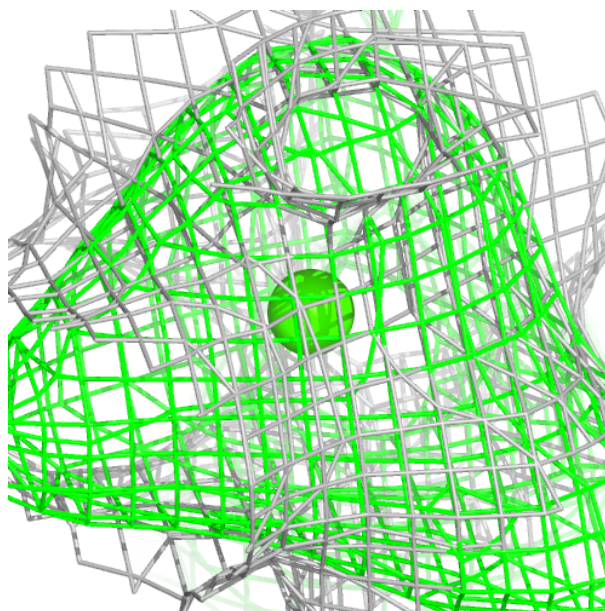
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and green (positive)



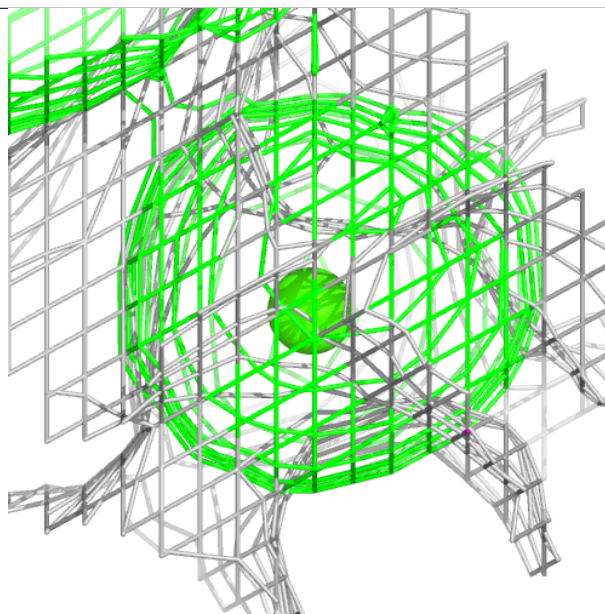
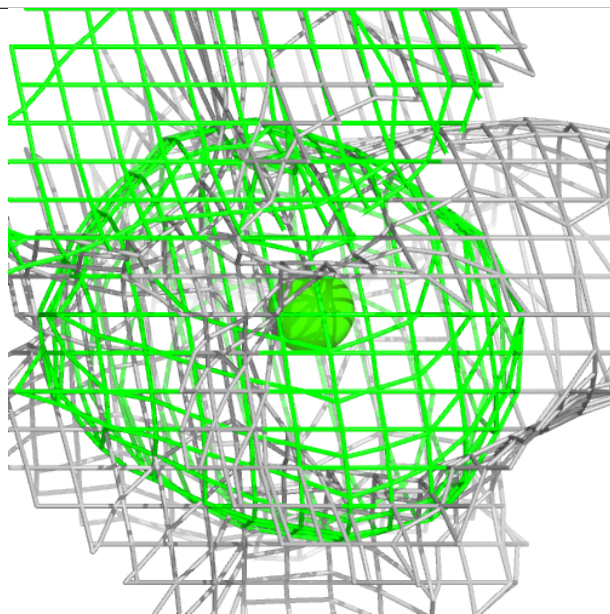
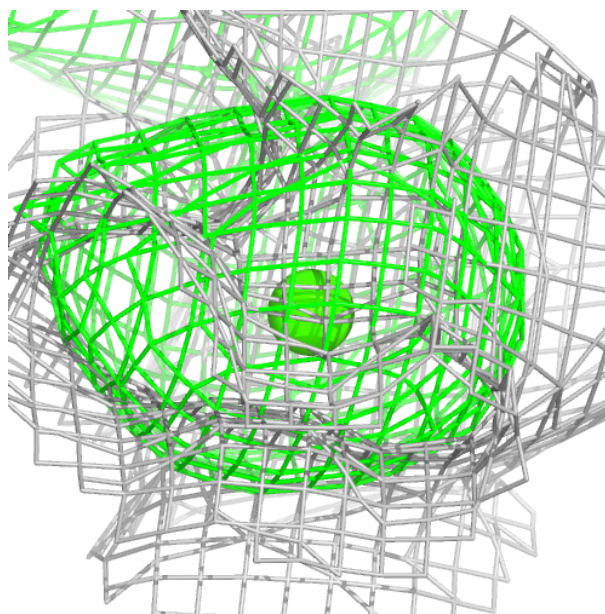
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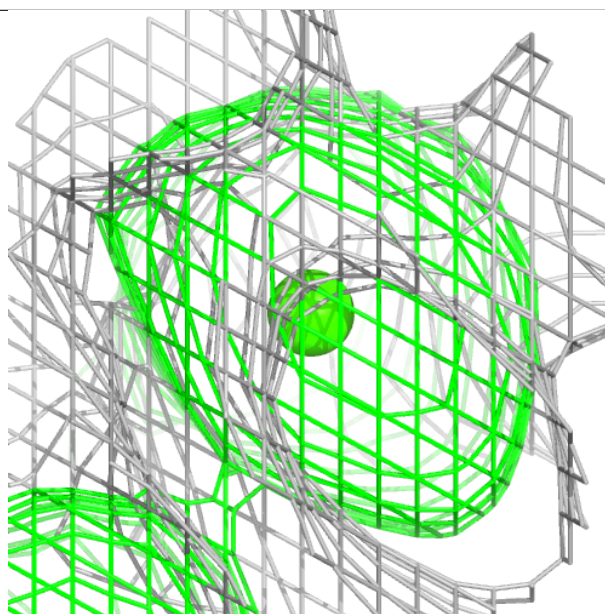
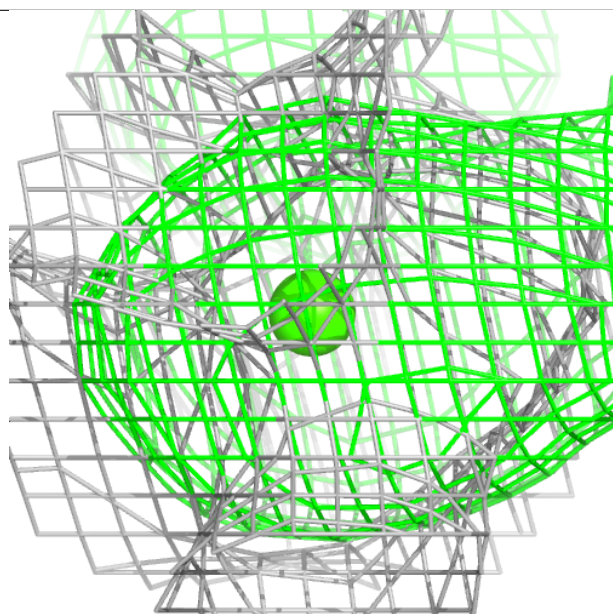
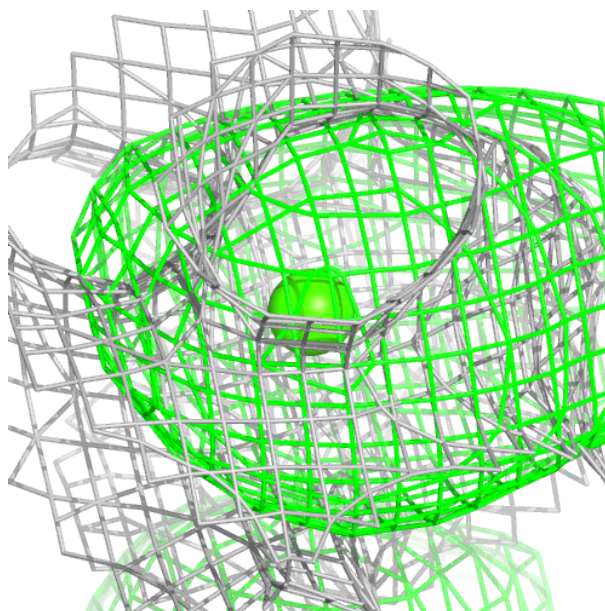
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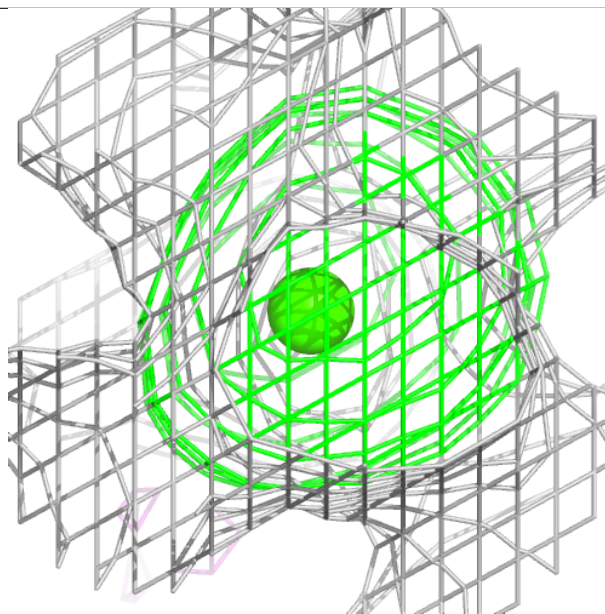
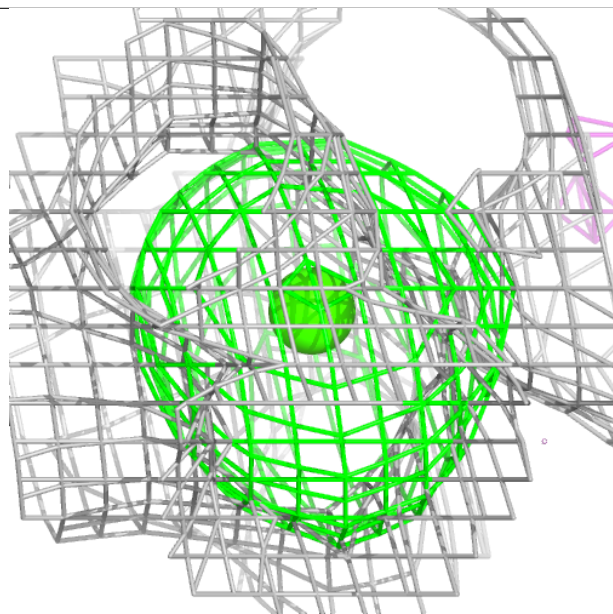
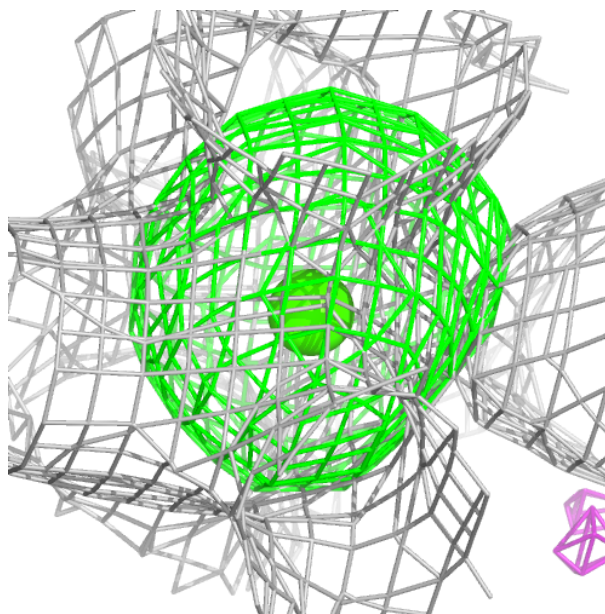
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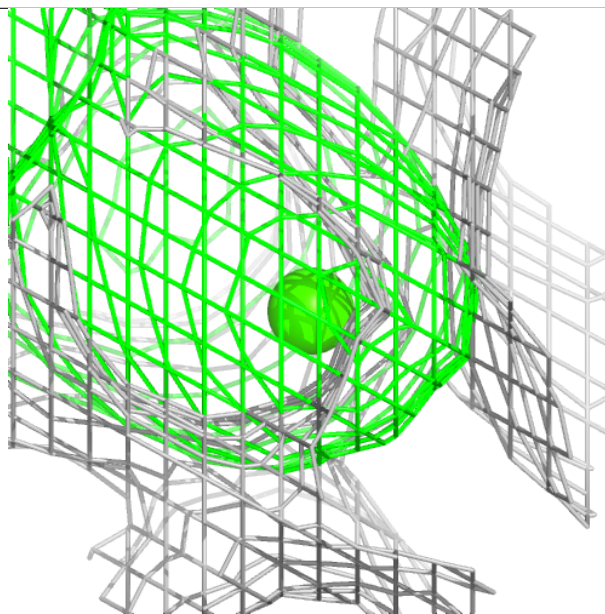
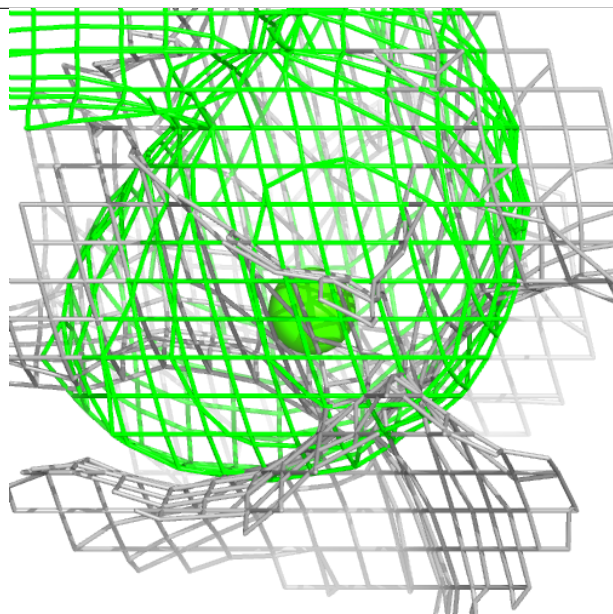
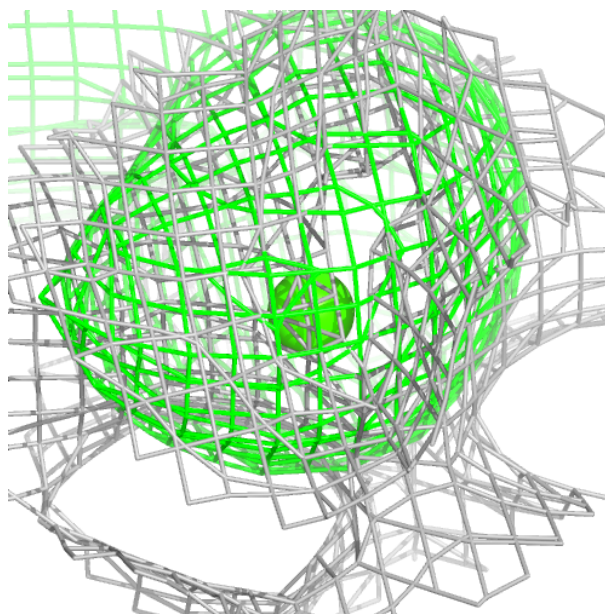
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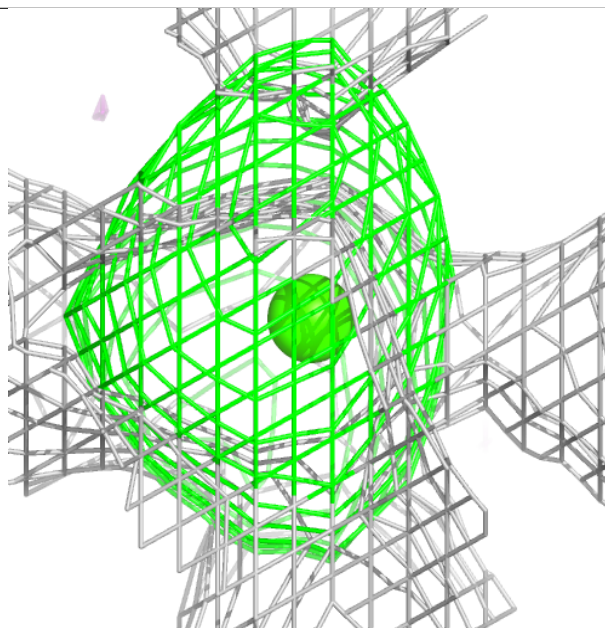
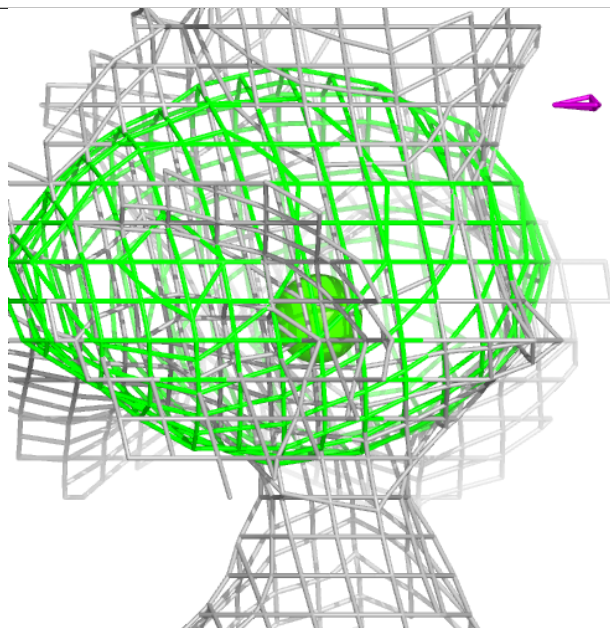
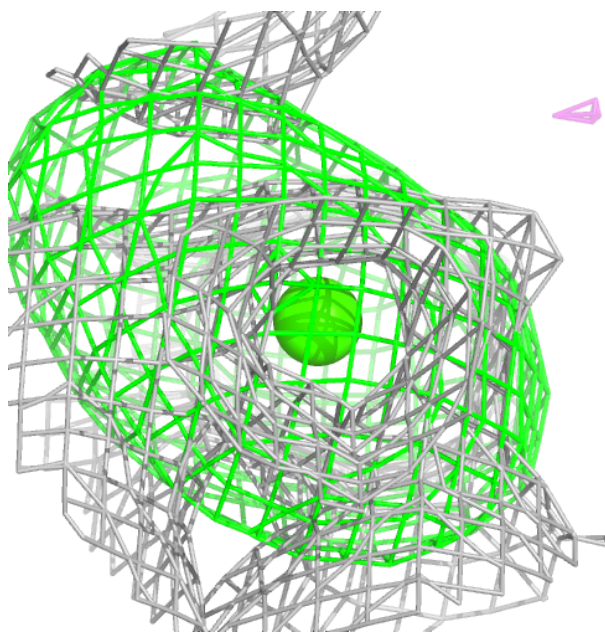
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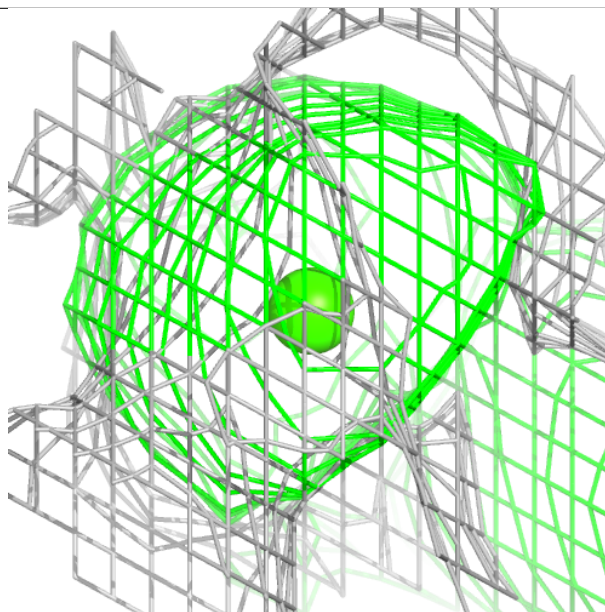
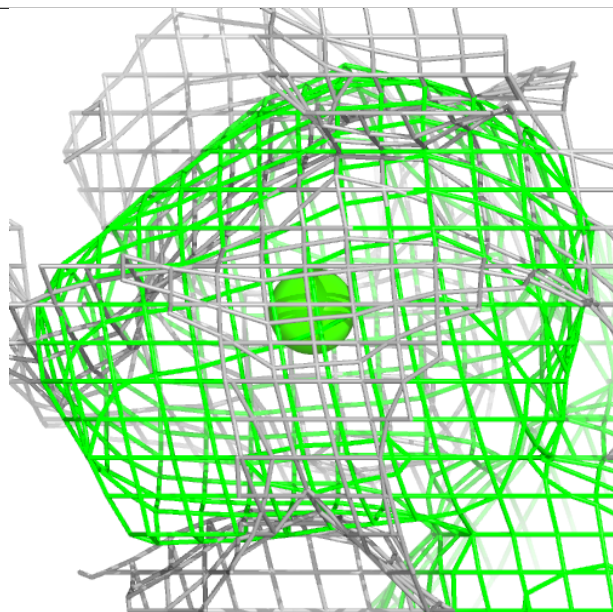
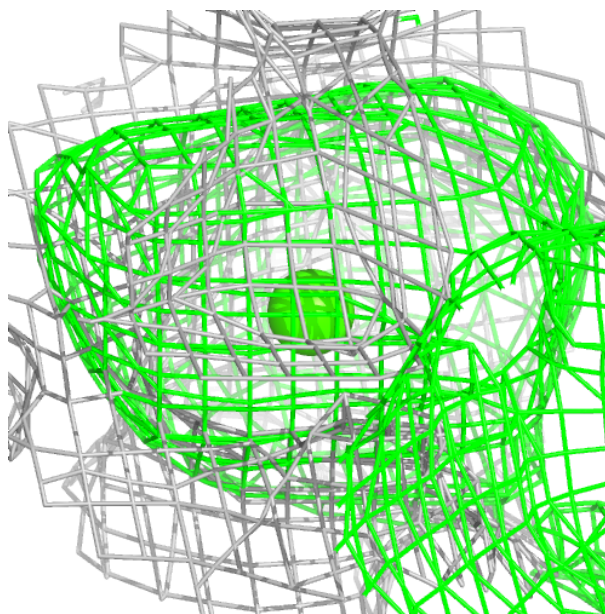
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and green (positive)



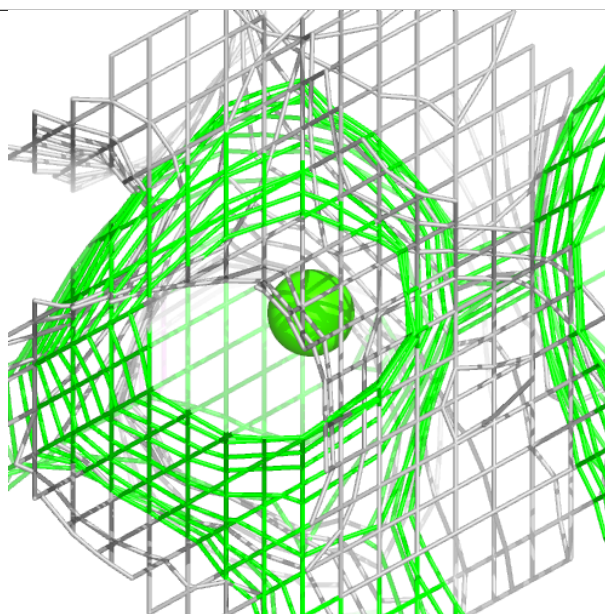
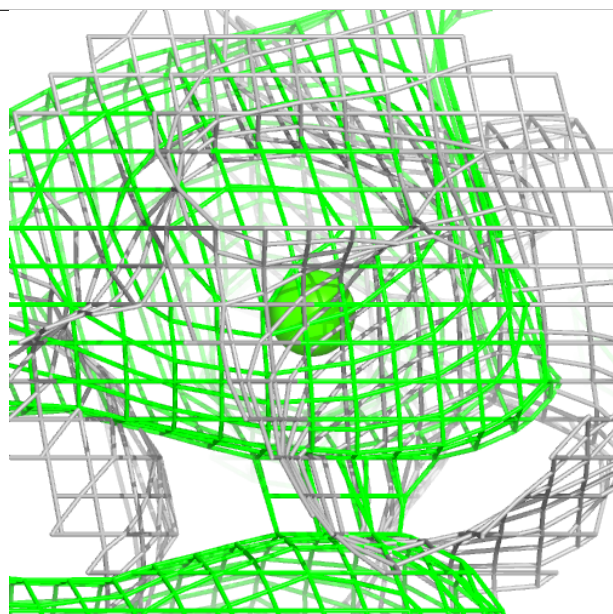
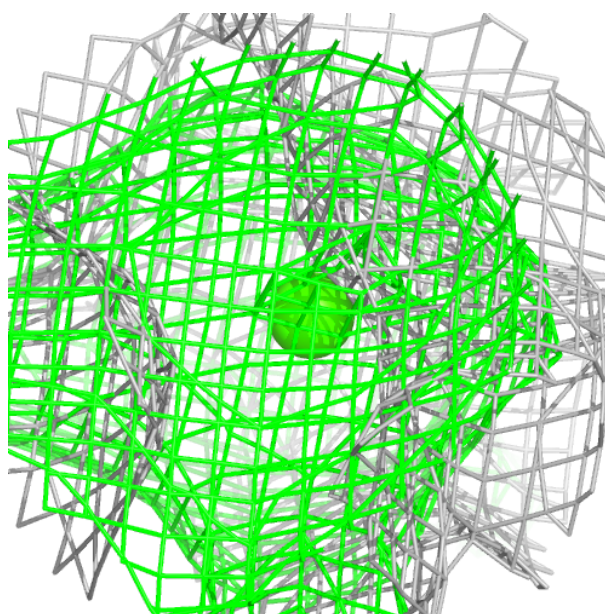
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and green (positive)



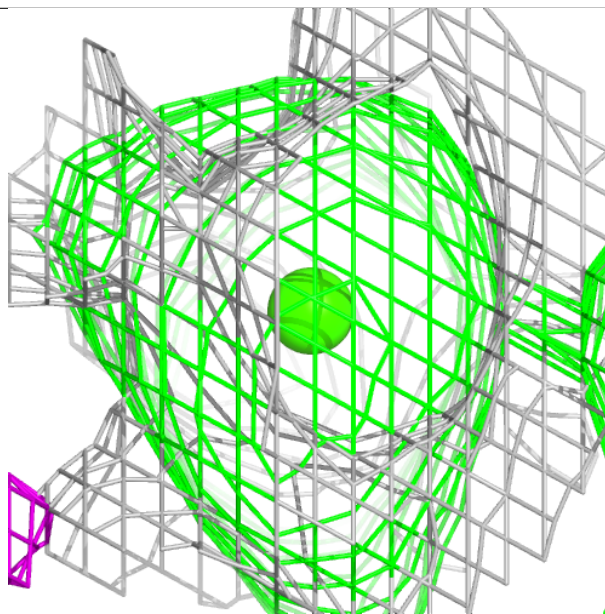
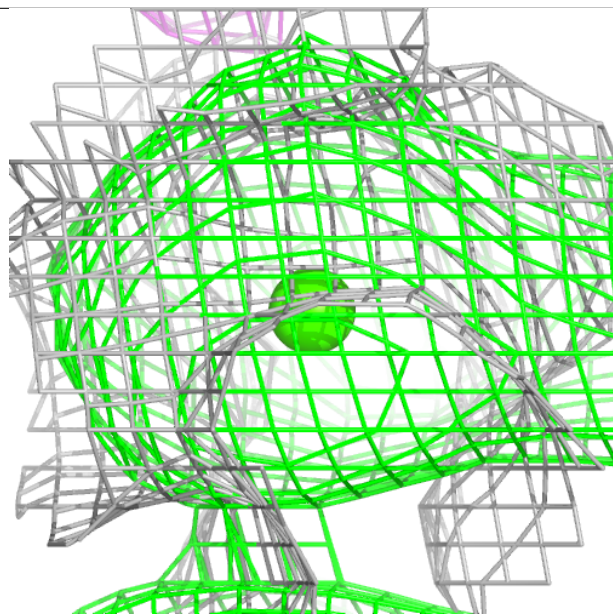
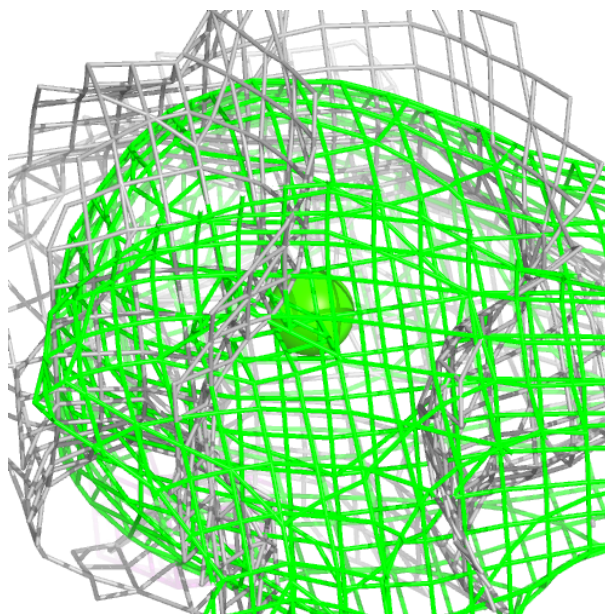
Electron density around CA B 405:

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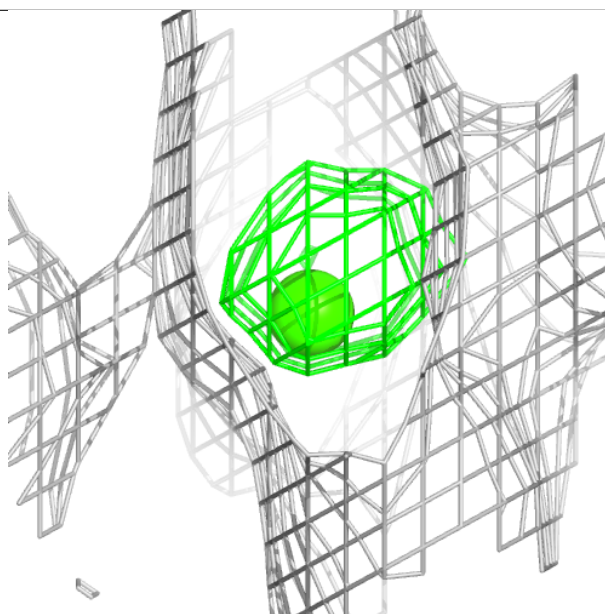
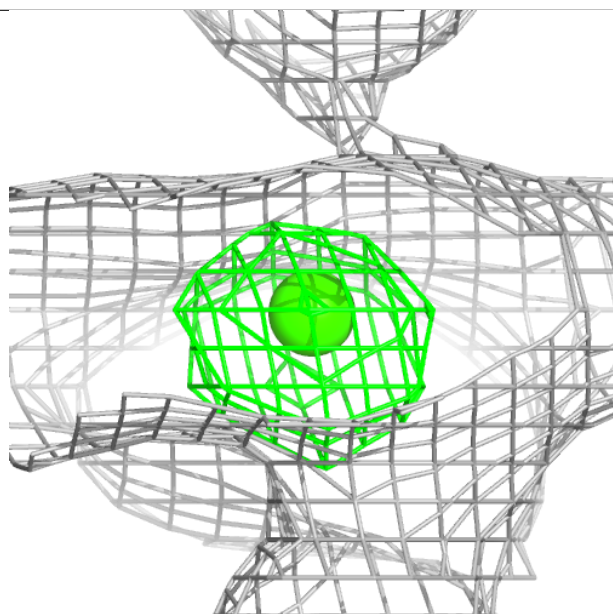
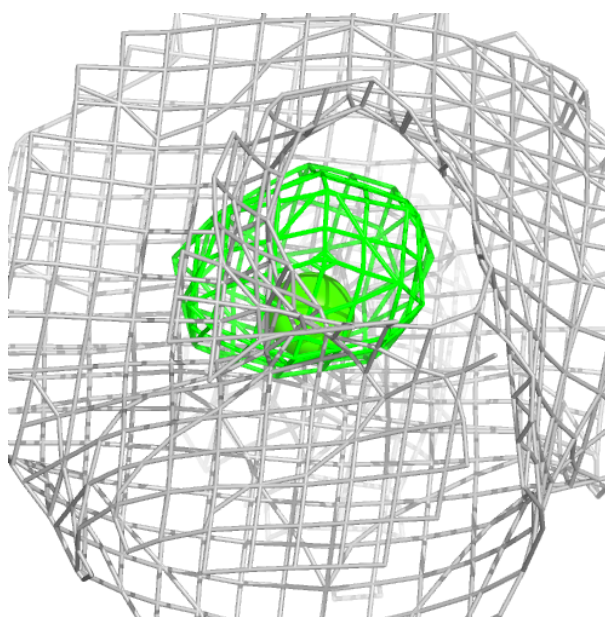
Electron density around CA B 406:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



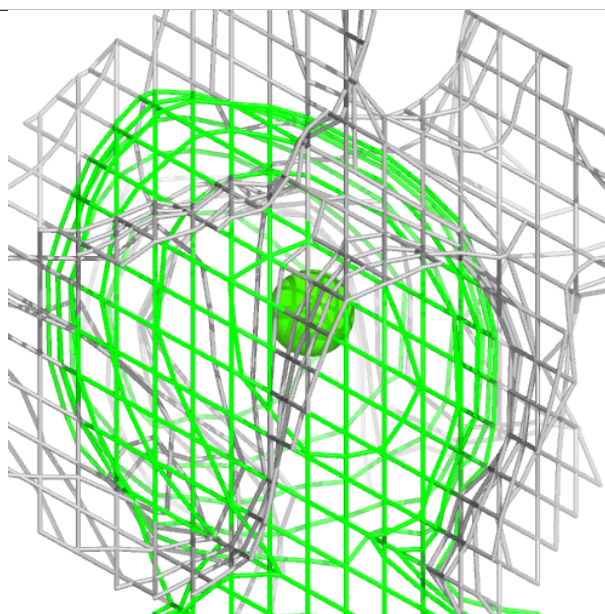
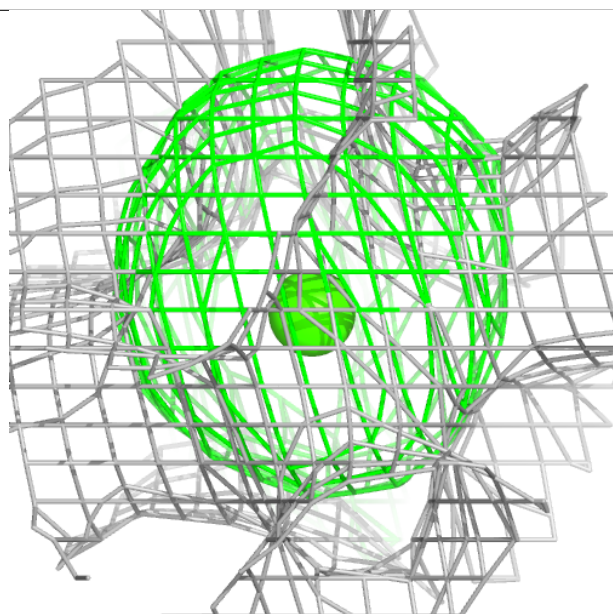
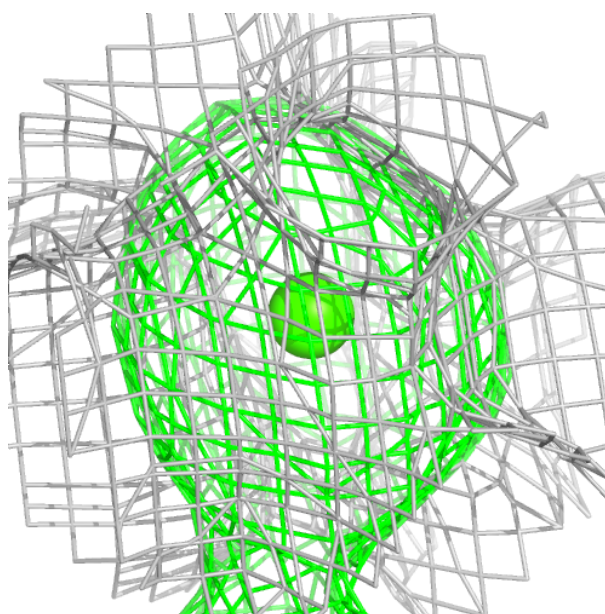
Electron density around CA E 401:

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



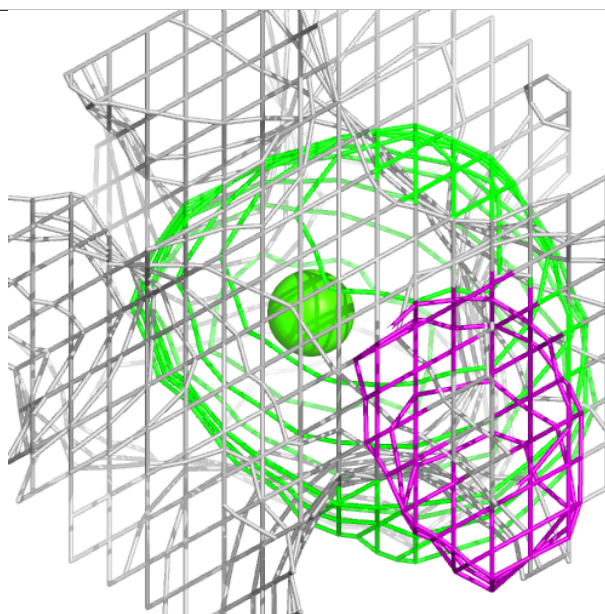
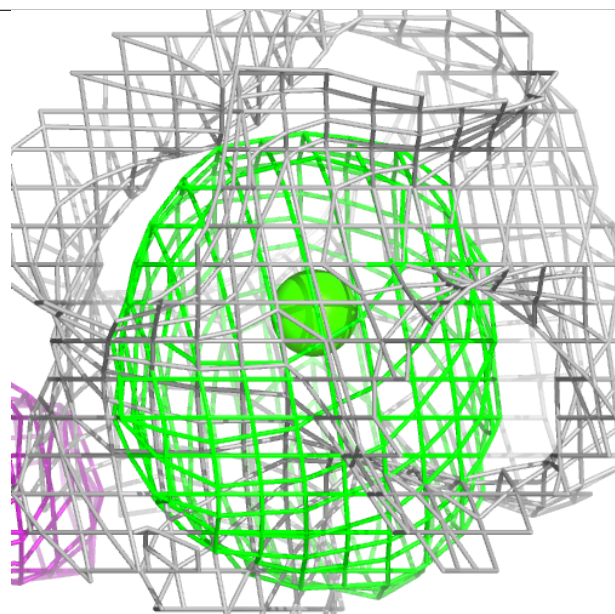
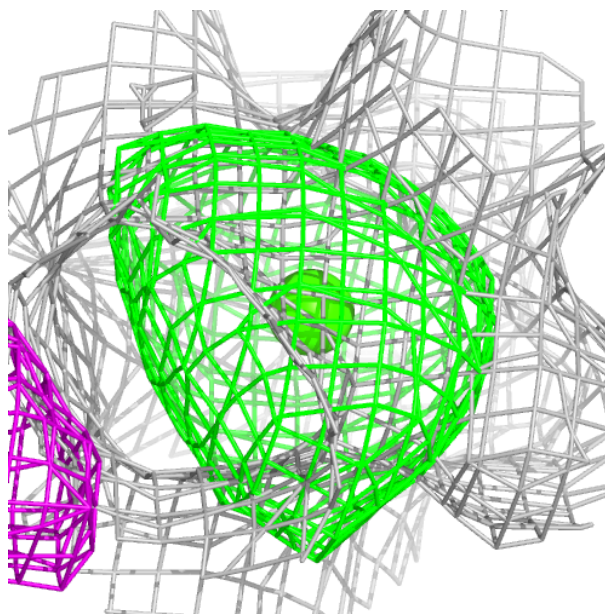
Electron density around CA E 402:

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



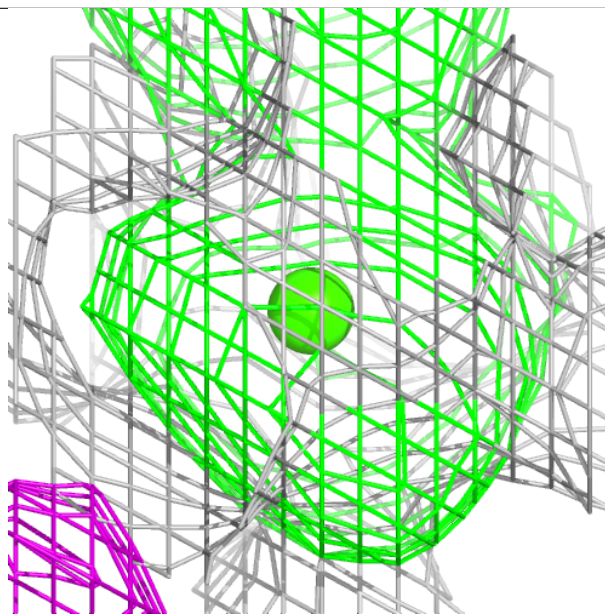
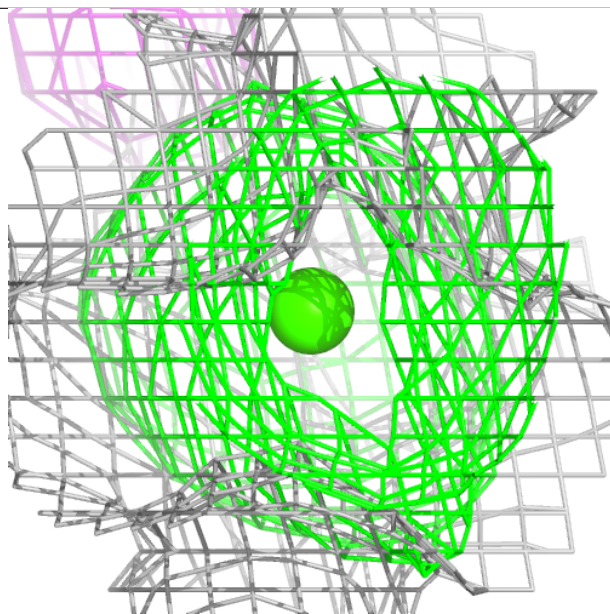
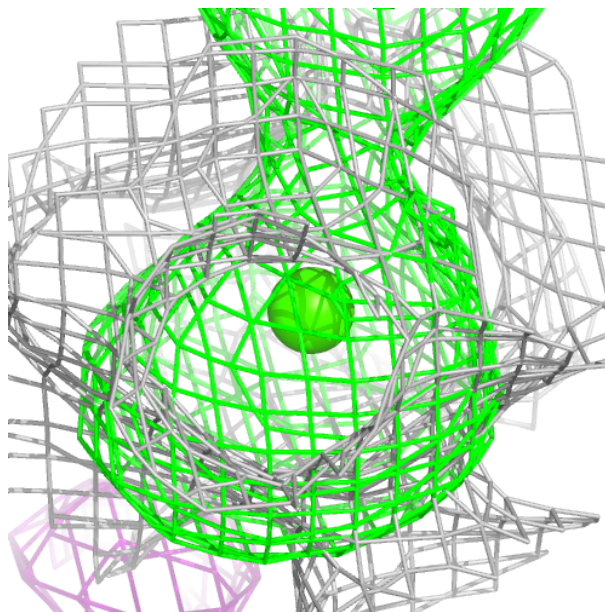
Electron density around CA E 403:

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



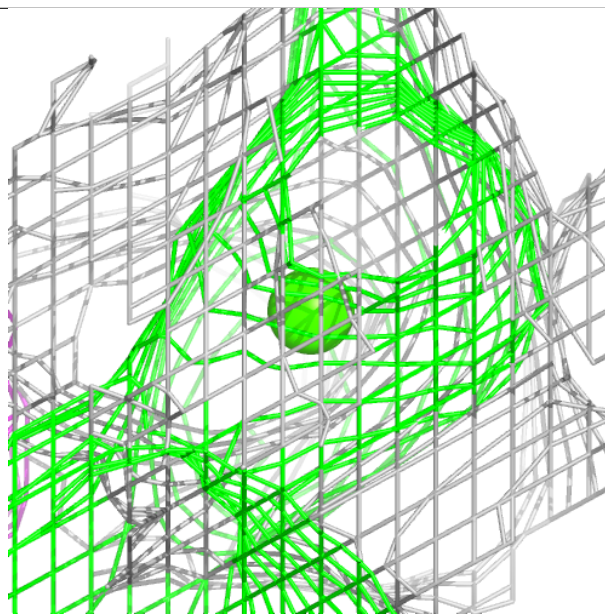
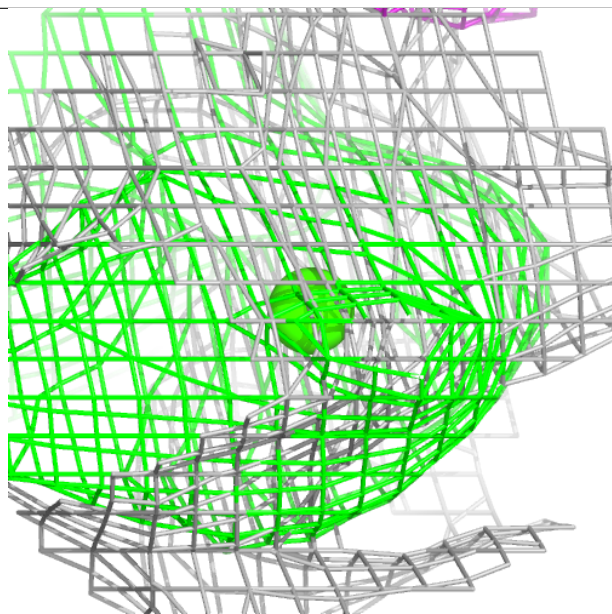
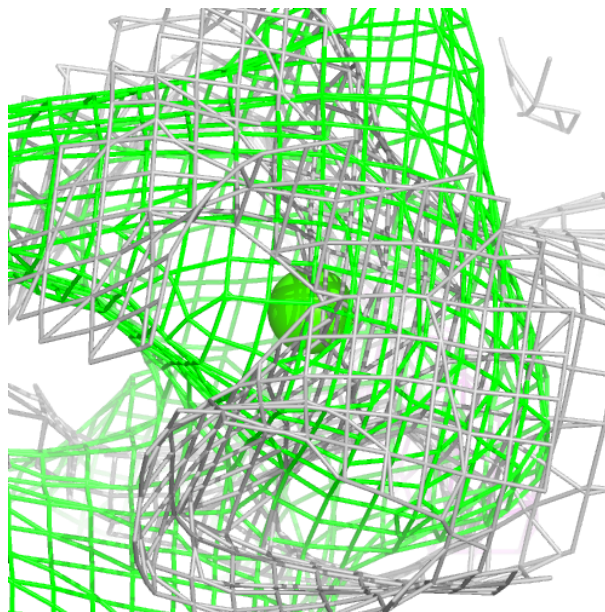
Electron density around CA E 404:

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



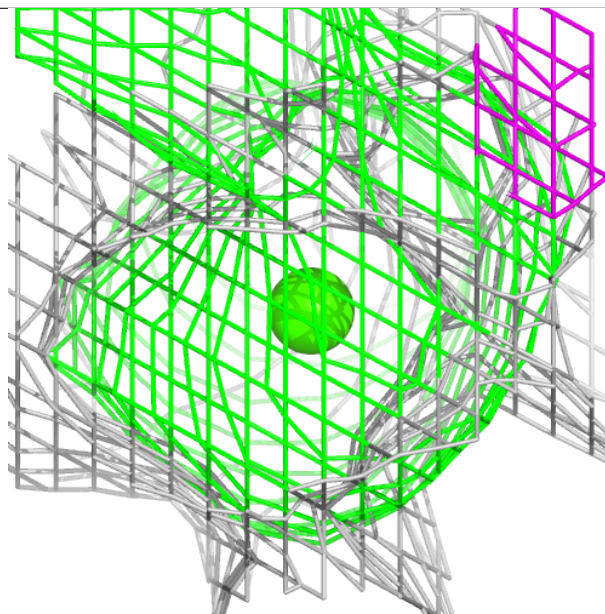
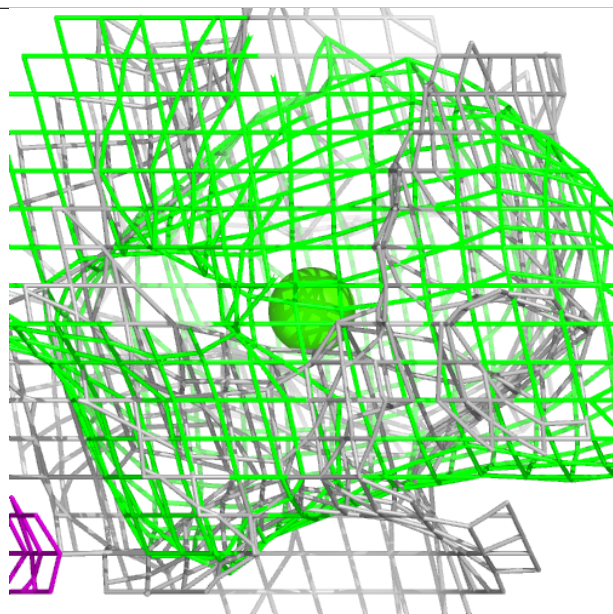
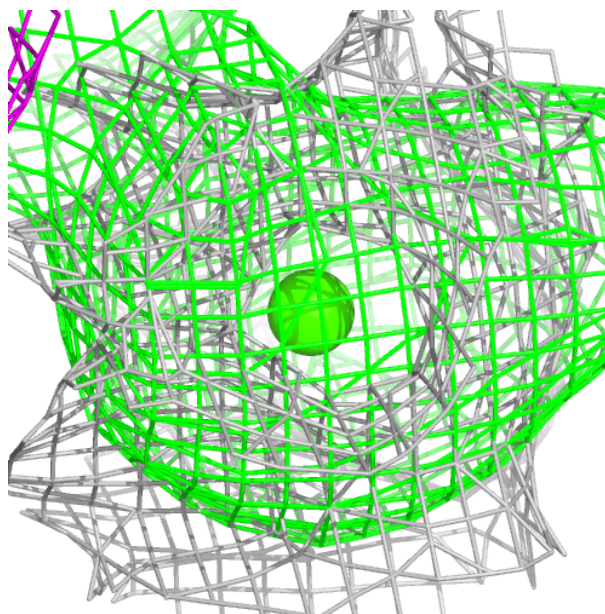
Electron density around CA E 405:

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



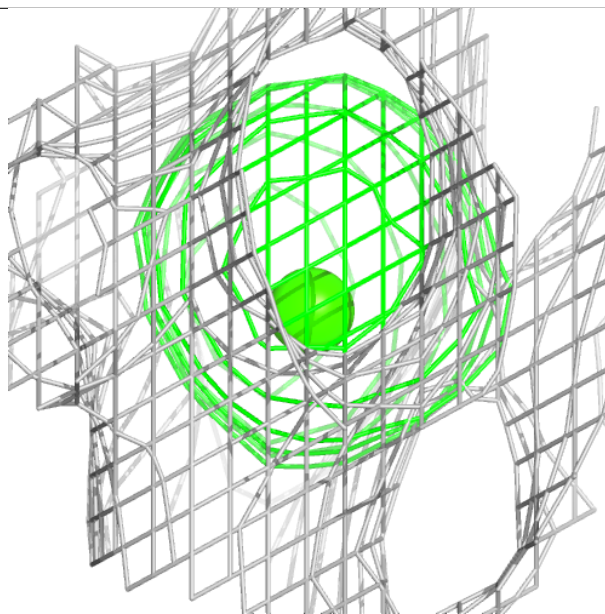
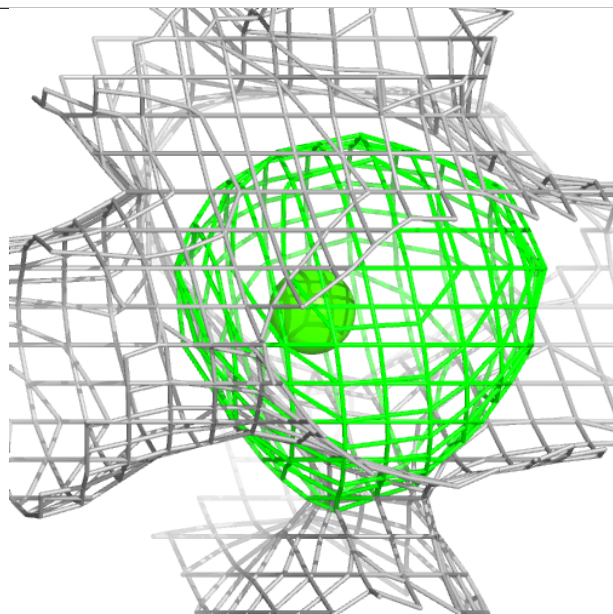
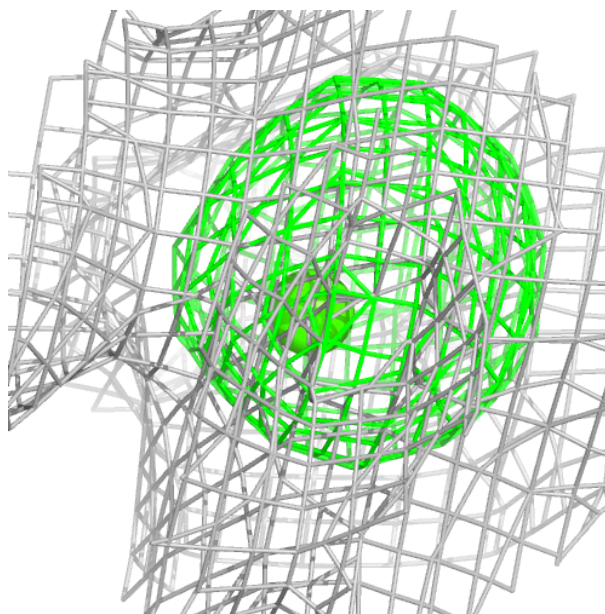
Electron density around CA E 406:

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



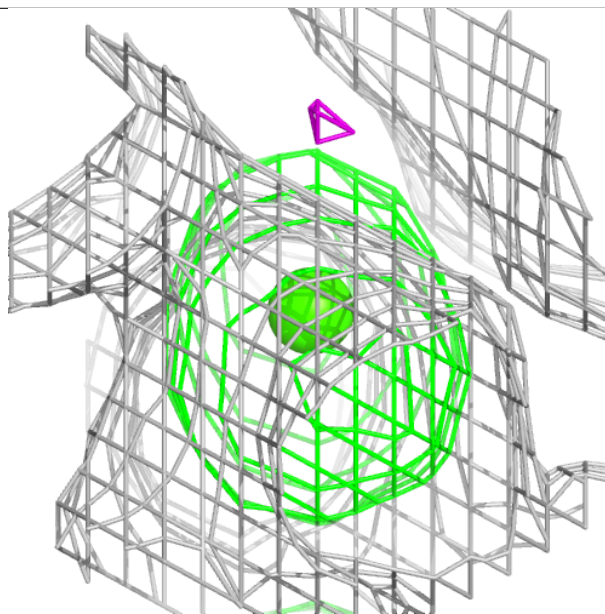
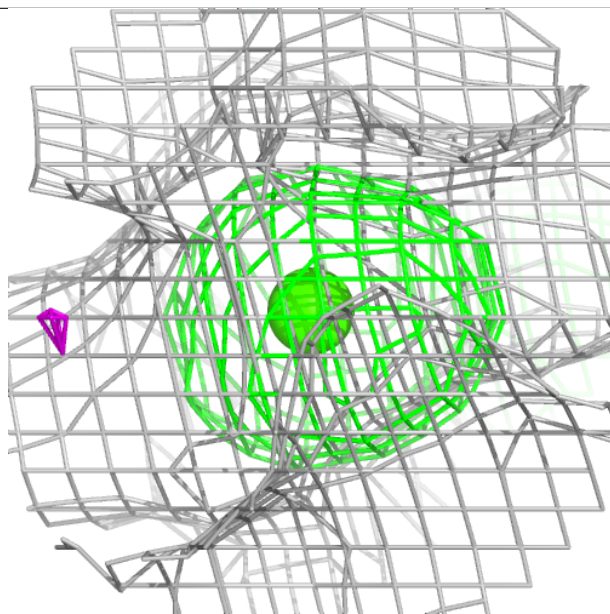
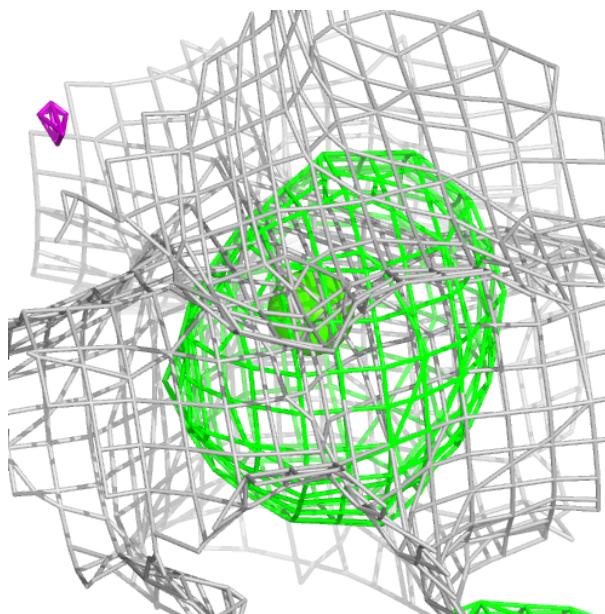
Electron density around CA G 401:

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



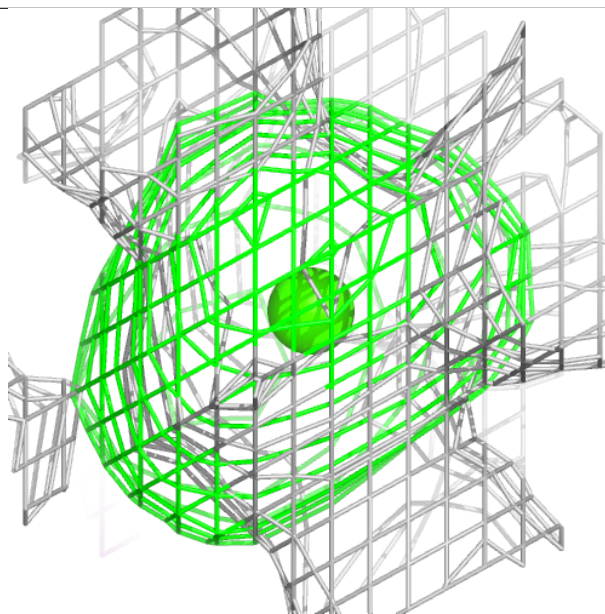
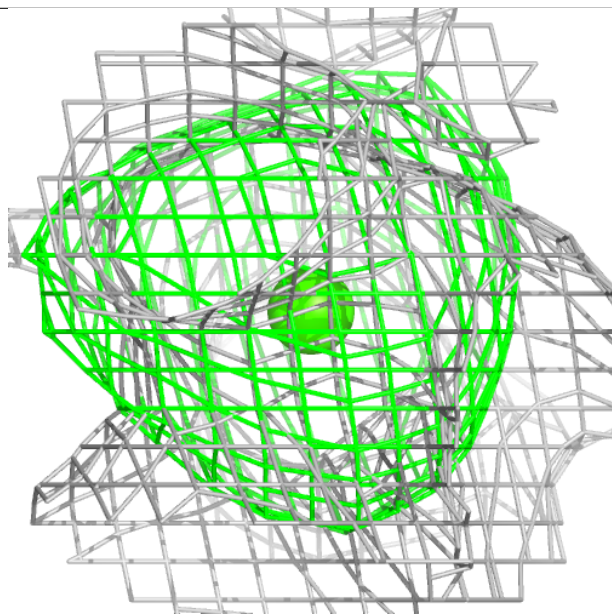
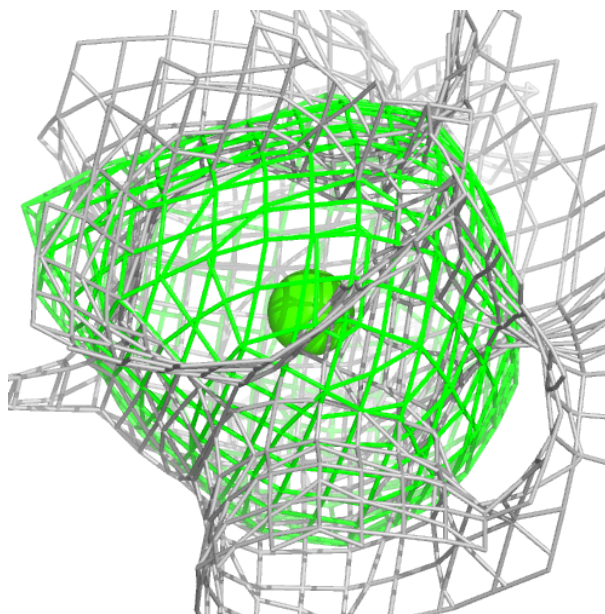
Electron density around CA G 402:

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



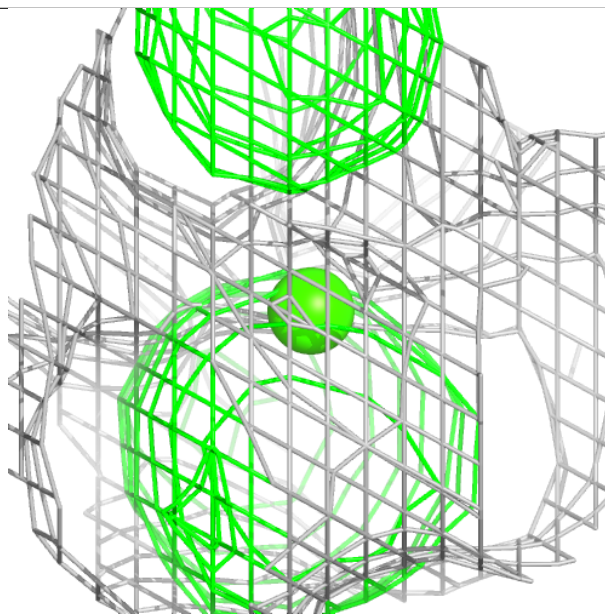
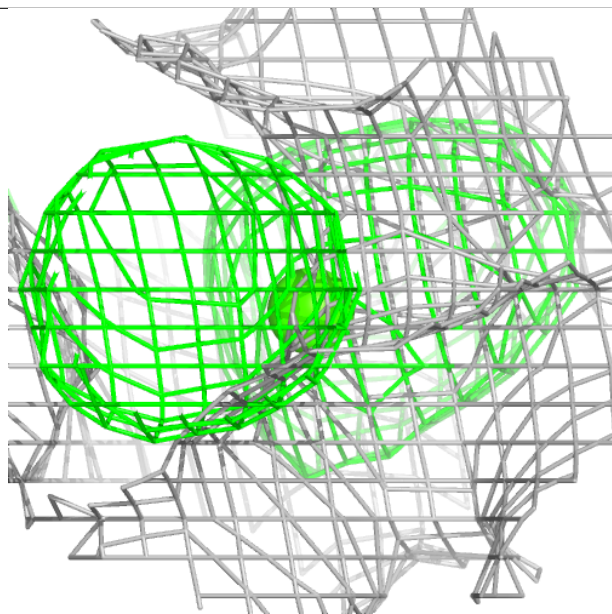
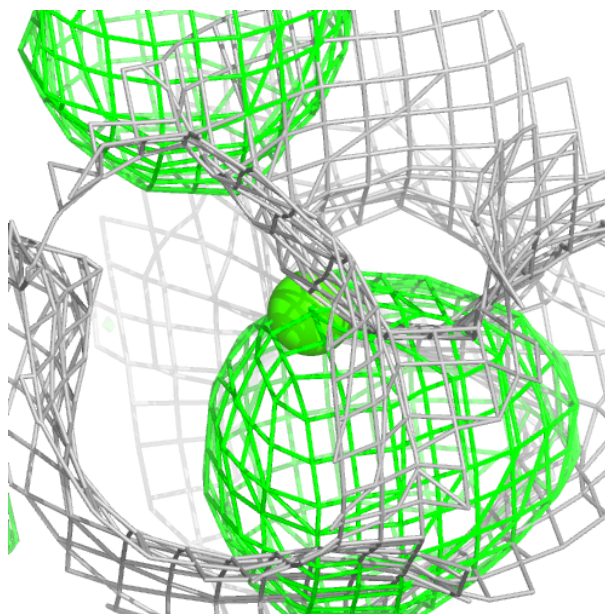
Electron density around CA G 403:

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



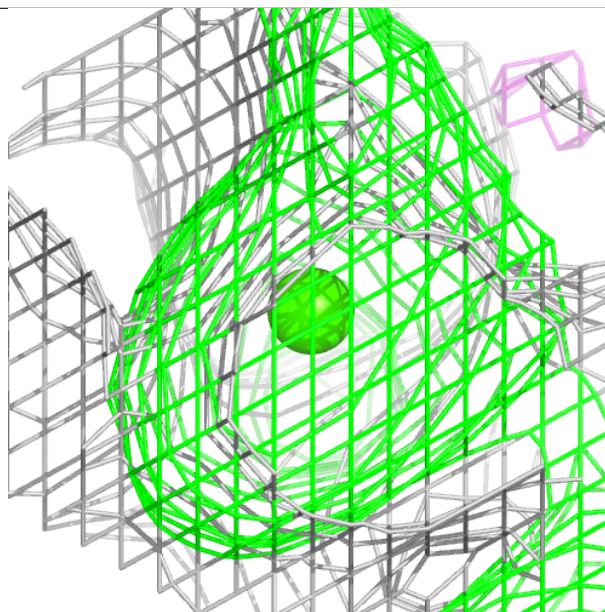
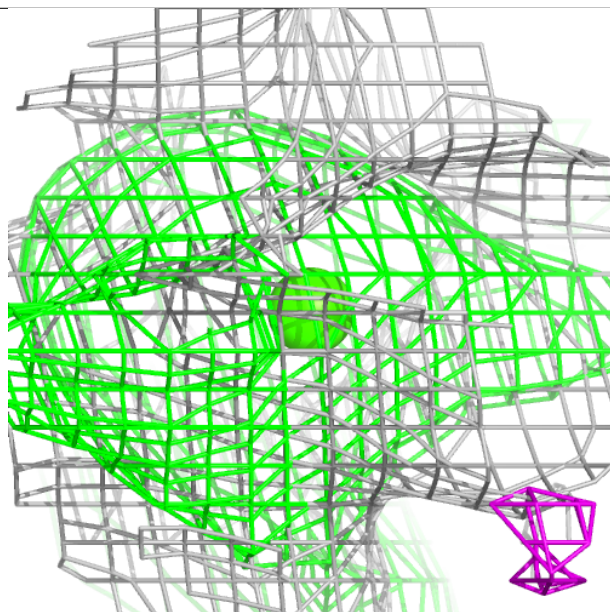
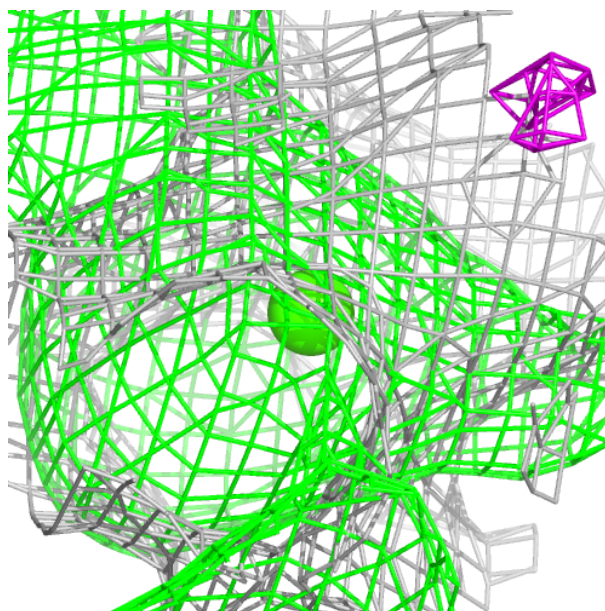
Electron density around CA G 404:

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



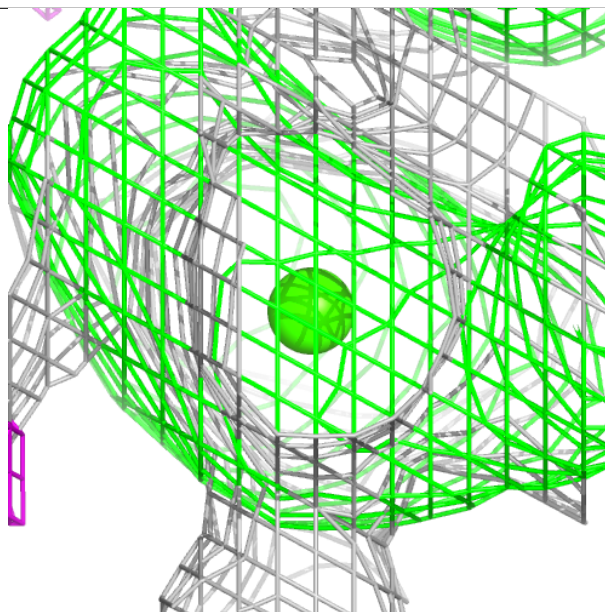
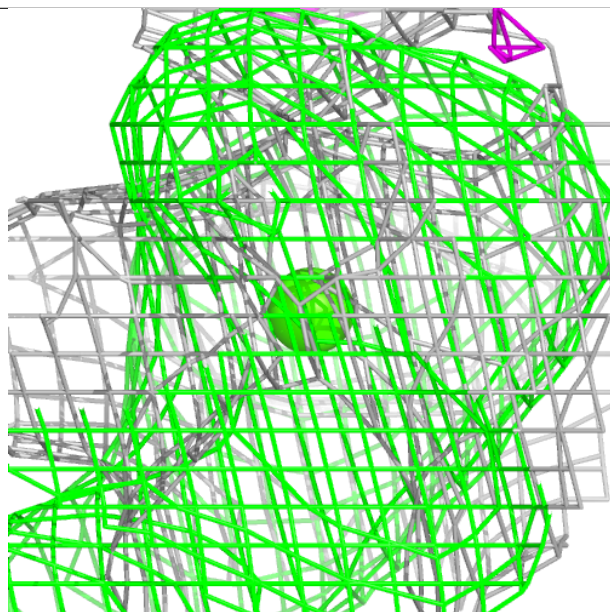
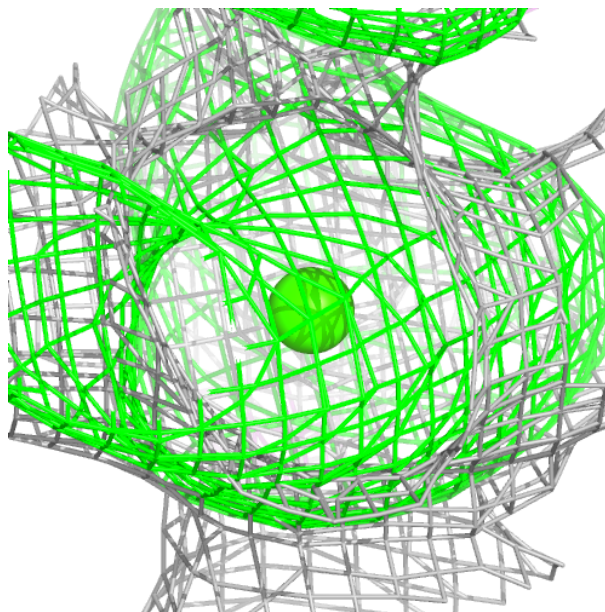
Electron density around CA G 405:

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



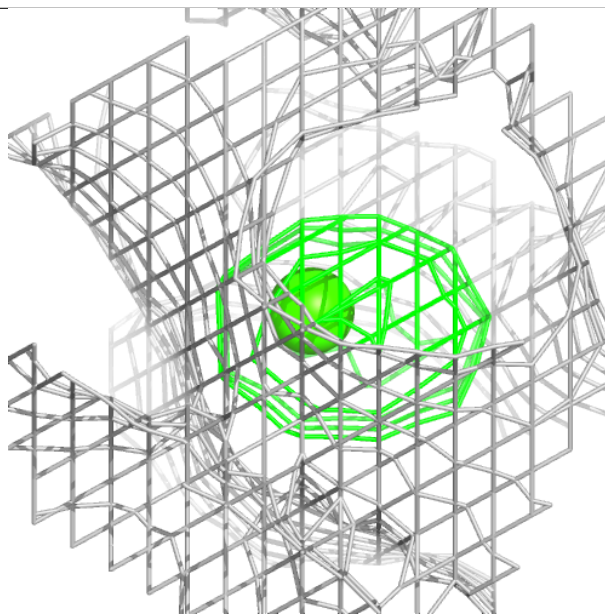
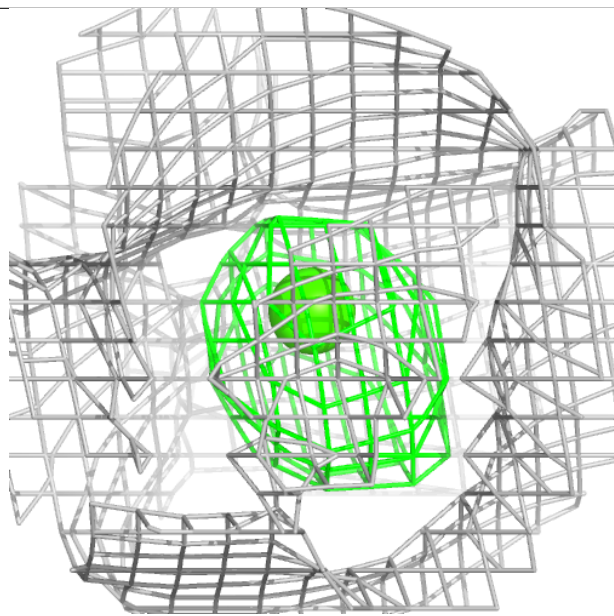
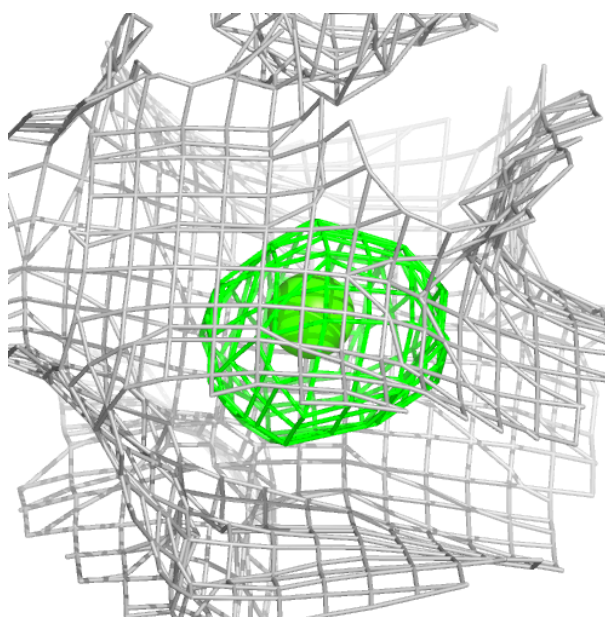
Electron density around CA G 406:

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



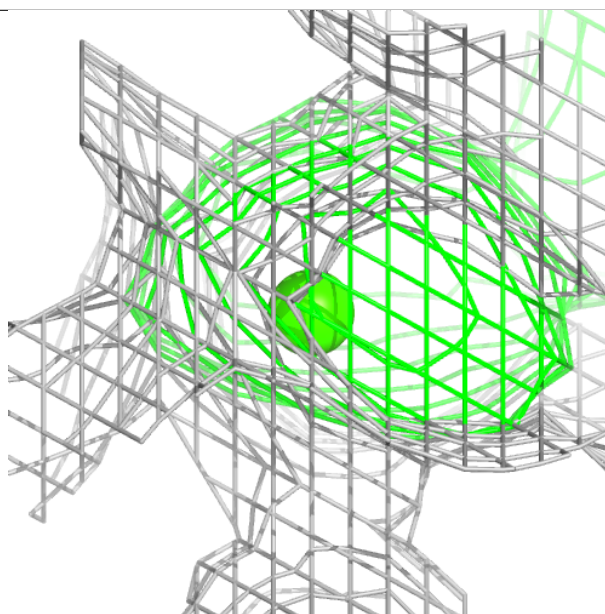
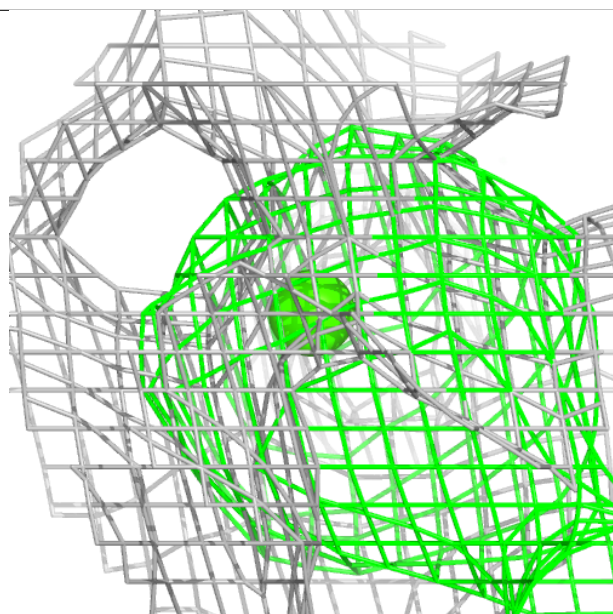
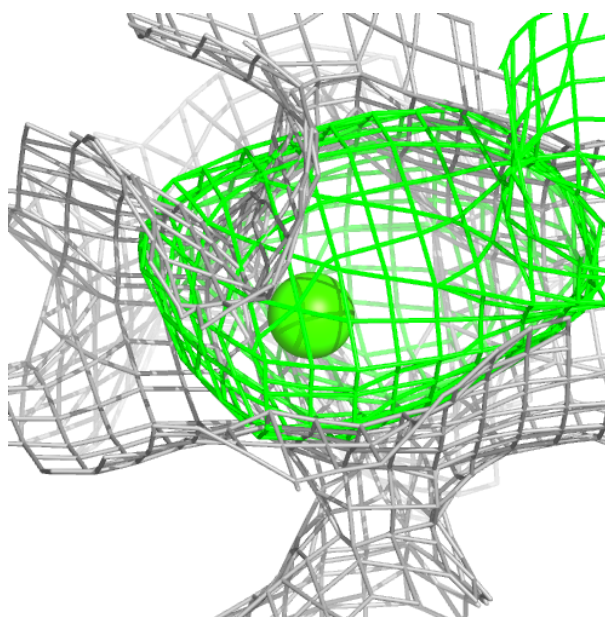
Electron density around CA I 401:

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



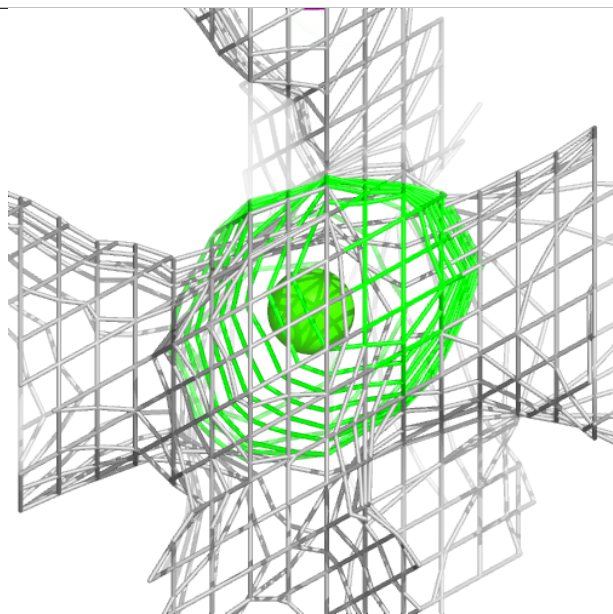
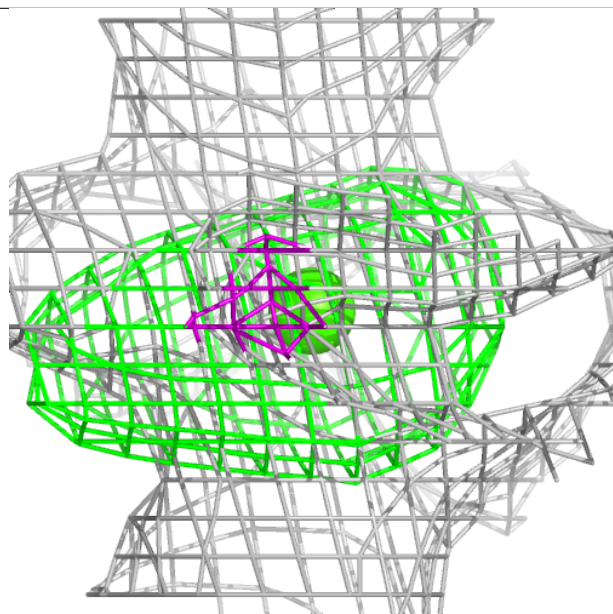
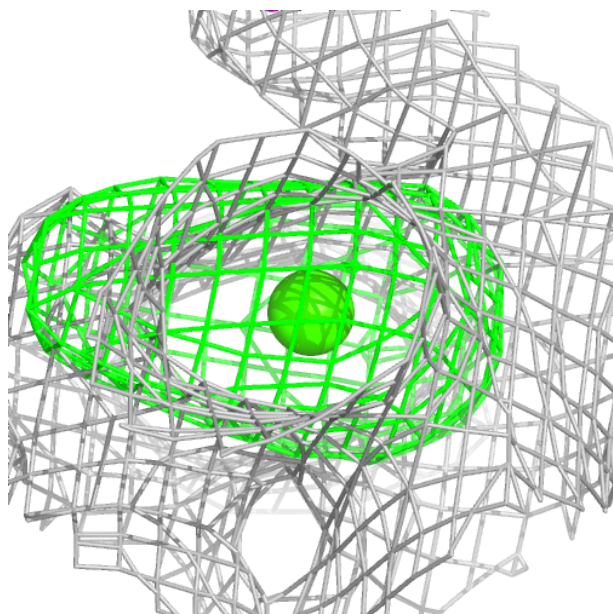
Electron density around CA I 402:

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



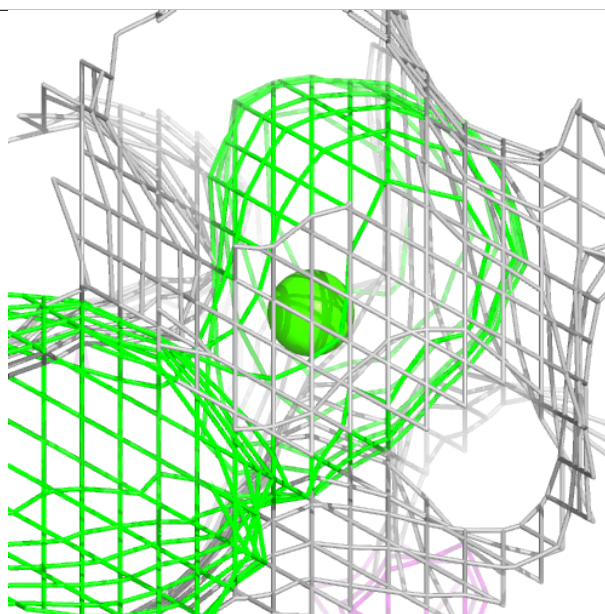
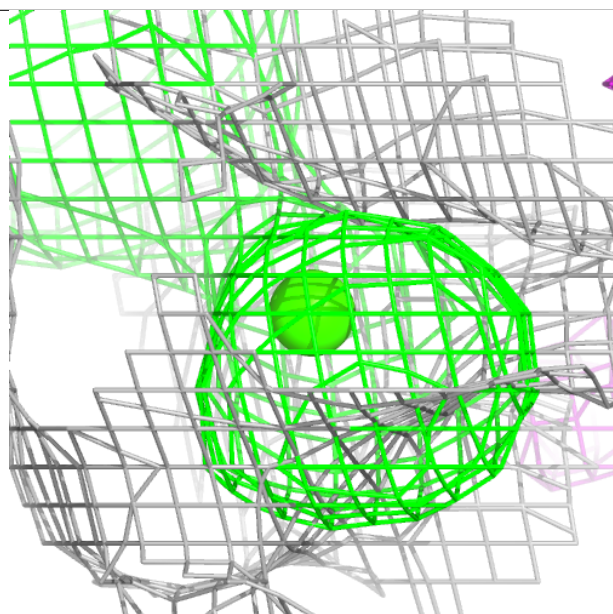
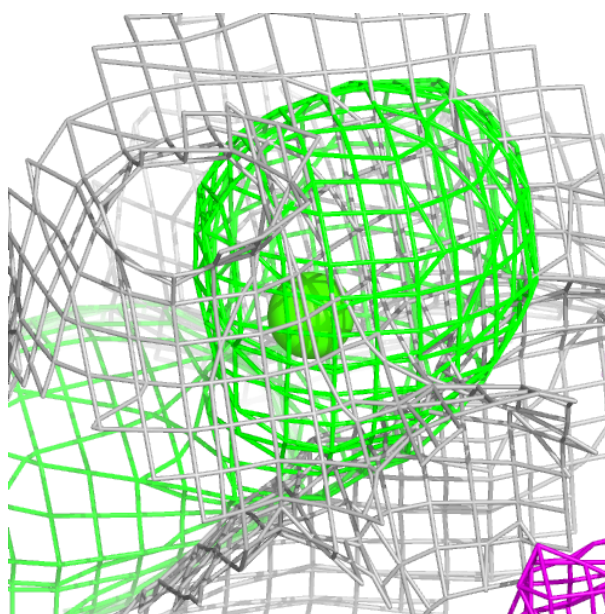
Electron density around CA I 403:

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



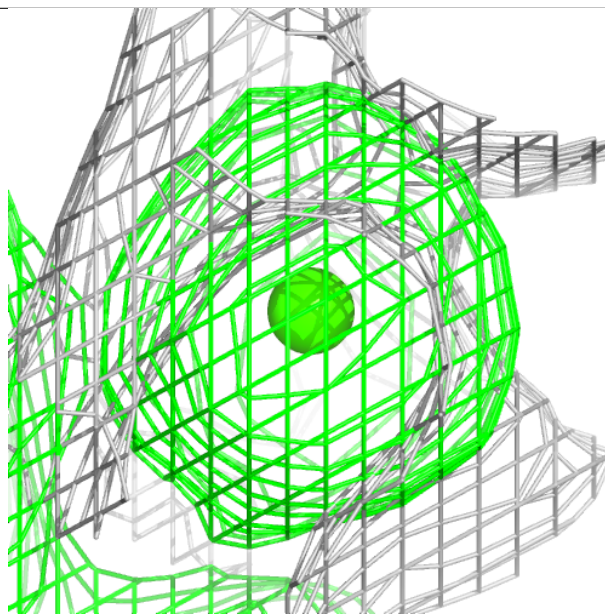
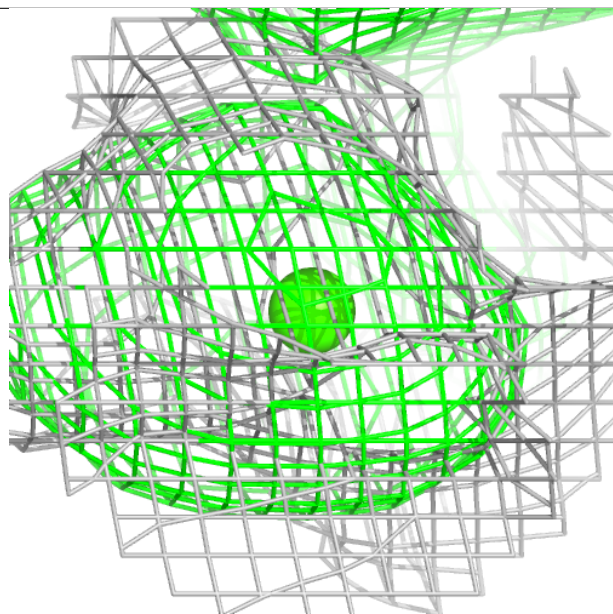
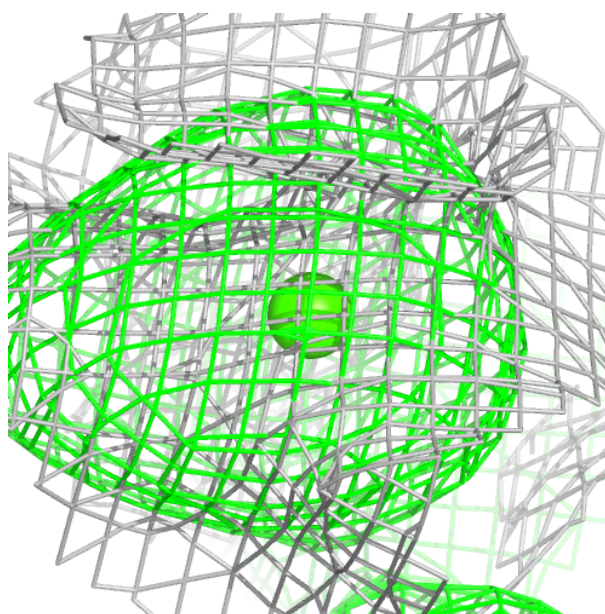
Electron density around CA I 404:

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



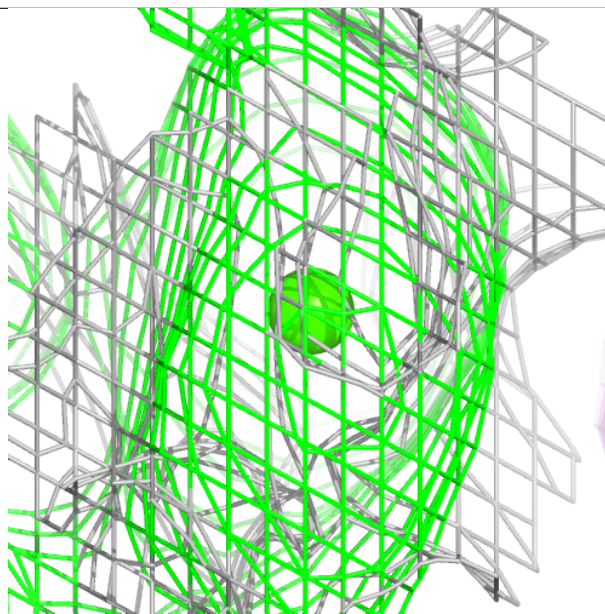
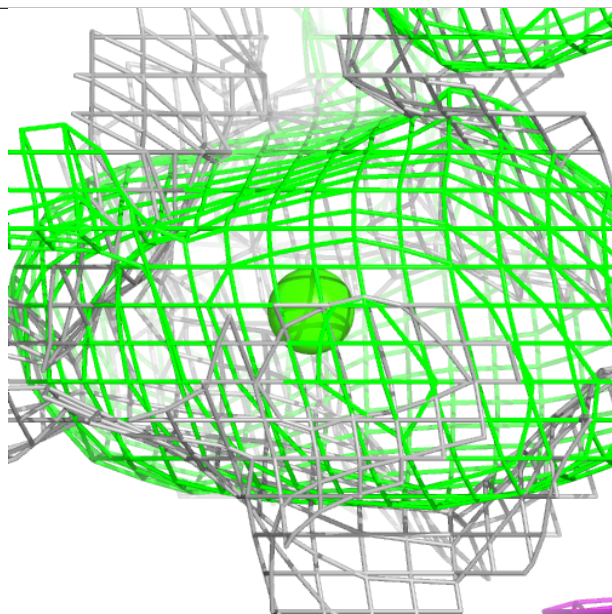
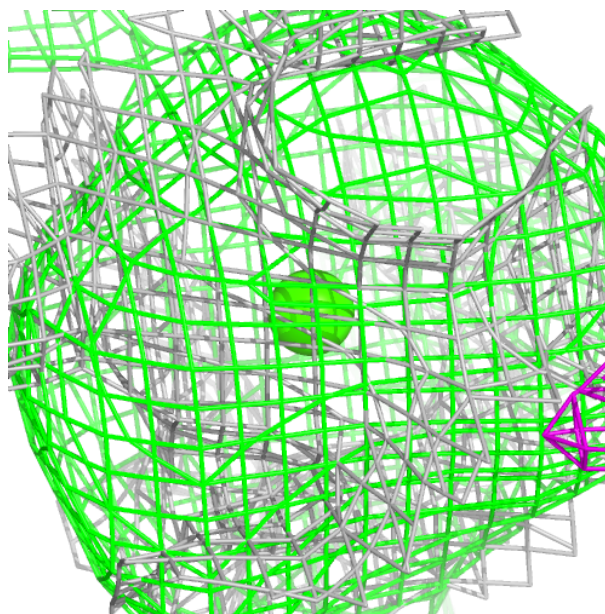
Electron density around CA I 405:

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



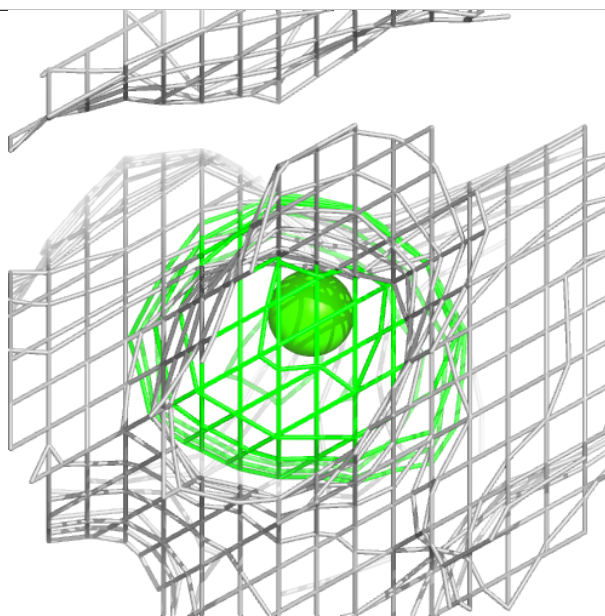
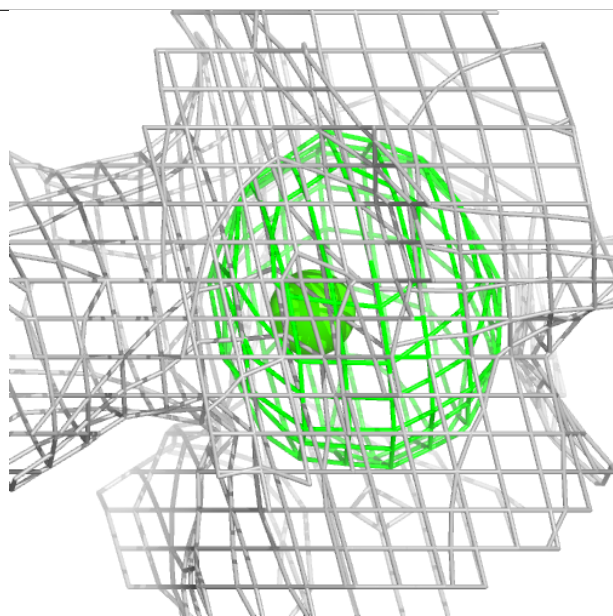
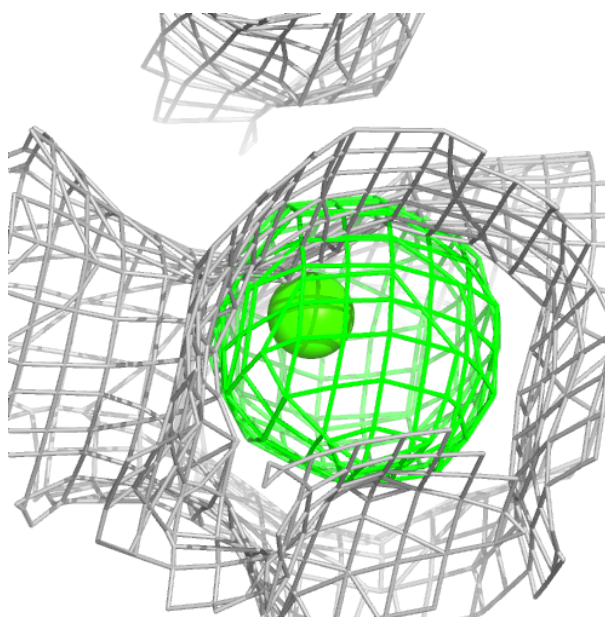
Electron density around CA I 406:

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



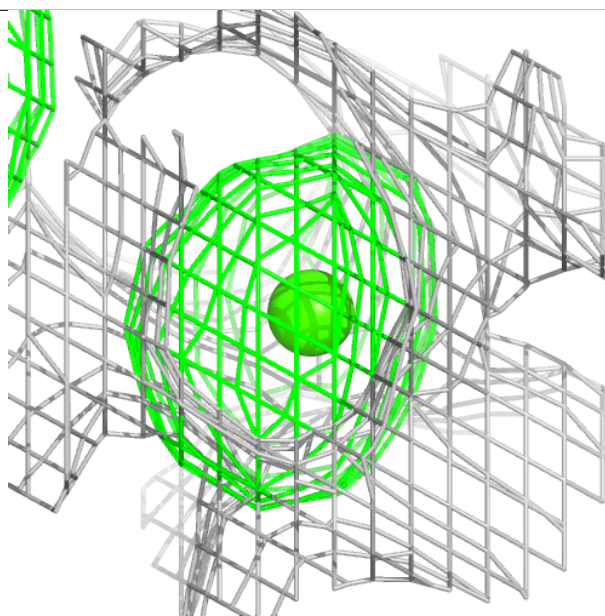
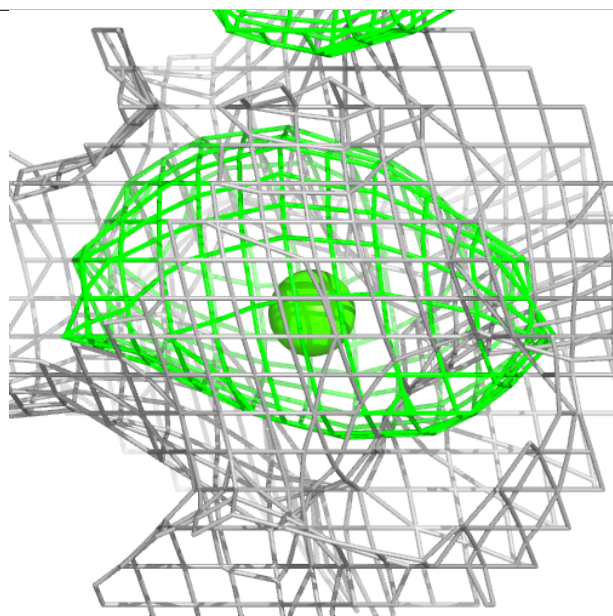
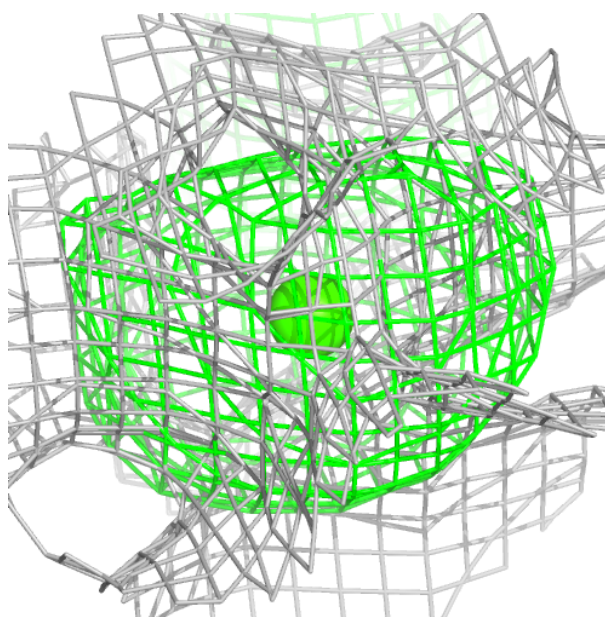
Electron density around CA K 401:

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



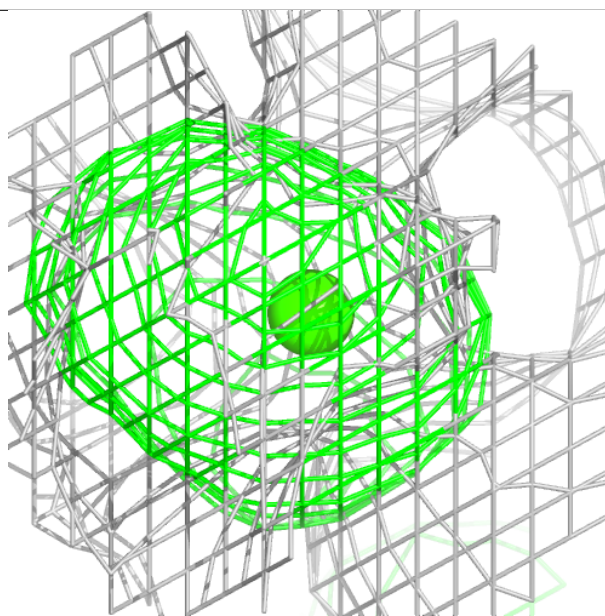
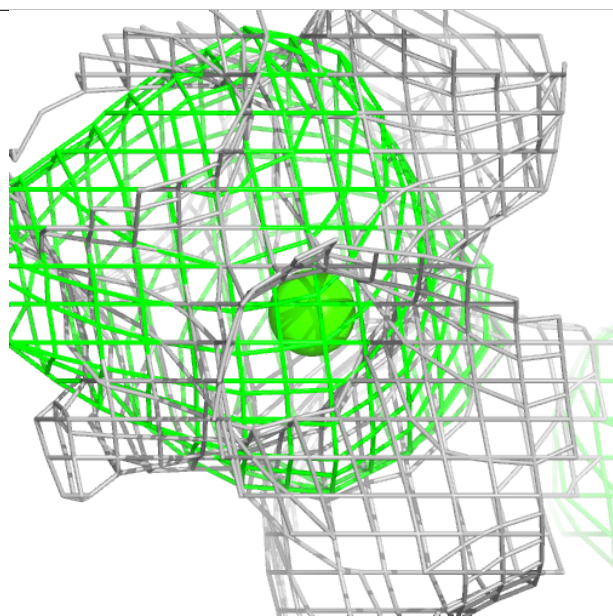
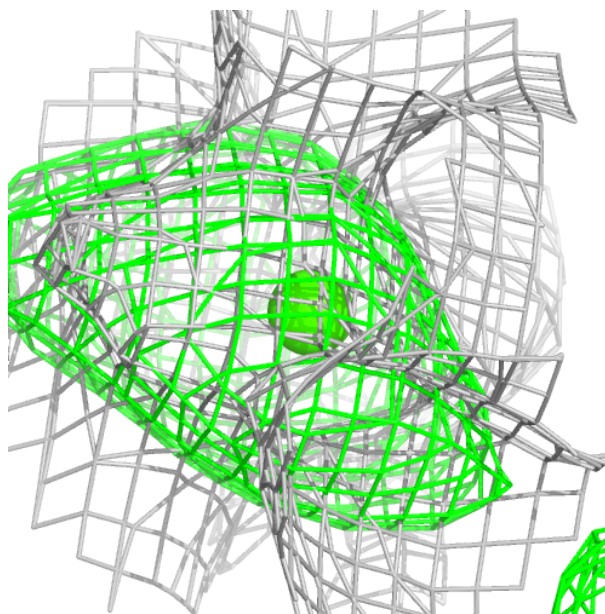
Electron density around CA K 402:

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



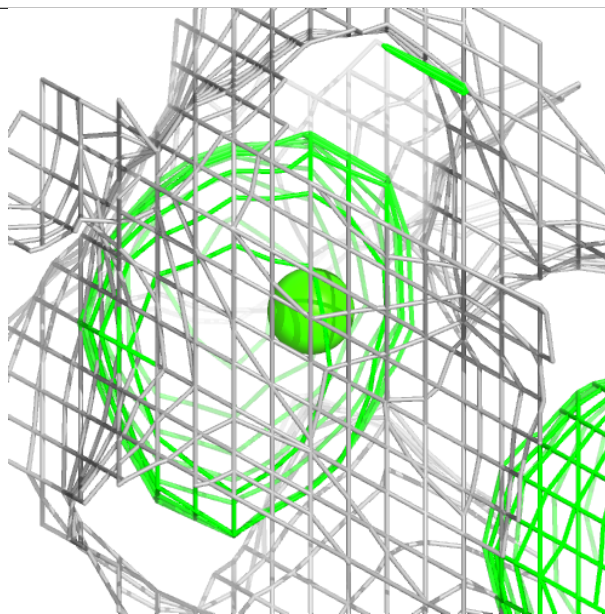
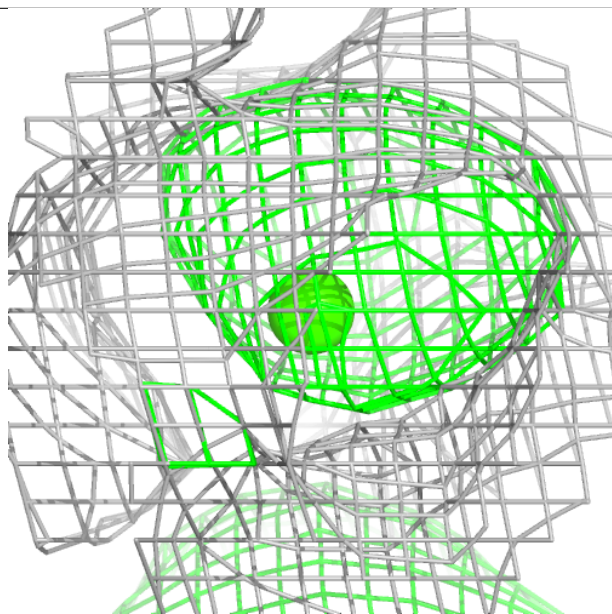
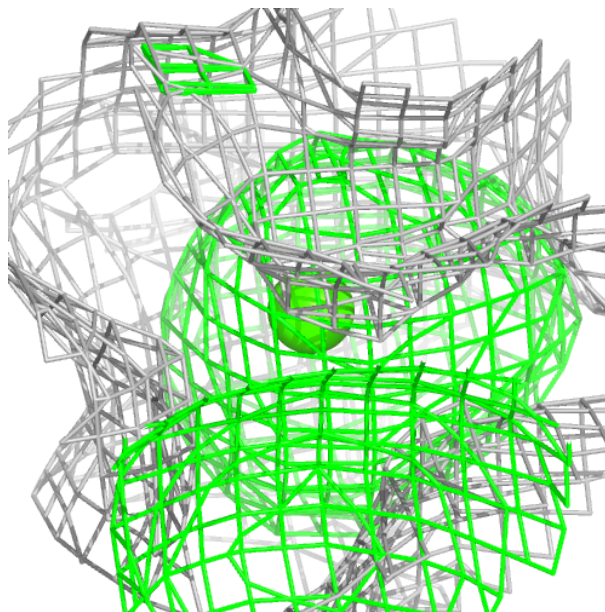
Electron density around CA K 403:

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



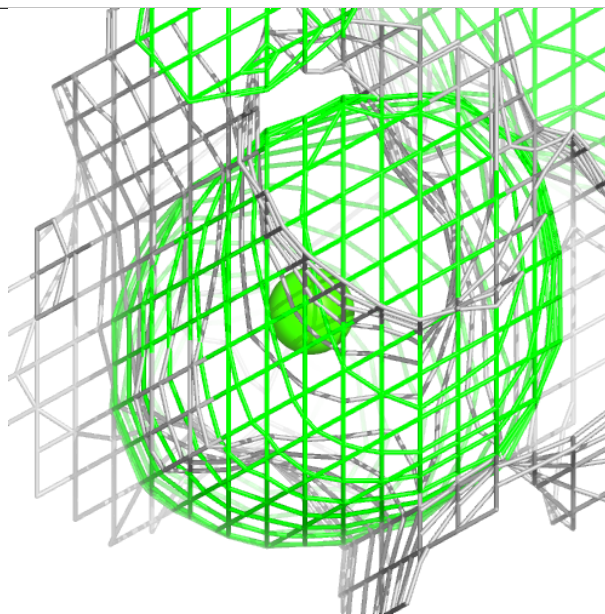
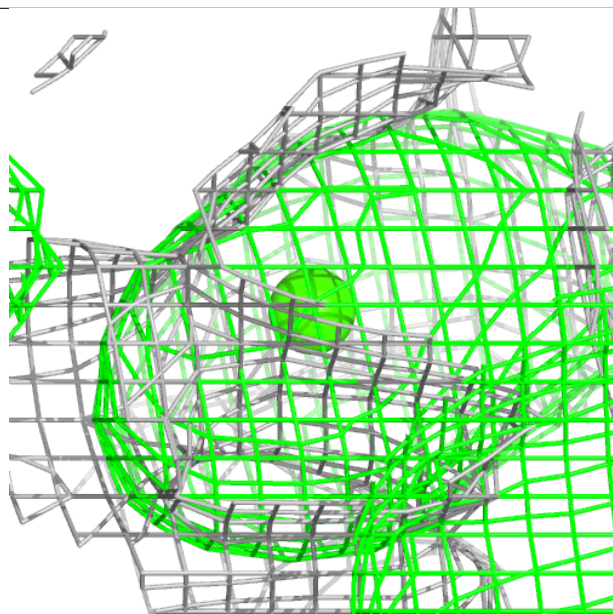
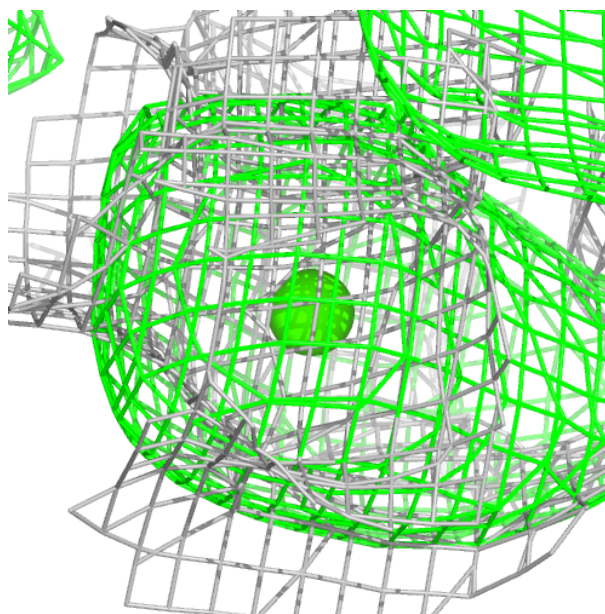
Electron density around CA K 404:

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



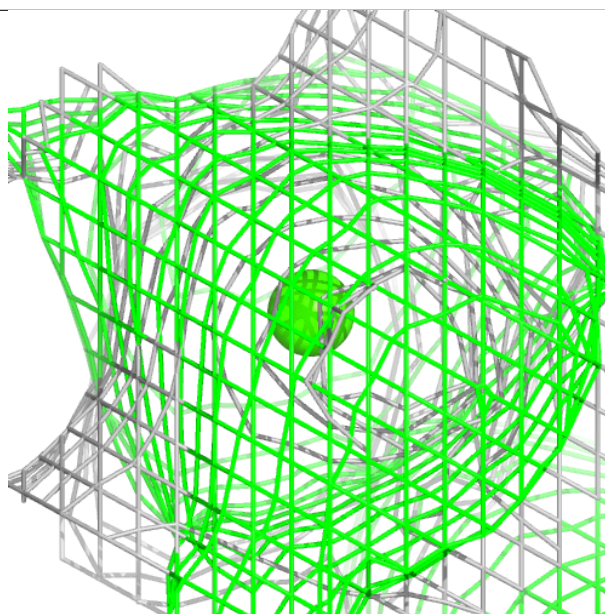
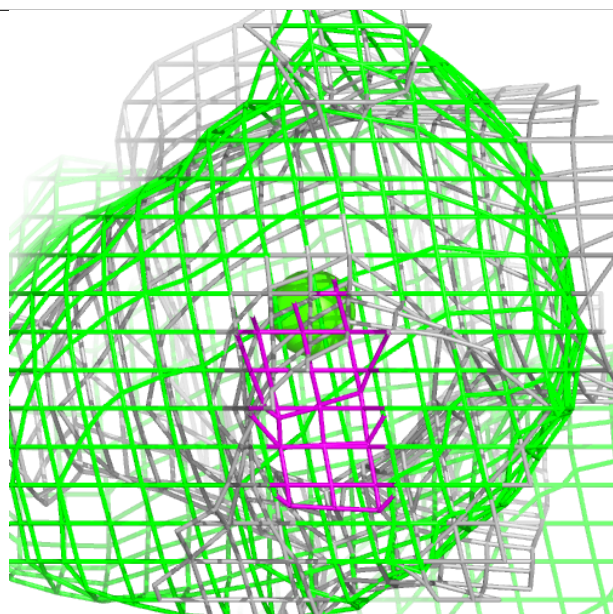
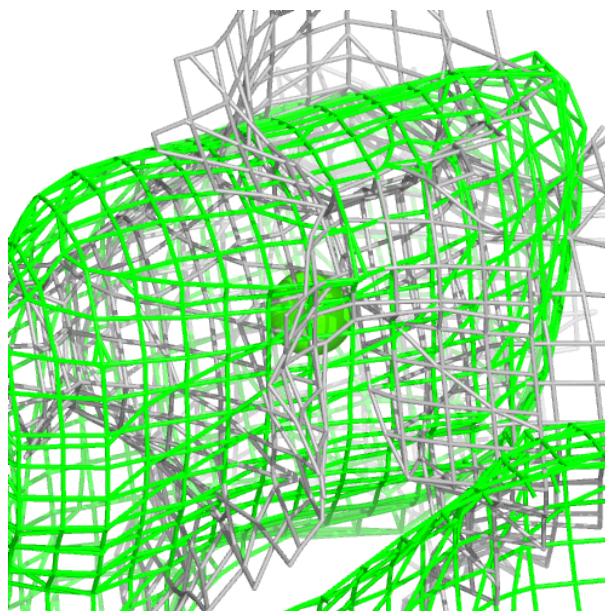
Electron density around CA K 405:

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



Electron density around CA K 406:

$2mF_o-DF_c$ (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.