



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 15, 2024 – 07:22 pm GMT

PDB ID : 6TXA
Title : Crystal structure of tetrameric human D137N-SAMHD1 (residues 109-626) with XTP, dGMPNPP and Mg
Authors : Morris, E.R.; Kunzelmann, S.; Caswell, S.J.; Arnold, L.H.; Purkiss, A.; Kelly, G.; Taylor, I.A.
Deposited on : 2020-01-13
Resolution : 2.85 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

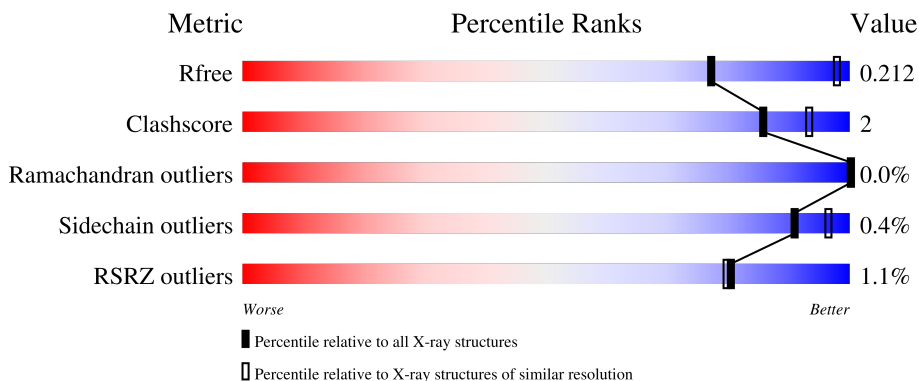
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.













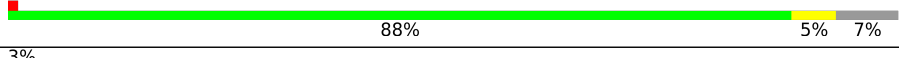

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	520	86% 6% 8%
1	B	520	88% 6% 8%
1	C	520	87% 5% 8%
1	D	520	88% 5% 8%

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Mol	Chain	Length	Quality of chain
1	E	520	 % 88% 5% 8%
1	F	520	 % 86% 6% 8%
1	G	520	 % 87% 5% 8%
1	H	520	 % 87% 5% 8%
1	I	520	 % 88% 5% 8%
1	J	520	 % 87% 5% 8%
1	K	520	 % 87% 5% 8%
1	L	520	 3% 86% 6% 8%
1	M	520	 2% 87% 5% 8%
1	N	520	 % 88% 5% 8%
1	O	520	 % 88% 5% 7%
1	P	520	 3% 87% 5% 8%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 62976 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Deoxynucleoside triphosphate triphosphohydrolase SAMHD1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	480	Total 3862	C 2472	N 667	O 703	S 20	0	0	0
1	B	479	Total 3845	C 2461	N 665	O 699	S 20	0	0	0
1	C	480	Total 3853	C 2467	N 667	O 699	S 20	0	0	0
1	D	481	Total 3852	C 2465	N 667	O 700	S 20	0	0	0
1	E	479	Total 3845	C 2461	N 665	O 699	S 20	0	0	0
1	F	478	Total 3831	C 2452	N 659	O 700	S 20	0	0	0
1	G	479	Total 3830	C 2450	N 660	O 700	S 20	0	0	0
1	H	480	Total 3870	C 2478	N 670	O 702	S 20	0	0	0
1	I	479	Total 3843	C 2460	N 664	O 699	S 20	0	0	0
1	J	478	Total 3827	C 2451	N 662	O 694	S 20	0	0	0
1	K	478	Total 3828	C 2450	N 659	O 699	S 20	0	0	0
1	L	478	Total 3789	C 2425	N 648	O 696	S 20	0	0	0
1	M	476	Total 3780	C 2419	N 648	O 693	S 20	0	0	0
1	N	477	Total 3818	C 2444	N 656	O 698	S 20	0	0	0
1	O	486	Total 3867	C 2472	N 665	O 710	S 20	0	0	0
1	P	478	Total 3793	C 2431	N 651	O 691	S 20	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	GLY	-	expression tag	UNP Q9Y3Z3
A	108	SER	-	expression tag	UNP Q9Y3Z3
A	137	ASN	ASP	engineered mutation	UNP Q9Y3Z3
B	107	GLY	-	expression tag	UNP Q9Y3Z3
B	108	SER	-	expression tag	UNP Q9Y3Z3
B	137	ASN	ASP	engineered mutation	UNP Q9Y3Z3
C	107	GLY	-	expression tag	UNP Q9Y3Z3
C	108	SER	-	expression tag	UNP Q9Y3Z3
C	137	ASN	ASP	engineered mutation	UNP Q9Y3Z3
D	107	GLY	-	expression tag	UNP Q9Y3Z3
D	108	SER	-	expression tag	UNP Q9Y3Z3
D	137	ASN	ASP	engineered mutation	UNP Q9Y3Z3
E	107	GLY	-	expression tag	UNP Q9Y3Z3
E	108	SER	-	expression tag	UNP Q9Y3Z3
E	137	ASN	ASP	engineered mutation	UNP Q9Y3Z3
F	107	GLY	-	expression tag	UNP Q9Y3Z3
F	108	SER	-	expression tag	UNP Q9Y3Z3
F	137	ASN	ASP	engineered mutation	UNP Q9Y3Z3
G	107	GLY	-	expression tag	UNP Q9Y3Z3
G	108	SER	-	expression tag	UNP Q9Y3Z3
G	137	ASN	ASP	engineered mutation	UNP Q9Y3Z3
H	107	GLY	-	expression tag	UNP Q9Y3Z3
H	108	SER	-	expression tag	UNP Q9Y3Z3
H	137	ASN	ASP	engineered mutation	UNP Q9Y3Z3
I	107	GLY	-	expression tag	UNP Q9Y3Z3
I	108	SER	-	expression tag	UNP Q9Y3Z3
I	137	ASN	ASP	engineered mutation	UNP Q9Y3Z3
J	107	GLY	-	expression tag	UNP Q9Y3Z3
J	108	SER	-	expression tag	UNP Q9Y3Z3
J	137	ASN	ASP	engineered mutation	UNP Q9Y3Z3
K	107	GLY	-	expression tag	UNP Q9Y3Z3
K	108	SER	-	expression tag	UNP Q9Y3Z3
K	137	ASN	ASP	engineered mutation	UNP Q9Y3Z3
L	107	GLY	-	expression tag	UNP Q9Y3Z3
L	108	SER	-	expression tag	UNP Q9Y3Z3
L	137	ASN	ASP	engineered mutation	UNP Q9Y3Z3
M	107	GLY	-	expression tag	UNP Q9Y3Z3
M	108	SER	-	expression tag	UNP Q9Y3Z3
M	137	ASN	ASP	engineered mutation	UNP Q9Y3Z3
N	107	GLY	-	expression tag	UNP Q9Y3Z3
N	108	SER	-	expression tag	UNP Q9Y3Z3
N	137	ASN	ASP	engineered mutation	UNP Q9Y3Z3

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Chain	Residue	Modelled	Actual	Comment	Reference
O	107	GLY	-	expression tag	UNP Q9Y3Z3
O	108	SER	-	expression tag	UNP Q9Y3Z3
O	137	ASN	ASP	engineered mutation	UNP Q9Y3Z3
P	107	GLY	-	expression tag	UNP Q9Y3Z3
P	108	SER	-	expression tag	UNP Q9Y3Z3
P	137	ASN	ASP	engineered mutation	UNP Q9Y3Z3

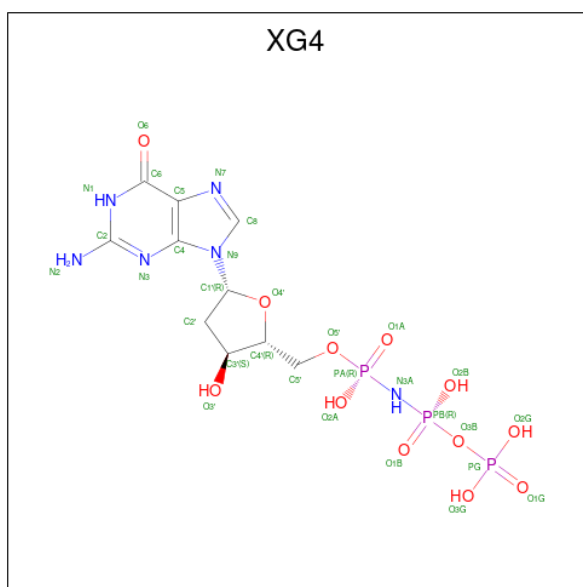
- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Fe 1 1	0	0
2	B	1	Total Fe 1 1	0	0
2	C	1	Total Fe 1 1	0	0
2	D	1	Total Fe 1 1	0	0
2	E	1	Total Fe 1 1	0	0
2	F	1	Total Fe 1 1	0	0
2	G	1	Total Fe 1 1	0	0
2	H	1	Total Fe 1 1	0	0
2	I	1	Total Fe 1 1	0	0
2	J	1	Total Fe 1 1	0	0
2	K	1	Total Fe 1 1	0	0
2	L	1	Total Fe 1 1	0	0
2	M	1	Total Fe 1 1	0	0
2	N	1	Total Fe 1 1	0	0
2	O	1	Total Fe 1 1	0	0
2	P	1	Total Fe 1 1	0	0

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

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

- Molecule 4 is 2'-deoxy-5'-O-[(R)-hydroxy{[(R)-hydroxy(phosphonoxy)phosphoryl]amino}phosphoryl]guanosine (three-letter code: XG4) (formula: C₁₀H₁₇N₆O₁₂P₃) (labeled as "Ligand of Interest" by depositor).



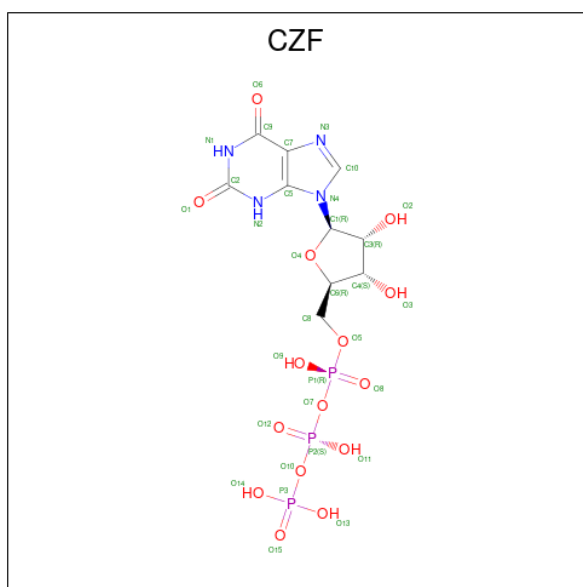
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	C	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	C	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	D	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	D	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	E	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	E	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	F	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	F	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	G	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	G	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	H	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	H	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	I	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	I	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	I	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	J	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	J	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	K	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	K	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	L	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	M	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	M	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	N	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	N	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	O	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	O	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	P	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	P	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 5 is [[[2 {R},3 {S},4 {R},5 {R}]-5-[2,6-bis(oxidanylidene)-3 {H}-purin-9-yl]-3,4-bis(oxidanyl)oxolan-2-yl]methoxy-oxidanyl-phosphoryl] phosphono hydrogen phosphate (three-letter code: CZF) (formula: C₁₀H₁₅N₄O₁₅P₃) (labeled as "Ligand of Interest" by depositor).



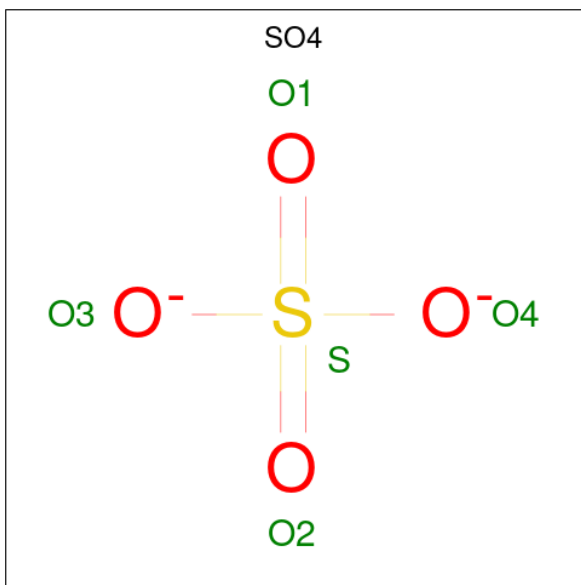
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
5	A	1	Total 32	C 10	N 4	O 15	P 3	0	0
5	B	1	Total 32	C 10	N 4	O 15	P 3	0	0
5	C	1	Total 32	C 10	N 4	O 15	P 3	0	0
5	C	1	Total 32	C 10	N 4	O 15	P 3	0	0
5	E	1	Total 32	C 10	N 4	O 15	P 3	0	0
5	F	1	Total 32	C 10	N 4	O 15	P 3	0	0
5	G	1	Total 32	C 10	N 4	O 15	P 3	0	0
5	H	1	Total 32	C 10	N 4	O 15	P 3	0	0
5	J	1	Total 32	C 10	N 4	O 15	P 3	0	0
5	J	1	Total 32	C 10	N 4	O 15	P 3	0	0
5	K	1	Total 32	C 10	N 4	O 15	P 3	0	0
5	L	1	Total 32	C 10	N 4	O 15	P 3	0	0
5	M	1	Total 32	C 10	N 4	O 15	P 3	0	0
5	N	1	Total 32	C 10	N 4	O 15	P 3	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
5	O	1	Total	C	N	O	P	0	0
			32	10	4	15	3		
5	P	1	Total	C	N	O	P	0	0
			32	10	4	15	3		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
			O	S			
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	C	1	Total	O	S	0	0
			5	4	1		
6	D	1	Total	O	S	0	0
			5	4	1		
6	E	1	Total	O	S	0	0
			5	4	1		
6	F	1	Total	O	S	0	0
			5	4	1		
6	G	1	Total	O	S	0	0
			5	4	1		
6	H	1	Total	O	S	0	0
			5	4	1		
6	I	1	Total	O	S	0	0
			5	4	1		

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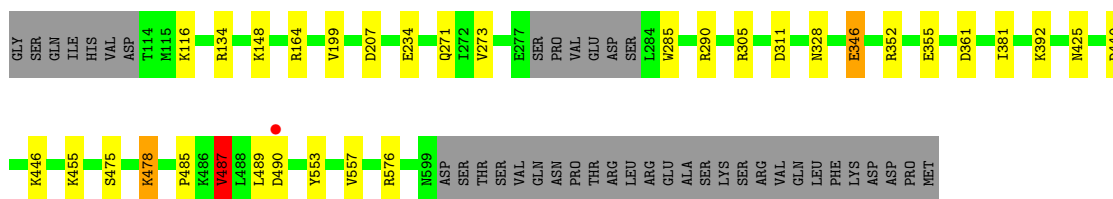
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	J	1	Total	O	S	0	0
			5	4	1		
6	K	1	Total	O	S	0	0
			5	4	1		
6	L	1	Total	O	S	0	0
			5	4	1		
6	M	1	Total	O	S	0	0
			5	4	1		
6	N	1	Total	O	S	0	0
			5	4	1		
6	O	1	Total	O	S	0	0
			5	4	1		

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.

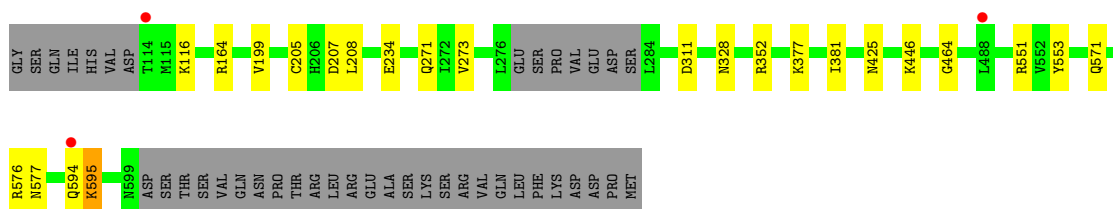
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

Chain A: 



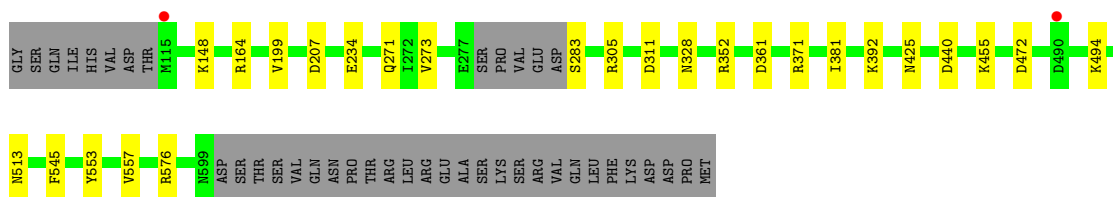
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

Chain B: 




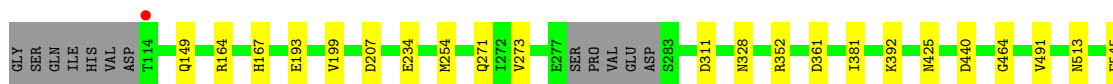
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

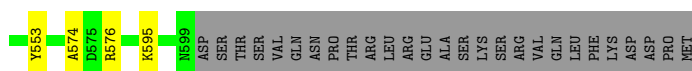
Chain C: 



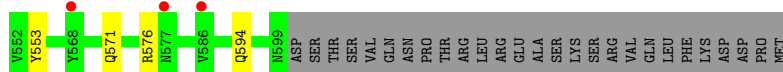
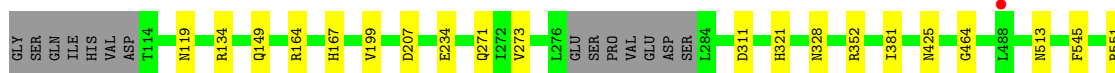
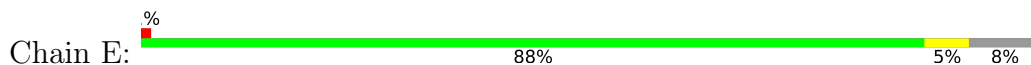
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

Chain D: 

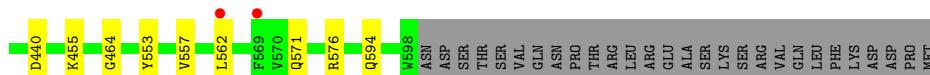
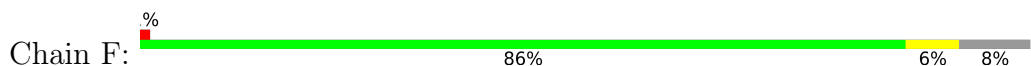




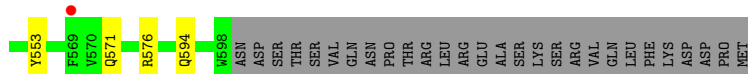
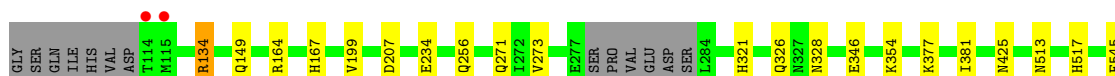
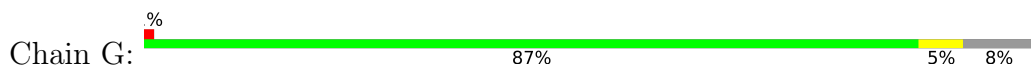
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



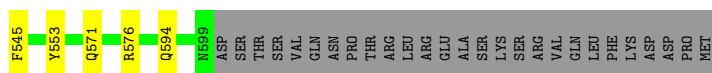
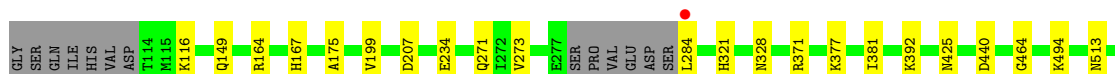
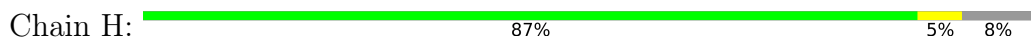
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



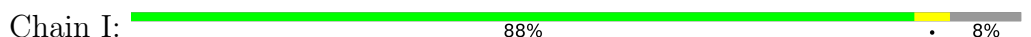
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

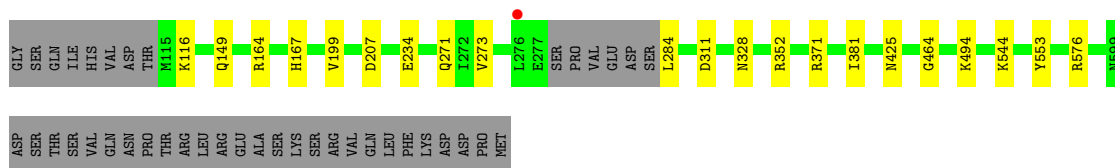


- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



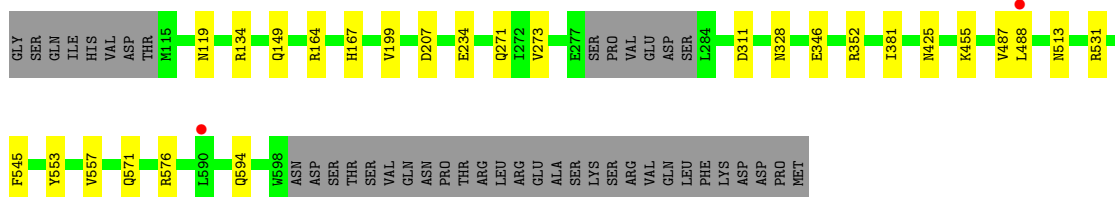
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1





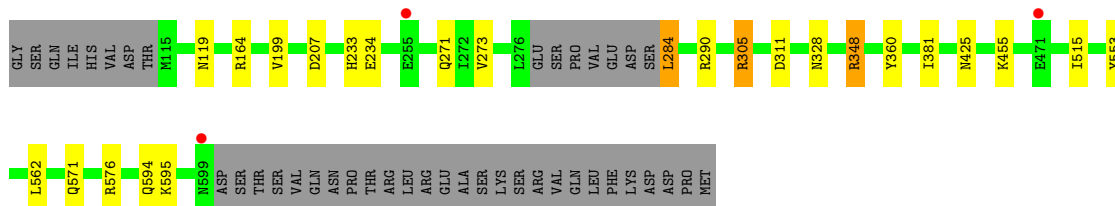
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

Chain J: 87% 5% 8%



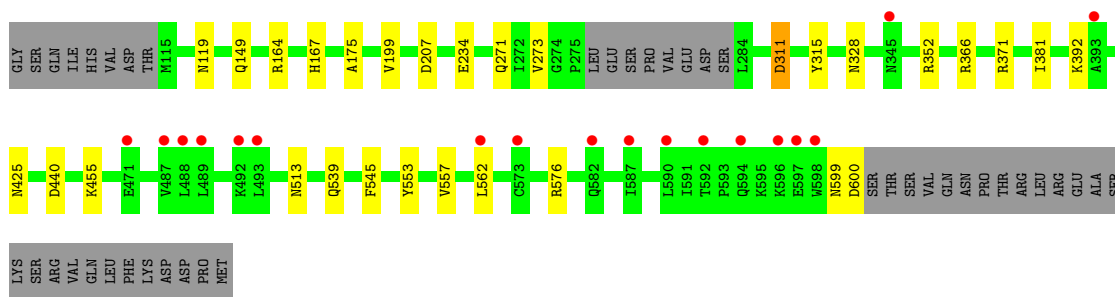
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

Chain K: 87% 8%



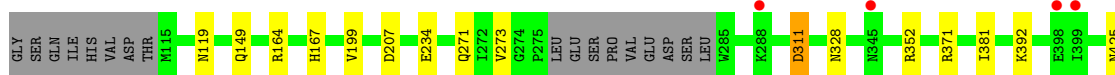
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

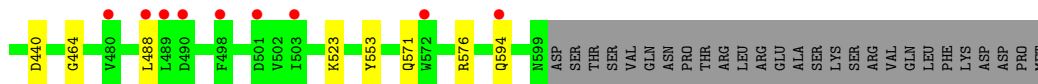
Chain L: 3% 86% 6% 8%



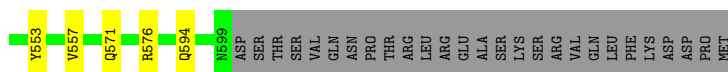
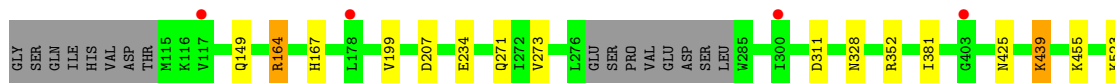
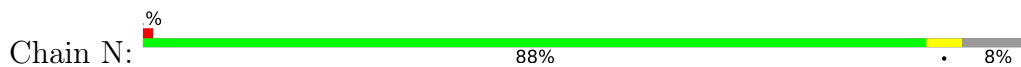
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

Chain M: 2% 87% 8%

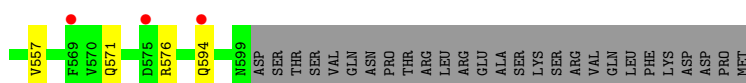
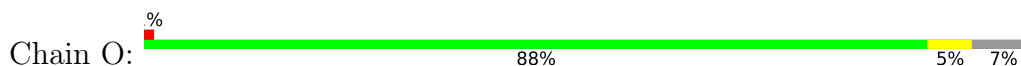




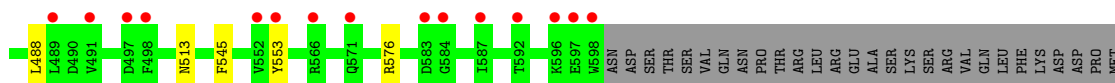
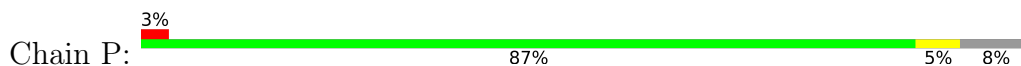
● Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



● Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



● Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	97.78Å 172.90Å 275.89Å 90.00° 95.20° 90.00°	Depositor
Resolution (Å)	146.24 – 2.85 274.75 – 2.84	Depositor EDS
% Data completeness (in resolution range)	66.4 (146.24-2.85) 65.8 (274.75-2.84)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 2.86Å)	Xtrriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.194 , 0.212 0.196 , 0.212	Depositor DCC
R_{free} test set	7031 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	49.5	Xtrriage
Anisotropy	0.060	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 37.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	62976	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.27% 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 i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: MG, XG4, FE, SO4, CZF

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	0.64	1/3955 (0.0%)	0.84	11/5356 (0.2%)
1	B	0.59	0/3938	0.79	6/5336 (0.1%)
1	C	0.60	0/3946	0.80	8/5344 (0.1%)
1	D	0.62	0/3945	0.81	7/5346 (0.1%)
1	E	0.57	0/3938	0.78	7/5336 (0.1%)
1	F	0.58	1/3924 (0.0%)	0.80	6/5320 (0.1%)
1	G	0.57	0/3923	0.79	5/5321 (0.1%)
1	H	0.60	0/3963	0.80	6/5364 (0.1%)
1	I	0.55	0/3936	0.77	5/5333 (0.1%)
1	J	0.57	0/3920	0.80	8/5313 (0.2%)
1	K	0.56	1/3921 (0.0%)	0.83	9/5316 (0.2%)
1	L	0.56	0/3882	0.78	6/5272 (0.1%)
1	M	0.53	0/3873	0.76	6/5258 (0.1%)
1	N	0.57	0/3911	0.78	5/5302 (0.1%)
1	O	0.54	0/3962	0.78	6/5379 (0.1%)
1	P	0.54	0/3886	0.80	8/5275 (0.2%)
All	All	0.57	3/62823 (0.0%)	0.79	109/85171 (0.1%)

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	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	K	305	ARG	NE-CZ	-5.57	1.25	1.33
1	F	346	GLU	CD-OE2	-5.17	1.20	1.25
1	A	355	GLU	CD-OE1	5.03	1.31	1.25

All (109) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	305	ARG	NE-CZ-NH2	16.28	128.44	120.30
1	D	164	ARG	NE-CZ-NH1	11.82	126.21	120.30
1	J	164	ARG	NE-CZ-NH1	11.38	125.99	120.30
1	L	164	ARG	NE-CZ-NH1	11.24	125.92	120.30
1	H	164	ARG	NE-CZ-NH1	11.13	125.86	120.30
1	P	164	ARG	NE-CZ-NH1	10.88	125.74	120.30
1	N	164	ARG	NE-CZ-NH1	10.73	125.67	120.30
1	H	164	ARG	NE-CZ-NH2	-9.36	115.62	120.30
1	N	164	ARG	NE-CZ-NH2	-9.32	115.64	120.30
1	L	164	ARG	NE-CZ-NH2	-9.29	115.66	120.30
1	P	164	ARG	NE-CZ-NH2	-9.25	115.68	120.30
1	D	164	ARG	NE-CZ-NH2	-8.93	115.83	120.30
1	J	164	ARG	NE-CZ-NH2	-8.80	115.90	120.30
1	G	164	ARG	NE-CZ-NH2	8.52	124.56	120.30
1	C	164	ARG	NE-CZ-NH2	8.29	124.45	120.30
1	K	164	ARG	NE-CZ-NH2	8.22	124.41	120.30
1	E	164	ARG	NE-CZ-NH2	8.09	124.35	120.30
1	I	164	ARG	NE-CZ-NH2	8.07	124.33	120.30
1	F	290	ARG	NE-CZ-NH2	8.04	124.32	120.30
1	F	164	ARG	NE-CZ-NH2	8.00	124.30	120.30
1	O	164	ARG	NE-CZ-NH2	7.89	124.25	120.30
1	G	164	ARG	NE-CZ-NH1	-7.87	116.36	120.30
1	I	164	ARG	NE-CZ-NH1	-7.79	116.40	120.30
1	M	164	ARG	NE-CZ-NH2	7.77	124.18	120.30
1	M	164	ARG	NE-CZ-NH1	-7.70	116.45	120.30
1	F	207	ASP	CB-CG-OD1	7.66	125.19	118.30
1	A	164	ARG	NE-CZ-NH2	7.64	124.12	120.30
1	F	164	ARG	NE-CZ-NH1	-7.64	116.48	120.30
1	O	164	ARG	NE-CZ-NH1	-7.63	116.48	120.30
1	D	207	ASP	CB-CG-OD1	7.61	125.14	118.30
1	E	164	ARG	NE-CZ-NH1	-7.58	116.51	120.30
1	G	207	ASP	CB-CG-OD1	7.56	125.10	118.30
1	D	254	MET	CG-SD-CE	7.54	112.27	100.20
1	H	207	ASP	CB-CG-OD1	7.53	125.08	118.30
1	K	164	ARG	NE-CZ-NH1	-7.53	116.54	120.30
1	B	207	ASP	CB-CG-OD1	7.51	125.06	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	164	ARG	NE-CZ-NH2	7.51	124.05	120.30
1	A	305	ARG	NE-CZ-NH1	7.50	124.05	120.30
1	C	207	ASP	CB-CG-OD1	7.49	125.04	118.30
1	K	207	ASP	CB-CG-OD1	7.46	125.01	118.30
1	I	207	ASP	CB-CG-OD1	7.44	125.00	118.30
1	O	207	ASP	CB-CG-OD1	7.39	124.95	118.30
1	E	207	ASP	CB-CG-OD1	7.38	124.94	118.30
1	J	207	ASP	CB-CG-OD1	7.34	124.91	118.30
1	A	207	ASP	CB-CG-OD1	7.31	124.88	118.30
1	P	290	ARG	NE-CZ-NH2	7.27	123.94	120.30
1	P	207	ASP	CB-CG-OD1	7.26	124.83	118.30
1	L	207	ASP	CB-CG-OD1	7.24	124.81	118.30
1	K	290	ARG	NE-CZ-NH2	7.23	123.92	120.30
1	N	207	ASP	CB-CG-OD1	7.21	124.78	118.30
1	M	207	ASP	CB-CG-OD1	7.18	124.77	118.30
1	A	164	ARG	NE-CZ-NH1	-7.17	116.72	120.30
1	A	290	ARG	NE-CZ-NH2	7.16	123.88	120.30
1	F	148	LYS	CD-CE-NZ	7.10	128.03	111.70
1	B	164	ARG	NE-CZ-NH1	-7.03	116.78	120.30
1	C	164	ARG	NE-CZ-NH1	-6.99	116.80	120.30
1	K	305	ARG	CD-NE-CZ	6.98	133.38	123.60
1	A	490	ASP	CB-CG-OD2	6.97	124.57	118.30
1	P	134	ARG	NE-CZ-NH1	6.92	123.76	120.30
1	C	371	ARG	NE-CZ-NH2	-6.76	116.92	120.30
1	A	134	ARG	NE-CZ-NH1	6.60	123.60	120.30
1	C	371	ARG	NE-CZ-NH1	6.57	123.58	120.30
1	K	305	ARG	NH1-CZ-NH2	-6.56	112.18	119.40
1	O	531	ARG	NE-CZ-NH1	-6.50	117.05	120.30
1	E	134	ARG	NE-CZ-NH1	6.49	123.54	120.30
1	P	429	GLU	CG-CD-OE1	-6.15	106.01	118.30
1	L	366	ARG	NE-CZ-NH2	-6.14	117.23	120.30
1	K	348	ARG	NE-CZ-NH2	-6.04	117.28	120.30
1	A	148	LYS	CD-CE-NZ	5.95	125.39	111.70
1	M	371	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	P	429	GLU	OE1-CD-OE2	5.91	130.39	123.30
1	E	551	ARG	NE-CZ-NH1	-5.85	117.38	120.30
1	A	490	ASP	CB-CG-OD1	-5.82	113.06	118.30
1	N	439	LYS	CD-CE-NZ	5.77	124.98	111.70
1	J	346	GLU	OE1-CD-OE2	-5.73	116.42	123.30
1	A	346	GLU	OE1-CD-OE2	-5.70	116.46	123.30
1	G	346	GLU	OE1-CD-OE2	-5.66	116.51	123.30
1	B	595	LYS	CD-CE-NZ	5.65	124.69	111.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	305	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	H	371	ARG	NE-CZ-NH2	-5.55	117.52	120.30
1	B	551	ARG	NE-CZ-NH1	-5.54	117.53	120.30
1	C	148	LYS	CD-CE-NZ	5.52	124.39	111.70
1	A	361	ASP	CB-CG-OD2	-5.49	113.36	118.30
1	E	207	ASP	CB-CG-OD2	-5.40	113.44	118.30
1	K	305	ARG	CG-CD-NE	-5.36	100.56	111.80
1	G	134	ARG	NE-CZ-NH2	-5.31	117.64	120.30
1	J	531	ARG	NE-CZ-NH1	5.31	122.95	120.30
1	L	371	ARG	NE-CZ-NH2	-5.29	117.66	120.30
1	P	488	LEU	CB-CG-CD2	5.28	119.98	111.00
1	D	464	GLY	N-CA-C	-5.27	99.92	113.10
1	O	361	ASP	CB-CG-OD1	5.23	123.00	118.30
1	J	134	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	J	207	ASP	CB-CG-OD2	-5.20	113.62	118.30
1	M	464	GLY	N-CA-C	-5.20	100.10	113.10
1	L	311	ASP	CB-CG-OD2	-5.18	113.64	118.30
1	F	464	GLY	N-CA-C	-5.18	100.15	113.10
1	M	311	ASP	CB-CG-OD2	-5.17	113.64	118.30
1	N	207	ASP	CB-CG-OD2	-5.16	113.66	118.30
1	I	464	GLY	N-CA-C	-5.14	100.24	113.10
1	D	193	GLU	OE1-CD-OE2	-5.13	117.14	123.30
1	H	284	LEU	CB-CG-CD2	-5.13	102.28	111.00
1	D	361	ASP	CB-CG-OD1	5.12	122.91	118.30
1	E	464	GLY	N-CA-C	-5.10	100.36	113.10
1	B	464	GLY	N-CA-C	-5.07	100.42	113.10
1	O	551	ARG	NE-CZ-NH1	-5.06	117.77	120.30
1	H	464	GLY	N-CA-C	-5.05	100.47	113.10
1	I	371	ARG	NE-CZ-NH1	5.05	122.83	120.30
1	J	134	ARG	NE-CZ-NH2	-5.03	117.78	120.30
1	C	361	ASP	CB-CG-OD1	5.02	122.82	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	487	VAL	Mainchain
1	C	283	SER	Peptide

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	3862	0	3768	18	0
1	B	3845	0	3742	16	0
1	C	3853	0	3758	11	1
1	D	3852	0	3745	14	0
1	E	3845	0	3742	17	0
1	F	3831	0	3713	21	0
1	G	3830	0	3698	15	0
1	H	3870	0	3792	16	0
1	I	3843	0	3735	14	0
1	J	3827	0	3716	24	0
1	K	3828	0	3706	23	0
1	L	3789	0	3621	23	0
1	M	3780	0	3621	25	0
1	N	3818	0	3695	16	0
1	O	3867	0	3722	21	0
1	P	3793	0	3650	15	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
2	M	1	0	0	0	0
2	N	1	0	0	0	0
2	O	1	0	0	0	0
2	P	1	0	0	0	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
3	M	3	0	0	0	0
3	N	3	0	0	0	0
3	O	3	0	0	0	0
3	P	3	0	0	0	0
4	A	62	0	26	2	0
4	B	62	0	26	3	0
4	C	62	0	26	5	0
4	D	62	0	26	3	0
4	E	62	0	26	3	0
4	F	62	0	26	3	0
4	G	62	0	26	5	0
4	H	62	0	26	1	0
4	I	93	0	39	9	0
4	J	62	0	26	4	0
4	K	62	0	26	4	0
4	L	31	0	13	2	0
4	M	62	0	26	6	0
4	N	62	0	26	6	0
4	O	62	0	26	4	0
4	P	62	0	26	5	0
5	A	32	0	0	2	0
5	B	32	0	0	1	0
5	C	64	0	0	1	0
5	E	32	0	0	1	0
5	F	32	0	0	1	0
5	G	32	0	0	0	0
5	H	32	0	0	2	0
5	J	64	0	0	3	0
5	K	32	0	0	1	0
5	L	32	0	0	0	0
5	M	32	0	0	0	0
5	N	32	0	0	1	0
5	O	32	0	0	2	0
5	P	32	0	0	2	0
6	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	5	0	0	0	0
6	C	5	0	0	0	0
6	D	5	0	0	0	0
6	E	5	0	0	0	0
6	F	5	0	0	0	0
6	G	5	0	0	1	0
6	H	5	0	0	0	0
6	I	5	0	0	0	0
6	J	5	0	0	0	0
6	K	5	0	0	0	0
6	L	5	0	0	0	0
6	M	5	0	0	0	0
6	N	5	0	0	0	0
6	O	5	0	0	0	0
All	All	62976	0	59840	270	1

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 2.

All (270) 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:N:352:ARG:NH2	4:N:708:XG4:O2G	2.08	0.85
1:K:305:ARG:HH11	1:K:348:ARG:CD	1.97	0.78
1:J:488:LEU:N	1:M:488:LEU:HB2	1.99	0.77
1:M:523:LYS:NZ	5:O:707:CZF:O13	2.16	0.77
1:K:305:ARG:NH1	1:K:348:ARG:NE	2.34	0.75
1:K:305:ARG:HH11	1:K:348:ARG:HD3	1.53	0.74
1:I:116:LYS:NZ	5:J:701:CZF:O1	2.21	0.72
1:B:577:ASN:OD1	1:B:595:LYS:NZ	2.18	0.72
1:F:326:GLN:HE21	1:G:326:GLN:CB	2.03	0.71
1:M:352:ARG:NH2	4:M:708:XG4:O3G	2.24	0.71
1:P:311:ASP:OD2	4:P:706:XG4:N3A	2.26	0.69
1:N:523:LYS:NZ	5:P:707:CZF:O14	2.26	0.69
1:M:352:ARG:NH1	4:M:708:XG4:O3G	2.26	0.68
1:G:517:HIS:ND1	6:G:708:SO4:O3	2.21	0.67
1:C:311:ASP:OD2	4:C:706:XG4:N3A	2.28	0.67
1:H:116:LYS:HE2	5:H:707:CZF:O9	1.94	0.67
1:B:116:LYS:NZ	5:B:706:CZF:O1	2.28	0.67
5:E:706:CZF:O12	4:G:701:XG4:O3G	2.12	0.66
1:E:425:ASN:OD1	1:F:425:ASN:ND2	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:328:ASN:HB2	1:L:328:ASN:HB2	1.79	0.64
4:E:708:XG4:O2B	1:H:377:LYS:NZ	2.29	0.64
1:I:311:ASP:OD2	4:I:705:XG4:N3A	2.31	0.64
1:K:455:LYS:CB	1:K:562:LEU:HD21	2.28	0.64
1:I:425:ASN:OD1	1:J:425:ASN:ND2	2.30	0.63
1:O:425:ASN:ND2	1:P:425:ASN:OD1	2.32	0.62
1:L:599:ASN:O	1:L:600:ASP:CB	2.47	0.62
1:E:119:ASN:HD21	4:G:701:XG4:HN2A	1.48	0.62
1:F:455:LYS:CB	1:F:562:LEU:HD21	2.29	0.62
1:K:233:HIS:CE1	4:K:706:XG4:O1A	2.52	0.61
4:I:707:XG4:O3G	1:L:352:ARG:NH1	2.33	0.61
1:K:425:ASN:ND2	1:L:425:ASN:OD1	2.33	0.61
1:G:425:ASN:ND2	1:H:425:ASN:OD1	2.34	0.61
1:M:425:ASN:ND2	1:N:425:ASN:OD1	2.33	0.61
4:N:708:XG4:H2'A	1:O:157:PHE:CE1	2.36	0.61
1:E:352:ARG:NH2	4:E:708:XG4:O2G	2.32	0.60
1:L:455:LYS:CB	1:L:562:LEU:HD21	2.31	0.60
1:J:352:ARG:NH2	4:J:709:XG4:O2G	2.34	0.60
1:K:305:ARG:NH1	1:K:348:ARG:CD	2.65	0.60
1:G:199:VAL:HG22	1:G:271:GLN:HE22	1.67	0.60
5:J:701:CZF:O12	4:K:701:XG4:O1G	2.18	0.60
1:B:199:VAL:HG22	1:B:271:GLN:HE22	1.67	0.59
1:C:199:VAL:HG22	1:C:271:GLN:HE22	1.68	0.59
1:K:199:VAL:HG22	1:K:271:GLN:HE22	1.68	0.59
1:A:199:VAL:HG22	1:A:271:GLN:HE22	1.68	0.59
1:D:199:VAL:HG22	1:D:271:GLN:HE22	1.67	0.59
1:I:352:ARG:NH1	4:I:708:XG4:O2G	2.23	0.59
1:A:352:ARG:NH1	4:A:708:XG4:O2G	2.35	0.59
1:F:199:VAL:HG22	1:F:271:GLN:HE22	1.68	0.59
4:M:708:XG4:HN2A	1:O:119:ASN:ND2	2.00	0.59
1:H:199:VAL:HG22	1:H:271:GLN:HE22	1.67	0.59
1:L:199:VAL:HG22	1:L:271:GLN:HE22	1.68	0.59
1:O:199:VAL:HG22	1:O:271:GLN:HE22	1.67	0.58
1:D:491:VAL:HG13	1:G:256:GLN:O	2.03	0.58
1:J:199:VAL:HG22	1:J:271:GLN:HE22	1.68	0.58
1:M:119:ASN:ND2	4:O:701:XG4:HN2A	2.01	0.58
1:N:199:VAL:HG22	1:N:271:GLN:HE22	1.67	0.58
1:E:199:VAL:HG22	1:E:271:GLN:HE22	1.68	0.58
1:G:571:GLN:HE22	1:G:594:GLN:NE2	2.02	0.58
1:N:571:GLN:HE22	1:N:594:GLN:HE22	1.52	0.58
1:P:199:VAL:HG22	1:P:271:GLN:HE22	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:199:VAL:HG22	1:M:271:GLN:HE22	1.67	0.57
1:E:119:ASN:ND2	4:G:701:XG4:HN2A	2.02	0.57
1:H:571:GLN:HE22	1:H:594:GLN:NE2	2.02	0.57
1:J:328:ASN:HB2	1:K:328:ASN:HB2	1.86	0.57
1:F:311:ASP:OD2	4:F:705:XG4:N3A	2.33	0.57
1:A:485:PRO:HG2	1:A:489:LEU:HD11	1.87	0.57
1:K:455:LYS:HB2	1:K:562:LEU:HD21	1.86	0.57
1:I:199:VAL:HG22	1:I:271:GLN:HE22	1.68	0.57
1:L:455:LYS:HB2	1:L:562:LEU:HD21	1.87	0.57
1:K:233:HIS:NE2	4:K:706:XG4:O1A	2.38	0.56
1:B:352:ARG:NH1	4:B:708:XG4:O3G	2.36	0.56
1:F:571:GLN:HE22	1:F:594:GLN:HE22	1.54	0.56
4:I:707:XG4:O3G	1:L:352:ARG:NH2	2.38	0.56
1:D:392:LYS:HD3	1:D:440:ASP:HB3	1.87	0.56
1:M:352:ARG:CZ	4:M:708:XG4:O3G	2.53	0.56
1:G:354:LYS:NZ	4:G:701:XG4:O2A	2.26	0.56
1:F:352:ARG:NH2	4:F:708:XG4:O2G	2.32	0.55
1:F:455:LYS:HB2	1:F:562:LEU:HD21	1.86	0.55
1:B:328:ASN:HB2	1:C:328:ASN:HB2	1.89	0.54
1:B:571:GLN:HE22	1:B:594:GLN:HE22	1.55	0.54
4:I:708:XG4:HN2A	1:K:119:ASN:ND2	2.05	0.54
4:B:708:XG4:O1B	5:C:709:CZF:O3	2.26	0.54
1:C:425:ASN:OD1	1:D:425:ASN:ND2	2.40	0.54
1:N:311:ASP:OD2	4:N:705:XG4:N3A	2.40	0.54
1:A:485:PRO:HG2	1:A:489:LEU:CD1	2.38	0.54
1:J:571:GLN:HE22	1:J:594:GLN:HE22	1.56	0.54
1:N:328:ASN:HB2	1:O:328:ASN:HB2	1.90	0.54
1:O:571:GLN:HE22	1:O:594:GLN:HE22	1.55	0.54
4:J:709:XG4:HN2A	1:L:119:ASN:ND2	2.07	0.53
1:K:571:GLN:NE2	1:K:594:GLN:HE22	2.07	0.53
1:E:571:GLN:HE22	1:E:594:GLN:HE22	1.55	0.53
1:A:116:LYS:NZ	5:A:706:CZF:O1	2.35	0.53
4:D:706:XG4:O1G	4:D:706:XG4:O2B	2.27	0.53
1:D:311:ASP:OD2	4:D:706:XG4:N3A	2.43	0.52
1:M:571:GLN:HE22	1:M:594:GLN:HE22	1.55	0.52
1:F:392:LYS:HD3	1:F:440:ASP:HB3	1.91	0.52
1:A:475:SER:HA	1:A:478:LYS:HD3	1.91	0.52
1:E:328:ASN:HB2	1:H:328:ASN:HB2	1.90	0.52
1:J:311:ASP:OD2	4:J:706:XG4:N3A	2.42	0.51
1:A:478:LYS:H	1:A:478:LYS:HD2	1.75	0.51
1:H:392:LYS:HD3	1:H:440:ASP:HB3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:328:ASN:HB2	1:P:328:ASN:HB2	1.91	0.51
1:A:328:ASN:HB2	1:D:328:ASN:HB2	1.93	0.51
1:O:311:ASP:OD2	4:O:706:XG4:N3A	2.41	0.51
1:O:116:LYS:NZ	5:O:707:CZF:O1	2.38	0.50
1:M:571:GLN:NE2	1:M:594:GLN:HE22	2.10	0.50
1:B:571:GLN:NE2	1:B:594:GLN:HE22	2.10	0.50
1:H:234:GLU:HB3	1:H:273:VAL:HG12	1.94	0.50
1:L:234:GLU:HB3	1:L:273:VAL:HG12	1.93	0.49
1:F:571:GLN:NE2	1:F:594:GLN:HE22	2.09	0.49
1:L:315:TYR:CG	4:L:705:XG4:H3'	2.47	0.49
1:N:234:GLU:HB3	1:N:273:VAL:HG12	1.94	0.49
1:H:116:LYS:CE	5:H:707:CZF:O9	2.59	0.49
1:J:381:ILE:HD13	1:J:553:TYR:CG	2.47	0.49
1:N:571:GLN:NE2	1:N:594:GLN:HE22	2.09	0.49
1:J:488:LEU:HB2	1:M:488:LEU:HA	1.93	0.49
1:A:381:ILE:HD13	1:A:553:TYR:CG	2.47	0.49
1:C:381:ILE:HD13	1:C:553:TYR:CG	2.48	0.49
1:P:234:GLU:HB3	1:P:273:VAL:HG12	1.95	0.49
1:E:571:GLN:NE2	1:E:594:GLN:HE22	2.10	0.49
4:I:707:XG4:HN2A	1:J:119:ASN:ND2	2.10	0.49
1:J:488:LEU:HB2	1:M:488:LEU:CA	2.43	0.49
1:B:311:ASP:OD2	4:B:705:XG4:N3A	2.46	0.49
1:D:381:ILE:HD13	1:D:553:TYR:CG	2.48	0.49
1:I:381:ILE:HD13	1:I:553:TYR:CG	2.48	0.49
1:J:234:GLU:HB3	1:J:273:VAL:HG12	1.95	0.49
1:K:594:GLN:HG3	1:K:595:LYS:N	2.27	0.49
1:M:381:ILE:HD13	1:M:553:TYR:CG	2.47	0.48
1:M:234:GLU:HB3	1:M:273:VAL:HG12	1.95	0.48
1:P:381:ILE:HD13	1:P:553:TYR:CG	2.48	0.48
1:O:571:GLN:NE2	1:O:594:GLN:HE22	2.10	0.48
1:J:488:LEU:HA	1:M:488:LEU:HD13	1.94	0.48
1:K:381:ILE:HD13	1:K:553:TYR:CG	2.48	0.48
1:L:311:ASP:OD2	4:L:705:XG4:N3A	2.44	0.48
1:O:381:ILE:HD13	1:O:553:TYR:CG	2.49	0.48
1:B:381:ILE:HD13	1:B:553:TYR:CG	2.49	0.48
1:F:381:ILE:HD13	1:F:553:TYR:CG	2.48	0.48
1:L:381:ILE:HD13	1:L:553:TYR:CG	2.49	0.48
1:P:352:ARG:NH1	4:P:701:XG4:O3G	2.37	0.48
1:E:381:ILE:HD13	1:E:553:TYR:CG	2.49	0.47
1:H:381:ILE:HD13	1:H:553:TYR:CG	2.48	0.47
1:E:234:GLU:HB3	1:E:273:VAL:HG12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:455:LYS:HE3	1:F:557:VAL:HG13	1.96	0.47
1:J:571:GLN:NE2	1:J:594:GLN:HE22	2.11	0.47
1:N:381:ILE:HD13	1:N:553:TYR:CG	2.49	0.47
1:F:326:GLN:NE2	1:G:326:GLN:CB	2.75	0.47
1:G:234:GLU:HB3	1:G:273:VAL:HG12	1.95	0.47
1:G:381:ILE:HD13	1:G:553:TYR:CG	2.49	0.47
1:I:234:GLU:HB3	1:I:273:VAL:HG12	1.96	0.47
4:M:708:XG4:HN2A	1:O:119:ASN:HD21	1.63	0.47
1:A:392:LYS:HD3	1:A:440:ASP:HB3	1.97	0.47
1:F:234:GLU:HB3	1:F:273:VAL:HG12	1.96	0.47
1:K:234:GLU:HB3	1:K:273:VAL:HG12	1.96	0.47
1:B:234:GLU:HB3	1:B:273:VAL:HG12	1.97	0.46
4:I:708:XG4:O3G	5:K:707:CZF:O12	2.32	0.46
1:J:488:LEU:CA	1:M:488:LEU:HB2	2.44	0.46
4:N:708:XG4:H2'A	1:O:157:PHE:CD1	2.49	0.46
4:C:706:XG4:H5'	4:C:706:XG4:H8	1.97	0.46
1:O:234:GLU:HB3	1:O:273:VAL:HG12	1.96	0.46
1:O:455:LYS:HE3	1:O:557:VAL:HG13	1.97	0.46
1:K:284:LEU:HD12	1:K:284:LEU:N	2.31	0.46
1:M:311:ASP:OD2	4:M:705:XG4:N3A	2.47	0.46
1:A:234:GLU:HB3	1:A:273:VAL:HG12	1.98	0.46
1:J:487:VAL:C	1:M:488:LEU:HB2	2.36	0.46
1:O:233:HIS:NE2	4:O:706:XG4:O1A	2.49	0.45
5:A:706:CZF:O12	4:C:701:XG4:O1G	2.35	0.45
1:C:352:ARG:NH2	4:C:701:XG4:O2G	2.37	0.45
1:N:571:GLN:HE22	1:N:594:GLN:NE2	2.14	0.45
1:A:311:ASP:OD2	4:A:705:XG4:N3A	2.49	0.45
1:C:381:ILE:HD13	1:C:553:TYR:CD2	2.52	0.45
1:D:574:ALA:HB1	1:D:595:LYS:HD3	1.98	0.45
1:I:116:LYS:HE2	5:J:701:CZF:O9	2.17	0.45
4:H:706:XG4:O2B	4:H:706:XG4:O1G	2.35	0.45
1:A:425:ASN:ND2	1:B:425:ASN:OD1	2.50	0.45
1:J:488:LEU:HB2	1:M:488:LEU:N	2.32	0.45
1:P:513:ASN:HB2	1:P:545:PHE:CE2	2.52	0.45
1:B:571:GLN:HE22	1:B:594:GLN:NE2	2.16	0.45
1:K:311:ASP:OD2	4:K:706:XG4:N3A	2.44	0.44
1:F:381:ILE:HD13	1:F:553:TYR:CD2	2.52	0.44
4:J:709:XG4:HN2A	1:L:119:ASN:HD21	1.65	0.44
1:E:321:HIS:CE1	1:F:321:HIS:CE1	3.05	0.44
1:I:284:LEU:N	1:I:284:LEU:HD12	2.33	0.44
1:M:381:ILE:HD13	1:M:553:TYR:CD2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:513:ASN:HB2	1:C:545:PHE:CE2	2.53	0.44
1:K:381:ILE:HD13	1:K:553:TYR:CD2	2.53	0.44
1:E:311:ASP:OD2	4:E:705:XG4:N3A	2.41	0.44
1:F:157:PHE:CE1	4:G:701:XG4:H1'	2.53	0.44
1:C:234:GLU:HB3	1:C:273:VAL:HG12	2.00	0.44
1:O:381:ILE:HD13	1:O:553:TYR:CD2	2.53	0.44
1:A:381:ILE:HD13	1:A:553:TYR:CD2	2.52	0.44
1:C:392:LYS:HD3	1:C:440:ASP:HB3	2.00	0.44
1:L:513:ASN:HB2	1:L:545:PHE:CE2	2.53	0.44
1:F:571:GLN:HE22	1:F:594:GLN:NE2	2.15	0.43
1:L:381:ILE:HD13	1:L:553:TYR:CD2	2.54	0.43
1:E:571:GLN:HE22	1:E:594:GLN:NE2	2.16	0.43
1:H:513:ASN:HB2	1:H:545:PHE:CE2	2.54	0.43
1:B:381:ILE:HD13	1:B:553:TYR:CD2	2.53	0.43
1:I:381:ILE:HD13	1:I:553:TYR:CD2	2.53	0.43
1:J:513:ASN:HB2	1:J:545:PHE:CE2	2.53	0.43
1:P:381:ILE:HD13	1:P:553:TYR:CD2	2.53	0.43
1:I:544:LYS:HD2	1:L:539:GLN:HB3	2.00	0.43
1:J:381:ILE:HD13	1:J:553:TYR:CD2	2.53	0.43
1:H:381:ILE:HD13	1:H:553:TYR:CD2	2.53	0.43
1:D:381:ILE:HD13	1:D:553:TYR:CD2	2.53	0.43
1:M:571:GLN:HE22	1:M:594:GLN:NE2	2.16	0.43
1:A:485:PRO:CG	1:A:489:LEU:HD11	2.48	0.43
1:D:234:GLU:HB3	1:D:273:VAL:HG12	2.00	0.43
1:D:513:ASN:HB2	1:D:545:PHE:CE2	2.53	0.43
1:E:513:ASN:HB2	1:E:545:PHE:CE2	2.53	0.43
4:F:708:XG4:O2B	1:G:377:LYS:NZ	2.50	0.43
1:O:352:ARG:NH1	4:O:701:XG4:O3G	2.40	0.43
1:G:513:ASN:HB2	1:G:545:PHE:CE2	2.53	0.43
1:H:199:VAL:HG22	1:H:271:GLN:NE2	2.34	0.43
1:F:116:LYS:NZ	5:F:706:CZF:O1	2.40	0.43
1:P:117:VAL:O	5:P:707:CZF:O2	2.37	0.43
1:P:315:TYR:CG	4:P:706:XG4:H3'	2.54	0.43
1:B:199:VAL:HG22	1:B:271:GLN:NE2	2.34	0.42
1:G:381:ILE:HD13	1:G:553:TYR:CD2	2.53	0.42
1:J:571:GLN:HE22	1:J:594:GLN:NE2	2.17	0.42
1:E:199:VAL:HG22	1:E:271:GLN:NE2	2.34	0.42
1:K:284:LEU:N	1:K:284:LEU:CD1	2.82	0.42
1:N:381:ILE:HD13	1:N:553:TYR:CD2	2.54	0.42
1:A:487:VAL:O	1:A:489:LEU:HG	2.20	0.42
1:E:381:ILE:HD13	1:E:553:TYR:CD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:455:LYS:HE3	1:J:557:VAL:HG13	2.00	0.42
1:M:199:VAL:HG22	1:M:271:GLN:NE2	2.34	0.42
4:N:708:XG4:O1A	1:O:376:HIS:NE2	2.42	0.42
1:M:392:LYS:HD3	1:M:440:ASP:HB3	2.00	0.42
1:N:164:ARG:NH1	4:N:705:XG4:O2A	2.43	0.42
5:N:706:CZF:O12	4:P:701:XG4:O1G	2.38	0.42
1:K:360:TYR:CE1	1:K:515:ILE:HG21	2.55	0.42
1:I:199:VAL:HG22	1:I:271:GLN:NE2	2.34	0.42
1:O:571:GLN:HE22	1:O:594:GLN:NE2	2.16	0.42
4:I:707:XG4:O3G	1:L:352:ARG:CZ	2.67	0.42
1:K:199:VAL:HG22	1:K:271:GLN:NE2	2.34	0.42
4:I:707:XG4:HN2A	1:J:119:ASN:HD21	1.68	0.41
1:L:392:LYS:HD3	1:L:440:ASP:HB3	2.02	0.41
1:A:455:LYS:HE3	1:A:557:VAL:HG13	2.02	0.41
1:B:377:LYS:NZ	4:C:701:XG4:O2B	2.48	0.41
1:N:455:LYS:HE2	1:N:557:VAL:HG13	2.01	0.41
1:F:199:VAL:HG22	1:F:271:GLN:NE2	2.34	0.41
1:A:285:TRP:HZ3	1:A:346:GLU:OE2	2.03	0.41
1:N:199:VAL:HG22	1:N:271:GLN:NE2	2.34	0.41
1:D:352:ARG:NH2	4:D:701:XG4:O2G	2.49	0.41
1:P:199:VAL:HG22	1:P:271:GLN:NE2	2.34	0.41
1:M:149:GLN:HE22	1:M:167:HIS:CG	2.39	0.41
1:O:199:VAL:HG22	1:O:271:GLN:NE2	2.34	0.41
1:E:149:GLN:HE22	1:E:167:HIS:CG	2.39	0.41
1:G:149:GLN:HE22	1:G:167:HIS:CG	2.39	0.41
1:H:175:ALA:HB1	1:H:199:VAL:HG12	2.03	0.41
1:J:149:GLN:HE22	1:J:167:HIS:CG	2.39	0.41
1:L:149:GLN:HE22	1:L:167:HIS:CG	2.39	0.41
1:P:175:ALA:HB1	1:P:199:VAL:HG12	2.03	0.41
1:H:149:GLN:HE22	1:H:167:HIS:CG	2.39	0.41
1:K:594:GLN:CG	1:K:595:LYS:N	2.84	0.41
1:L:199:VAL:HG22	1:L:271:GLN:NE2	2.34	0.41
1:L:455:LYS:HE3	1:L:557:VAL:HG13	2.03	0.41
1:N:149:GLN:HE22	1:N:167:HIS:CG	2.39	0.41
1:J:199:VAL:HG22	1:J:271:GLN:NE2	2.34	0.40
1:O:149:GLN:HE22	1:O:167:HIS:CG	2.39	0.40
1:P:149:GLN:HE22	1:P:167:HIS:CG	2.39	0.40
1:P:315:TYR:CD1	4:P:706:XG4:H3'	2.56	0.40
1:I:149:GLN:HE22	1:I:167:HIS:CG	2.39	0.40
1:D:574:ALA:O	1:D:595:LYS:HE2	2.20	0.40
1:F:149:GLN:HE22	1:F:167:HIS:CG	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:175:ALA:HB1	1:L:199:VAL:HG12	2.04	0.40
1:D:149:GLN:HE22	1:D:167:HIS:CG	2.39	0.40
1:B:205:CYS:HB3	1:B:208:LEU:HD12	2.04	0.40
1:C:455:LYS:HE3	1:C:557:VAL:HG13	2.02	0.40
1:G:321:HIS:CE1	1:H:321:HIS:CE1	3.09	0.40

All (1) 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:C:472:ASP:OD1	1:P:396:TYR:OH[1_565]	1.78	0.42

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	476/520 (92%)	459 (96%)	16 (3%)	1 (0%)	47	75
1	B	475/520 (91%)	460 (97%)	15 (3%)	0	100	100
1	C	476/520 (92%)	459 (96%)	17 (4%)	0	100	100
1	D	477/520 (92%)	461 (97%)	16 (3%)	0	100	100
1	E	475/520 (91%)	460 (97%)	15 (3%)	0	100	100
1	F	474/520 (91%)	459 (97%)	15 (3%)	0	100	100
1	G	475/520 (91%)	461 (97%)	14 (3%)	0	100	100
1	H	476/520 (92%)	461 (97%)	15 (3%)	0	100	100
1	I	475/520 (91%)	461 (97%)	14 (3%)	0	100	100
1	J	474/520 (91%)	462 (98%)	12 (2%)	0	100	100
1	K	474/520 (91%)	460 (97%)	14 (3%)	0	100	100
1	L	474/520 (91%)	460 (97%)	14 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	M	472/520 (91%)	456 (97%)	16 (3%)	0	100	100
1	N	473/520 (91%)	460 (97%)	13 (3%)	0	100	100
1	O	484/520 (93%)	466 (96%)	17 (4%)	1 (0%)	47	75
1	P	474/520 (91%)	459 (97%)	15 (3%)	0	100	100
All	All	7604/8320 (91%)	7364 (97%)	238 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	487	VAL
1	O	280	VAL

5.3.2 Protein sidechains [i](#)

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	411/464 (89%)	408 (99%)	3 (1%)	84	94
1	B	408/464 (88%)	406 (100%)	2 (0%)	88	96
1	C	409/464 (88%)	407 (100%)	2 (0%)	88	96
1	D	408/464 (88%)	407 (100%)	1 (0%)	93	98
1	E	408/464 (88%)	407 (100%)	1 (0%)	93	98
1	F	406/464 (88%)	405 (100%)	1 (0%)	93	98
1	G	404/464 (87%)	401 (99%)	3 (1%)	84	94
1	H	413/464 (89%)	411 (100%)	2 (0%)	88	96
1	I	407/464 (88%)	405 (100%)	2 (0%)	88	96
1	J	404/464 (87%)	403 (100%)	1 (0%)	93	98
1	K	405/464 (87%)	403 (100%)	2 (0%)	88	96
1	L	396/464 (85%)	395 (100%)	1 (0%)	92	97
1	M	396/464 (85%)	395 (100%)	1 (0%)	92	97
1	N	404/464 (87%)	402 (100%)	2 (0%)	88	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	O	408/464 (88%)	407 (100%)	1 (0%)	93	98
1	P	397/464 (86%)	396 (100%)	1 (0%)	92	97
All	All	6484/7424 (87%)	6458 (100%)	26 (0%)	91	96

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	446	LYS
1	A	478	LYS
1	A	576	ARG
1	B	446	LYS
1	B	576	ARG
1	C	494	LYS
1	C	576	ARG
1	D	576	ARG
1	E	576	ARG
1	F	576	ARG
1	G	134	ARG
1	G	328	ASN
1	G	576	ARG
1	H	494	LYS
1	H	576	ARG
1	I	494	LYS
1	I	576	ARG
1	J	576	ARG
1	K	284	LEU
1	K	576	ARG
1	L	576	ARG
1	M	576	ARG
1	N	439	LYS
1	N	576	ARG
1	O	576	ARG
1	P	576	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (69) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	271	GLN
1	A	375	GLN
1	A	380	ASN

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Mol	Chain	Res	Type
1	B	271	GLN
1	B	375	GLN
1	B	380	ASN
1	B	571	GLN
1	B	594	GLN
1	C	271	GLN
1	C	375	GLN
1	C	380	ASN
1	D	271	GLN
1	D	375	GLN
1	D	380	ASN
1	E	271	GLN
1	E	375	GLN
1	E	380	ASN
1	E	571	GLN
1	E	594	GLN
1	F	271	GLN
1	F	326	GLN
1	F	375	GLN
1	F	380	ASN
1	F	571	GLN
1	F	594	GLN
1	G	271	GLN
1	G	328	ASN
1	G	375	GLN
1	G	380	ASN
1	G	594	GLN
1	H	271	GLN
1	H	375	GLN
1	H	380	ASN
1	H	594	GLN
1	I	271	GLN
1	I	375	GLN
1	I	380	ASN
1	J	271	GLN
1	J	375	GLN
1	J	380	ASN
1	J	571	GLN
1	J	594	GLN
1	K	271	GLN
1	K	375	GLN
1	K	380	ASN

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Mol	Chain	Res	Type
1	K	571	GLN
1	K	594	GLN
1	L	271	GLN
1	L	375	GLN
1	L	380	ASN
1	M	271	GLN
1	M	375	GLN
1	M	380	ASN
1	M	571	GLN
1	M	594	GLN
1	N	271	GLN
1	N	375	GLN
1	N	380	ASN
1	N	571	GLN
1	N	594	GLN
1	O	163	ASN
1	O	271	GLN
1	O	375	GLN
1	O	380	ASN
1	O	571	GLN
1	O	594	GLN
1	P	271	GLN
1	P	375	GLN
1	P	380	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 127 ligands modelled in this entry, 64 are monoatomic - leaving 63 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
4	XG4	M	705	3,2	29,33,33	1.40	5 (17%)	35,52,52	1.42	4 (11%)
4	XG4	H	706	3,2	29,33,33	2.04	8 (27%)	35,52,52	2.06	8 (22%)
4	XG4	D	701	3	29,33,33	1.49	7 (24%)	35,52,52	1.72	6 (17%)
4	XG4	N	705	3,2	29,33,33	1.34	4 (13%)	35,52,52	1.67	7 (20%)
4	XG4	O	701	3	29,33,33	1.36	5 (17%)	35,52,52	1.53	5 (14%)
6	SO4	A	707	-	4,4,4	0.64	0	6,6,6	0.64	0
4	XG4	M	708	3	29,33,33	1.27	5 (17%)	35,52,52	1.31	4 (11%)
5	CZF	A	706	3	24,34,34	1.03	2 (8%)	33,54,54	1.55	4 (12%)
4	XG4	J	706	3,2	29,33,33	1.62	6 (20%)	35,52,52	2.13	7 (20%)
5	CZF	L	706	3	24,34,34	0.82	1 (4%)	33,54,54	1.75	5 (15%)
4	XG4	B	705	3,2	29,33,33	1.56	2 (6%)	35,52,52	1.62	8 (22%)
4	XG4	L	705	3,2	29,33,33	1.53	7 (24%)	35,52,52	1.51	6 (17%)
4	XG4	P	706	3,2	29,33,33	1.46	4 (13%)	35,52,52	1.97	8 (22%)
4	XG4	I	707	3	29,33,33	1.48	10 (34%)	35,52,52	1.34	4 (11%)
4	XG4	D	706	3,2	29,33,33	1.89	7 (24%)	35,52,52	2.22	9 (25%)
5	CZF	C	707	3	24,34,34	1.03	2 (8%)	33,54,54	1.69	4 (12%)
5	CZF	H	707	3	24,34,34	1.06	2 (8%)	33,54,54	1.38	3 (9%)
5	CZF	M	706	3	24,34,34	1.00	1 (4%)	33,54,54	1.54	4 (12%)
4	XG4	B	708	3	29,33,33	1.37	5 (17%)	35,52,52	1.98	5 (14%)
6	SO4	C	708	-	4,4,4	0.41	0	6,6,6	0.58	0
4	XG4	F	705	3,2	29,33,33	1.60	3 (10%)	35,52,52	1.71	6 (17%)
4	XG4	O	706	3,2	29,33,33	1.50	3 (10%)	35,52,52	1.67	7 (20%)
5	CZF	J	707	3	24,34,34	1.00	2 (8%)	33,54,54	1.62	3 (9%)
6	SO4	J	708	-	4,4,4	0.51	0	6,6,6	0.44	0
4	XG4	A	705	3,2	29,33,33	1.82	5 (17%)	35,52,52	2.20	7 (20%)
4	XG4	K	701	3	29,33,33	1.33	3 (10%)	35,52,52	1.94	9 (25%)
5	CZF	J	701	3	24,34,34	0.78	1 (4%)	33,54,54	1.57	4 (12%)
5	CZF	O	707	3	24,34,34	0.92	2 (8%)	33,54,54	1.62	4 (12%)
4	XG4	J	709	3	29,33,33	1.59	5 (17%)	35,52,52	1.71	5 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	XG4	G	701	3	29,33,33	1.52	5 (17%)	35,52,52	1.67	5 (14%)
5	CZF	C	709	3	24,34,34	0.99	2 (8%)	33,54,54	1.57	4 (12%)
5	CZF	P	707	3	24,34,34	0.94	2 (8%)	33,54,54	1.30	3 (9%)
5	CZF	F	706	3	24,34,34	0.91	2 (8%)	33,54,54	1.64	4 (12%)
6	SO4	E	707	-	4,4,4	0.48	0	6,6,6	0.76	0
6	SO4	L	707	-	4,4,4	0.42	0	6,6,6	0.51	0
6	SO4	O	708	-	4,4,4	0.61	0	6,6,6	0.44	0
6	SO4	F	707	-	4,4,4	0.57	0	6,6,6	0.71	0
6	SO4	H	708	-	4,4,4	0.72	0	6,6,6	0.29	0
6	SO4	K	708	-	4,4,4	0.34	0	6,6,6	0.27	0
6	SO4	N	707	-	4,4,4	0.38	0	6,6,6	0.43	0
5	CZF	B	706	3	24,34,34	1.03	2 (8%)	33,54,54	1.81	6 (18%)
5	CZF	E	706	3	24,34,34	0.90	2 (8%)	33,54,54	1.55	4 (12%)
4	XG4	E	708	3	29,33,33	1.48	6 (20%)	35,52,52	1.44	6 (17%)
5	CZF	N	706	3	24,34,34	0.85	1 (4%)	33,54,54	1.52	3 (9%)
6	SO4	G	708	-	4,4,4	0.50	0	6,6,6	0.60	0
4	XG4	N	708	3	29,33,33	1.41	6 (20%)	35,52,52	1.59	5 (14%)
5	CZF	G	707	3	24,34,34	1.04	2 (8%)	33,54,54	1.49	4 (12%)
4	XG4	H	701	3	29,33,33	1.36	4 (13%)	35,52,52	2.00	6 (17%)
4	XG4	C	706	3,2	29,33,33	1.88	7 (24%)	35,52,52	2.04	6 (17%)
4	XG4	C	701	3	29,33,33	1.45	7 (24%)	35,52,52	1.62	6 (17%)
4	XG4	E	705	3,2	29,33,33	1.63	6 (20%)	35,52,52	2.00	7 (20%)
4	XG4	P	701	3	29,33,33	1.34	5 (17%)	35,52,52	1.54	4 (11%)
6	SO4	M	707	-	4,4,4	0.50	0	6,6,6	0.55	0
4	XG4	F	708	3	29,33,33	1.28	5 (17%)	35,52,52	1.55	5 (14%)
4	XG4	I	705	3,2	29,33,33	1.51	4 (13%)	35,52,52	1.74	6 (17%)
4	XG4	K	706	3,2	29,33,33	1.41	4 (13%)	35,52,52	1.36	3 (8%)
4	XG4	G	706	3,2	29,33,33	1.74	6 (20%)	35,52,52	1.91	6 (17%)
4	XG4	I	708	3	29,33,33	1.35	6 (20%)	35,52,52	1.40	4 (11%)
4	XG4	A	708	3	29,33,33	1.49	5 (17%)	35,52,52	1.60	7 (20%)
5	CZF	K	707	3	24,34,34	1.02	2 (8%)	33,54,54	1.33	4 (12%)
6	SO4	B	707	-	4,4,4	0.43	0	6,6,6	0.50	0
6	SO4	D	707	-	4,4,4	0.47	0	6,6,6	0.40	0
6	SO4	I	706	-	4,4,4	0.50	0	6,6,6	0.44	0

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
4	XG4	M	705	3,2	-	4/15/34/34	0/3/3/3
4	XG4	H	706	3,2	-	4/15/34/34	0/3/3/3
4	XG4	D	701	3	-	2/15/34/34	0/3/3/3
4	XG4	N	705	3,2	-	2/15/34/34	0/3/3/3
4	XG4	O	701	3	-	4/15/34/34	0/3/3/3
4	XG4	M	708	3	-	6/15/34/34	0/3/3/3
5	CZF	A	706	3	-	4/18/38/38	0/3/3/3
4	XG4	J	706	3,2	-	5/15/34/34	0/3/3/3
5	CZF	L	706	3	-	5/18/38/38	0/3/3/3
4	XG4	B	705	3,2	-	4/15/34/34	0/3/3/3
4	XG4	L	705	3,2	-	4/15/34/34	0/3/3/3
4	XG4	P	706	3,2	-	3/15/34/34	0/3/3/3
4	XG4	I	707	3	-	4/15/34/34	0/3/3/3
4	XG4	D	706	3,2	-	3/15/34/34	0/3/3/3
5	CZF	C	707	3	-	7/18/38/38	0/3/3/3
5	CZF	H	707	3	-	6/18/38/38	0/3/3/3
5	CZF	M	706	3	-	6/18/38/38	0/3/3/3
4	XG4	B	708	3	-	4/15/34/34	0/3/3/3
4	XG4	F	705	3,2	-	3/15/34/34	0/3/3/3
4	XG4	O	706	3,2	-	4/15/34/34	0/3/3/3
5	CZF	J	707	3	-	3/18/38/38	0/3/3/3
4	XG4	A	705	3,2	-	2/15/34/34	0/3/3/3
4	XG4	K	701	3	-	1/15/34/34	0/3/3/3
5	CZF	J	701	3	-	6/18/38/38	0/3/3/3
5	CZF	O	707	3	-	2/18/38/38	0/3/3/3
4	XG4	J	709	3	-	2/15/34/34	0/3/3/3
4	XG4	G	701	3	-	6/15/34/34	0/3/3/3
5	CZF	C	709	3	-	3/18/38/38	0/3/3/3
5	CZF	P	707	3	-	3/18/38/38	0/3/3/3
5	CZF	F	706	3	-	5/18/38/38	0/3/3/3
5	CZF	B	706	3	-	5/18/38/38	0/3/3/3
5	CZF	E	706	3	-	5/18/38/38	0/3/3/3
4	XG4	E	708	3	-	3/15/34/34	0/3/3/3
5	CZF	N	706	3	-	4/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	XG4	N	708	3	-	6/15/34/34	0/3/3/3
5	CZF	G	707	3	-	6/18/38/38	0/3/3/3
4	XG4	H	701	3	-	2/15/34/34	0/3/3/3
4	XG4	C	706	3,2	-	2/15/34/34	0/3/3/3
4	XG4	C	701	3	-	3/15/34/34	0/3/3/3
4	XG4	E	705	3,2	-	2/15/34/34	0/3/3/3
4	XG4	P	701	3	-	3/15/34/34	0/3/3/3
4	XG4	F	708	3	-	2/15/34/34	0/3/3/3
4	XG4	I	705	3,2	-	2/15/34/34	0/3/3/3
4	XG4	K	706	3,2	-	2/15/34/34	0/3/3/3
4	XG4	G	706	3,2	-	2/15/34/34	0/3/3/3
4	XG4	I	708	3	-	6/15/34/34	0/3/3/3
4	XG4	A	708	3	-	3/15/34/34	0/3/3/3
5	CZF	K	707	3	-	4/18/38/38	0/3/3/3

All (198) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	706	XG4	PA-O1A	6.61	1.56	1.46
4	D	706	XG4	PA-O1A	6.60	1.56	1.46
4	H	706	XG4	PA-O1A	6.50	1.56	1.46
4	A	705	XG4	PA-O1A	6.49	1.56	1.46
4	F	705	XG4	PA-O1A	5.64	1.55	1.46
4	B	705	XG4	PA-O1A	5.30	1.54	1.46
4	G	706	XG4	PA-O1A	5.05	1.54	1.46
4	J	706	XG4	PA-O1A	4.80	1.53	1.46
4	O	706	XG4	PA-O1A	4.64	1.53	1.46
4	H	706	XG4	PB-O1B	4.54	1.53	1.46
4	I	705	XG4	PA-O1A	4.48	1.53	1.46
4	D	706	XG4	PB-O1B	4.25	1.52	1.46
4	E	705	XG4	PB-O1B	4.22	1.52	1.46
4	J	709	XG4	PA-O1A	4.18	1.52	1.46
4	J	709	XG4	PB-O1B	4.14	1.52	1.46
4	C	706	XG4	PB-O1B	4.06	1.52	1.46
4	L	705	XG4	PA-O1A	4.05	1.52	1.46
4	E	705	XG4	PA-O1A	4.05	1.52	1.46
4	D	701	XG4	PB-O1B	4.03	1.52	1.46
4	A	708	XG4	PB-O1B	4.00	1.52	1.46
4	B	705	XG4	PB-O1B	3.91	1.52	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	706	XG4	PB-O1B	3.87	1.52	1.46
4	M	705	XG4	PA-O1A	3.86	1.52	1.46
4	H	701	XG4	PB-O1B	3.84	1.52	1.46
4	G	701	XG4	PA-O1A	3.84	1.52	1.46
4	G	701	XG4	PB-O1B	3.82	1.52	1.46
4	A	705	XG4	PB-O1B	3.79	1.52	1.46
4	A	708	XG4	PA-O1A	3.75	1.52	1.46
4	K	701	XG4	PB-O1B	3.71	1.52	1.46
5	H	707	CZF	C7-C9	-3.65	1.40	1.47
4	J	706	XG4	PB-O1B	3.62	1.51	1.46
5	G	707	CZF	C7-C9	-3.56	1.40	1.47
4	F	705	XG4	PB-O1B	3.55	1.51	1.46
4	H	706	XG4	PG-O1G	3.51	1.61	1.50
4	K	706	XG4	PB-O1B	3.50	1.51	1.46
4	E	708	XG4	PB-O1B	3.45	1.51	1.46
4	O	706	XG4	PB-O1B	3.45	1.51	1.46
5	C	707	CZF	C7-C9	-3.43	1.40	1.47
5	B	706	CZF	C7-C9	-3.42	1.40	1.47
4	P	706	XG4	PB-O3B	3.42	1.63	1.59
4	E	708	XG4	PA-O1A	3.40	1.51	1.46
4	I	705	XG4	PB-O1B	3.39	1.51	1.46
5	M	706	CZF	C7-C9	-3.34	1.40	1.47
4	D	701	XG4	PA-O1A	3.34	1.51	1.46
4	C	701	XG4	PB-O1B	3.34	1.51	1.46
4	K	706	XG4	PA-O1A	3.31	1.51	1.46
5	J	707	CZF	C7-C9	-3.31	1.40	1.47
4	N	705	XG4	PB-O1B	3.28	1.51	1.46
4	F	708	XG4	PB-O1B	3.27	1.51	1.46
4	O	701	XG4	PA-O1A	3.26	1.51	1.46
4	L	705	XG4	PB-O1B	3.25	1.51	1.46
4	P	701	XG4	PA-O1A	3.23	1.51	1.46
4	N	705	XG4	PA-O1A	3.19	1.51	1.46
4	C	706	XG4	C5-C6	-3.16	1.41	1.47
4	H	701	XG4	PA-O1A	3.15	1.51	1.46
5	K	707	CZF	C7-C9	-3.14	1.41	1.47
4	P	706	XG4	PA-O1A	3.12	1.51	1.46
4	O	701	XG4	PB-O1B	3.11	1.51	1.46
4	G	706	XG4	C5-C6	-3.03	1.41	1.47
4	N	708	XG4	PA-O1A	3.02	1.51	1.46
4	I	707	XG4	PA-O1A	3.01	1.50	1.46
4	K	701	XG4	PA-O1A	3.01	1.50	1.46
4	M	705	XG4	PB-O1B	3.00	1.50	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P	706	XG4	PB-O1B	2.99	1.50	1.46
4	H	706	XG4	C5-C6	-2.99	1.41	1.47
4	B	708	XG4	PA-O1A	2.97	1.50	1.46
5	A	706	CZF	C7-C9	-2.96	1.41	1.47
4	I	708	XG4	PB-O1B	2.95	1.50	1.46
4	I	707	XG4	PB-O1B	2.95	1.50	1.46
4	P	701	XG4	PB-O1B	2.94	1.50	1.46
4	I	708	XG4	PA-O1A	2.92	1.50	1.46
4	A	705	XG4	PB-O3B	2.91	1.62	1.59
4	G	701	XG4	C5-C6	-2.90	1.41	1.47
4	N	708	XG4	C5-C6	-2.89	1.41	1.47
4	N	708	XG4	PB-O1B	2.89	1.50	1.46
5	C	709	CZF	C7-C9	-2.88	1.41	1.47
4	J	709	XG4	C5-C6	-2.86	1.41	1.47
4	M	708	XG4	PB-O1B	2.82	1.50	1.46
4	E	705	XG4	PB-O3B	2.82	1.62	1.59
4	F	708	XG4	PA-O2A	-2.78	1.49	1.56
4	E	708	XG4	C5-C6	-2.78	1.41	1.47
4	C	701	XG4	PA-O1A	2.77	1.50	1.46
4	D	706	XG4	PG-O1G	2.75	1.59	1.50
4	B	708	XG4	PB-O1B	2.75	1.50	1.46
4	F	705	XG4	C5-C6	-2.68	1.42	1.47
4	A	705	XG4	C5-C6	-2.65	1.42	1.47
4	F	708	XG4	C5-C6	-2.64	1.42	1.47
4	I	708	XG4	C5-C6	-2.64	1.42	1.47
4	B	708	XG4	C5-C6	-2.62	1.42	1.47
4	J	706	XG4	C5-C6	-2.60	1.42	1.47
5	P	707	CZF	C7-C9	-2.60	1.42	1.47
4	B	708	XG4	PB-O2B	-2.59	1.49	1.56
5	E	706	CZF	C7-C9	-2.58	1.42	1.47
4	C	701	XG4	PA-O2A	-2.58	1.49	1.56
4	I	707	XG4	C5-C6	-2.58	1.42	1.47
4	E	708	XG4	PA-O2A	-2.56	1.49	1.56
4	D	701	XG4	C5-C6	-2.55	1.42	1.47
4	H	706	XG4	PA-O5'	2.54	1.67	1.57
4	D	706	XG4	PB-O3B	2.53	1.62	1.59
4	G	701	XG4	PA-O2A	-2.52	1.50	1.56
5	F	706	CZF	C7-C9	-2.50	1.42	1.47
4	I	707	XG4	C1'-N9	-2.50	1.42	1.49
4	H	701	XG4	PA-O2A	-2.50	1.50	1.56
4	N	705	XG4	PA-O2A	-2.49	1.50	1.56
4	I	708	XG4	PA-O2A	-2.49	1.50	1.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	O	706	XG4	C5-C6	-2.49	1.42	1.47
5	O	707	CZF	C7-C9	-2.49	1.42	1.47
4	C	701	XG4	C5-C6	-2.48	1.42	1.47
4	L	705	XG4	C5-C6	-2.48	1.42	1.47
4	N	708	XG4	PA-O2A	-2.47	1.50	1.56
4	M	708	XG4	PA-O2A	-2.44	1.50	1.56
4	L	705	XG4	C6-N1	2.44	1.41	1.37
5	C	707	CZF	C10-N3	-2.42	1.30	1.35
4	K	701	XG4	PA-O2A	-2.41	1.50	1.56
4	M	705	XG4	C5-C6	-2.41	1.42	1.47
4	P	706	XG4	C5-C6	-2.40	1.42	1.47
4	M	708	XG4	PA-O1A	2.40	1.50	1.46
4	H	706	XG4	PB-O3B	2.40	1.62	1.59
4	G	706	XG4	PG-O1G	2.36	1.58	1.50
4	D	701	XG4	PA-O2A	-2.36	1.50	1.56
4	B	708	XG4	PA-O2A	-2.35	1.50	1.56
4	P	701	XG4	PA-O2A	-2.34	1.50	1.56
4	L	705	XG4	PB-O3B	2.34	1.62	1.59
4	G	701	XG4	PB-O2B	-2.33	1.50	1.56
4	E	705	XG4	C5-C6	-2.32	1.42	1.47
4	M	708	XG4	PB-O2B	-2.32	1.50	1.56
4	M	708	XG4	C5-C6	-2.32	1.42	1.47
4	J	709	XG4	PB-N3A	2.31	1.69	1.63
5	A	706	CZF	C10-N3	-2.31	1.31	1.35
5	J	707	CZF	C10-N3	-2.28	1.31	1.35
5	G	707	CZF	C10-N3	-2.28	1.31	1.35
4	D	701	XG4	PB-O2B	-2.27	1.50	1.56
4	I	705	XG4	C5-C6	-2.27	1.42	1.47
4	A	708	XG4	PA-O2A	-2.27	1.50	1.56
4	J	706	XG4	PB-O3B	2.27	1.61	1.59
5	K	707	CZF	C10-N3	-2.26	1.31	1.35
4	A	705	XG4	C5-C4	-2.26	1.37	1.43
4	D	706	XG4	C5-C6	-2.26	1.42	1.47
4	K	706	XG4	C5-C6	-2.25	1.42	1.47
4	O	701	XG4	PB-O2B	-2.25	1.50	1.56
4	P	701	XG4	C5-C6	-2.25	1.42	1.47
4	I	707	XG4	PG-O3G	-2.25	1.46	1.54
4	D	701	XG4	PG-O1G	2.24	1.57	1.50
4	M	705	XG4	PA-O2A	-2.23	1.50	1.56
4	J	706	XG4	PA-O5'	2.22	1.66	1.57
4	A	708	XG4	C5-C6	-2.21	1.42	1.47
4	E	705	XG4	C6-N1	2.21	1.41	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	O	701	XG4	PA-O2A	-2.21	1.50	1.56
4	I	707	XG4	C5-C4	-2.21	1.37	1.43
4	H	701	XG4	C5-C6	-2.19	1.43	1.47
4	I	707	XG4	C6-N1	2.19	1.41	1.37
5	B	706	CZF	C10-N3	-2.19	1.31	1.35
4	C	706	XG4	PB-O3B	2.19	1.61	1.59
5	C	709	CZF	C10-N3	-2.18	1.31	1.35
4	H	706	XG4	C5-C4	-2.18	1.37	1.43
5	N	706	CZF	C7-C9	-2.16	1.43	1.47
4	E	708	XG4	C5-C4	-2.16	1.37	1.43
4	G	706	XG4	PB-O3B	2.16	1.61	1.59
5	P	707	CZF	C10-N3	-2.16	1.31	1.35
4	N	708	XG4	PB-O2B	-2.16	1.50	1.56
4	E	708	XG4	PB-O2B	-2.15	1.51	1.56
4	I	705	XG4	PA-O2A	-2.14	1.51	1.56
4	C	701	XG4	C5-C4	-2.12	1.37	1.43
4	I	707	XG4	PB-O2B	-2.12	1.51	1.56
4	G	706	XG4	C6-N1	2.12	1.41	1.37
4	N	705	XG4	C5-C6	-2.10	1.43	1.47
4	K	706	XG4	PA-O2A	-2.10	1.51	1.56
4	D	706	XG4	C6-N1	2.10	1.41	1.37
4	J	706	XG4	C6-N1	2.09	1.41	1.37
4	C	706	XG4	PA-O5'	2.09	1.65	1.57
5	E	706	CZF	C10-N3	-2.09	1.31	1.35
4	F	708	XG4	PA-O1A	2.09	1.49	1.46
4	C	701	XG4	C8-N7	-2.09	1.31	1.35
5	J	701	CZF	C10-N3	-2.09	1.31	1.35
4	A	708	XG4	PB-O2B	-2.08	1.51	1.56
4	C	706	XG4	C5-C4	-2.07	1.37	1.43
4	O	701	XG4	C5-C6	-2.07	1.43	1.47
5	F	706	CZF	C10-N3	-2.07	1.31	1.35
4	I	708	XG4	C5-C4	-2.07	1.37	1.43
4	M	705	XG4	C5-C4	-2.06	1.37	1.43
4	L	705	XG4	C5-C4	-2.06	1.37	1.43
4	I	707	XG4	C8-N7	-2.06	1.31	1.35
5	L	706	CZF	C7-C9	-2.06	1.43	1.47
4	P	701	XG4	C5-C4	-2.06	1.37	1.43
4	F	708	XG4	C5-C4	-2.06	1.37	1.43
4	I	707	XG4	PA-O2A	-2.05	1.51	1.56
5	H	707	CZF	C10-N3	-2.05	1.31	1.35
5	O	707	CZF	C10-N3	-2.05	1.31	1.35
4	J	709	XG4	PA-O2A	-2.05	1.51	1.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	N	708	XG4	C5-C4	-2.05	1.37	1.43
4	C	701	XG4	C1'-N9	-2.04	1.43	1.49
4	I	708	XG4	PB-O2B	-2.03	1.51	1.56
4	C	706	XG4	C1'-N9	-2.03	1.43	1.49
4	H	706	XG4	O5'-C5'	2.02	1.52	1.44
4	D	706	XG4	C5-C4	-2.01	1.37	1.43
4	L	705	XG4	PG-O1G	2.01	1.57	1.50
4	D	701	XG4	C5-C4	-2.01	1.38	1.43
4	E	705	XG4	PA-O5'	2.00	1.65	1.57

All (254) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	705	XG4	O1A-PA-N3A	-7.32	101.00	111.77
4	C	706	XG4	O1A-PA-N3A	-7.08	101.34	111.77
4	J	706	XG4	O2A-PA-O5'	-6.69	88.60	106.75
4	B	708	XG4	O1B-PB-N3A	6.49	121.33	111.77
4	A	705	XG4	O2A-PA-O1A	6.29	123.11	109.92
4	G	706	XG4	O1B-PB-N3A	-6.17	102.69	111.77
4	P	706	XG4	O1B-PB-N3A	-6.03	102.89	111.77
4	H	706	XG4	O2A-PA-O5'	-6.01	90.46	106.75
4	H	701	XG4	O1A-PA-N3A	5.86	120.40	111.77
4	D	706	XG4	O2B-PB-O1B	5.80	122.08	109.92
4	F	705	XG4	O2B-PB-O1B	5.75	121.98	109.92
4	E	705	XG4	O2B-PB-O1B	5.66	121.79	109.92
4	A	705	XG4	O2A-PA-O5'	-5.48	91.89	106.75
4	D	701	XG4	O1B-PB-N3A	5.46	119.81	111.77
4	K	701	XG4	O3B-PB-N3A	-5.46	91.44	106.59
5	C	707	CZF	C5-N2-C2	-5.34	119.76	128.11
4	C	706	XG4	O2B-PB-O1B	5.26	120.95	109.92
4	A	705	XG4	O2B-PB-O1B	5.17	120.76	109.92
4	H	706	XG4	O2B-PB-O1B	5.16	120.73	109.92
4	N	708	XG4	O2B-PB-O1B	5.12	120.66	109.92
4	O	706	XG4	O2B-PB-O1B	5.11	120.64	109.92
4	P	701	XG4	O2B-PB-O1B	5.10	120.62	109.92
5	M	706	CZF	C5-N2-C2	-5.10	120.14	128.11
4	H	706	XG4	O5'-PA-O1A	5.08	133.79	114.24
4	B	708	XG4	O3B-PB-N3A	-5.07	92.51	106.59
4	H	701	XG4	O2B-PB-O1B	5.06	120.53	109.92
4	J	709	XG4	O1B-PB-N3A	5.06	119.22	111.77
4	F	708	XG4	O2B-PB-O1B	5.01	120.42	109.92
4	I	705	XG4	O2B-PB-O1B	4.97	120.33	109.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	705	XG4	O1A-PA-N3A	-4.96	104.47	111.77
4	F	705	XG4	O2A-PA-O1A	4.94	120.29	109.92
5	L	706	CZF	N2-C2-N1	4.94	118.77	115.90
4	M	705	XG4	O2B-PB-O1B	4.93	120.25	109.92
4	L	705	XG4	O2A-PA-O1A	4.92	120.23	109.92
4	J	709	XG4	O2B-PB-O1B	4.88	120.16	109.92
5	A	706	CZF	C5-N2-C2	-4.87	120.49	128.11
4	K	706	XG4	O2B-PB-O1B	4.85	120.08	109.92
4	J	706	XG4	O2B-PB-O1B	4.84	120.07	109.92
4	D	706	XG4	O2A-PA-O5'	-4.83	93.65	106.75
5	L	706	CZF	C5-N2-C2	-4.82	120.58	128.11
4	P	706	XG4	O1A-PA-N3A	-4.79	104.71	111.77
4	G	701	XG4	O2B-PB-O1B	4.79	119.97	109.92
4	G	706	XG4	O2B-PB-O1B	4.79	119.96	109.92
4	C	701	XG4	O1A-PA-N3A	4.79	118.82	111.77
4	D	706	XG4	O1A-PA-N3A	-4.78	104.72	111.77
5	B	706	CZF	C5-N2-C2	-4.78	120.64	128.11
4	D	706	XG4	O5'-PA-O1A	4.75	132.53	114.24
4	D	701	XG4	O2B-PB-O1B	4.75	119.87	109.92
4	D	706	XG4	O2A-PA-O1A	4.73	119.85	109.92
4	C	706	XG4	O2A-PA-O1A	4.71	119.79	109.92
5	O	707	CZF	C5-N2-C2	-4.70	120.77	128.11
5	K	707	CZF	C5-N2-C2	-4.69	120.77	128.11
4	K	701	XG4	O2A-PA-O1A	4.66	119.69	109.92
5	N	706	CZF	C5-N2-C2	-4.65	120.84	128.11
5	H	707	CZF	C5-N2-C2	-4.65	120.85	128.11
5	O	707	CZF	N2-C2-N1	4.64	118.60	115.90
5	C	709	CZF	C5-N2-C2	-4.64	120.86	128.11
5	F	706	CZF	C5-N2-C2	-4.62	120.89	128.11
5	C	707	CZF	N2-C2-N1	4.61	118.57	115.90
5	J	701	CZF	C5-N2-C2	-4.60	120.92	128.11
5	N	706	CZF	N2-C2-N1	4.60	118.57	115.90
5	J	707	CZF	C5-N2-C2	-4.58	120.95	128.11
5	P	707	CZF	C5-N2-C2	-4.58	120.95	128.11
4	I	705	XG4	O2A-PA-O5'	-4.57	94.35	106.75
5	G	707	CZF	C5-N2-C2	-4.57	120.96	128.11
5	F	706	CZF	N2-C2-N1	4.56	118.55	115.90
4	B	708	XG4	O2A-PA-O5'	-4.55	94.41	106.75
4	J	706	XG4	O5'-PA-O1A	4.52	131.64	114.24
4	B	705	XG4	O2B-PB-O1B	4.52	119.39	109.92
4	H	701	XG4	O2A-PA-O1A	4.46	119.27	109.92
4	P	706	XG4	O2B-PB-O1B	4.44	119.23	109.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	J	707	CZF	N2-C2-N1	4.40	118.46	115.90
5	E	706	CZF	C5-N2-C2	-4.40	121.23	128.11
5	J	701	CZF	N2-C2-N1	4.40	118.45	115.90
4	F	708	XG4	O2A-PA-O1A	4.39	119.13	109.92
5	C	709	CZF	N2-C2-N1	4.37	118.44	115.90
4	J	706	XG4	O2A-PA-O1A	4.34	119.02	109.92
4	K	701	XG4	O2B-PB-O1B	4.34	119.01	109.92
4	C	701	XG4	O2B-PB-O1B	4.33	118.99	109.92
4	A	708	XG4	O2B-PB-O1B	4.32	118.99	109.92
5	B	706	CZF	N2-C2-N1	4.32	118.41	115.90
4	E	708	XG4	O2B-PB-O1B	4.32	118.97	109.92
4	G	706	XG4	O2A-PA-O1A	4.31	118.96	109.92
4	B	705	XG4	O2A-PA-O1A	4.30	118.95	109.92
4	A	705	XG4	O5'-PA-O1A	4.30	130.79	114.24
4	I	705	XG4	O2A-PA-O1A	4.28	118.89	109.92
5	J	707	CZF	C9-N1-C2	-4.27	123.51	126.88
4	I	708	XG4	O2B-PB-O1B	4.26	118.86	109.92
4	N	705	XG4	O2B-PB-O1B	4.26	118.86	109.92
4	I	707	XG4	O2B-PB-O1B	4.25	118.84	109.92
4	A	708	XG4	O3B-PB-N3A	-4.23	94.85	106.59
4	E	708	XG4	O2A-PA-O1A	4.23	118.78	109.92
5	A	706	CZF	N2-C2-N1	4.22	118.35	115.90
4	O	701	XG4	O1A-PA-N3A	4.17	117.92	111.77
4	N	705	XG4	O2A-PA-O5'	-4.17	95.45	106.75
4	H	701	XG4	O1B-PB-N3A	4.16	117.90	111.77
4	N	708	XG4	O2A-PA-O1A	4.16	118.64	109.92
5	M	706	CZF	N2-C2-N1	4.11	118.29	115.90
4	O	706	XG4	O2A-PA-O1A	4.10	118.53	109.92
4	L	705	XG4	O2B-PB-O1B	4.08	118.48	109.92
4	O	701	XG4	O2A-PA-O1A	4.05	118.41	109.92
4	P	701	XG4	O2A-PA-O1A	3.99	118.29	109.92
4	G	701	XG4	O2A-PA-O1A	3.98	118.27	109.92
4	D	701	XG4	O2G-PG-O3B	-3.98	91.28	104.64
4	P	706	XG4	O2A-PA-O1A	3.96	118.21	109.92
4	M	708	XG4	O2B-PB-O1B	3.95	118.20	109.92
4	K	701	XG4	O1A-PA-N3A	3.94	117.57	111.77
4	H	706	XG4	PB-O3B-PG	-3.93	118.76	132.62
4	O	706	XG4	O1B-PB-N3A	3.88	117.49	111.77
4	O	701	XG4	O2B-PB-O1B	3.81	117.91	109.92
4	G	701	XG4	O1B-PB-N3A	3.74	117.28	111.77
5	G	707	CZF	P2-O7-P1	-3.72	120.04	132.83
4	A	708	XG4	O2A-PA-O1A	3.72	117.71	109.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	N	705	XG4	O2A-PA-O1A	3.69	117.67	109.92
4	H	701	XG4	O5'-PA-O1A	-3.68	100.09	114.24
4	E	705	XG4	O2A-PA-O1A	3.63	117.54	109.92
5	F	706	CZF	C9-N1-C2	-3.60	124.04	126.88
4	I	705	XG4	O1B-PB-N3A	-3.58	106.49	111.77
5	C	709	CZF	C9-N1-C2	-3.58	124.06	126.88
5	L	706	CZF	P2-O7-P1	-3.58	120.55	132.83
4	G	706	XG4	O1A-PA-N3A	-3.57	106.51	111.77
4	J	709	XG4	O2A-PA-O1A	3.56	117.38	109.92
4	M	705	XG4	O2A-PA-O1A	3.55	117.36	109.92
4	B	708	XG4	O2B-PB-O1B	3.53	117.31	109.92
5	E	706	CZF	N2-C2-N1	3.50	117.93	115.90
4	I	708	XG4	O2A-PA-O1A	3.50	117.25	109.92
4	P	701	XG4	O1A-PA-N3A	3.49	116.91	111.77
5	B	706	CZF	C9-N1-C2	-3.48	124.13	126.88
5	C	707	CZF	C9-N1-C2	-3.48	124.13	126.88
4	P	706	XG4	O2A-PA-O5'	3.48	116.18	106.75
4	B	708	XG4	O2A-PA-O1A	3.47	117.21	109.92
5	O	707	CZF	C9-N1-C2	-3.43	124.17	126.88
4	N	705	XG4	O3B-PB-N3A	-3.41	97.12	106.59
4	M	708	XG4	O2A-PA-O1A	3.39	117.02	109.92
4	G	701	XG4	O2A-PA-O5'	-3.38	97.58	106.75
4	D	706	XG4	O1B-PB-N3A	-3.38	106.80	111.77
5	B	706	CZF	P2-O7-P1	-3.38	121.24	132.83
4	J	709	XG4	O2B-PB-O3B	-3.37	93.38	104.64
4	F	705	XG4	O1A-PA-N3A	-3.36	106.83	111.77
4	J	706	XG4	O1A-PA-N3A	-3.33	106.87	111.77
4	C	701	XG4	O3B-PB-N3A	-3.32	97.39	106.59
4	F	708	XG4	O5'-PA-O1A	-3.30	101.56	114.24
4	C	701	XG4	O2A-PA-O1A	3.27	116.78	109.92
4	H	706	XG4	O2A-PA-O1A	3.22	116.68	109.92
4	C	701	XG4	O2A-PA-O5'	-3.20	98.08	106.75
5	F	706	CZF	P2-O7-P1	-3.19	121.86	132.83
5	A	706	CZF	C9-N1-C2	-3.19	124.36	126.88
5	G	707	CZF	C9-N1-C2	-3.16	124.39	126.88
4	C	706	XG4	O5'-PA-O1A	3.16	126.39	114.24
5	E	706	CZF	C9-N1-C2	-3.12	124.42	126.88
5	H	707	CZF	N2-C2-N1	3.10	117.70	115.90
5	L	706	CZF	C9-N1-C2	-3.02	124.49	126.88
5	H	707	CZF	C9-N1-C2	-3.02	124.50	126.88
5	K	707	CZF	N2-C2-N1	3.00	117.64	115.90
4	I	707	XG4	O3G-PG-O3B	-2.99	94.59	104.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	O	706	XG4	O3B-PB-N3A	-2.99	98.29	106.59
4	C	706	XG4	O2A-PA-O5'	-2.98	98.67	106.75
4	N	708	XG4	O5'-PA-O1A	-2.97	102.81	114.24
4	I	707	XG4	O2A-PA-O1A	2.93	116.07	109.92
5	P	707	CZF	N2-C2-N1	2.91	117.59	115.90
4	H	706	XG4	O1A-PA-N3A	-2.90	107.50	111.77
4	J	709	XG4	O2G-PG-O3B	-2.88	94.98	104.64
4	B	705	XG4	O6-C6-C5	2.87	129.99	124.37
4	K	701	XG4	O1B-PB-N3A	2.87	116.00	111.77
4	N	705	XG4	O1A-PA-N3A	-2.87	107.54	111.77
4	G	706	XG4	O2A-PA-O5'	-2.86	98.99	106.75
5	A	706	CZF	P2-O7-P1	-2.86	123.01	132.83
4	D	701	XG4	O2B-PB-O3B	-2.84	95.15	104.64
4	M	705	XG4	O2A-PA-O5'	-2.84	99.04	106.75
4	B	705	XG4	O1B-PB-N3A	-2.84	107.59	111.77
4	E	708	XG4	O2A-PA-O5'	-2.84	99.05	106.75
4	G	701	XG4	O1A-PA-N3A	2.81	115.90	111.77
4	J	706	XG4	O1B-PB-N3A	-2.80	107.64	111.77
4	G	706	XG4	PB-O3B-PG	-2.80	122.77	132.62
5	J	701	CZF	C9-N1-C2	-2.78	124.69	126.88
4	L	705	XG4	O1A-PA-N3A	2.77	115.86	111.77
4	I	708	XG4	O3B-PB-N3A	-2.76	98.93	106.59
4	P	706	XG4	O5'-PA-O1A	-2.75	103.66	114.24
4	K	706	XG4	O2A-PA-O1A	2.73	115.64	109.92
5	E	706	CZF	P2-O7-P1	-2.71	123.53	132.83
4	N	708	XG4	O2A-PA-O5'	-2.69	99.46	106.75
4	H	701	XG4	O6-C6-C5	2.66	129.56	124.37
4	K	701	XG4	O2G-PG-O3B	-2.65	95.75	104.64
5	N	706	CZF	C9-N1-C2	-2.64	124.80	126.88
5	B	706	CZF	O10-P3-O15	-2.61	96.71	111.19
4	D	701	XG4	O2A-PA-O1A	2.60	115.36	109.92
4	E	708	XG4	O1B-PB-N3A	2.59	115.59	111.77
4	N	708	XG4	O1A-PA-N3A	2.58	115.57	111.77
4	E	705	XG4	PB-O3B-PG	-2.58	123.55	132.62
4	F	708	XG4	O1A-PA-N3A	2.56	115.54	111.77
5	J	701	CZF	O6-C9-N1	-2.56	117.62	120.65
5	L	706	CZF	O6-C9-N1	-2.55	117.63	120.65
4	D	706	XG4	PB-O3B-PG	-2.55	123.62	132.62
5	C	709	CZF	P2-O7-P1	-2.53	124.13	132.83
5	B	706	CZF	O14-P3-O10	2.53	113.13	104.64
4	O	706	XG4	O2B-PB-O3B	2.53	113.10	104.64
4	I	708	XG4	O6-C6-C5	2.52	129.30	124.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	K	701	XG4	O5'-PA-O1A	-2.50	104.61	114.24
4	I	705	XG4	O5'-PA-O1A	2.44	123.63	114.24
4	J	706	XG4	PB-O3B-PG	-2.43	124.07	132.62
4	A	708	XG4	O3G-PG-O2G	2.43	116.91	107.64
4	A	705	XG4	O3G-PG-O2G	2.40	116.82	107.64
4	K	706	XG4	O6-C6-C5	2.40	129.06	124.37
5	K	707	CZF	C9-N1-C2	-2.39	124.99	126.88
4	A	708	XG4	PB-O3B-PG	-2.38	124.22	132.62
4	E	705	XG4	O5'-PA-O1A	2.38	123.39	114.24
4	F	708	XG4	O1B-PB-N3A	-2.37	108.27	111.77
4	B	705	XG4	O2A-PA-O5'	-2.36	100.33	106.75
4	M	708	XG4	O1B-PB-N3A	2.36	115.24	111.77
4	A	708	XG4	O1A-PA-N3A	2.34	115.22	111.77
4	C	706	XG4	O3B-PB-N3A	-2.33	100.12	106.59
4	K	701	XG4	O6-C6-C5	2.32	128.91	124.37
4	B	705	XG4	O2B-PB-O3B	2.30	112.31	104.64
4	F	705	XG4	O2A-PA-O5'	-2.30	100.52	106.75
4	A	708	XG4	C2'-C1'-N9	2.29	119.56	114.27
4	B	705	XG4	PB-O3B-PG	-2.29	124.57	132.62
4	O	706	XG4	O6-C6-C5	2.27	128.81	124.37
5	M	706	CZF	C9-N1-C2	-2.26	125.10	126.88
4	N	705	XG4	O5'-PA-O1A	2.26	122.93	114.24
4	B	705	XG4	O5'-PA-O1A	2.24	122.88	114.24
4	M	708	XG4	O6-C6-C5	2.24	128.74	124.37
5	G	707	CZF	N2-C2-N1	2.20	117.17	115.90
4	A	705	XG4	O3B-PB-N3A	-2.19	100.51	106.59
4	H	706	XG4	O3B-PB-N3A	-2.18	100.55	106.59
4	D	706	XG4	O6-C6-C5	2.17	128.61	124.37
4	P	706	XG4	O6-C6-C5	2.17	128.60	124.37
5	P	707	CZF	C9-N1-C2	-2.15	125.18	126.88
4	D	706	XG4	O3B-PB-N3A	-2.15	100.63	106.59
5	M	706	CZF	C4-C3-C1	2.14	104.21	100.98
4	I	705	XG4	O6-C6-C5	2.14	128.56	124.37
4	C	701	XG4	O1B-PB-N3A	2.14	114.92	111.77
4	D	701	XG4	O3G-PG-O2G	2.14	115.81	107.64
4	O	706	XG4	O3G-PG-O2G	2.13	115.77	107.64
4	F	705	XG4	O2B-PB-O3B	2.12	111.72	104.64
4	L	705	XG4	PB-O3B-PG	-2.12	125.16	132.62
5	C	707	CZF	O9-P1-O8	2.11	122.69	112.24
4	E	708	XG4	O3B-PB-N3A	-2.11	100.73	106.59
4	H	706	XG4	O2B-PB-O3B	2.11	111.69	104.64
4	P	701	XG4	O3B-PB-N3A	-2.11	100.75	106.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	K	701	XG4	O3G-PG-O2G	2.10	115.64	107.64
4	E	708	XG4	O3G-PG-O2G	2.09	115.64	107.64
4	O	701	XG4	O3G-PG-O2G	2.09	115.63	107.64
5	K	707	CZF	C4-C3-C1	2.08	104.10	100.98
4	F	705	XG4	O6-C6-C5	2.07	128.42	124.37
4	P	706	XG4	O2B-PB-O3B	2.07	111.54	104.64
4	M	705	XG4	O6-C6-C5	2.06	128.40	124.37
4	L	705	XG4	O2B-PB-O3B	2.06	111.52	104.64
4	E	705	XG4	O2A-PA-O5'	-2.06	101.16	106.75
4	L	705	XG4	O1B-PB-N3A	-2.05	108.76	111.77
4	E	705	XG4	O3B-PG-O1G	-2.04	99.87	111.19
4	I	707	XG4	O1B-PB-N3A	2.04	114.77	111.77
4	N	705	XG4	O6-C6-C5	2.04	128.35	124.37
4	O	701	XG4	O6-C6-C5	2.03	128.34	124.37
5	O	707	CZF	C4-C3-C1	2.00	104.00	100.98

There are no chirality outliers.

All (179) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	705	XG4	PB-N3A-PA-O1A
4	A	708	XG4	PG-O3B-PB-O1B
4	A	708	XG4	PG-O3B-PB-O2B
4	B	705	XG4	PB-N3A-PA-O1A
4	B	705	XG4	PG-O3B-PB-O1B
4	B	705	XG4	PG-O3B-PB-O2B
4	B	708	XG4	PG-O3B-PB-O2B
4	C	701	XG4	PA-N3A-PB-O1B
4	C	701	XG4	PG-O3B-PB-O1B
4	C	701	XG4	PG-O3B-PB-O2B
4	C	706	XG4	PB-N3A-PA-O1A
4	D	701	XG4	PA-N3A-PB-O1B
4	D	706	XG4	PB-N3A-PA-O1A
4	D	706	XG4	PG-O3B-PB-O1B
4	E	705	XG4	PB-N3A-PA-O1A
4	E	708	XG4	PG-O3B-PB-O1B
4	E	708	XG4	PG-O3B-PB-O2B
4	F	705	XG4	PB-N3A-PA-O1A
4	F	708	XG4	PA-N3A-PB-O1B
4	G	701	XG4	PB-N3A-PA-O1A
4	G	701	XG4	PB-N3A-PA-O5'
4	G	701	XG4	PA-N3A-PB-O1B

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Mol	Chain	Res	Type	Atoms
4	G	701	XG4	PB-O3B-PG-O3G
4	G	706	XG4	PB-N3A-PA-O1A
4	H	701	XG4	PB-N3A-PA-O5'
4	H	701	XG4	PA-N3A-PB-O1B
4	H	706	XG4	PB-N3A-PA-O1A
4	H	706	XG4	PG-O3B-PB-O1B
4	H	706	XG4	PG-O3B-PB-O2B
4	I	705	XG4	PB-N3A-PA-O1A
4	I	707	XG4	PG-O3B-PB-O1B
4	I	707	XG4	PG-O3B-PB-O2B
4	I	708	XG4	PA-N3A-PB-O3B
4	I	708	XG4	PB-O3B-PG-O2G
4	I	708	XG4	PB-O3B-PG-O3G
4	J	706	XG4	PB-N3A-PA-O1A
4	J	706	XG4	PG-O3B-PB-O1B
4	J	706	XG4	PG-O3B-PB-O2B
4	J	709	XG4	PB-N3A-PA-O5'
4	J	709	XG4	PA-N3A-PB-O1B
4	K	701	XG4	PB-O3B-PG-O2G
4	K	706	XG4	PB-N3A-PA-O1A
4	L	705	XG4	PB-N3A-PA-O1A
4	L	705	XG4	PG-O3B-PB-O1B
4	L	705	XG4	PG-O3B-PB-O2B
4	M	705	XG4	PB-N3A-PA-O1A
4	M	705	XG4	PG-O3B-PB-O1B
4	M	705	XG4	PG-O3B-PB-O2B
4	M	708	XG4	PA-N3A-PB-O1B
4	M	708	XG4	PG-O3B-PB-O1B
4	M	708	XG4	PG-O3B-PB-O2B
4	N	705	XG4	PB-N3A-PA-O1A
4	N	708	XG4	PA-N3A-PB-O1B
4	N	708	XG4	PB-O3B-PG-O2G
4	N	708	XG4	PB-O3B-PG-O3G
4	O	701	XG4	PA-N3A-PB-O1B
4	O	701	XG4	PG-O3B-PB-O1B
4	O	701	XG4	PG-O3B-PB-O2B
4	O	706	XG4	PB-N3A-PA-O1A
4	O	706	XG4	PG-O3B-PB-O1B
4	P	701	XG4	PG-O3B-PB-O1B
4	P	701	XG4	PG-O3B-PB-O2B
4	P	706	XG4	PG-O3B-PB-O1B
4	P	706	XG4	PG-O3B-PB-O2B

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Mol	Chain	Res	Type	Atoms
5	A	706	CZF	P2-O10-P3-O14
5	B	706	CZF	P2-O10-P3-O14
5	C	707	CZF	C8-O5-P1-O9
5	C	707	CZF	P2-O10-P3-O14
5	E	706	CZF	P2-O10-P3-O14
5	F	706	CZF	P2-O10-P3-O13
5	F	706	CZF	P2-O10-P3-O14
5	H	707	CZF	P2-O10-P3-O14
5	K	707	CZF	P2-O10-P3-O14
5	L	706	CZF	P2-O10-P3-O14
5	M	706	CZF	P2-O10-P3-O14
5	N	706	CZF	P2-O10-P3-O13
4	N	708	XG4	C3'-C4'-C5'-O5'
4	N	708	XG4	O4'-C4'-C5'-O5'
4	I	708	XG4	C5'-O5'-PA-O1A
4	I	708	XG4	C5'-O5'-PA-N3A
4	F	705	XG4	PB-O3B-PG-O1G
4	J	706	XG4	PB-O3B-PG-O1G
5	A	706	CZF	P2-O10-P3-O15
5	G	707	CZF	P2-O10-P3-O15
5	J	701	CZF	P2-O10-P3-O15
5	C	707	CZF	C6-C8-O5-P1
5	K	707	CZF	P2-O10-P3-O15
5	F	706	CZF	C6-C8-O5-P1
5	G	707	CZF	C6-C8-O5-P1
5	L	706	CZF	C6-C8-O5-P1
5	M	706	CZF	C6-C8-O5-P1
4	G	701	XG4	PB-O3B-PG-O2G
5	G	707	CZF	P2-O10-P3-O14
5	J	701	CZF	P2-O10-P3-O14
5	C	707	CZF	C8-O5-P1-O7
5	B	706	CZF	P2-O7-P1-O9
5	E	706	CZF	P3-O10-P2-O12
5	J	701	CZF	P3-O10-P2-O12
5	L	706	CZF	P2-O7-P1-O9
5	M	706	CZF	P2-O7-P1-O9
5	P	707	CZF	P3-O10-P2-O12
4	M	708	XG4	C5'-O5'-PA-O1A
5	C	709	CZF	C6-C8-O5-P1
5	N	706	CZF	C6-C8-O5-P1
4	B	705	XG4	C4'-C5'-O5'-PA
4	N	705	XG4	C4'-C5'-O5'-PA

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Mol	Chain	Res	Type	Atoms
4	O	706	XG4	C4'-C5'-O5'-PA
4	O	706	XG4	PB-O3B-PG-O1G
5	E	706	CZF	P2-O10-P3-O15
5	O	707	CZF	C6-C8-O5-P1
4	D	706	XG4	C4'-C5'-O5'-PA
4	E	705	XG4	C4'-C5'-O5'-PA
4	F	705	XG4	C4'-C5'-O5'-PA
4	I	705	XG4	C4'-C5'-O5'-PA
5	C	707	CZF	P2-O7-P1-O9
5	F	706	CZF	P2-O7-P1-O9
5	H	707	CZF	P2-O7-P1-O9
5	K	707	CZF	P2-O7-P1-O9
5	O	707	CZF	P2-O7-P1-O9
5	P	707	CZF	P2-O7-P1-O9
5	B	706	CZF	C6-C8-O5-P1
5	K	707	CZF	C6-C8-O5-P1
4	C	706	XG4	C4'-C5'-O5'-PA
5	P	707	CZF	C6-C8-O5-P1
4	H	706	XG4	C4'-C5'-O5'-PA
5	B	706	CZF	P2-O10-P3-O15
4	B	708	XG4	PA-N3A-PB-O1B
5	G	707	CZF	P2-O7-P1-O9
5	J	707	CZF	P3-O10-P2-O12
5	M	706	CZF	P3-O10-P2-O12
5	E	706	CZF	C6-C8-O5-P1
4	A	705	XG4	C4'-C5'-O5'-PA
4	J	706	XG4	C4'-C5'-O5'-PA
4	K	706	XG4	C4'-C5'-O5'-PA
4	M	705	XG4	C4'-C5'-O5'-PA
4	P	706	XG4	C4'-C5'-O5'-PA
4	G	701	XG4	PB-O3B-PG-O1G
4	I	708	XG4	PB-O3B-PG-O1G
5	F	706	CZF	P2-O10-P3-O15
5	L	706	CZF	P2-O10-P3-O15
4	L	705	XG4	C4'-C5'-O5'-PA
4	I	707	XG4	PB-O3B-PG-O3G
4	M	708	XG4	PB-O3B-PG-O3G
5	C	709	CZF	P2-O10-P3-O14
5	M	706	CZF	P2-O10-P3-O13
4	G	706	XG4	C4'-C5'-O5'-PA
5	A	706	CZF	P2-O7-P1-O9
5	B	706	CZF	P3-O10-P2-O11

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Mol	Chain	Res	Type	Atoms
5	E	706	CZF	P3-O10-P2-O11
5	G	707	CZF	P2-O7-P1-O8
5	G	707	CZF	P3-O10-P2-O12
5	H	707	CZF	P2-O7-P1-O8
5	H	707	CZF	P3-O10-P2-O12
5	J	701	CZF	P2-O7-P1-O8
5	J	701	CZF	P2-O7-P1-O9
5	J	701	CZF	P3-O10-P2-O11
5	J	707	CZF	P2-O7-P1-O8
5	L	706	CZF	P2-O7-P1-O8
5	M	706	CZF	P2-O7-P1-O8
5	N	706	CZF	P2-O7-P1-O8
5	N	706	CZF	P2-O7-P1-O9
5	A	706	CZF	C6-C8-O5-P1
5	J	707	CZF	C6-C8-O5-P1
5	C	707	CZF	C8-O5-P1-O8
4	N	708	XG4	PB-O3B-PG-O1G
5	C	707	CZF	P2-O10-P3-O15
5	C	709	CZF	P2-O10-P3-O15
5	H	707	CZF	P2-O10-P3-O15
4	A	708	XG4	PA-N3A-PB-O3B
4	B	708	XG4	PB-N3A-PA-O5'
4	D	701	XG4	PB-N3A-PA-O5'
4	E	708	XG4	PA-N3A-PB-O3B
4	F	708	XG4	PB-N3A-PA-O5'
4	I	707	XG4	PA-N3A-PB-O3B
4	O	701	XG4	PB-N3A-PA-O5'
4	P	701	XG4	PA-N3A-PB-O3B
4	B	708	XG4	C5'-O5'-PA-N3A
4	M	708	XG4	C5'-O5'-PA-N3A
5	H	707	CZF	C6-C8-O5-P1

There are no ring outliers.

42 monomers are involved in 77 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	M	705	XG4	1	0
4	H	706	XG4	1	0
4	D	701	XG4	1	0
4	N	705	XG4	2	0
4	O	701	XG4	2	0
4	M	708	XG4	5	0

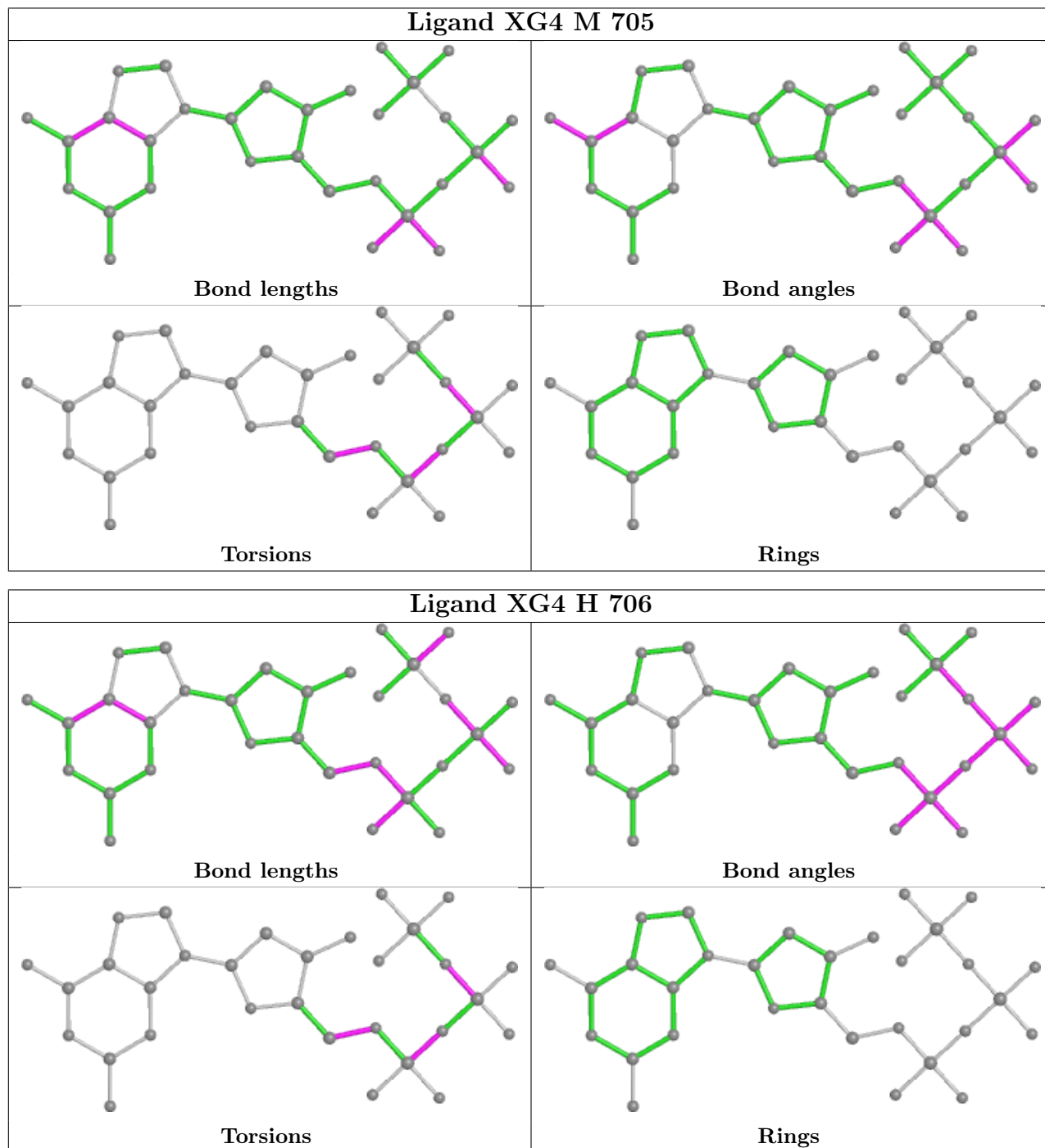
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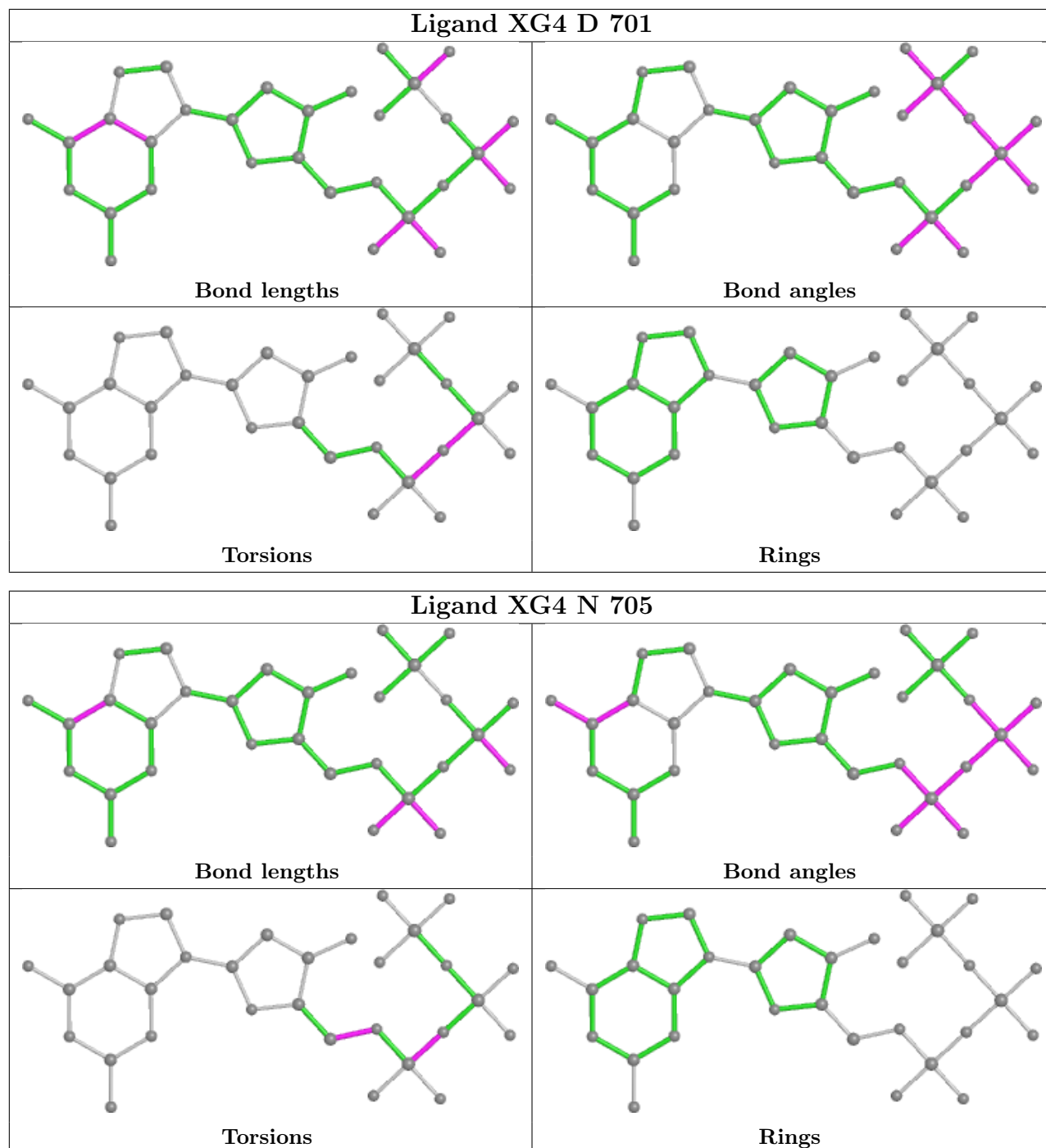
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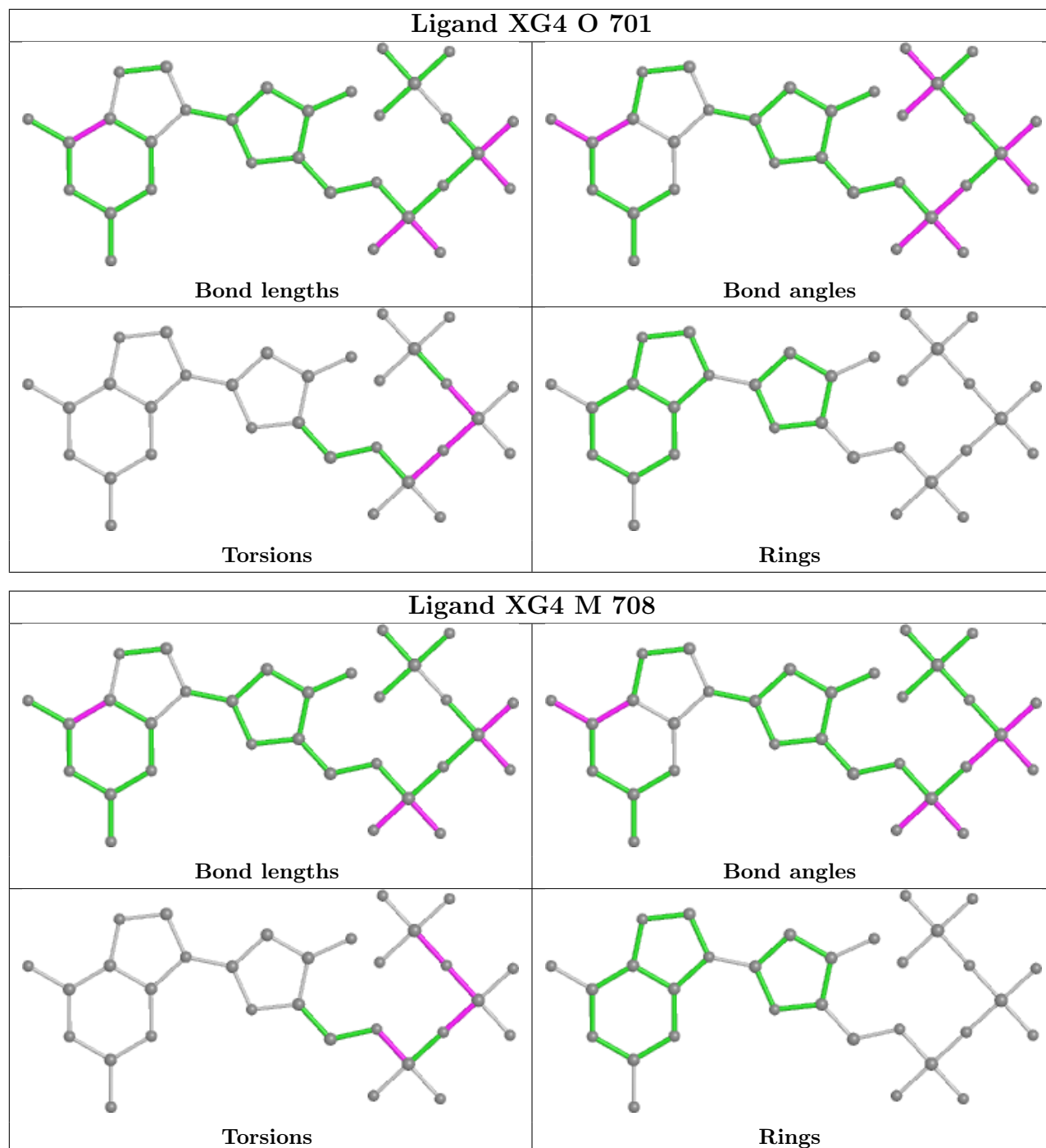
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	706	CZF	2	0
4	J	706	XG4	1	0
4	B	705	XG4	1	0
4	L	705	XG4	2	0
4	P	706	XG4	3	0
4	I	707	XG4	5	0
4	D	706	XG4	2	0
5	H	707	CZF	2	0
4	B	708	XG4	2	0
4	F	705	XG4	1	0
4	O	706	XG4	2	0
4	A	705	XG4	1	0
4	K	701	XG4	1	0
5	J	701	CZF	3	0
5	O	707	CZF	2	0
4	J	709	XG4	3	0
4	G	701	XG4	5	0
5	C	709	CZF	1	0
5	P	707	CZF	2	0
5	F	706	CZF	1	0
5	B	706	CZF	1	0
5	E	706	CZF	1	0
4	E	708	XG4	2	0
5	N	706	CZF	1	0
6	G	708	SO4	1	0
4	N	708	XG4	4	0
4	C	706	XG4	2	0
4	C	701	XG4	3	0
4	E	705	XG4	1	0
4	P	701	XG4	2	0
4	F	708	XG4	2	0
4	I	705	XG4	1	0
4	K	706	XG4	3	0
4	I	708	XG4	3	0
4	A	708	XG4	1	0
5	K	707	CZF	1	0

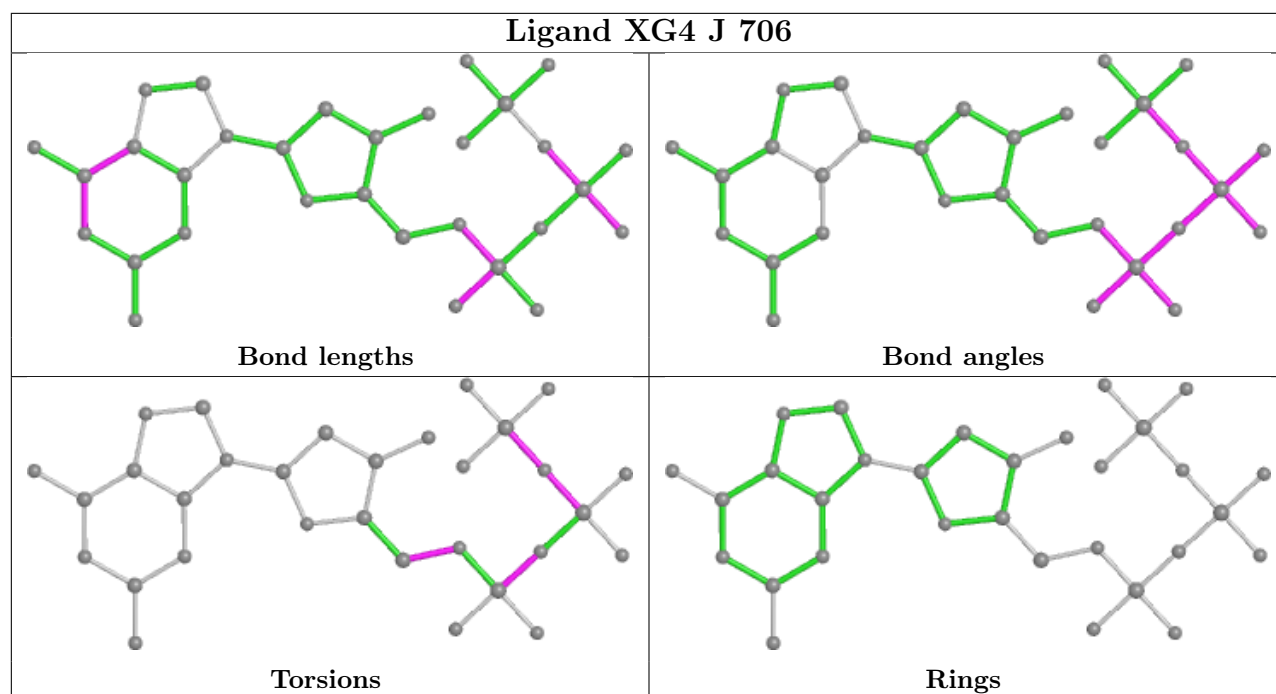
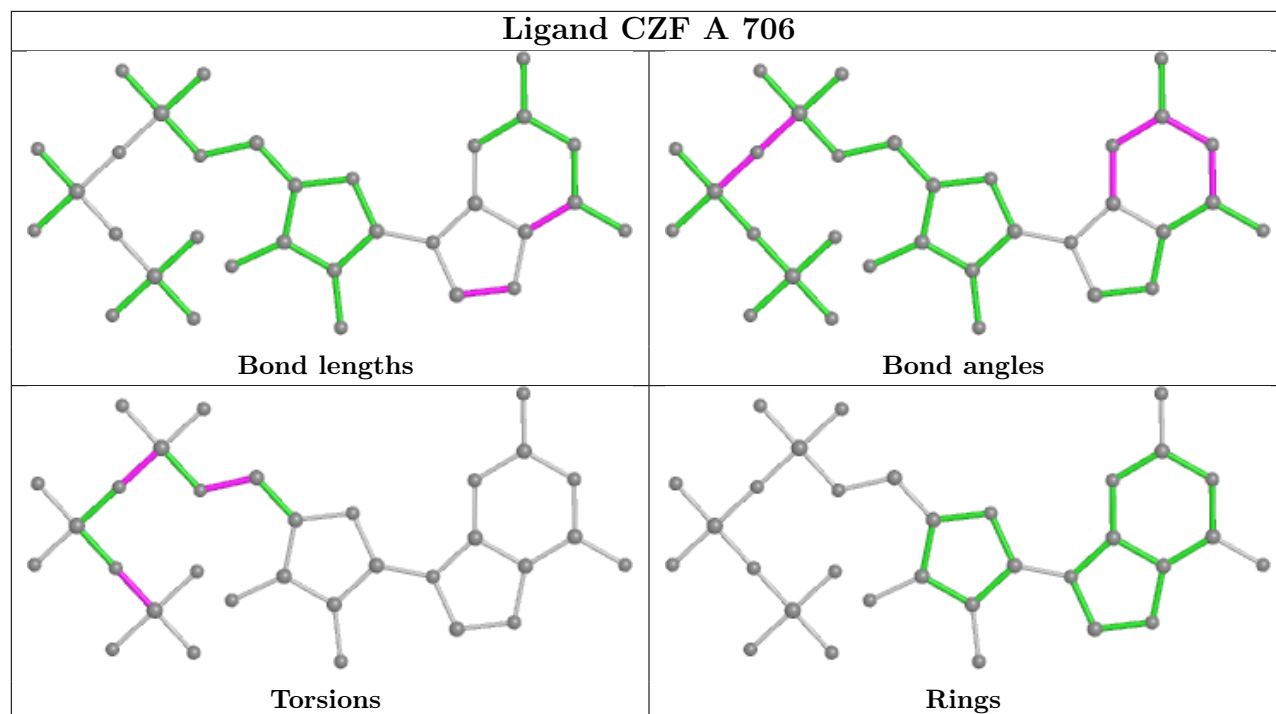
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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

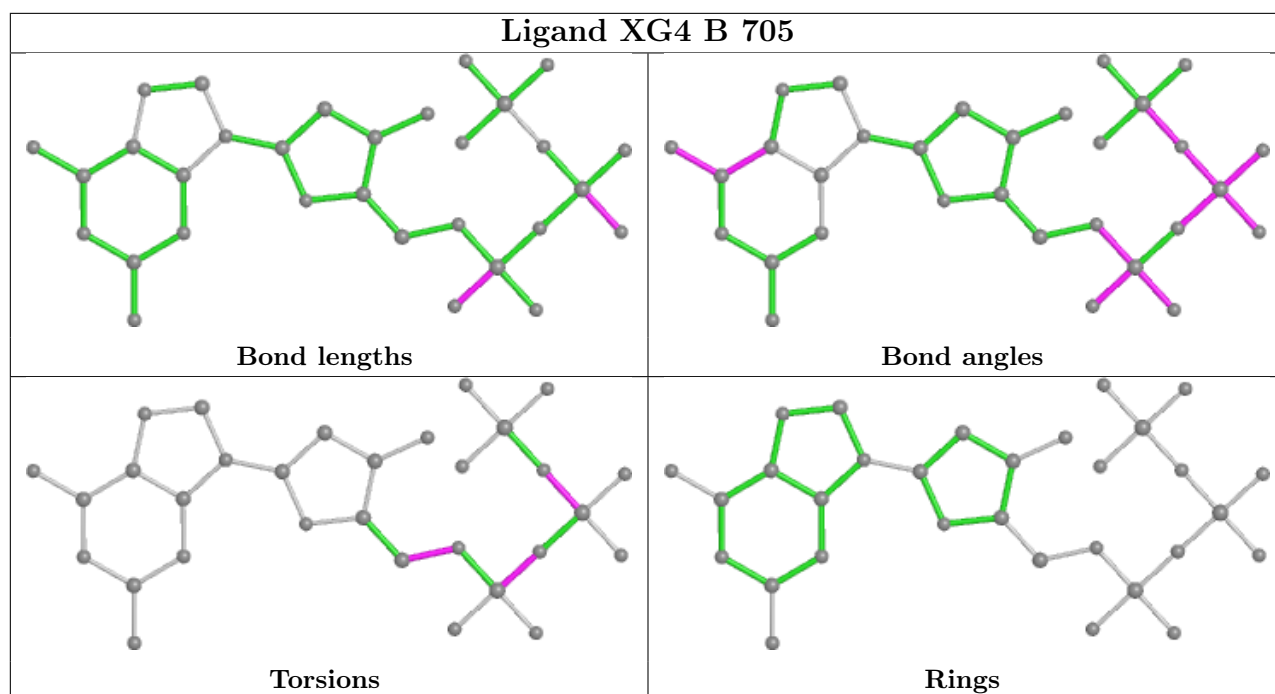
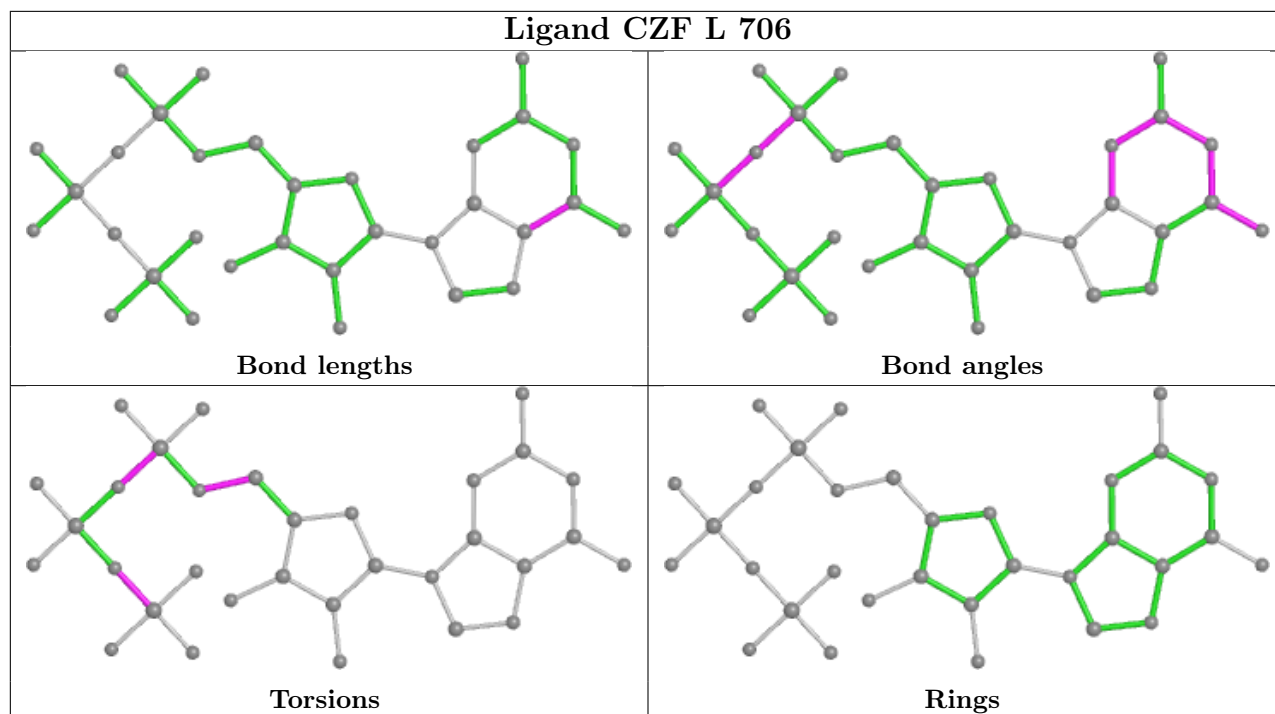
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified 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.

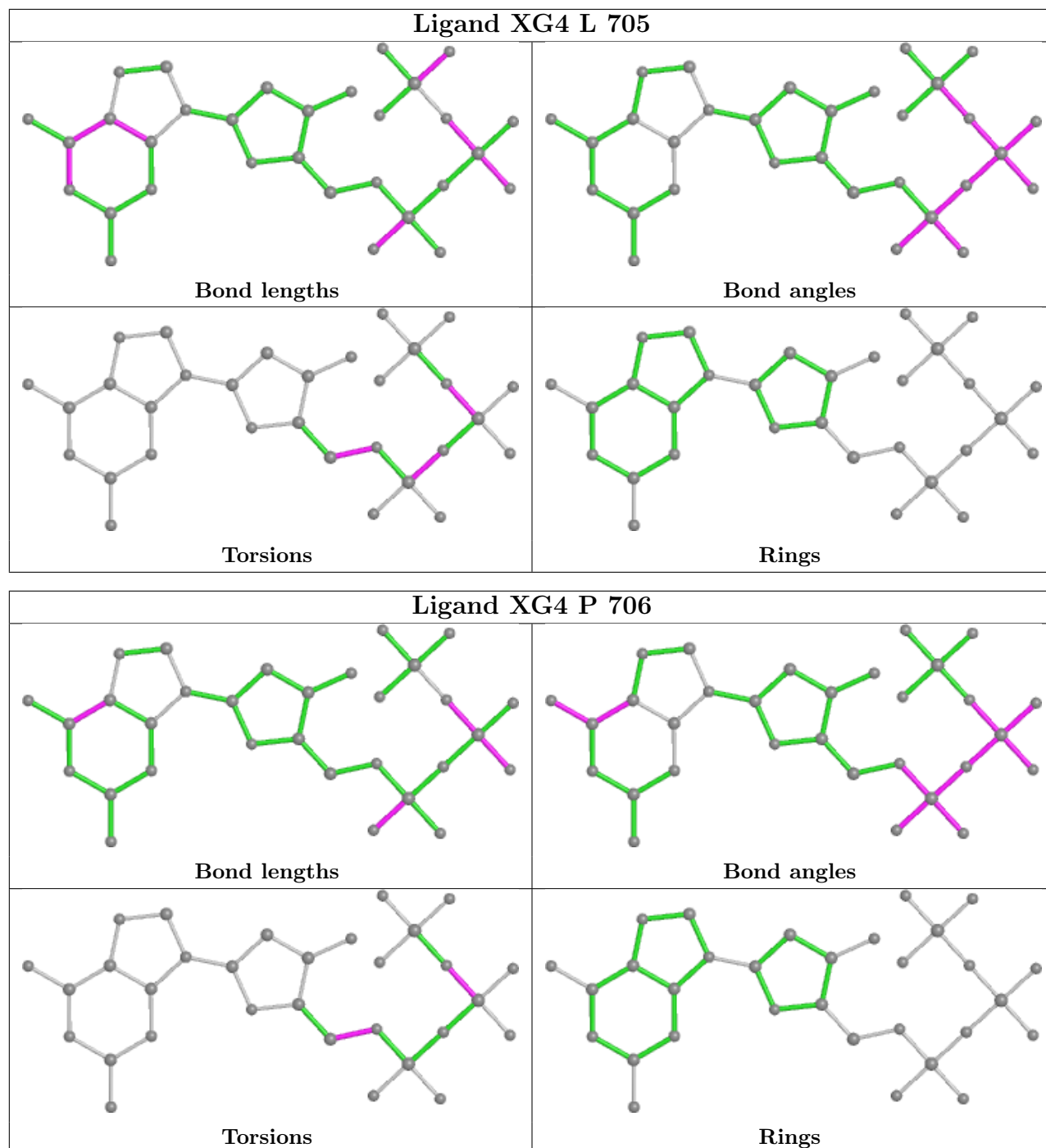


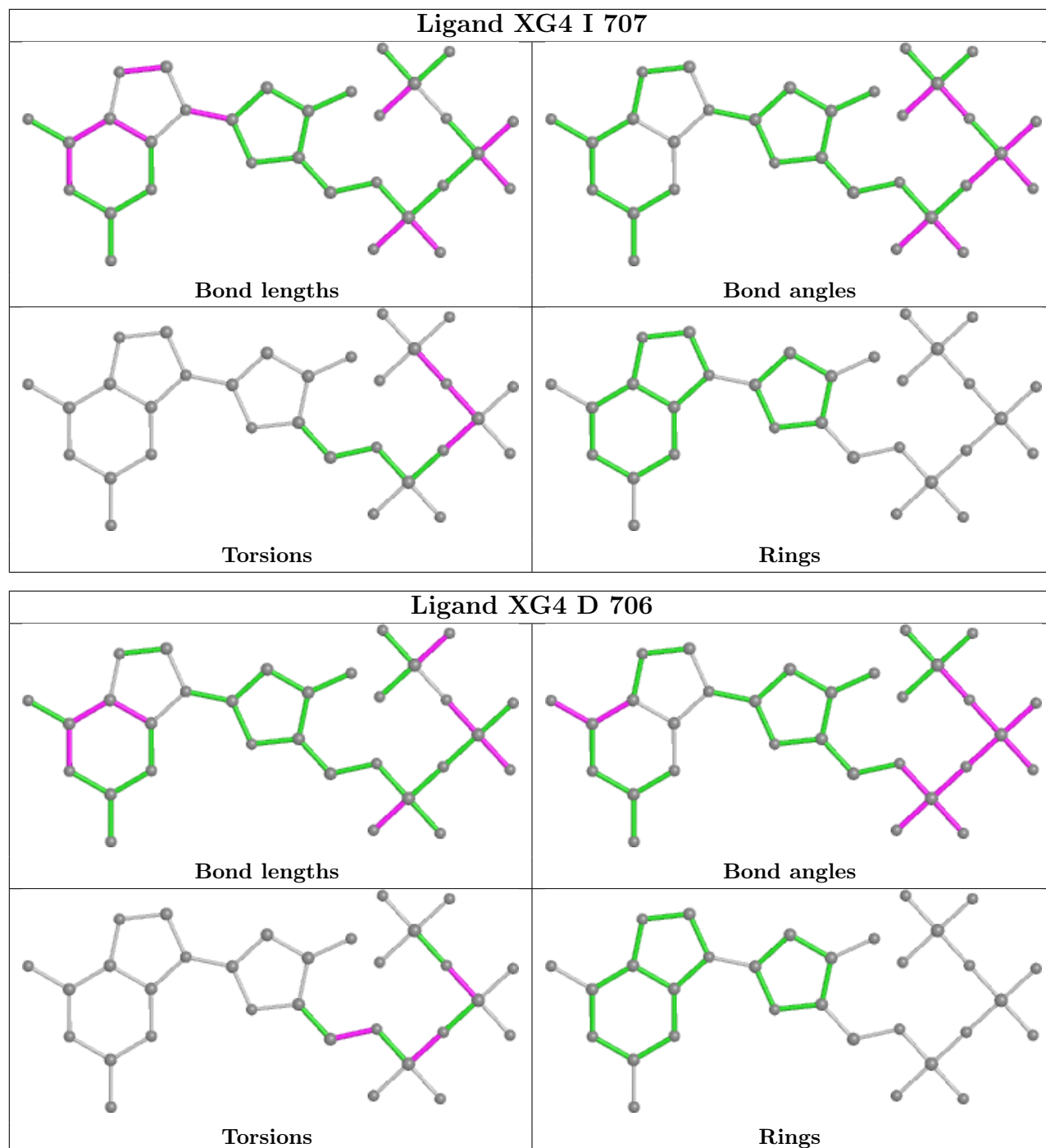


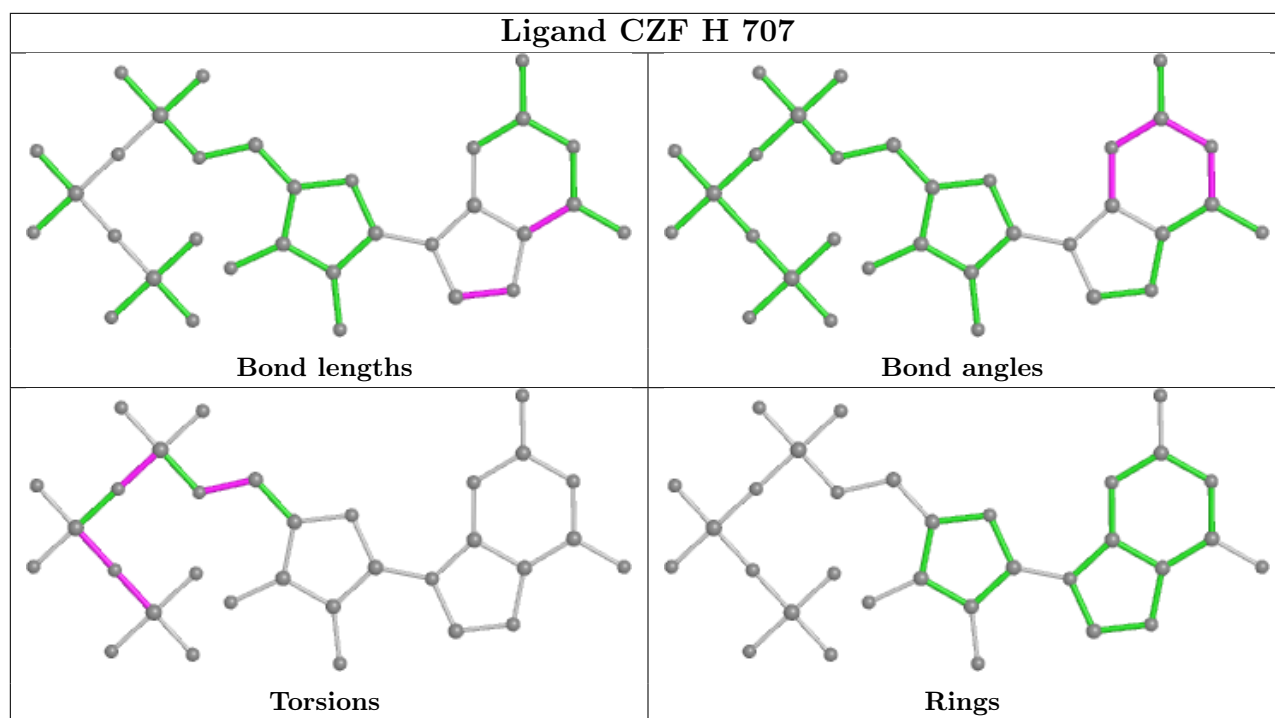
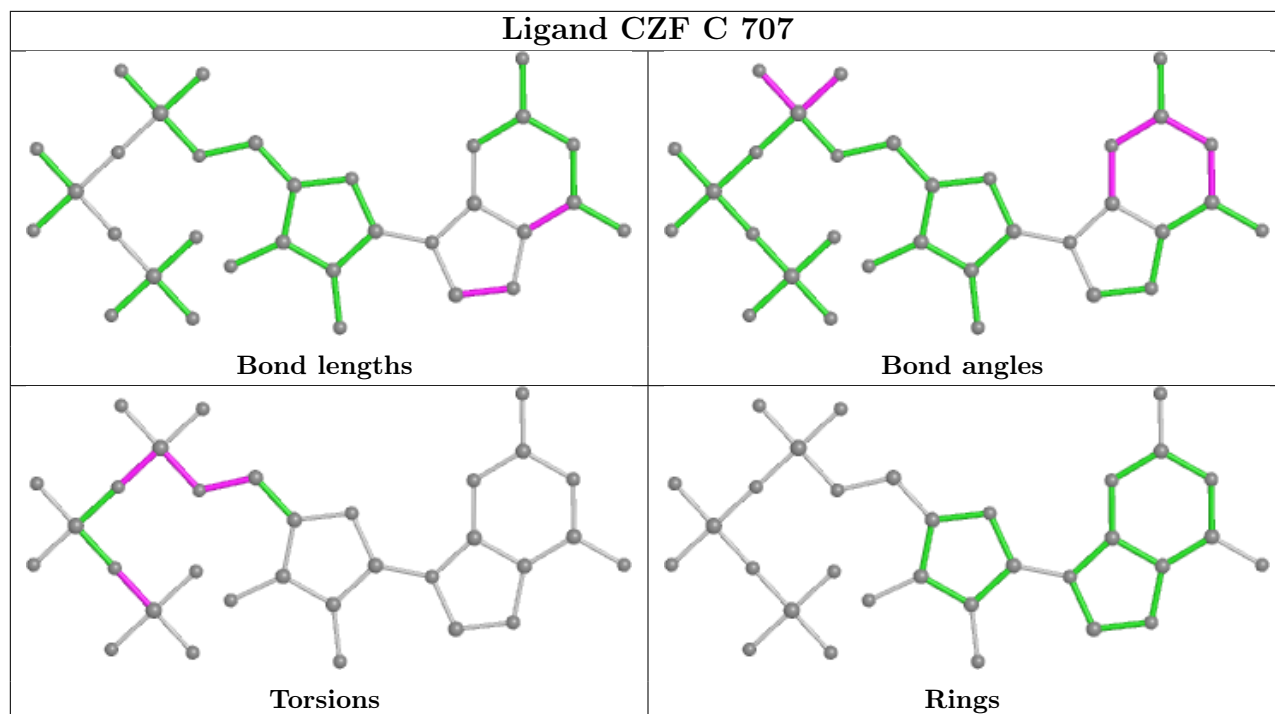


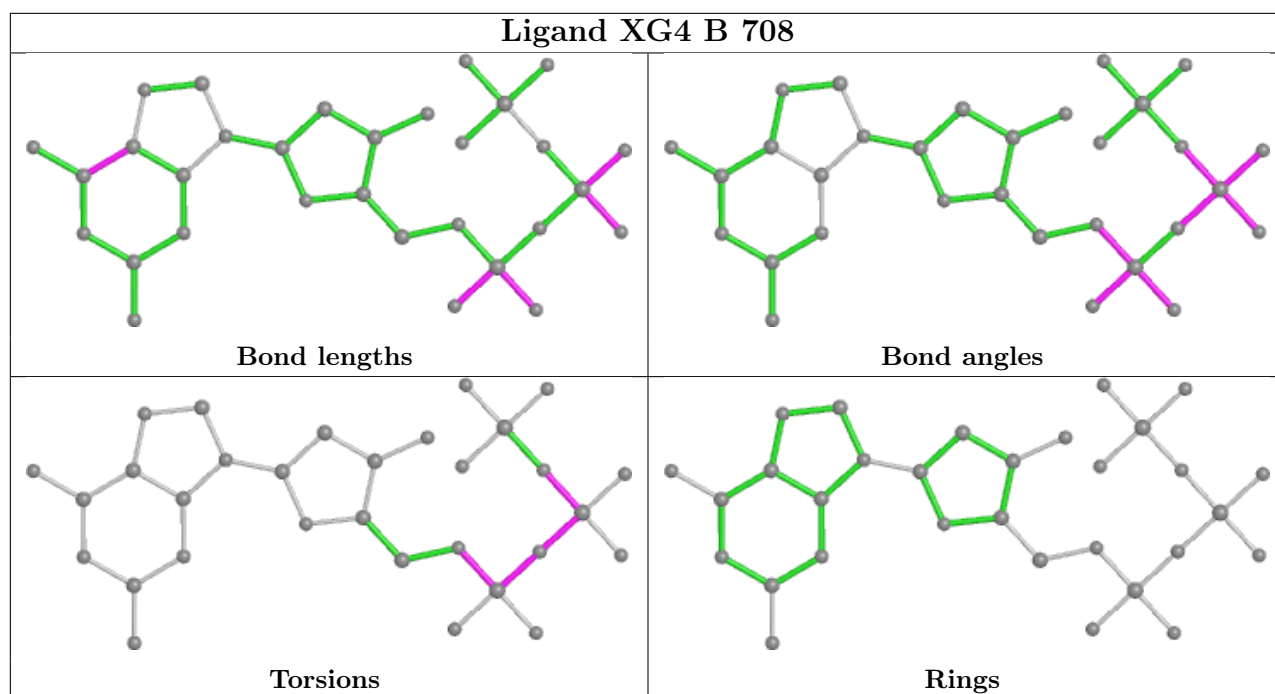
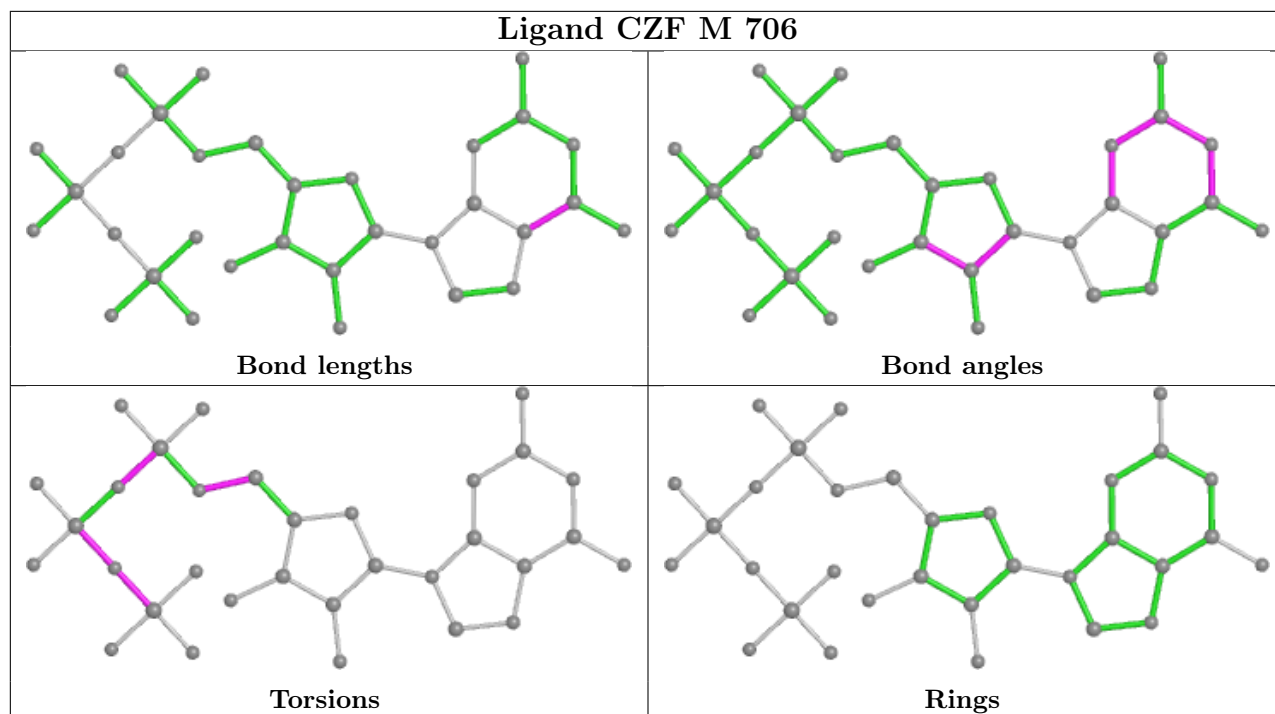


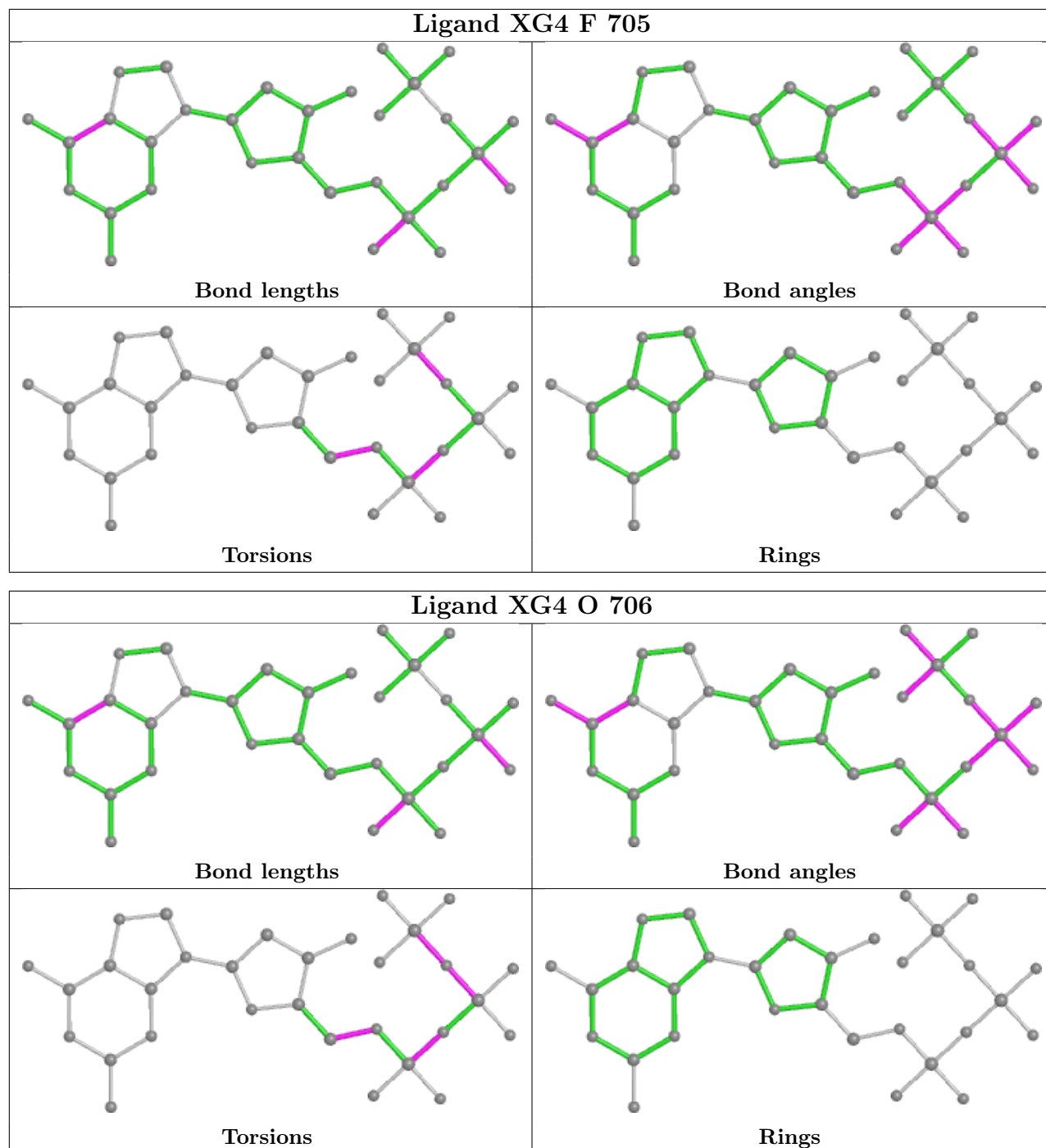


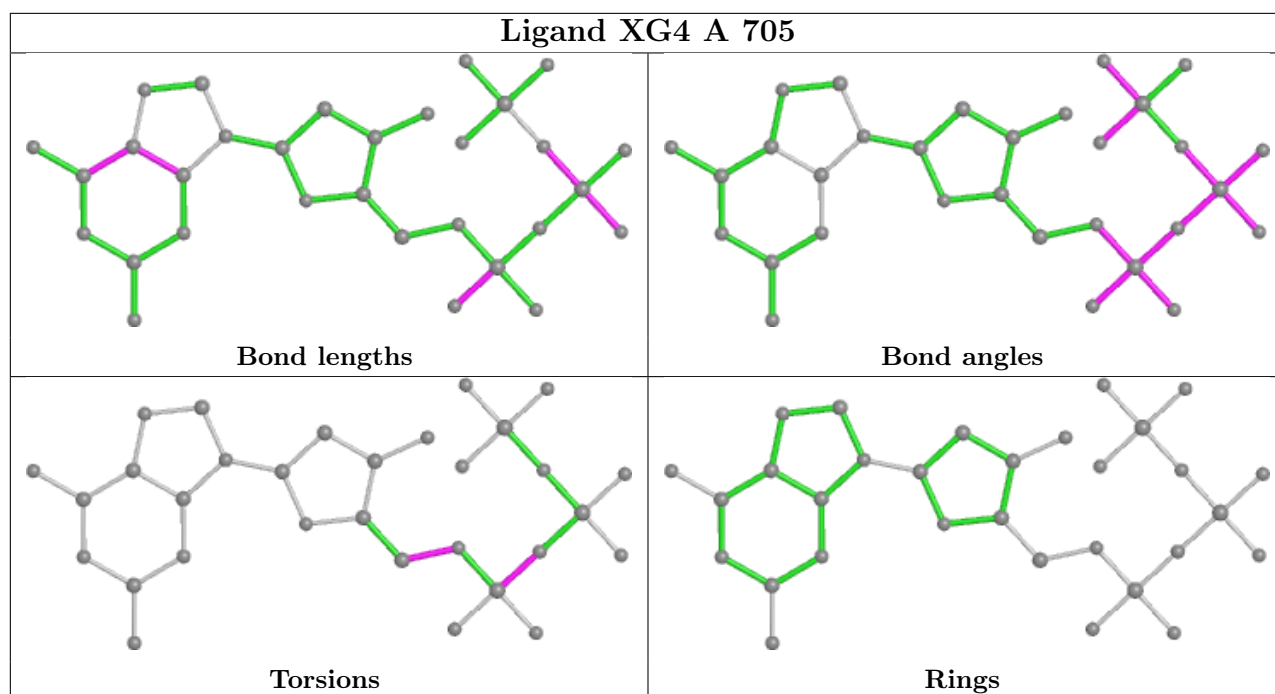
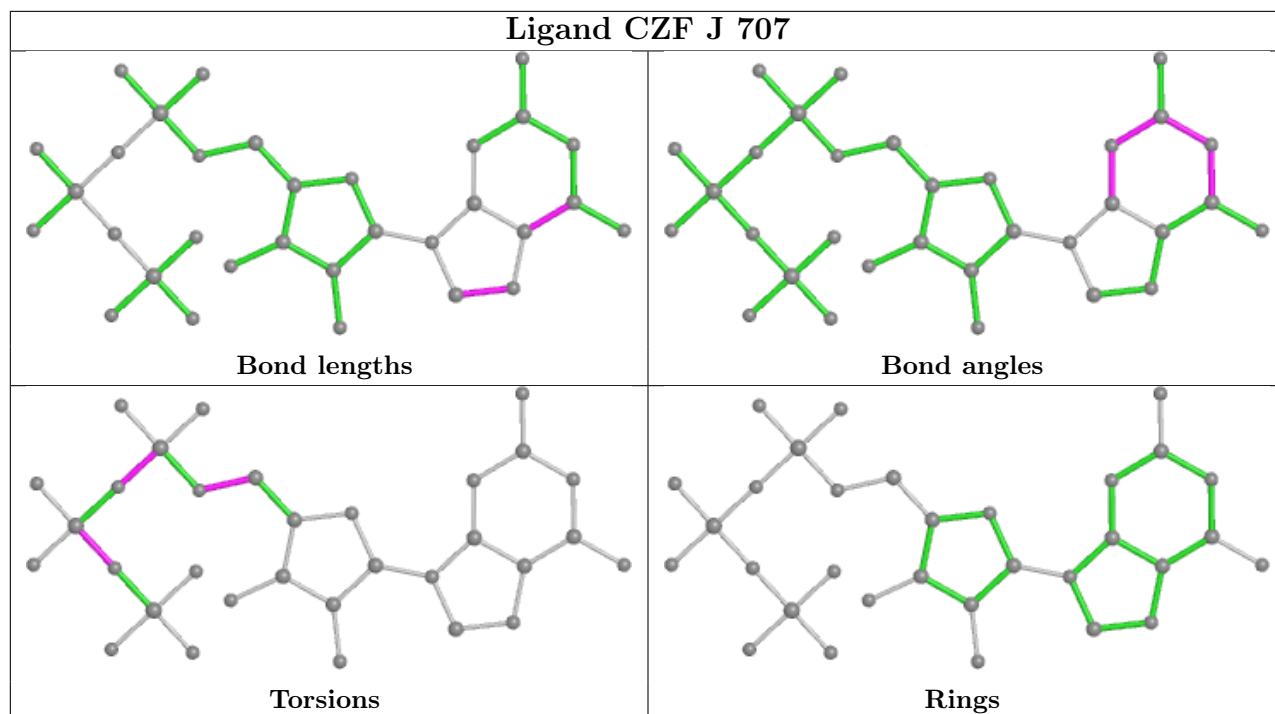


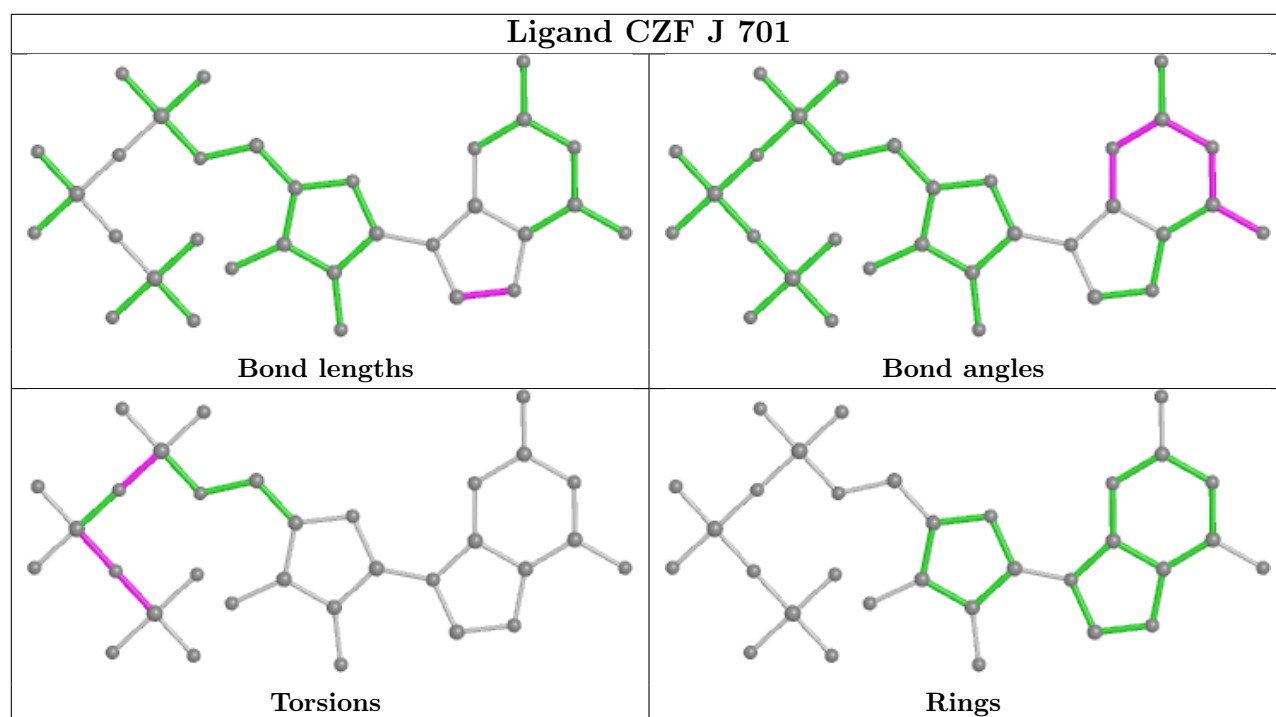
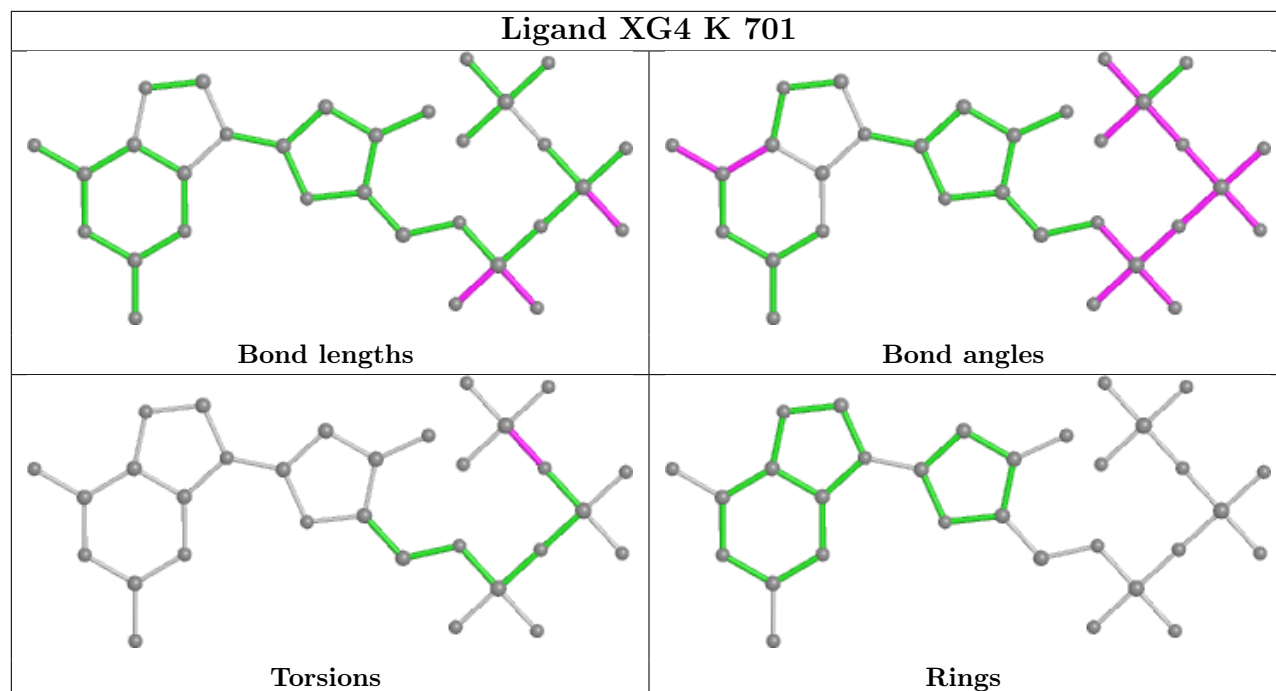


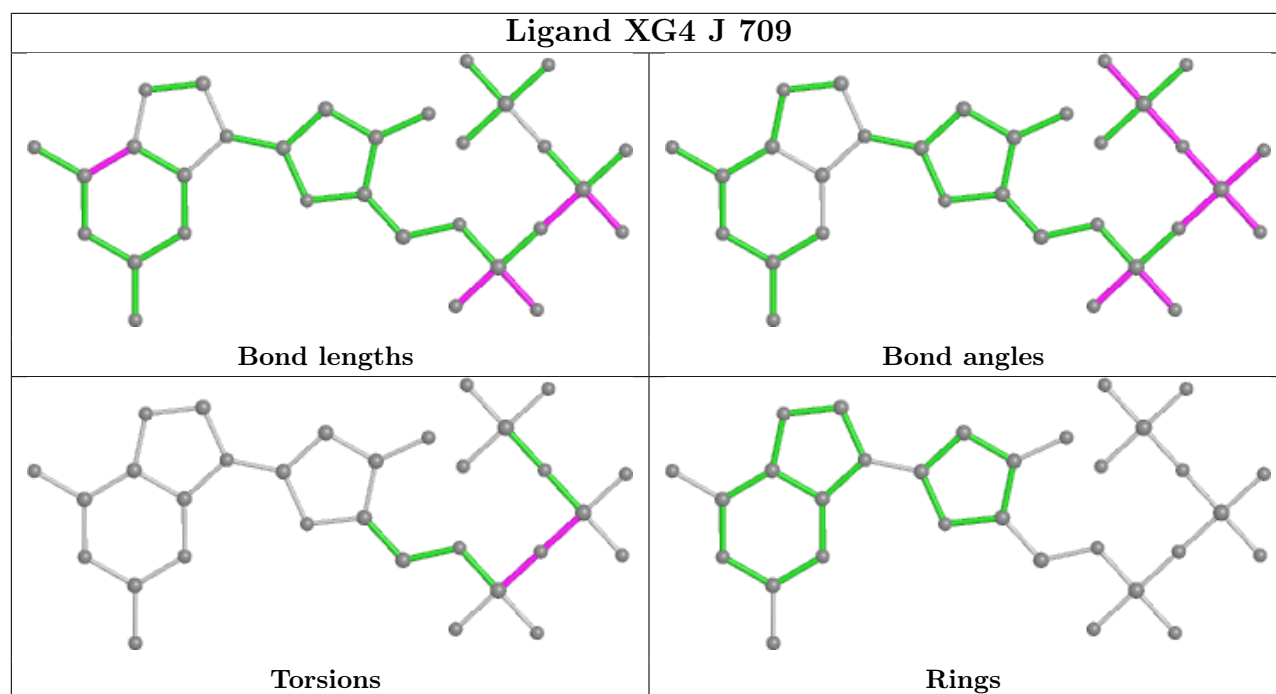
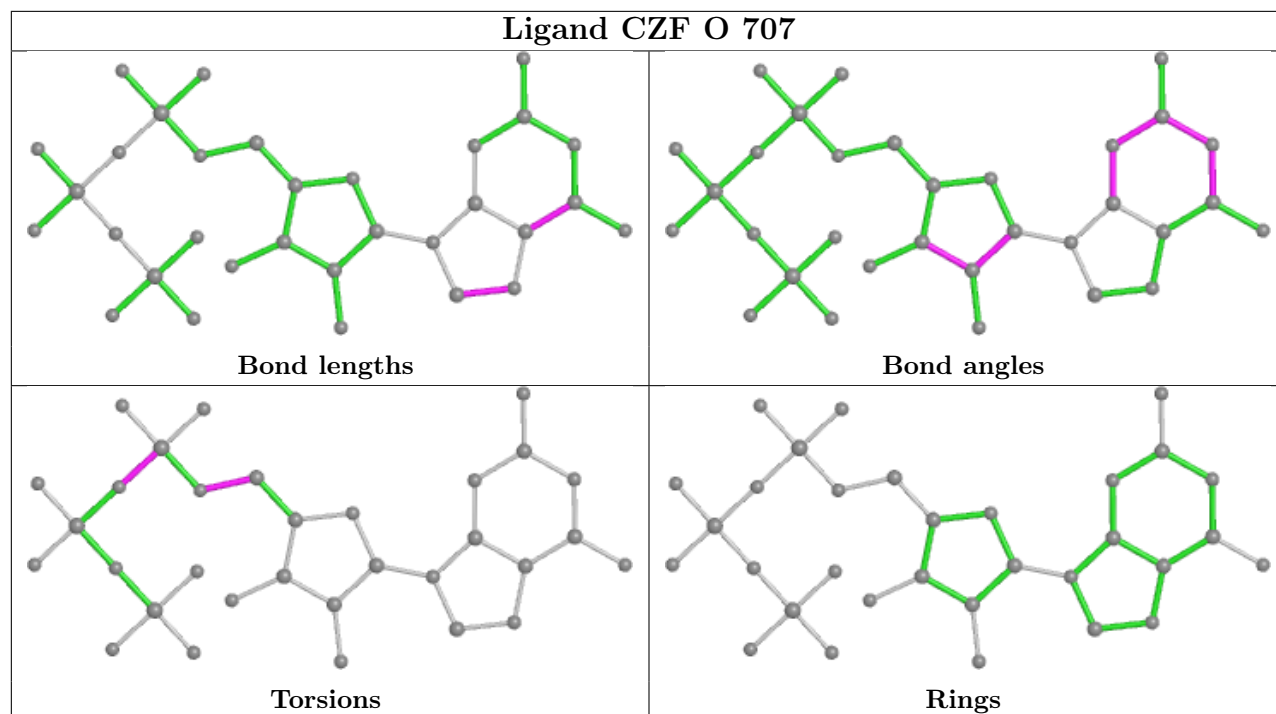


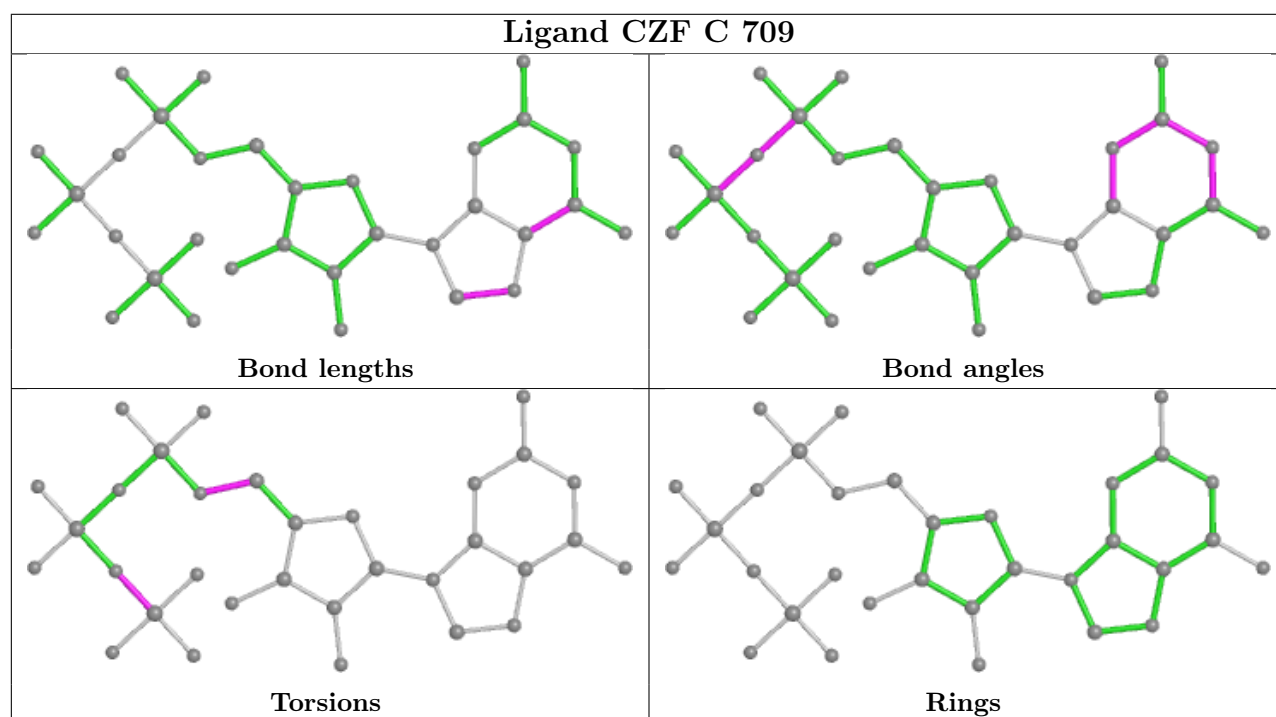
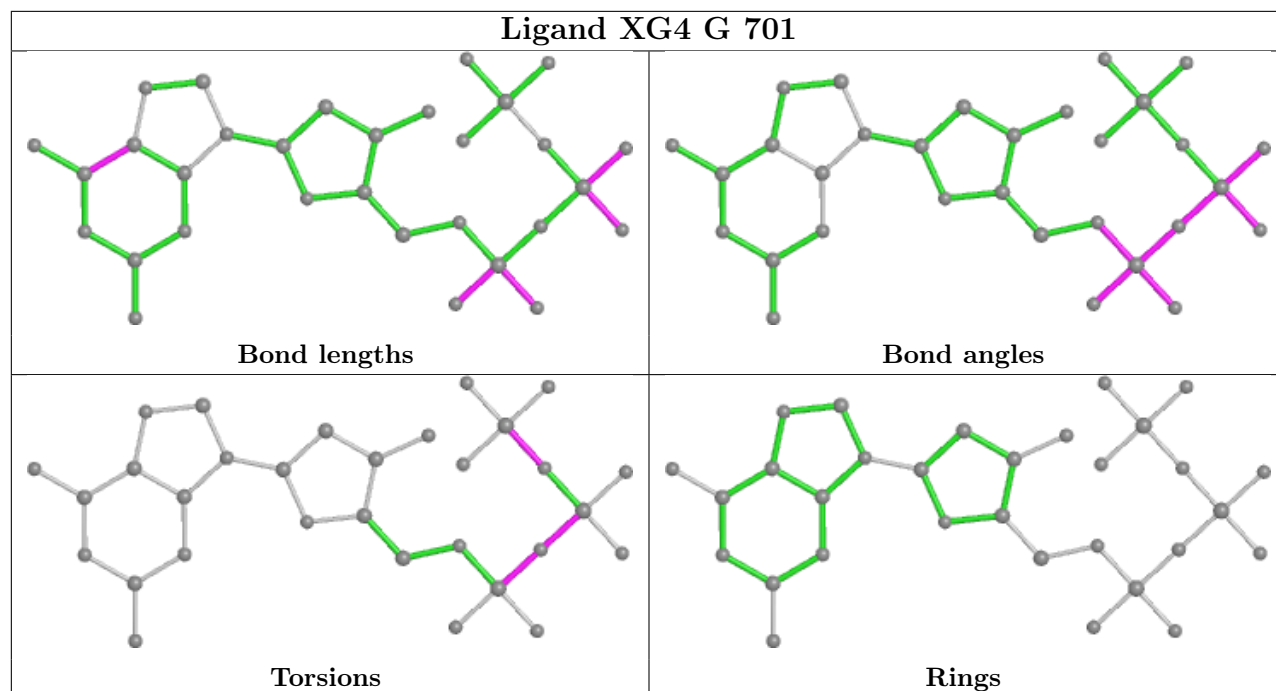


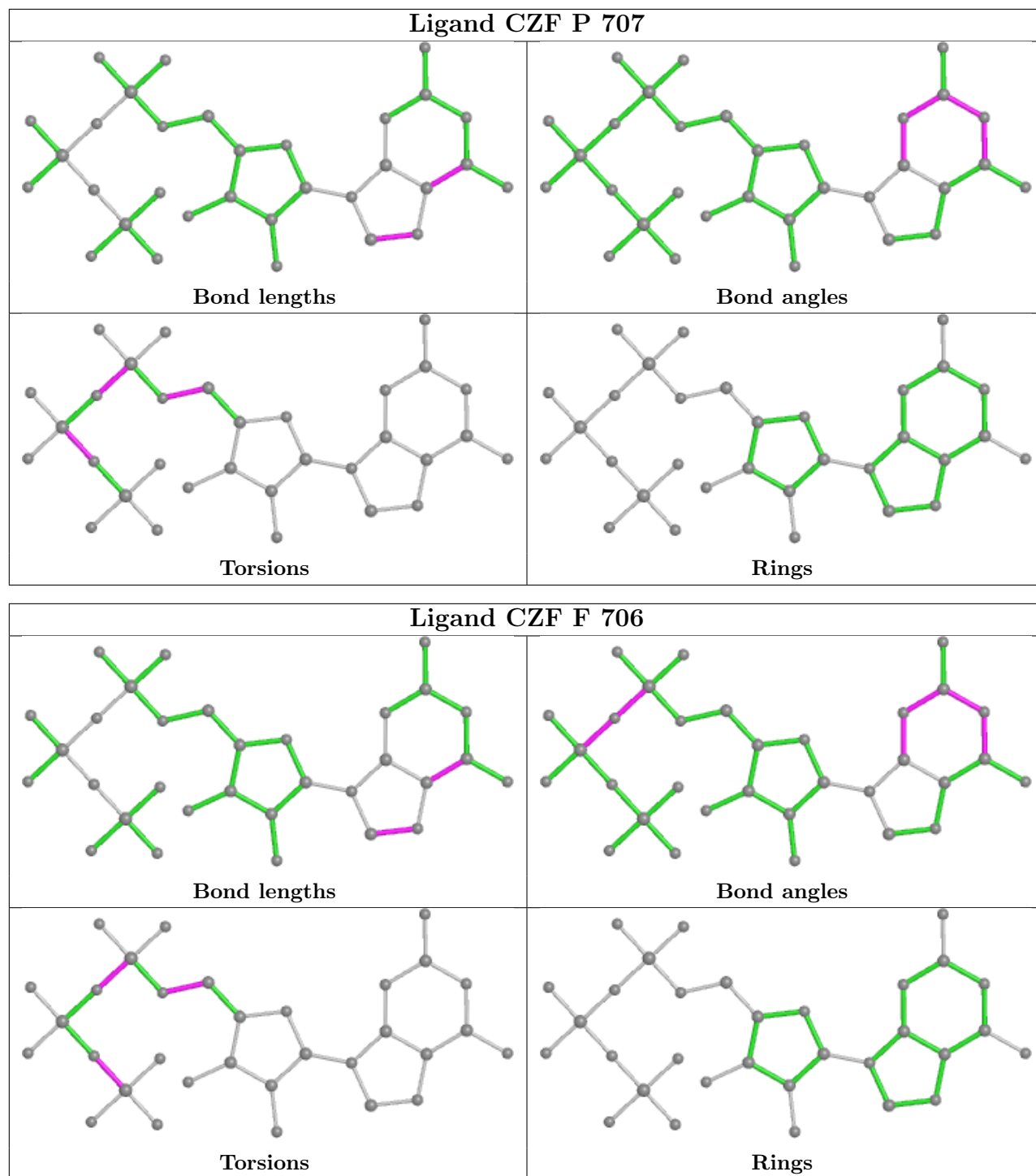


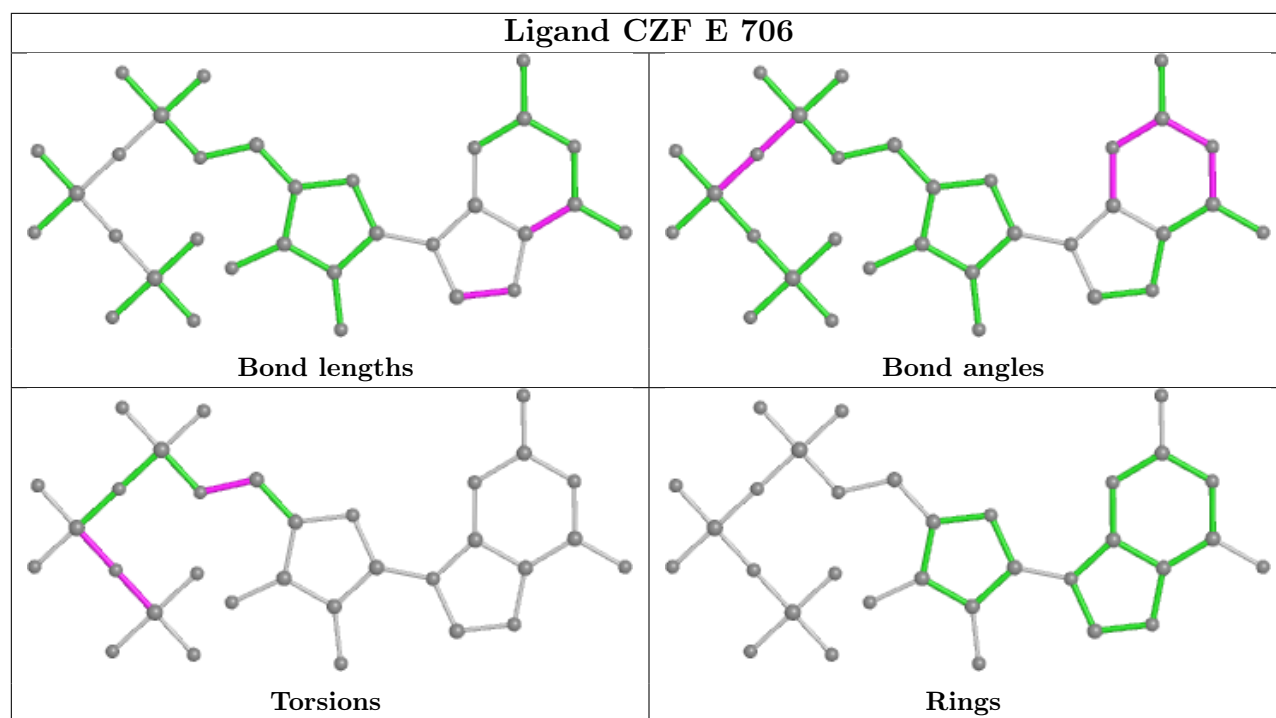
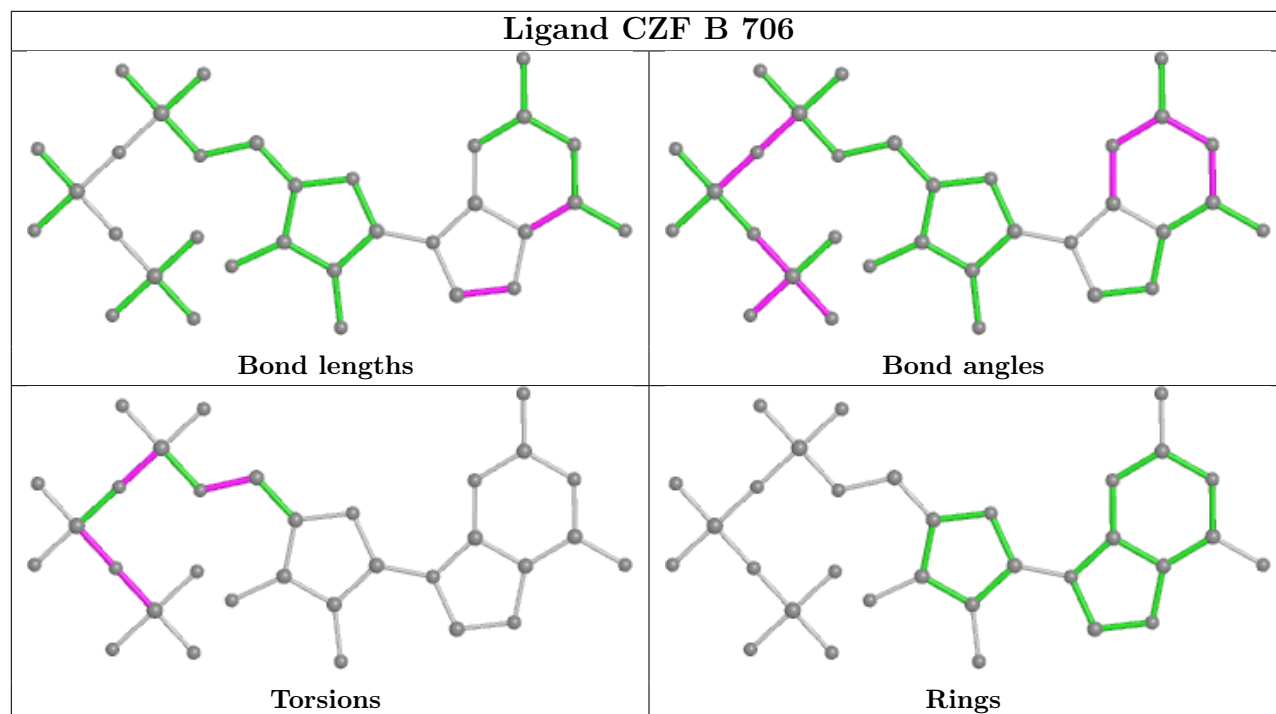


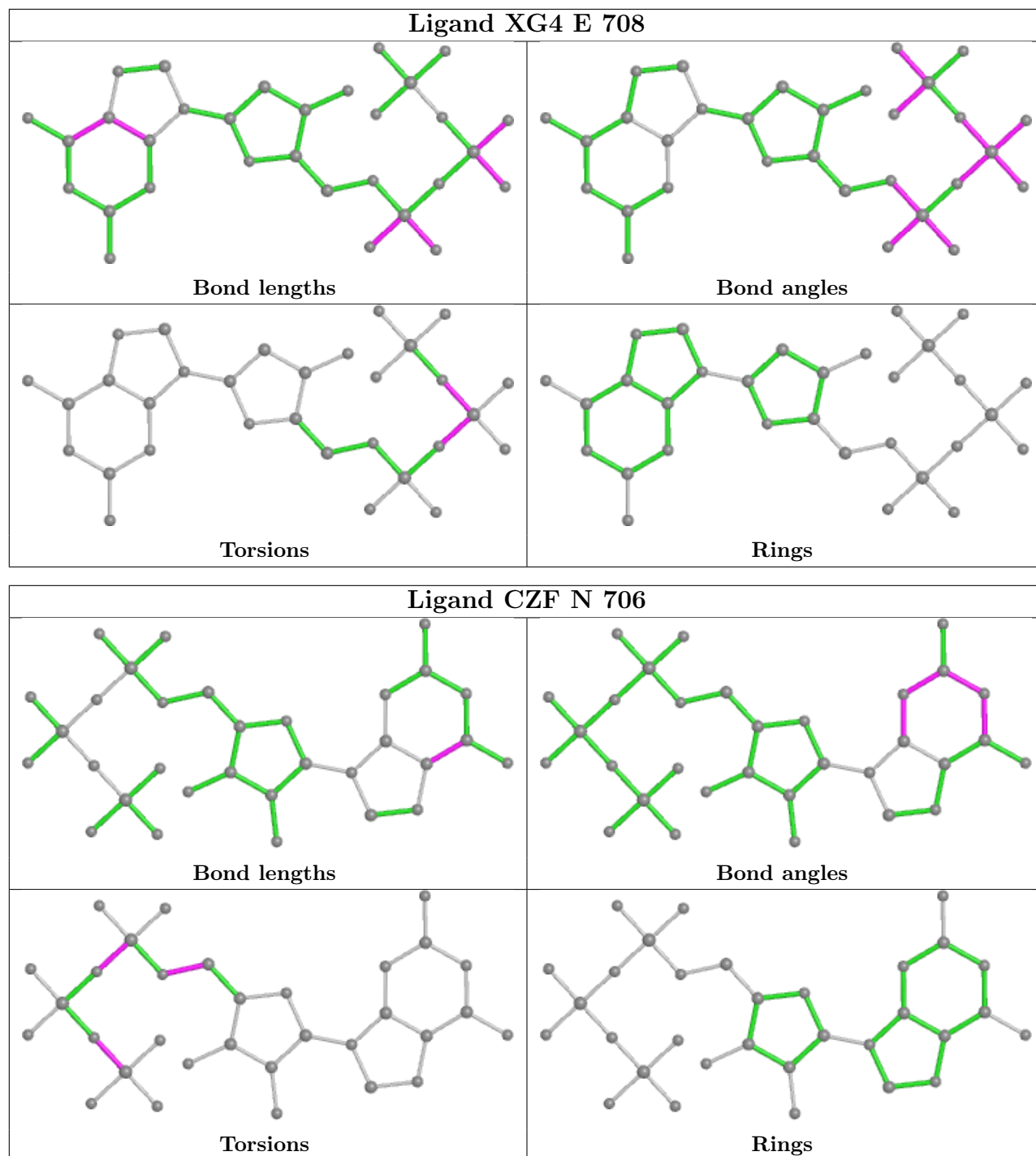


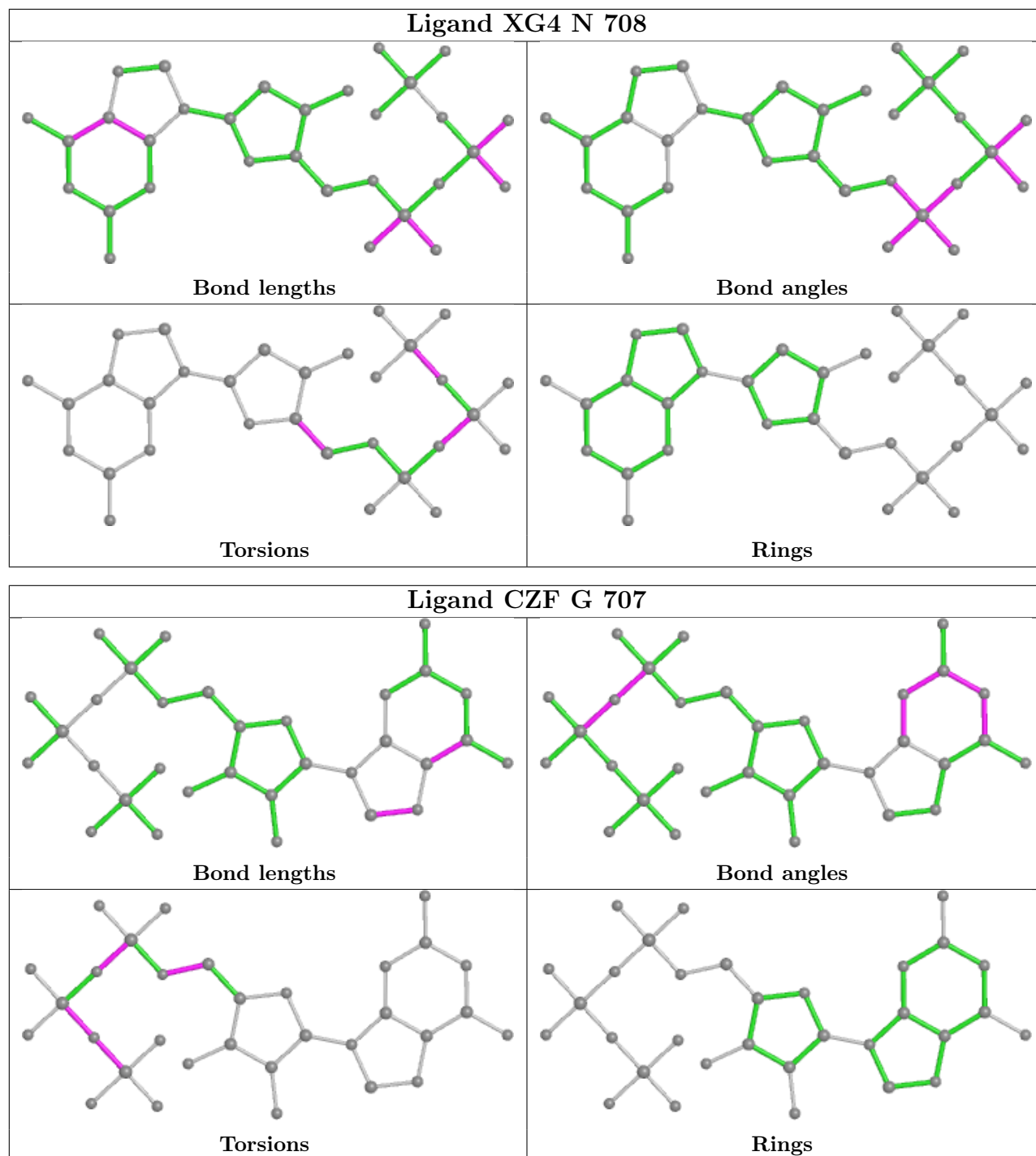


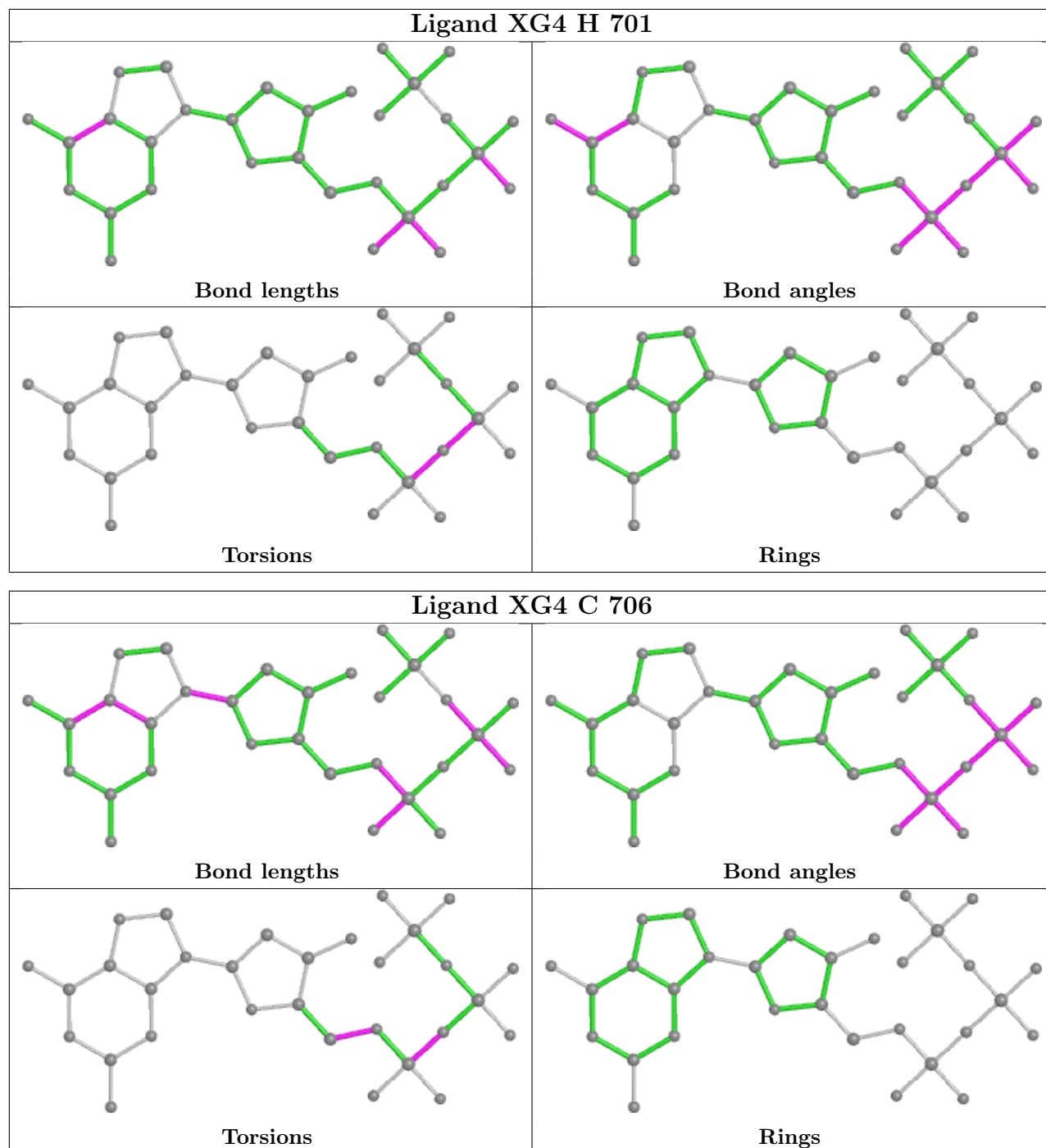


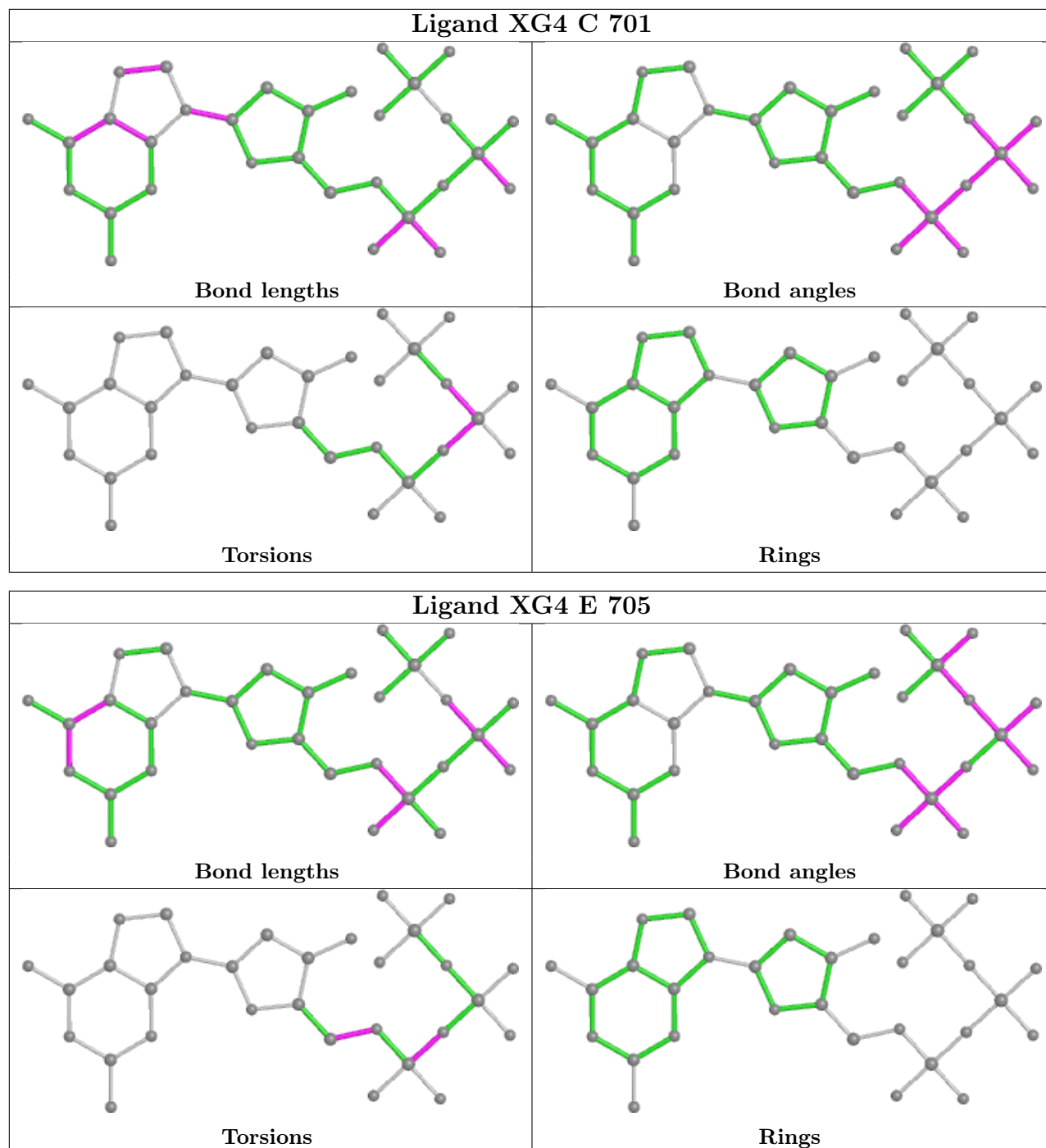


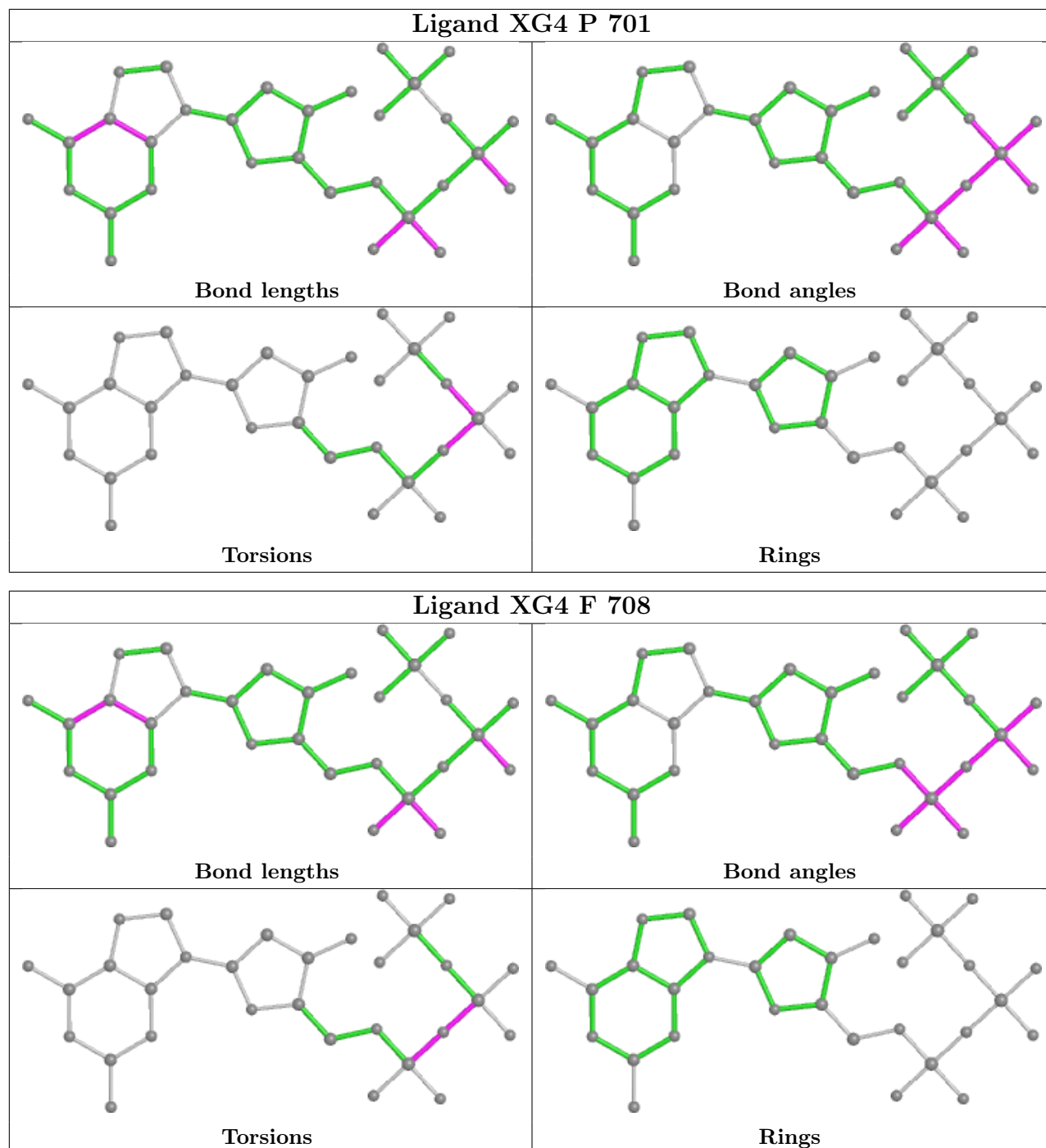


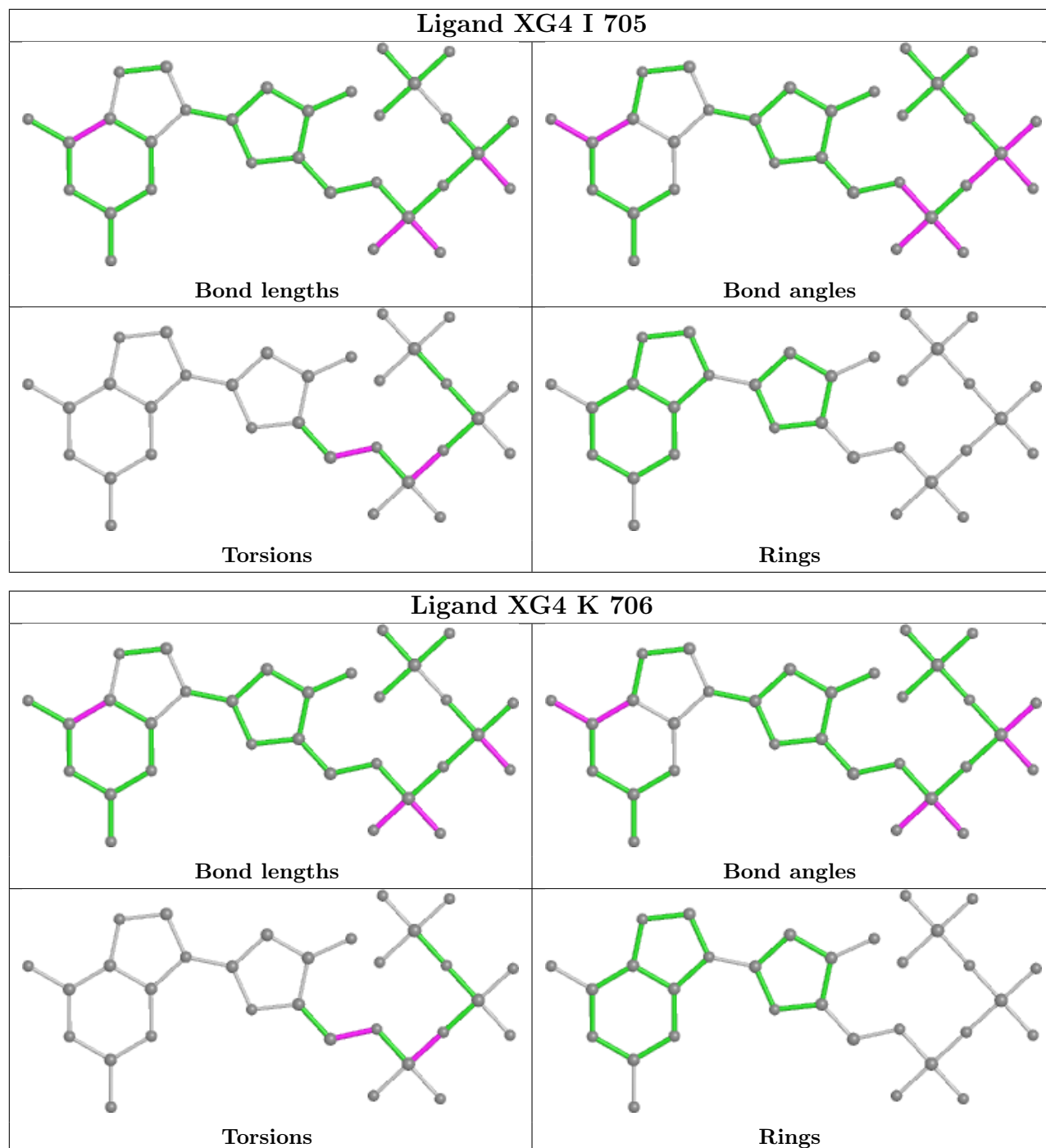


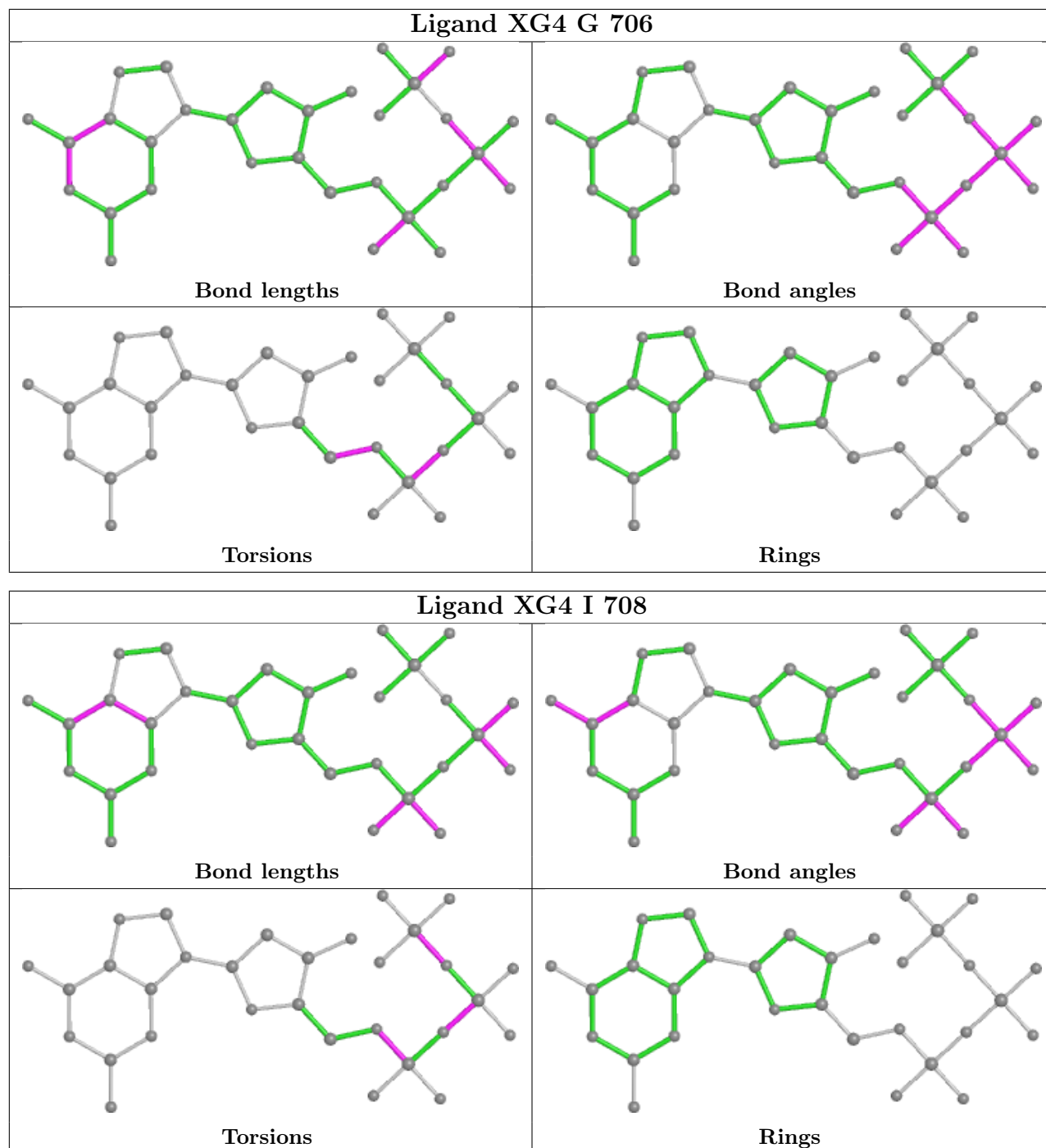


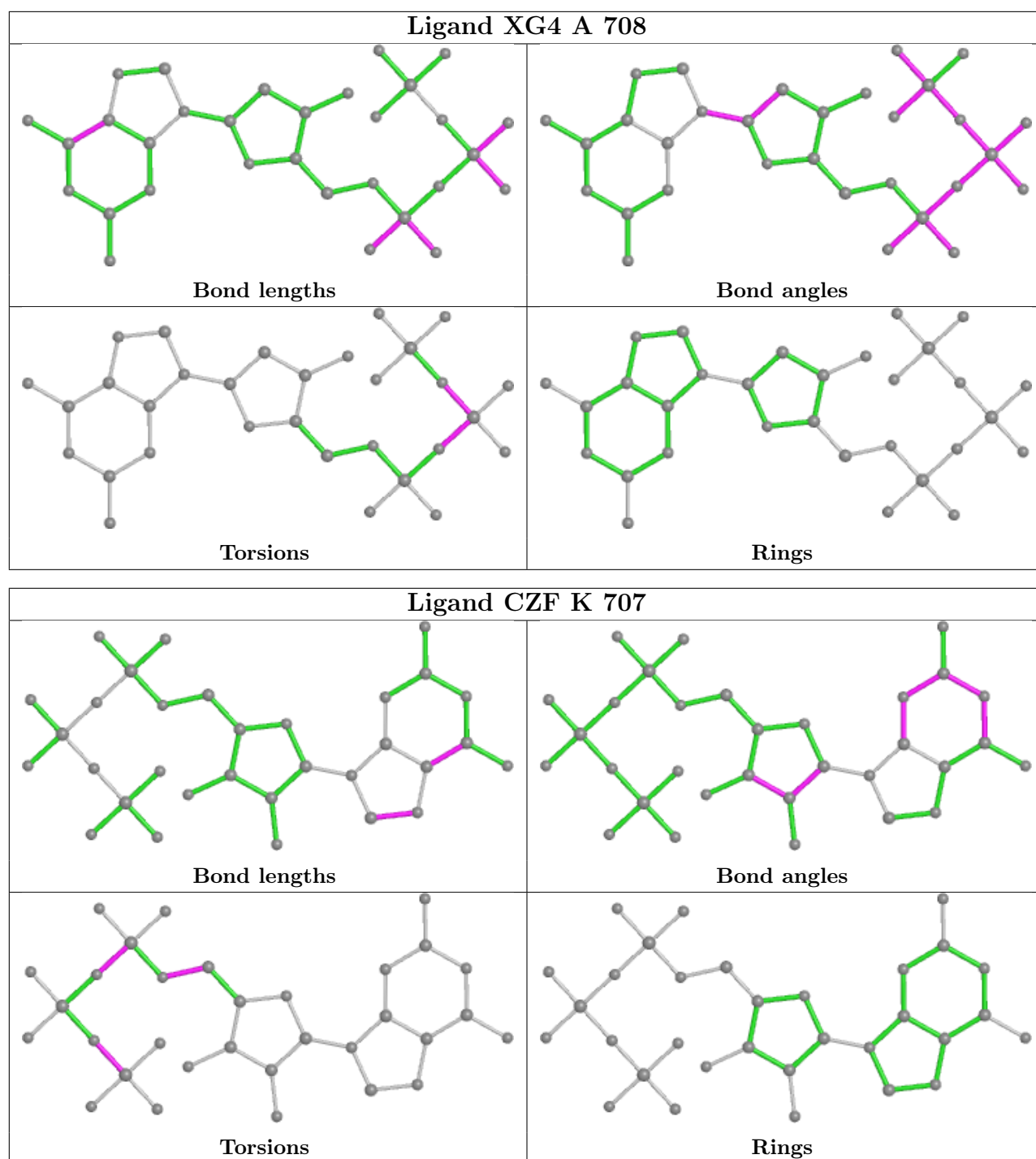












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	480/520 (92%)	-0.21	1 (0%) 95 95	11, 37, 68, 117	0
1	B	479/520 (92%)	-0.09	3 (0%) 89 89	17, 45, 87, 118	0
1	C	480/520 (92%)	-0.13	2 (0%) 92 92	17, 44, 80, 105	0
1	D	481/520 (92%)	-0.16	1 (0%) 95 95	12, 40, 70, 105	0
1	E	479/520 (92%)	-0.06	4 (0%) 86 85	19, 50, 90, 118	0
1	F	478/520 (91%)	0.01	5 (1%) 82 81	22, 53, 103, 133	0
1	G	479/520 (92%)	-0.08	3 (0%) 89 89	18, 47, 93, 118	0
1	H	480/520 (92%)	-0.25	1 (0%) 95 95	13, 38, 69, 99	0
1	I	479/520 (92%)	0.08	1 (0%) 95 95	23, 63, 97, 109	0
1	J	478/520 (91%)	-0.07	2 (0%) 92 92	19, 49, 87, 101	0
1	K	478/520 (91%)	0.07	3 (0%) 89 89	26, 63, 96, 114	0
1	L	478/520 (91%)	0.20	18 (3%) 40 35	23, 67, 121, 140	0
1	M	476/520 (91%)	0.31	13 (2%) 54 50	36, 77, 110, 126	0
1	N	477/520 (91%)	0.11	4 (0%) 86 85	33, 63, 93, 108	0
1	O	486/520 (93%)	0.22	7 (1%) 75 74	30, 67, 119, 140	0
1	P	478/520 (91%)	0.36	16 (3%) 46 41	37, 74, 140, 166	0
All	All	7666/8320 (92%)	0.02	84 (1%) 80 80	11, 54, 103, 166	0

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	480	VAL	4.0
1	B	594	GLN	4.0
1	M	572	TRP	3.8
1	P	583	ASP	3.6
1	M	345	ASN	3.4

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Mol	Chain	Res	Type	RSRZ
1	P	598	TRP	3.3
1	O	495	ALA	3.3
1	P	584	GLY	3.2
1	A	490	ASP	3.2
1	O	114	THR	3.1
1	P	489	LEU	3.1
1	L	488	LEU	3.0
1	G	114	THR	3.0
1	B	488	LEU	3.0
1	P	497	ASP	3.0
1	L	487	VAL	2.9
1	L	489	LEU	2.9
1	N	403	GLY	2.9
1	G	115	MET	2.8
1	O	594	GLN	2.8
1	M	498	PHE	2.8
1	P	571	GLN	2.8
1	K	599	ASN	2.8
1	K	255	GLU	2.8
1	L	471	GLU	2.8
1	L	345	ASN	2.7
1	L	493	LEU	2.7
1	P	553	TYR	2.7
1	M	399	ILE	2.7
1	O	499	ILE	2.7
1	L	597	GLU	2.6
1	L	594	GLN	2.6
1	L	587	ILE	2.5
1	M	503	ILE	2.5
1	B	114	THR	2.5
1	L	562	LEU	2.5
1	G	569	PHE	2.4
1	F	562	LEU	2.4
1	H	284	LEU	2.4
1	L	596	LYS	2.4
1	E	568	TYR	2.4
1	K	471	GLU	2.4
1	P	552	VAL	2.4
1	P	566	ARG	2.3
1	J	590	LEU	2.3
1	D	114	THR	2.3
1	L	590	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	P	587	ILE	2.3
1	E	577	ASN	2.2
1	L	592	THR	2.2
1	P	597	GLU	2.2
1	M	490	ASP	2.2
1	O	554	CYS	2.2
1	L	598	TRP	2.2
1	P	403	GLY	2.2
1	F	114	THR	2.2
1	M	398	GLU	2.2
1	J	488	LEU	2.2
1	I	276	LEU	2.2
1	L	492	LYS	2.1
1	L	582	GLN	2.1
1	M	501	ASP	2.1
1	F	347	LEU	2.1
1	N	117	VAL	2.1
1	O	569	PHE	2.1
1	O	575	ASP	2.1
1	F	569	PHE	2.1
1	C	490	ASP	2.1
1	E	488	LEU	2.1
1	M	488	LEU	2.1
1	L	573	CYS	2.1
1	M	594	GLN	2.0
1	M	288	LYS	2.0
1	P	498	PHE	2.0
1	N	300	ILE	2.0
1	F	184	GLU	2.0
1	C	115	MET	2.0
1	E	586	VAL	2.0
1	P	491	VAL	2.0
1	L	393	ALA	2.0
1	M	489	LEU	2.0
1	P	592	THR	2.0
1	N	178	LEU	2.0
1	P	596	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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
6	SO4	I	706	5/5	0.68	0.25	125,130,132,137	0
6	SO4	M	707	5/5	0.79	0.33	140,145,151,154	0
6	SO4	N	707	5/5	0.79	0.31	112,119,120,126	0
6	SO4	G	708	5/5	0.84	0.28	107,109,114,114	0
6	SO4	L	707	5/5	0.89	0.30	96,99,104,108	0
6	SO4	F	707	5/5	0.89	0.26	102,103,107,111	0
6	SO4	K	708	5/5	0.89	0.17	88,90,91,93	0
6	SO4	C	708	5/5	0.92	0.14	88,90,92,95	0
6	SO4	O	708	5/5	0.92	0.18	96,97,98,100	0
3	MG	O	704	1/1	0.93	0.08	13,13,13,13	0
6	SO4	E	707	5/5	0.93	0.18	76,79,81,86	0
3	MG	N	703	1/1	0.94	0.12	26,26,26,26	0
3	MG	K	704	1/1	0.94	0.08	21,21,21,21	0
5	CZF	N	706	32/32	0.95	0.15	49,53,56,57	0
6	SO4	D	707	5/5	0.95	0.19	72,73,74,75	0
6	SO4	H	708	5/5	0.95	0.17	79,81,83,83	0
6	SO4	B	707	5/5	0.95	0.13	84,85,86,88	0
6	SO4	J	708	5/5	0.95	0.16	77,78,80,81	0
4	XG4	P	706	31/31	0.96	0.15	49,58,72,75	0
3	MG	N	704	1/1	0.96	0.08	22,22,22,22	0
5	CZF	O	707	32/32	0.96	0.13	50,59,66,67	0
6	SO4	A	707	5/5	0.96	0.19	76,78,80,81	0
3	MG	D	704	1/1	0.96	0.18	11,11,11,11	0
4	XG4	L	705	31/31	0.96	0.15	38,47,57,59	0
4	XG4	M	705	31/31	0.96	0.13	49,54,61,66	0
4	XG4	M	708	31/31	0.96	0.15	45,53,70,74	0
4	XG4	P	701	31/31	0.96	0.16	45,49,57,58	0
4	XG4	F	705	31/31	0.97	0.14	19,23,25,27	0
5	CZF	P	707	32/32	0.97	0.14	39,46,59,61	0
4	XG4	G	706	31/31	0.97	0.14	16,18,20,21	0
4	XG4	H	706	31/31	0.97	0.13	11,13,14,14	0
4	XG4	I	705	31/31	0.97	0.14	34,38,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	XG4	I	708	31/31	0.97	0.14	37,45,67,70	0
4	XG4	J	706	31/31	0.97	0.13	15,16,19,19	0
4	XG4	K	706	31/31	0.97	0.13	32,35,41,42	0
3	MG	F	703	1/1	0.97	0.14	12,12,12,12	0
3	MG	H	703	1/1	0.97	0.25	11,11,11,11	0
3	MG	C	704	1/1	0.97	0.14	12,12,12,12	0
4	XG4	O	706	31/31	0.97	0.15	34,42,45,49	0
4	XG4	A	705	31/31	0.97	0.13	10,10,10,10	0
4	XG4	C	706	31/31	0.97	0.13	18,20,21,21	0
5	CZF	J	701	32/32	0.97	0.14	34,38,50,52	0
5	CZF	K	707	32/32	0.97	0.13	58,63,67,70	0
4	XG4	D	706	31/31	0.97	0.13	11,11,11,12	0
3	MG	B	704	1/1	0.98	0.10	13,13,13,13	0
4	XG4	J	709	31/31	0.98	0.13	14,15,21,21	0
4	XG4	K	701	31/31	0.98	0.12	26,27,37,38	0
3	MG	K	705	1/1	0.98	0.05	39,39,39,39	0
3	MG	M	703	1/1	0.98	0.07	21,21,21,21	0
3	MG	M	704	1/1	0.98	0.07	14,14,14,14	0
2	FE	M	701	1/1	0.98	0.07	61,61,61,61	0
4	XG4	N	705	31/31	0.98	0.12	37,41,46,47	0
4	XG4	N	708	31/31	0.98	0.13	38,41,54,55	0
4	XG4	O	701	31/31	0.98	0.13	28,31,35,37	0
2	FE	O	702	1/1	0.98	0.10	50,50,50,50	0
3	MG	D	705	1/1	0.98	0.10	15,15,15,15	0
3	MG	O	705	1/1	0.98	0.07	40,40,40,40	0
5	CZF	A	706	32/32	0.98	0.13	21,24,32,33	0
5	CZF	B	706	32/32	0.98	0.13	14,15,23,24	0
5	CZF	C	707	32/32	0.98	0.12	14,14,17,18	0
5	CZF	C	709	32/32	0.98	0.13	27,31,38,39	0
5	CZF	E	706	32/32	0.98	0.13	27,30,40,41	0
5	CZF	F	706	32/32	0.98	0.13	26,30,39,40	0
5	CZF	G	707	32/32	0.98	0.12	13,15,24,24	0
5	CZF	H	707	32/32	0.98	0.12	16,17,22,22	0
3	MG	P	703	1/1	0.98	0.19	15,15,15,15	0
5	CZF	J	707	32/32	0.98	0.13	22,27,34,35	0
3	MG	P	704	1/1	0.98	0.09	22,22,22,22	0
5	CZF	L	706	32/32	0.98	0.12	19,23,34,35	0
5	CZF	M	706	32/32	0.98	0.11	30,32,44,45	0
3	MG	E	702	1/1	0.98	0.22	11,11,11,11	0
4	XG4	A	708	31/31	0.98	0.12	12,13,19,19	0
4	XG4	B	705	31/31	0.98	0.12	13,15,19,20	0
4	XG4	B	708	31/31	0.98	0.14	26,27,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	MG	E	703	1/1	0.98	0.14	11,11,11,11	0
4	XG4	D	701	31/31	0.98	0.11	13,14,18,18	0
3	MG	A	703	1/1	0.98	0.16	10,10,10,10	0
4	XG4	E	705	31/31	0.98	0.13	15,19,28,29	0
4	XG4	E	708	31/31	0.98	0.12	15,16,23,23	0
3	MG	A	704	1/1	0.98	0.12	13,13,13,13	0
4	XG4	F	708	31/31	0.98	0.12	20,22,30,30	0
4	XG4	G	701	31/31	0.98	0.13	28,33,36,36	0
3	MG	H	704	1/1	0.98	0.20	11,11,11,11	0
4	XG4	H	701	31/31	0.98	0.13	22,24,29,29	0
3	MG	I	703	1/1	0.98	0.14	19,19,19,19	0
3	MG	J	704	1/1	0.98	0.18	10,10,10,10	0
4	XG4	I	707	31/31	0.98	0.14	26,27,43,44	0
3	MG	J	705	1/1	0.98	0.08	16,16,16,16	0
2	FE	L	701	1/1	0.99	0.11	40,40,40,40	0
2	FE	D	702	1/1	0.99	0.12	17,17,17,17	0
3	MG	P	705	1/1	0.99	0.06	16,16,16,16	0
3	MG	E	704	1/1	0.99	0.13	15,15,15,15	0
3	MG	F	702	1/1	0.99	0.28	12,12,12,12	0
2	FE	N	701	1/1	0.99	0.08	41,41,41,41	0
3	MG	F	704	1/1	0.99	0.12	15,15,15,15	0
4	XG4	C	701	31/31	0.99	0.13	21,22,33,33	0
3	MG	G	703	1/1	0.99	0.28	11,11,11,11	0
3	MG	G	704	1/1	0.99	0.13	11,11,11,11	0
3	MG	G	705	1/1	0.99	0.09	13,13,13,13	0
2	FE	E	701	1/1	0.99	0.11	24,24,24,24	0
3	MG	A	702	1/1	0.99	0.30	10,10,10,10	0
3	MG	H	705	1/1	0.99	0.08	14,14,14,14	0
3	MG	I	702	1/1	0.99	0.25	13,13,13,13	0
2	FE	F	701	1/1	0.99	0.12	28,28,28,28	0
3	MG	I	704	1/1	0.99	0.06	13,13,13,13	0
2	FE	G	702	1/1	0.99	0.11	19,19,19,19	0
3	MG	B	702	1/1	0.99	0.28	12,12,12,12	0
3	MG	K	703	1/1	0.99	0.22	13,13,13,13	0
3	MG	B	703	1/1	0.99	0.15	12,12,12,12	0
2	FE	H	702	1/1	0.99	0.10	13,13,13,13	0
3	MG	L	702	1/1	0.99	0.18	12,12,12,12	0
3	MG	L	703	1/1	0.99	0.10	12,12,12,12	0
3	MG	L	704	1/1	0.99	0.09	11,11,11,11	0
3	MG	M	702	1/1	0.99	0.17	14,14,14,14	0
3	MG	C	703	1/1	0.99	0.29	12,12,12,12	0
2	FE	I	701	1/1	0.99	0.09	37,37,37,37	0

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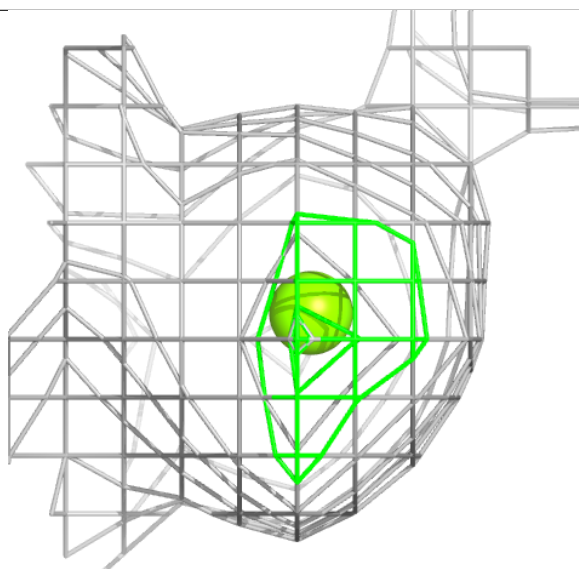
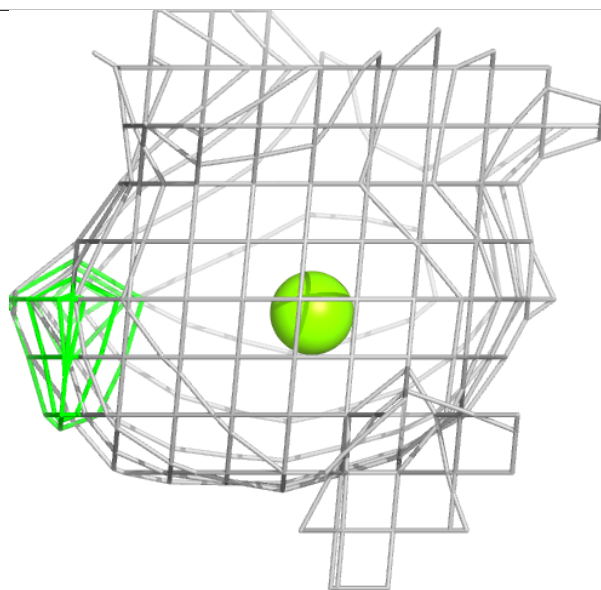
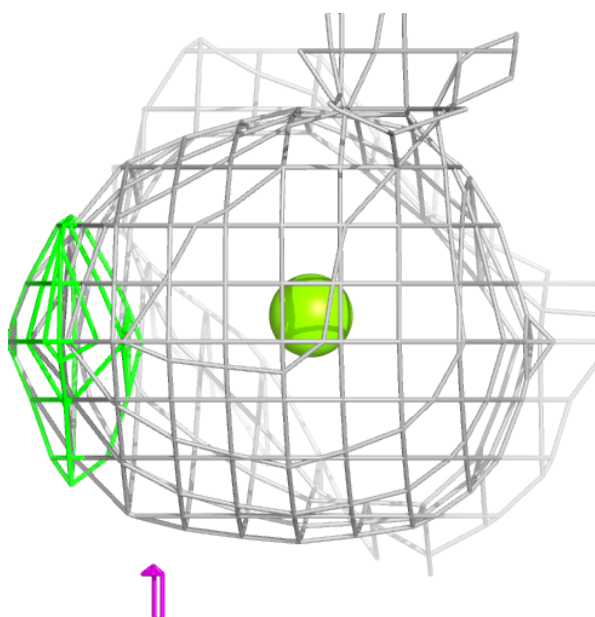
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å²)	Q<0.9
3	MG	N	702	1/1	0.99	0.20	14,14,14,14	0
3	MG	C	705	1/1	0.99	0.15	13,13,13,13	0
3	MG	D	703	1/1	0.99	0.26	12,12,12,12	0
2	FE	J	702	1/1	0.99	0.10	18,18,18,18	0
2	FE	K	702	1/1	0.99	0.12	50,50,50,50	0
2	FE	A	701	1/1	1.00	0.09	11,11,11,11	0
2	FE	B	701	1/1	1.00	0.12	20,20,20,20	0
2	FE	C	702	1/1	1.00	0.11	15,15,15,15	0
3	MG	O	703	1/1	1.00	0.25	13,13,13,13	0
3	MG	J	703	1/1	1.00	0.22	11,11,11,11	0
2	FE	P	702	1/1	1.00	0.13	48,48,48,48	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.

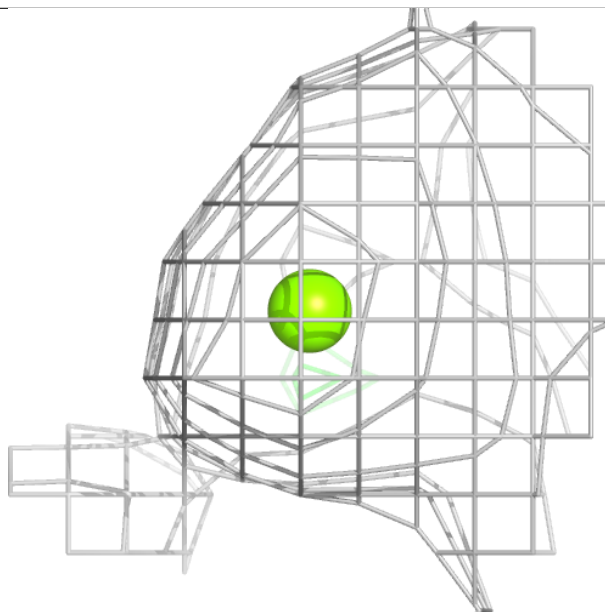
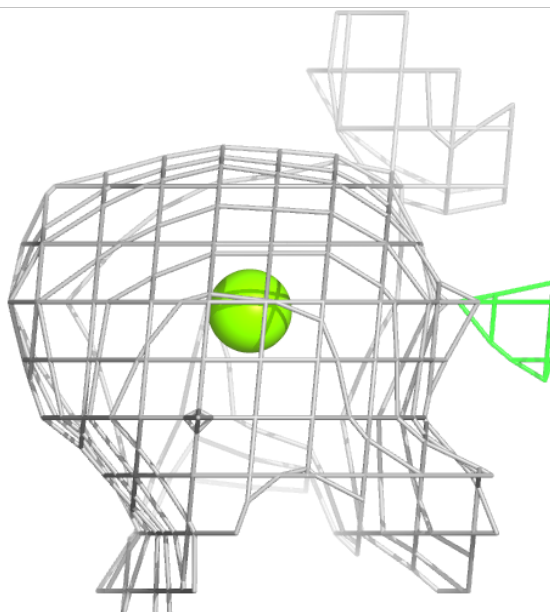
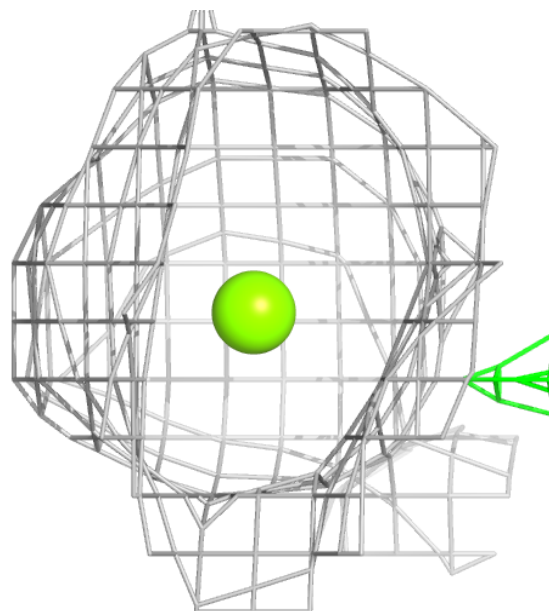
Electron density around MG O 704:

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



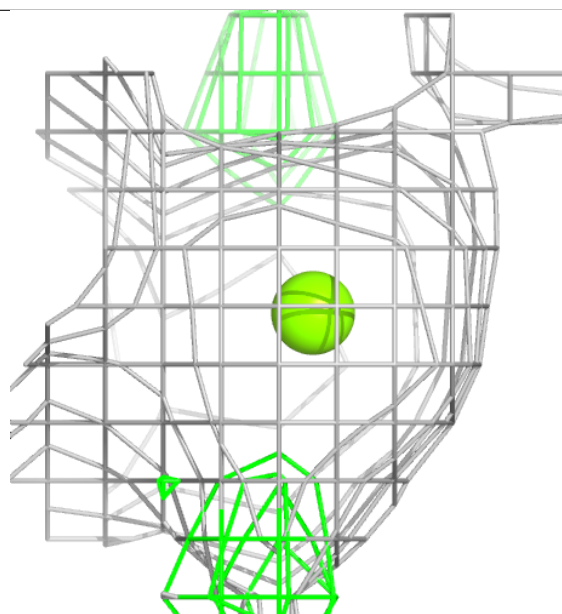
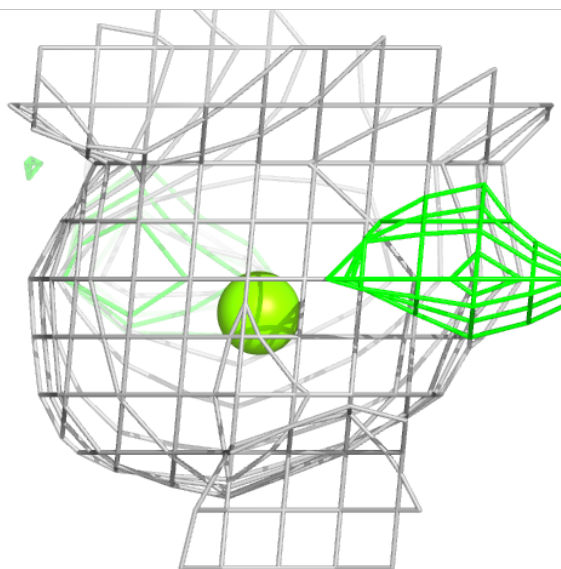
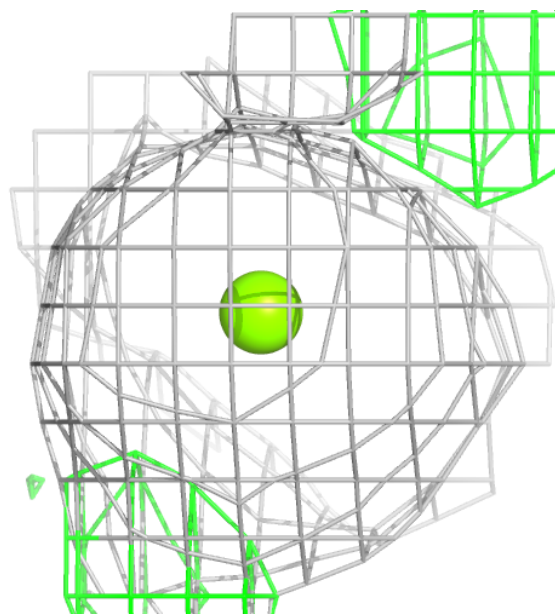
Electron density around MG N 703:

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



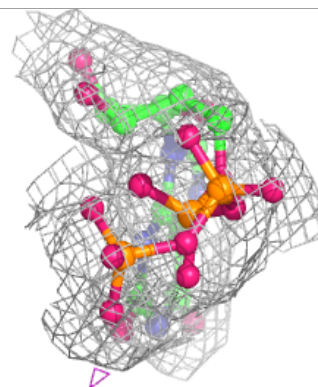
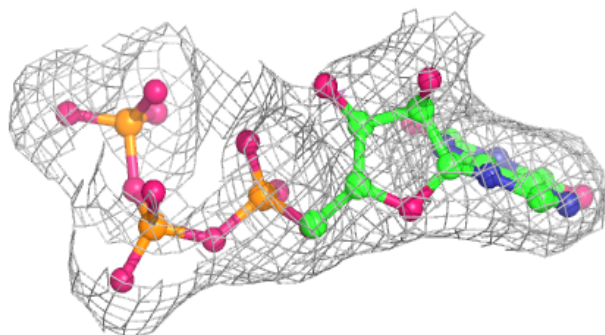
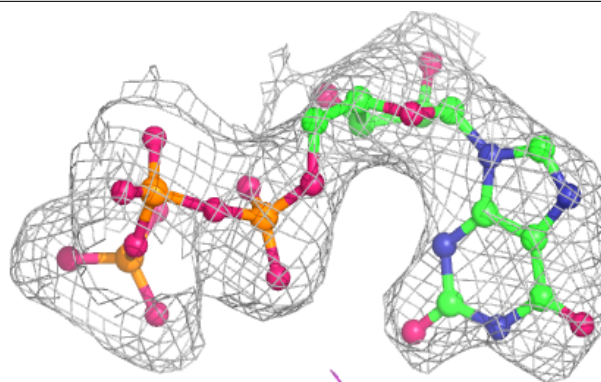
Electron density around MG K 704:

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

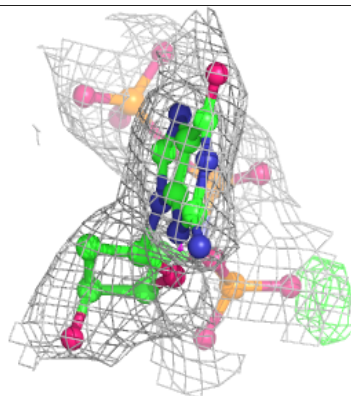
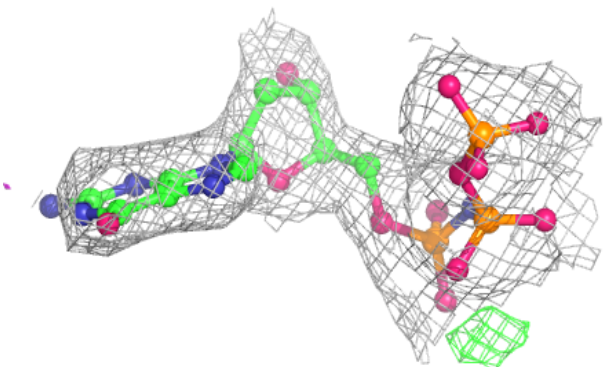
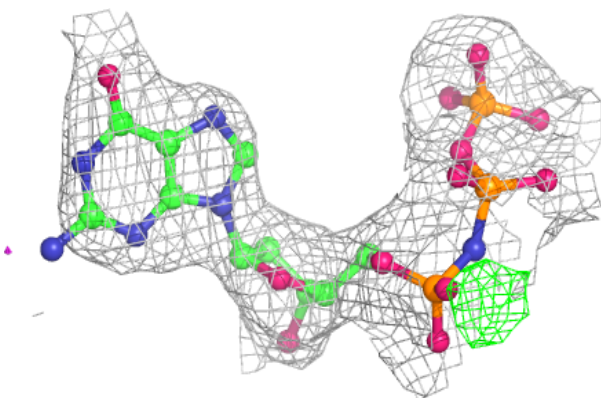


Electron density around CZF N 706:

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

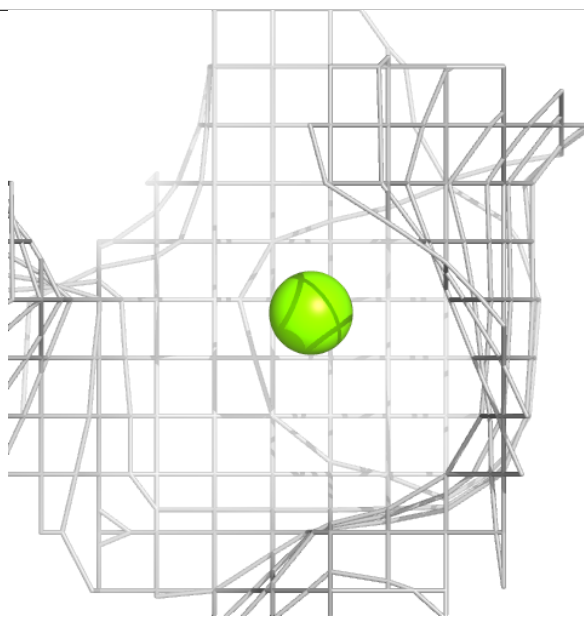
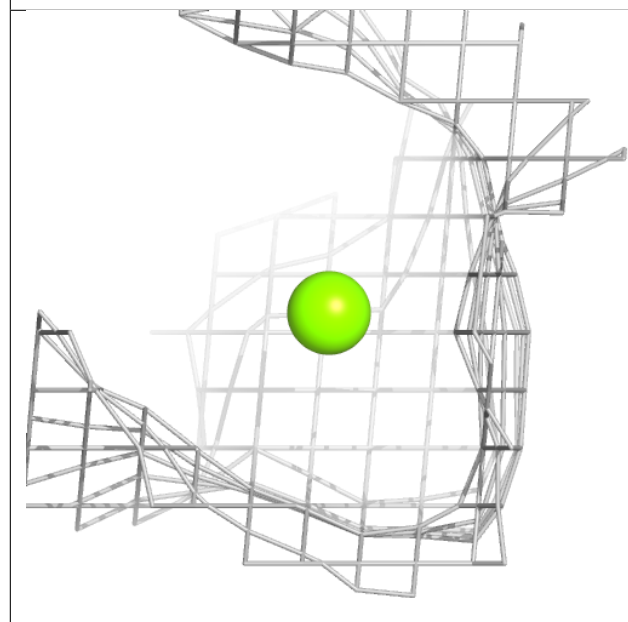
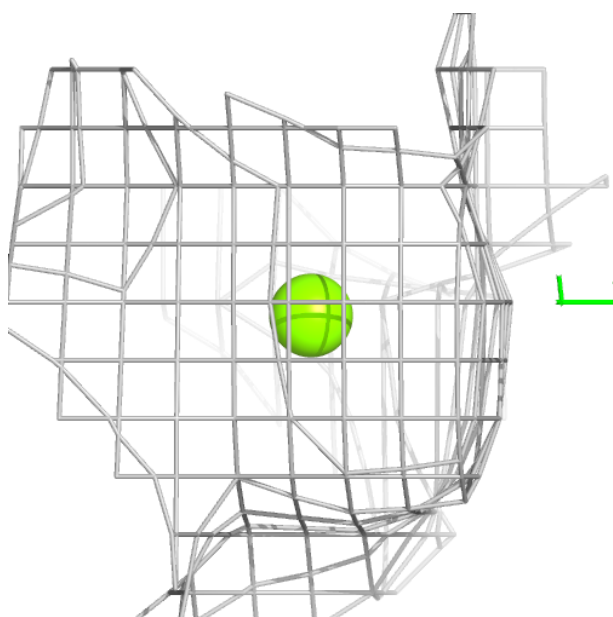
**Electron density around XG4 P 706:**

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



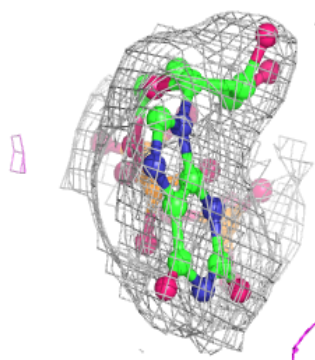
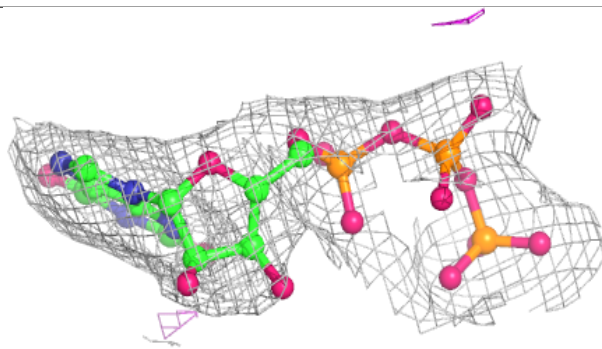
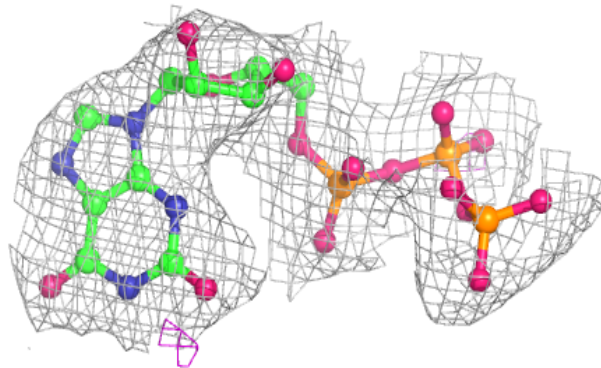
Electron density around MG N 704:

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



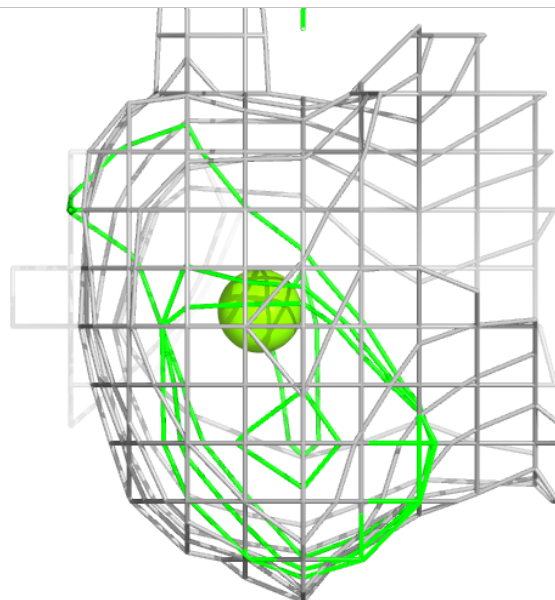
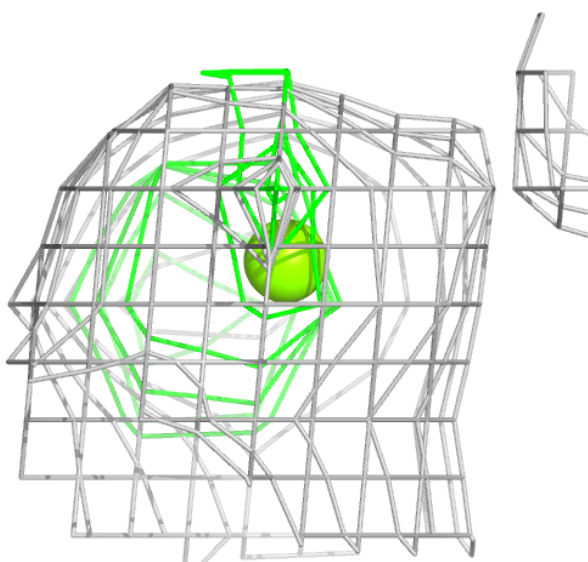
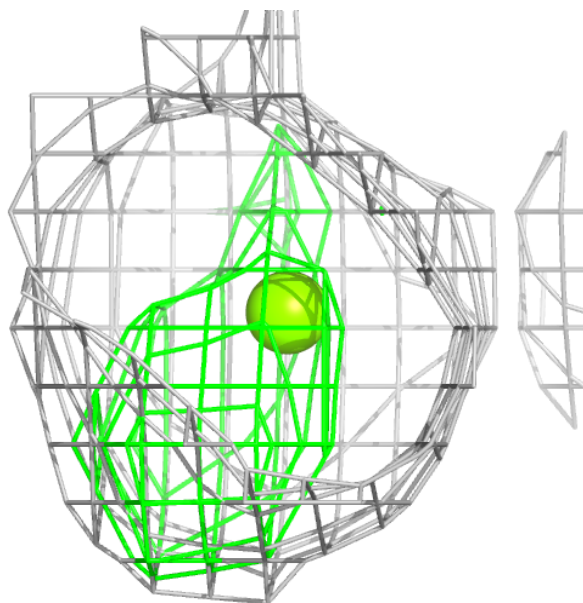
Electron density around CZF O 707:

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



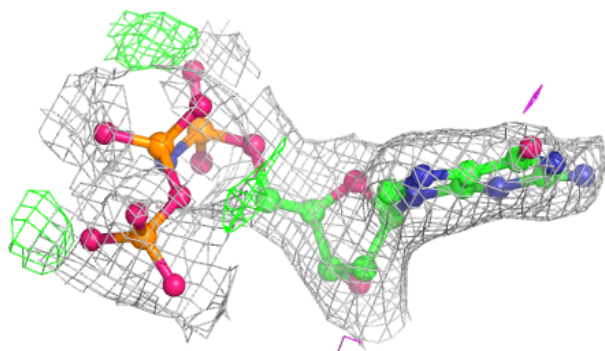
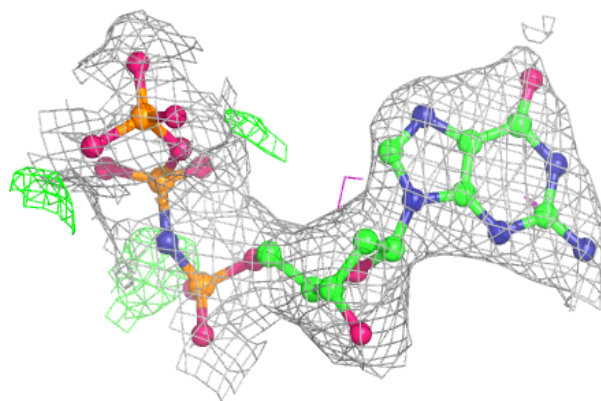
Electron density around MG D 704:

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and green (positive)

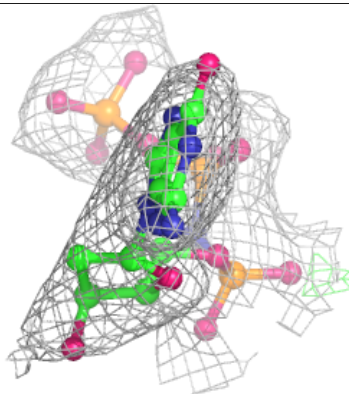
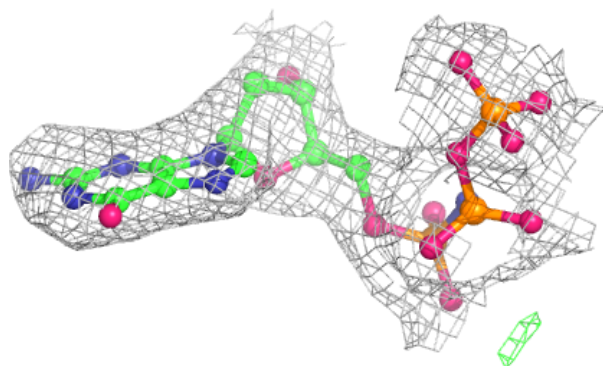
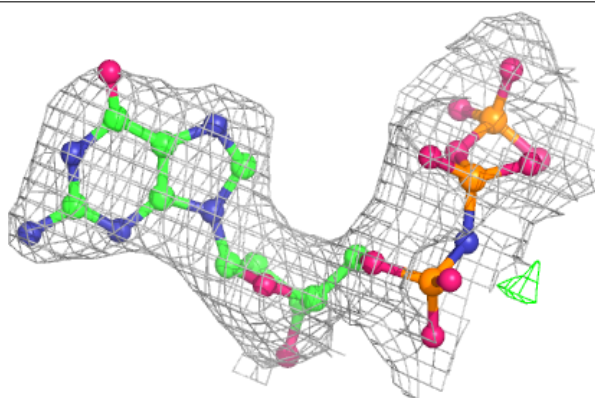


Electron density around XG4 L 705:

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

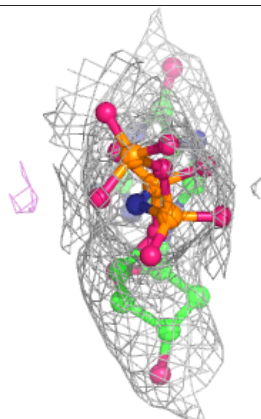
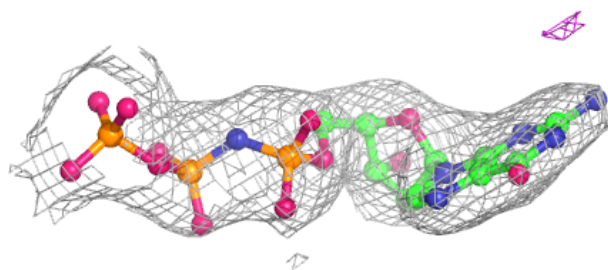
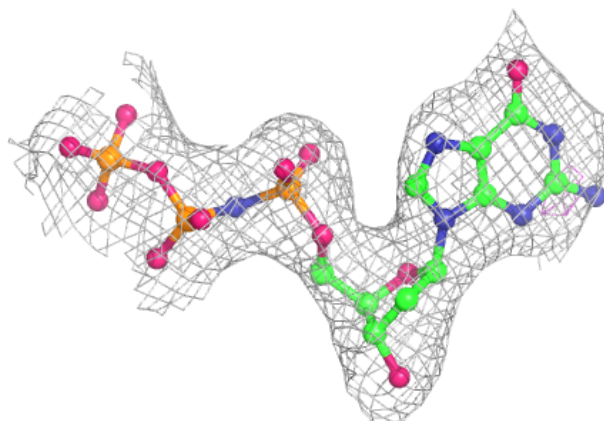
**Electron density around XG4 M 705:**

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

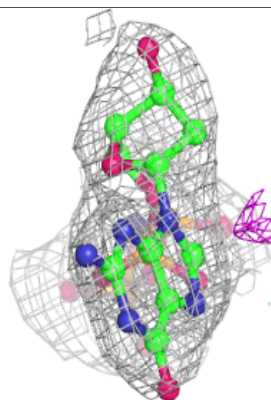
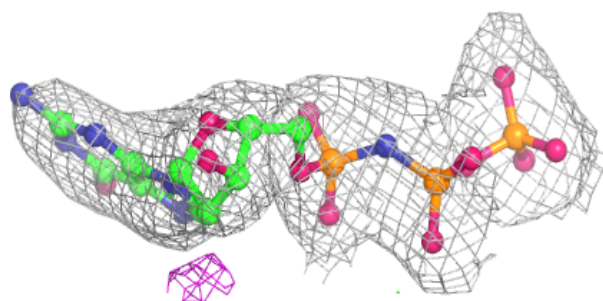
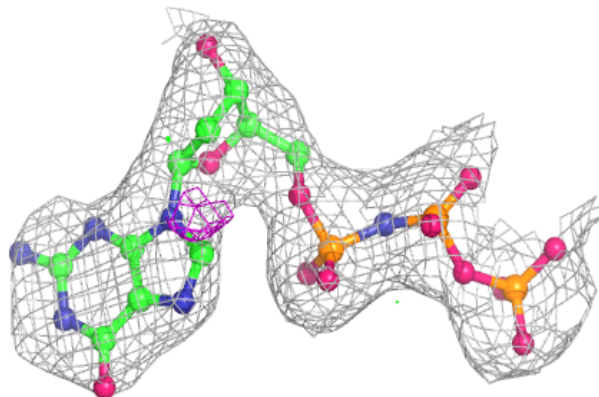


Electron density around XG4 M 708:

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

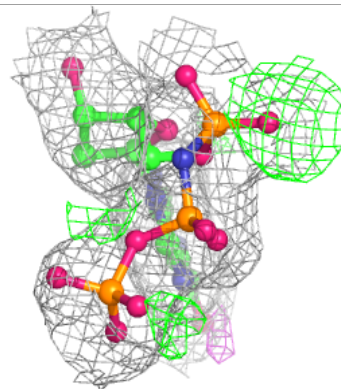
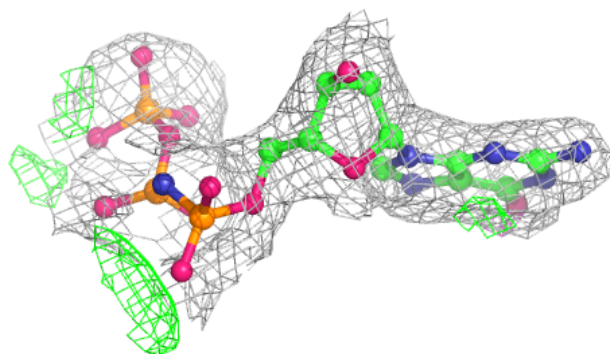
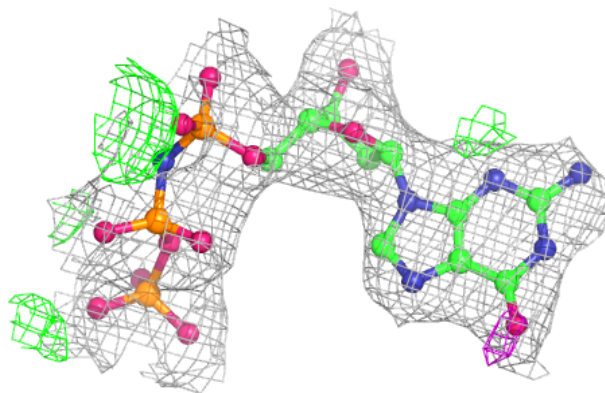
**Electron density around XG4 P 701:**

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

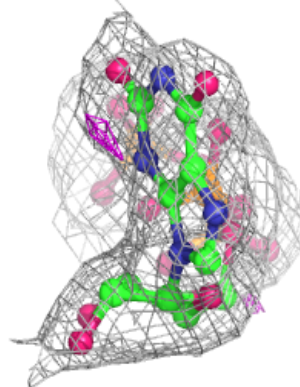
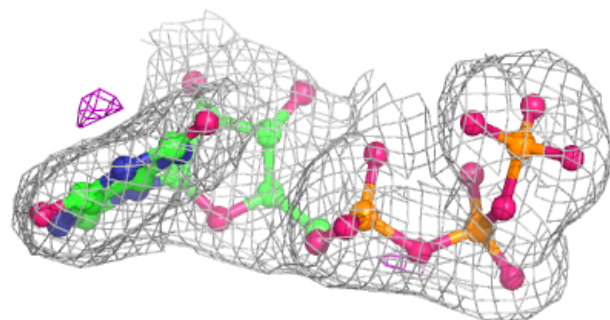
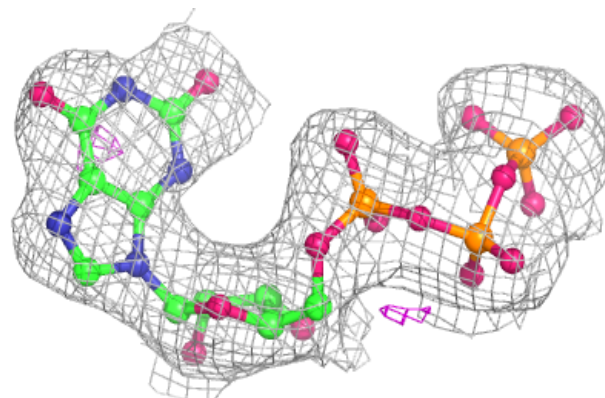


Electron density around XG4 F 705:

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

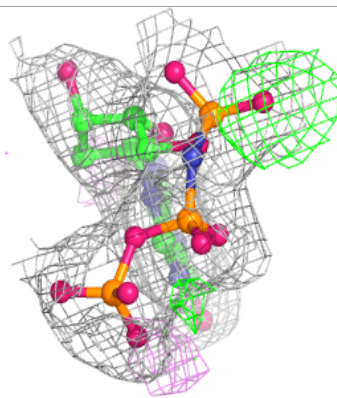
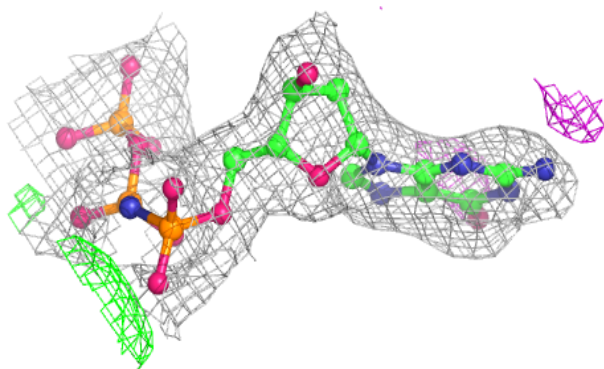
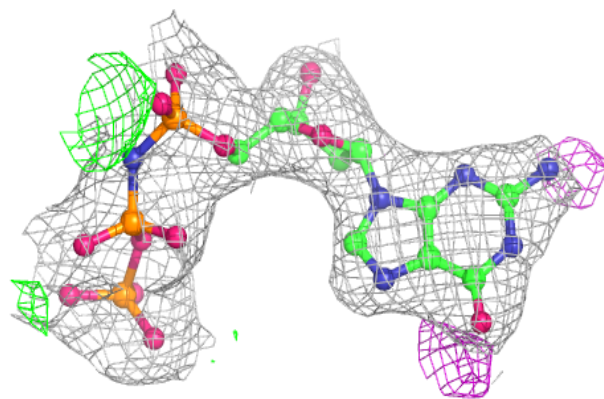
**Electron density around CZF P 707:**

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

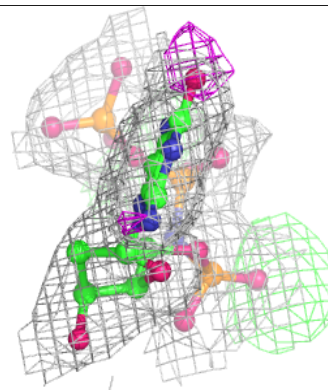
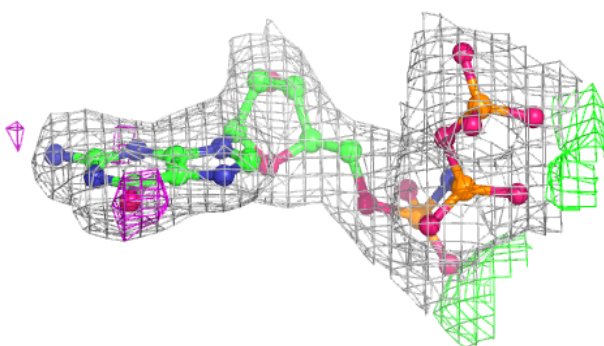
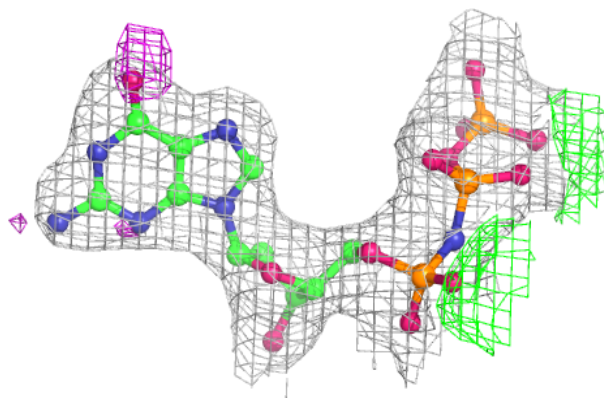


Electron density around XG4 G 706:

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

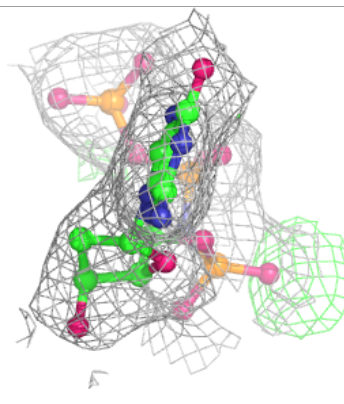
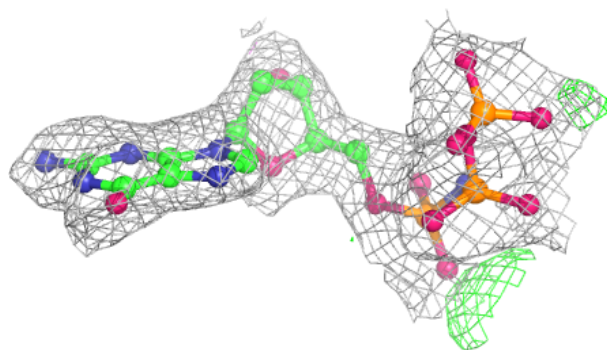
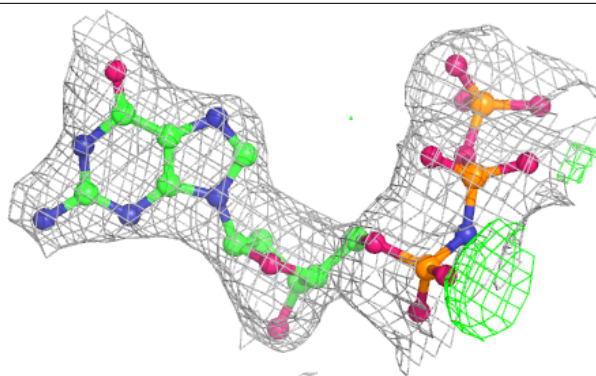
**Electron density around XG4 H 706:**

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

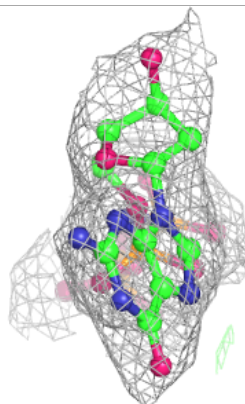
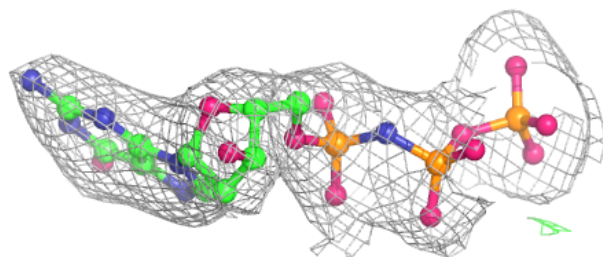
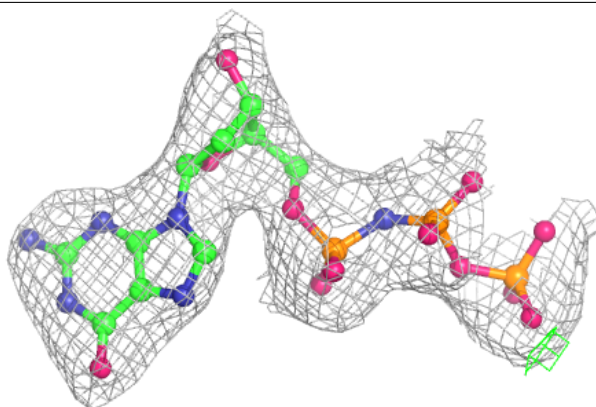


Electron density around XG4 I 705:

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

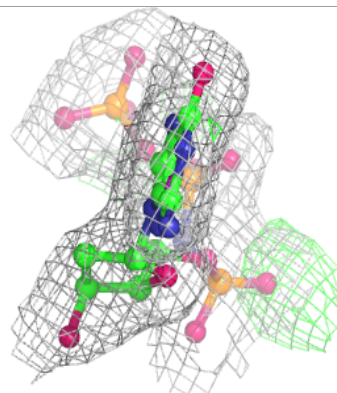
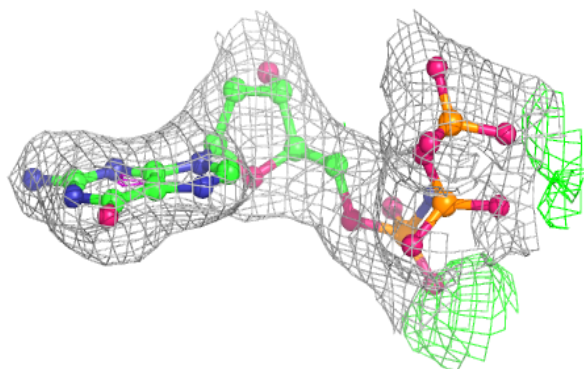
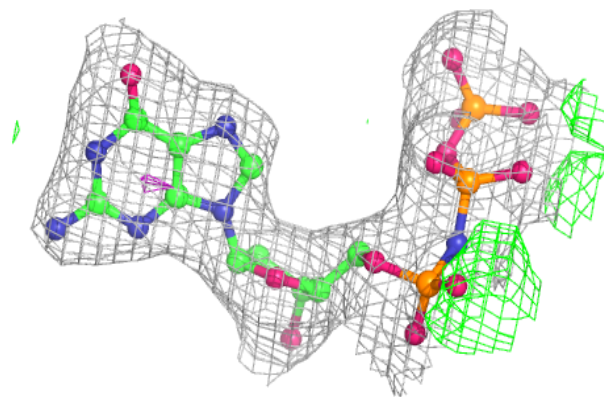
**Electron density around XG4 I 708:**

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

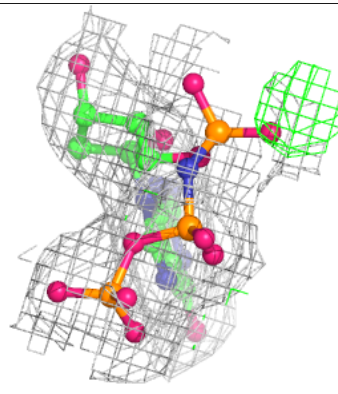
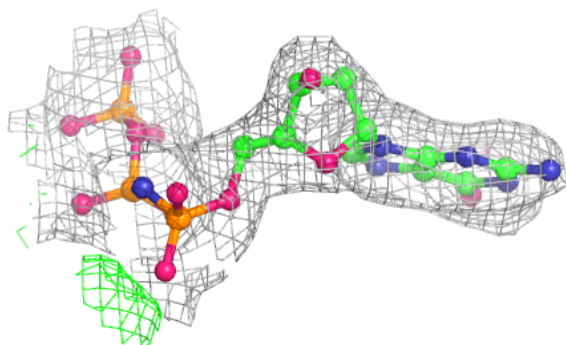
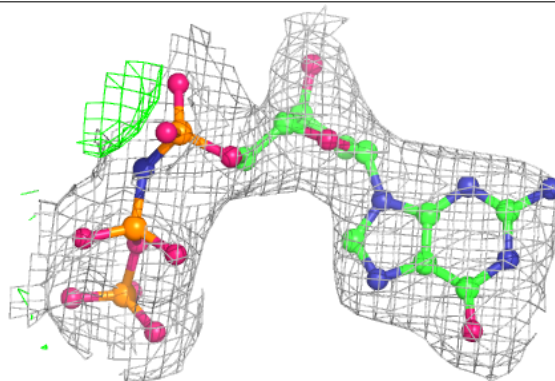


Electron density around XG4 J 706:

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

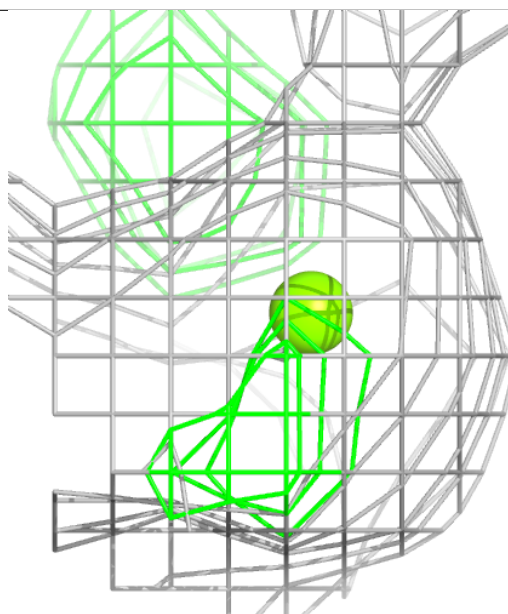
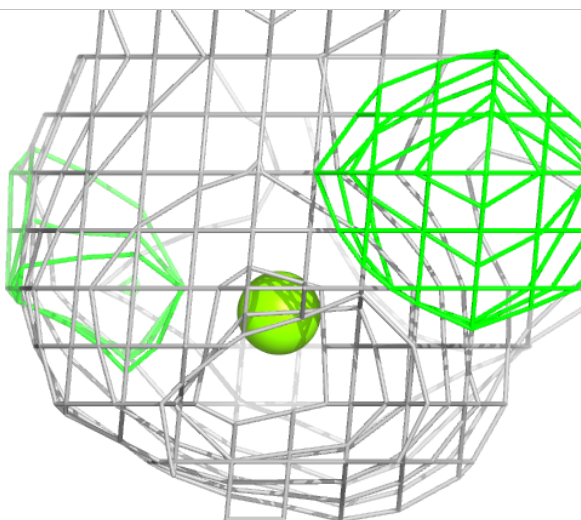
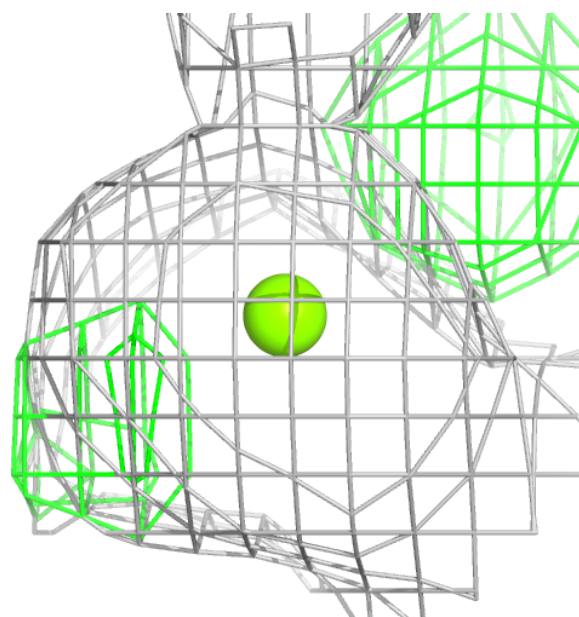
**Electron density around XG4 K 706:**

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



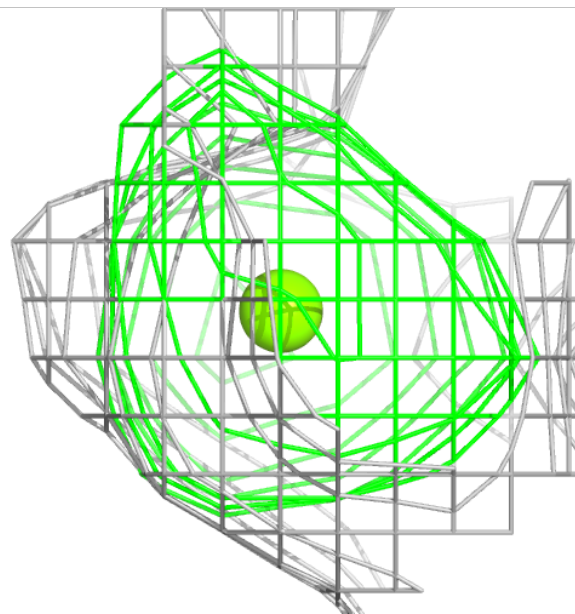
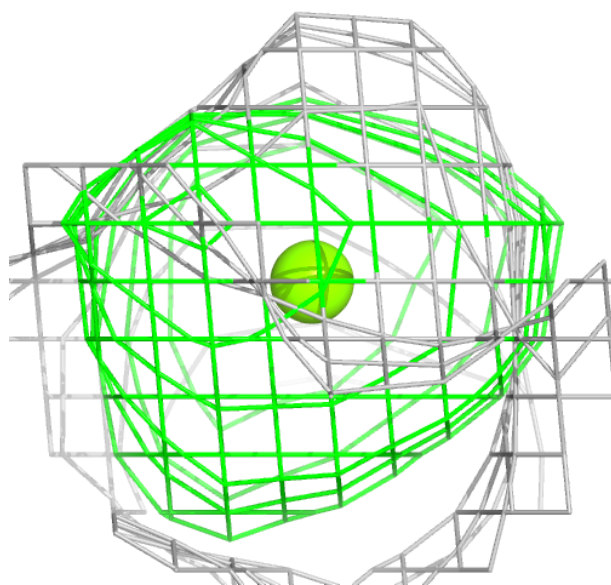
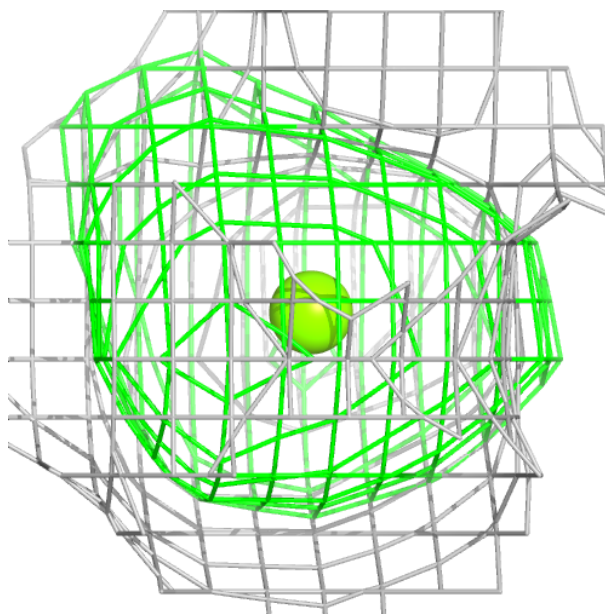
Electron density around MG F 703:

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



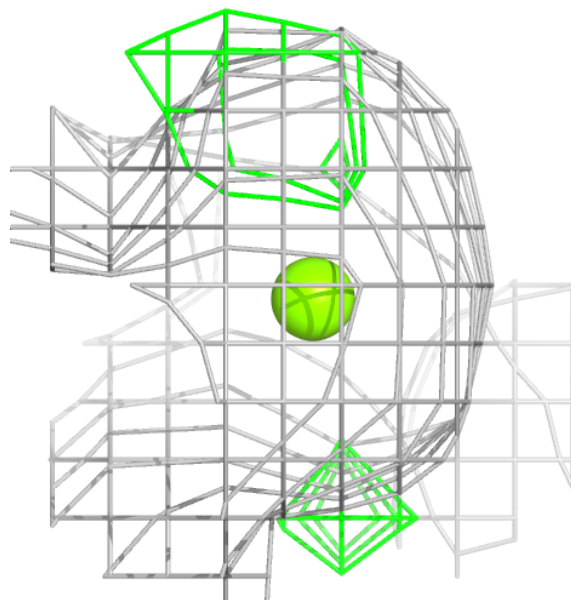
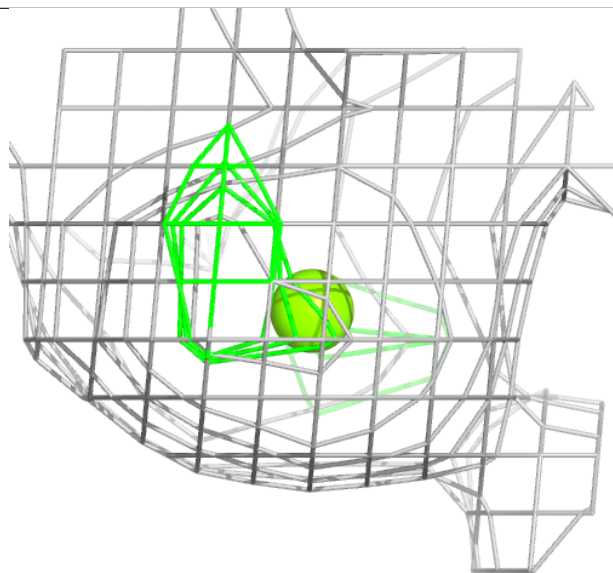
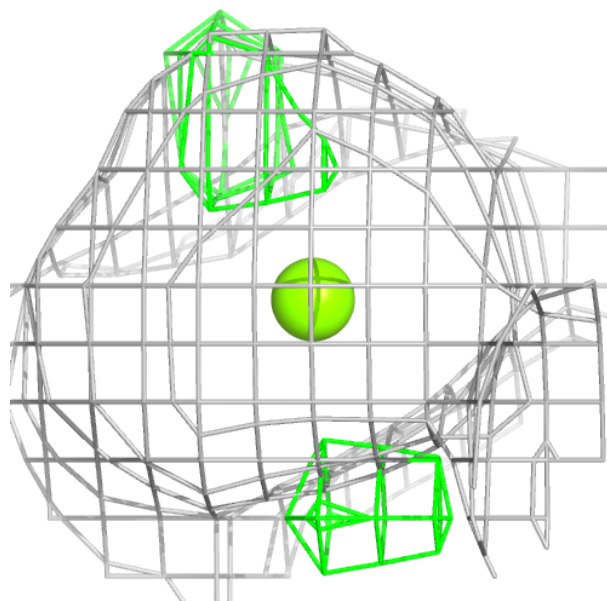
Electron density around MG H 703:

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



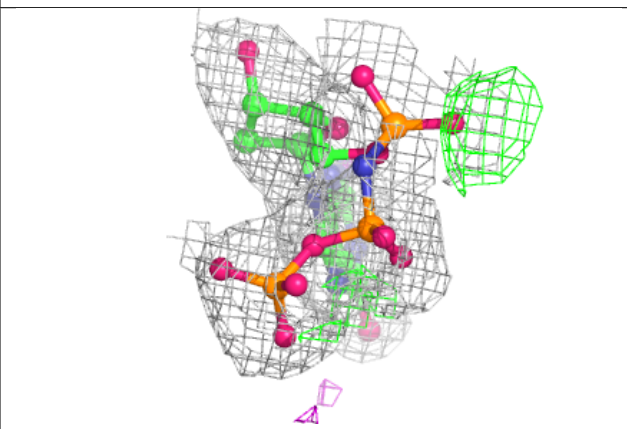
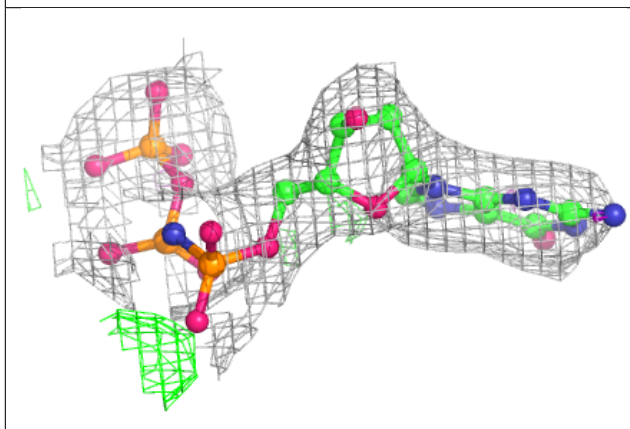
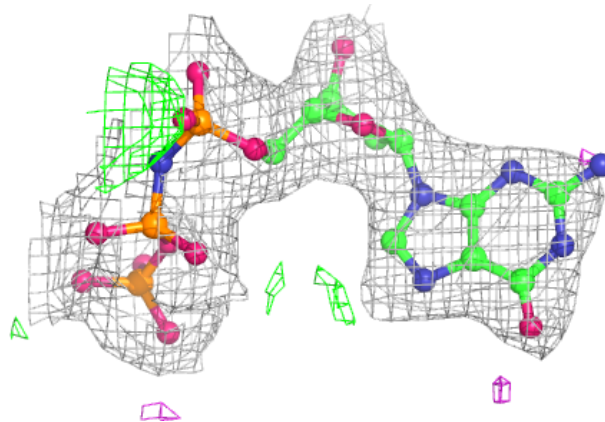
Electron density around MG C 704:

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

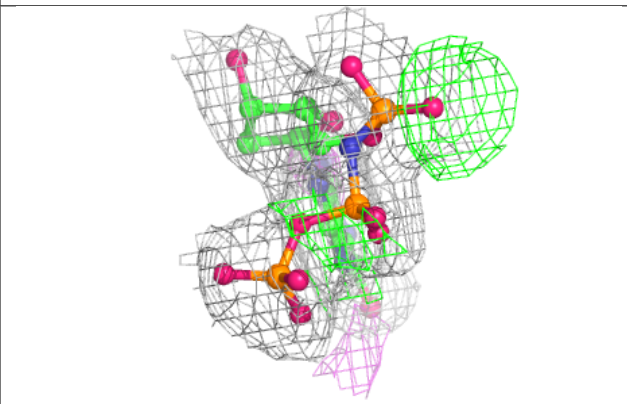
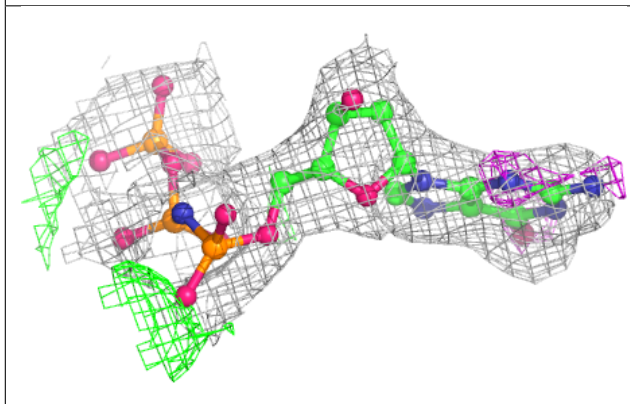
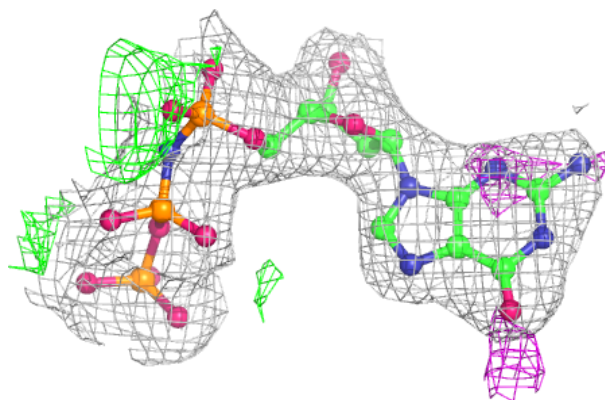


Electron density around XG4 O 706:

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

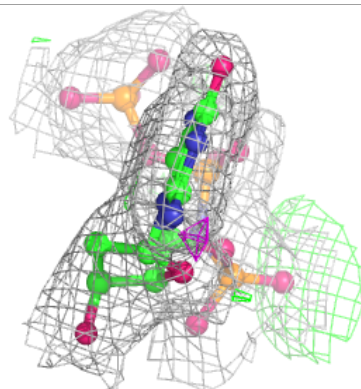
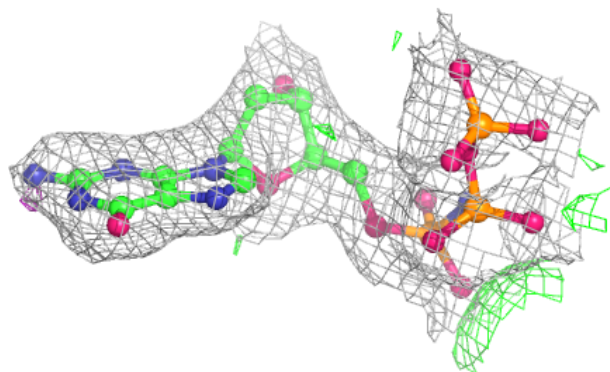
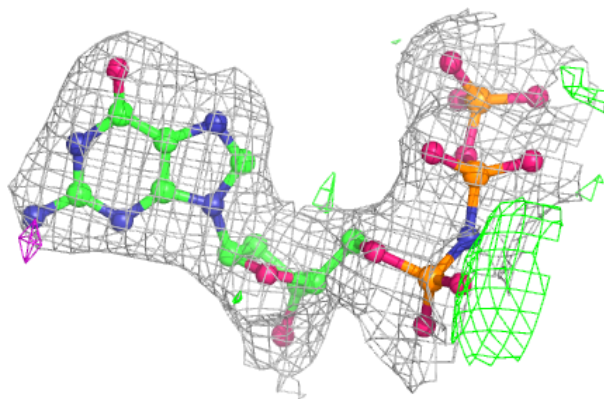
**Electron density around XG4 A 705:**

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

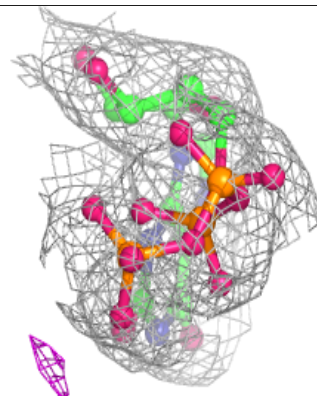
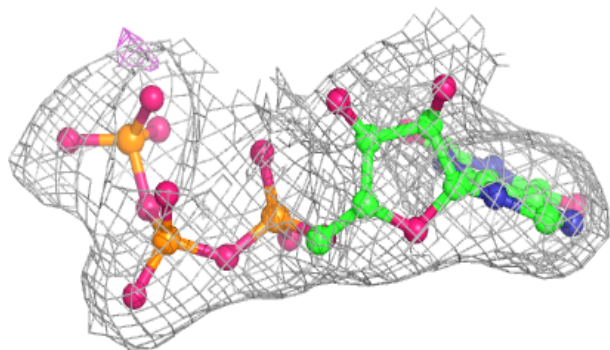
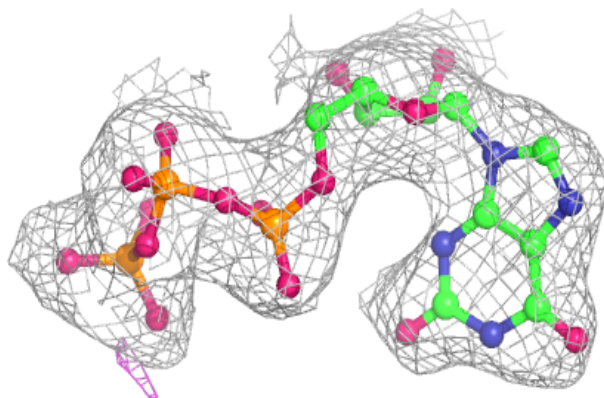


Electron density around XG4 C 706:

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

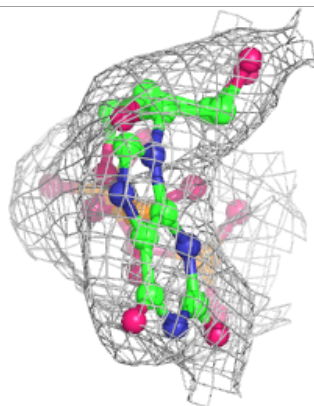
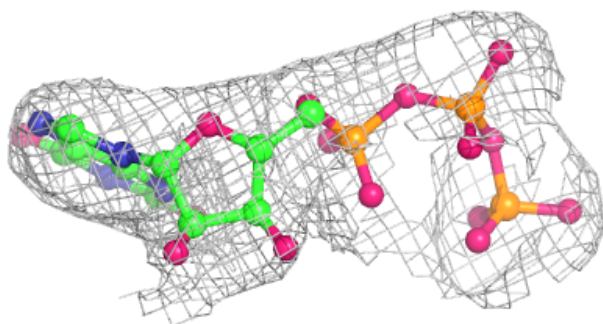
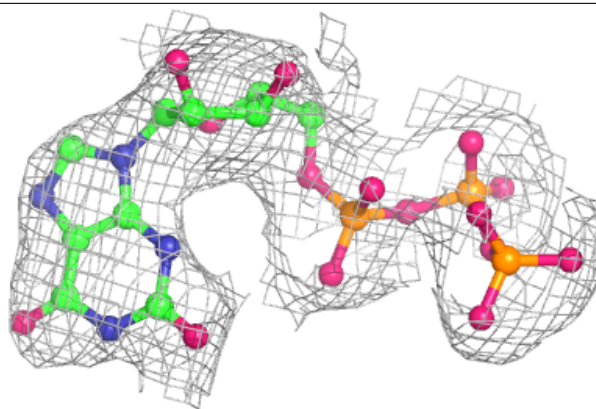
**Electron density around CZF J 701:**

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

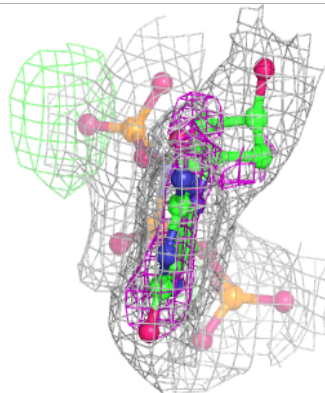
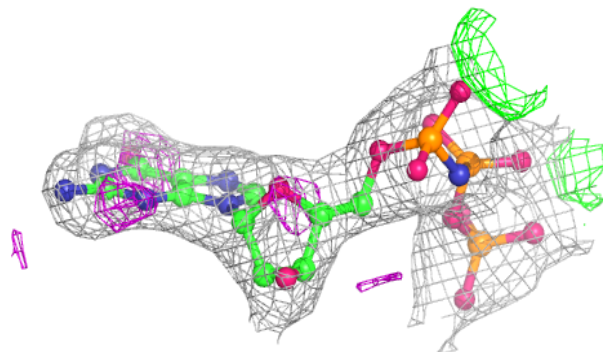
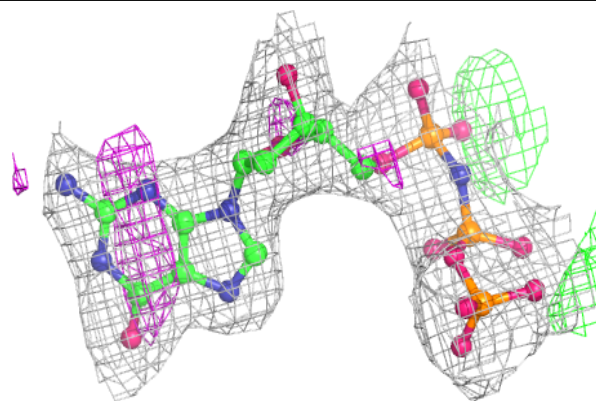


Electron density around CZF K 707:

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

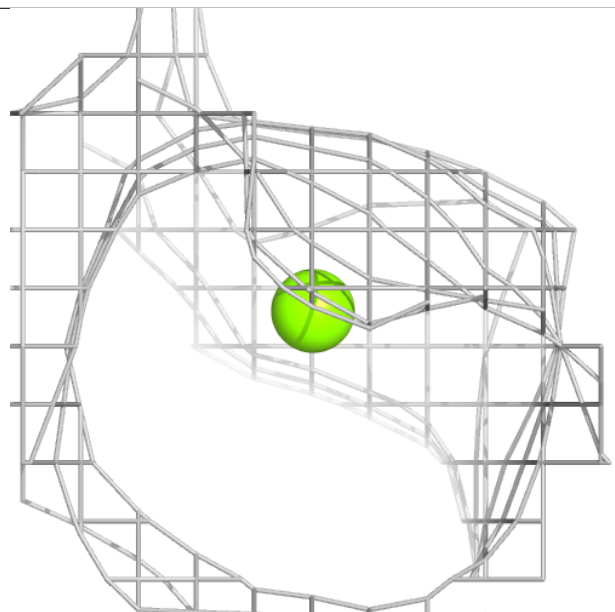
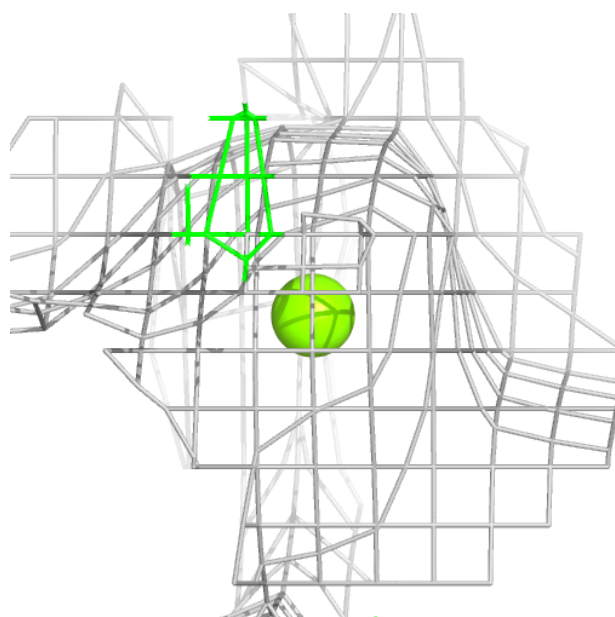
**Electron density around XG4 D 706:**

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



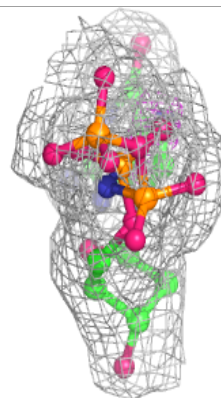
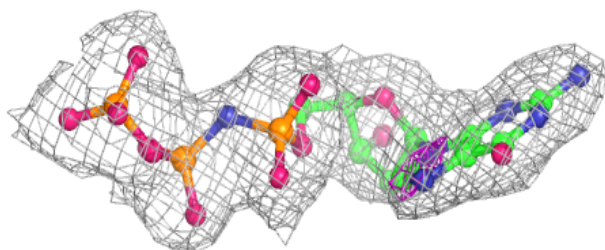
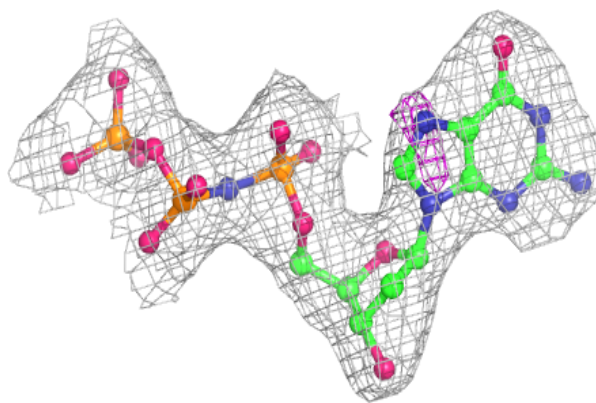
Electron density around MG B 704:

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

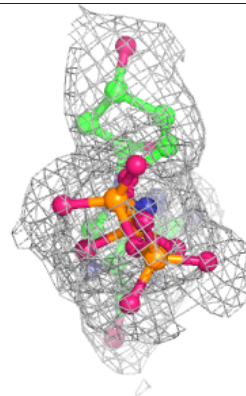
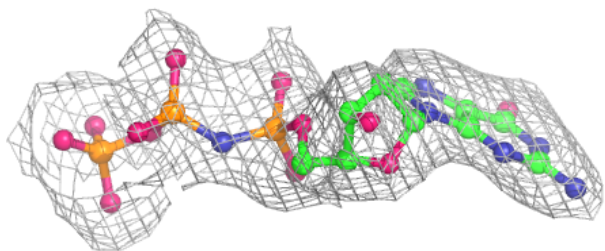
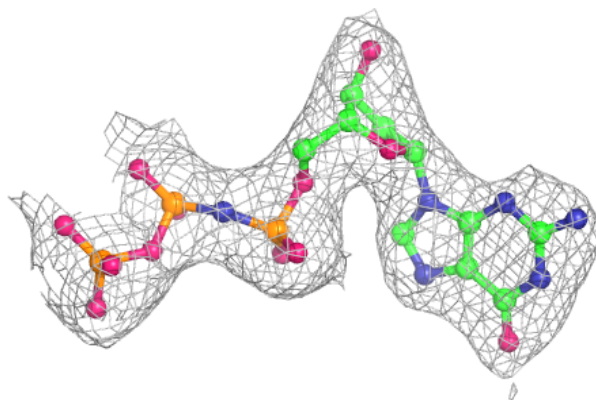


Electron density around XG4 J 709:

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

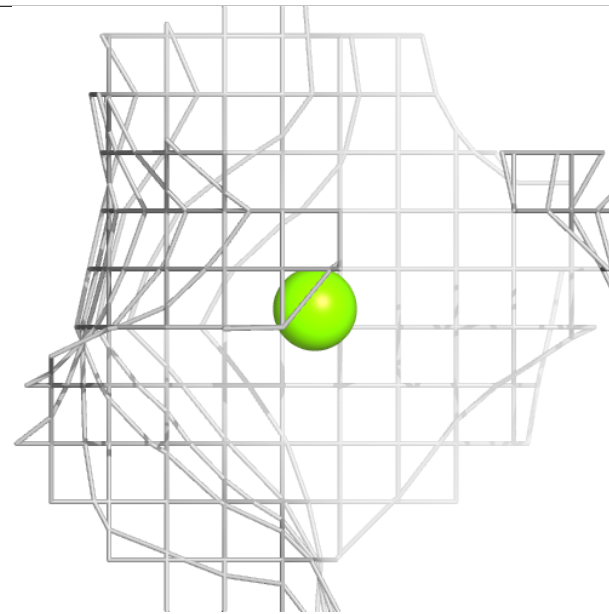
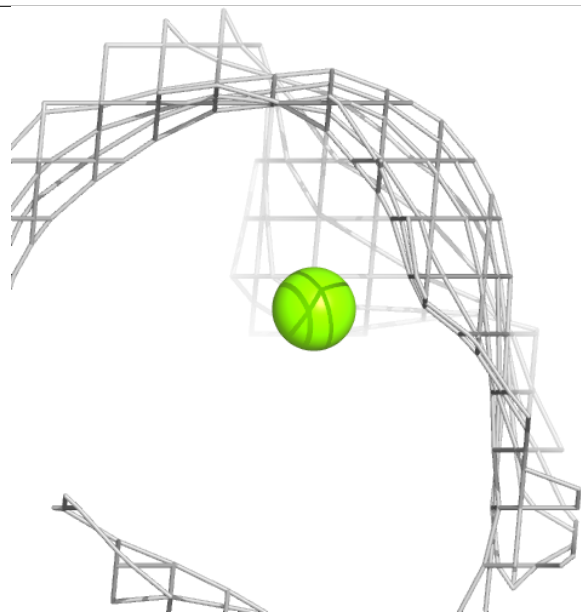
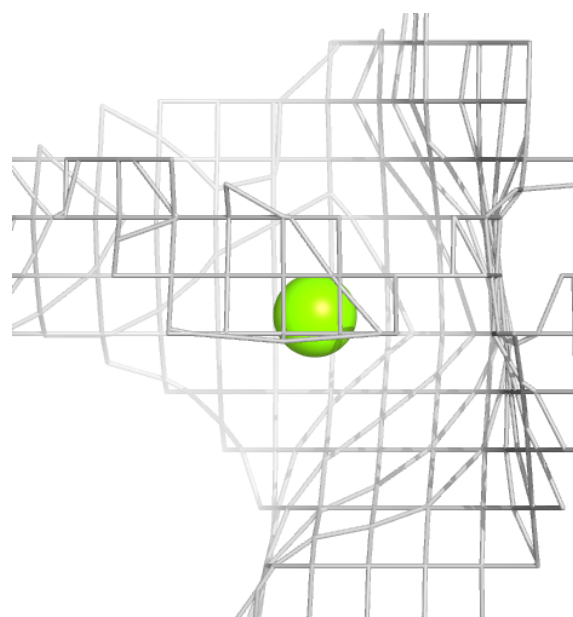
**Electron density around XG4 K 701:**

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



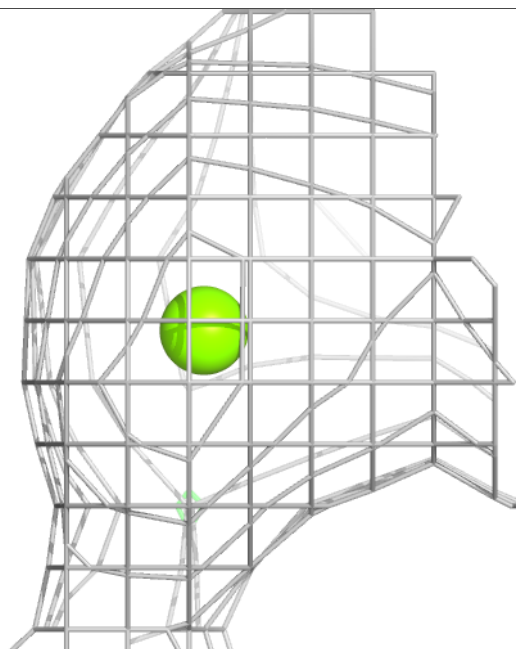
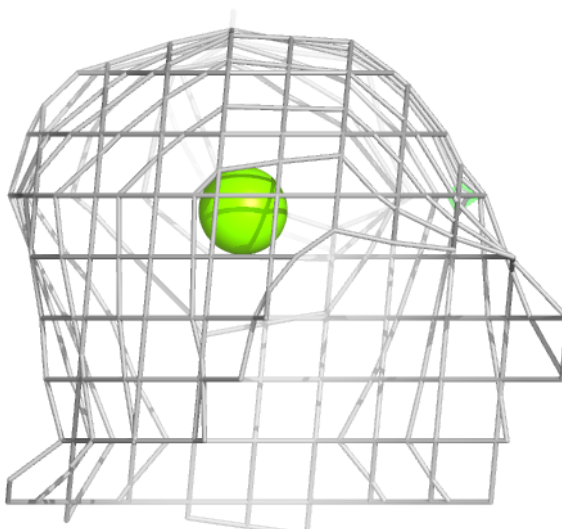
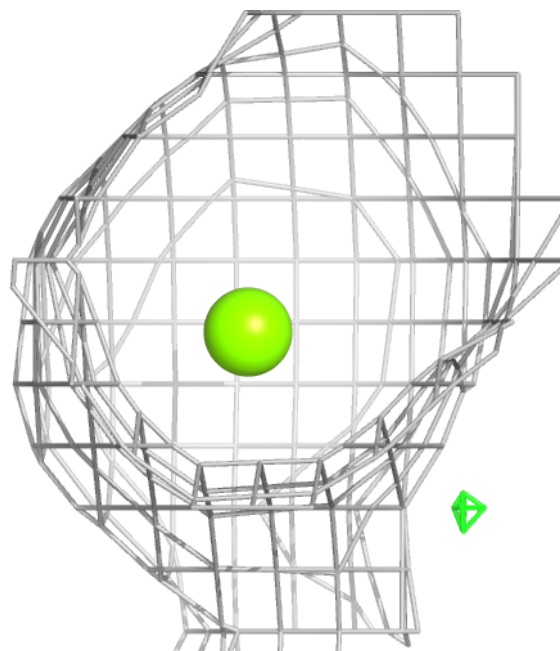
Electron density around MG K 705:

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



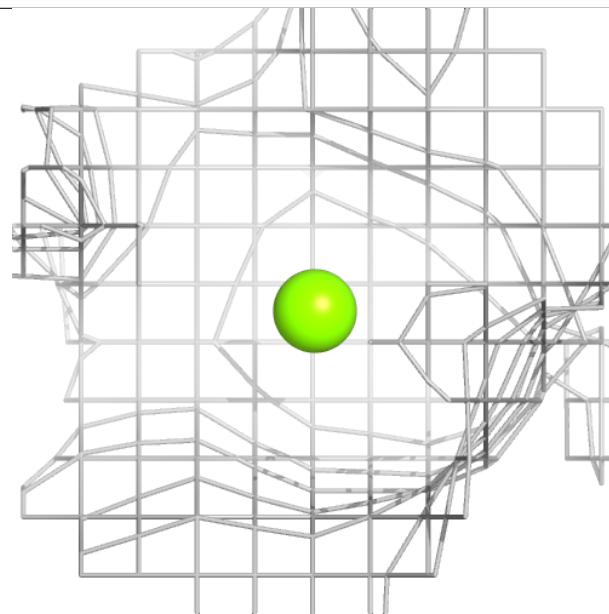
Electron density around MG M 703:

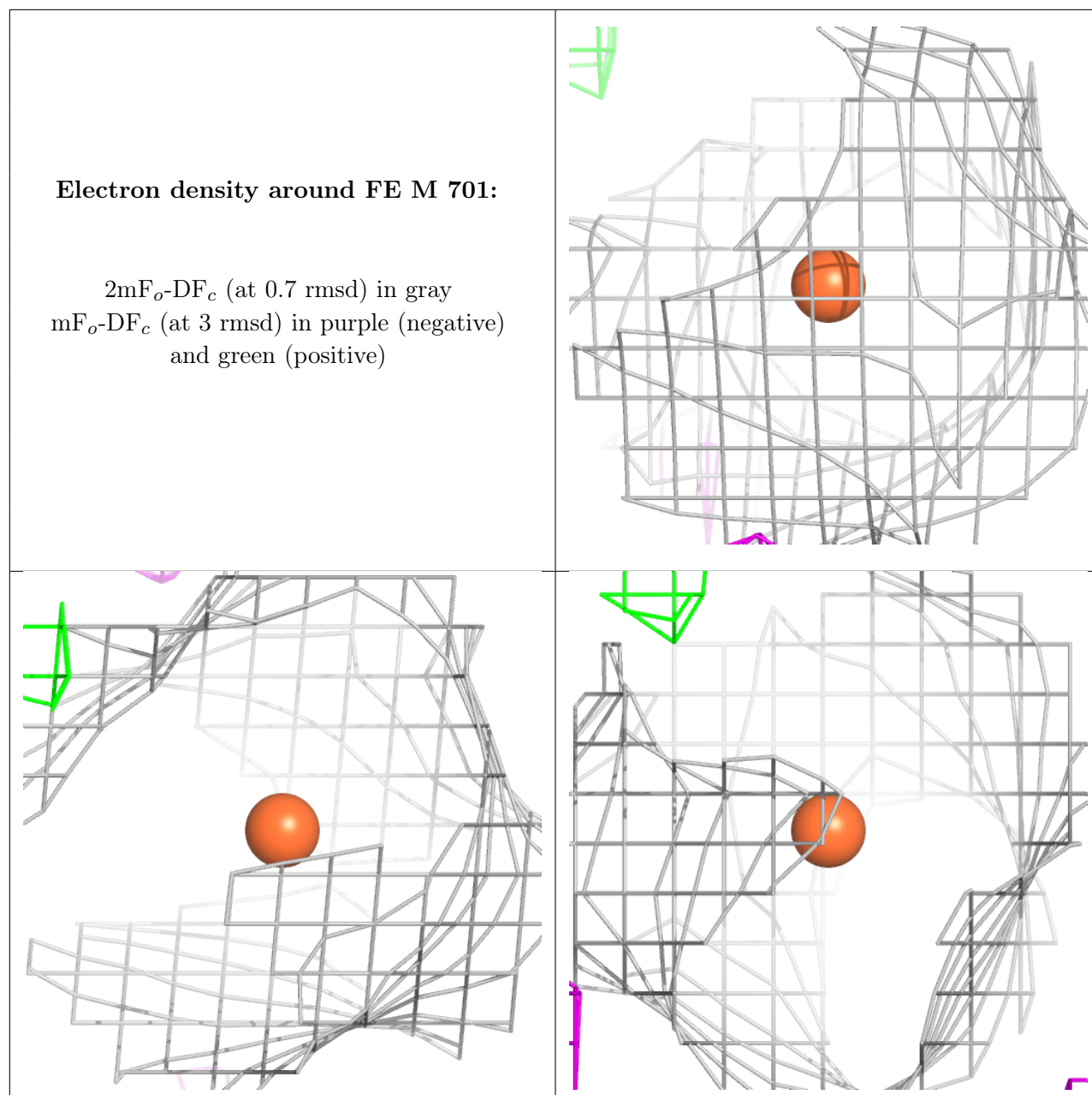
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around MG M 704:

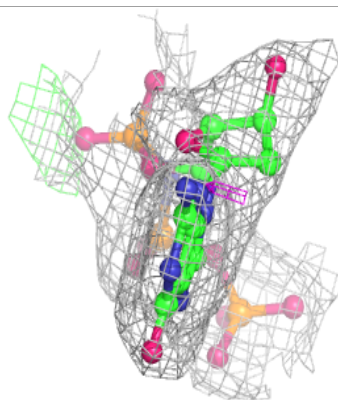
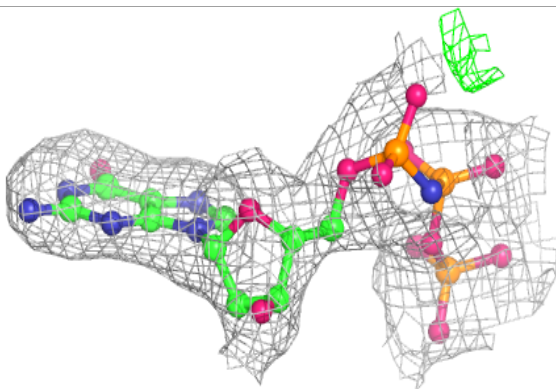
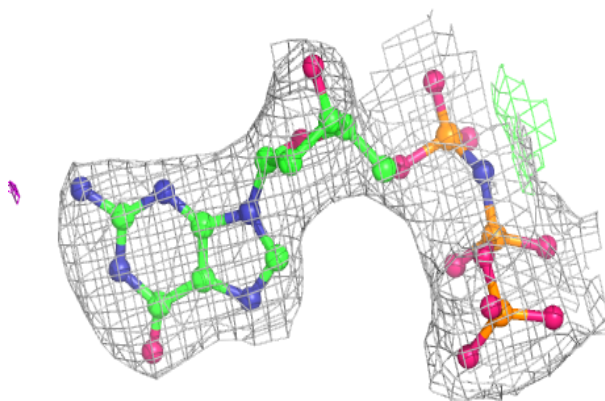
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



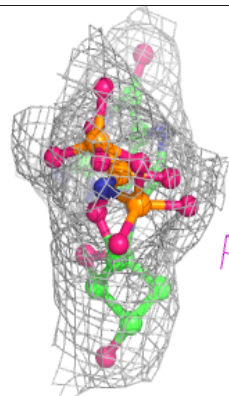
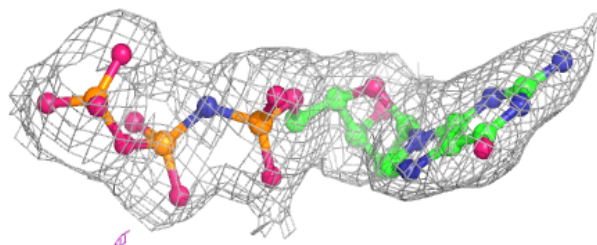
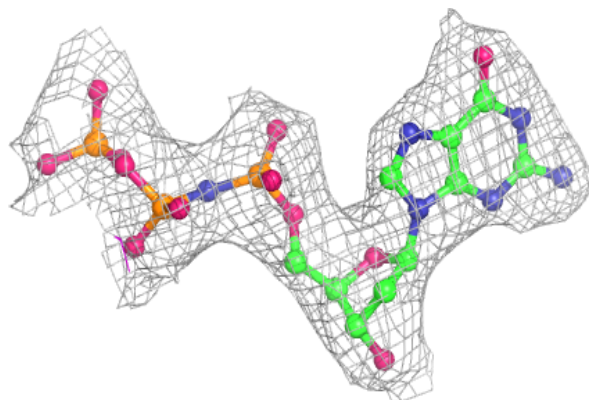


Electron density around XG4 N 705:

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

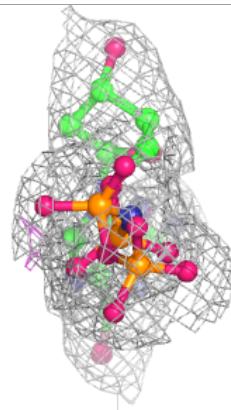
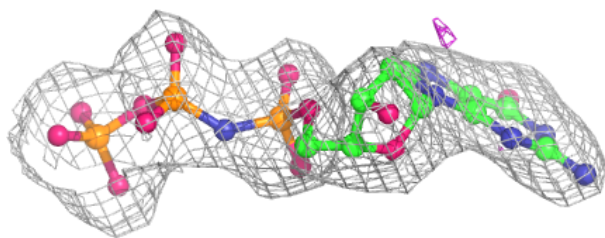
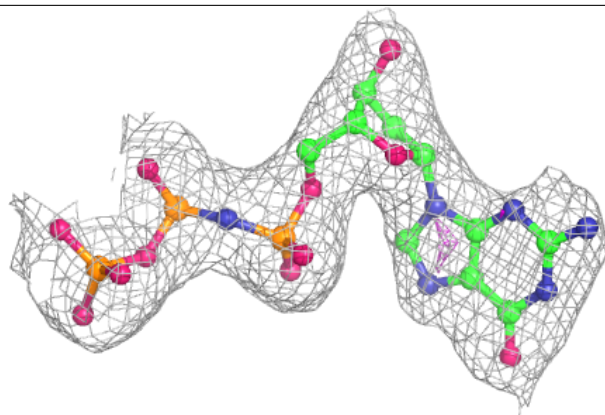
**Electron density around XG4 N 708:**

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



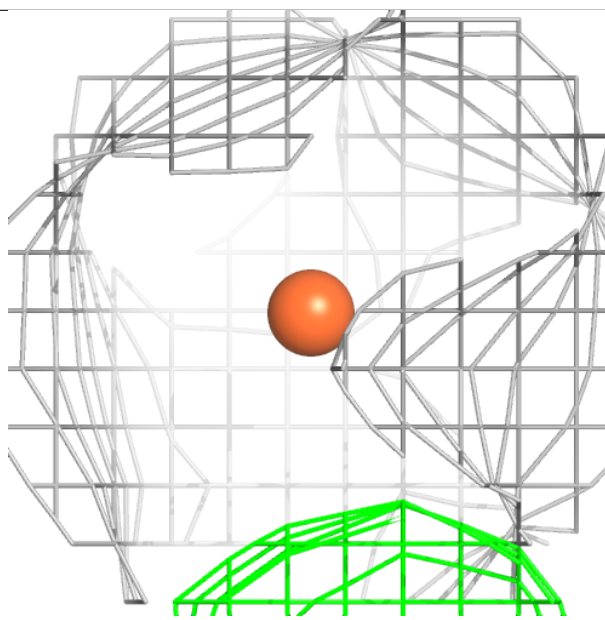
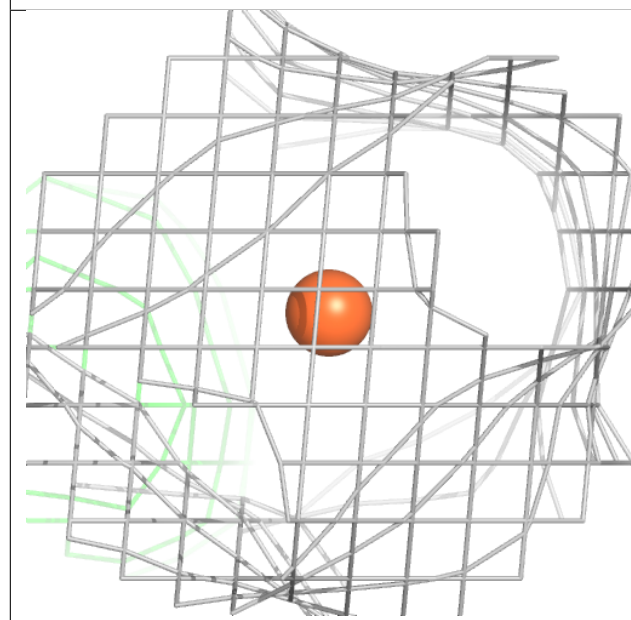
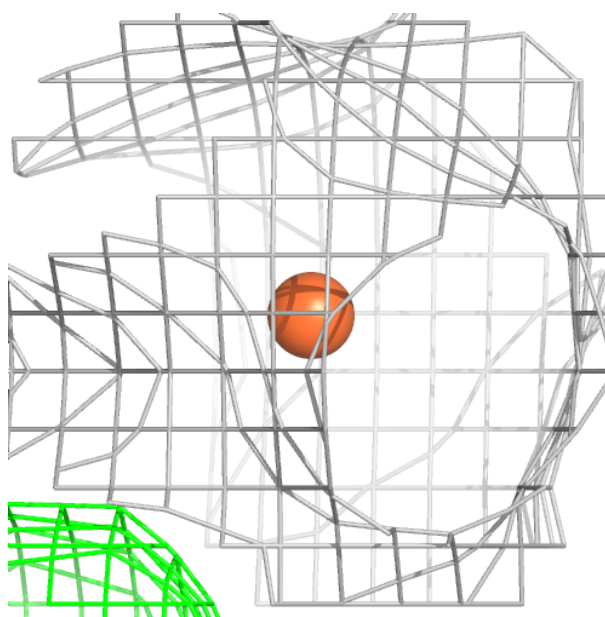
Electron density around XG4 O 701:

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



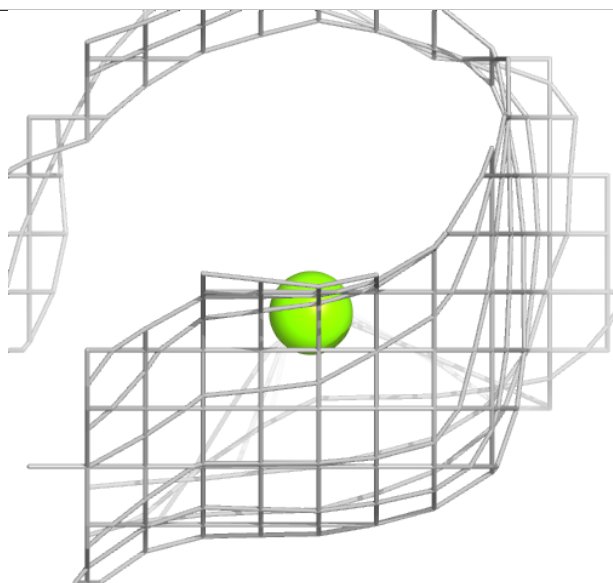
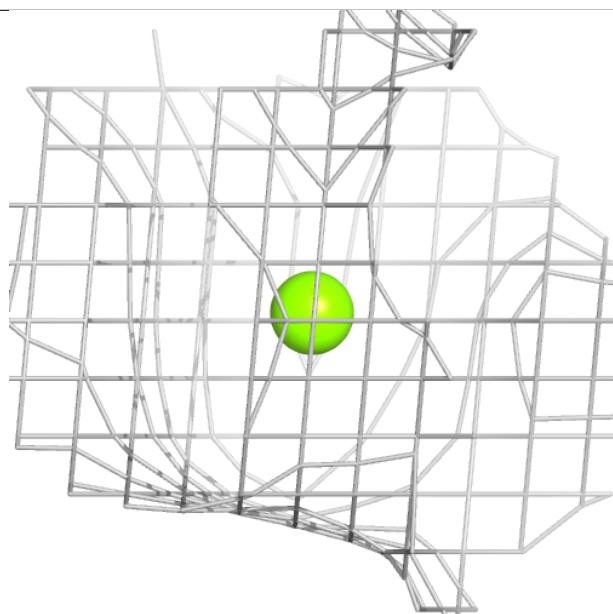
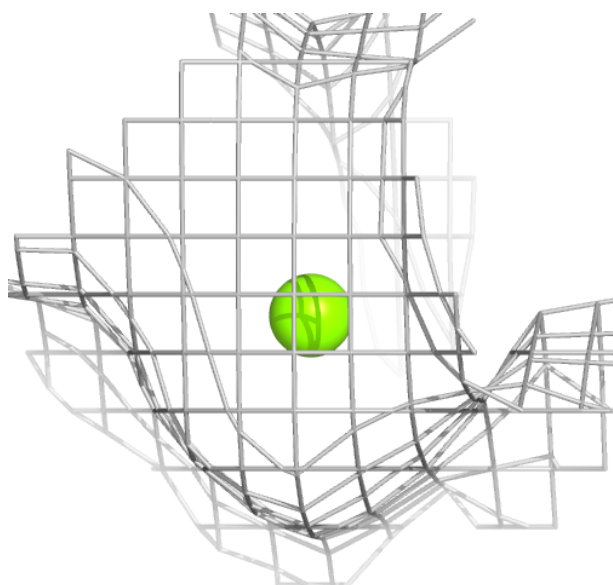
Electron density around FE O 702:

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



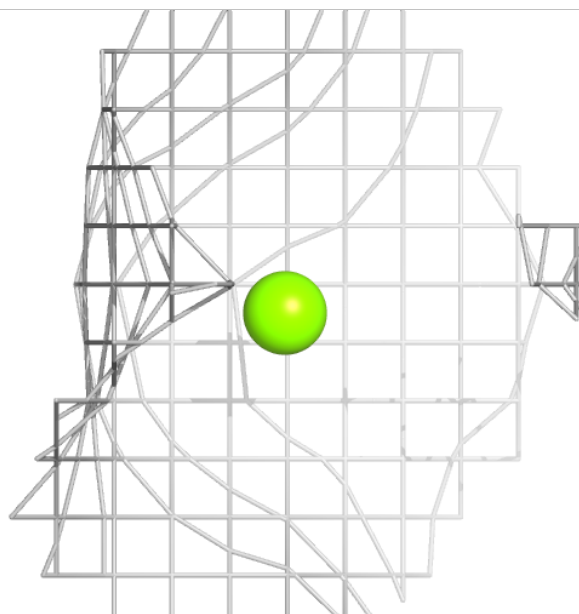
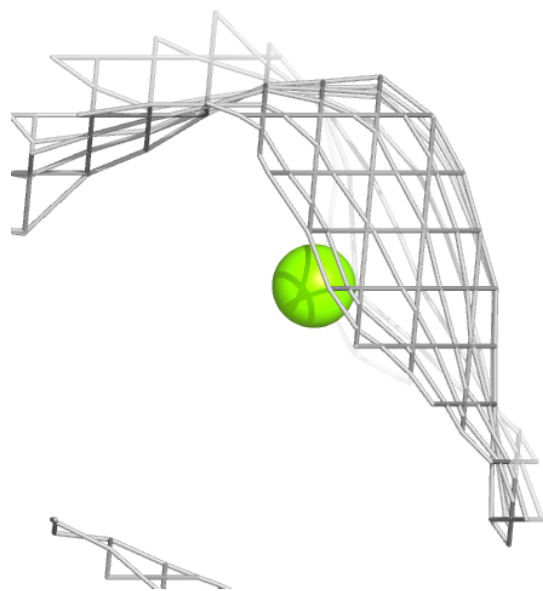
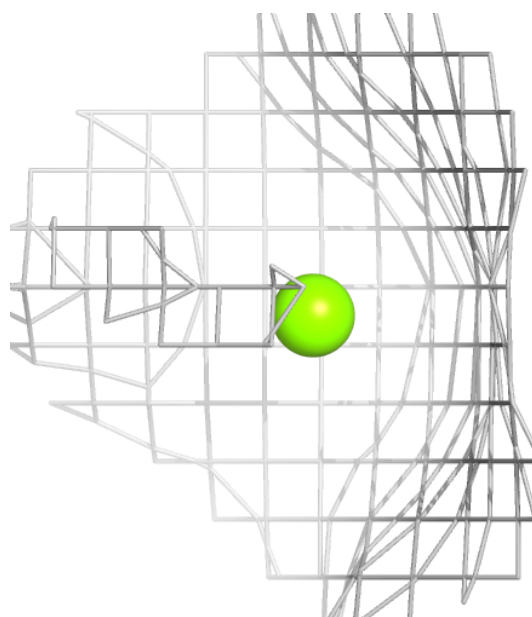
Electron density around MG D 705:

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



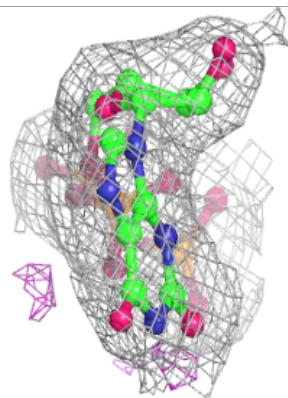
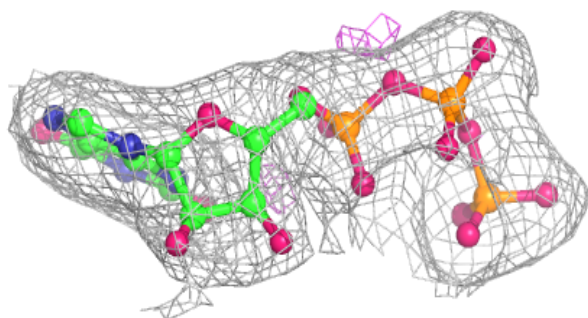
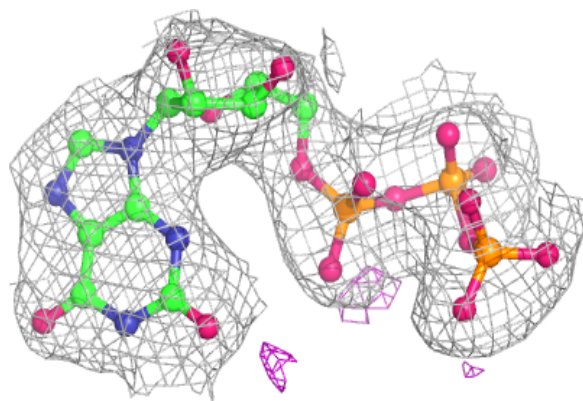
Electron density around MG O 705:

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

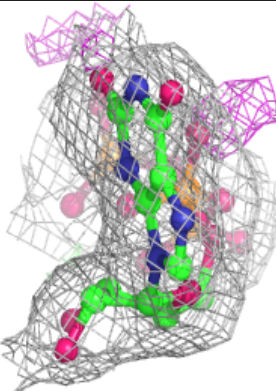
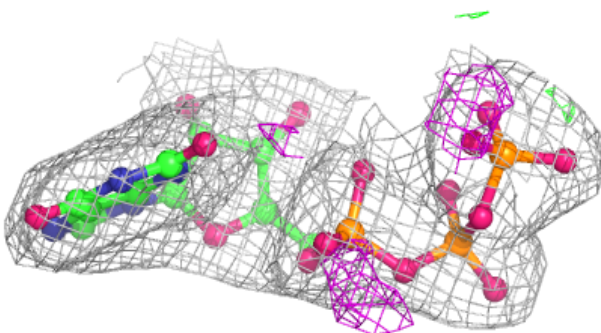
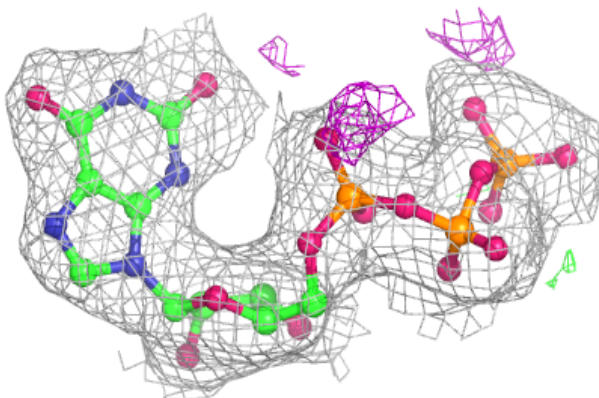


Electron density around CZF A 706:

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

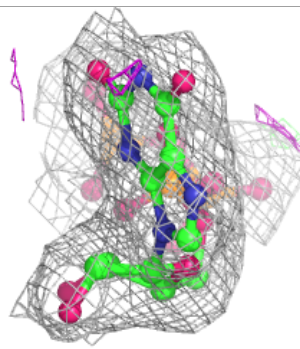
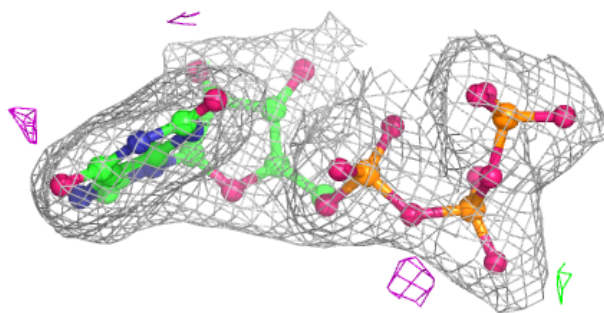
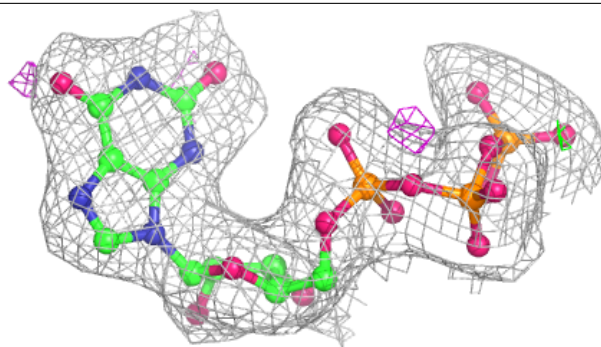
**Electron density around CZF B 706:**

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

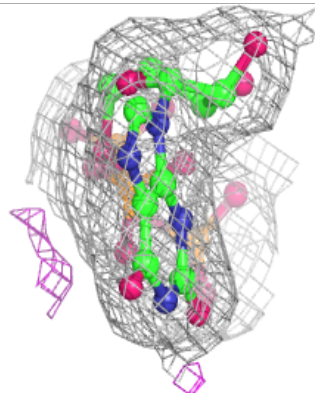
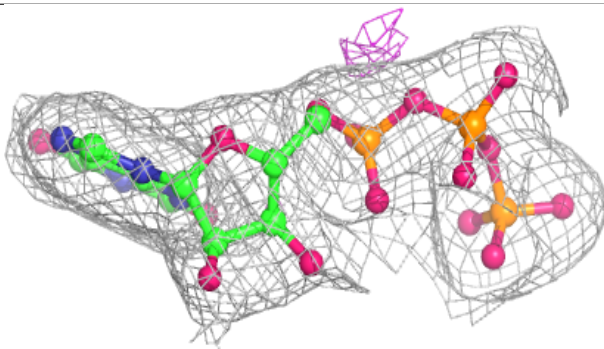
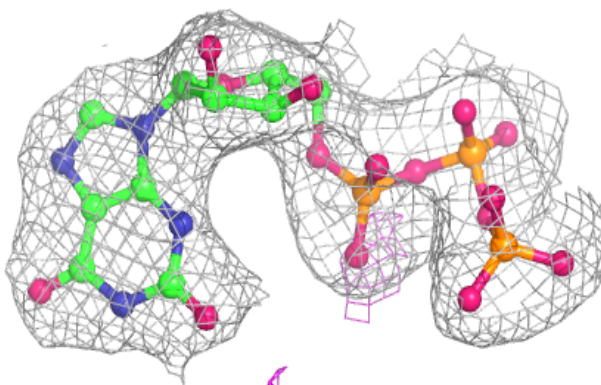


Electron density around CZF C 707:

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

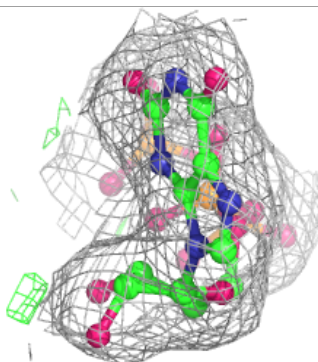
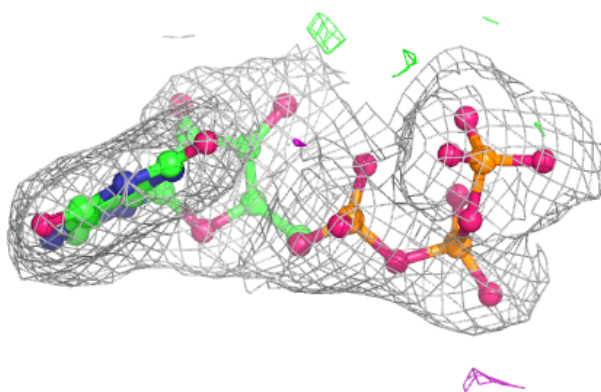
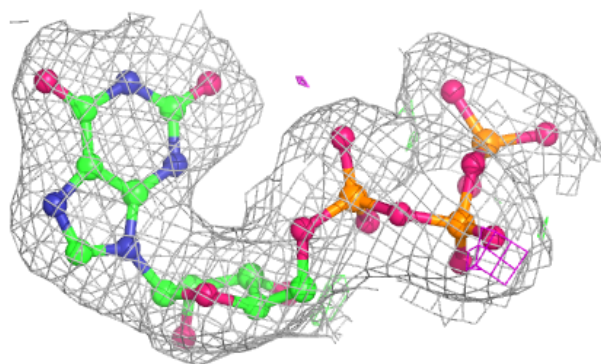
**Electron density around CZF C 709:**

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

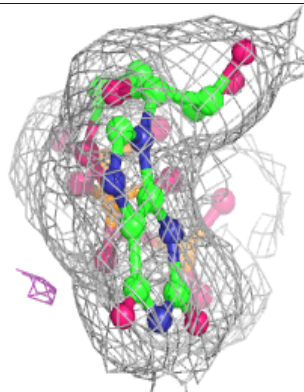
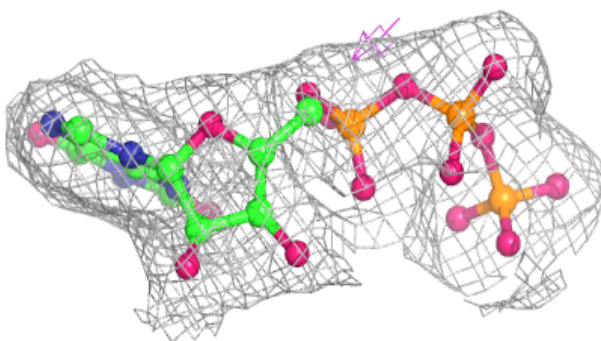
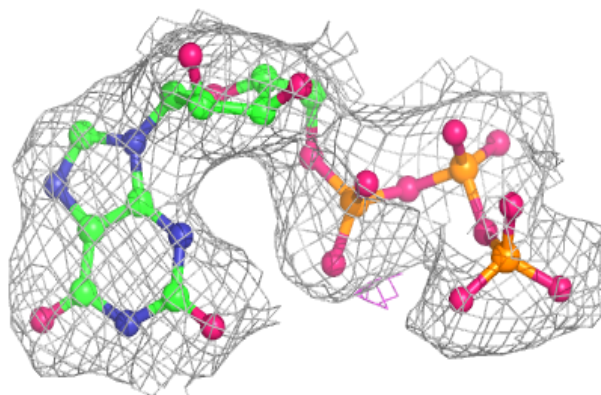


Electron density around CZF E 706:

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

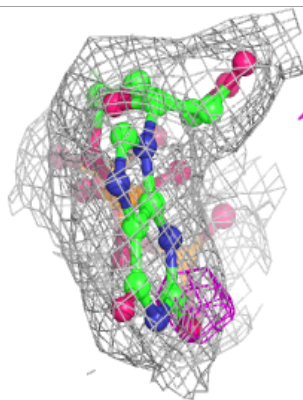
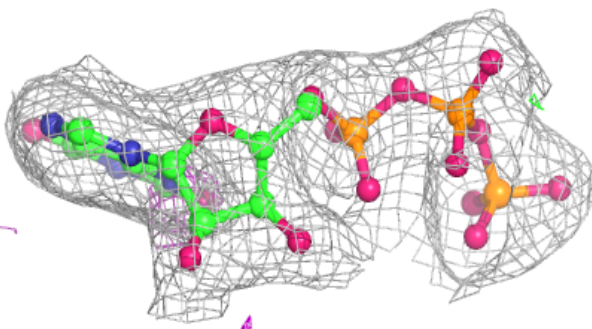
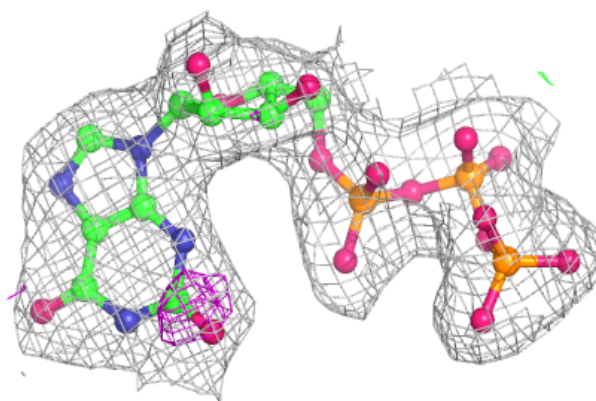
**Electron density around CZF F 706:**

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

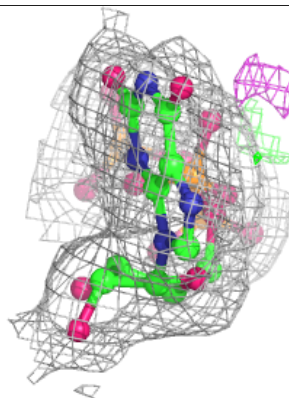
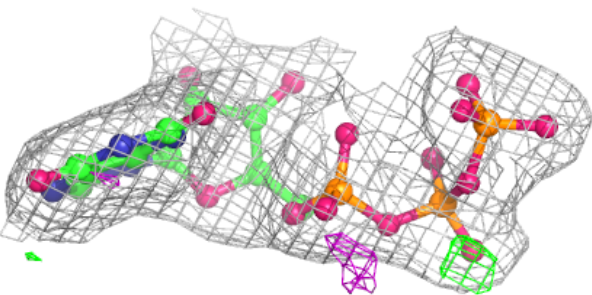
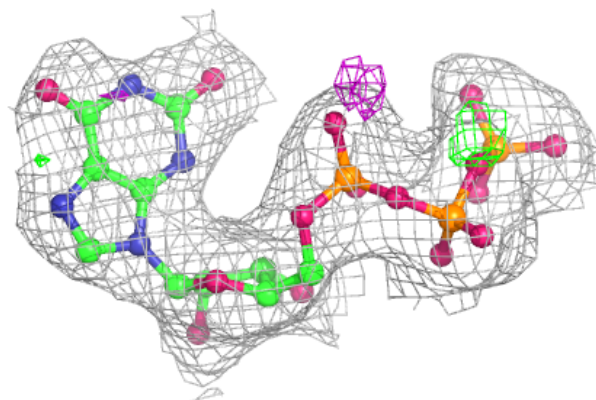


Electron density around CZF G 707:

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

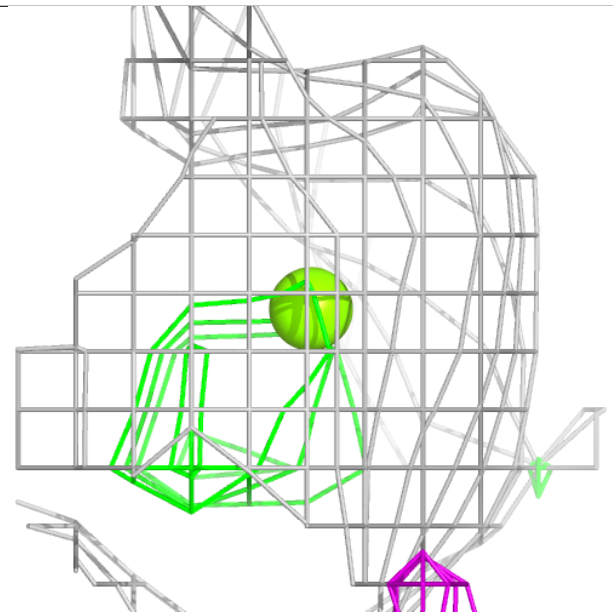
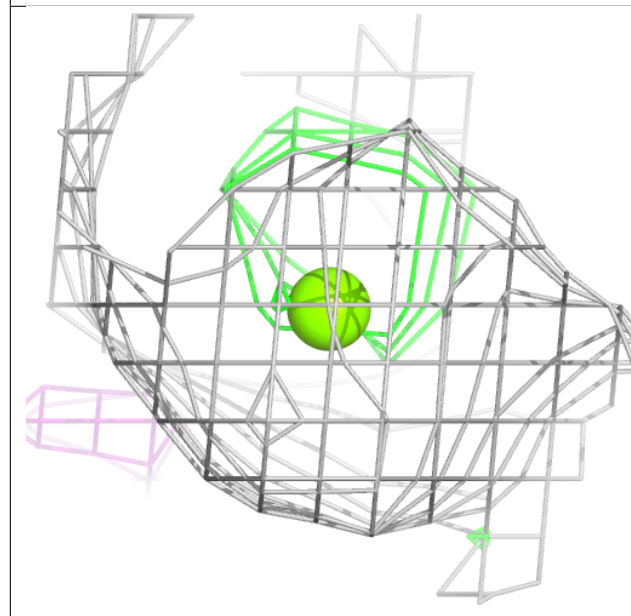
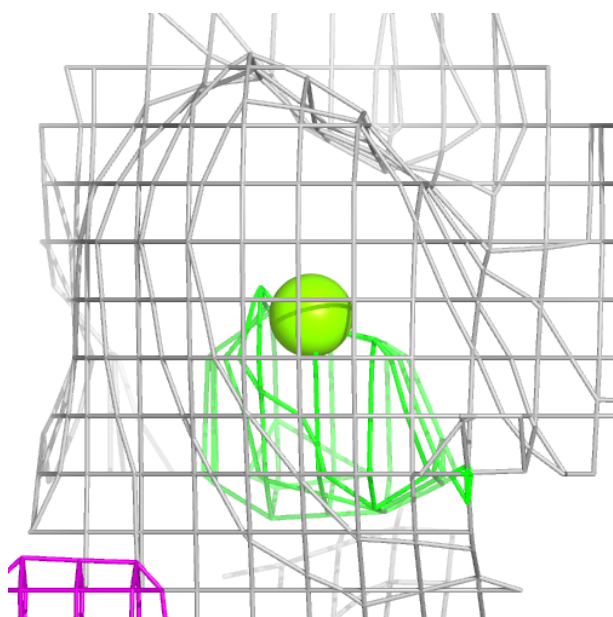
**Electron density around CZF H 707:**

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



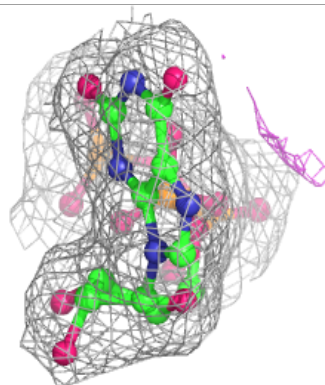
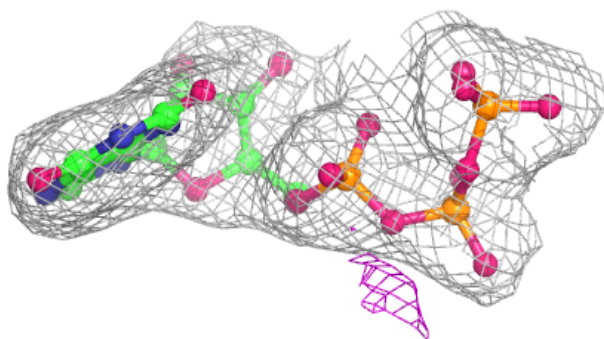
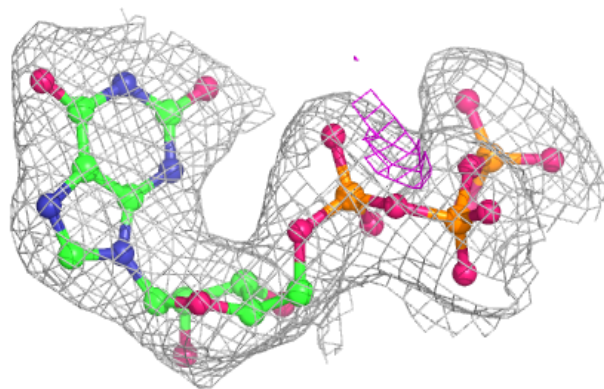
Electron density around MG P 703:

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



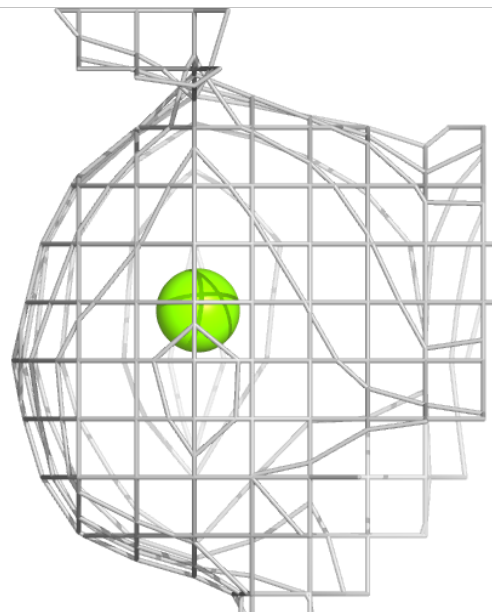
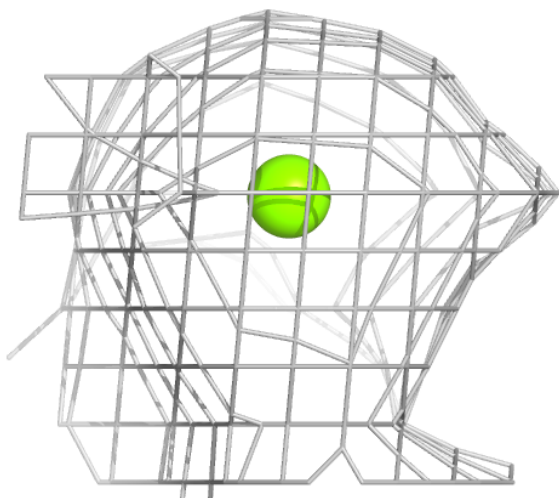
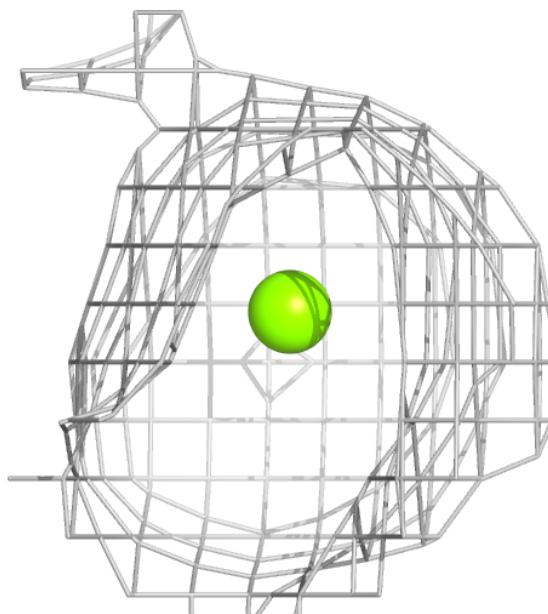
Electron density around CZF J 707:

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



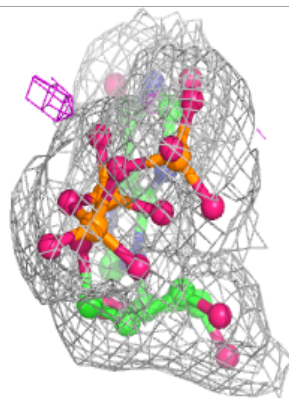
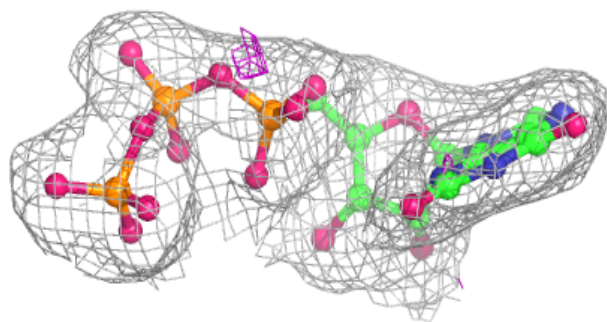
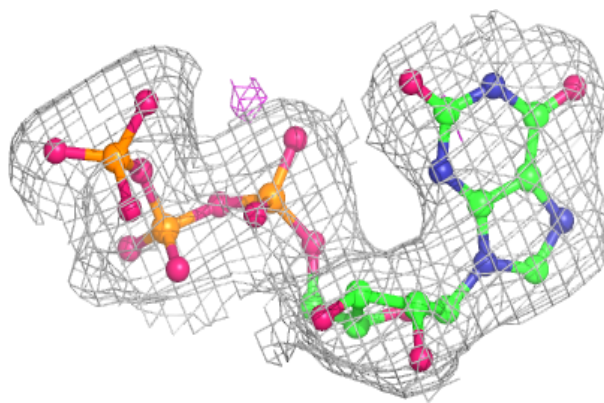
Electron density around MG P 704:

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

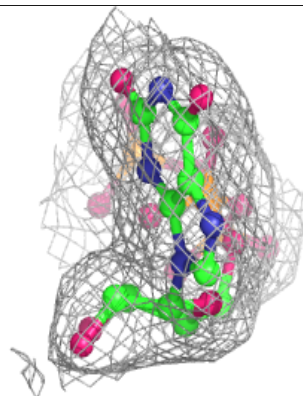
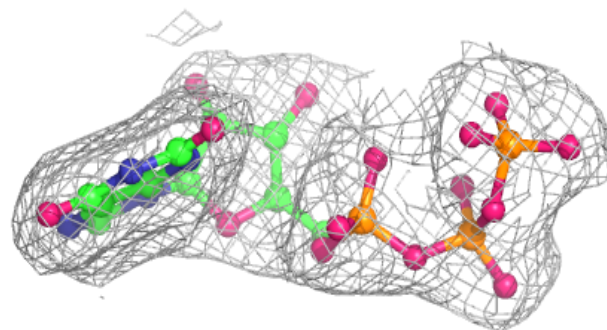
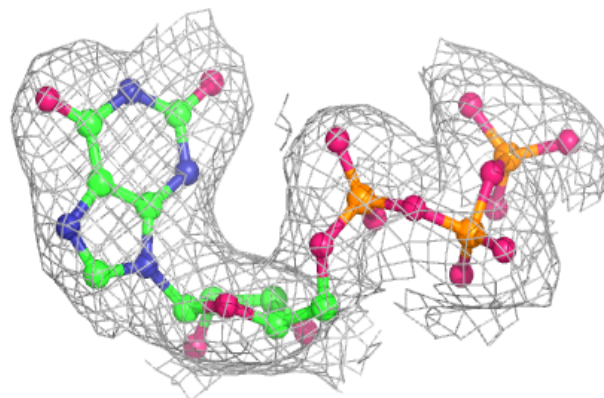


Electron density around CZF L 706:

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

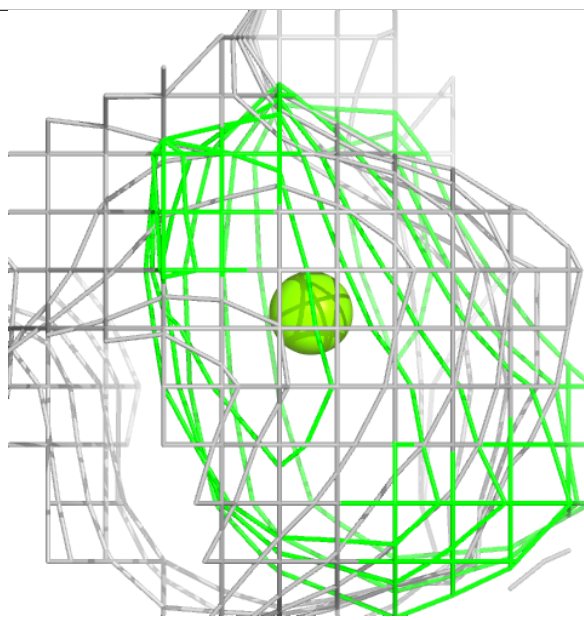
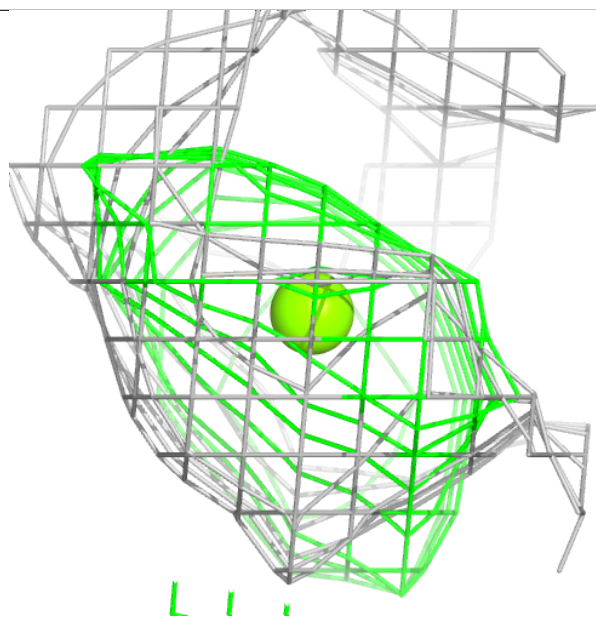
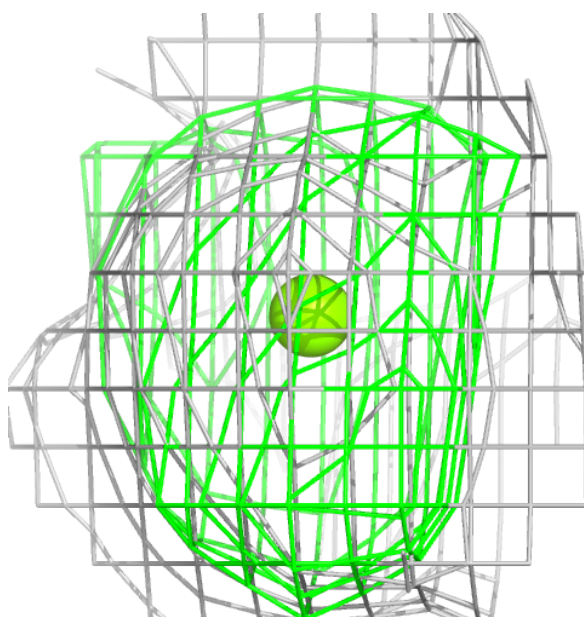
**Electron density around CZF M 706:**

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



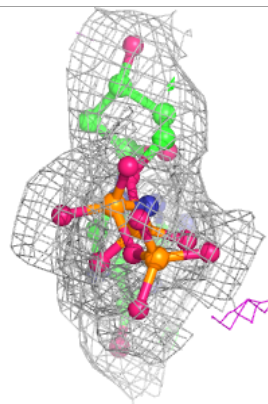
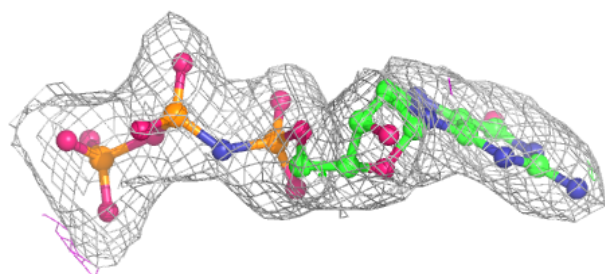
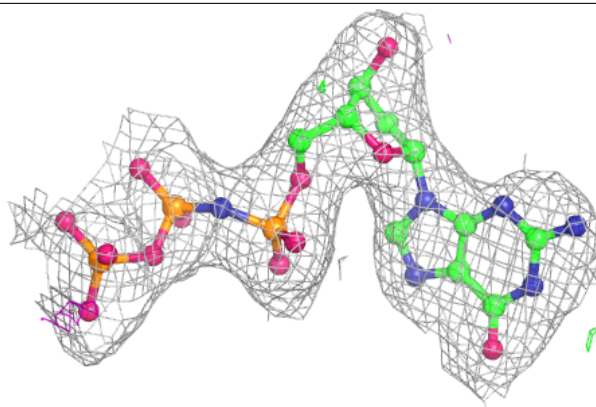
Electron density around MG E 702:

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

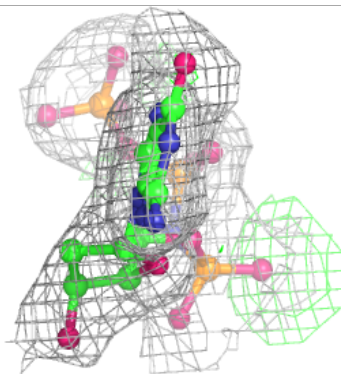
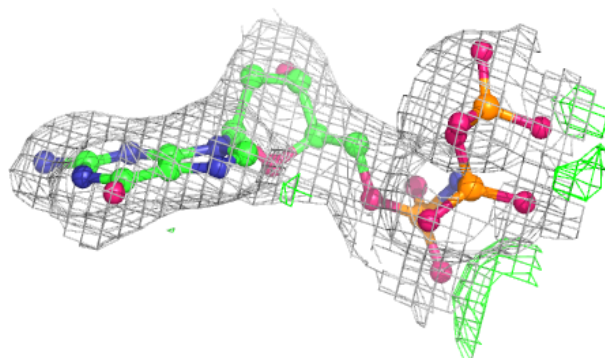
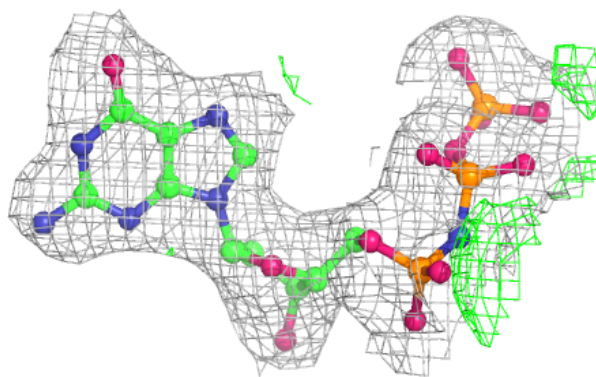


Electron density around XG4 A 708:

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

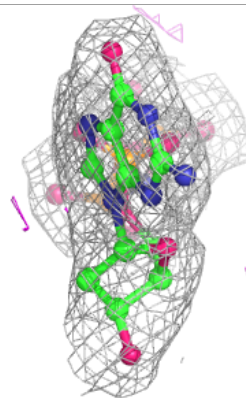
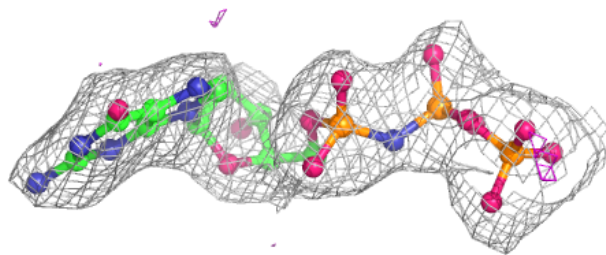
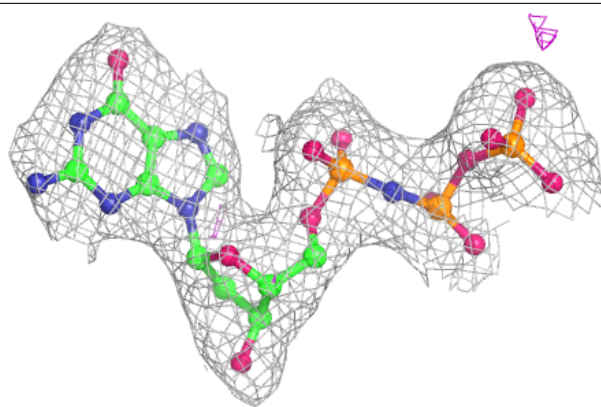
**Electron density around XG4 B 705:**

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



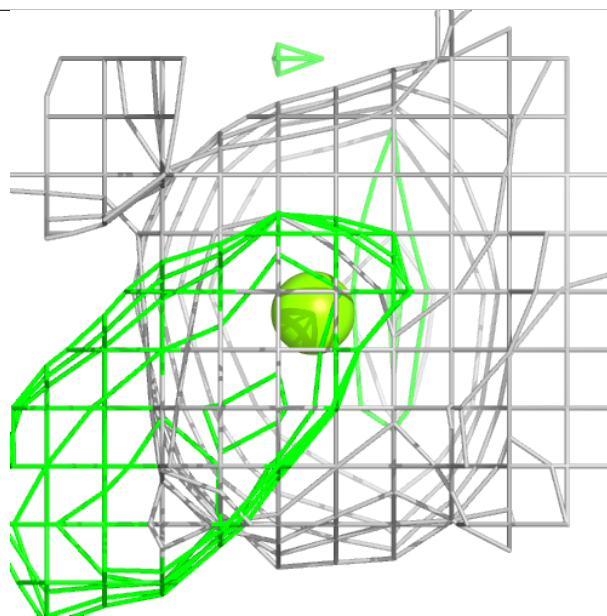
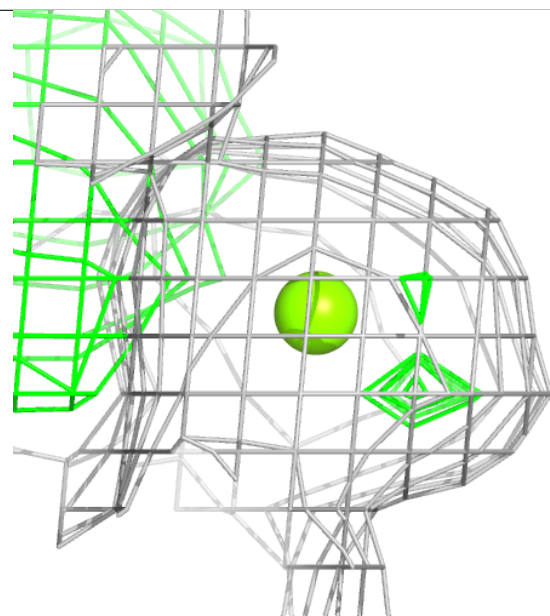
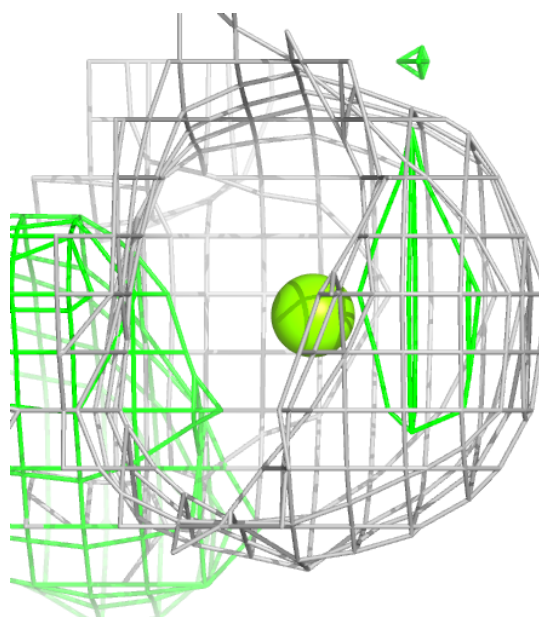
Electron density around XG4 B 708:

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



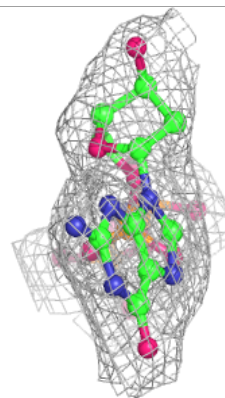
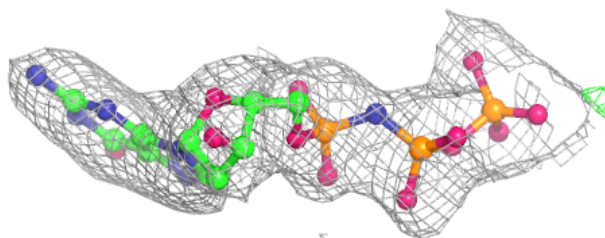
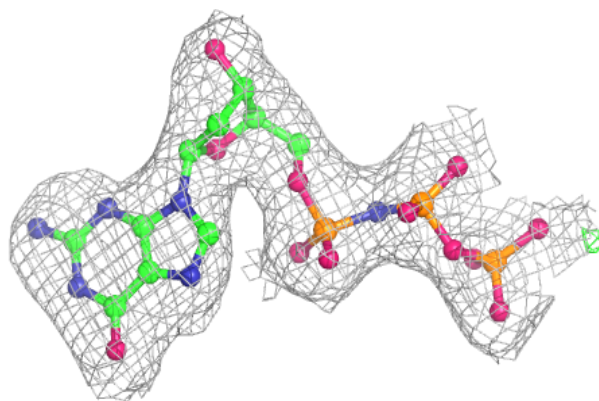
Electron density around MG E 703:

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



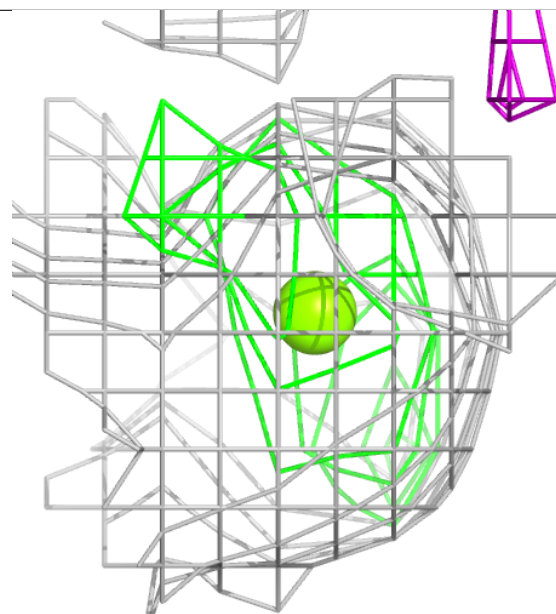
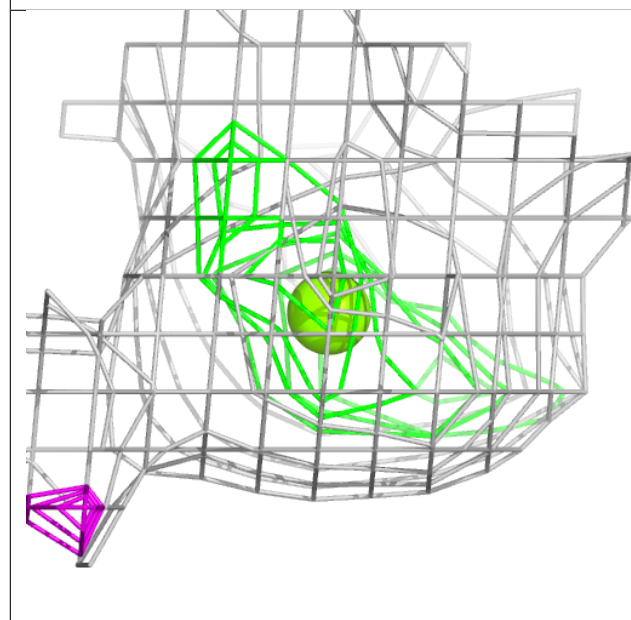
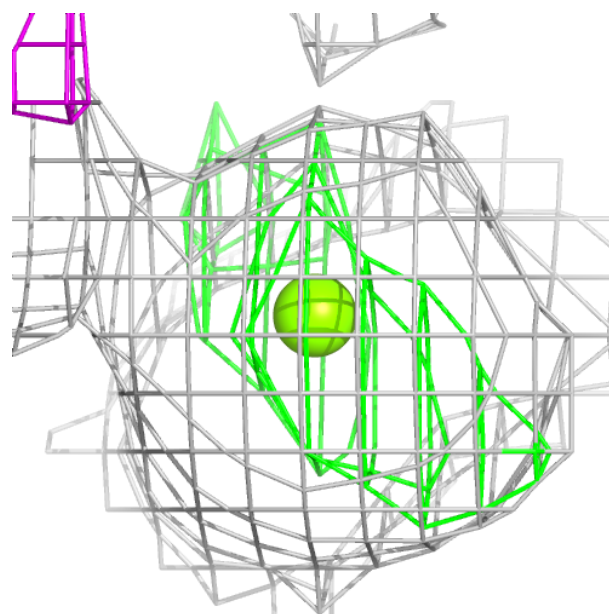
Electron density around XG4 D 701:

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



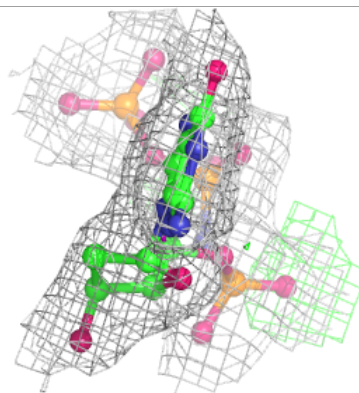
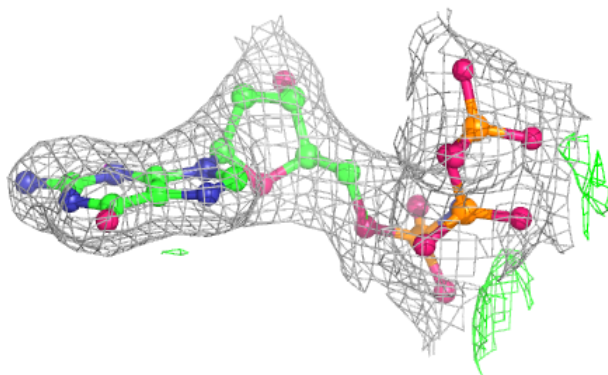
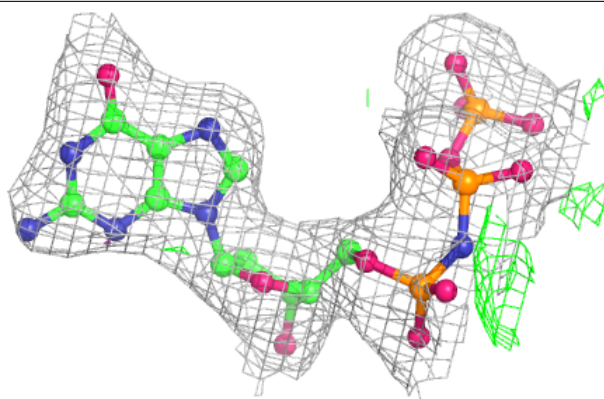
Electron density around MG A 703:

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

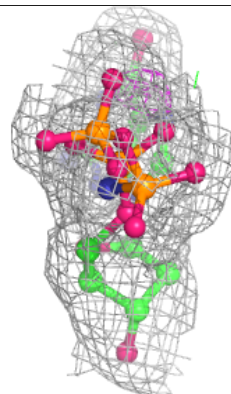
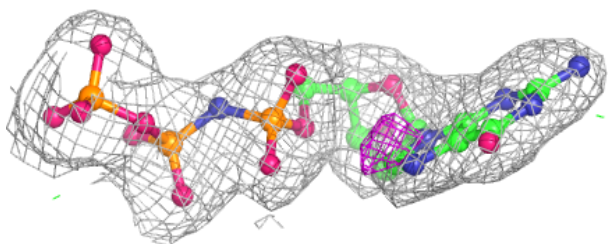
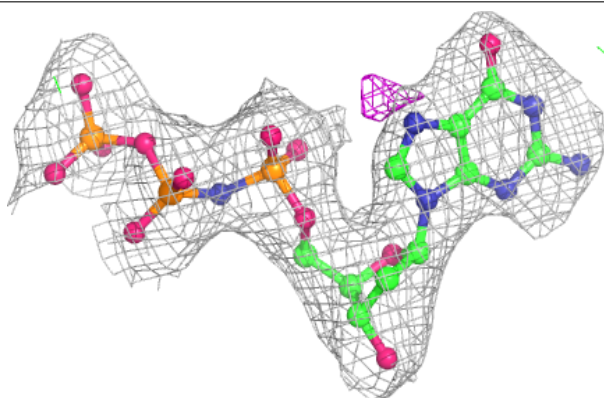


Electron density around XG4 E 705:

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

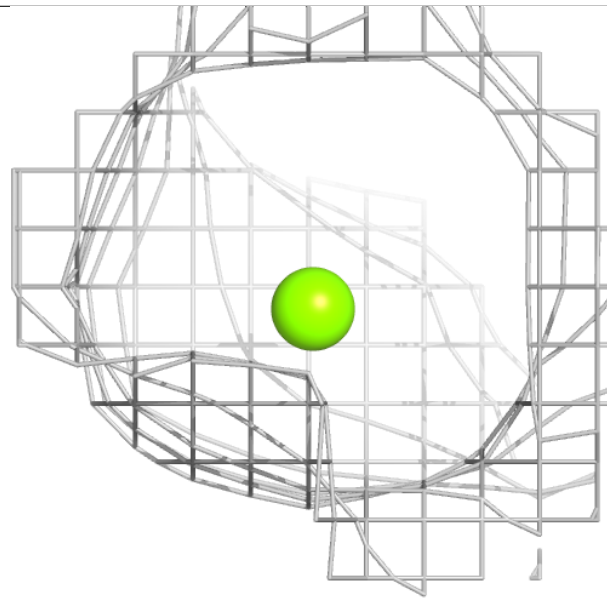
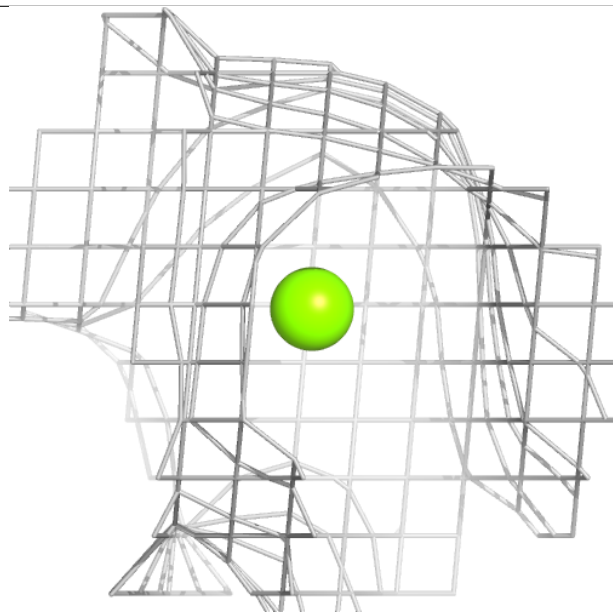
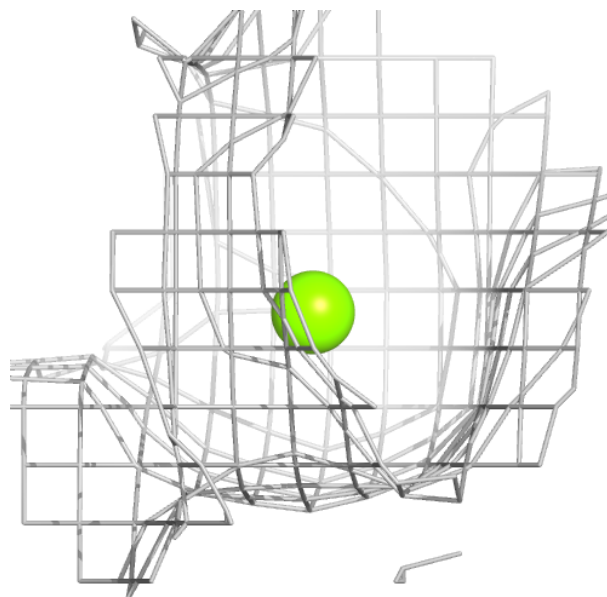
**Electron density around XG4 E 708:**

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



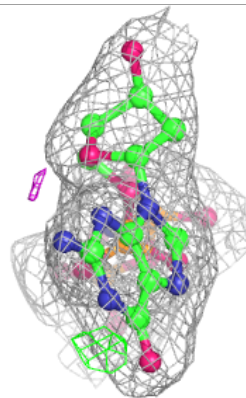
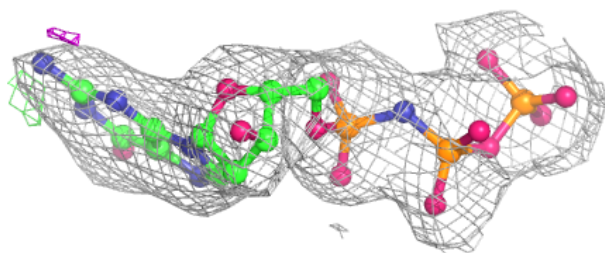
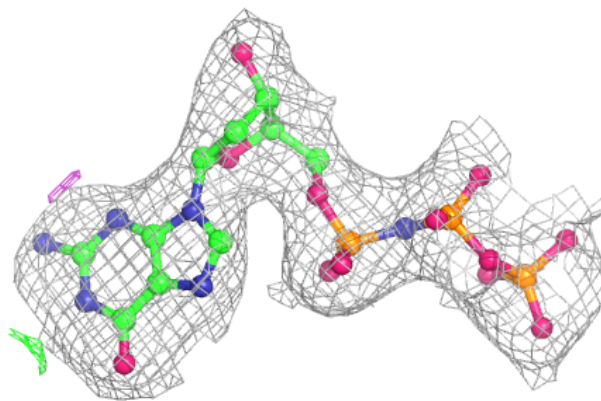
Electron density around MG A 704:

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

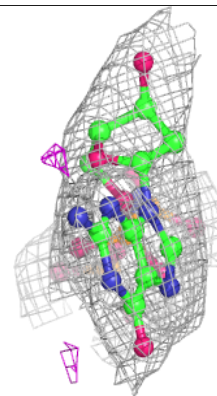
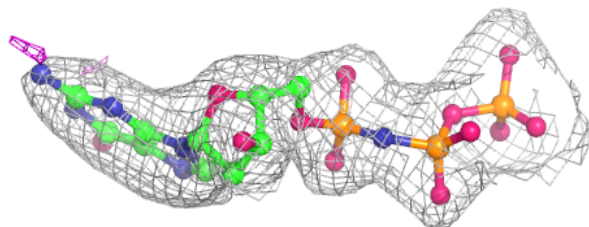
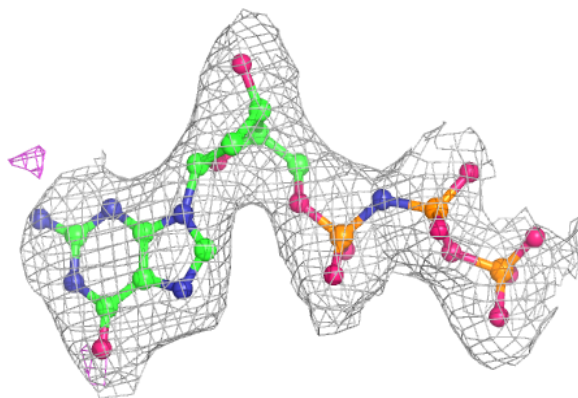


Electron density around XG4 F 708:

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

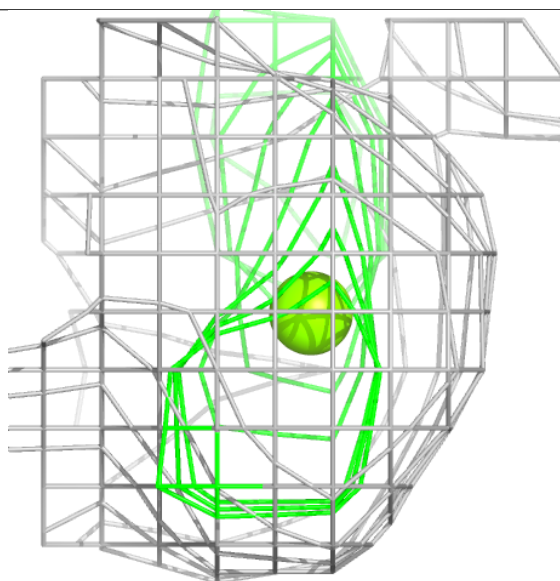
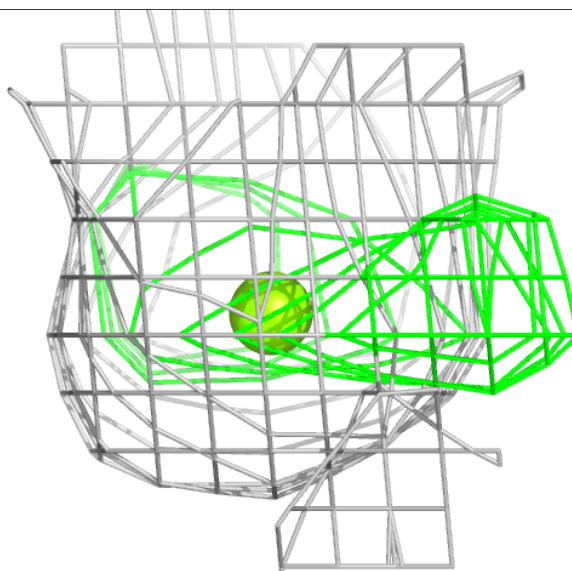
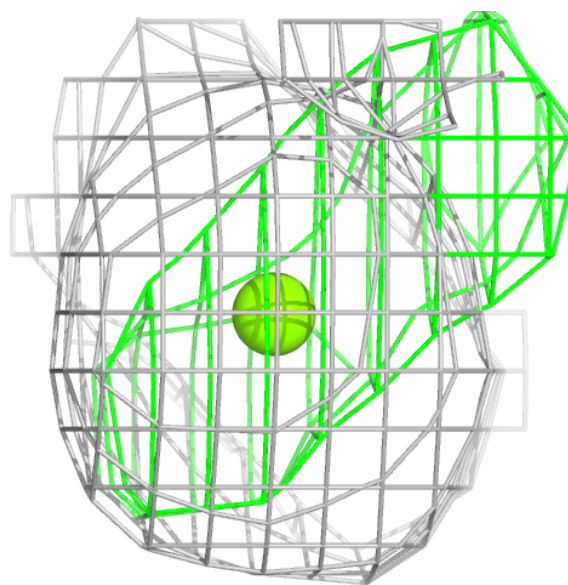
**Electron density around XG4 G 701:**

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



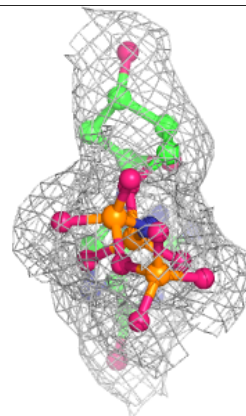
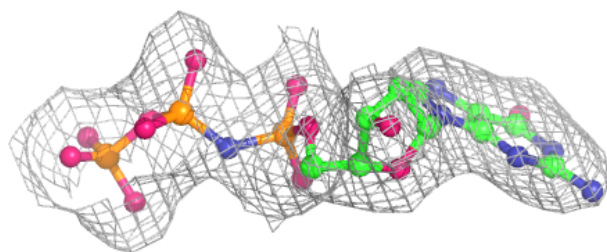
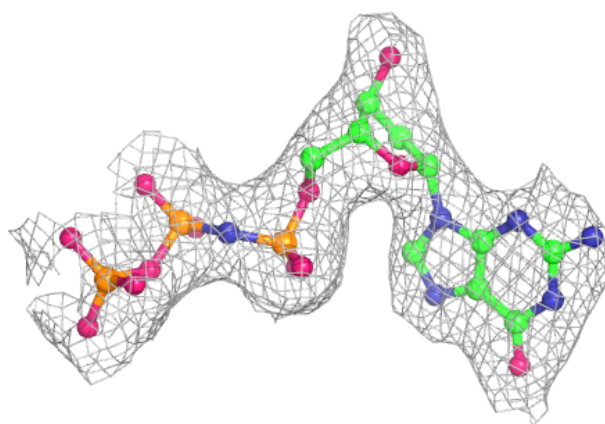
Electron density around MG H 704:

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



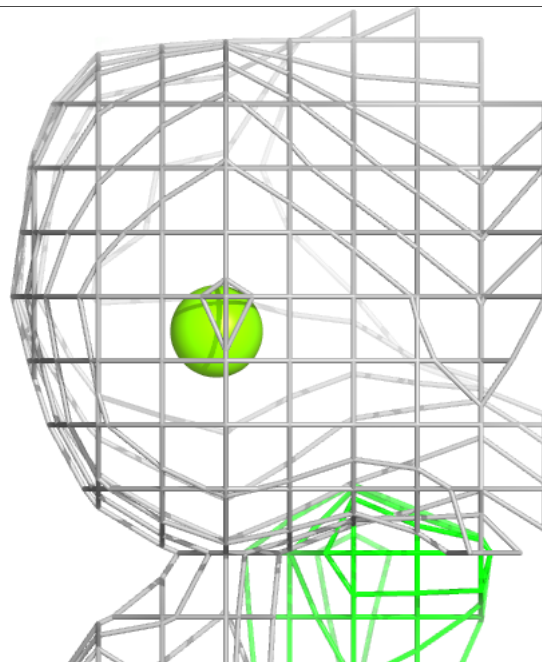
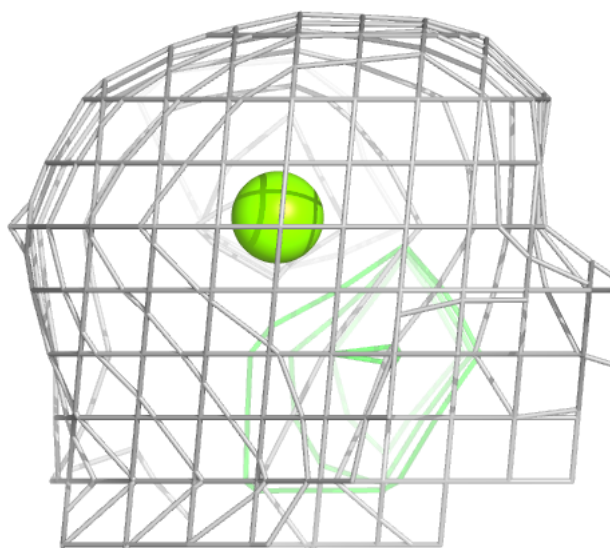
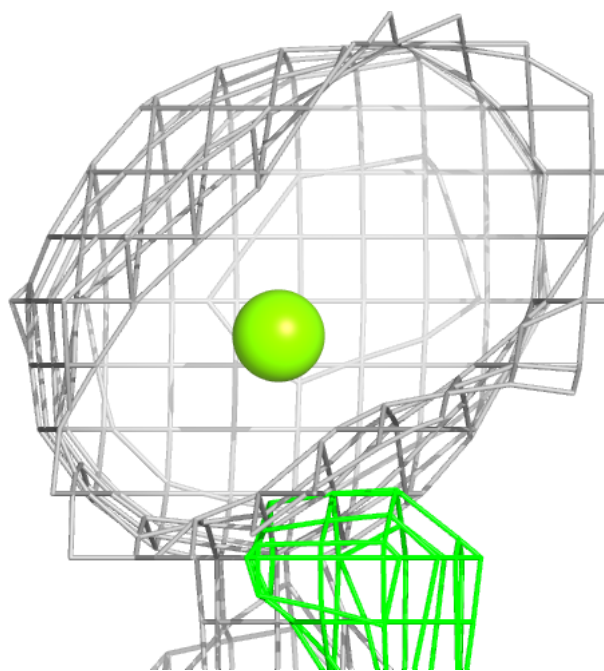
Electron density around XG4 H 701:

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



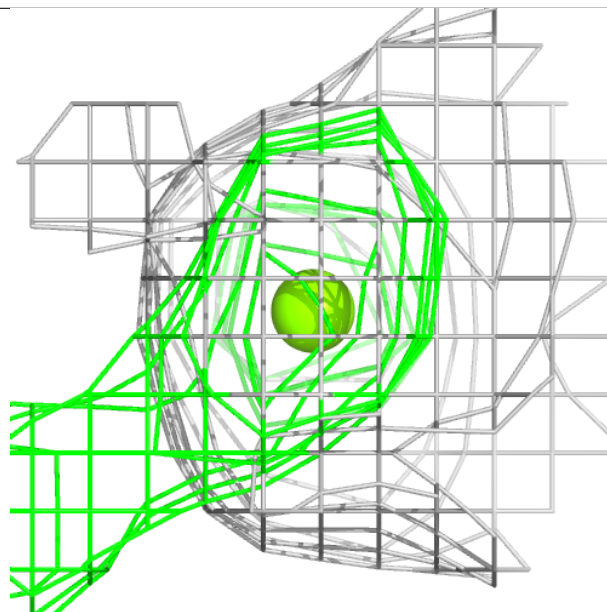
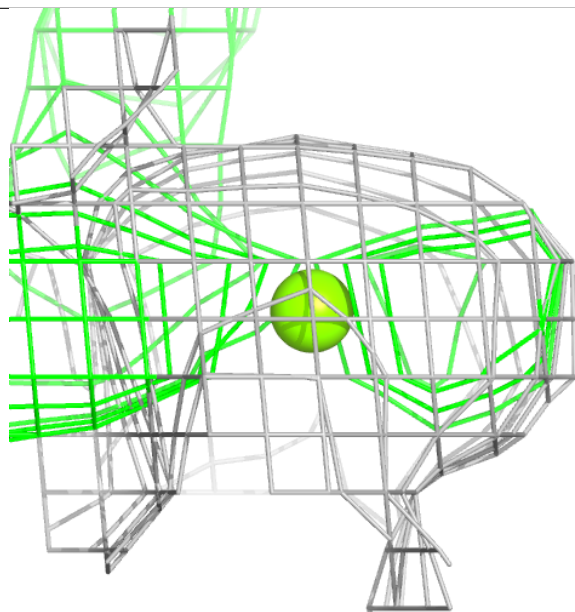
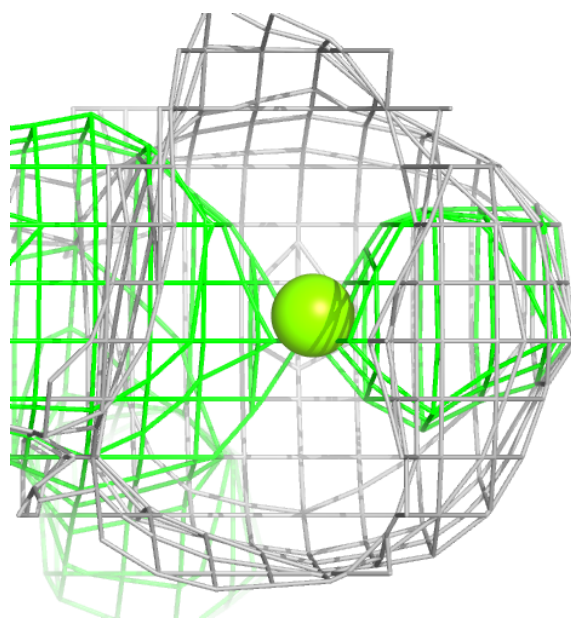
Electron density around MG I 703:

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



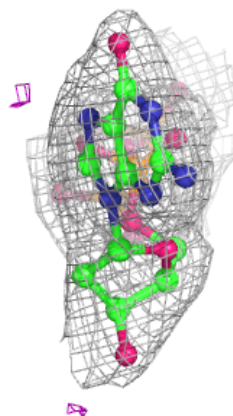
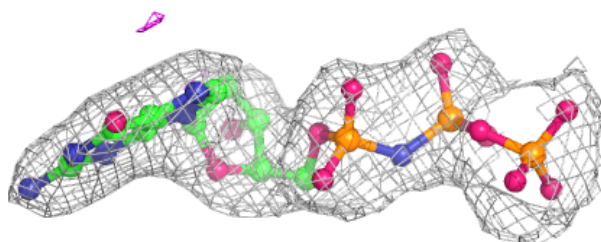
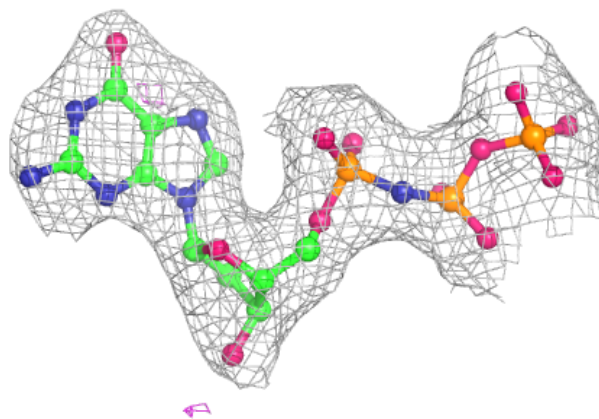
Electron density around MG J 704:

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



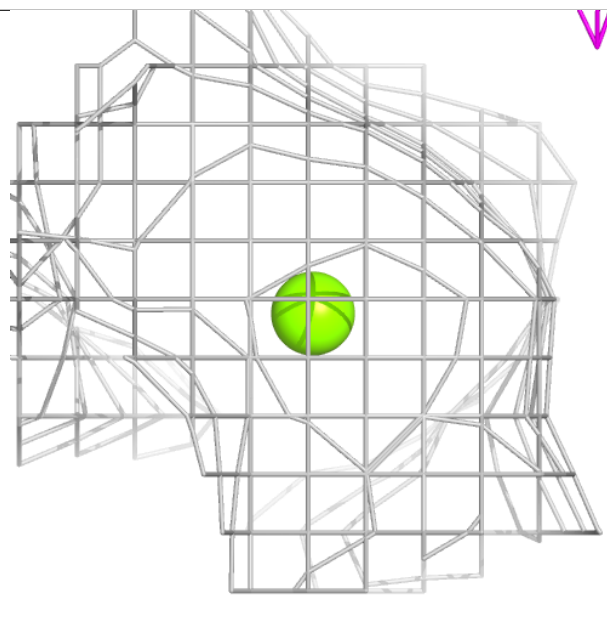
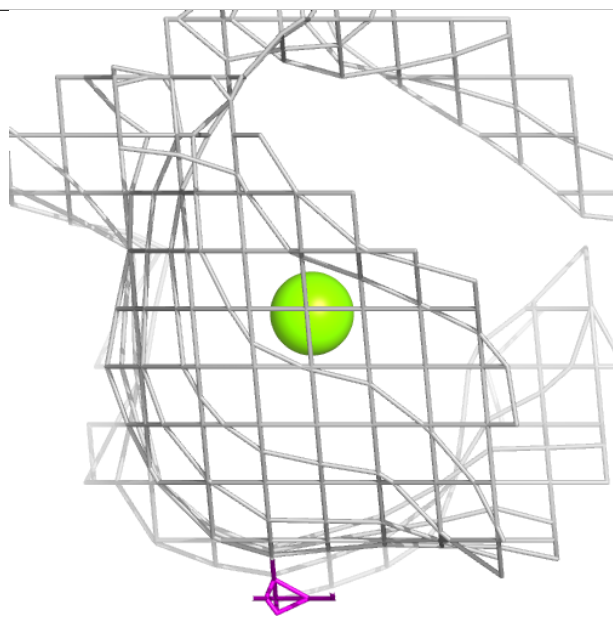
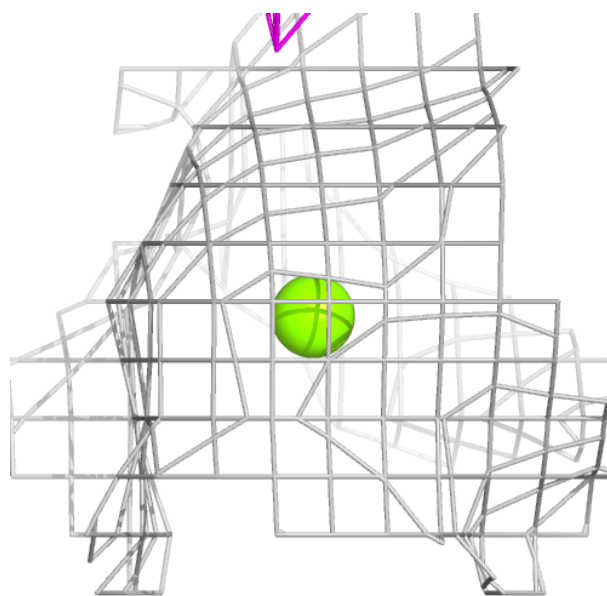
Electron density around XG4 I 707:

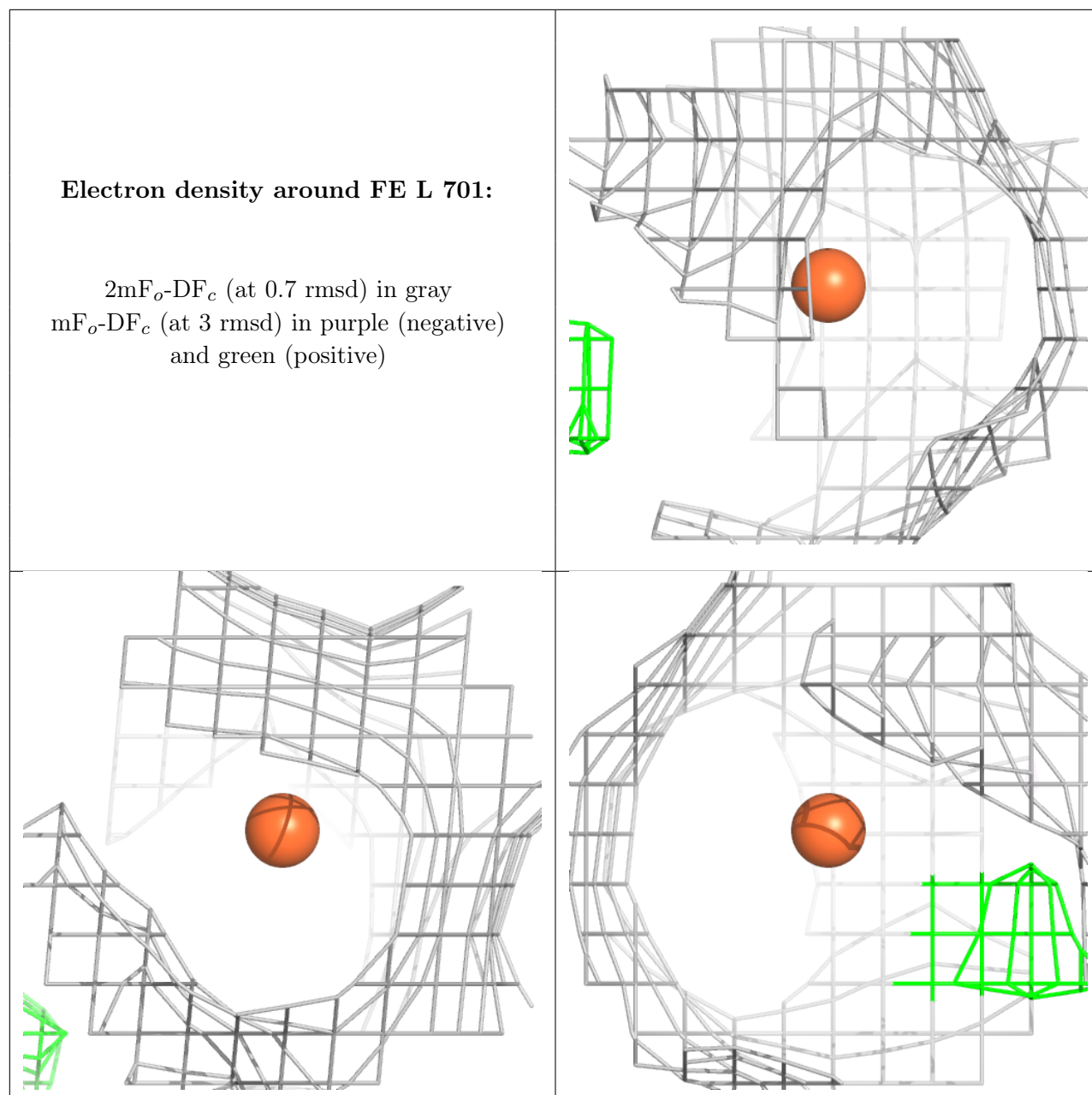
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around MG J 705:

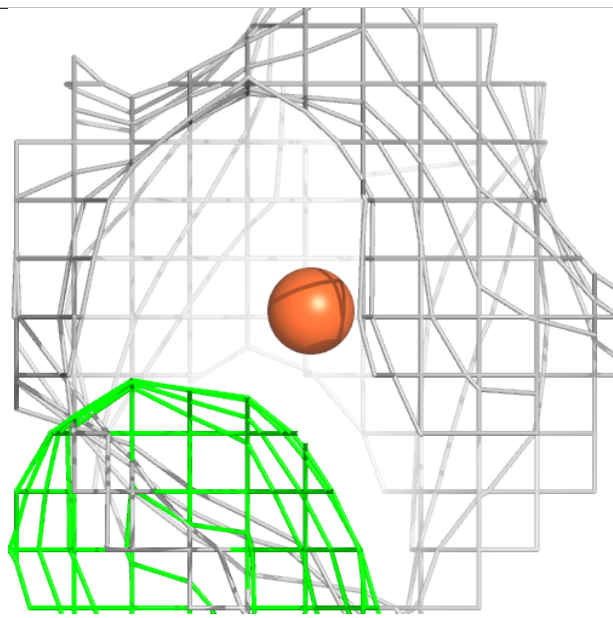
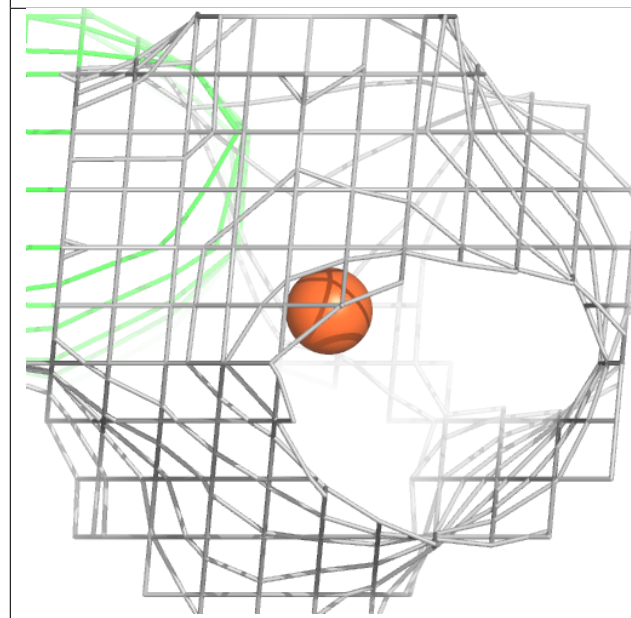
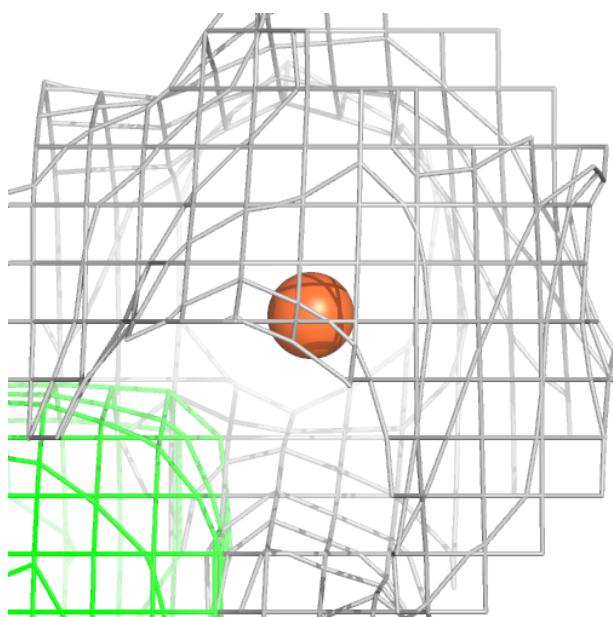
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

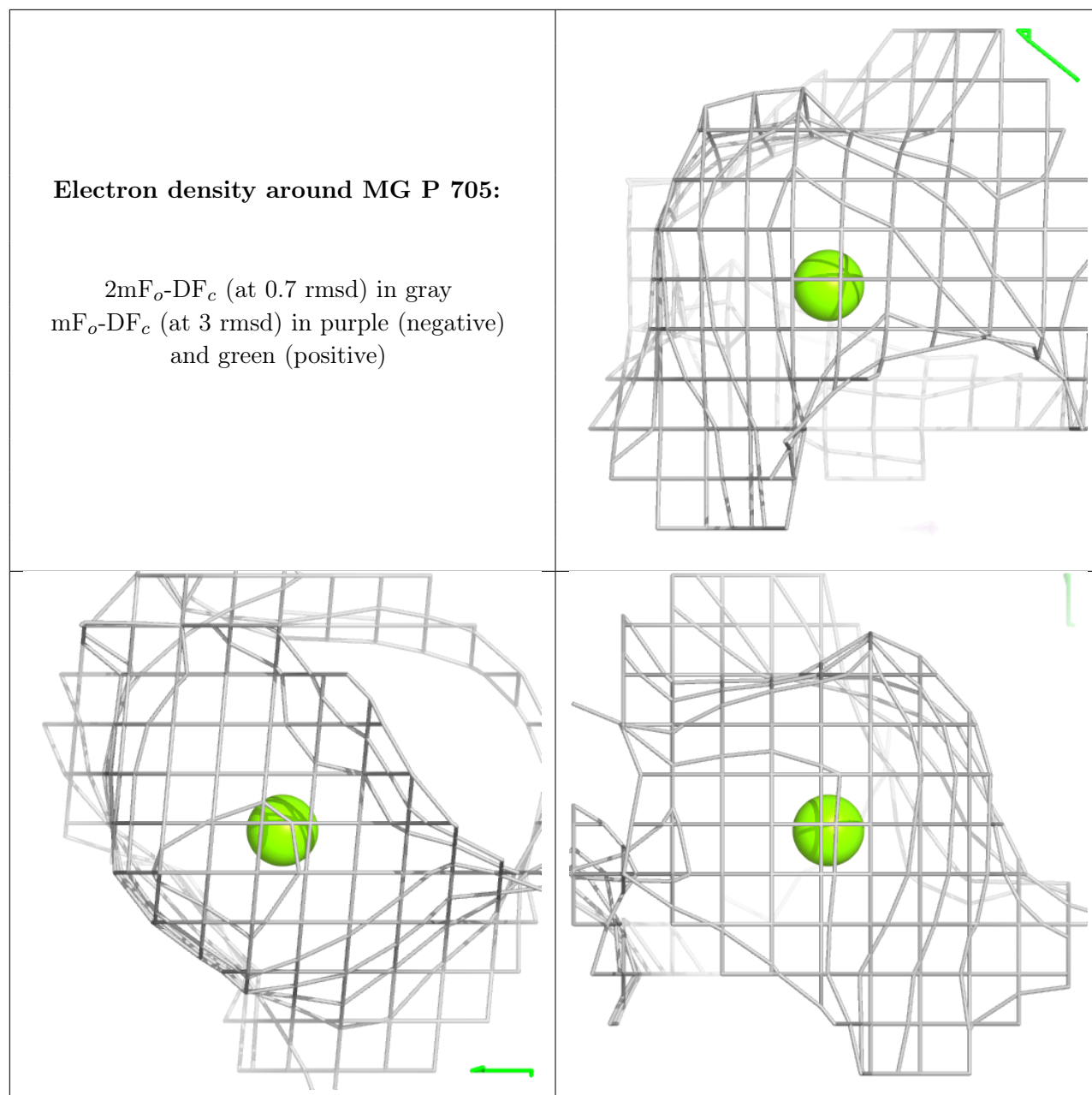




Electron density around FE D 702:

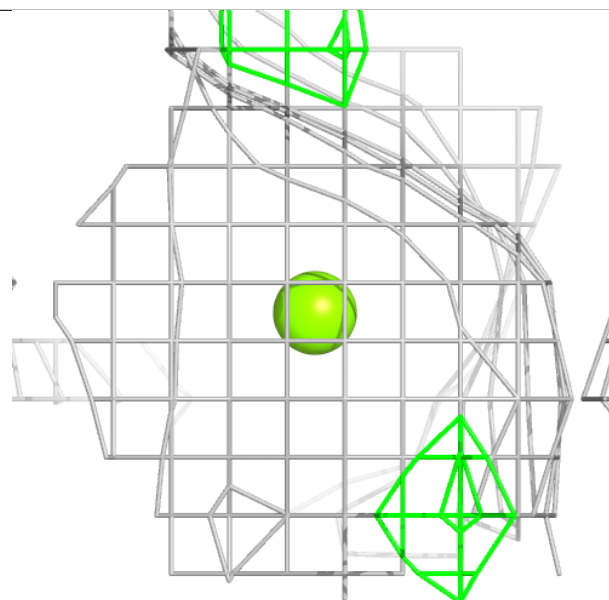
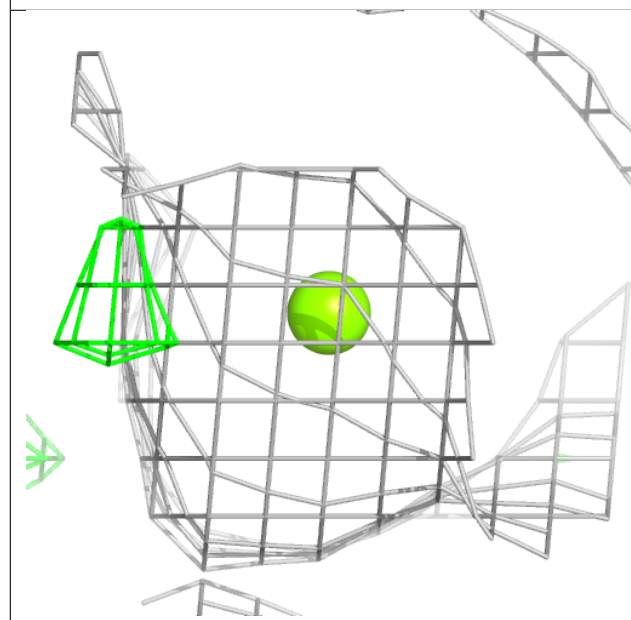
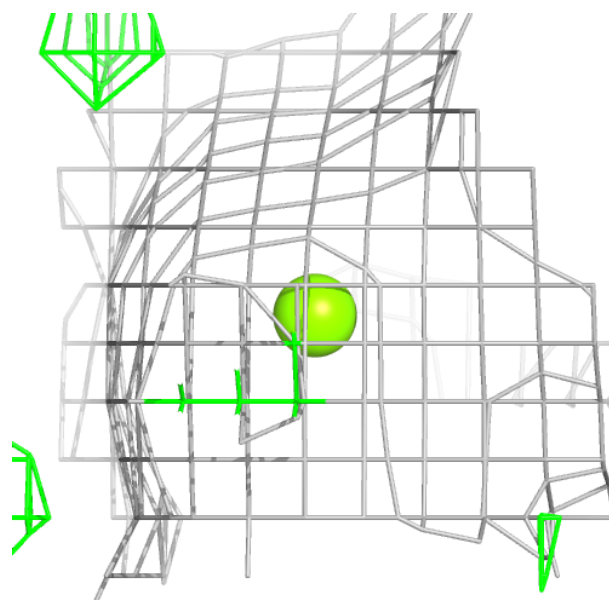
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





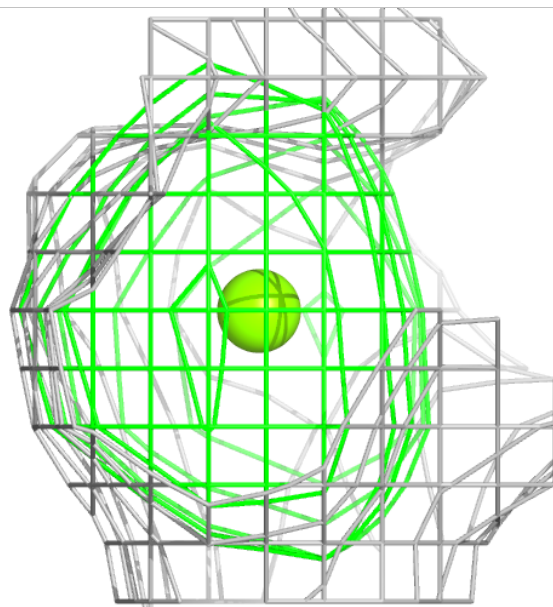
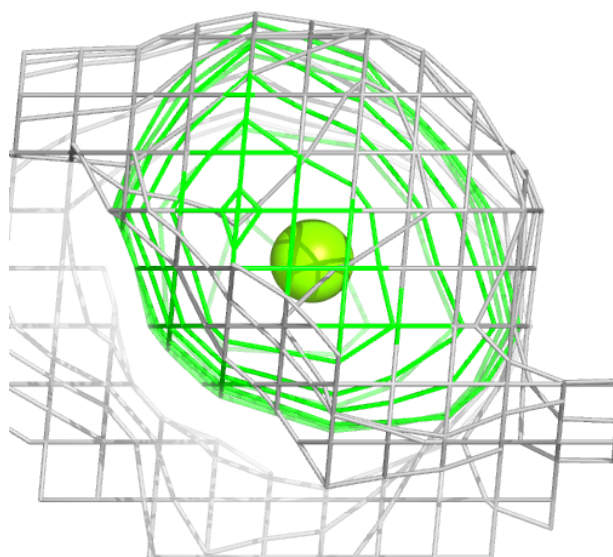
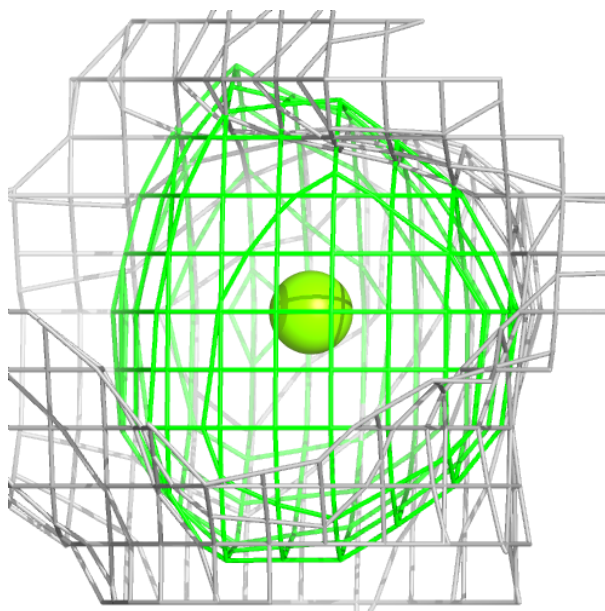
Electron density around MG E 704:

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



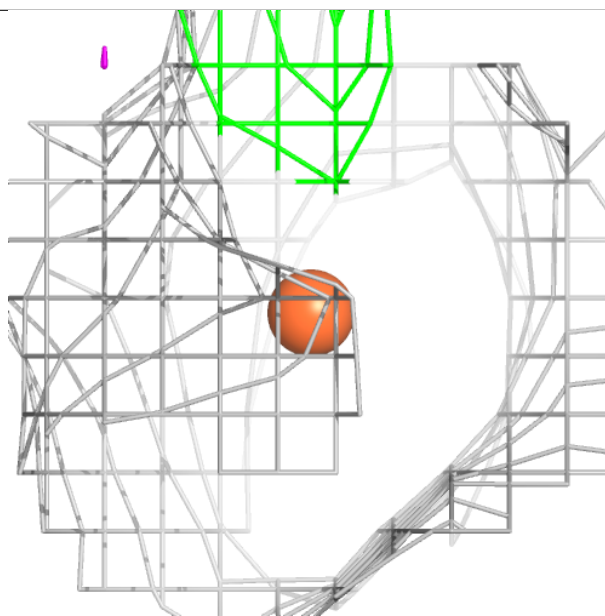
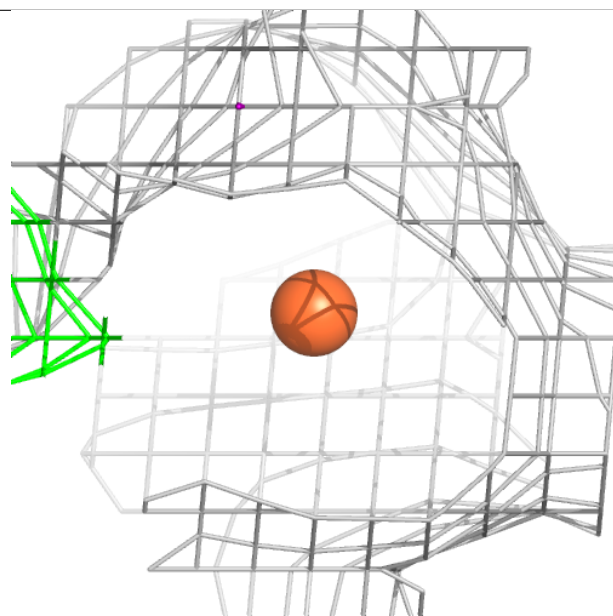
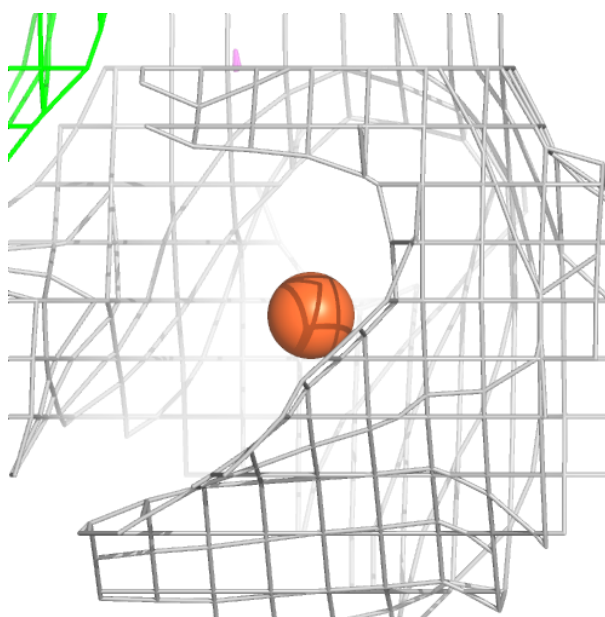
Electron density around MG F 702:

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



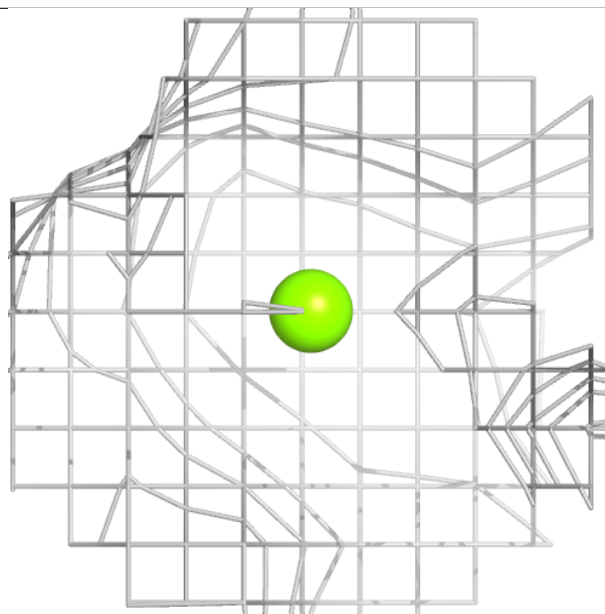
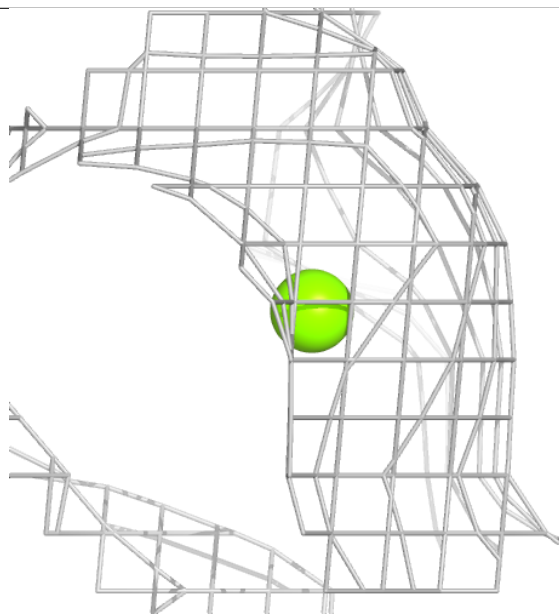
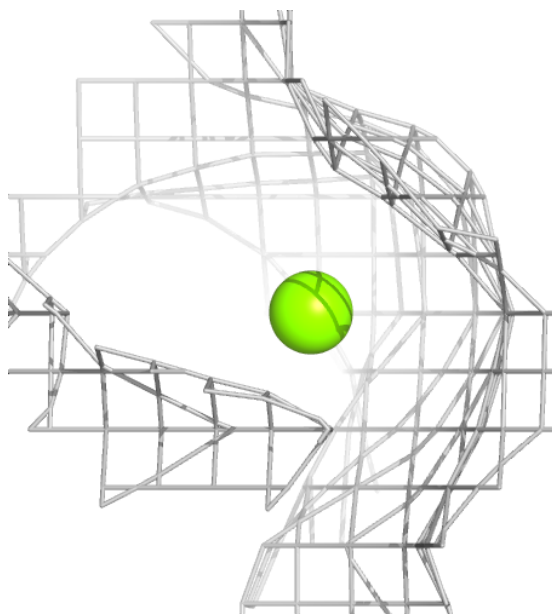
Electron density around FE N 701:

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



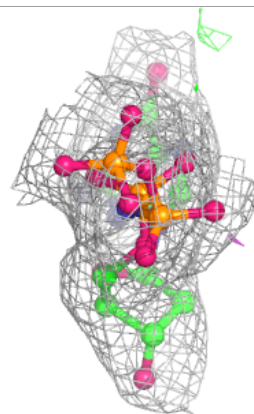
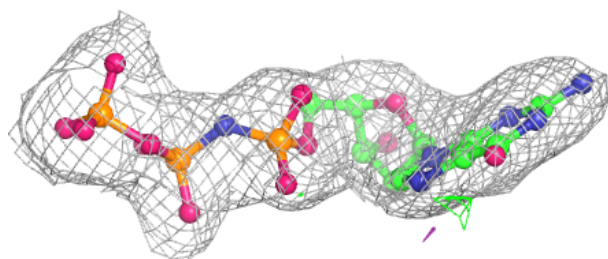
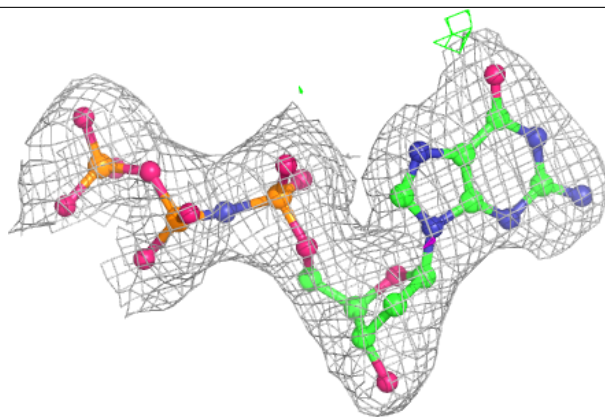
Electron density around MG F 704:

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



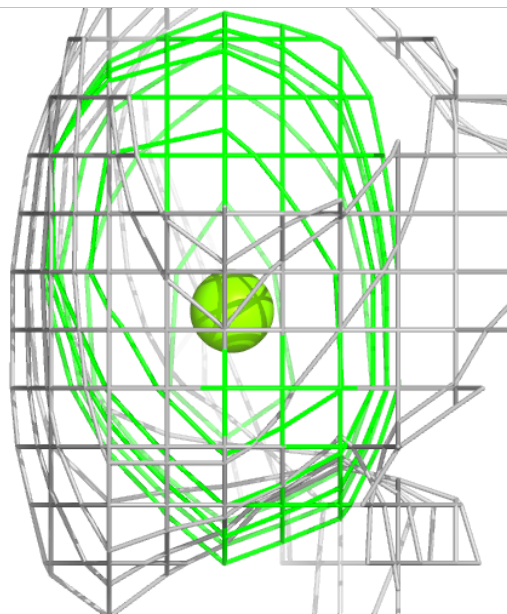
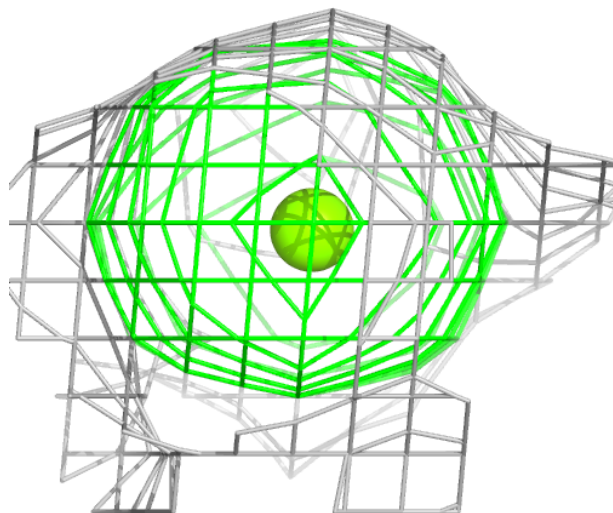
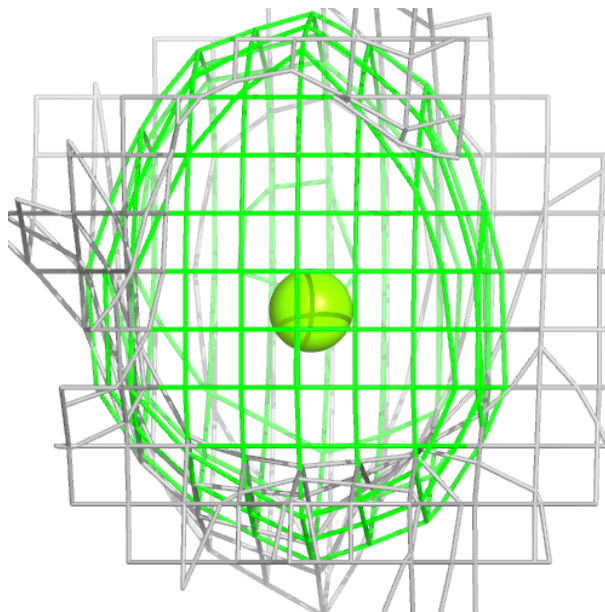
Electron density around XG4 C 701:

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



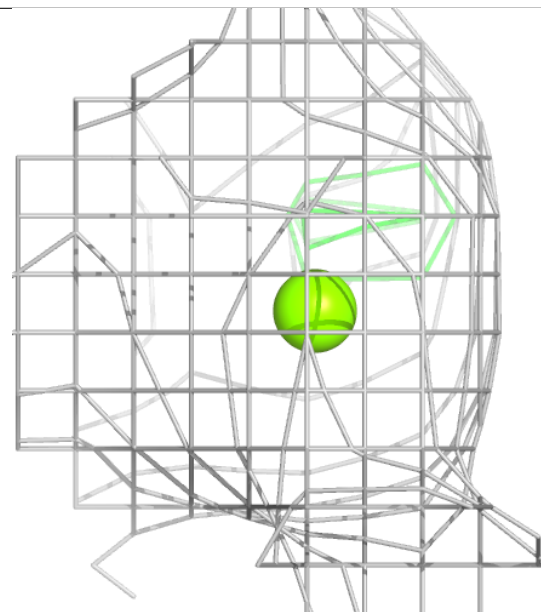
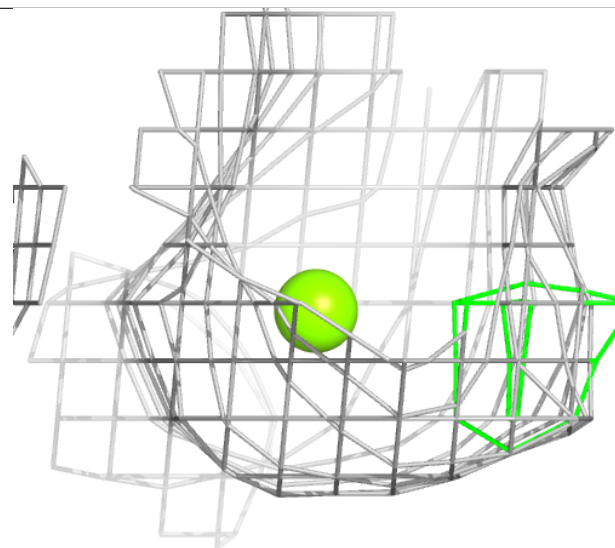
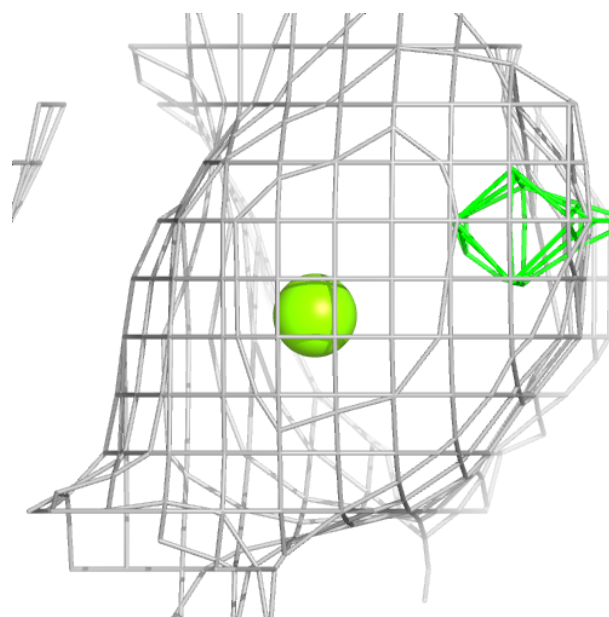
Electron density around MG G 703:

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



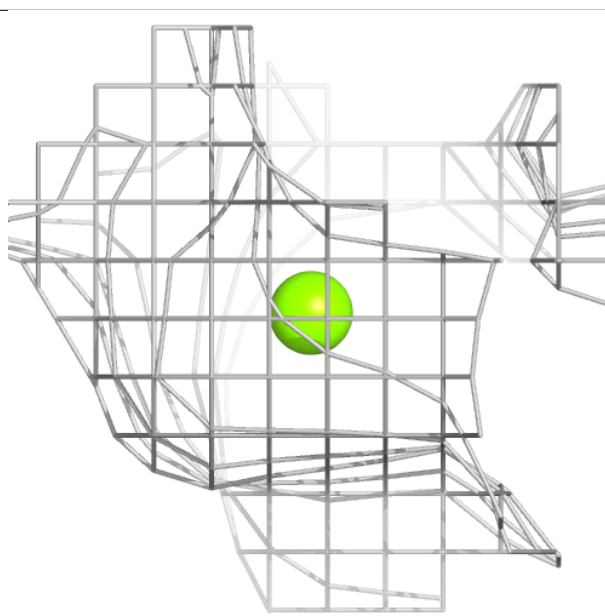
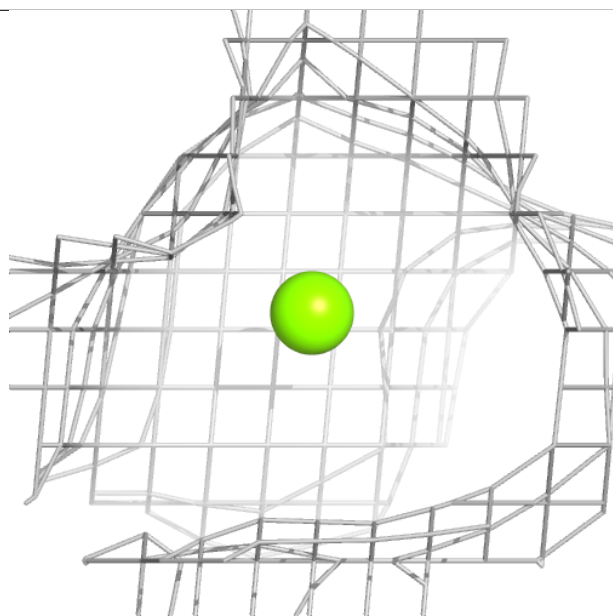
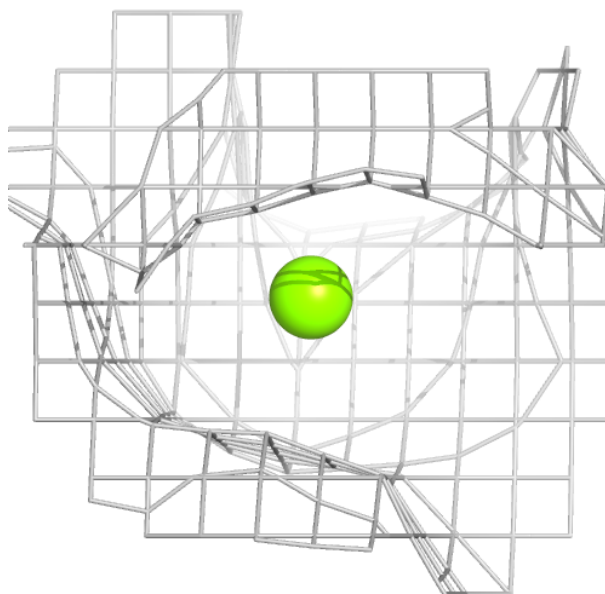
Electron density around MG G 704:

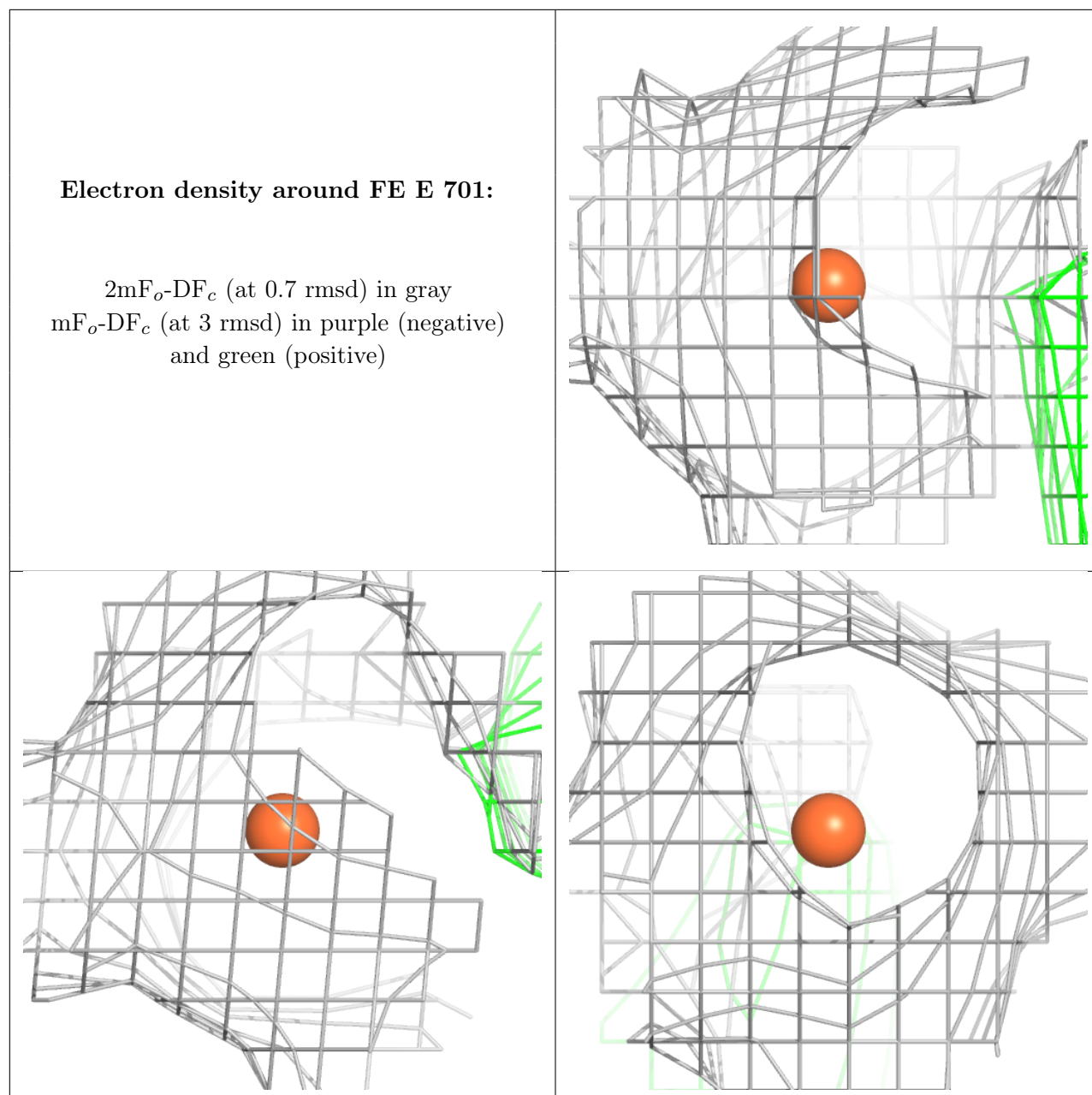
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around MG G 705:

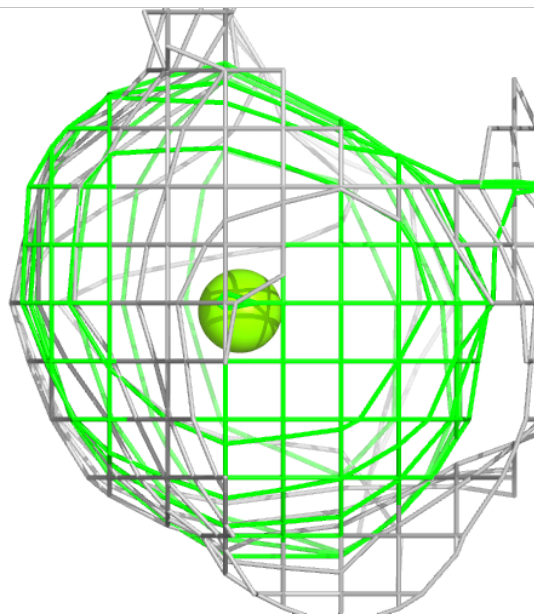
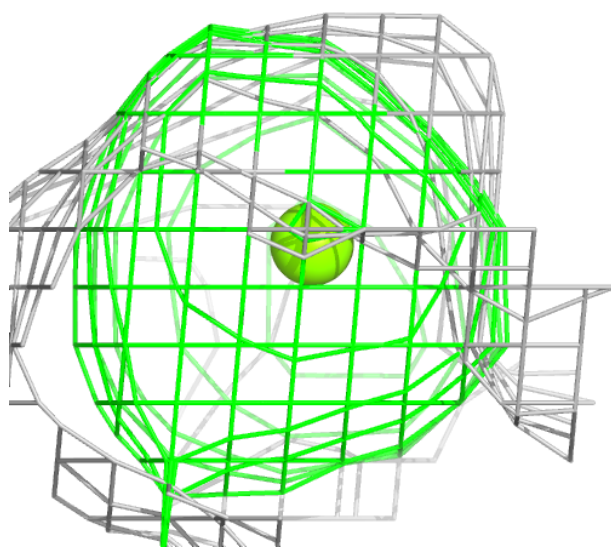
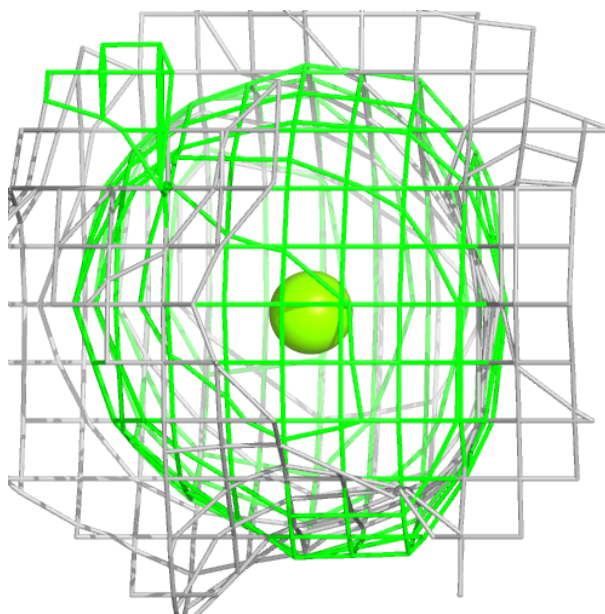
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





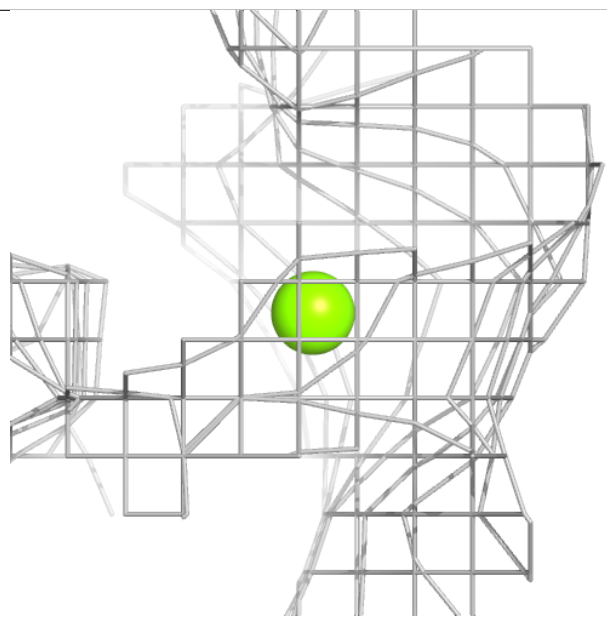
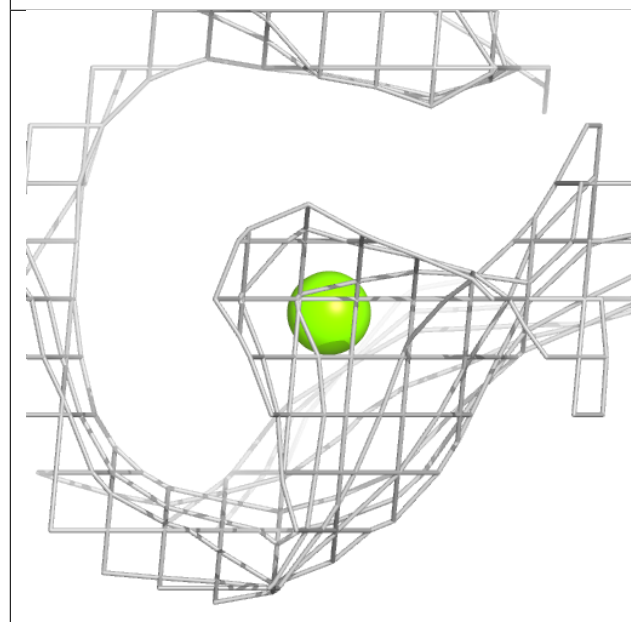
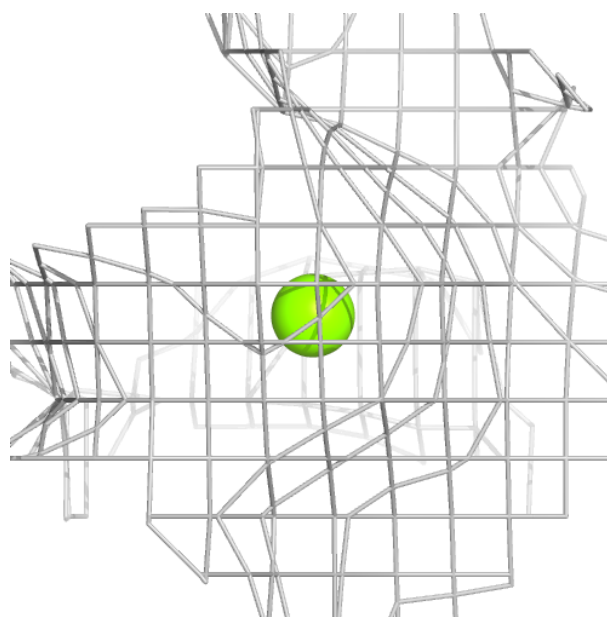
Electron density around MG A 702:

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



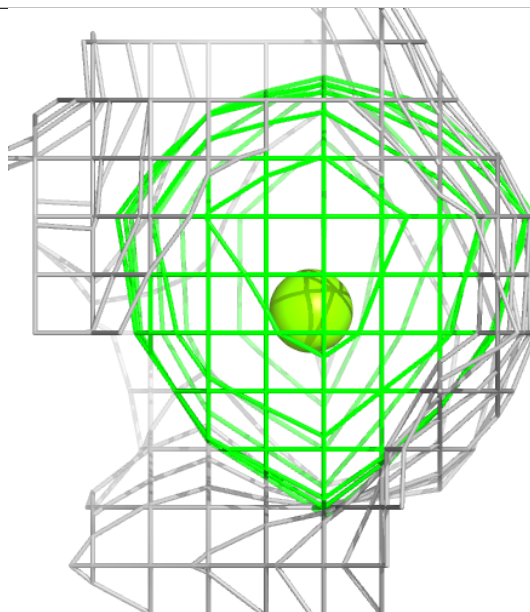
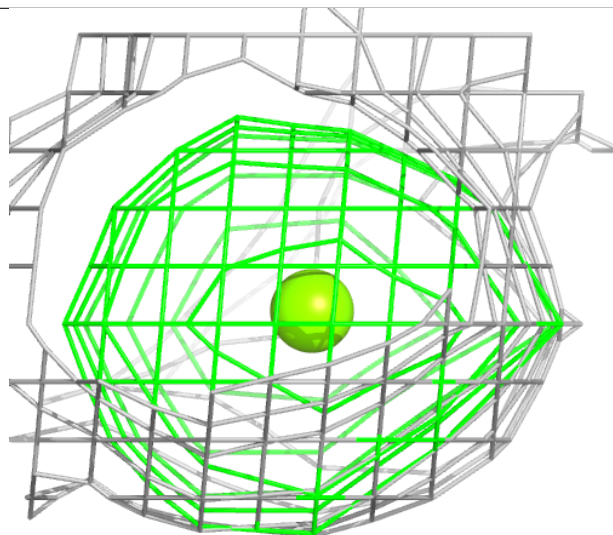
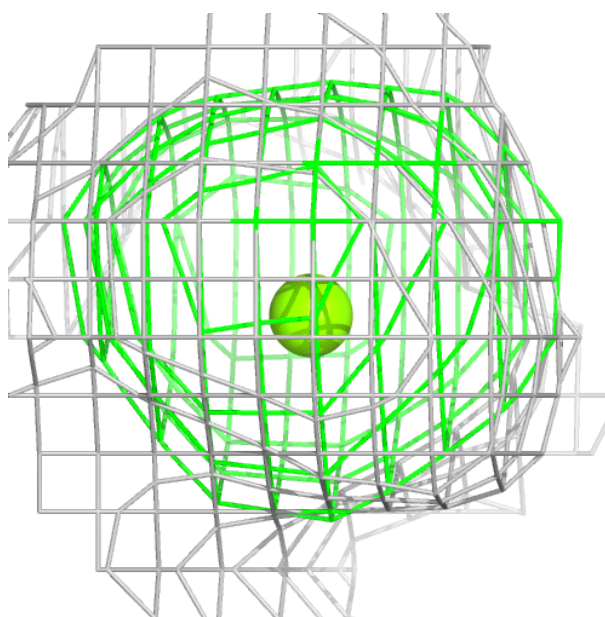
Electron density around MG H 705:

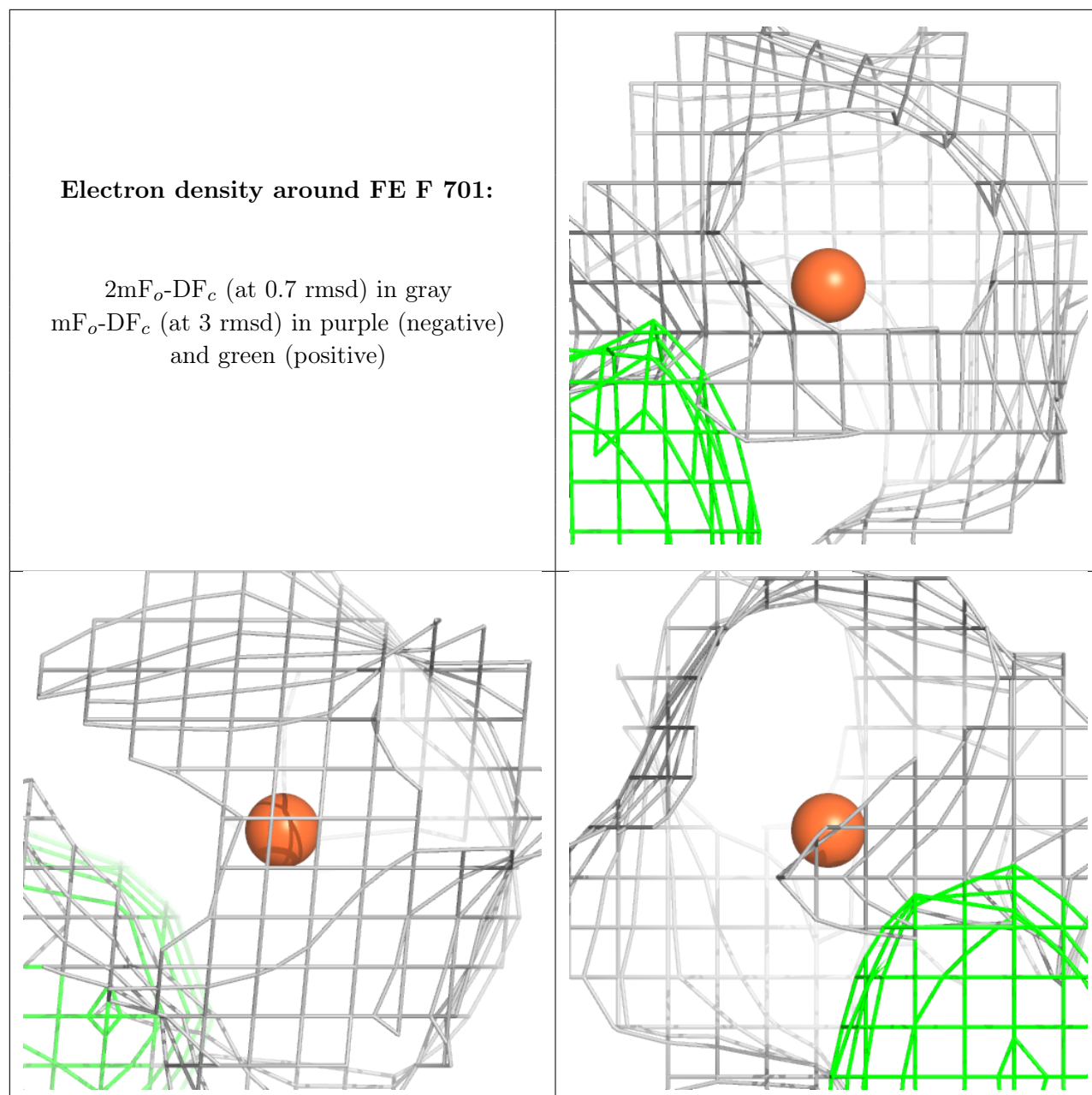
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around MG I 702:

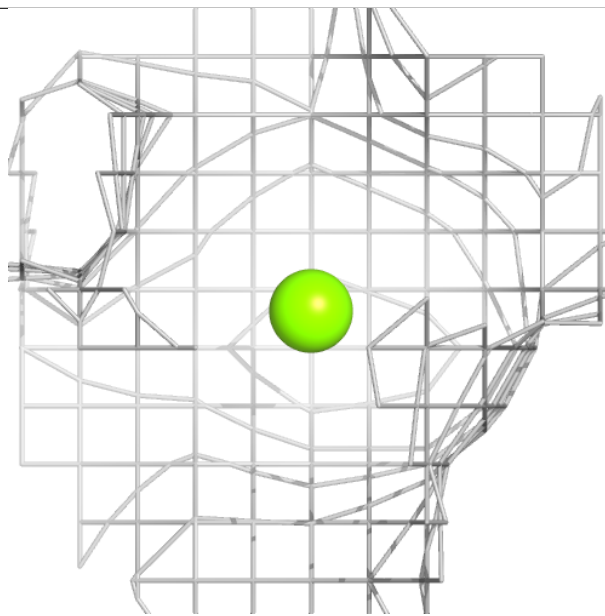
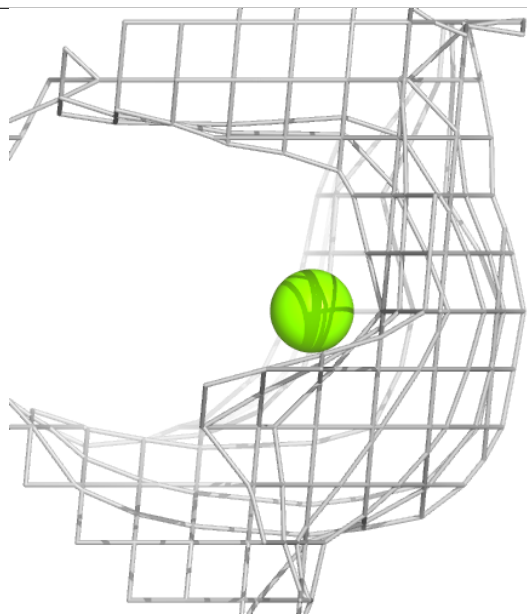
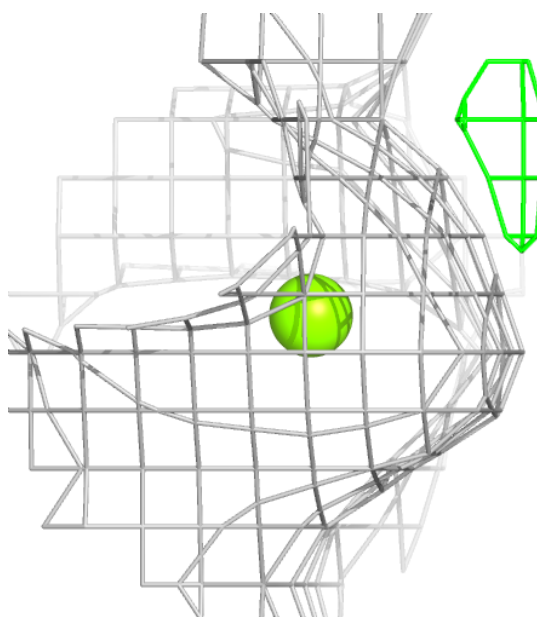
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





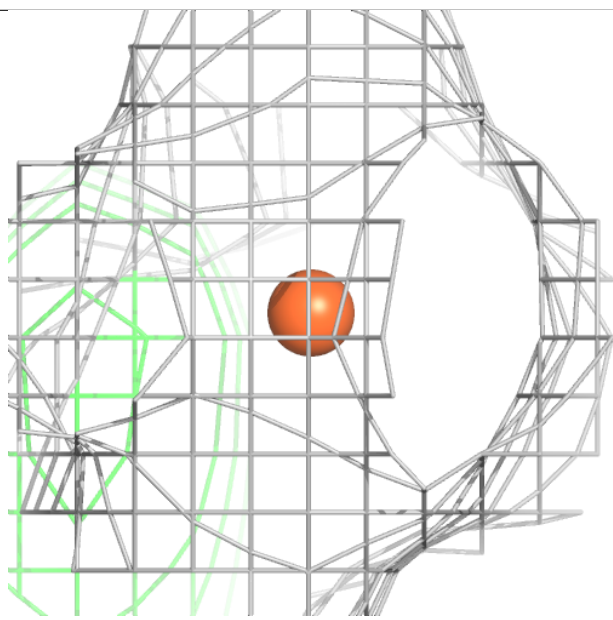
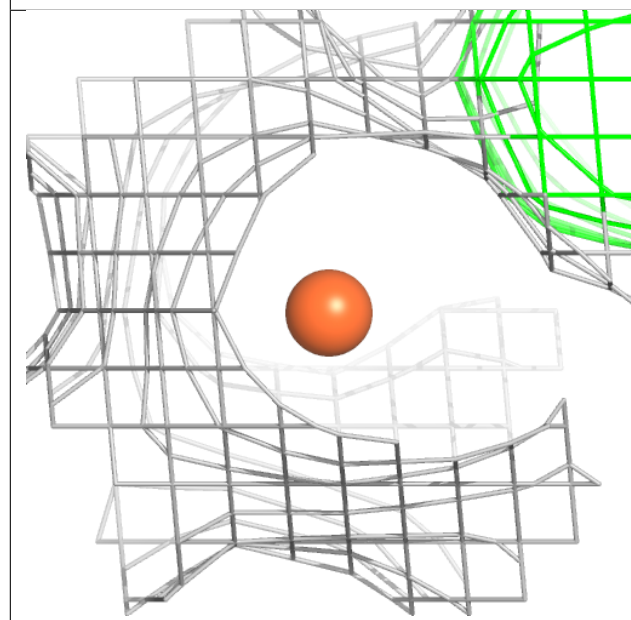
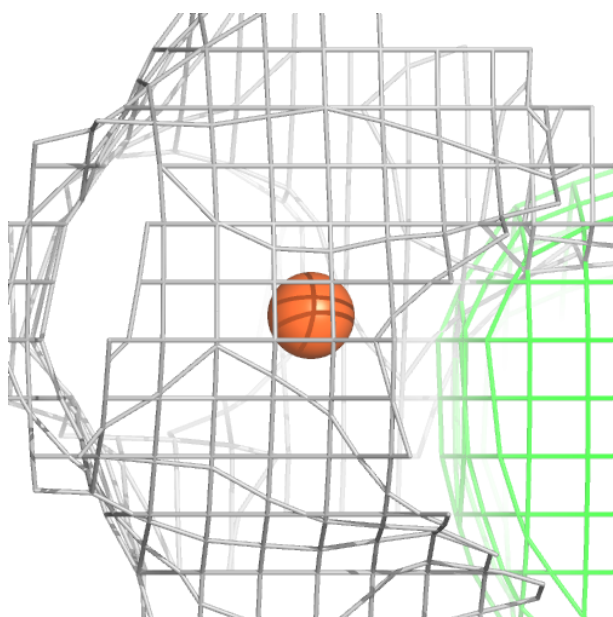
Electron density around MG I 704:

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



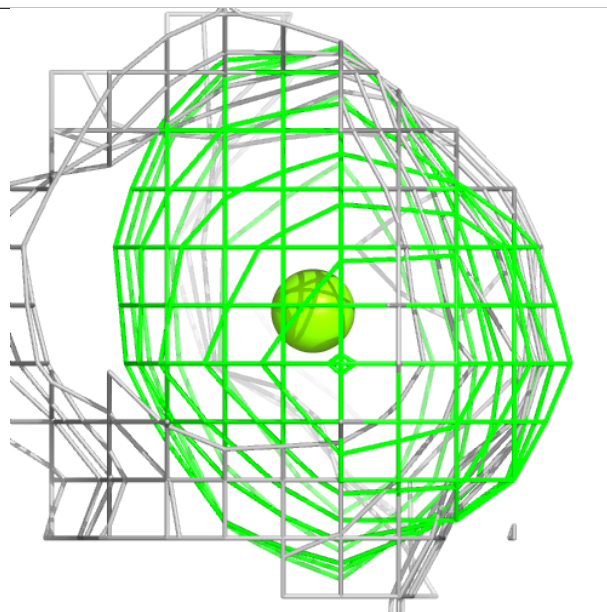
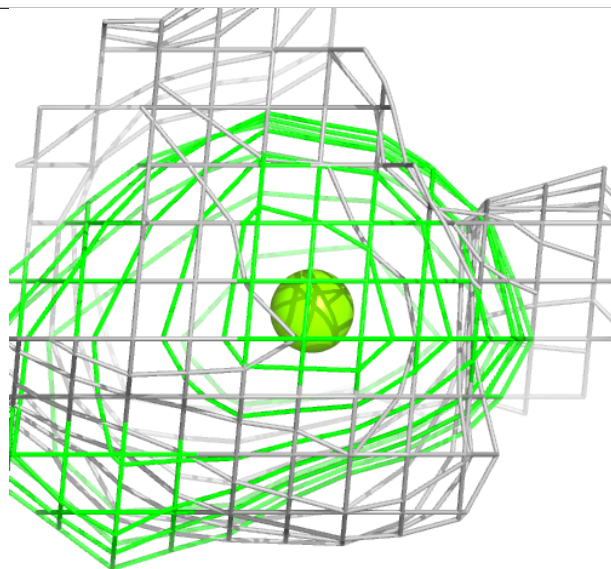
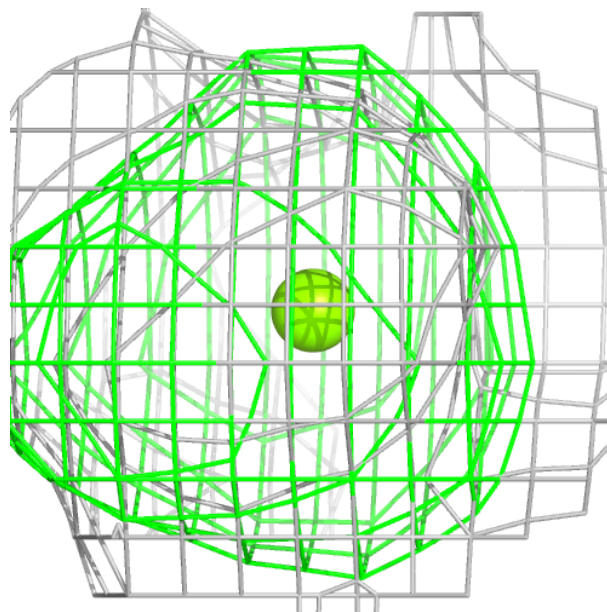
Electron density around FE G 702:

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



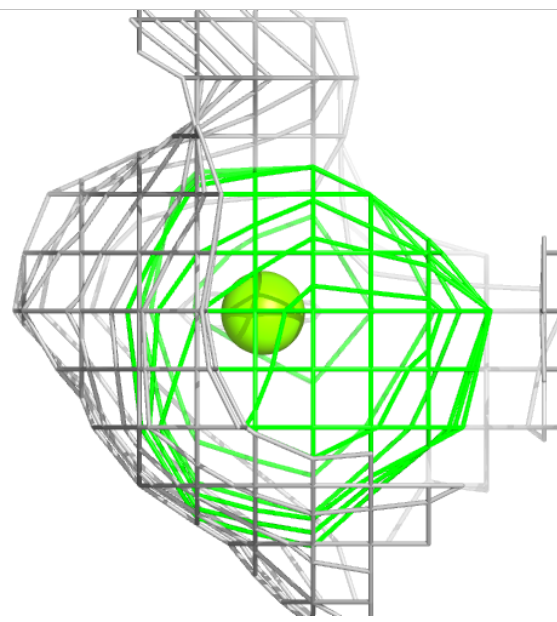
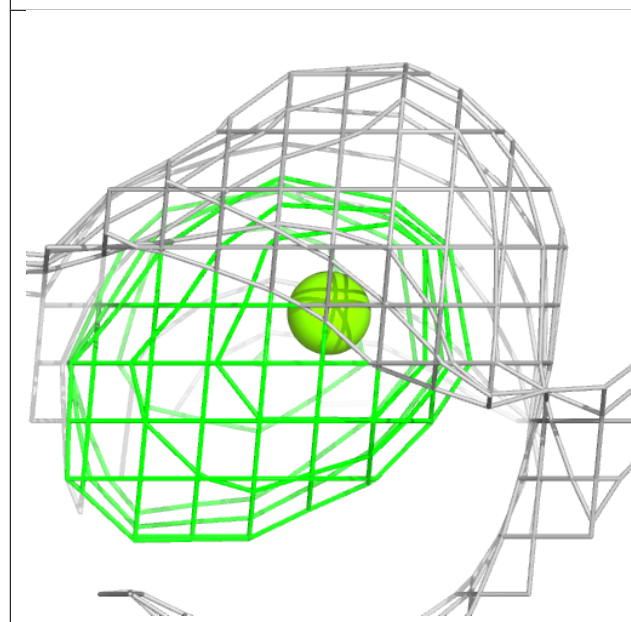
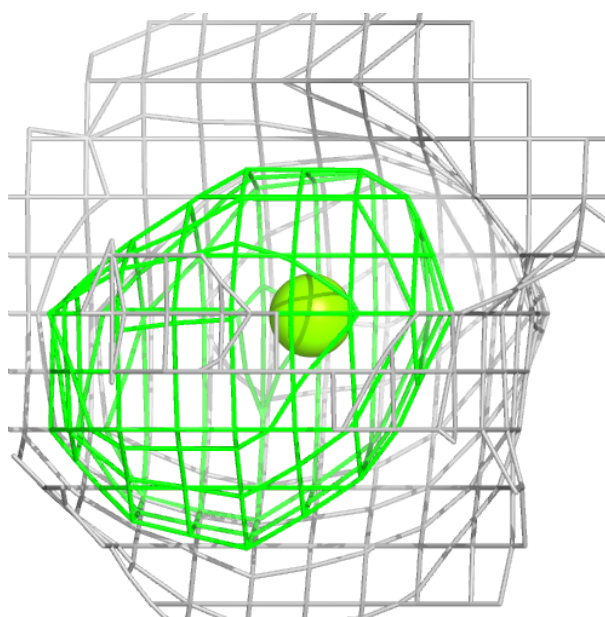
Electron density around MG B 702:

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



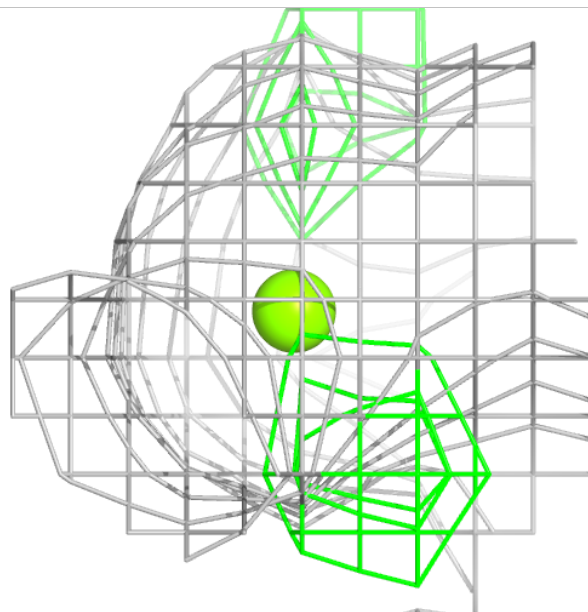
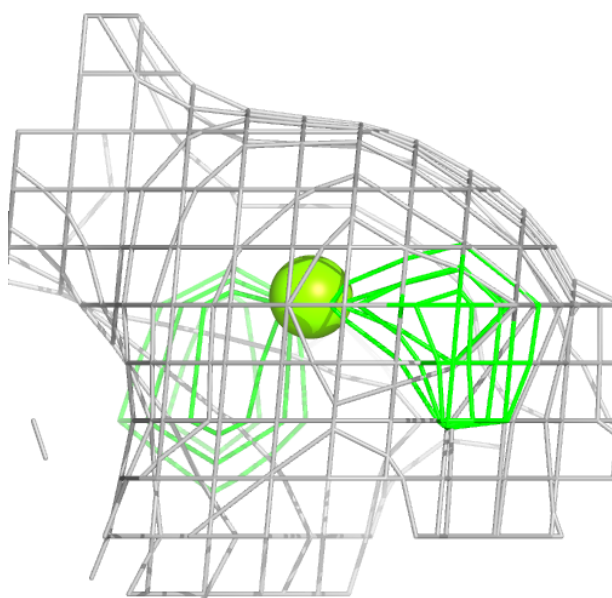
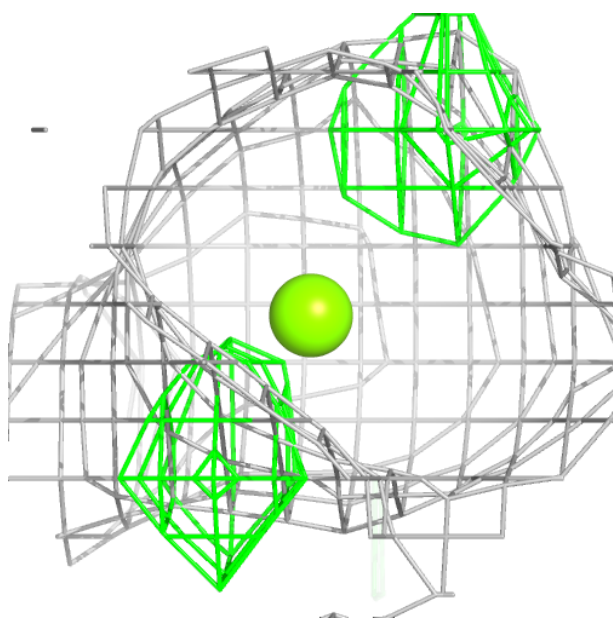
Electron density around MG K 703:

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



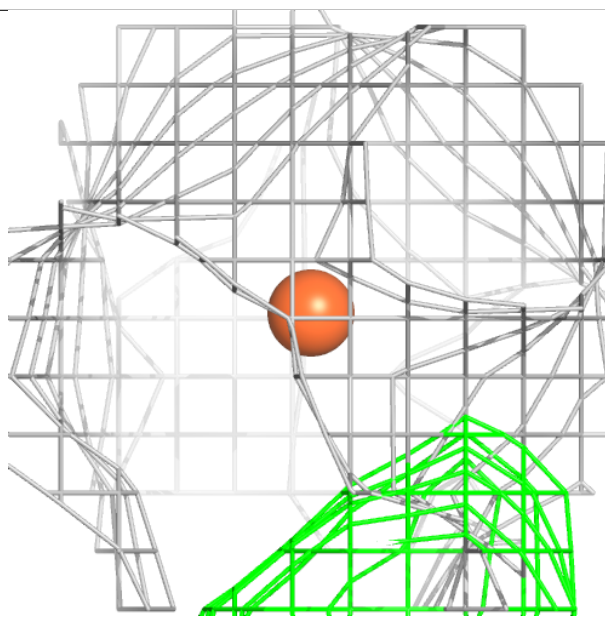
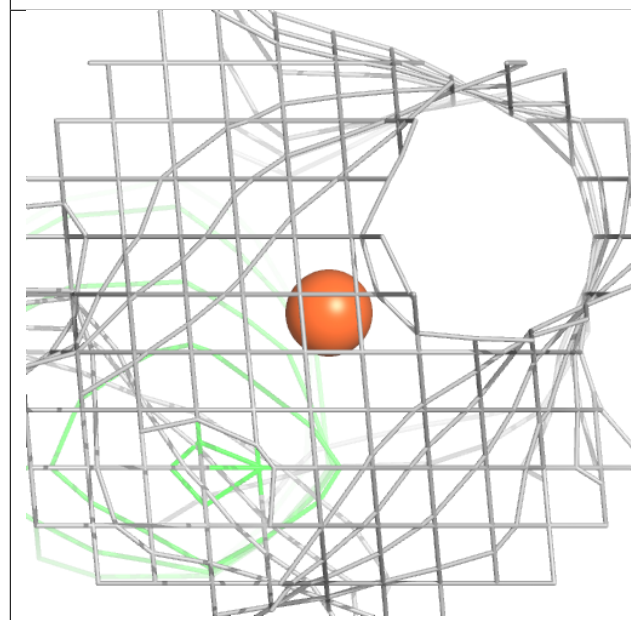
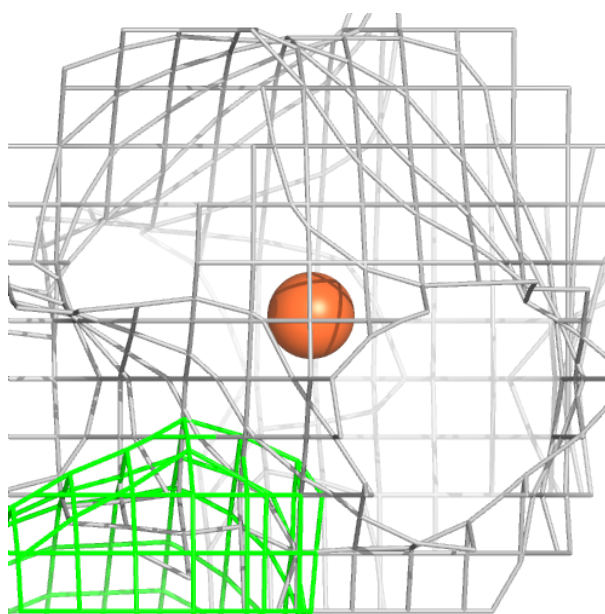
Electron density around MG B 703:

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



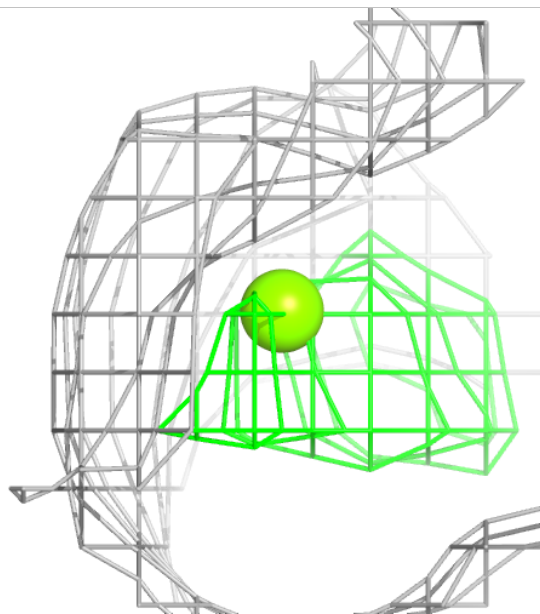
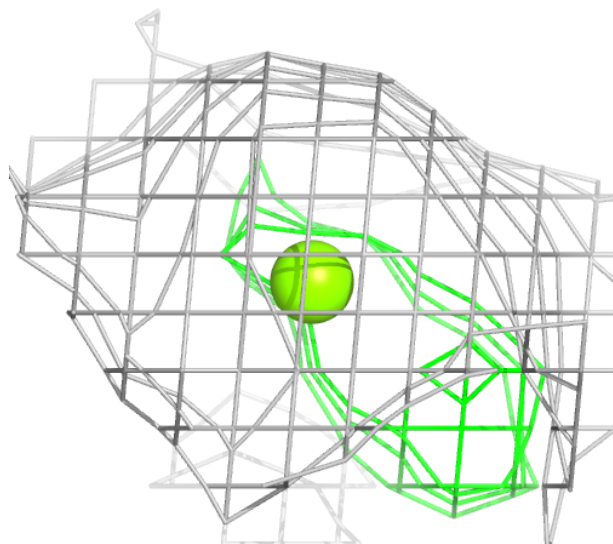
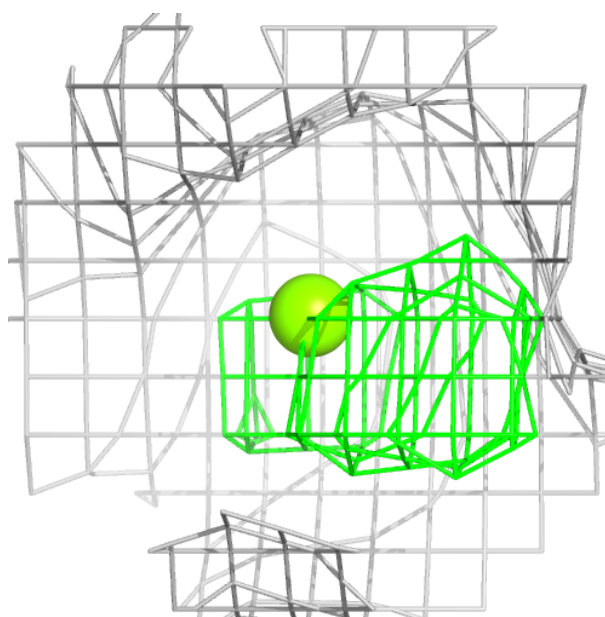
Electron density around FE H 702:

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



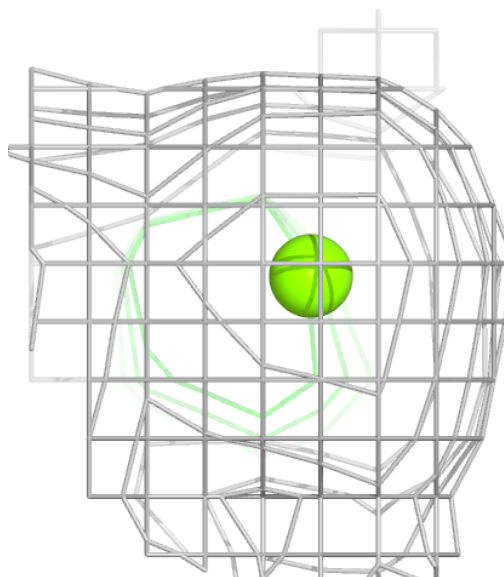
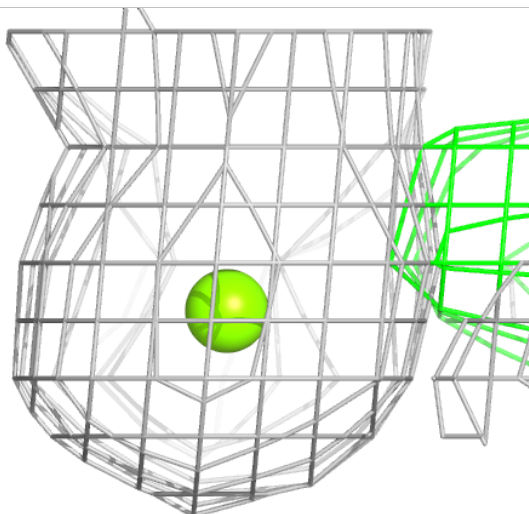
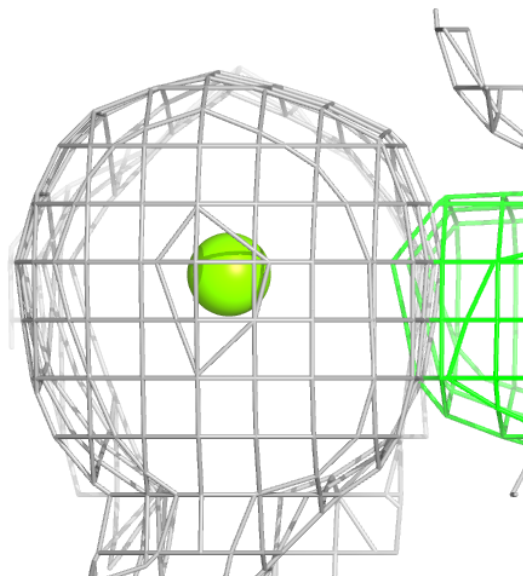
Electron density around MG L 702:

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



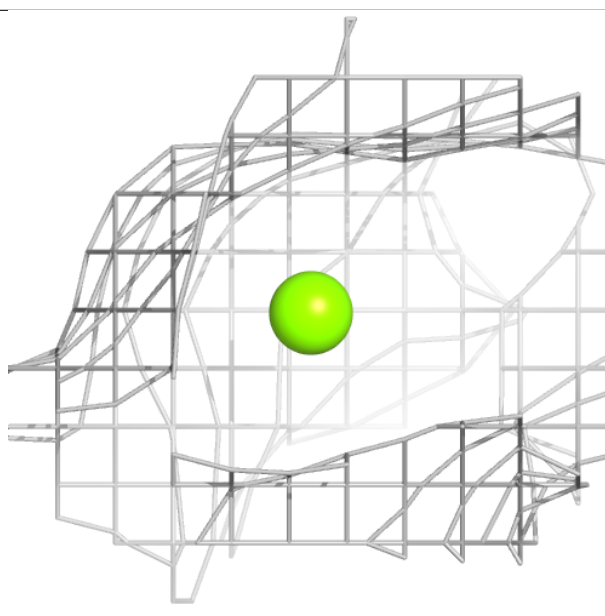
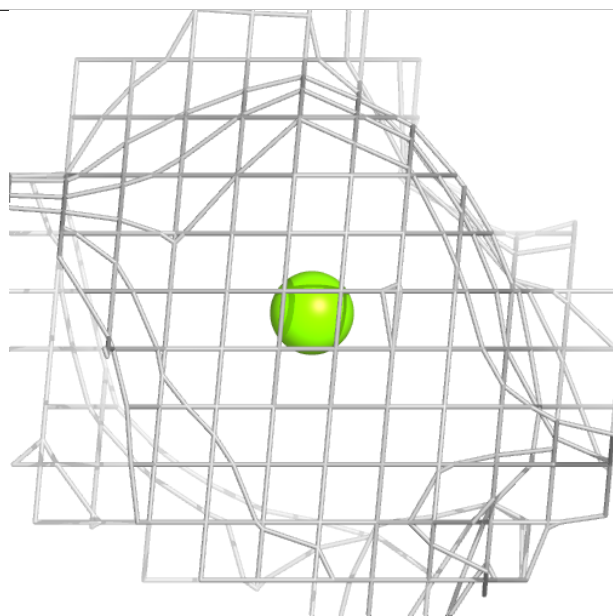
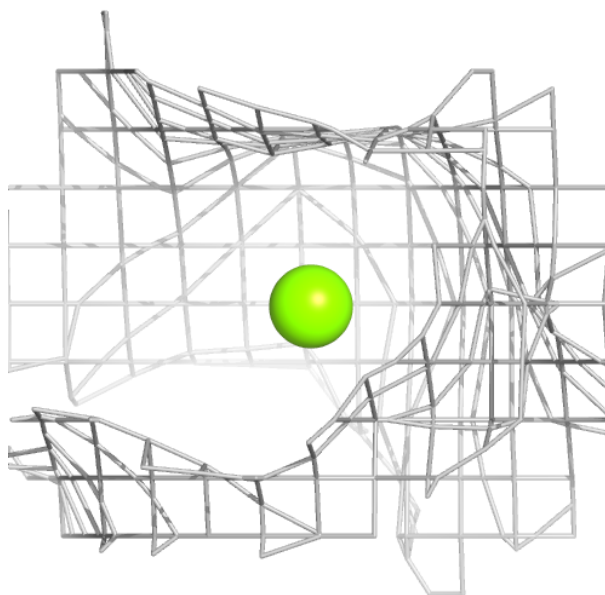
Electron density around MG L 703:

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



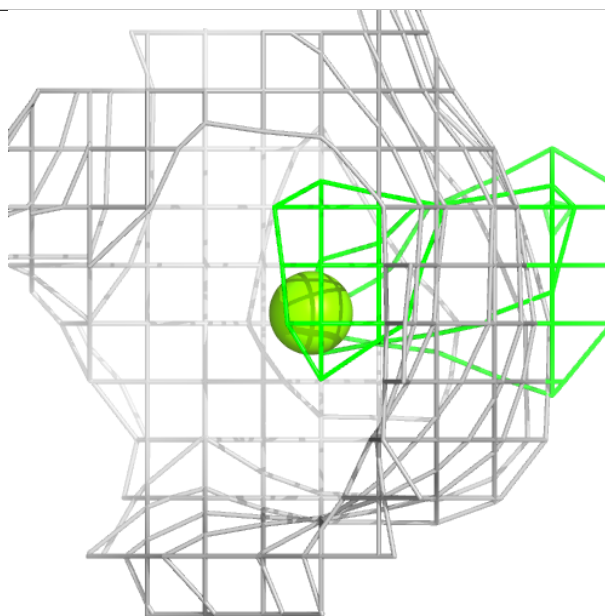
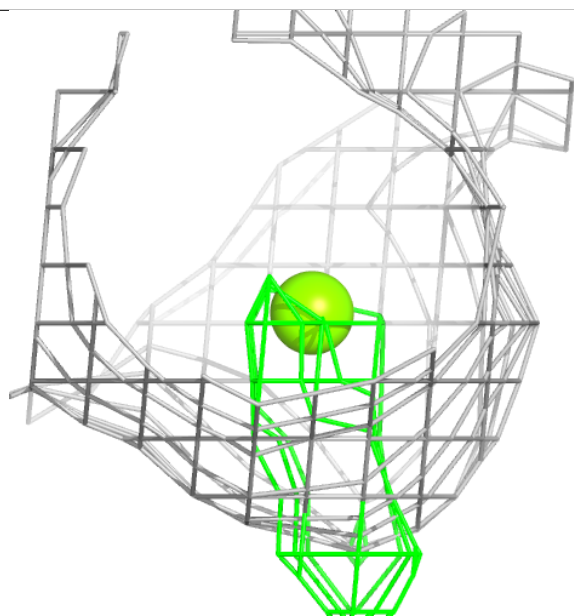
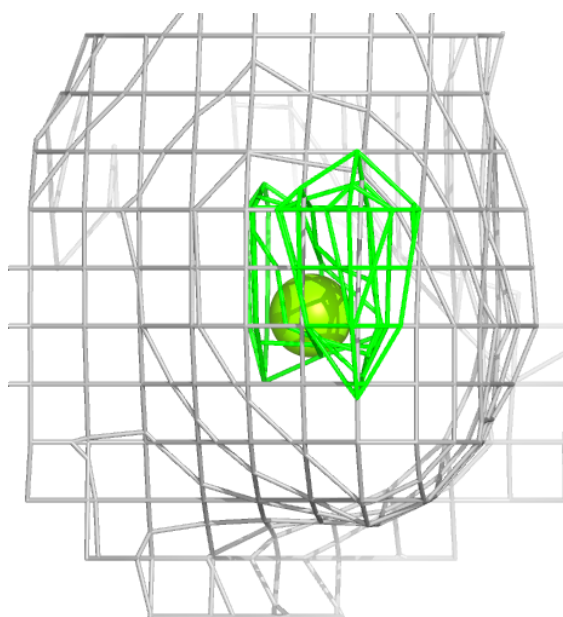
Electron density around MG L 704:

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



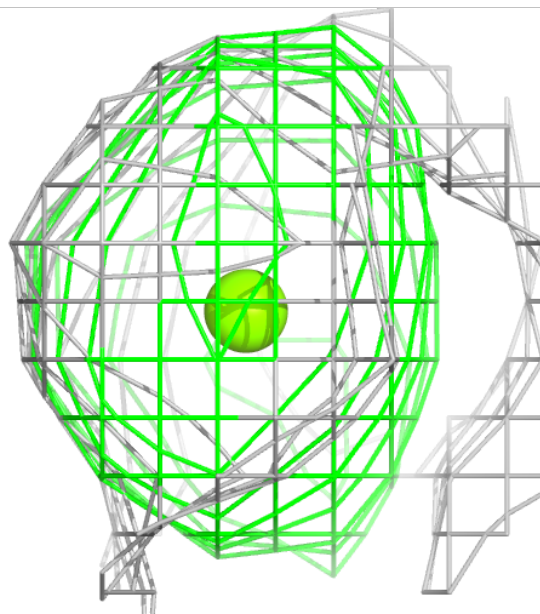
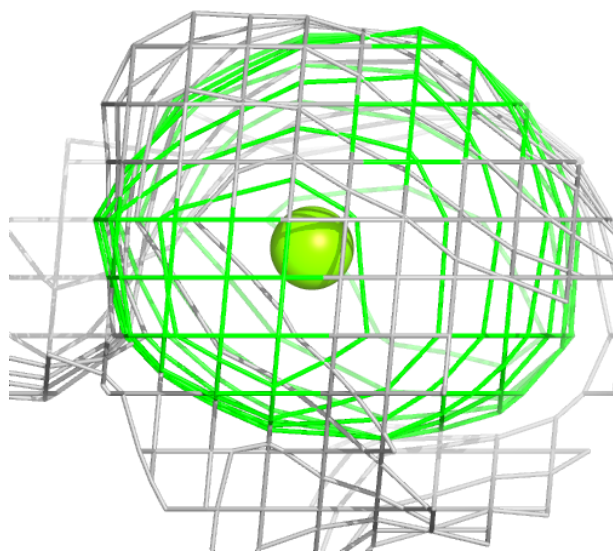
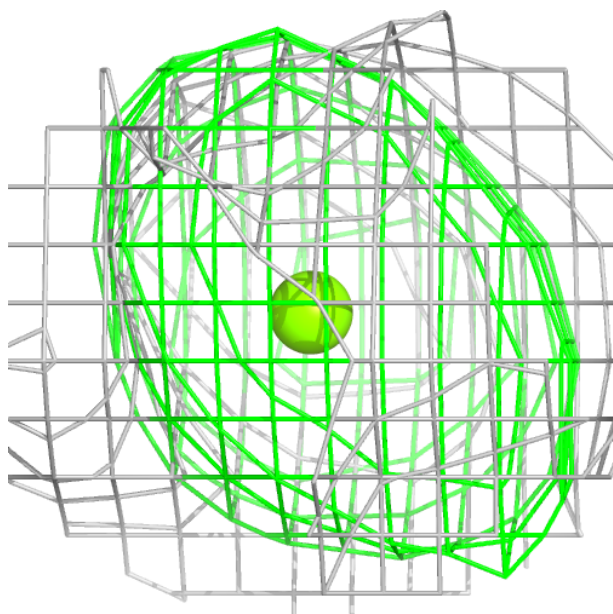
Electron density around MG M 702:

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



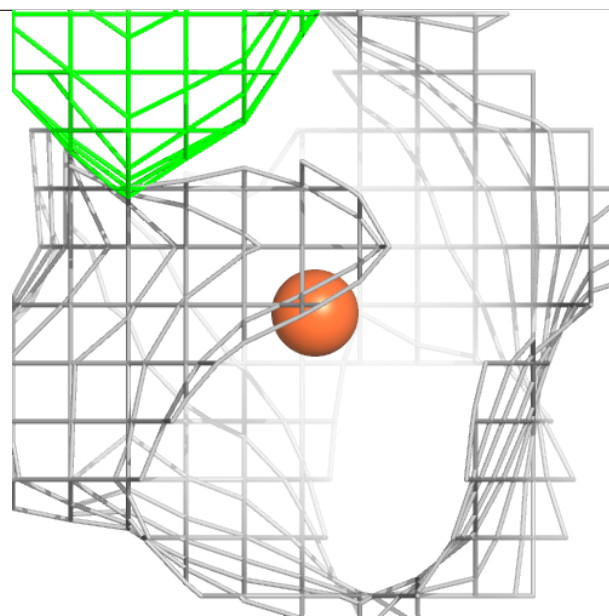
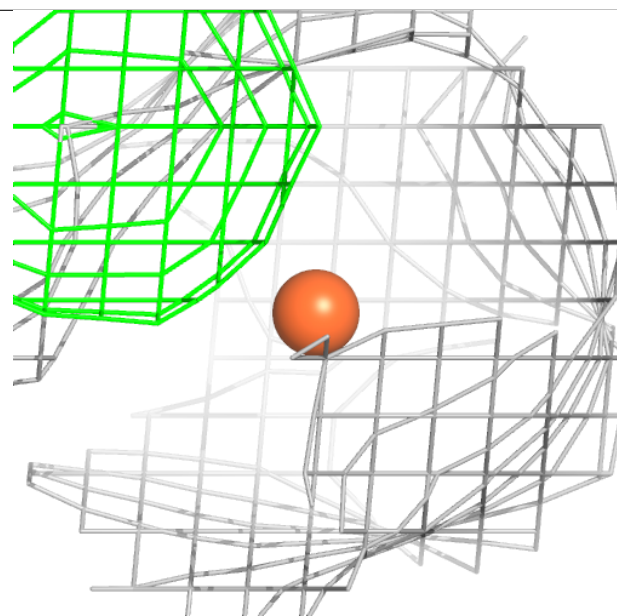
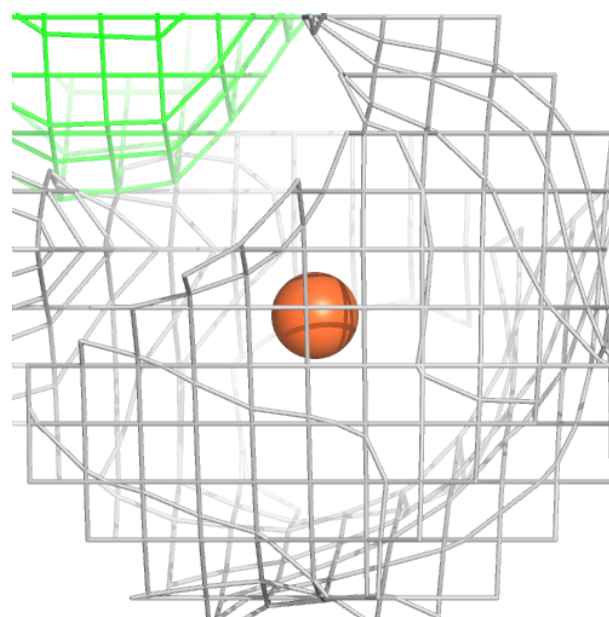
Electron density around MG C 703:

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



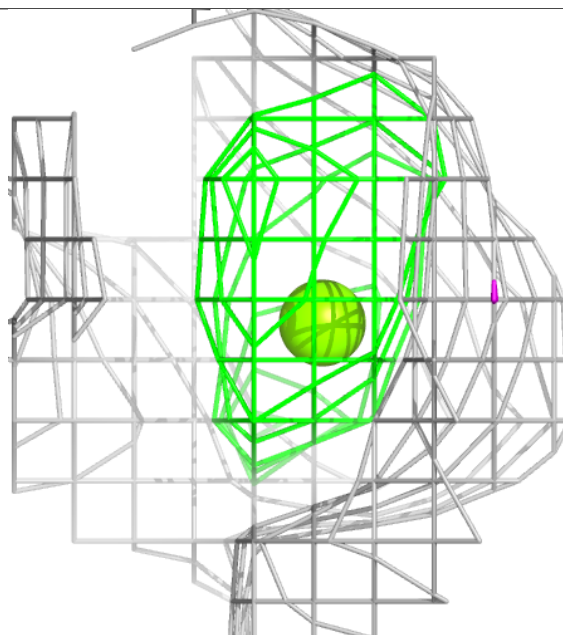
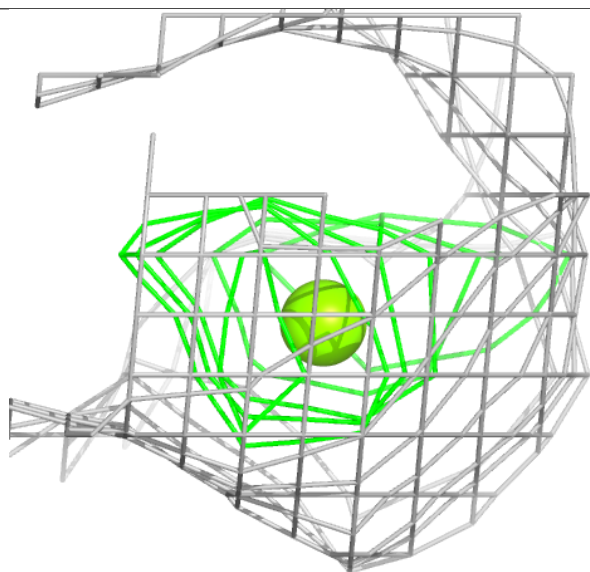
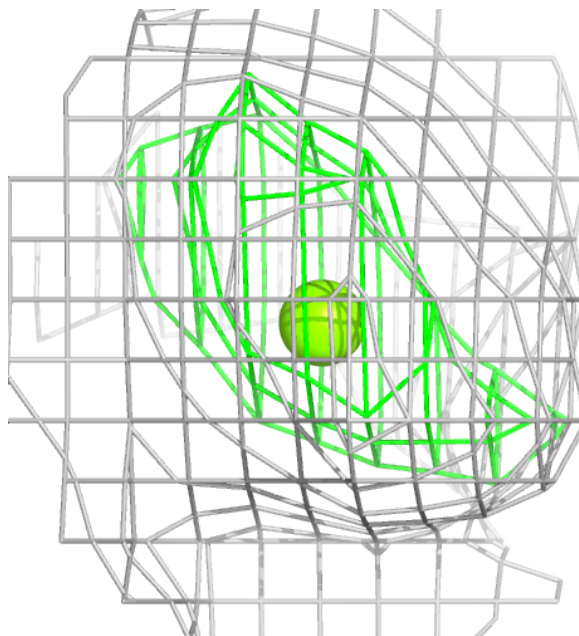
Electron density around FE I 701:

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



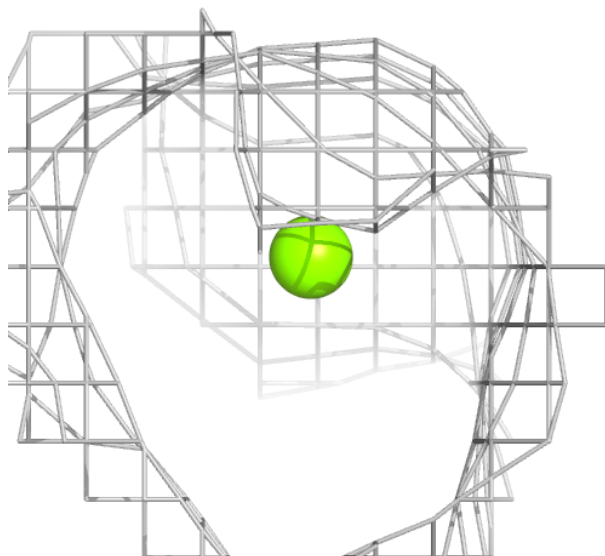
Electron density around MG N 702:

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



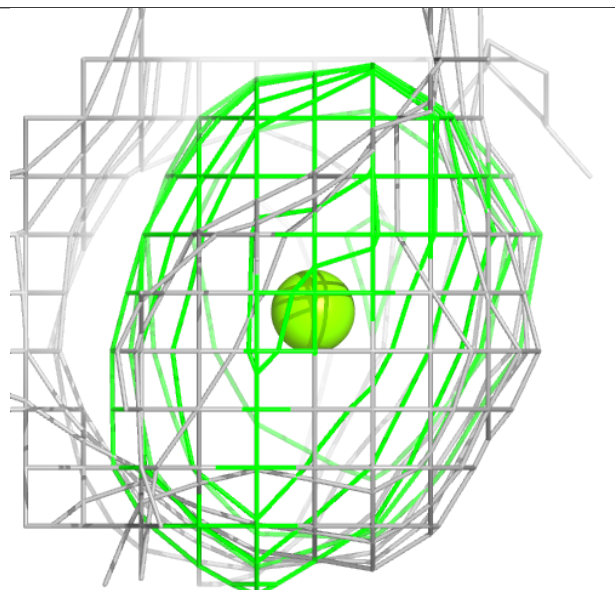
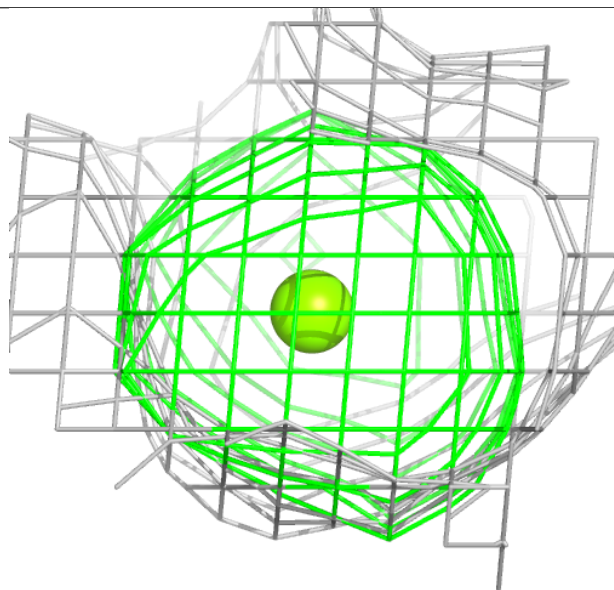
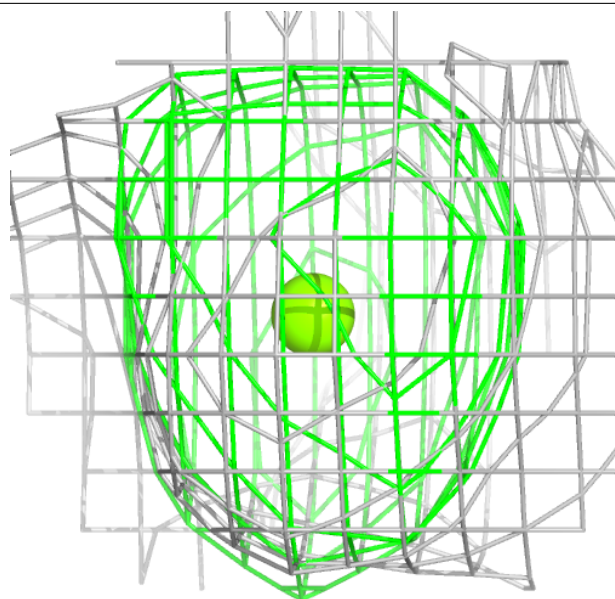
Electron density around MG C 705:

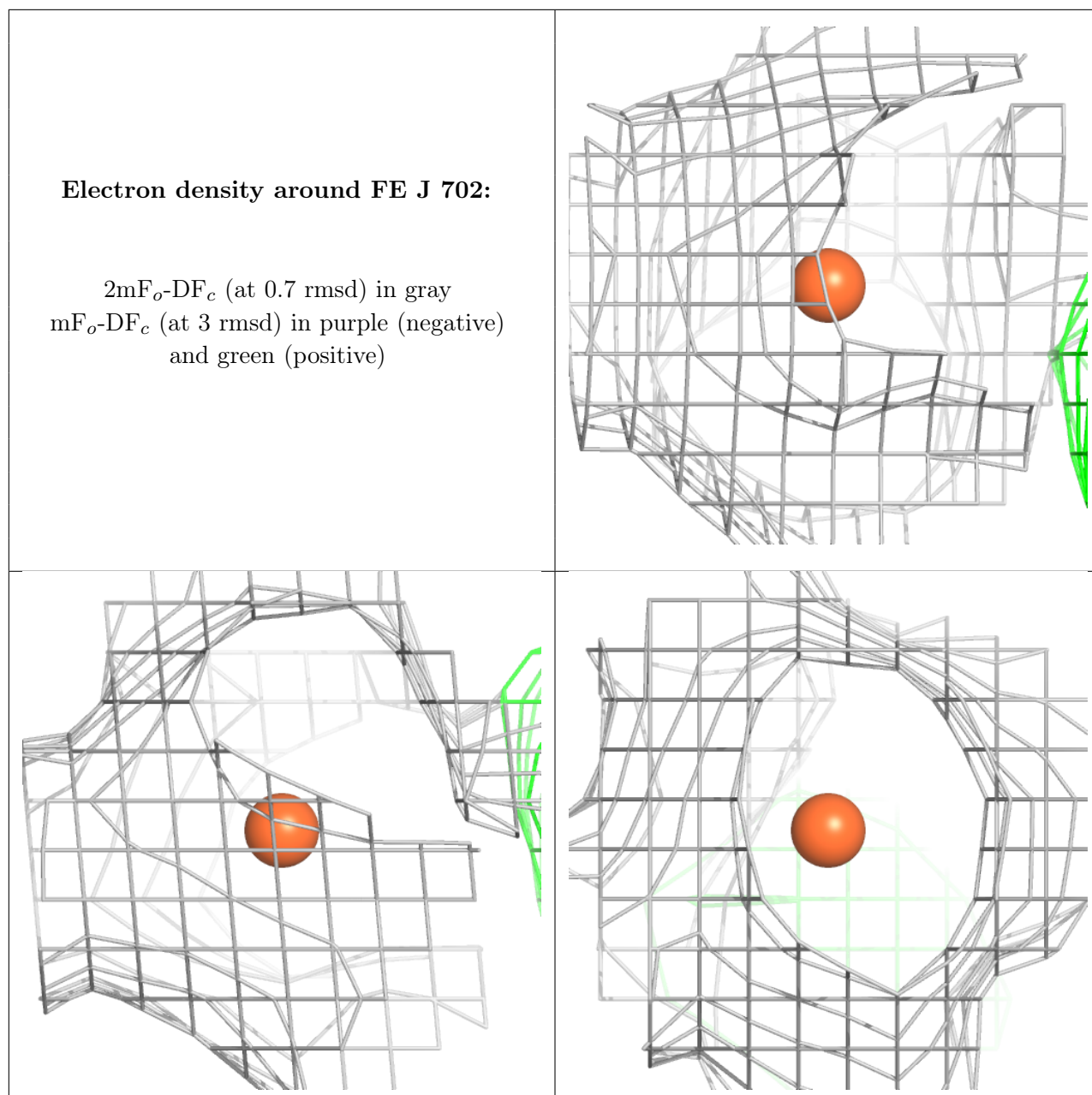
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around MG D 703:

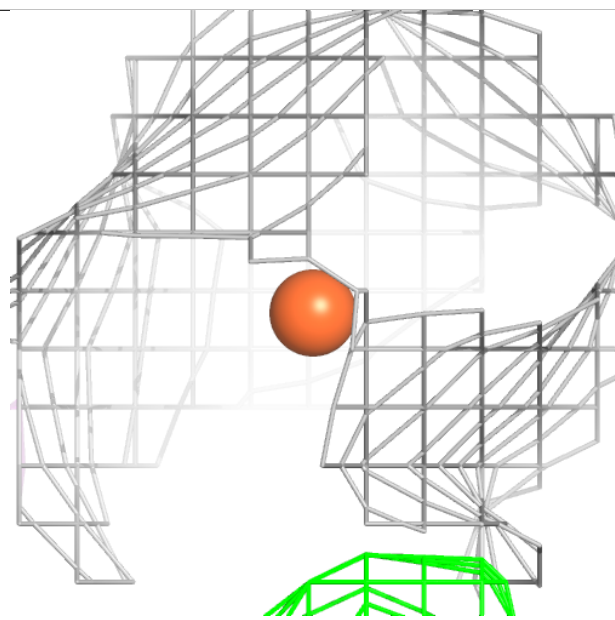
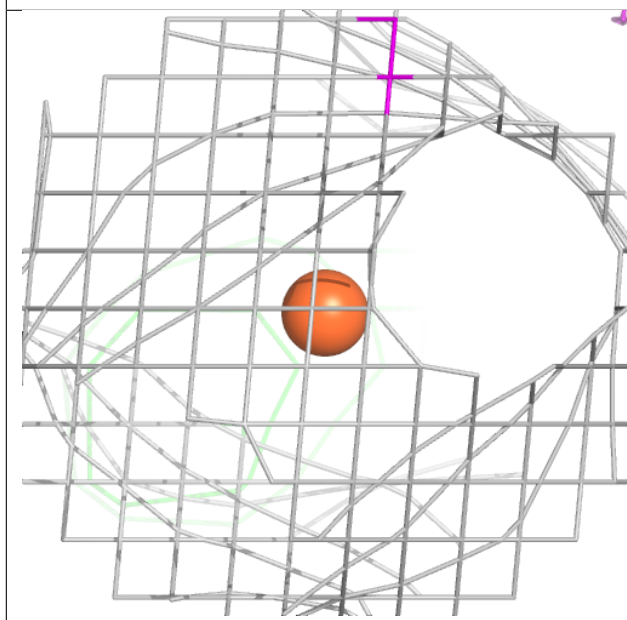
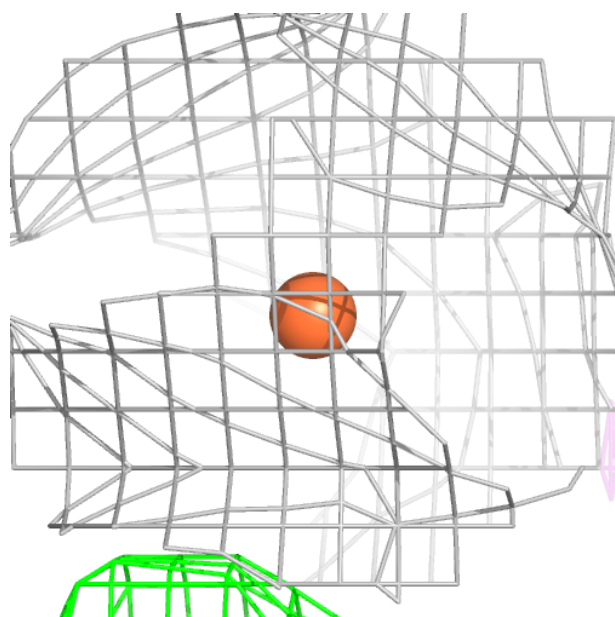
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





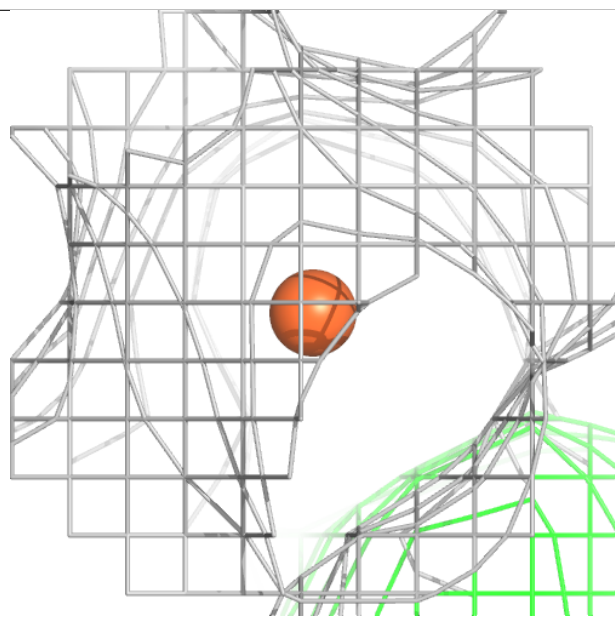
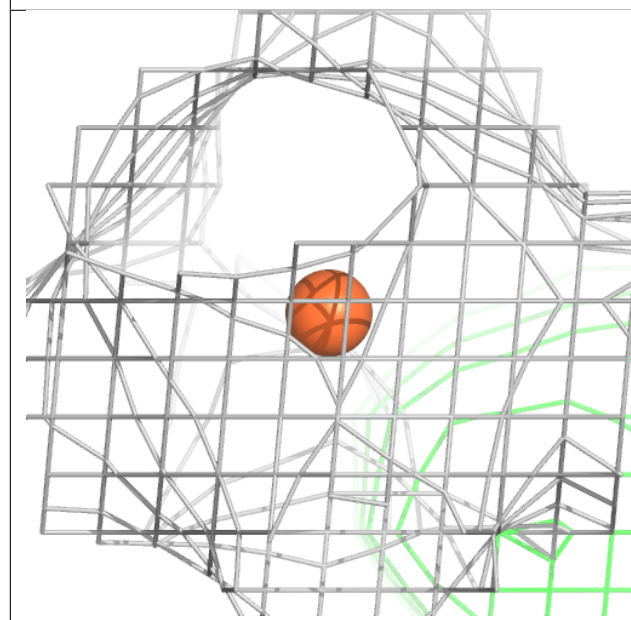
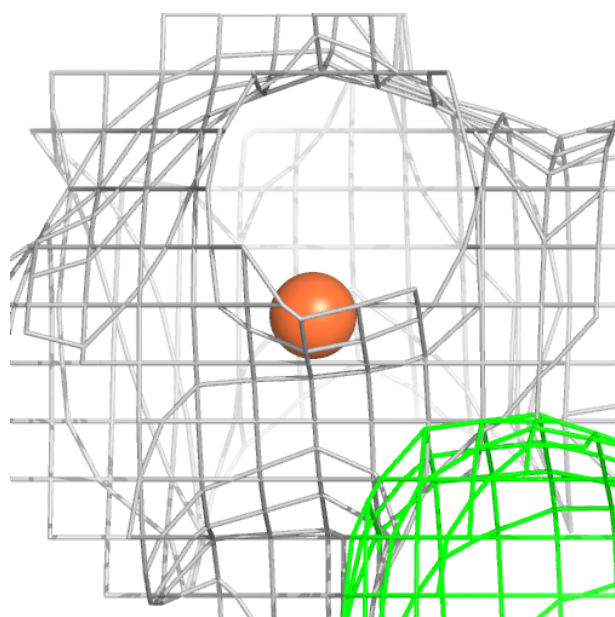
Electron density around FE K 702:

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



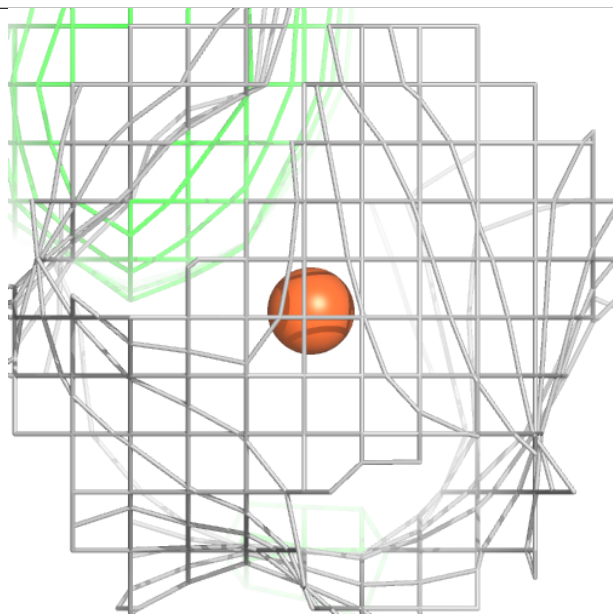
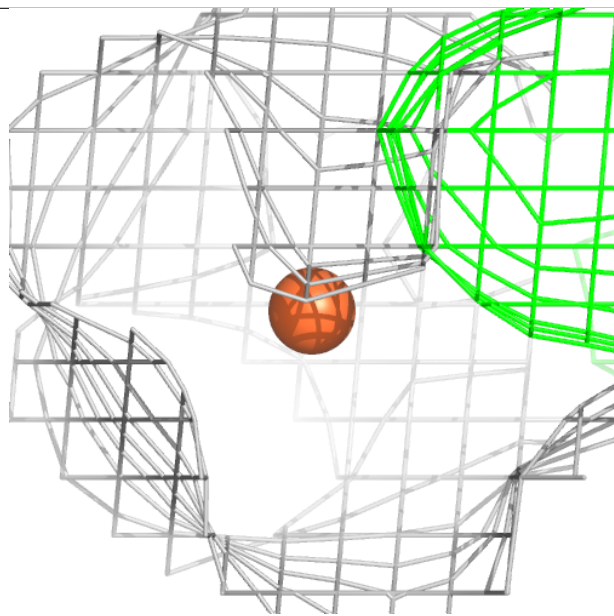
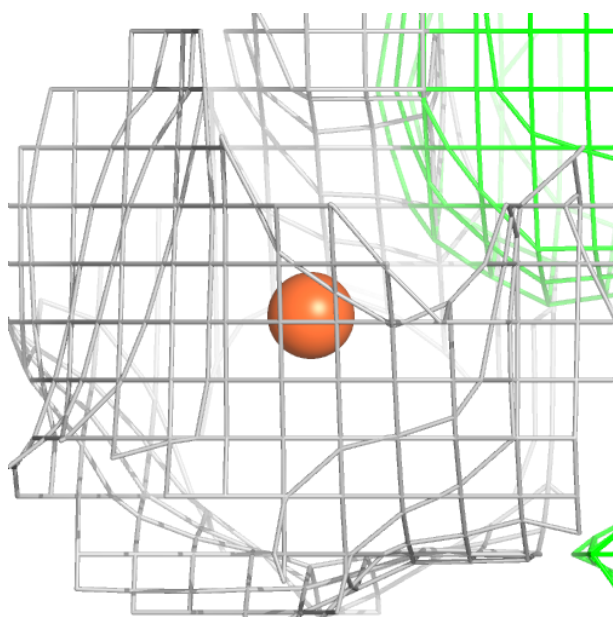
Electron density around FE A 701:

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



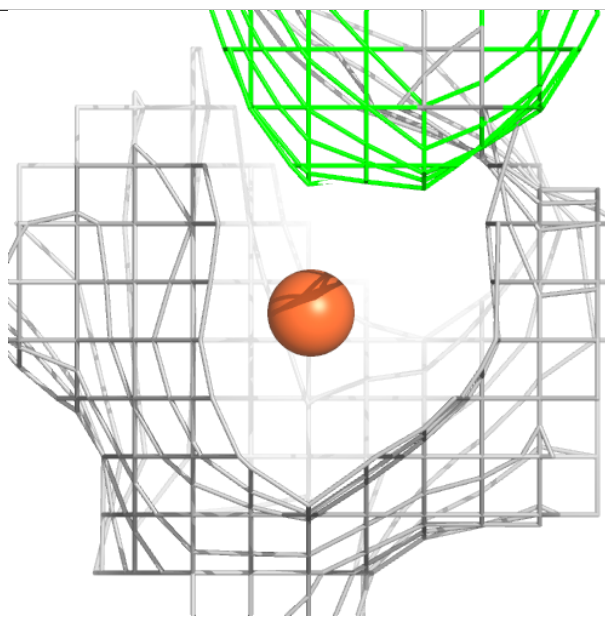
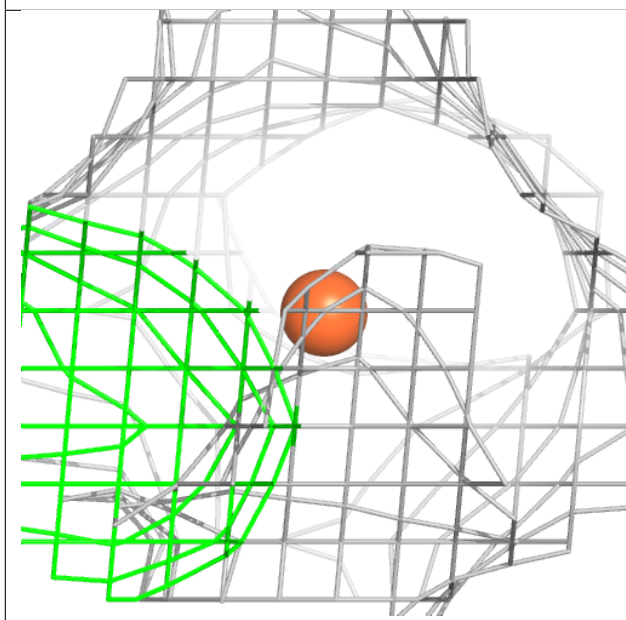
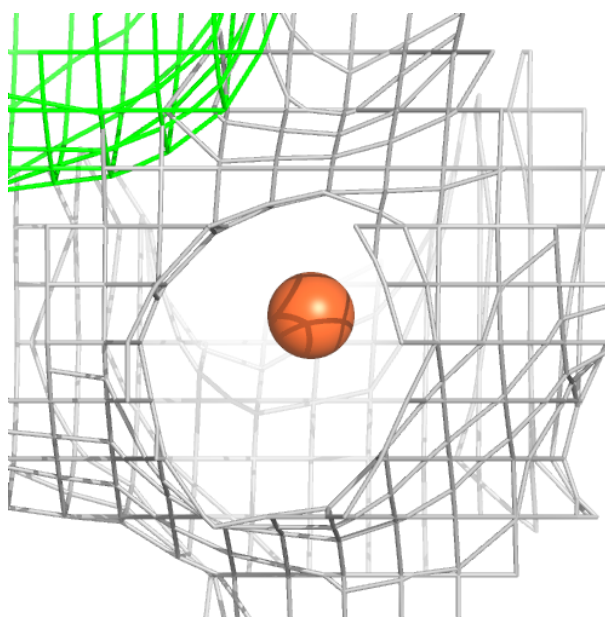
Electron density around FE B 701:

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



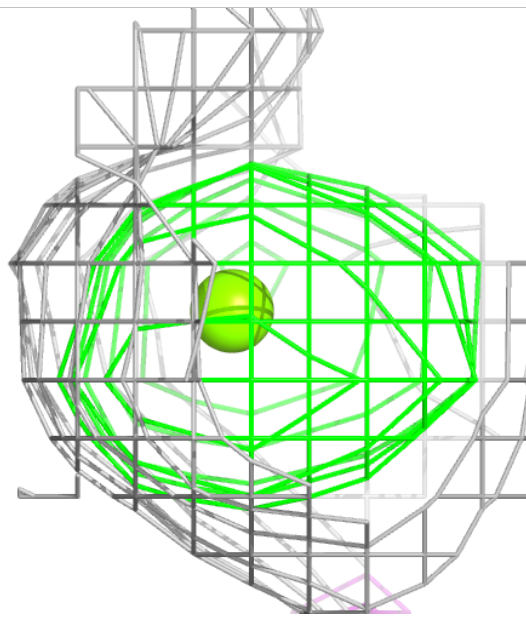
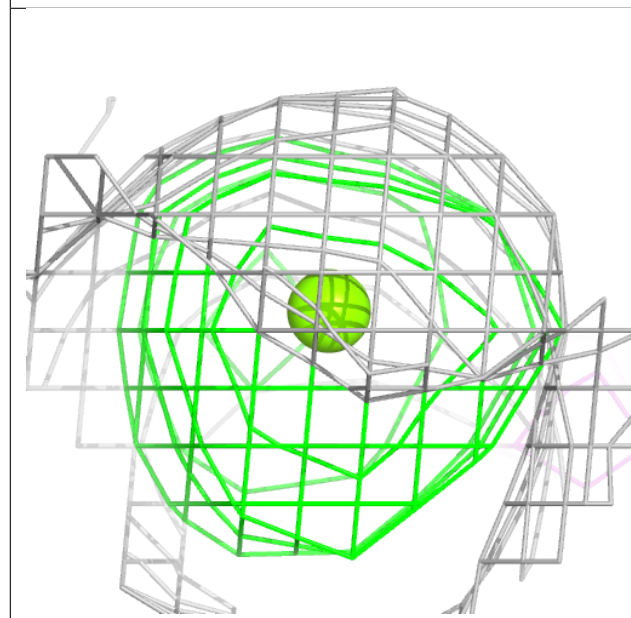
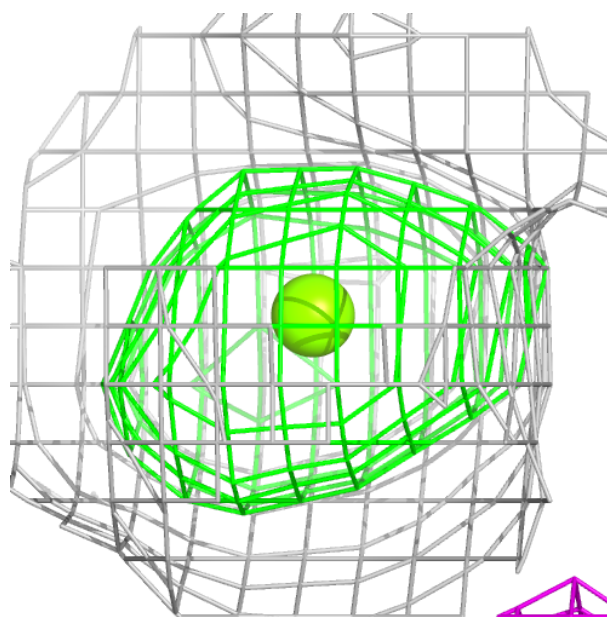
Electron density around FE C 702:

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



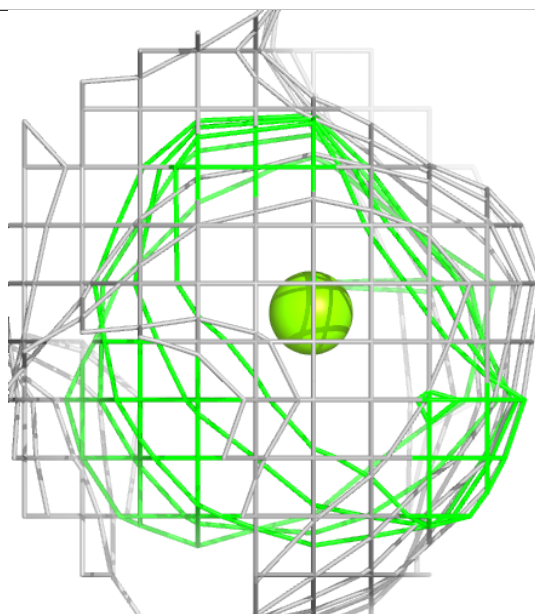
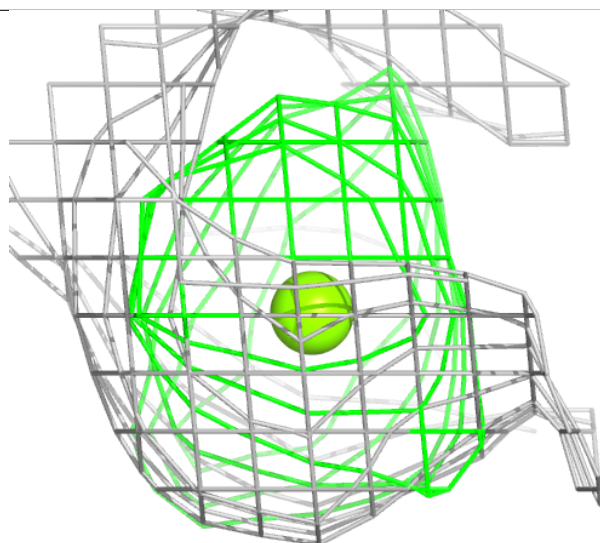
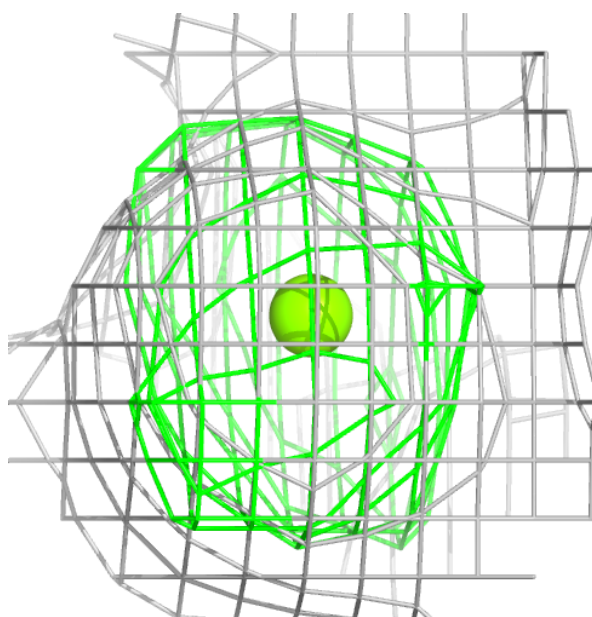
Electron density around MG O 703:

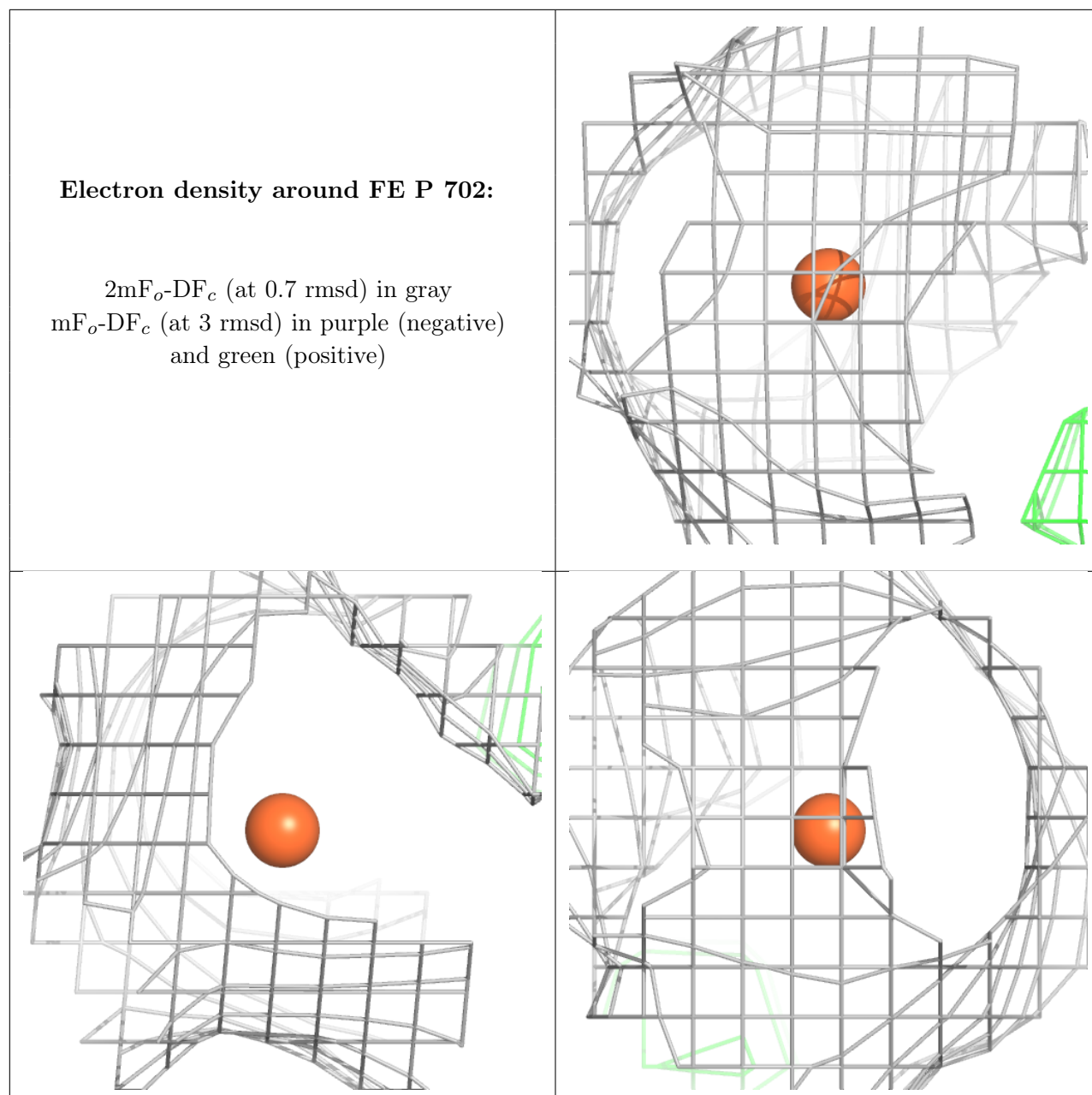
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around MG J 703:

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





6.5 Other polymers [i](#)

There are no such residues in this entry.