wwPDB X-ray Structure Validation Summary Report (i)

Jan 14, 2024 – 02:53 am GMT

PDB ID	:	6XU1
Title	:	Crystal structure of tetrameric human H215A-SAMHD1 (residues 109-626) with GTP, dAMPNPP and Mg
Authors	:	Morris, E.R.; Kunzelmann, S.; Caswell, S.J.; Arnold, L.H.; Purkiss, A.G.; Kelly, G.; Taylor, I.A.
Deposited on	:	2020-01-17
Resolution	:	2.20 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

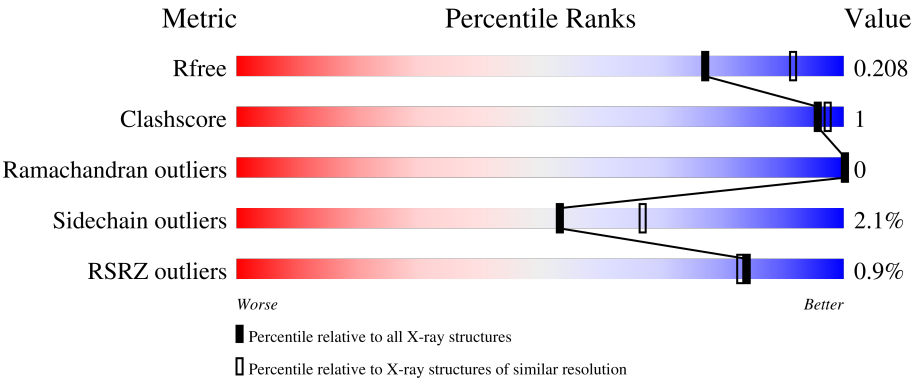
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 <=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	83% 8% • 8%
1	C	520	82% 9% 8%
1	D	520	82% 8% • 8%

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Mol	Chain	Length	Quality of chain
1	E	520	2% 81% 7% 11%
1	F	520	82% 10% 8%
1	G	520	% 84% 8% 8%
1	H	520	2% 85% 7% 8%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 32438 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
1	A	480	Total	C	N	O	S	0	0	0
			3882	2485	672	705	20			
1	B	479	Total	C	N	O	S	0	0	0
			3882	2487	673	702	20			
1	C	478	Total	C	N	O	S	0	0	0
			3864	2475	668	701	20			
1	D	478	Total	C	N	O	S	0	0	0
			3868	2479	668	701	20			
1	E	464	Total	C	N	O	S	0	0	0
			3757	2404	651	682	20			
1	F	480	Total	C	N	O	S	0	0	0
			3894	2494	676	704	20			
1	G	479	Total	C	N	O	S	0	0	0
			3882	2486	674	702	20			
1	H	478	Total	C	N	O	S	0	0	0
			3844	2467	667	690	20			

There are 24 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	215	ALA	HIS	engineered mutation	UNP Q9Y3Z3
B	107	GLY	-	expression tag	UNP Q9Y3Z3
B	108	SER	-	expression tag	UNP Q9Y3Z3
B	215	ALA	HIS	engineered mutation	UNP Q9Y3Z3
C	107	GLY	-	expression tag	UNP Q9Y3Z3
C	108	SER	-	expression tag	UNP Q9Y3Z3
C	215	ALA	HIS	engineered mutation	UNP Q9Y3Z3
D	107	GLY	-	expression tag	UNP Q9Y3Z3
D	108	SER	-	expression tag	UNP Q9Y3Z3
D	215	ALA	HIS	engineered mutation	UNP Q9Y3Z3
E	107	GLY	-	expression tag	UNP Q9Y3Z3

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Chain	Residue	Modelled	Actual	Comment	Reference
E	108	SER	-	expression tag	UNP Q9Y3Z3
E	215	ALA	HIS	engineered mutation	UNP Q9Y3Z3
F	107	GLY	-	expression tag	UNP Q9Y3Z3
F	108	SER	-	expression tag	UNP Q9Y3Z3
F	215	ALA	HIS	engineered mutation	UNP Q9Y3Z3
G	107	GLY	-	expression tag	UNP Q9Y3Z3
G	108	SER	-	expression tag	UNP Q9Y3Z3
G	215	ALA	HIS	engineered mutation	UNP Q9Y3Z3
H	107	GLY	-	expression tag	UNP Q9Y3Z3
H	108	SER	-	expression tag	UNP Q9Y3Z3
H	215	ALA	HIS	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

- 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

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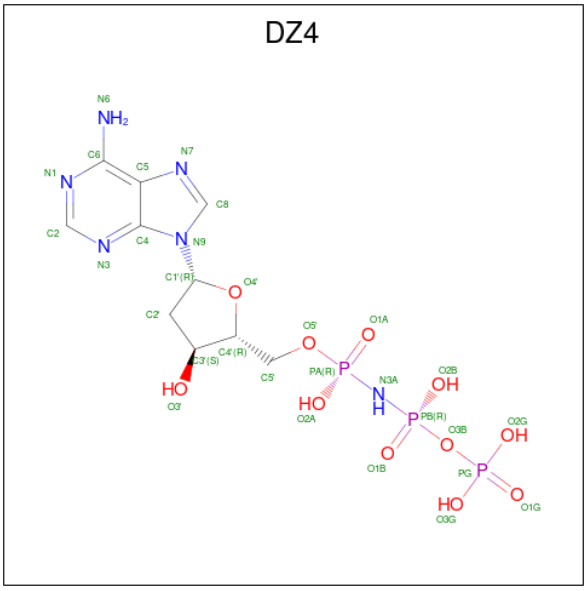
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	3	Total Mg 3 3	0	0
3	D	4	Total Mg 4 4	0	0
3	E	3	Total Mg 3 3	0	0
3	F	3	Total Mg 3 3	0	0
3	G	3	Total Mg 3 3	0	0
3	H	3	Total Mg 3 3	0	0

- Molecule 4 is 2'-deoxy-5'-O-[(R)-hydroxy{[(R)-hydroxy(phosphonooxy)phosphoryl]amino}phosphoryl]adenosine (three-letter code: DZ4) (formula: $C_{10}H_{17}N_6O_{11}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O P 30 10 6 11 3	0	0
4	A	1	Total C N O P 30 10 6 11 3	0	0
4	B	1	Total C N O P 30 10 6 11 3	0	0
4	C	1	Total C N O P 30 10 6 11 3	0	0

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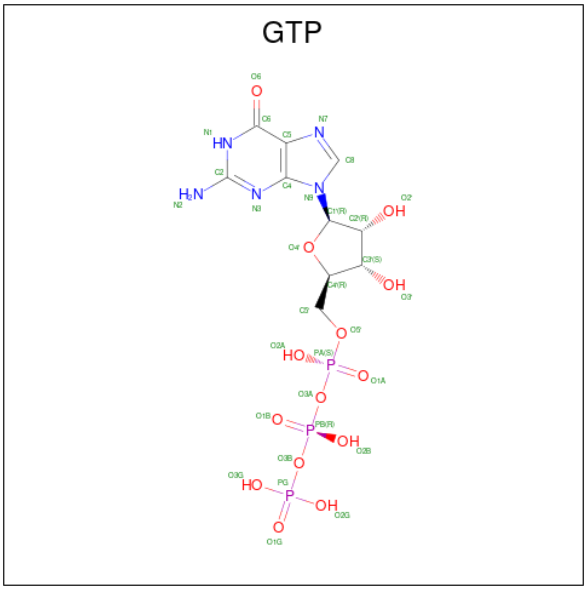
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	C	1	Total	C	N	O	P	0	0
			30	10	6	11	3		
4	C	1	Total	C	N	O	P	0	0
			30	10	6	11	3		
4	D	1	Total	C	N	O	P	0	0
			30	10	6	11	3		
4	D	1	Total	C	N	O	P	0	0
			30	10	6	11	3		
4	E	1	Total	C	N	O	P	0	0
			30	10	6	11	3		
4	E	1	Total	C	N	O	P	0	0
			30	10	6	11	3		
4	F	1	Total	C	N	O	P	0	0
			30	10	6	11	3		
4	F	1	Total	C	N	O	P	0	0
			30	10	6	11	3		
4	G	1	Total	C	N	O	P	0	0
			30	10	6	11	3		
4	G	1	Total	C	N	O	P	0	0
			30	10	6	11	3		
4	H	1	Total	C	N	O	P	0	0
			30	10	6	11	3		
4	H	1	Total	C	N	O	P	0	0
			30	10	6	11	3		

- Molecule 5 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
5	B	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
5	C	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
5	D	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
5	E	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
5	E	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
5	G	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
5	H	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- Molecule 6 is water.

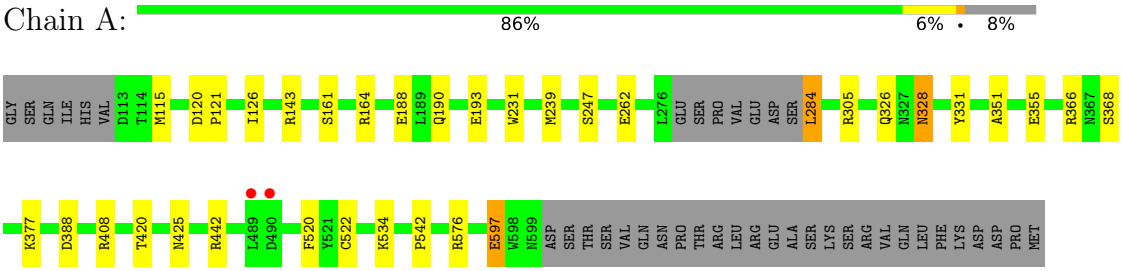
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	99	Total	O	0	0
			99	99		
6	B	113	Total	O	0	0
			113	113		
6	C	116	Total	O	0	0
			116	116		
6	D	99	Total	O	0	0
			99	99		
6	E	71	Total	O	0	0
			71	71		
6	F	124	Total	O	0	0
			124	124		
6	G	115	Total	O	0	0
			115	115		
6	H	59	Total	O	0	0
			59	59		

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.

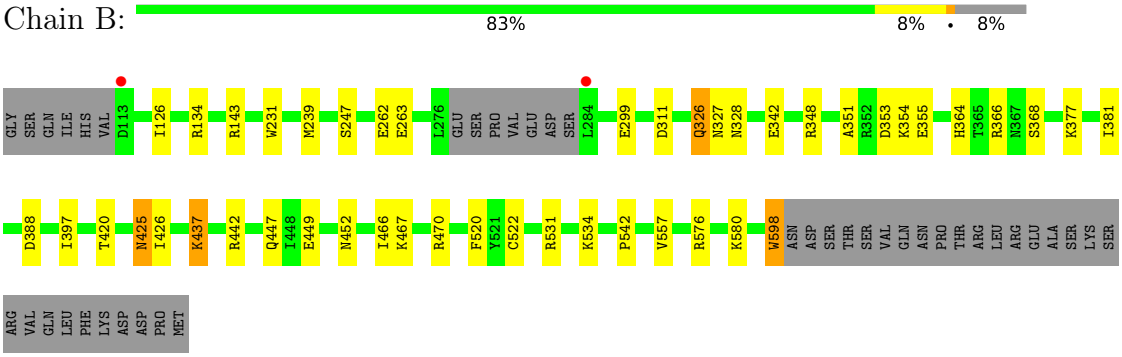
• Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

Chain A:



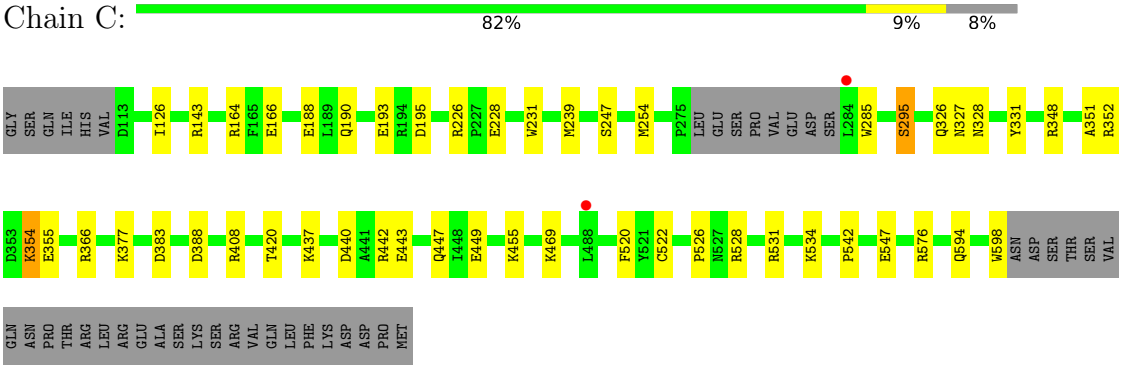
• Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

Chain B:



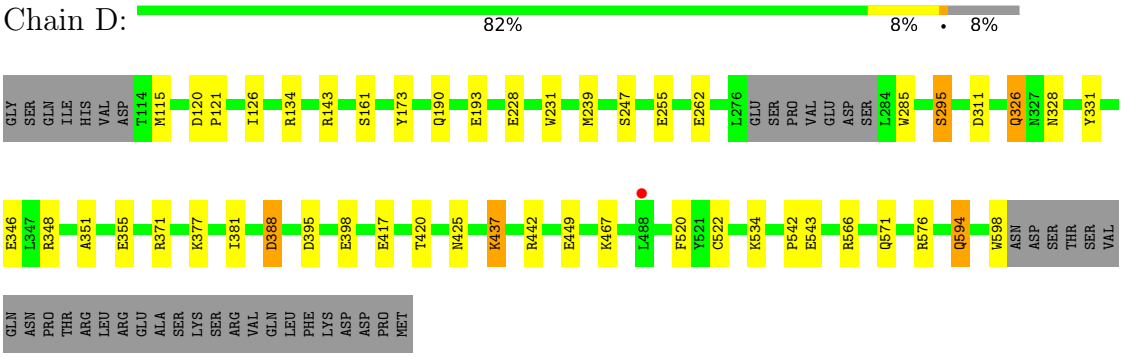
• Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

Chain C:



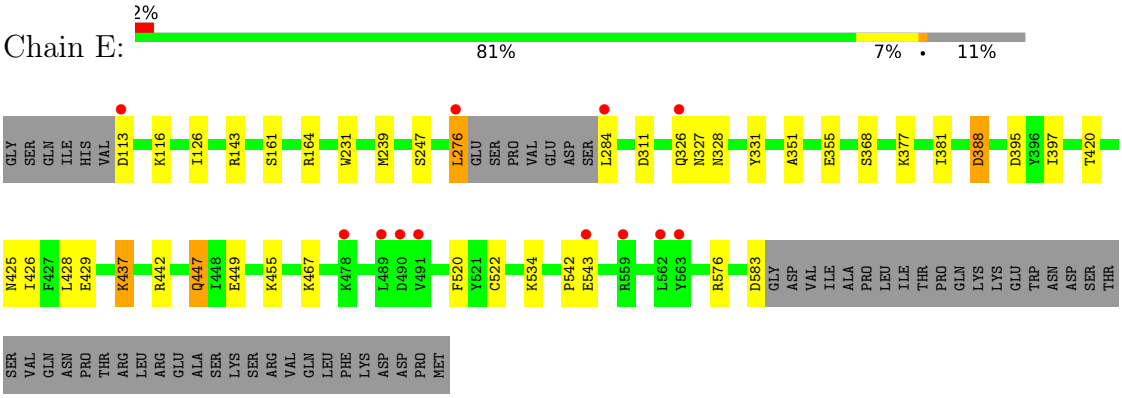
• Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

Chain D:



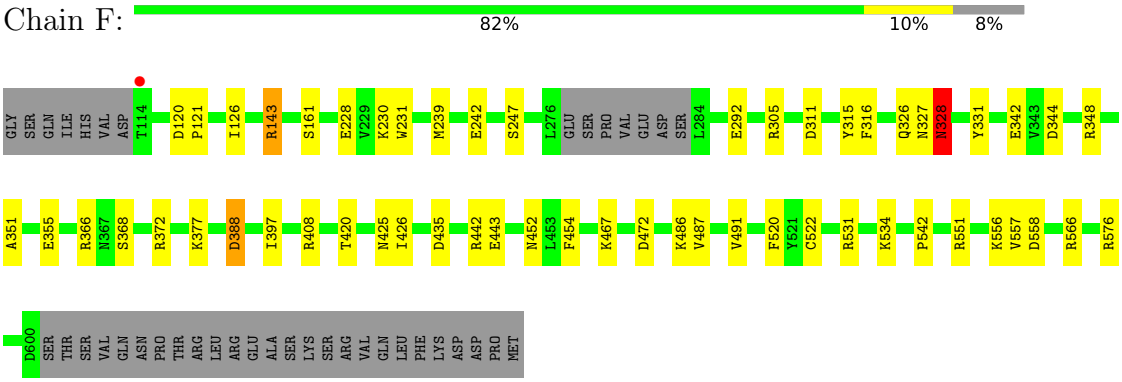
• Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

Chain E:



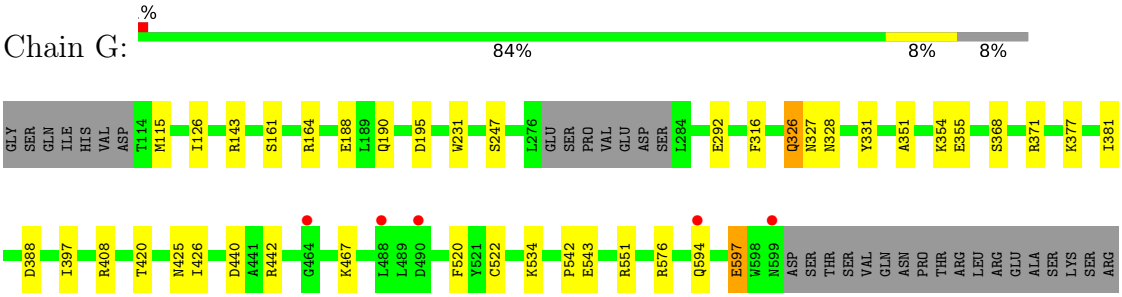
• Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

Chain F:



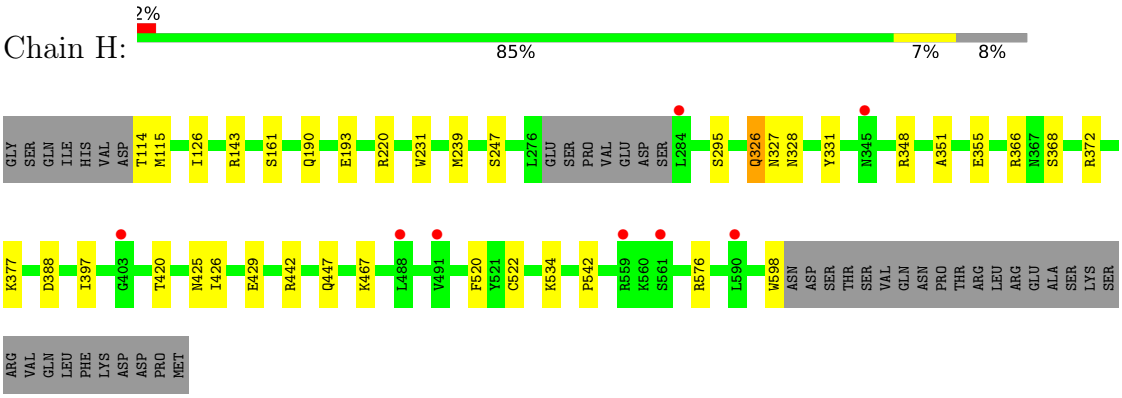
• Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

Chain G:



• Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	137.37Å 171.86Å 179.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	107.30 – 2.20 107.30 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.6 (107.30-2.20) 98.6 (107.30-2.20)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.71 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.176 , 0.202 0.183 , 0.208	Depositor DCC
R_{free} test set	10526 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å^2)	24.4	Xtriage
Anisotropy	0.268	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 39.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.008 for -h,l,k	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	32438	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.30% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, DZ4, MG, FE

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	1.13	11/3974 (0.3%)	1.07	15/5375 (0.3%)
1	B	1.11	12/3974 (0.3%)	1.07	20/5372 (0.4%)
1	C	1.11	18/3956 (0.5%)	1.06	21/5350 (0.4%)
1	D	1.09	16/3960 (0.4%)	1.03	19/5355 (0.4%)
1	E	1.02	10/3845 (0.3%)	1.05	16/5197 (0.3%)
1	F	1.17	16/3986 (0.4%)	1.11	28/5387 (0.5%)
1	G	1.07	10/3974 (0.3%)	1.02	16/5373 (0.3%)
1	H	0.99	12/3936 (0.3%)	0.98	12/5325 (0.2%)
All	All	1.09	105/31605 (0.3%)	1.05	147/42734 (0.3%)

The worst 5 of 105 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	161	SER	CB-OG	13.29	1.59	1.42
1	G	355	GLU	CD-OE1	12.10	1.39	1.25
1	B	355	GLU	CD-OE1	12.03	1.38	1.25
1	C	355	GLU	CD-OE1	11.73	1.38	1.25
1	F	355	GLU	CD-OE1	10.79	1.37	1.25

The worst 5 of 147 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	395	ASP	CB-CG-OD2	10.52	127.77	118.30
1	E	442	ARG	NE-CZ-NH1	9.37	124.99	120.30
1	E	164	ARG	NE-CZ-NH2	9.22	124.91	120.30
1	C	354	LYS	CD-CE-NZ	8.94	132.26	111.70
1	F	348	ARG	NE-CZ-NH2	8.94	124.77	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3882	0	3823	8	0
1	B	3882	0	3841	14	0
1	C	3864	0	3808	8	0
1	D	3868	0	3819	10	0
1	E	3757	0	3700	11	0
1	F	3894	0	3858	12	0
1	G	3882	0	3838	8	0
1	H	3844	0	3793	9	0
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
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	D	4	0	0	0	0
3	E	3	0	0	0	0
3	F	3	0	0	0	0
3	G	3	0	0	0	0
3	H	3	0	0	0	0
4	A	60	0	26	0	0
4	B	30	0	13	0	0
4	C	90	0	39	1	0
4	D	60	0	26	0	0
4	E	60	0	26	0	0
4	F	60	0	26	0	0
4	G	60	0	26	0	0
4	H	60	0	26	0	0
5	A	32	0	12	0	0
5	B	32	0	12	0	0
5	C	32	0	12	0	0
5	D	32	0	12	1	0
5	E	64	0	24	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	32	0	11	0	0
5	H	32	0	12	0	0
6	A	99	0	0	0	0
6	B	113	0	0	2	0
6	C	116	0	0	3	0
6	D	99	0	0	0	0
6	E	71	0	0	0	0
6	F	124	0	0	0	1
6	G	115	0	0	0	1
6	H	59	0	0	0	0
All	All	32438	0	30783	67	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 1.

The worst 5 of 67 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:F:328:ASN:N	1:F:328:ASN:OD1	2.05	0.85
1:B:437:LYS:NZ	6:B:802:HOH:O	2.26	0.68
1:E:425:ASN:OD1	1:F:425:ASN:ND2	2.28	0.66
1:A:425:ASN:OD1	1:B:425:ASN:ND2	2.26	0.61
1:D:534:LYS:HE3	1:D:542:PRO:O	2.04	0.58

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)
6:F:923:HOH:O	6:G:912:HOH:O[3_655]	2.08	0.12

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%)	466 (98%)	10 (2%)	0	100	100
1	B	475/520 (91%)	468 (98%)	7 (2%)	0	100	100
1	C	474/520 (91%)	464 (98%)	10 (2%)	0	100	100
1	D	474/520 (91%)	466 (98%)	8 (2%)	0	100	100
1	E	460/520 (88%)	452 (98%)	8 (2%)	0	100	100
1	F	476/520 (92%)	470 (99%)	6 (1%)	0	100	100
1	G	475/520 (91%)	466 (98%)	9 (2%)	0	100	100
1	H	474/520 (91%)	466 (98%)	8 (2%)	0	100	100
All	All	3784/4160 (91%)	3718 (98%)	66 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	416/463 (90%)	408 (98%)	8 (2%)	57	71
1	B	417/463 (90%)	410 (98%)	7 (2%)	60	74
1	C	414/463 (89%)	405 (98%)	9 (2%)	52	65
1	D	415/463 (90%)	405 (98%)	10 (2%)	49	62
1	E	403/463 (87%)	393 (98%)	10 (2%)	47	60
1	F	419/463 (90%)	412 (98%)	7 (2%)	60	74
1	G	417/463 (90%)	409 (98%)	8 (2%)	57	71
1	H	409/463 (88%)	400 (98%)	9 (2%)	52	65
All	All	3310/3704 (89%)	3242 (98%)	68 (2%)	53	67

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	594	GLN
1	H	114	THR

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Mol	Chain	Res	Type
1	H	388	ASP
1	D	126	ILE
1	C	594	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	328	ASN
1	H	328	ASN
1	G	375	GLN
1	G	571	GLN
1	H	380	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 57 ligands modelled in this entry, 33 are monoatomic - leaving 24 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	DZ4	G	701	3	29,32,32	1.56	5 (17%)	33,50,50	2.12	5 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	DZ4	F	706	3	29,32,32	1.36	5 (17%)	33,50,50	2.16	6 (18%)
4	DZ4	F	705	3,2	29,32,32	1.94	5 (17%)	33,50,50	1.64	5 (15%)
5	GTP	B	706	3	26,34,34	1.82	5 (19%)	32,54,54	1.76	9 (28%)
4	DZ4	G	706	3,2	29,32,32	1.60	4 (13%)	33,50,50	1.47	4 (12%)
4	DZ4	A	705	3,2	29,32,32	1.89	3 (10%)	33,50,50	1.49	4 (12%)
4	DZ4	C	706	3,2	29,32,32	1.50	4 (13%)	33,50,50	1.82	5 (15%)
5	GTP	E	707	3	26,34,34	1.23	1 (3%)	32,54,54	1.49	6 (18%)
4	DZ4	D	701	3	29,32,32	1.47	5 (17%)	33,50,50	1.90	6 (18%)
4	DZ4	H	706	3,2	29,32,32	2.95	7 (24%)	33,50,50	1.75	6 (18%)
4	DZ4	A	707	3	29,32,32	1.41	3 (10%)	33,50,50	1.81	4 (12%)
5	GTP	A	706	3	26,34,34	1.32	4 (15%)	32,54,54	1.78	10 (31%)
4	DZ4	C	701	3	29,32,32	1.24	5 (17%)	33,50,50	1.96	5 (15%)
5	GTP	C	707	3	26,34,34	1.67	8 (30%)	32,54,54	1.82	11 (34%)
5	GTP	E	706	3	26,34,34	1.51	6 (23%)	32,54,54	2.53	14 (43%)
4	DZ4	E	708	3	29,32,32	1.60	7 (24%)	33,50,50	1.93	8 (24%)
5	GTP	D	707	3	26,34,34	1.24	2 (7%)	32,54,54	2.01	12 (37%)
4	DZ4	D	706	3,2	29,32,32	1.49	5 (17%)	33,50,50	1.81	7 (21%)
4	DZ4	E	705	3,2	29,32,32	1.52	6 (20%)	33,50,50	1.73	7 (21%)
4	DZ4	H	701	3	29,32,32	1.41	4 (13%)	33,50,50	1.91	8 (24%)
4	DZ4	B	705	3,2	29,32,32	1.20	3 (10%)	33,50,50	1.37	3 (9%)
5	GTP	H	707	3	26,34,34	1.41	3 (11%)	32,54,54	1.63	9 (28%)
4	DZ4	C	708	3	29,32,32	1.54	6 (20%)	33,50,50	1.84	6 (18%)
5	GTP	G	707	3	26,34,34	1.91	5 (19%)	32,54,54	1.58	7 (21%)

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	DZ4	G	701	3	-	4/15/34/34	0/3/3/3
4	DZ4	F	706	3	-	2/15/34/34	0/3/3/3
4	DZ4	F	705	3,2	-	3/15/34/34	0/3/3/3
5	GTP	B	706	3	-	6/18/38/38	0/3/3/3
4	DZ4	G	706	3,2	-	1/15/34/34	0/3/3/3
4	DZ4	A	705	3,2	-	2/15/34/34	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	DZ4	C	706	3,2	-	2/15/34/34	0/3/3/3
5	GTP	E	707	3	-	8/18/38/38	0/3/3/3
4	DZ4	D	701	3	-	4/15/34/34	0/3/3/3
4	DZ4	H	706	3,2	-	2/15/34/34	0/3/3/3
4	DZ4	A	707	3	-	2/15/34/34	0/3/3/3
5	GTP	A	706	3	-	6/18/38/38	0/3/3/3
4	DZ4	C	701	3	-	2/15/34/34	0/3/3/3
5	GTP	C	707	3	-	7/18/38/38	0/3/3/3
5	GTP	E	706	3	-	9/18/38/38	0/3/3/3
4	DZ4	E	708	3	-	5/15/34/34	0/3/3/3
5	GTP	D	707	3	-	7/18/38/38	0/3/3/3
4	DZ4	D	706	3,2	-	1/15/34/34	0/3/3/3
4	DZ4	E	705	3,2	-	2/15/34/34	0/3/3/3
4	DZ4	H	701	3	-	4/15/34/34	0/3/3/3
4	DZ4	B	705	3,2	-	2/15/34/34	0/3/3/3
5	GTP	H	707	3	-	4/18/38/38	0/3/3/3
4	DZ4	C	708	3	-	5/15/34/34	0/3/3/3
5	GTP	G	707	3	-	8/18/38/38	0/3/3/3

The worst 5 of 111 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	706	DZ4	PA-O1A	7.61	1.58	1.46
4	A	705	DZ4	PB-O1B	6.99	1.57	1.46
4	H	706	DZ4	PB-O1B	6.83	1.57	1.46
5	B	706	GTP	O4'-C1'	6.34	1.49	1.41
4	H	706	DZ4	PB-O3B	-6.34	1.51	1.59

The worst 5 of 167 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	C	701	DZ4	O1A-PA-N3A	-7.77	100.33	111.77
5	E	706	GTP	O5'-C5'-C4'	7.41	134.50	108.99
4	E	705	DZ4	O2B-PB-O1B	6.49	123.52	109.92
4	G	701	DZ4	O1B-PB-N3A	-6.28	102.52	111.77
4	A	707	DZ4	O1A-PA-N3A	-6.22	102.61	111.77

There are no chirality outliers.

5 of 98 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	705	DZ4	PA-N3A-PB-O1B
4	A	707	DZ4	PB-N3A-PA-O1A
4	A	707	DZ4	PA-N3A-PB-O1B
4	B	705	DZ4	PA-N3A-PB-O1B
4	C	701	DZ4	PA-N3A-PB-O1B

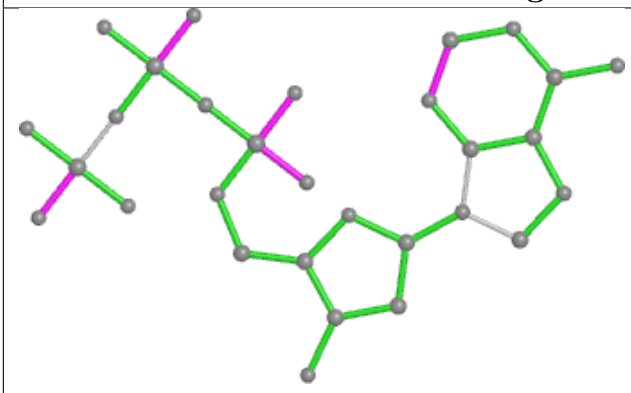
There are no ring outliers.

2 monomers are involved in 2 short contacts:

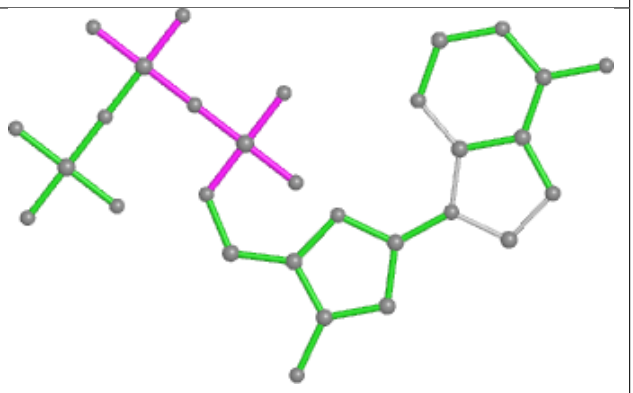
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	706	DZ4	1	0
5	D	707	GTP	1	0

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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

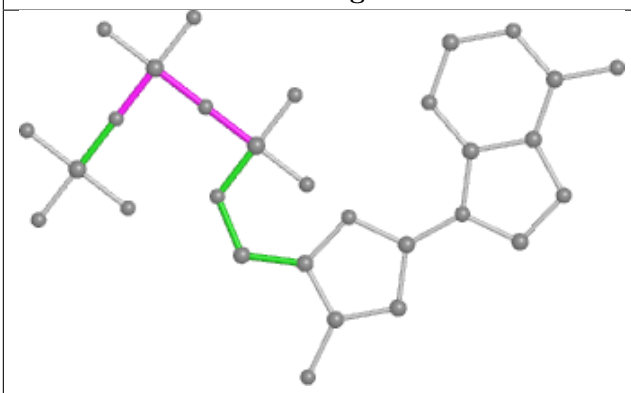
Ligand DZ4 G 701



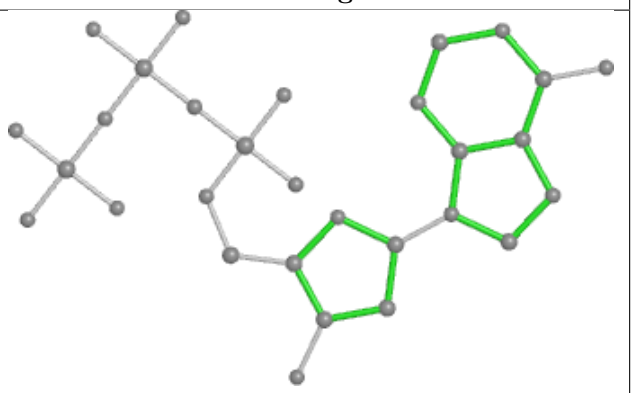
Bond lengths



Bond angles

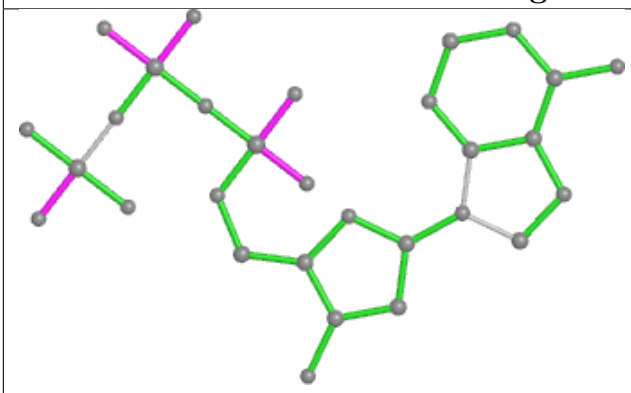


Torsions



Rings

Ligand DZ4 F 706



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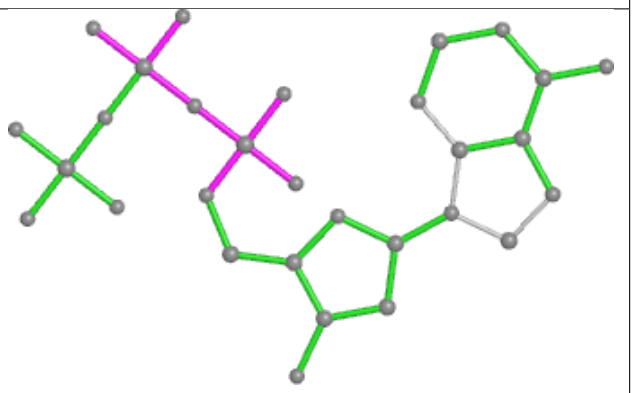

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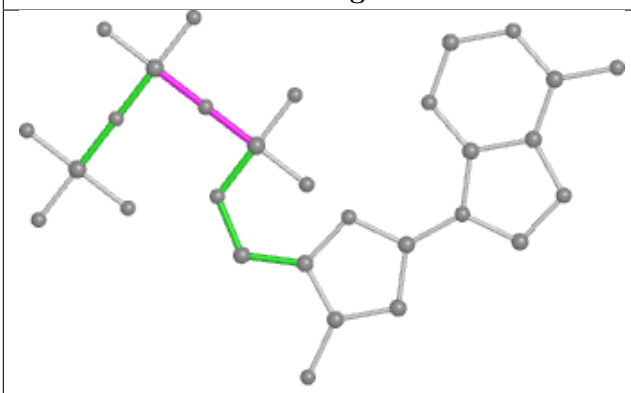

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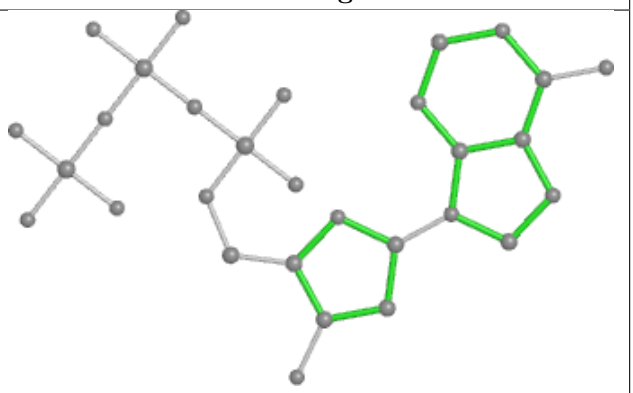
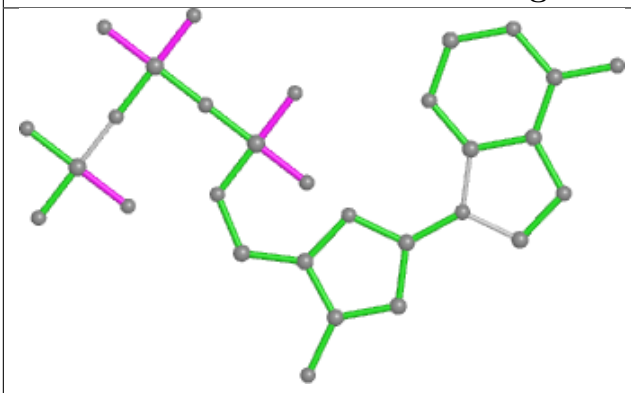


Rings

Ligand DZ4 F 705



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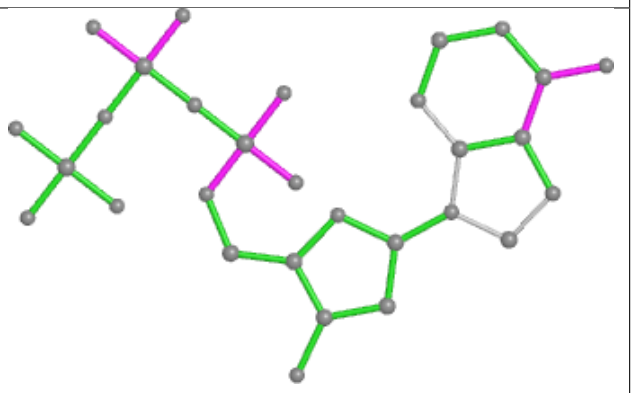

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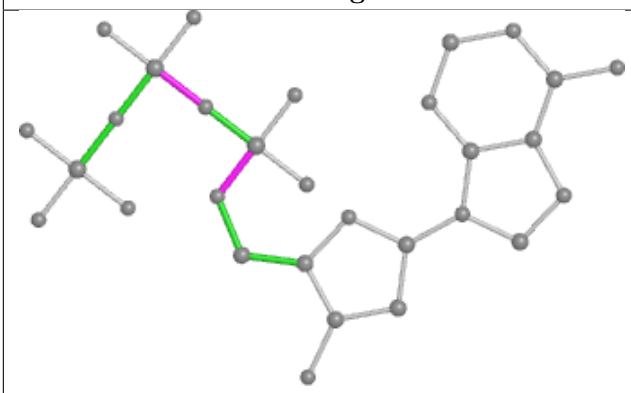

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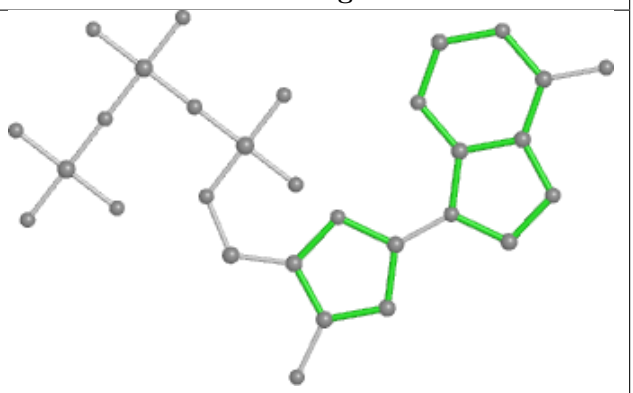
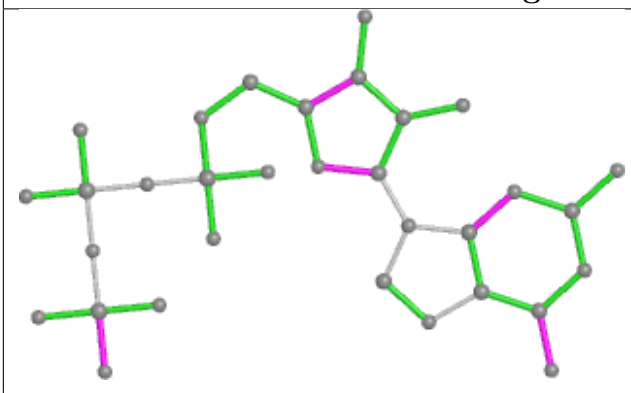


Rings

Ligand GTP B 706



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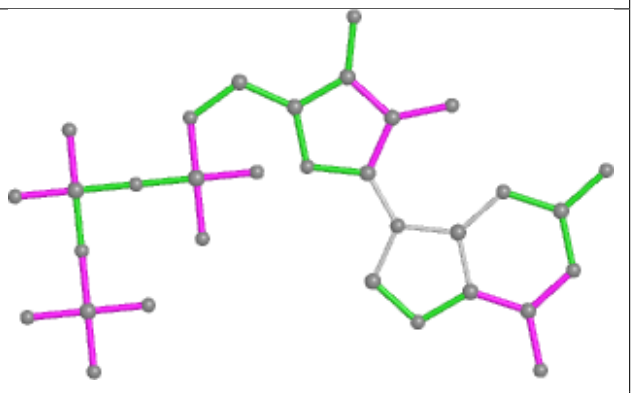
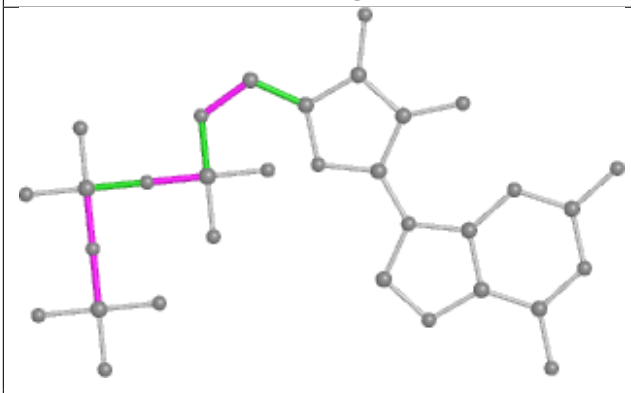


Bond angles



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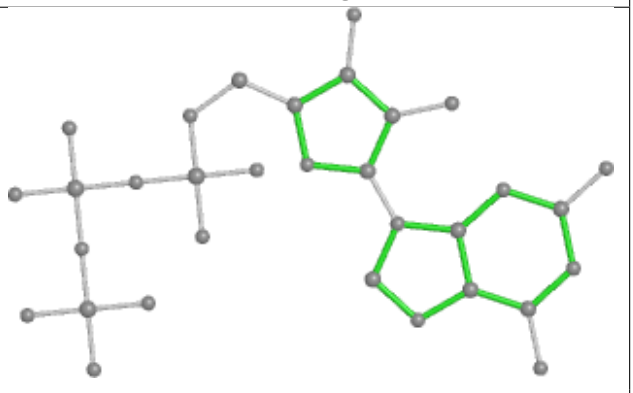
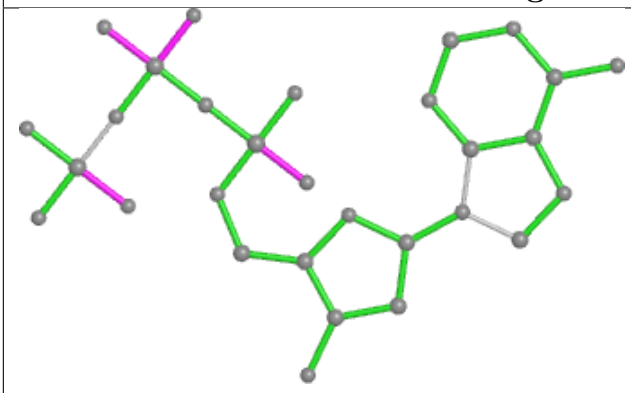


Rings

Ligand DZ4 G 706



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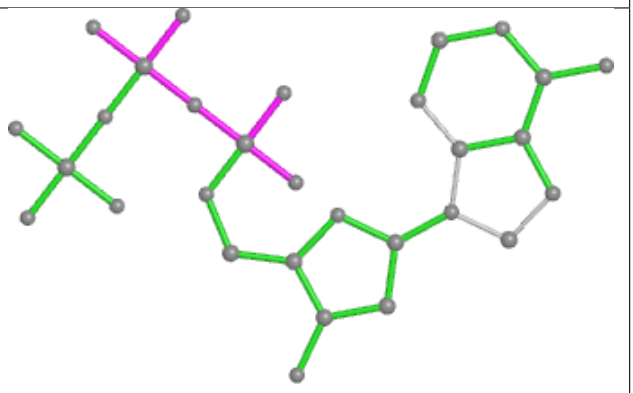

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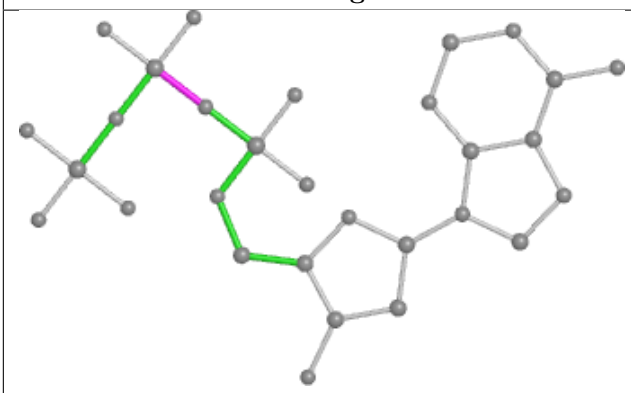

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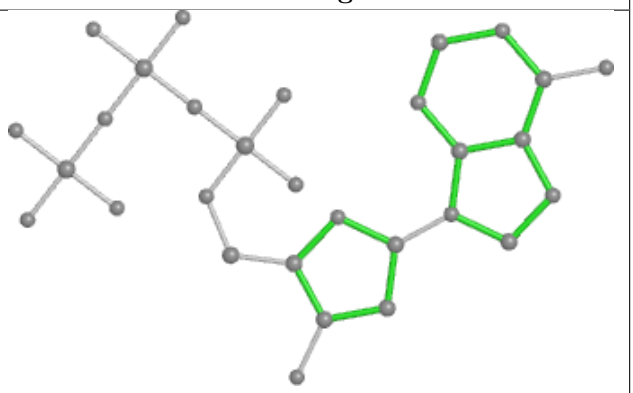
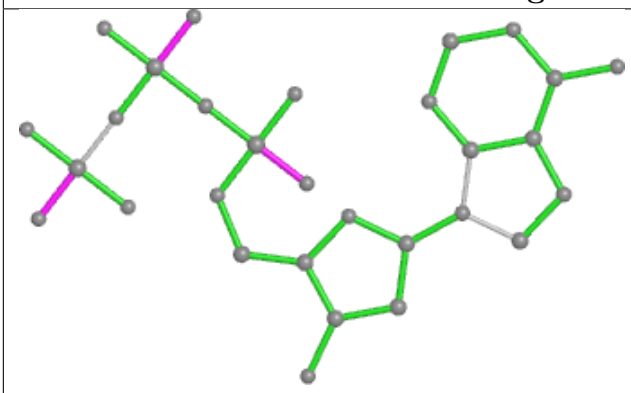


Rings

Ligand DZ4 A 705



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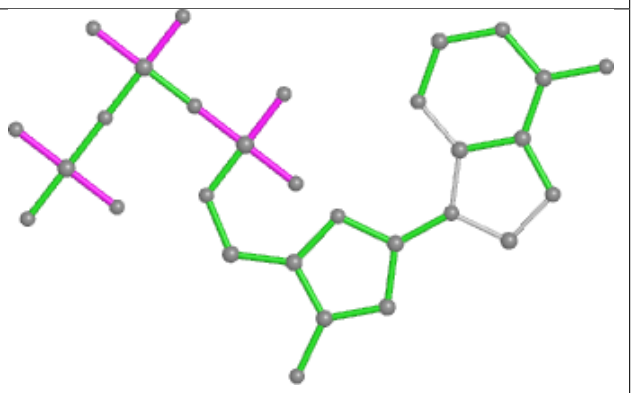
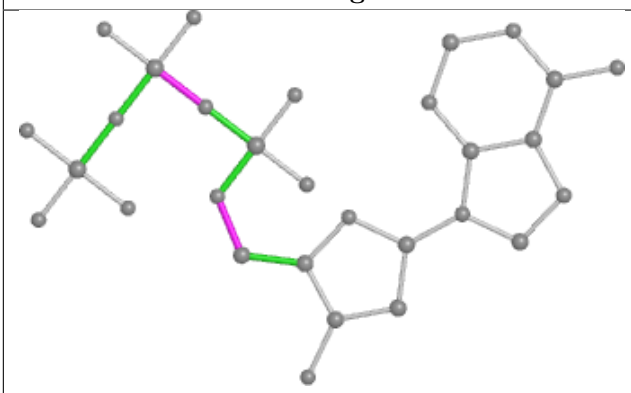


Bond angles



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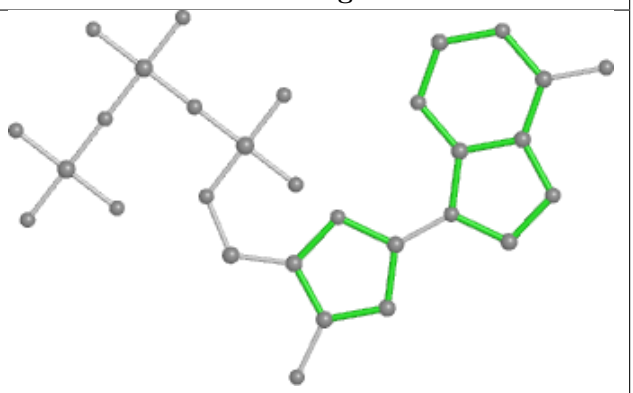
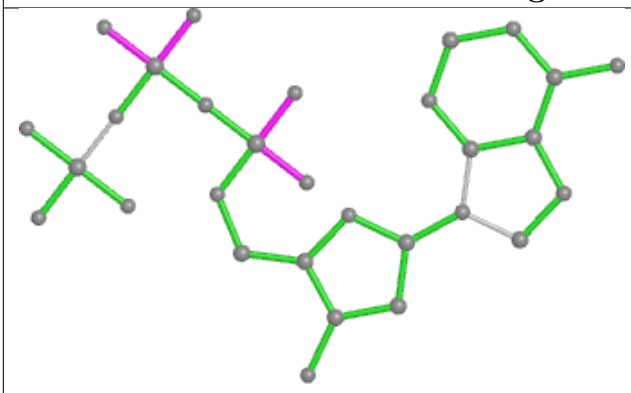
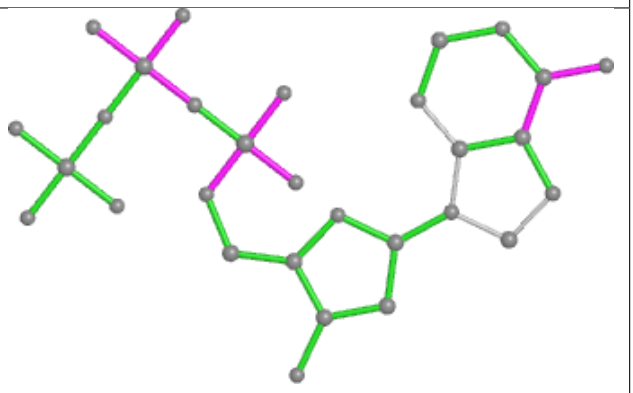


Rings

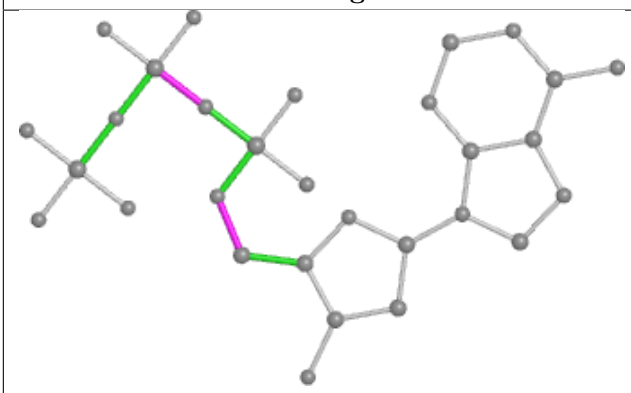
Ligand DZ4 C 706



Bond lengths



Bond angles



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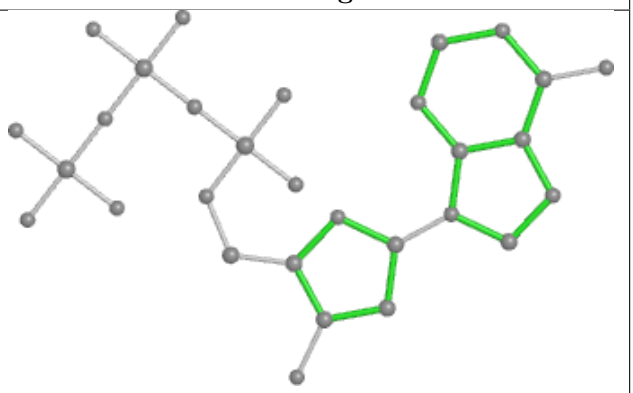
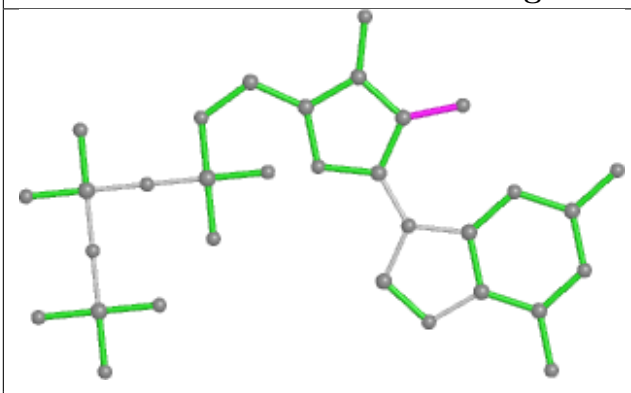
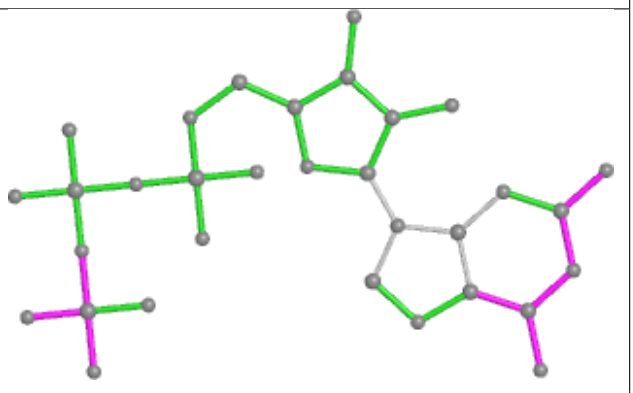


Rings

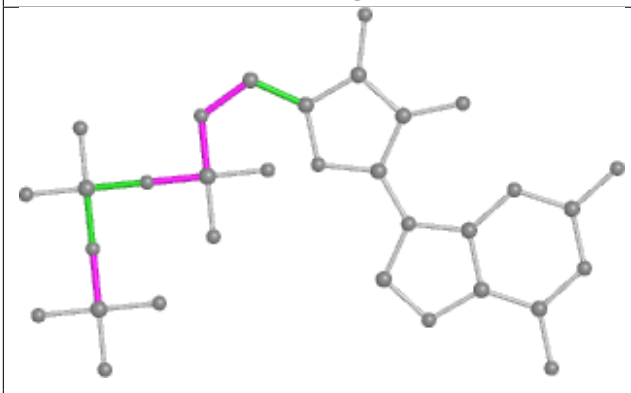
Ligand GTP E 707



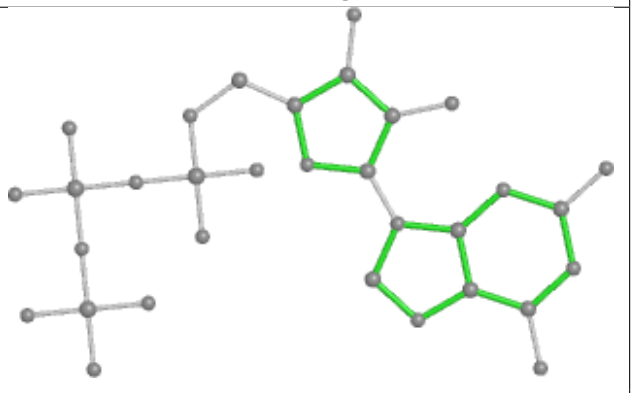
Bond lengths



Bond angles

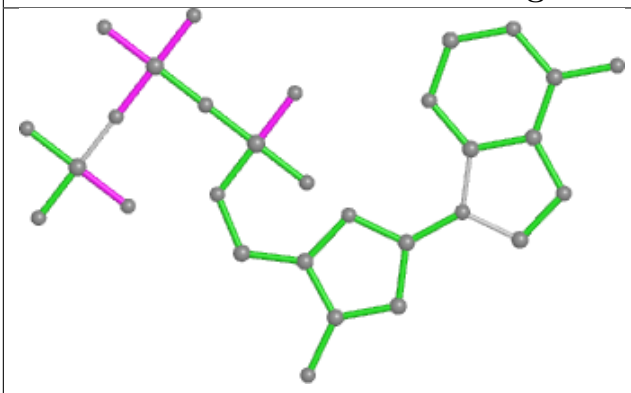


Torsions



Rings

Ligand DZ4 D 701



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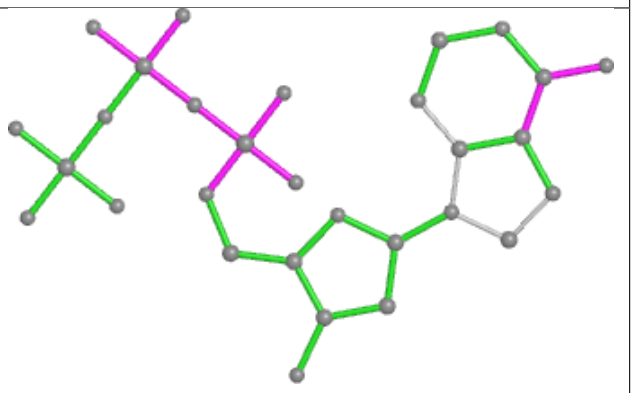

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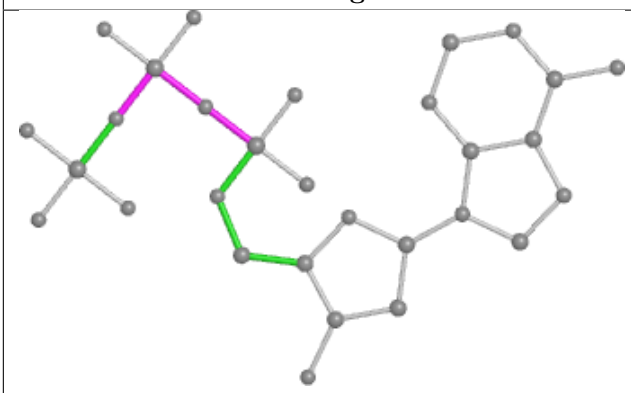

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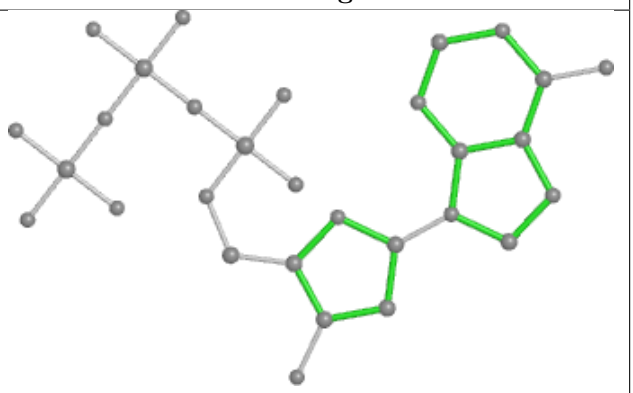
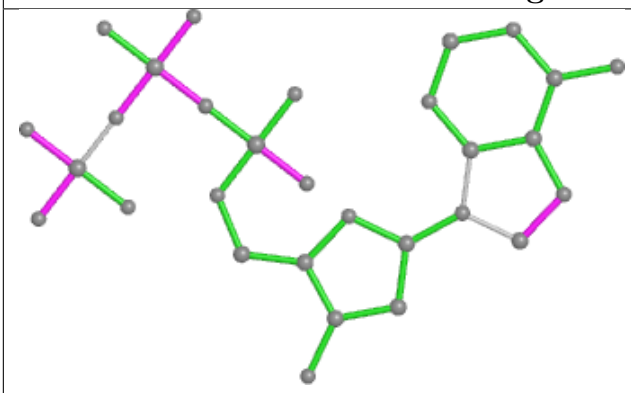


Rings

Ligand DZ4 H 706



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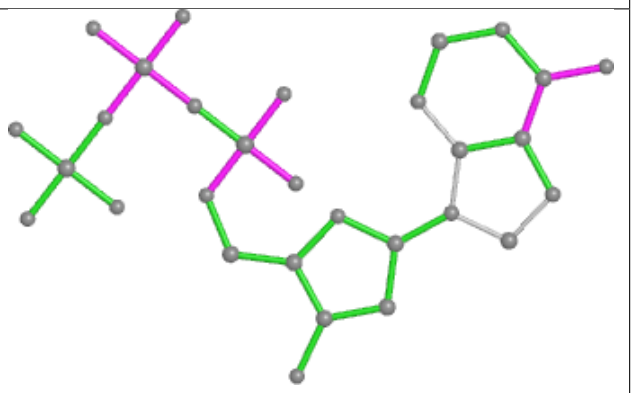

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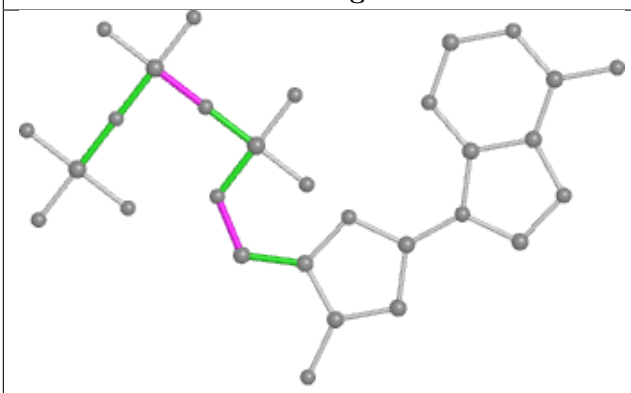

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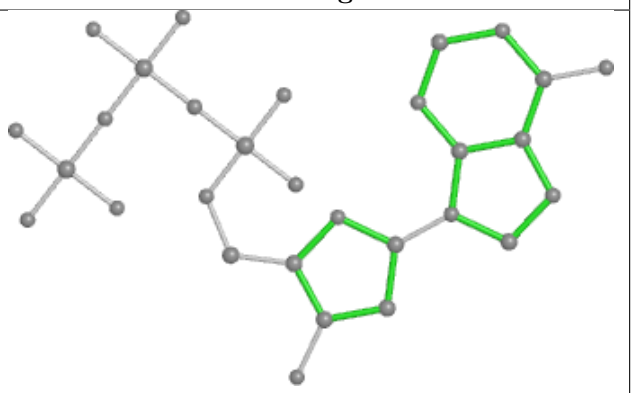
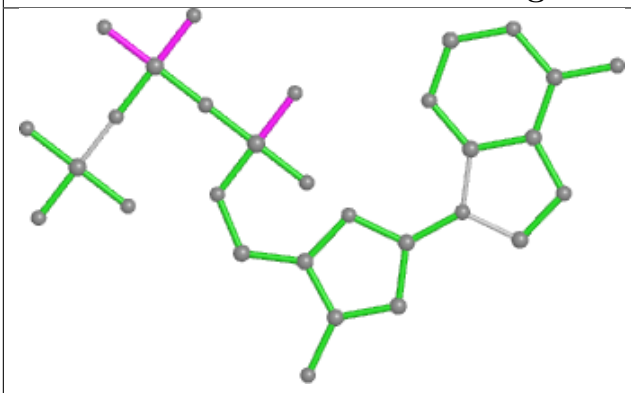


Rings

Ligand DZ4 A 707



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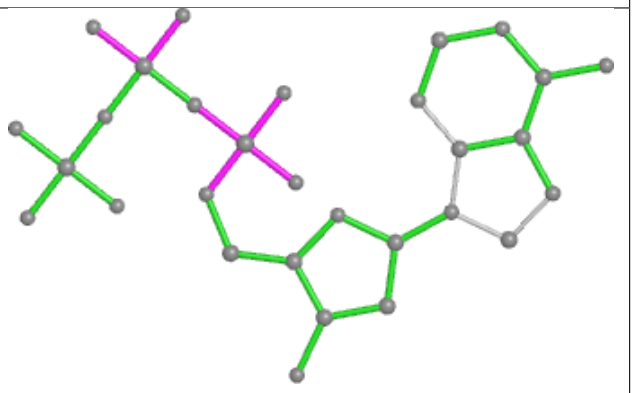

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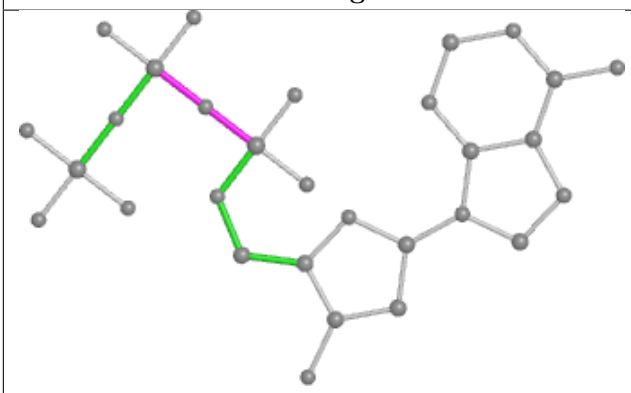

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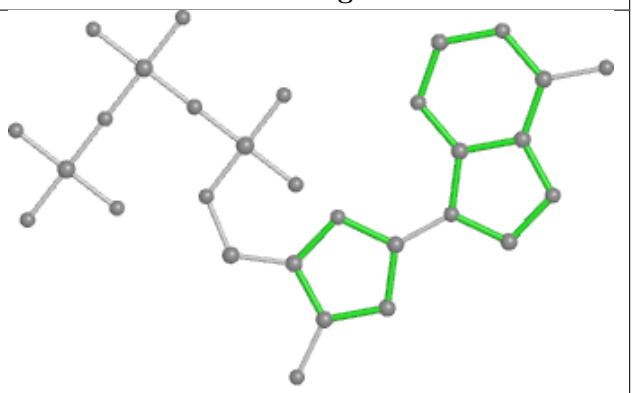
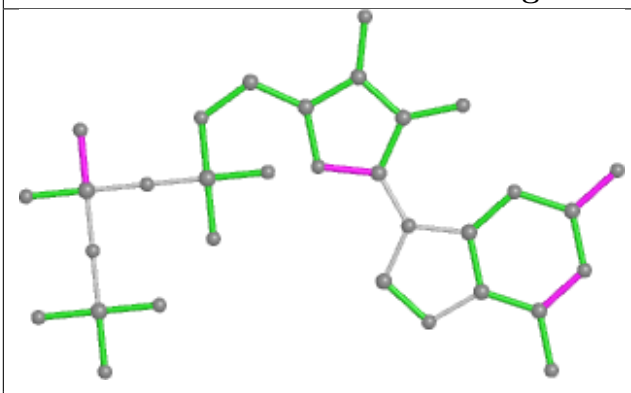


Rings

Ligand GTP A 706



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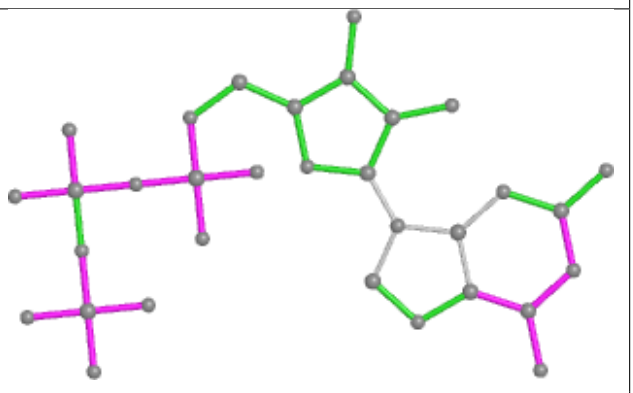

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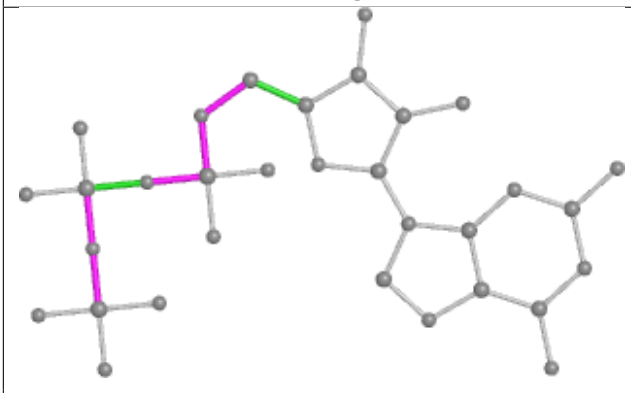

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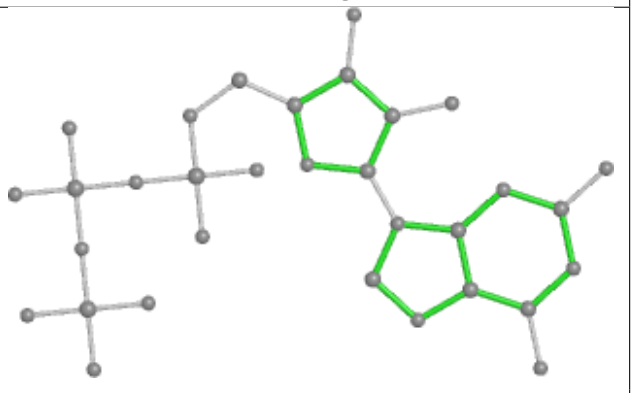
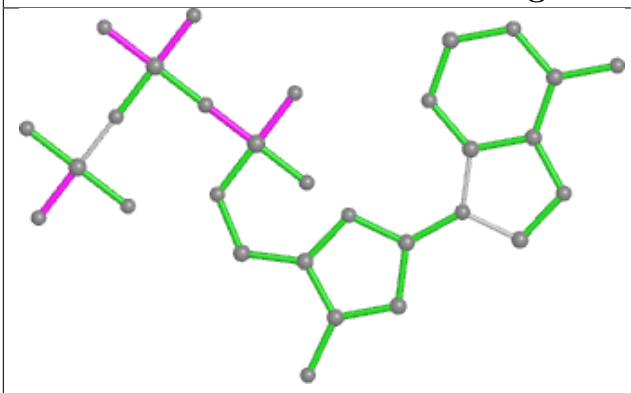


Rings

Ligand DZ4 C 701



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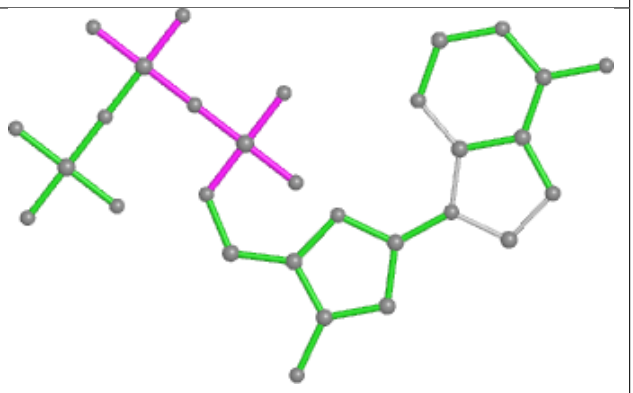

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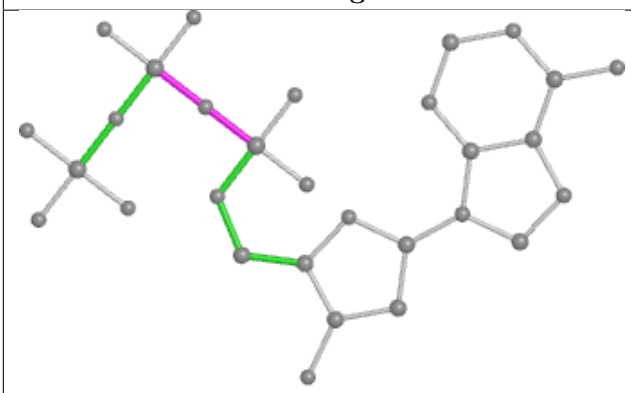

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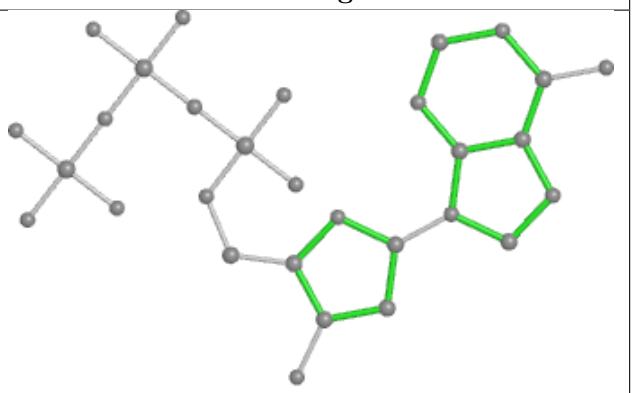
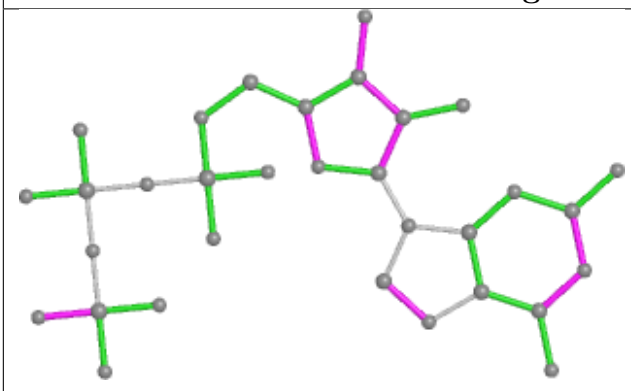


Rings

Ligand GTP C 707



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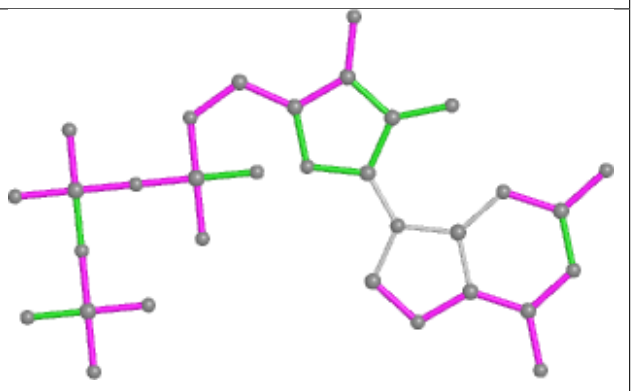

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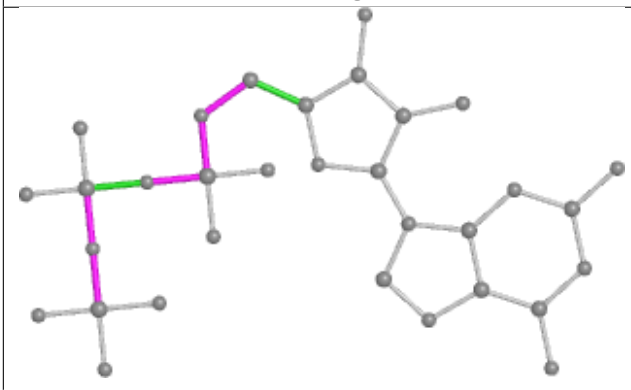

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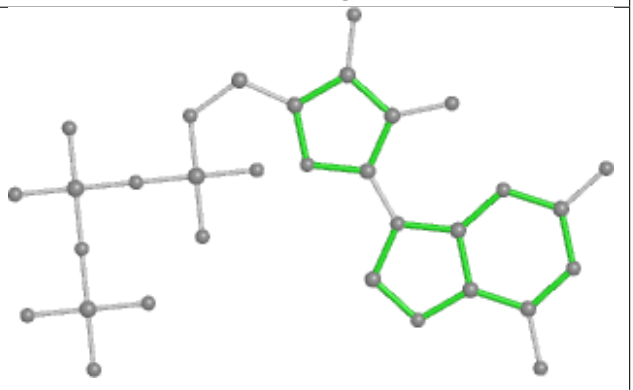
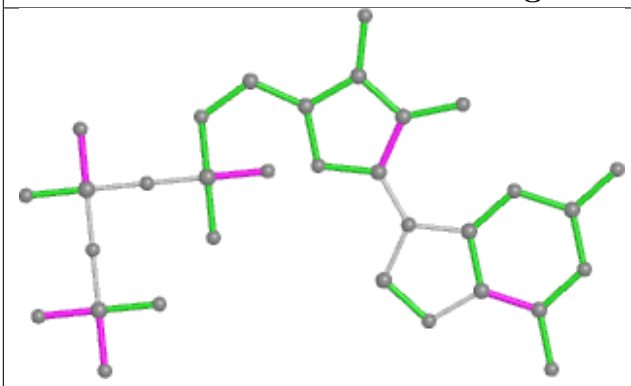


Rings

Ligand GTP E 706



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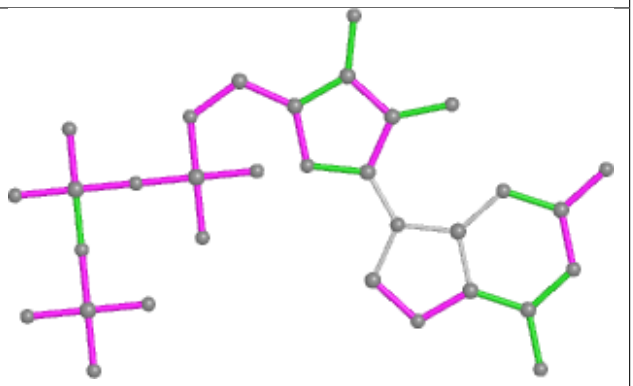

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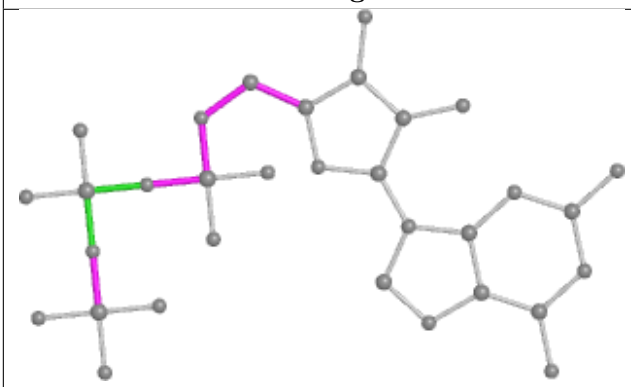

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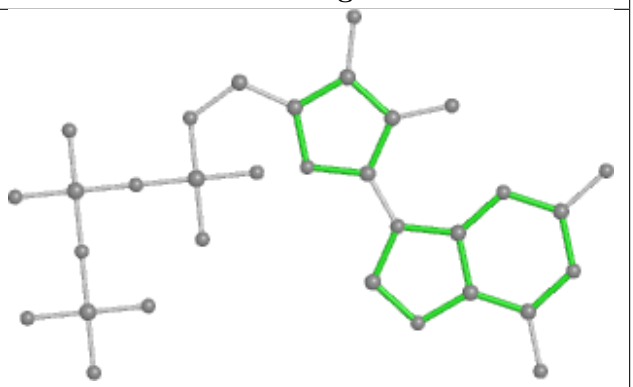
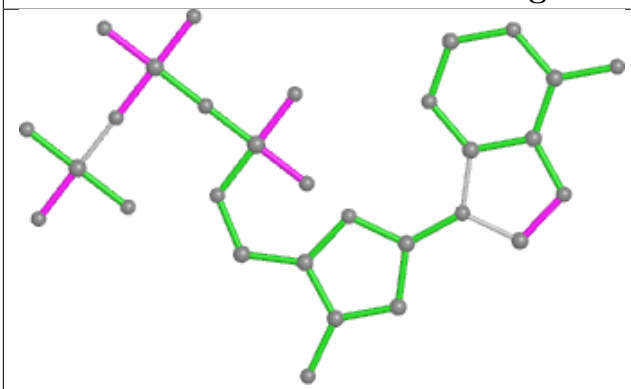


Rings

Ligand DZ4 E 708



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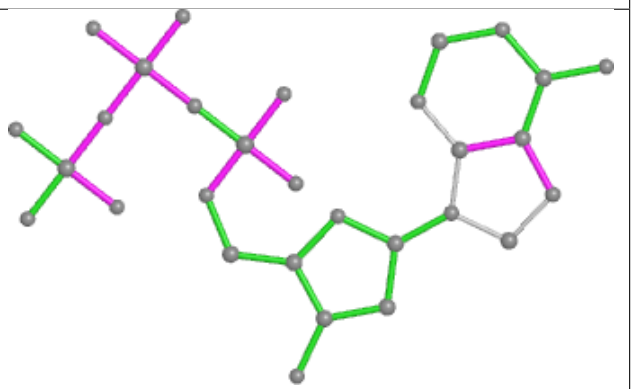

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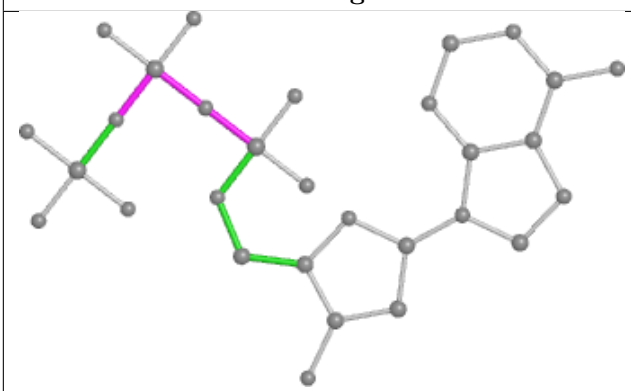

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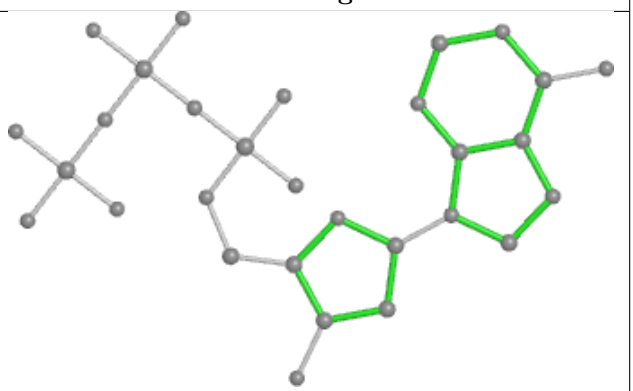
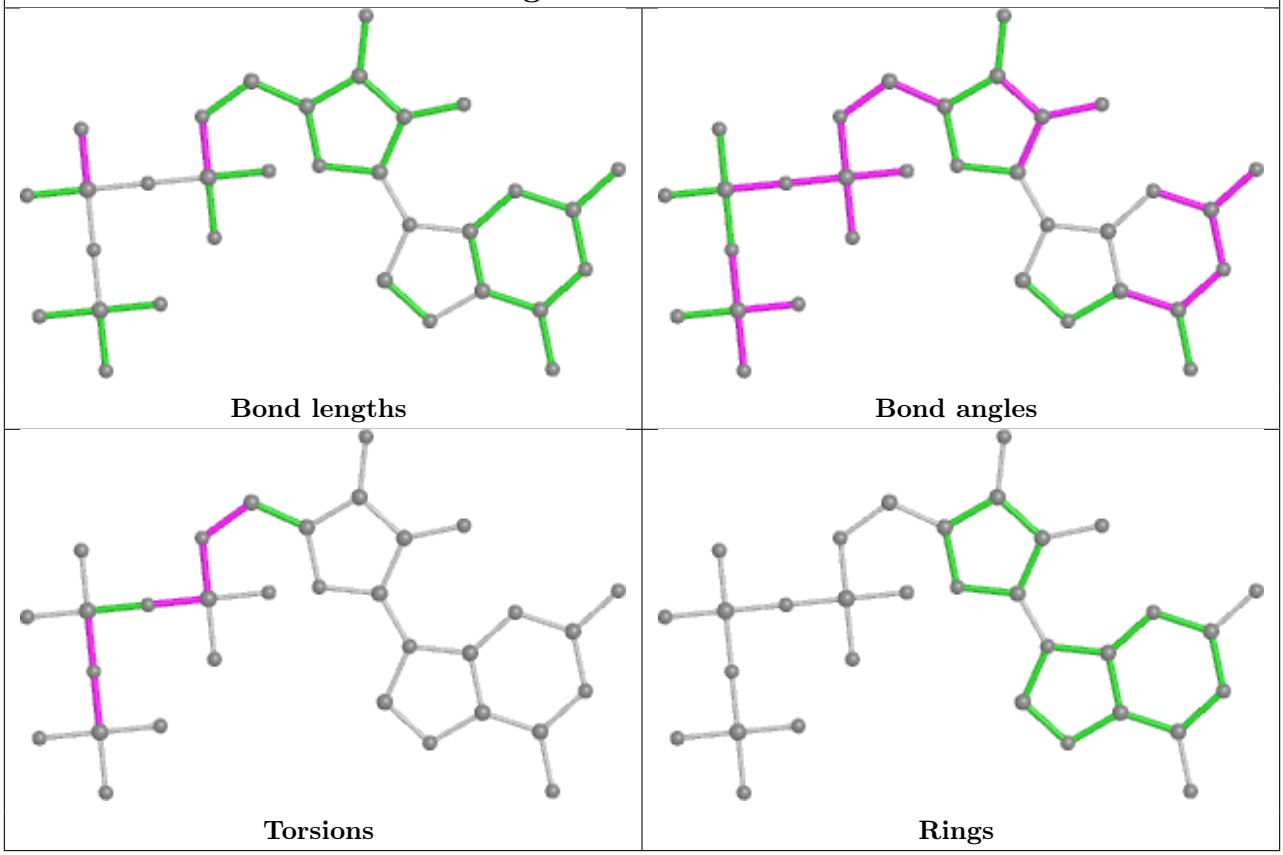


Rings

Ligand GTP D 707



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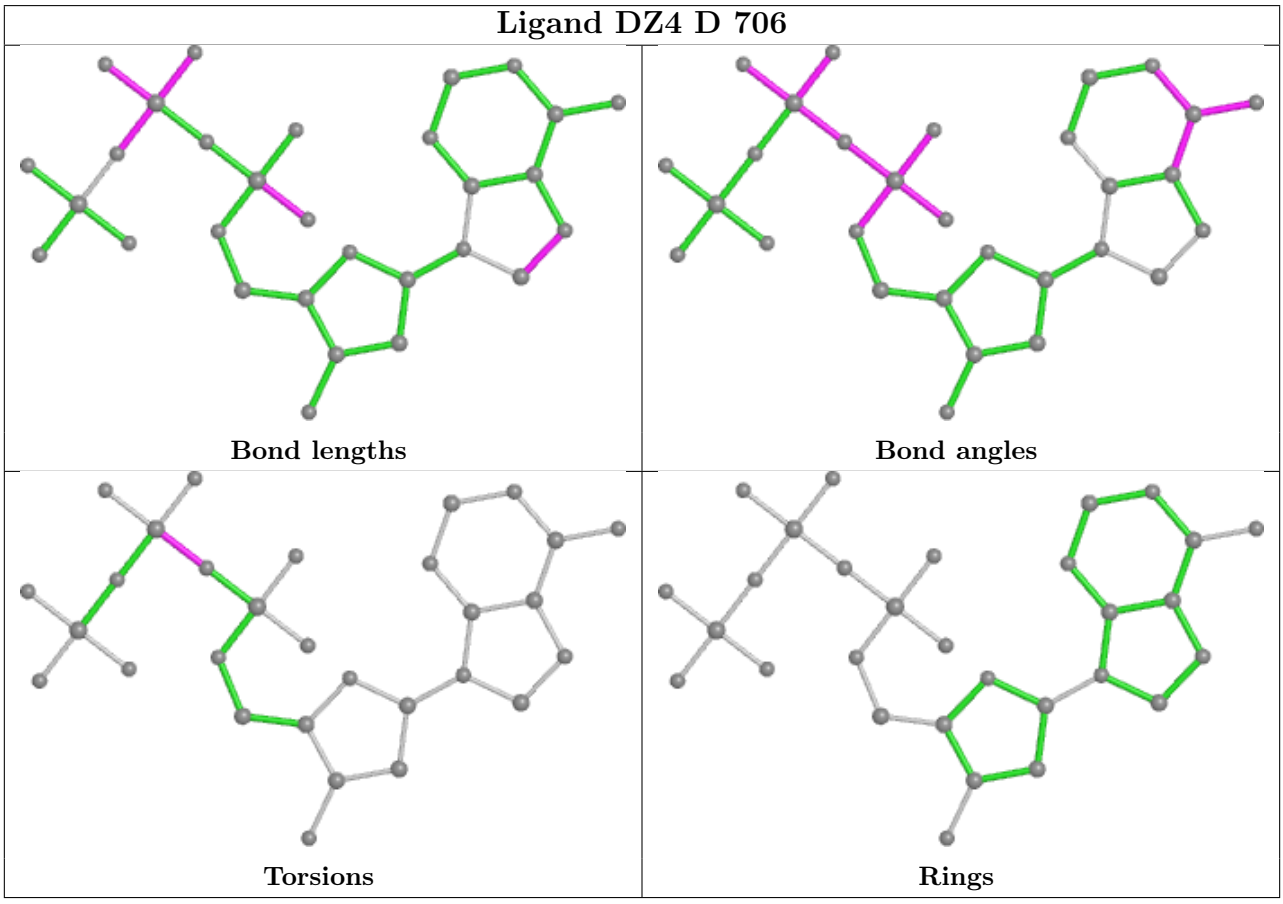

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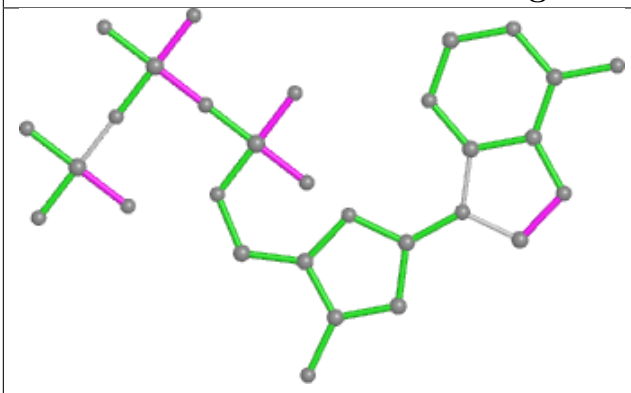

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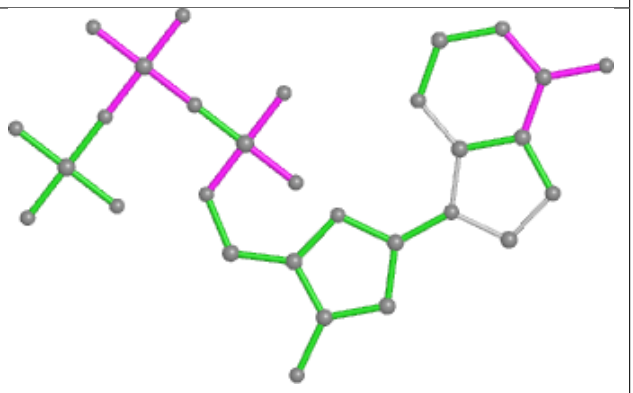
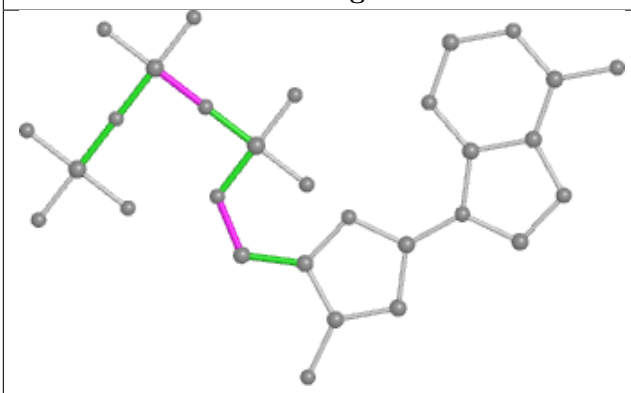


Bond angles



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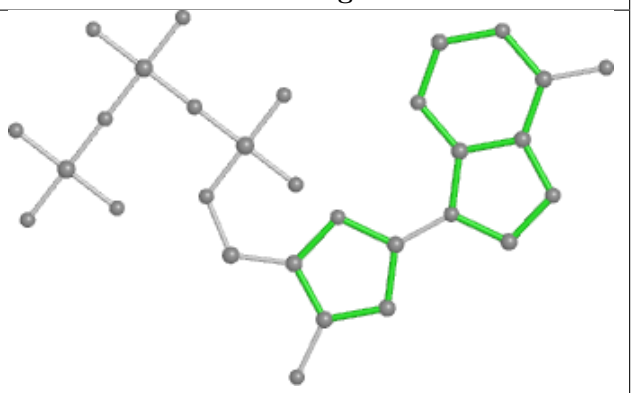
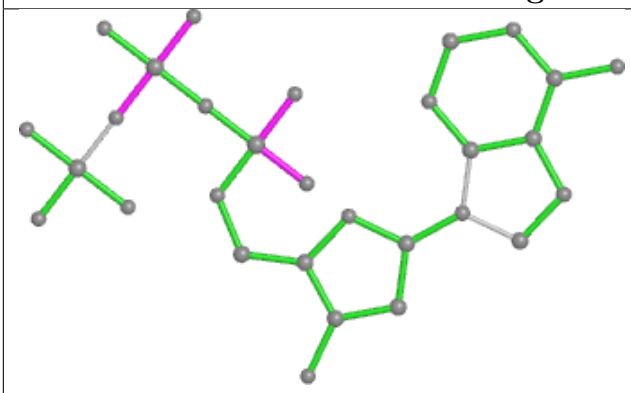


Rings

Ligand DZ4 H 701



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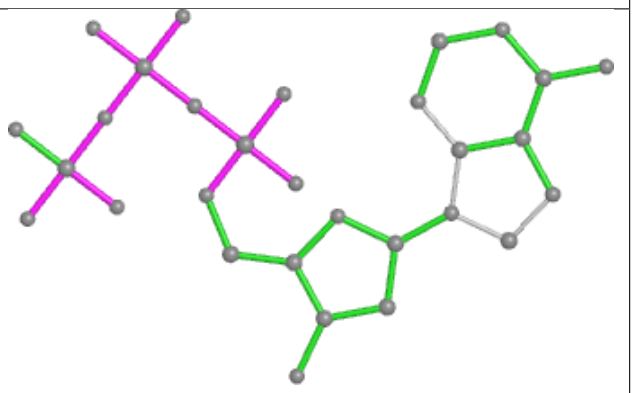
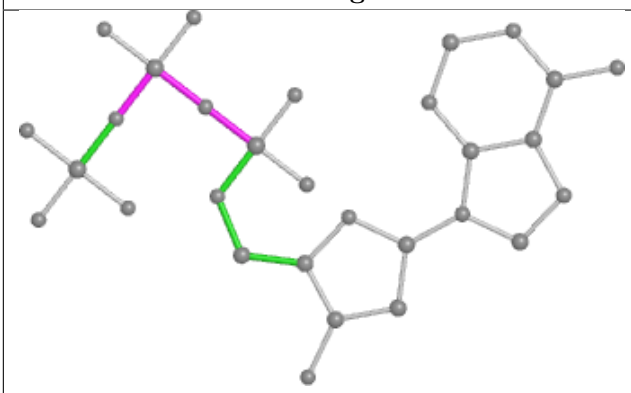


Bond angles



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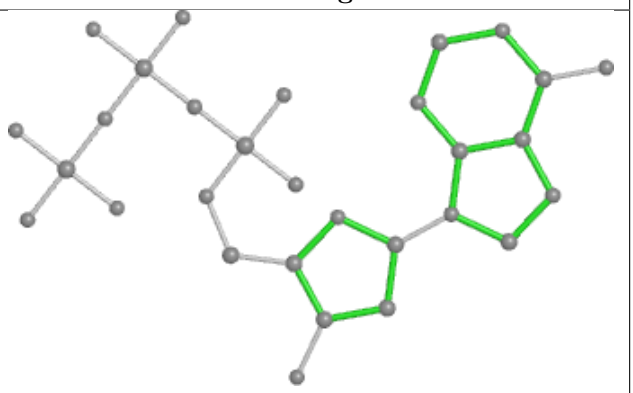
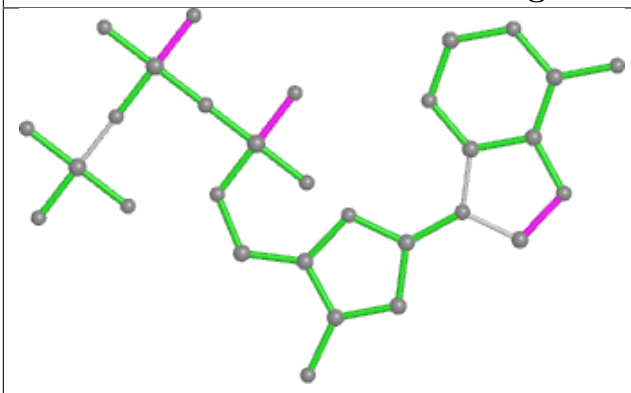


Rings

Ligand DZ4 B 705



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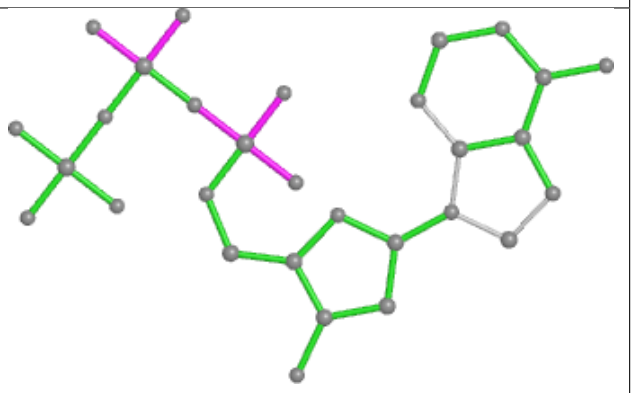
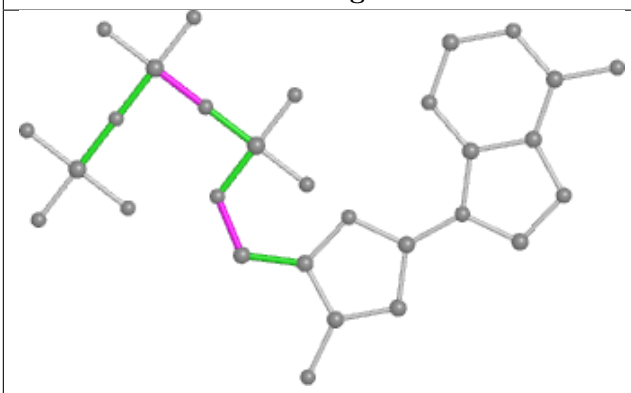


Bond angles



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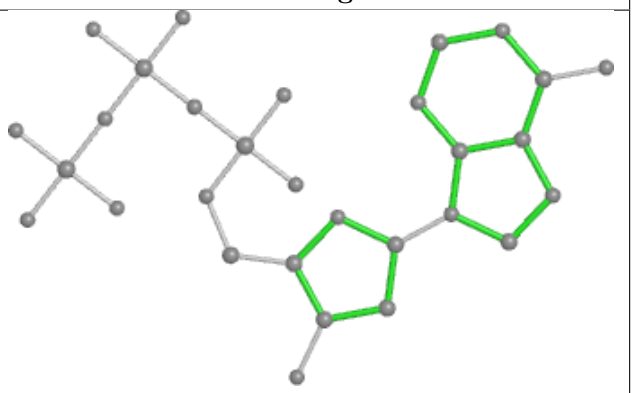
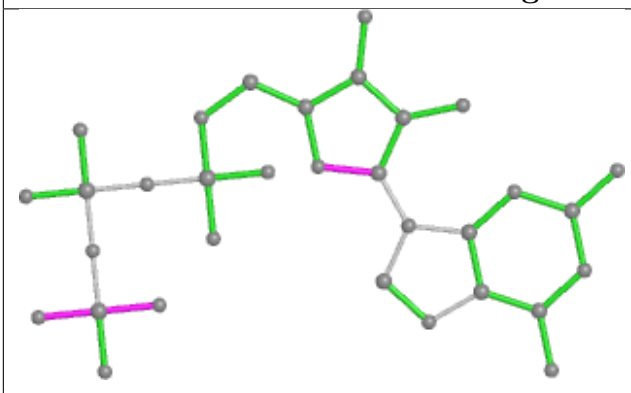


Rings

Ligand GTP H 707



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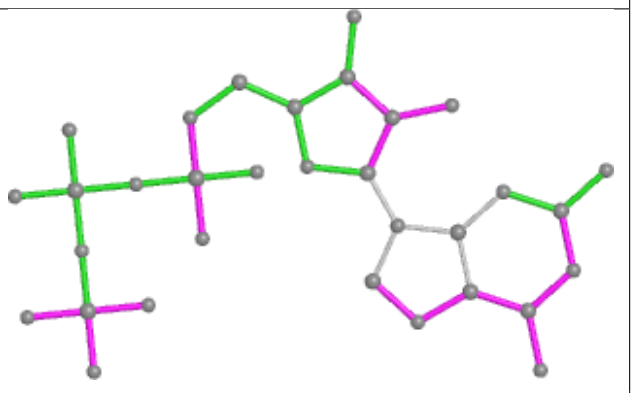
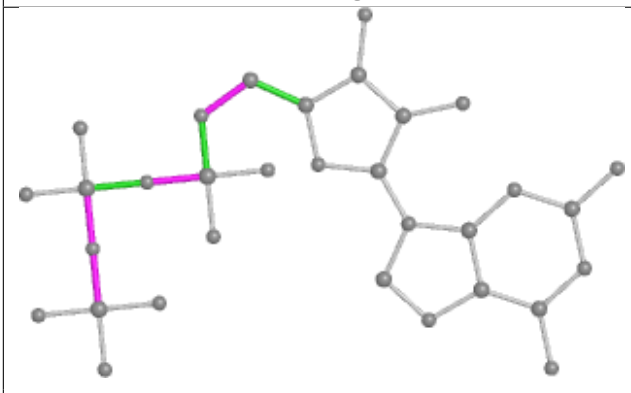


Bond angles



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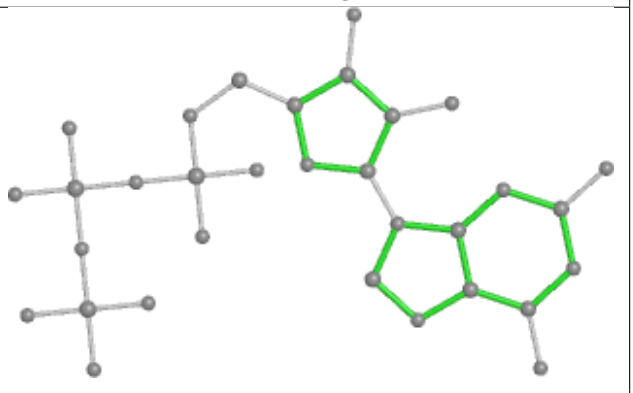
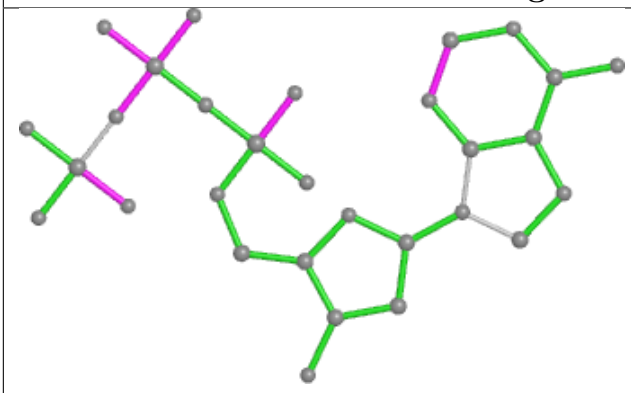


Rings

Ligand DZ4 C 708



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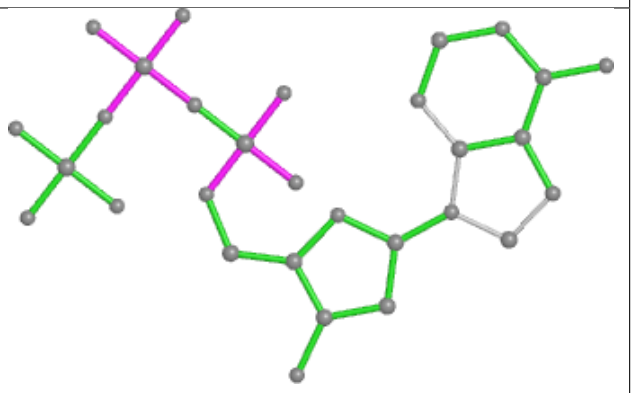
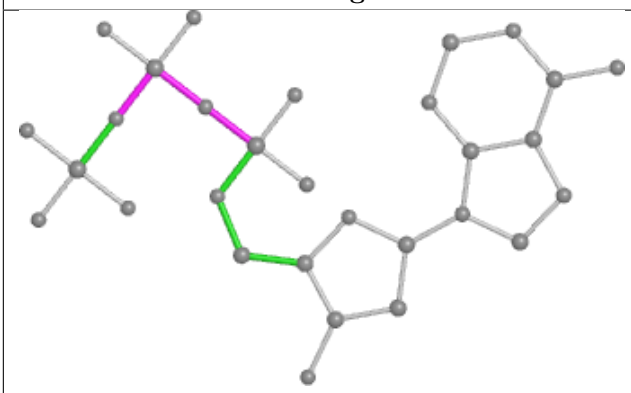


Bond angles



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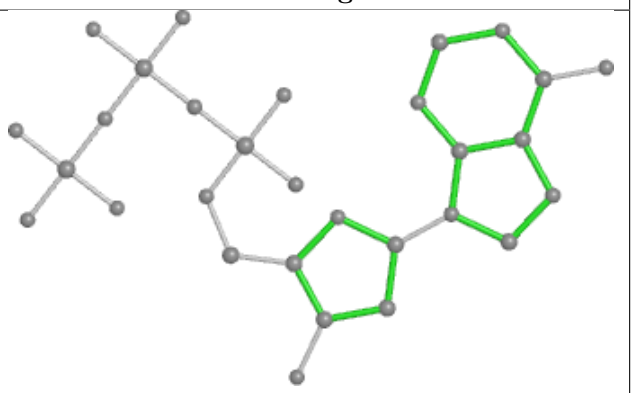
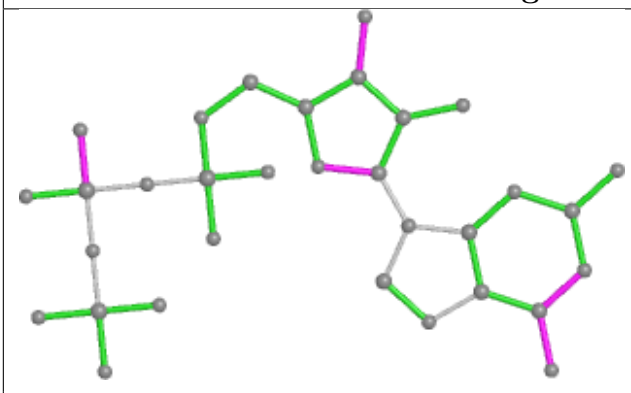
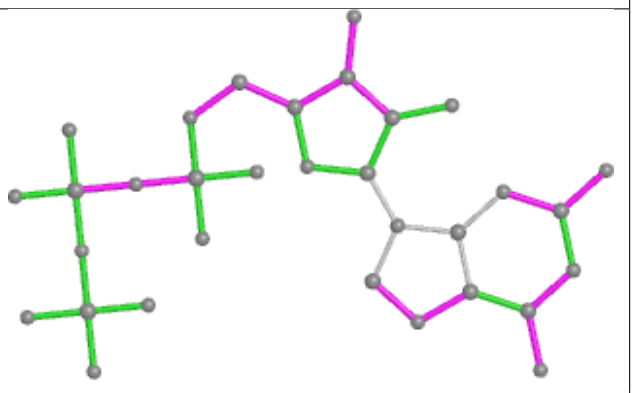


Rings

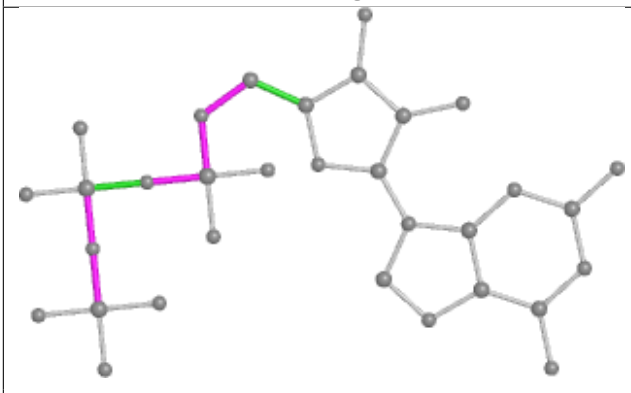
Ligand GTP G 707



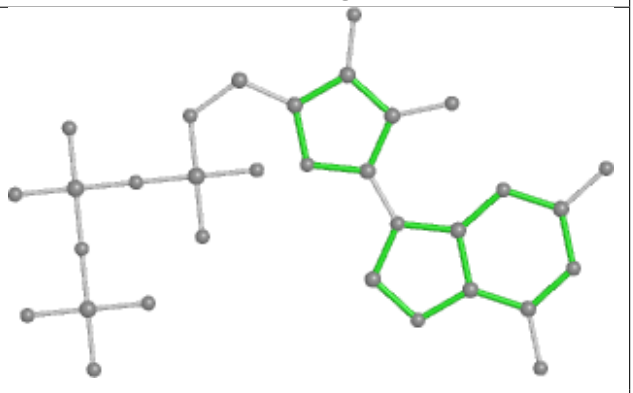
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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%)	-0.35	2 (0%)	92	91	12, 27, 59, 93	0
1	B	479/520 (92%)	-0.42	2 (0%)	92	91	12, 25, 53, 73	0
1	C	478/520 (91%)	-0.40	2 (0%)	92	91	12, 25, 57, 79	0
1	D	478/520 (91%)	-0.41	1 (0%)	95	94	13, 27, 54, 77	0
1	E	464/520 (89%)	-0.12	12 (2%)	56	53	14, 34, 70, 96	0
1	F	480/520 (92%)	-0.43	1 (0%)	95	94	11, 24, 47, 65	0
1	G	479/520 (92%)	-0.36	5 (1%)	82	81	13, 27, 56, 87	0
1	H	478/520 (91%)	-0.14	8 (1%)	70	68	17, 38, 75, 100	0
All	All	3816/4160 (91%)	-0.33	33 (0%)	84	83	11, 28, 60, 100	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	284	LEU	4.8
1	G	488	LEU	3.6
1	B	284	LEU	3.4
1	A	489	LEU	3.3
1	A	490	ASP	3.2

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

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

6.3 Carbohydrates

There are no 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, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	MG	H	704	1/1	0.86	0.07	32,32,32,32	0
3	MG	D	708	1/1	0.89	0.07	38,38,38,38	0
3	MG	H	703	1/1	0.90	0.12	15,15,15,15	0
3	MG	G	705	1/1	0.95	0.06	36,36,36,36	0
3	MG	E	703	1/1	0.96	0.03	26,26,26,26	0
3	MG	B	704	1/1	0.96	0.06	17,17,17,17	0
4	DZ4	H	706	30/30	0.96	0.11	18,22,27,34	0
3	MG	F	703	1/1	0.97	0.05	15,15,15,15	0
3	MG	F	704	1/1	0.97	0.04	28,28,28,28	0
3	MG	B	703	1/1	0.97	0.03	16,16,16,16	0
3	MG	D	704	1/1	0.98	0.04	19,19,19,19	0
3	MG	D	705	1/1	0.98	0.05	18,18,18,18	0
3	MG	C	705	1/1	0.98	0.07	17,17,17,17	0
4	DZ4	A	707	30/30	0.98	0.09	13,15,18,20	0
4	DZ4	C	701	30/30	0.98	0.09	11,13,16,18	0
4	DZ4	E	708	30/30	0.98	0.10	20,23,32,33	0
4	DZ4	F	706	30/30	0.98	0.10	11,15,19,20	0
4	DZ4	H	701	30/30	0.98	0.09	20,23,28,29	0
3	MG	G	704	1/1	0.98	0.05	20,20,20,20	0
5	GTP	E	707	32/32	0.98	0.09	18,20,30,33	0
5	GTP	G	707	32/32	0.98	0.09	20,23,32,36	0
3	MG	E	702	1/1	0.99	0.09	15,15,15,15	0
3	MG	H	705	1/1	0.99	0.08	17,17,17,17	0
4	DZ4	A	705	30/30	0.99	0.09	13,15,19,21	0
3	MG	C	704	1/1	0.99	0.02	13,13,13,13	0
4	DZ4	B	705	30/30	0.99	0.10	12,14,16,16	0
3	MG	E	704	1/1	0.99	0.05	16,16,16,16	0
4	DZ4	C	706	30/30	0.99	0.10	13,14,16,17	0
4	DZ4	C	708	30/30	0.99	0.09	14,16,20,23	0
4	DZ4	D	701	30/30	0.99	0.09	13,15,19,19	0
4	DZ4	D	706	30/30	0.99	0.09	13,16,19,20	0
4	DZ4	E	705	30/30	0.99	0.09	17,21,23,24	0
3	MG	A	704	1/1	0.99	0.04	14,14,14,14	0
4	DZ4	F	705	30/30	0.99	0.10	12,13,15,16	0
3	MG	D	703	1/1	0.99	0.08	8,8,8,8	0
4	DZ4	G	701	30/30	0.99	0.10	12,15,19,20	0
4	DZ4	G	706	30/30	0.99	0.10	12,13,15,16	0

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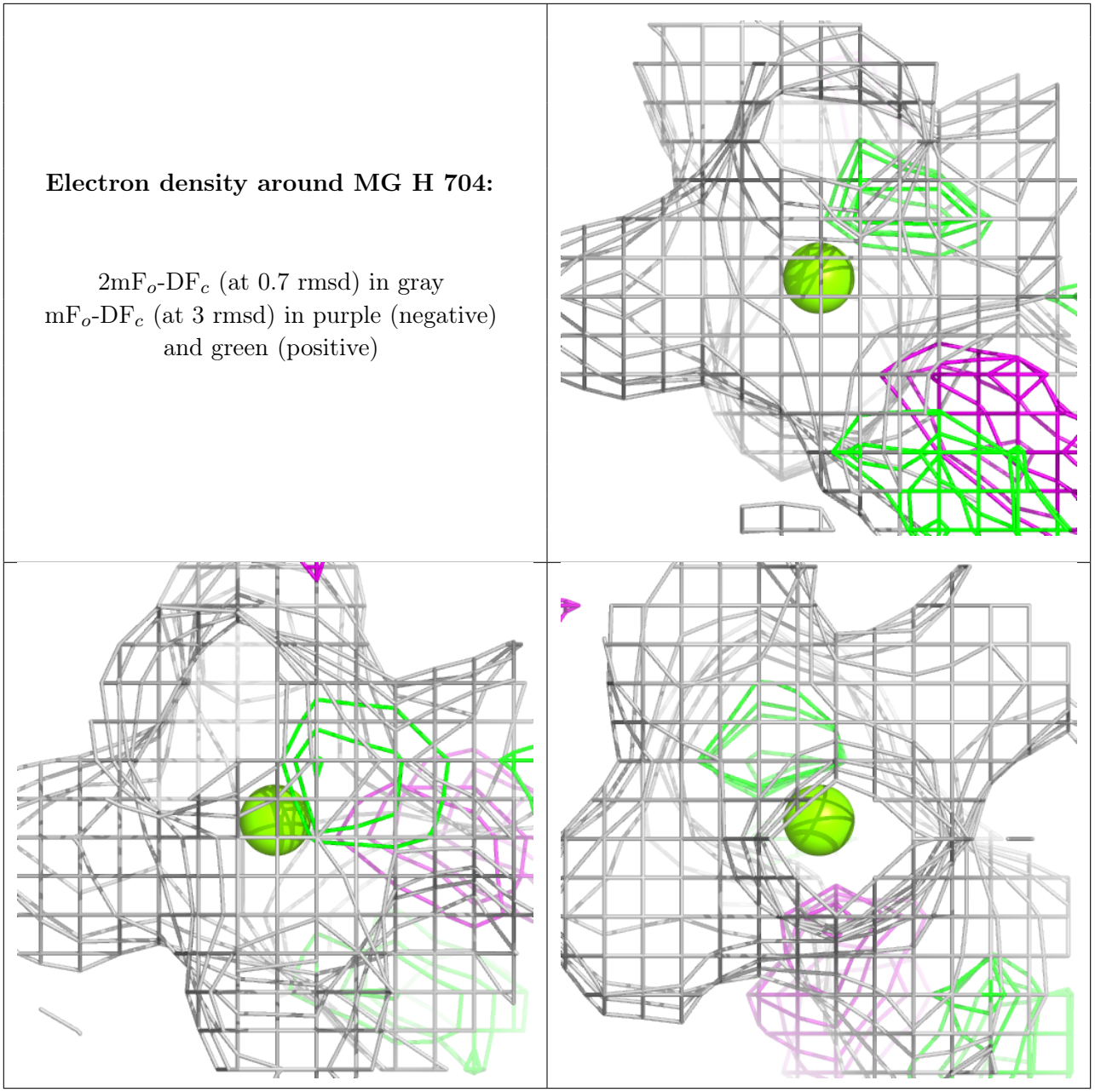
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	MG	G	703	1/1	0.99	0.09	11,11,11,11	0
3	MG	A	702	1/1	0.99	0.05	8,8,8,8	0
5	GTP	A	706	32/32	0.99	0.09	12,13,18,19	0
5	GTP	B	706	32/32	0.99	0.08	13,17,25,25	0
5	GTP	C	707	32/32	0.99	0.09	14,16,22,23	0
5	GTP	D	707	32/32	0.99	0.08	14,16,22,23	0
5	GTP	E	706	32/32	0.99	0.09	13,15,21,23	0
3	MG	A	703	1/1	0.99	0.05	14,14,14,14	0
3	MG	C	703	1/1	0.99	0.09	9,9,9,9	0
5	GTP	H	707	32/32	0.99	0.10	15,17,22,23	0
2	FE	A	701	1/1	1.00	0.11	14,14,14,14	0
2	FE	B	701	1/1	1.00	0.09	13,13,13,13	0
2	FE	C	702	1/1	1.00	0.10	13,13,13,13	0
3	MG	B	702	1/1	1.00	0.05	9,9,9,9	0
2	FE	D	702	1/1	1.00	0.10	15,15,15,15	0
2	FE	E	701	1/1	1.00	0.11	17,17,17,17	0
2	FE	F	701	1/1	1.00	0.09	14,14,14,14	0
3	MG	F	702	1/1	1.00	0.11	9,9,9,9	0
2	FE	G	702	1/1	1.00	0.10	13,13,13,13	0
2	FE	H	702	1/1	1.00	0.10	20,20,20,20	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.

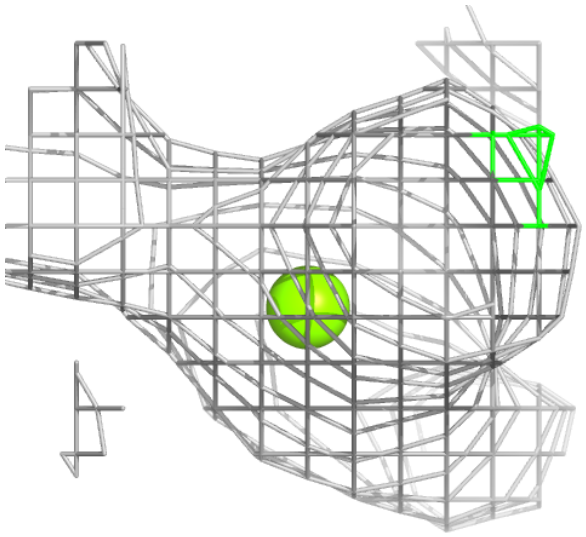
Electron density around MG H 704:

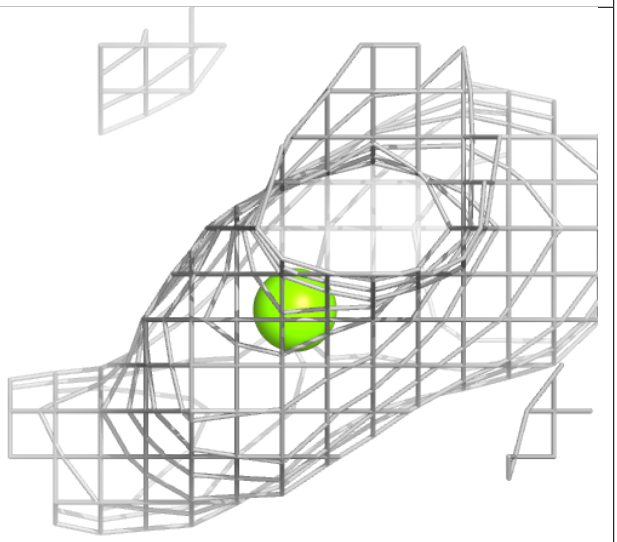
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around MG D 708:

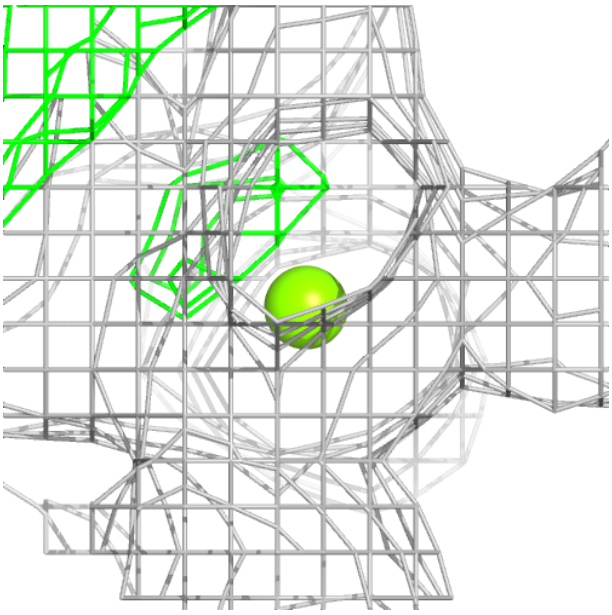
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

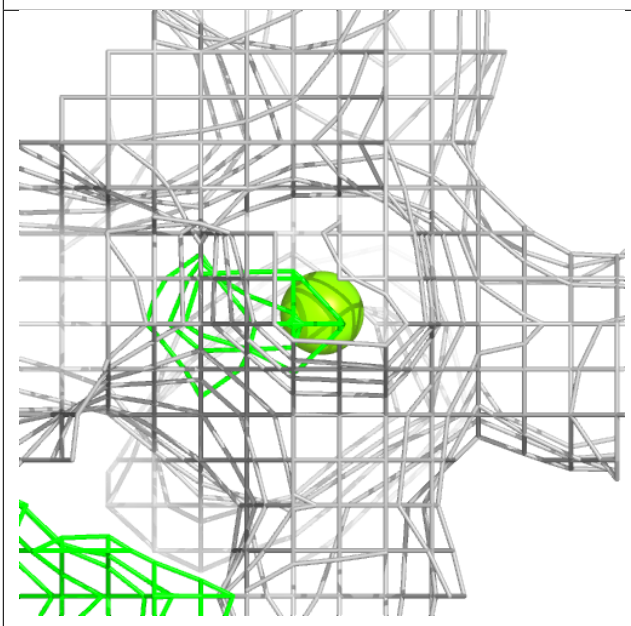


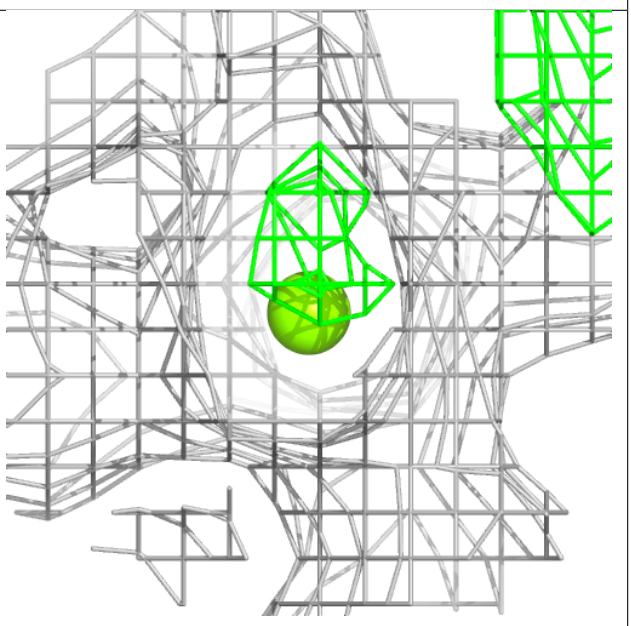


Electron density around MG H 703:

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

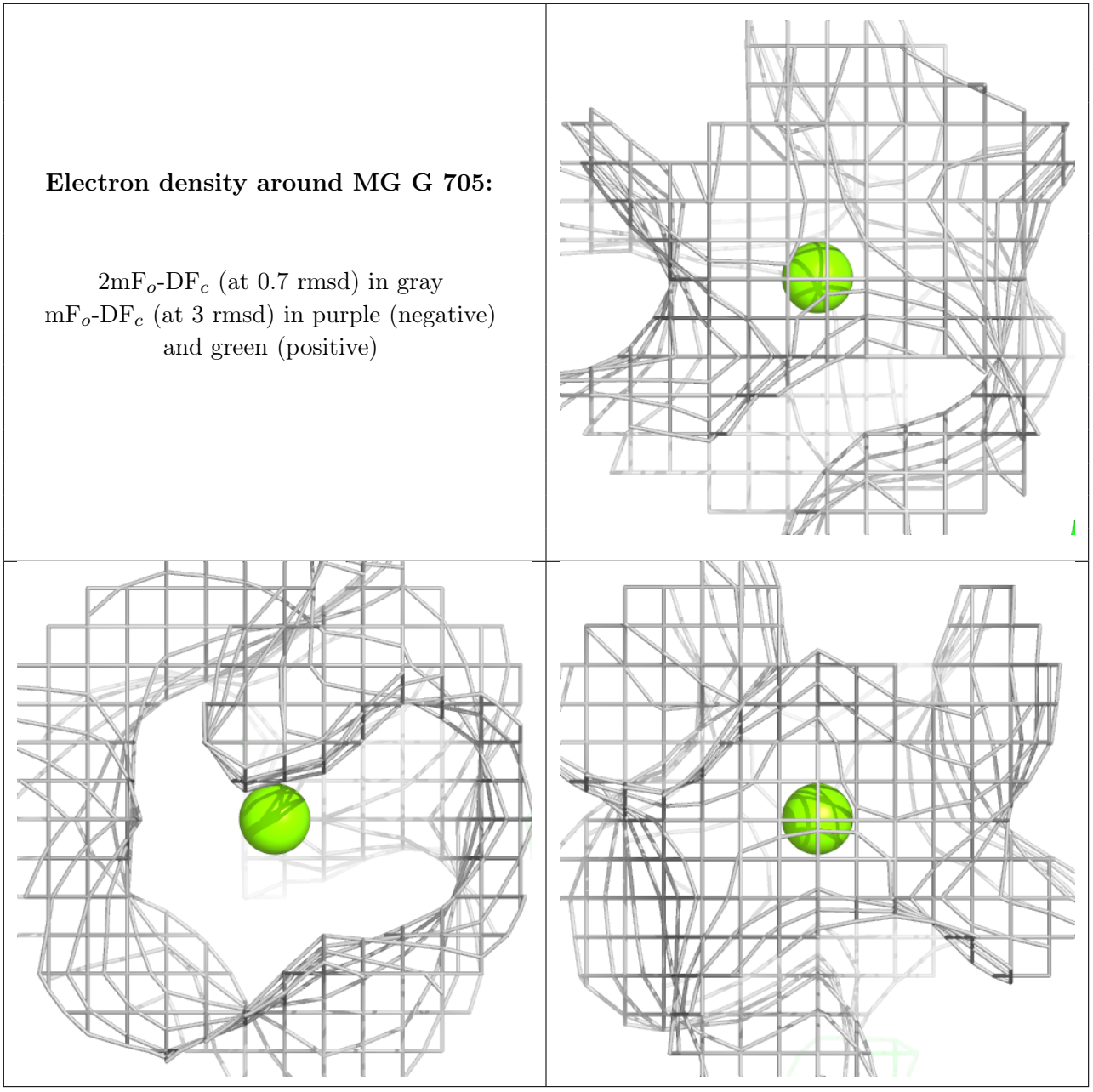






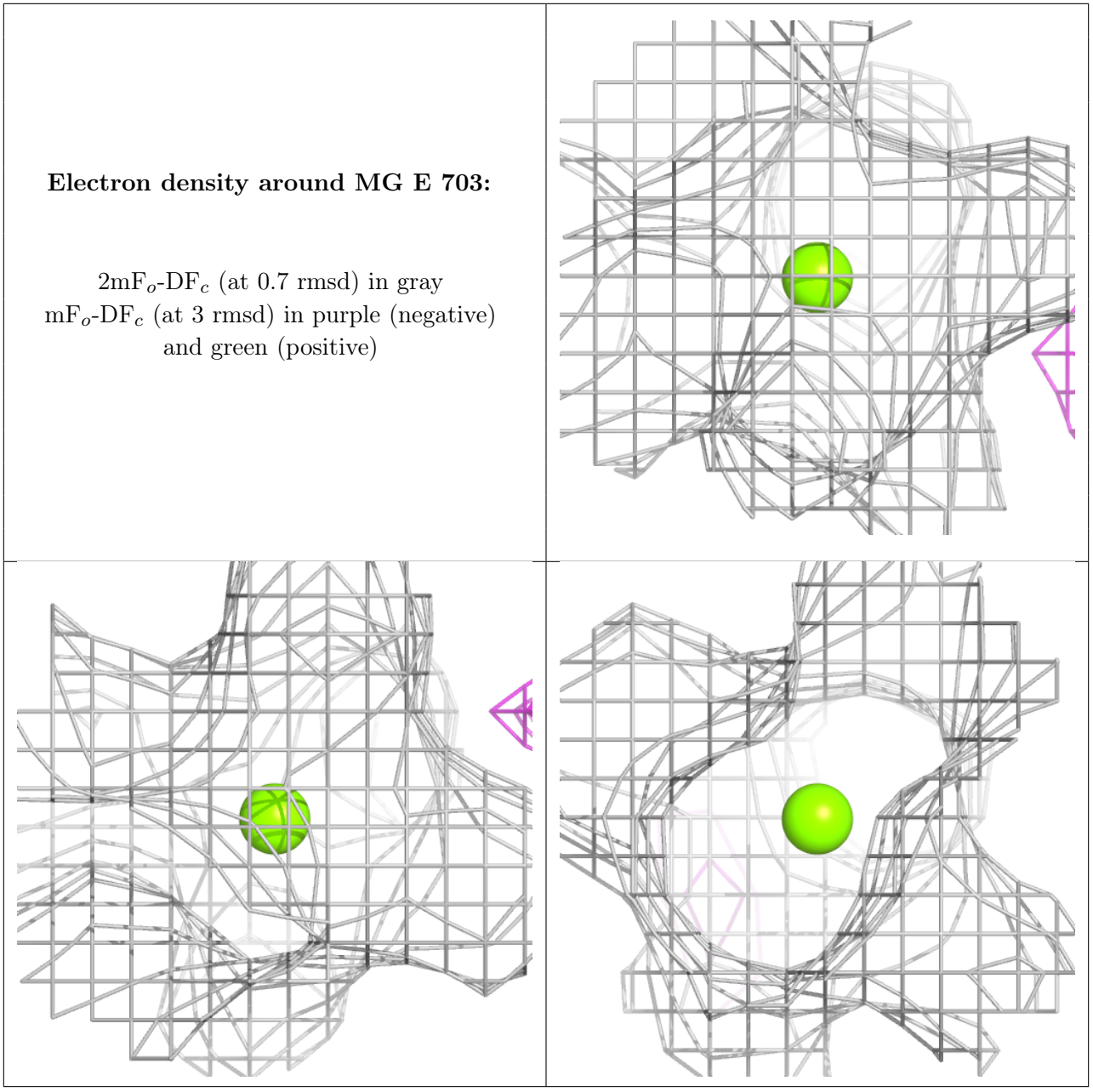
Electron density around MG G 705:

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



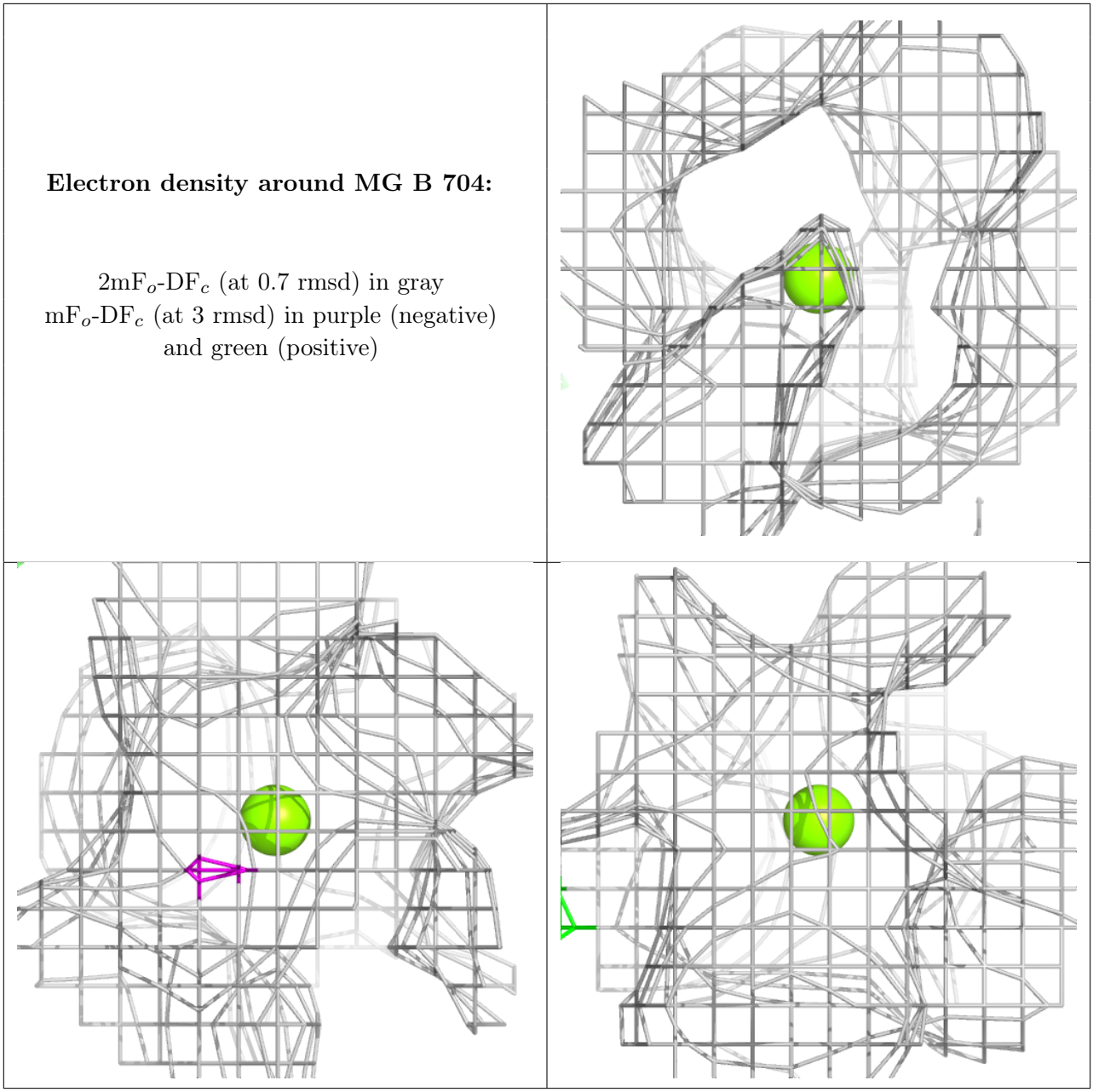
Electron density around MG E 703:

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



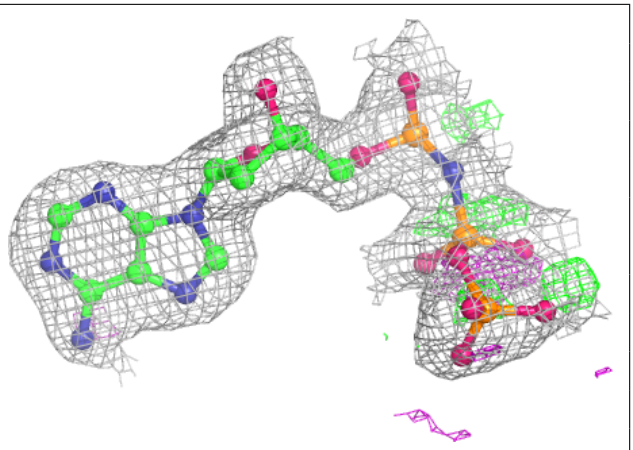
Electron density around MG B 704:

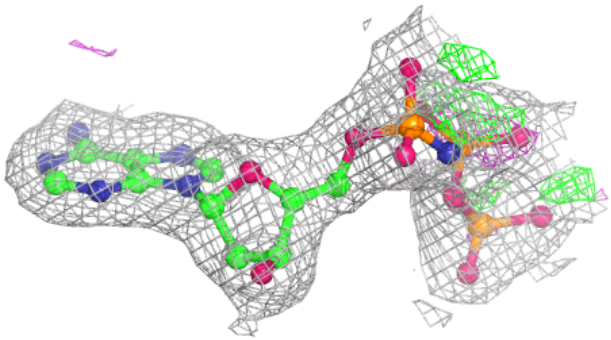
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

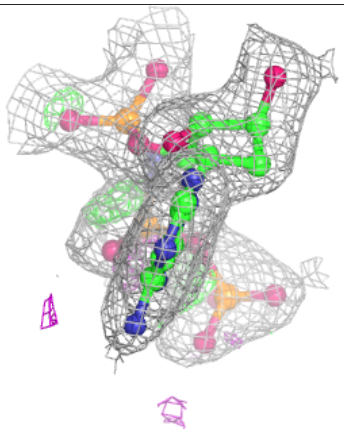


Electron density around DZ4 H 706:

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

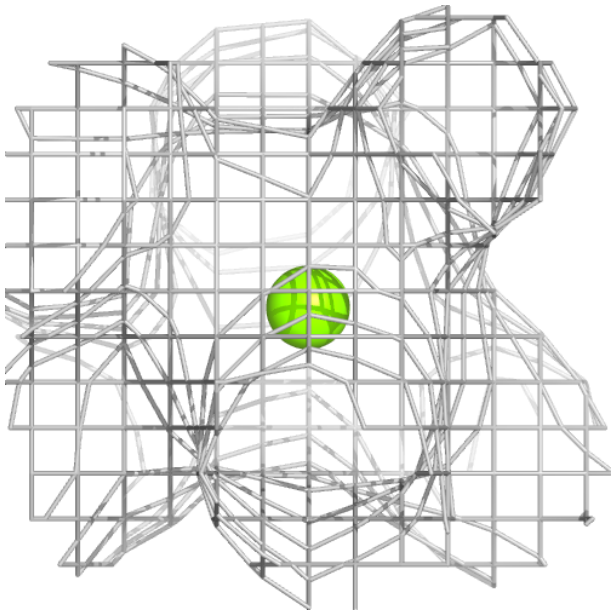


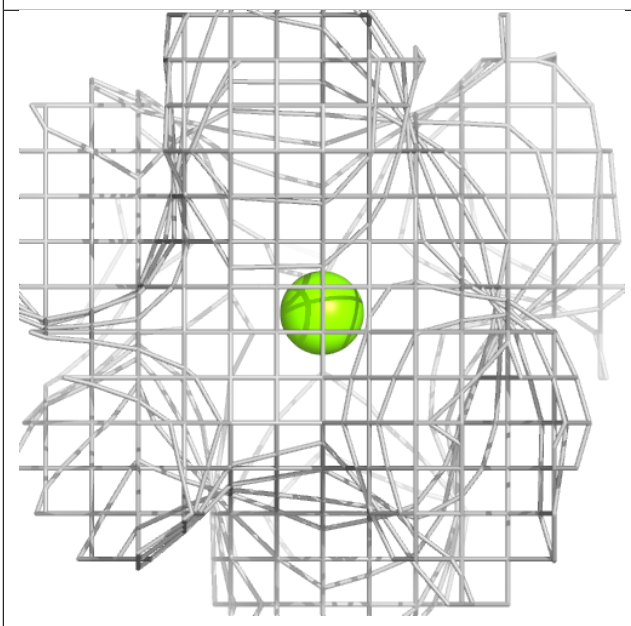


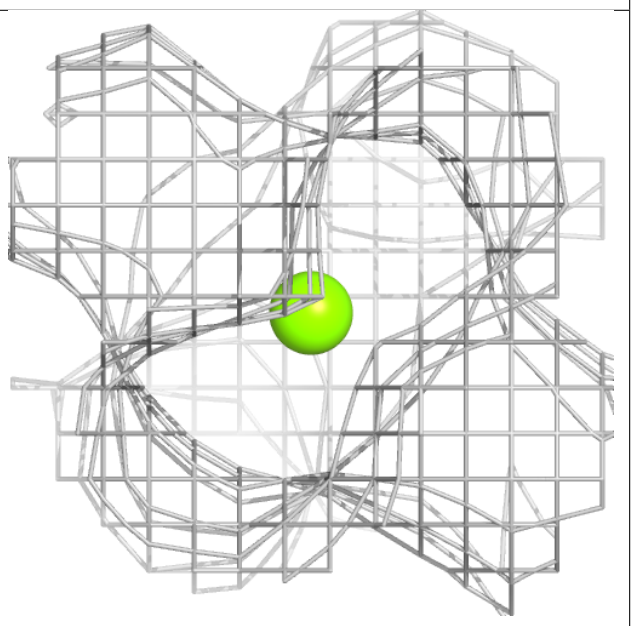


Electron density around MG F 703:

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

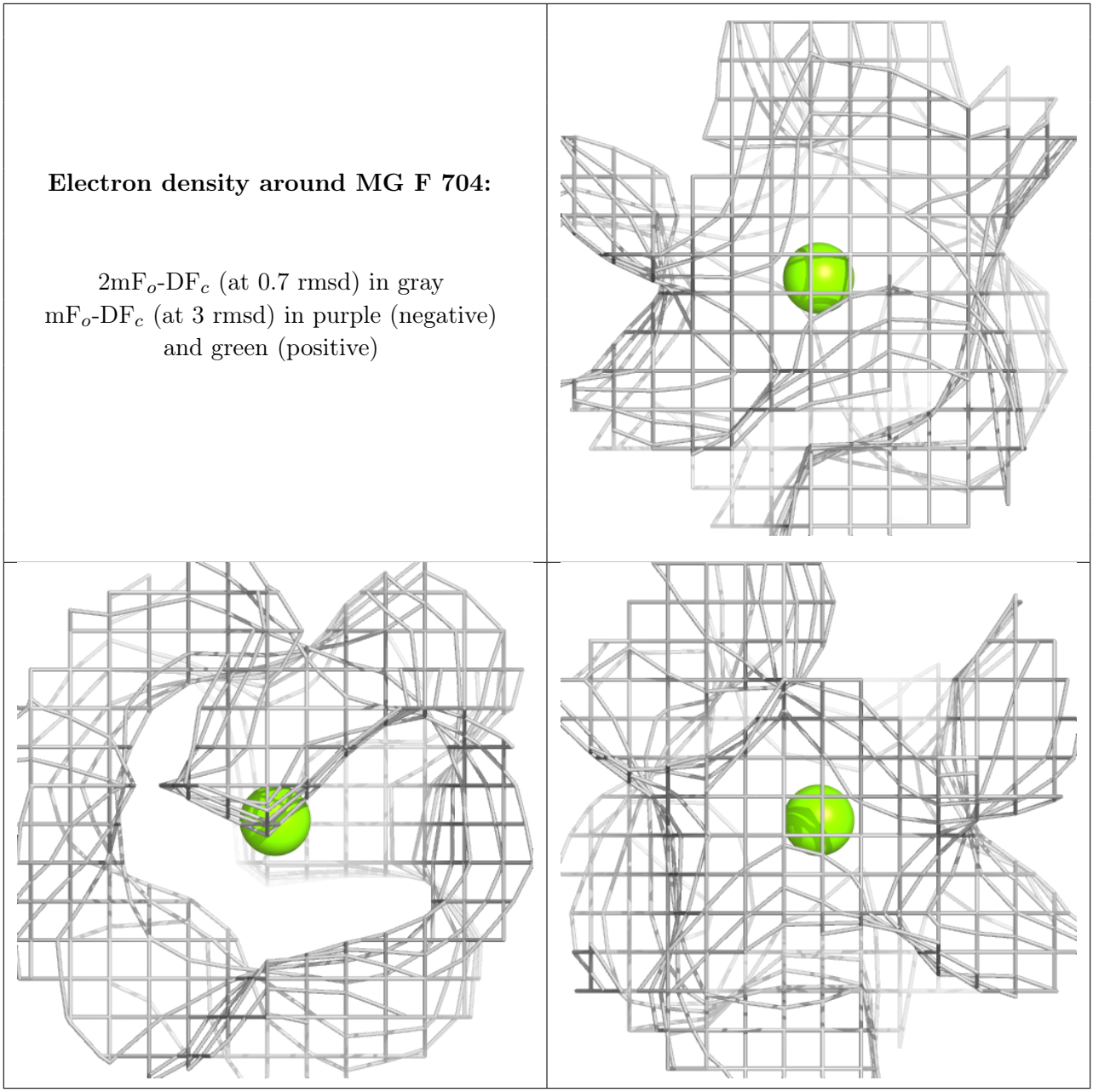






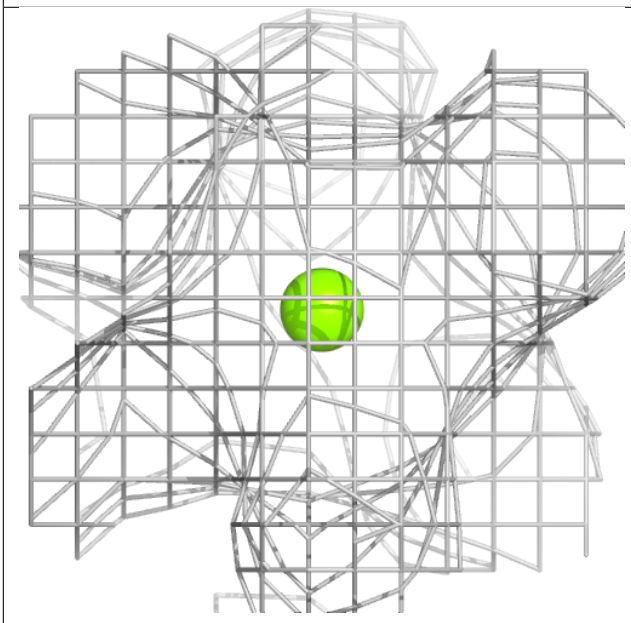
Electron density around MG F 704:

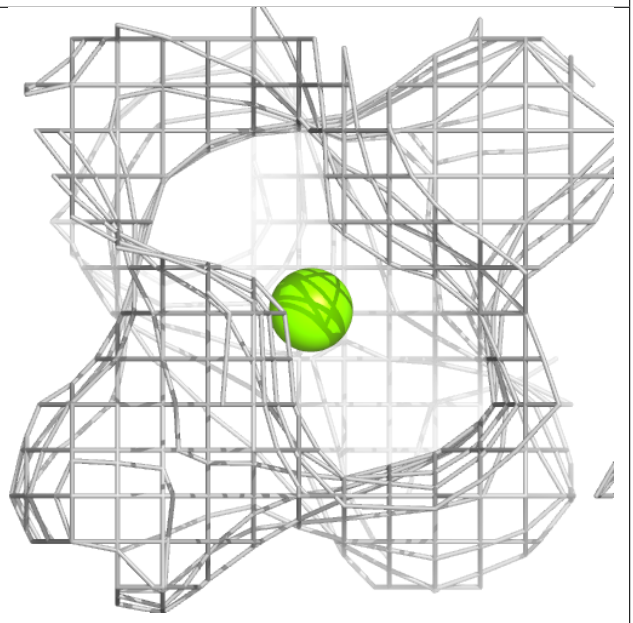
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around MG B 703:

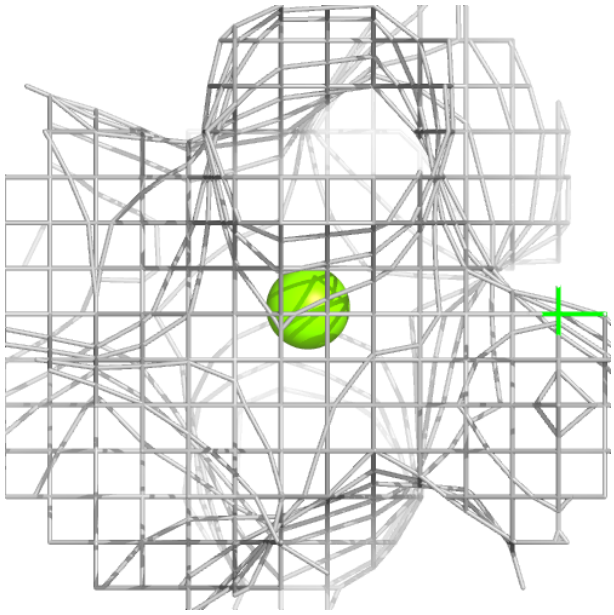
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

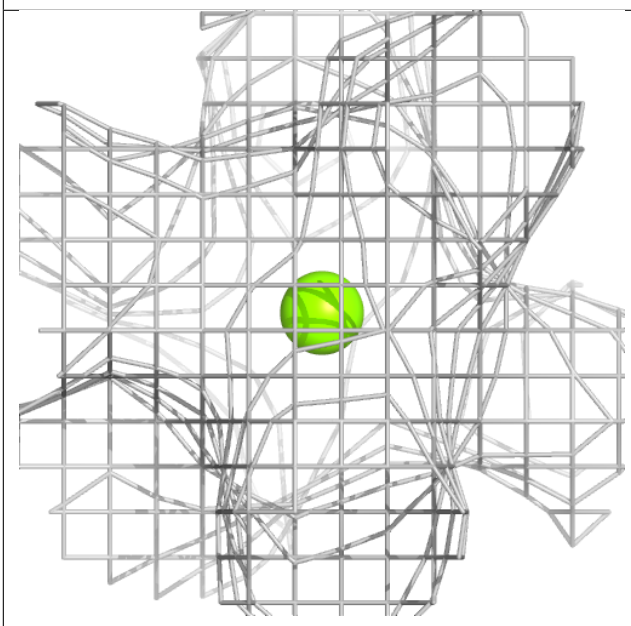


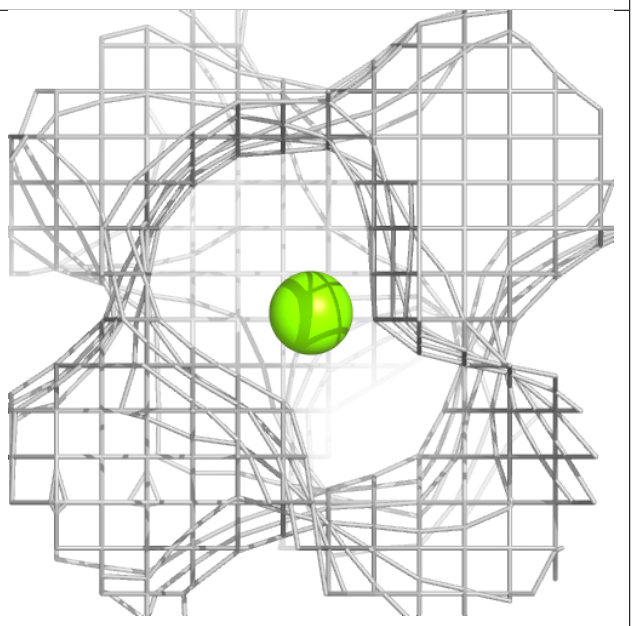


Electron density around MG D 704:

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

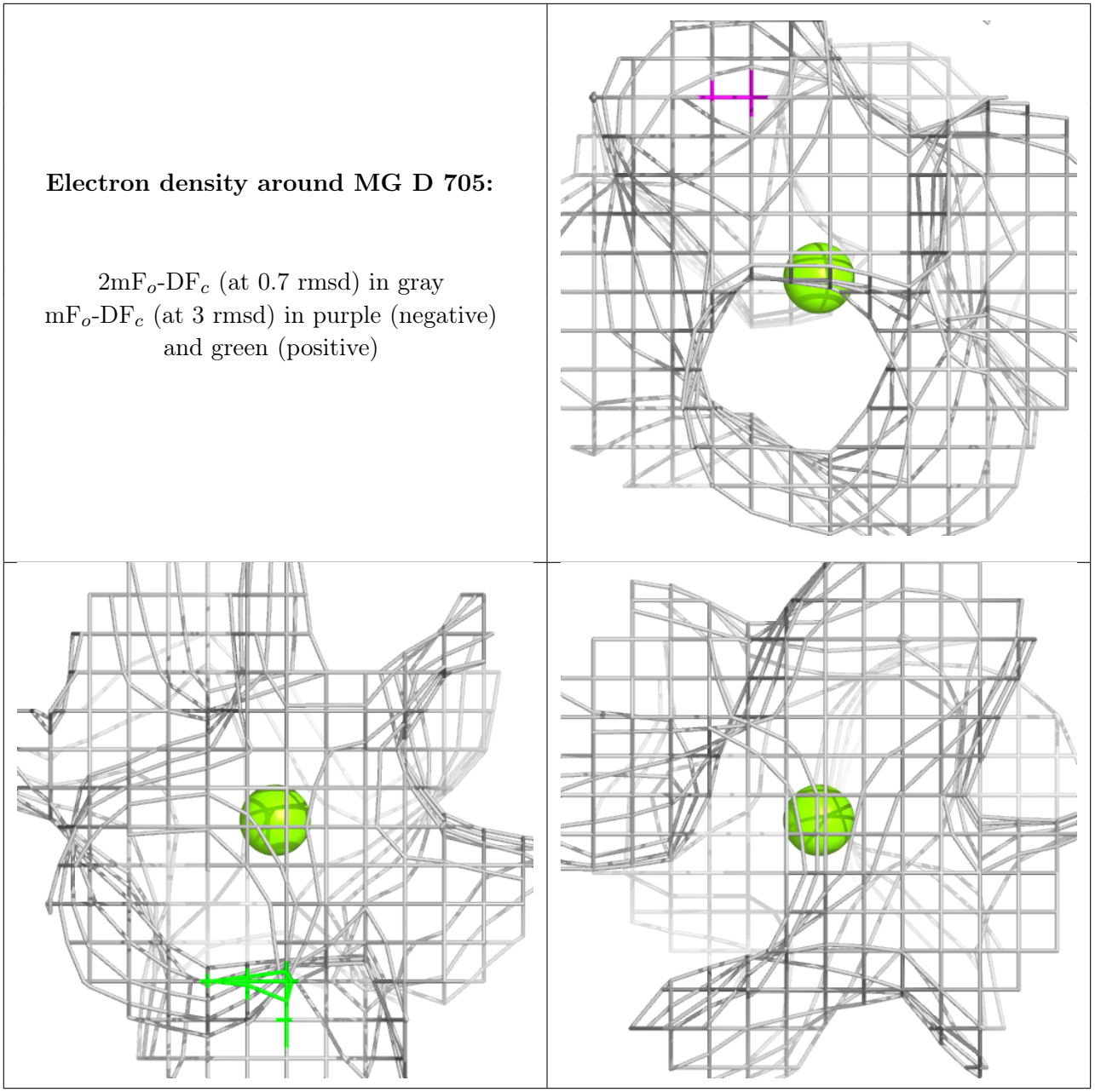






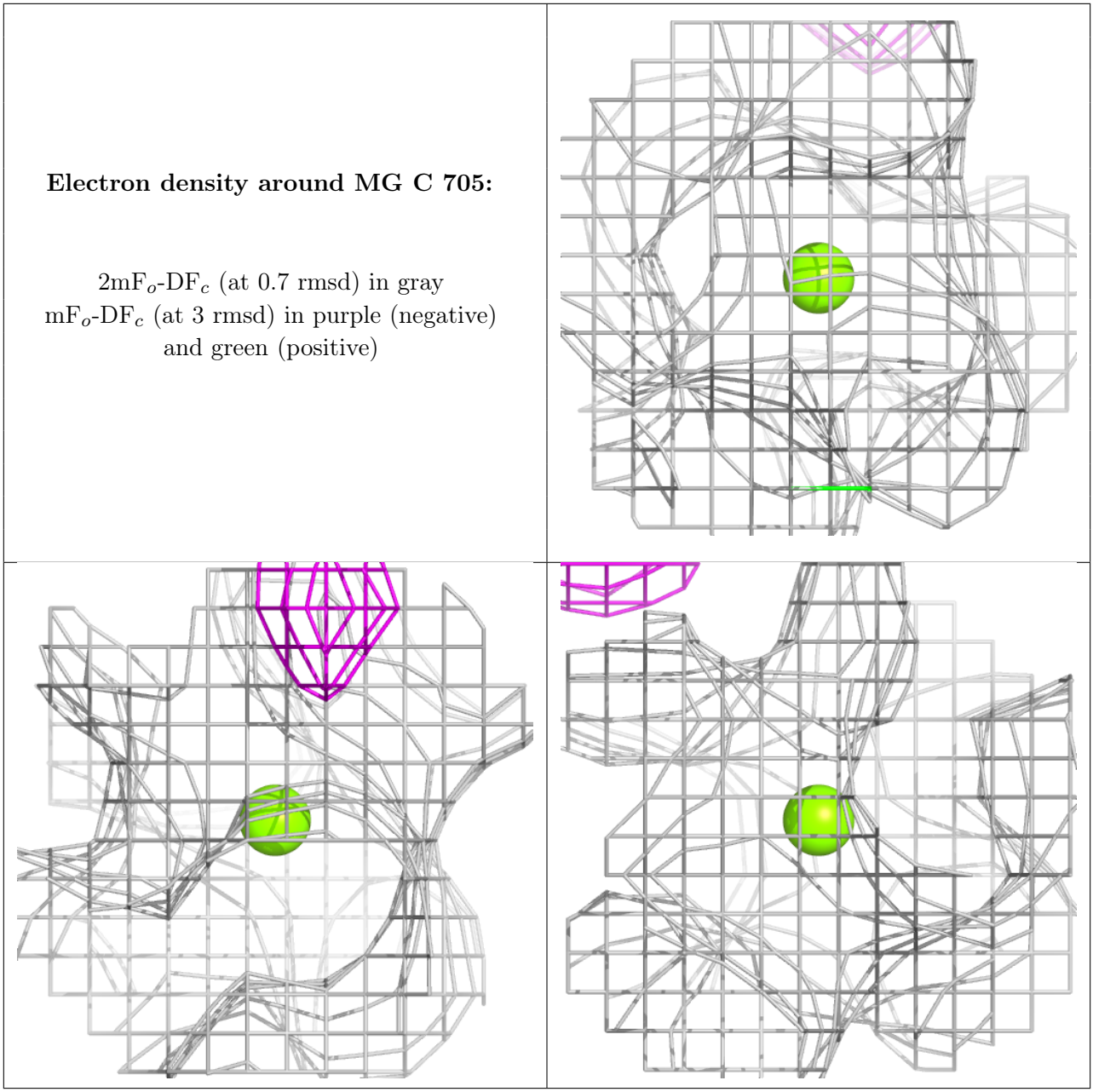
Electron density around MG D 705:

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



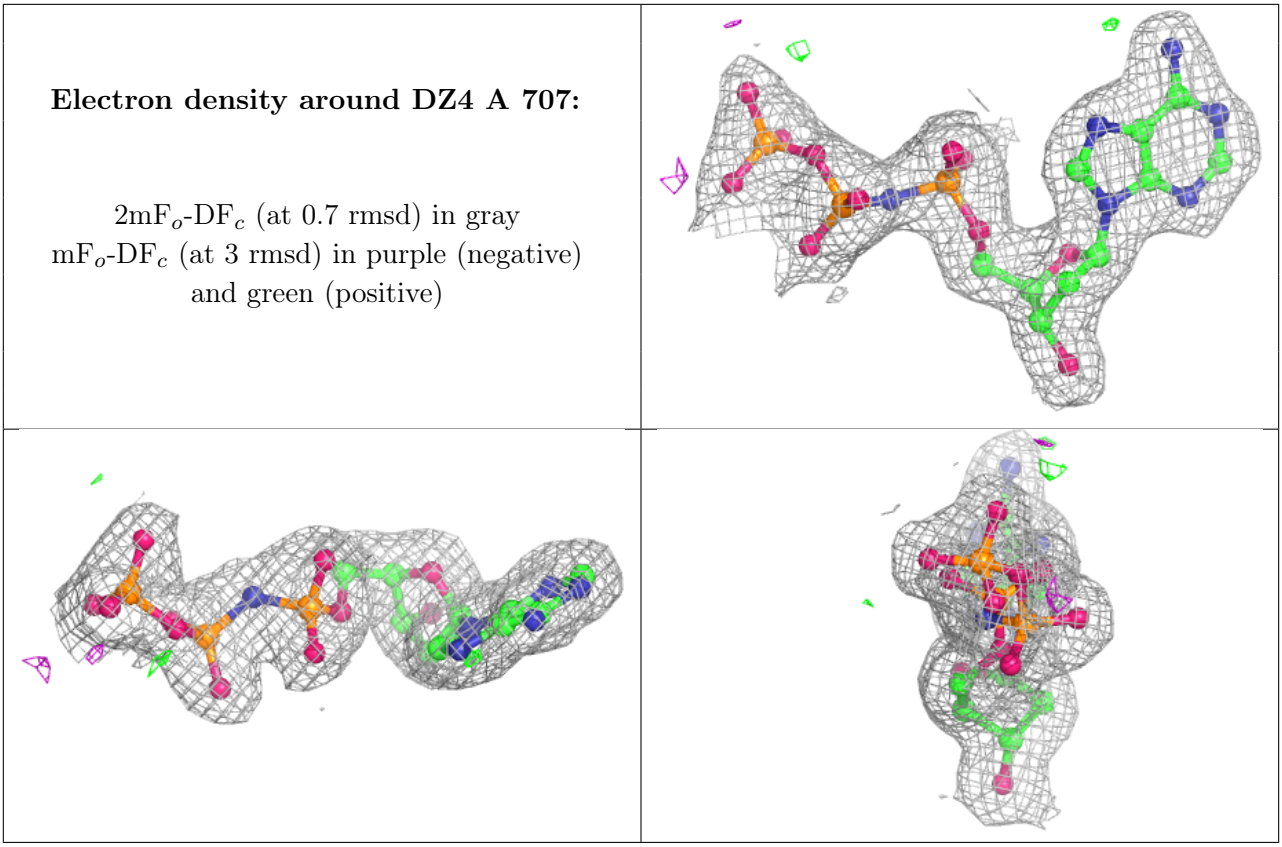
Electron density around MG C 705:

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



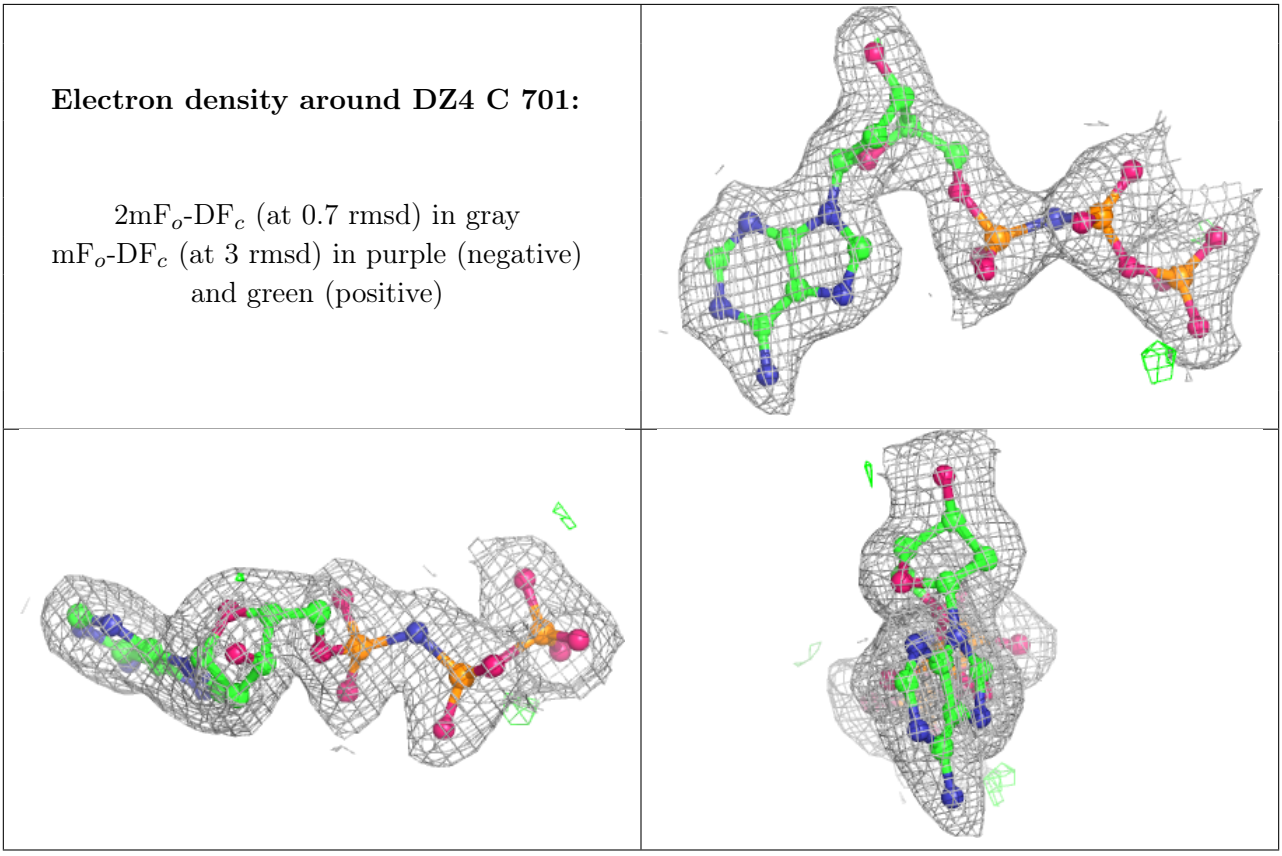
Electron density around DZ4 A 707:

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



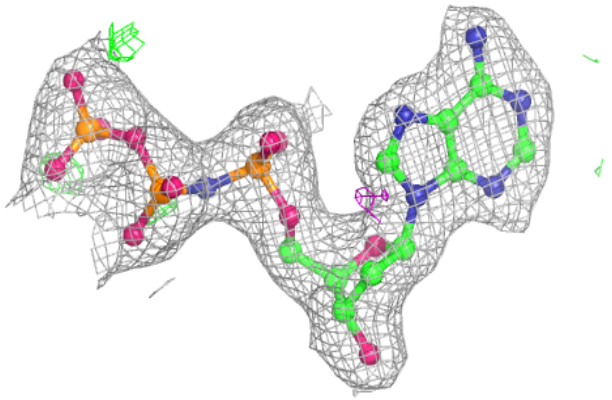
Electron density around DZ4 C 701:

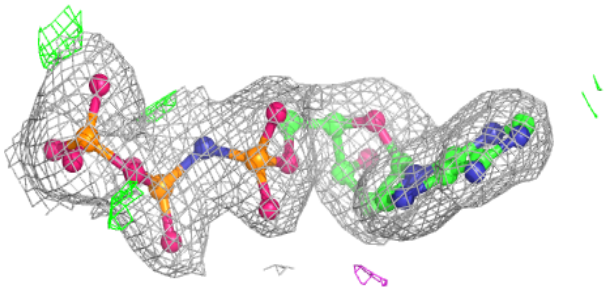
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

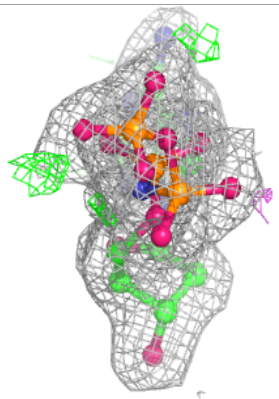


Electron density around DZ4 E 708:

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

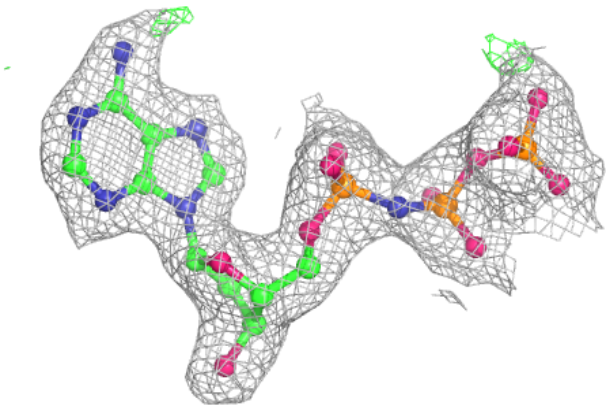


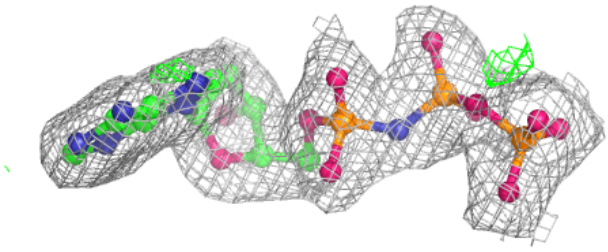


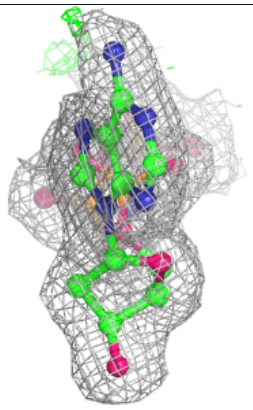


Electron density around DZ4 F 706:

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

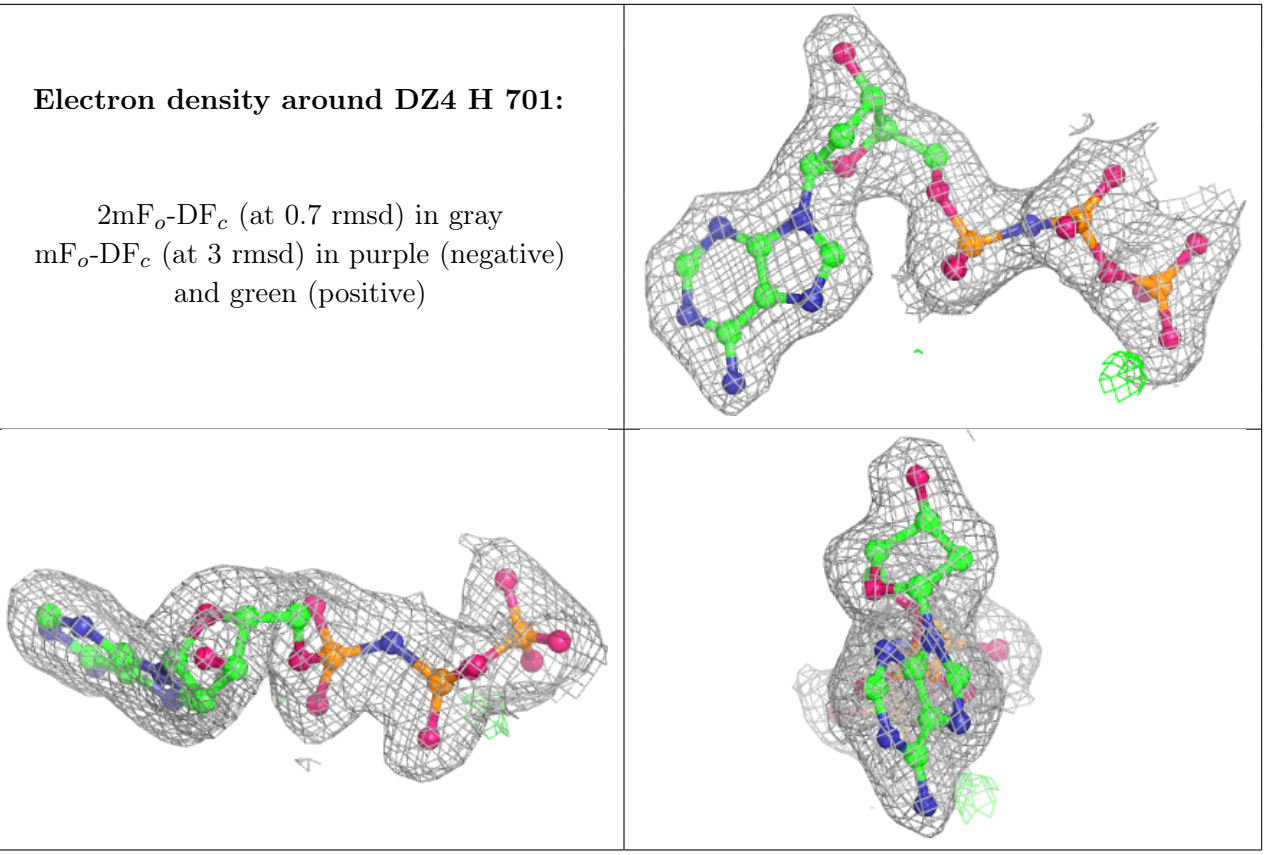






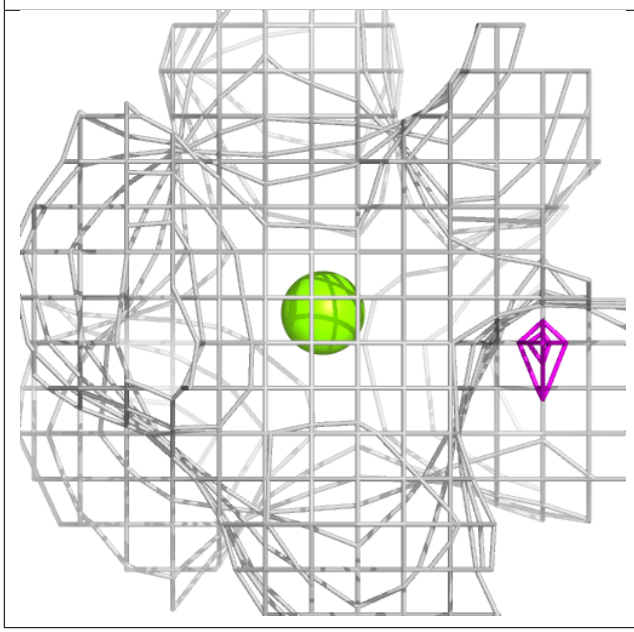
Electron density around DZ4 H 701:

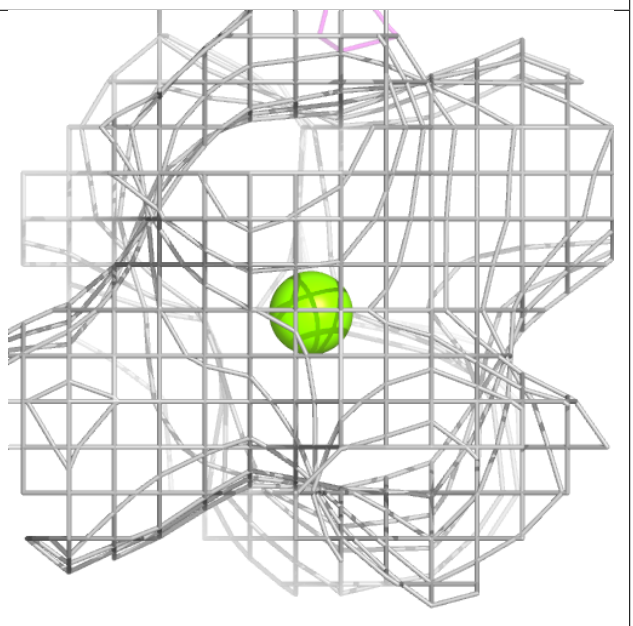
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around MG G 704:

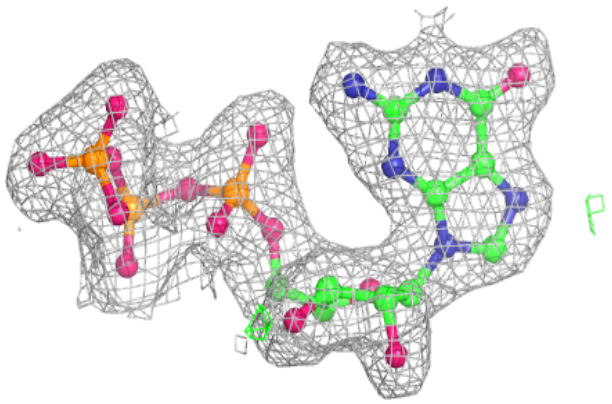
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

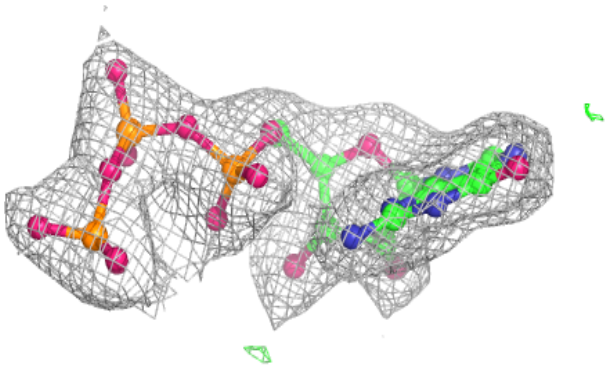


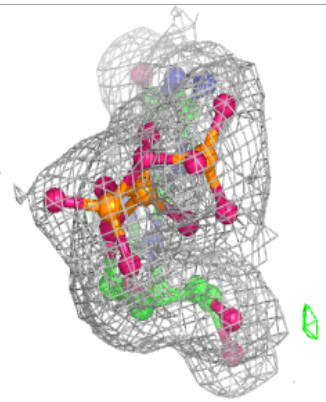


Electron density around GTP E 707:

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

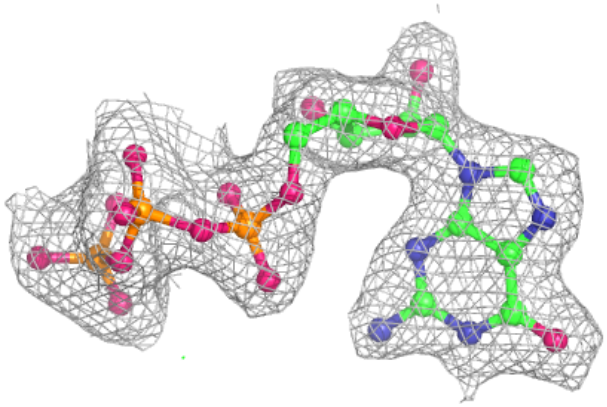


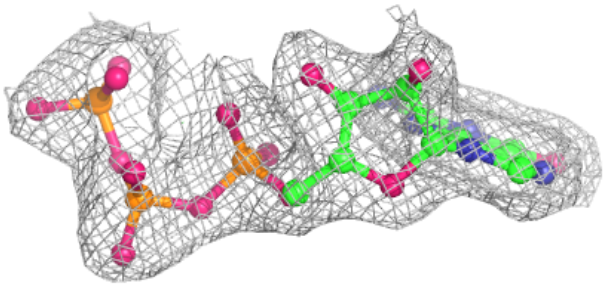


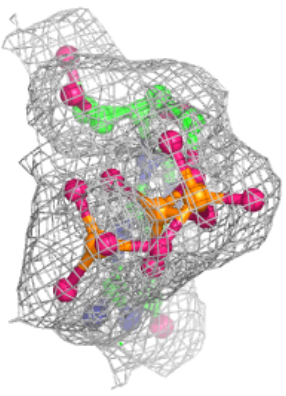


Electron density around GTP G 707:

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

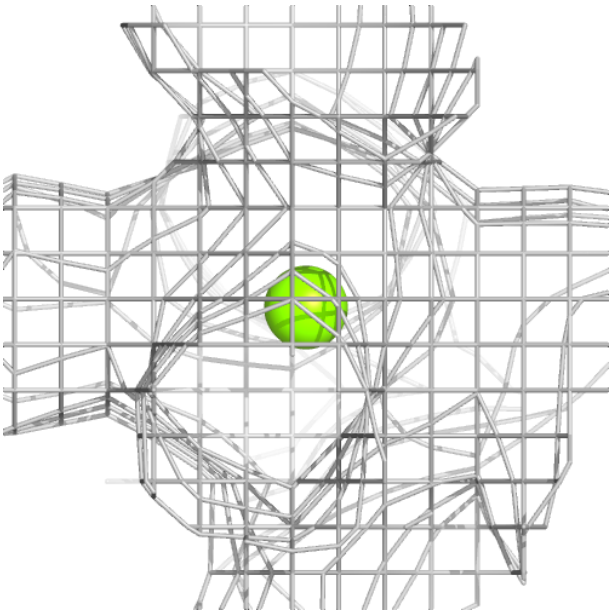


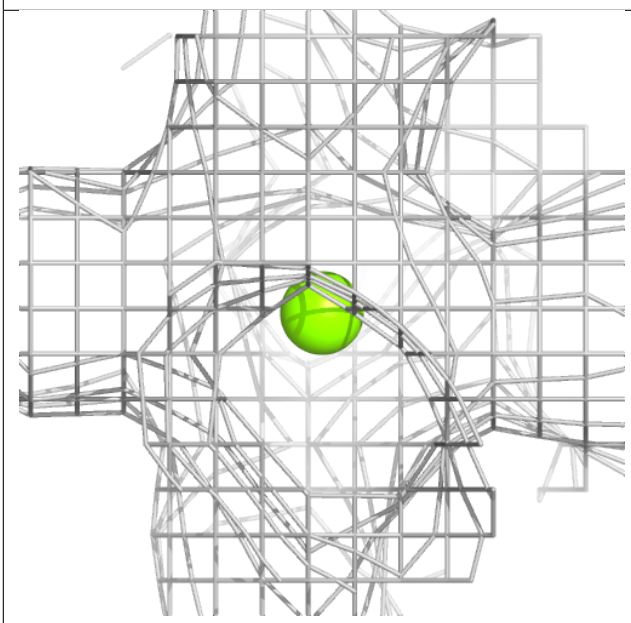


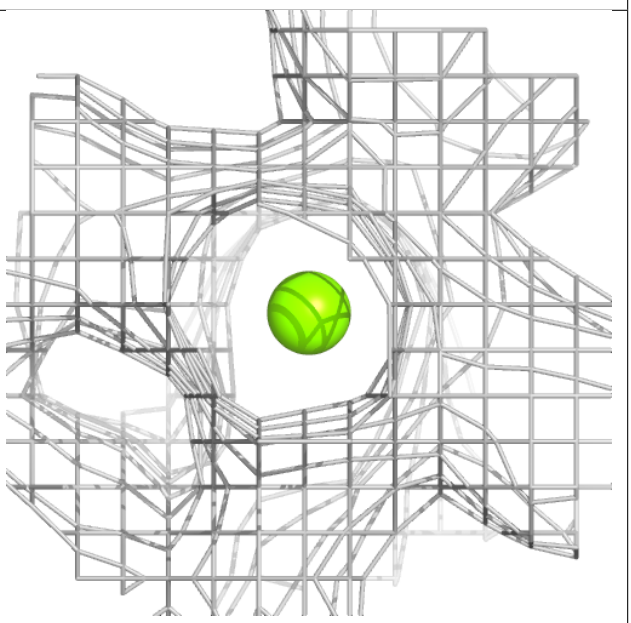


Electron density around MG E 702:

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

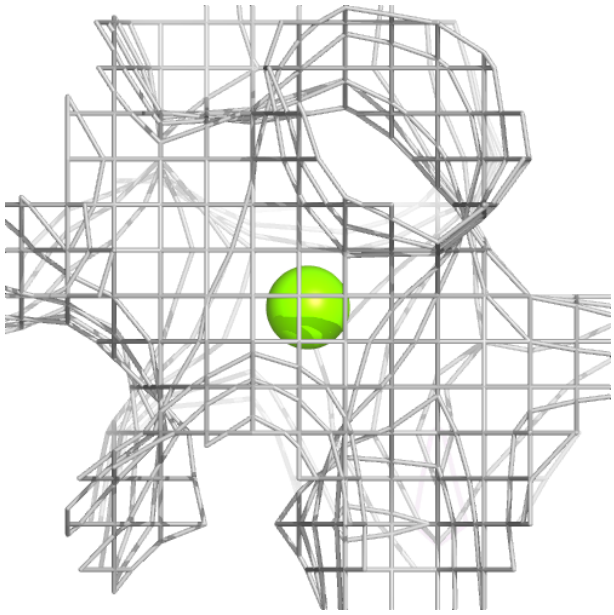


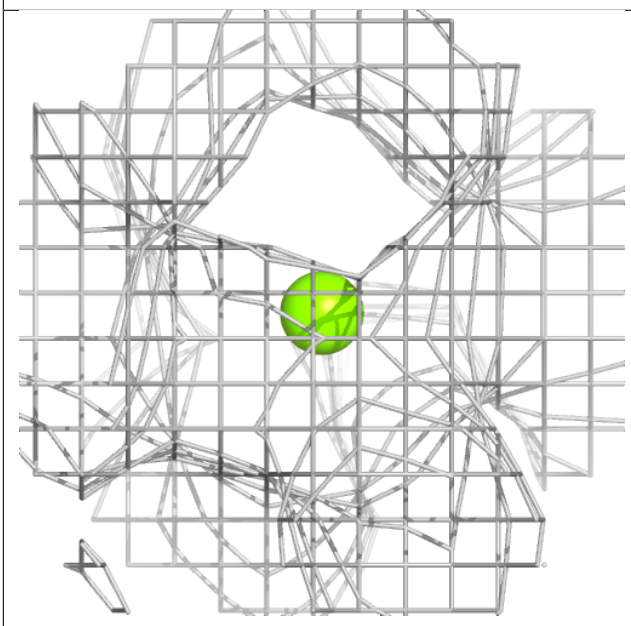


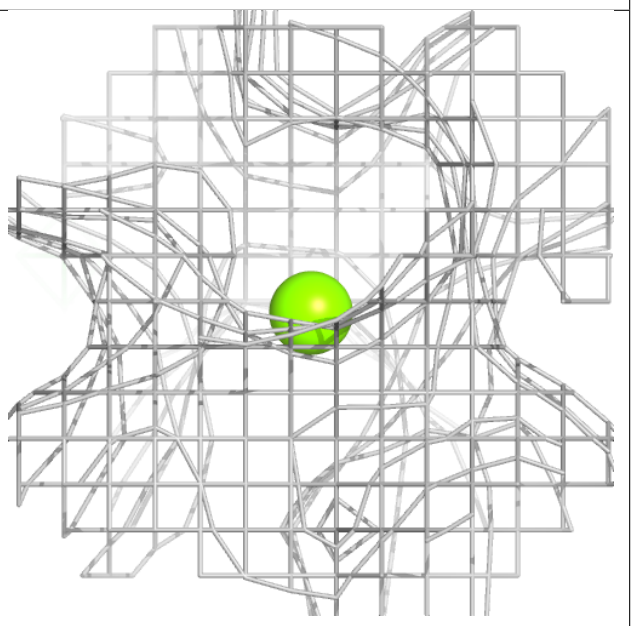


Electron density around MG H 705:

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

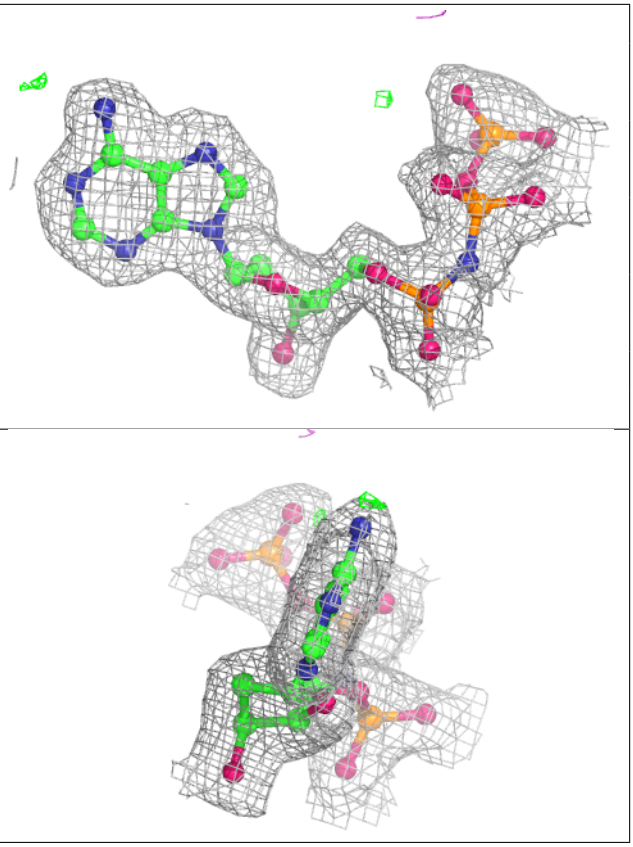






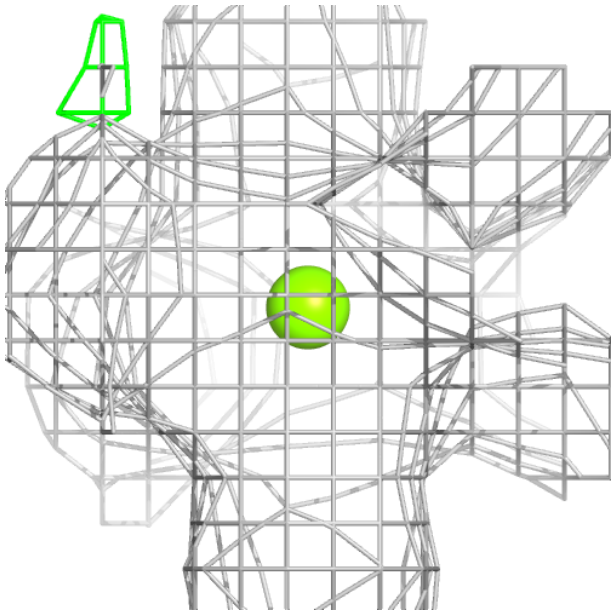
Electron density around DZ4 A 705:

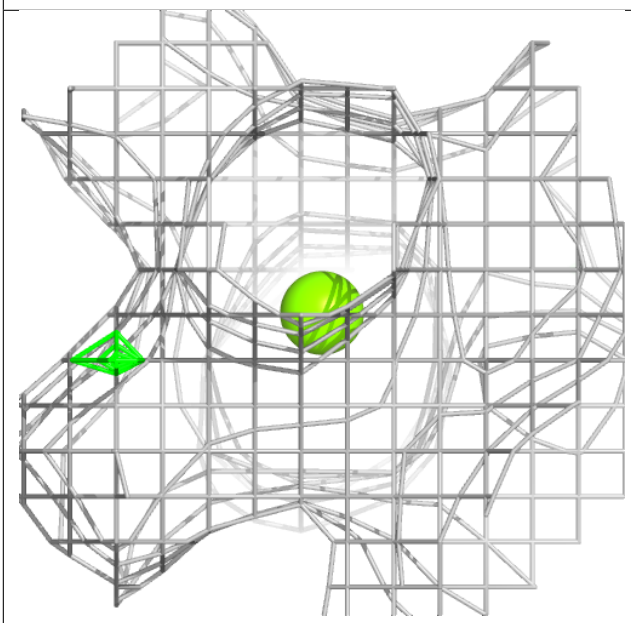
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

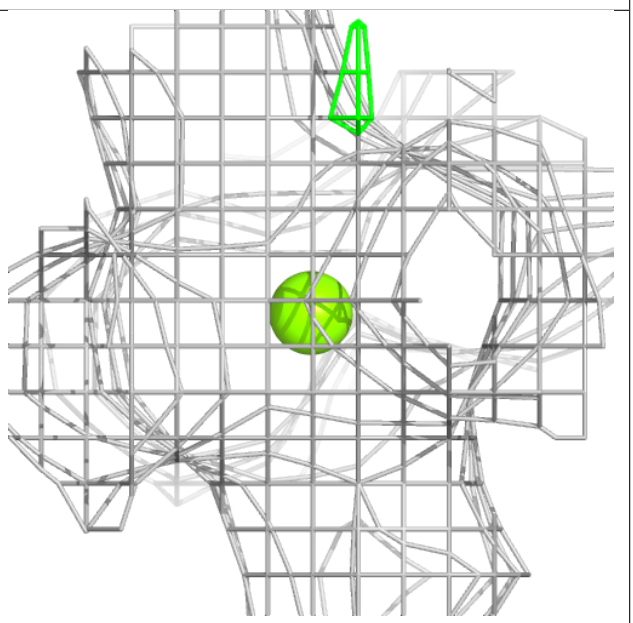


Electron density around MG C 704:

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

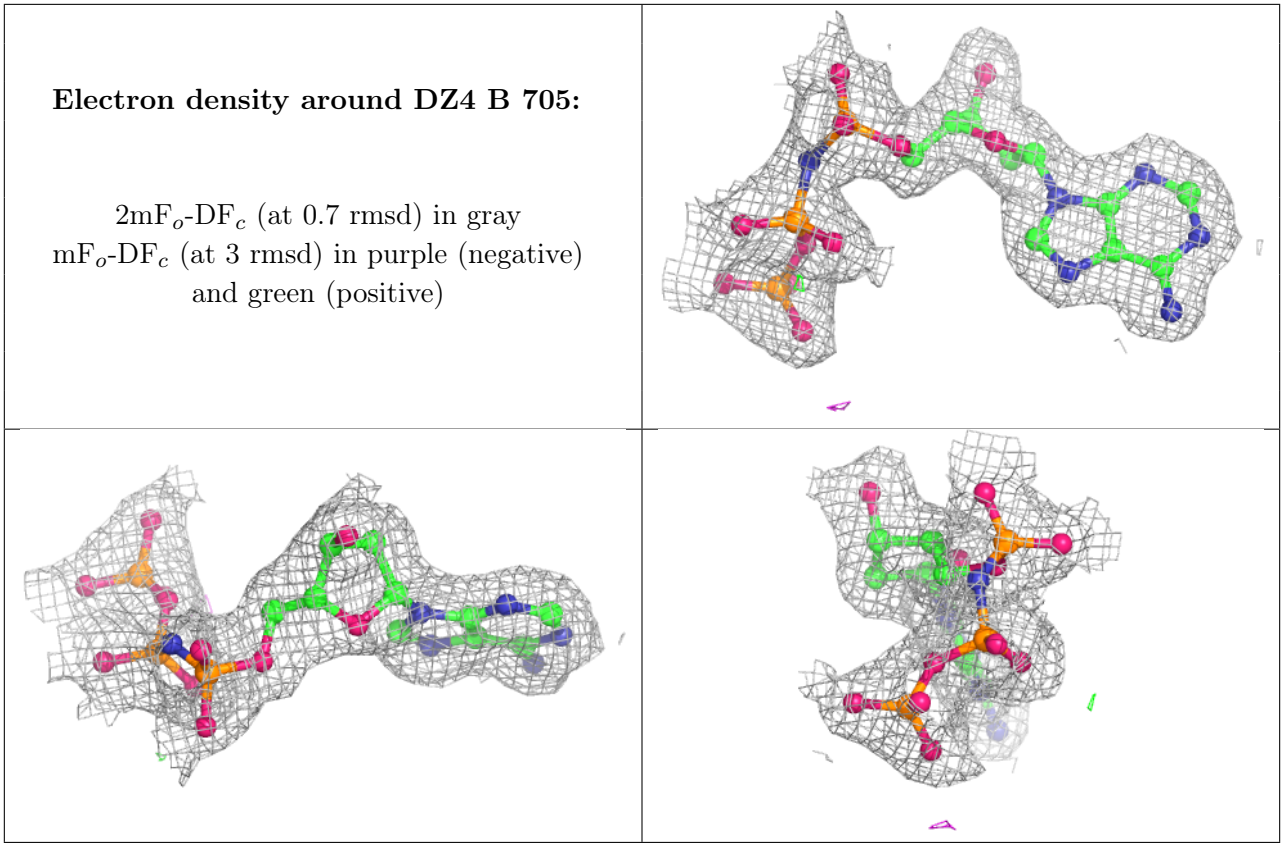






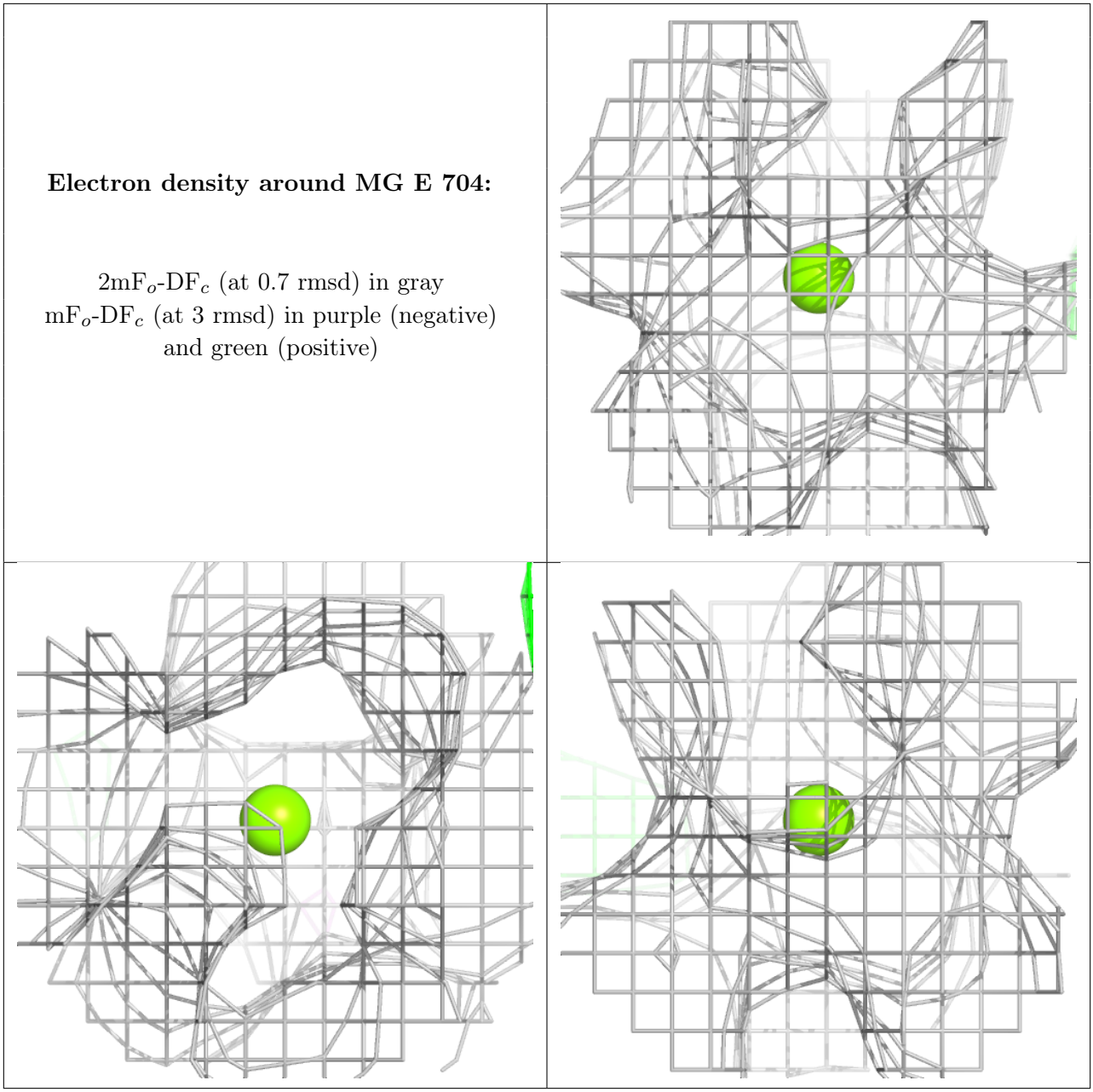
Electron density around DZ4 B 705:

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



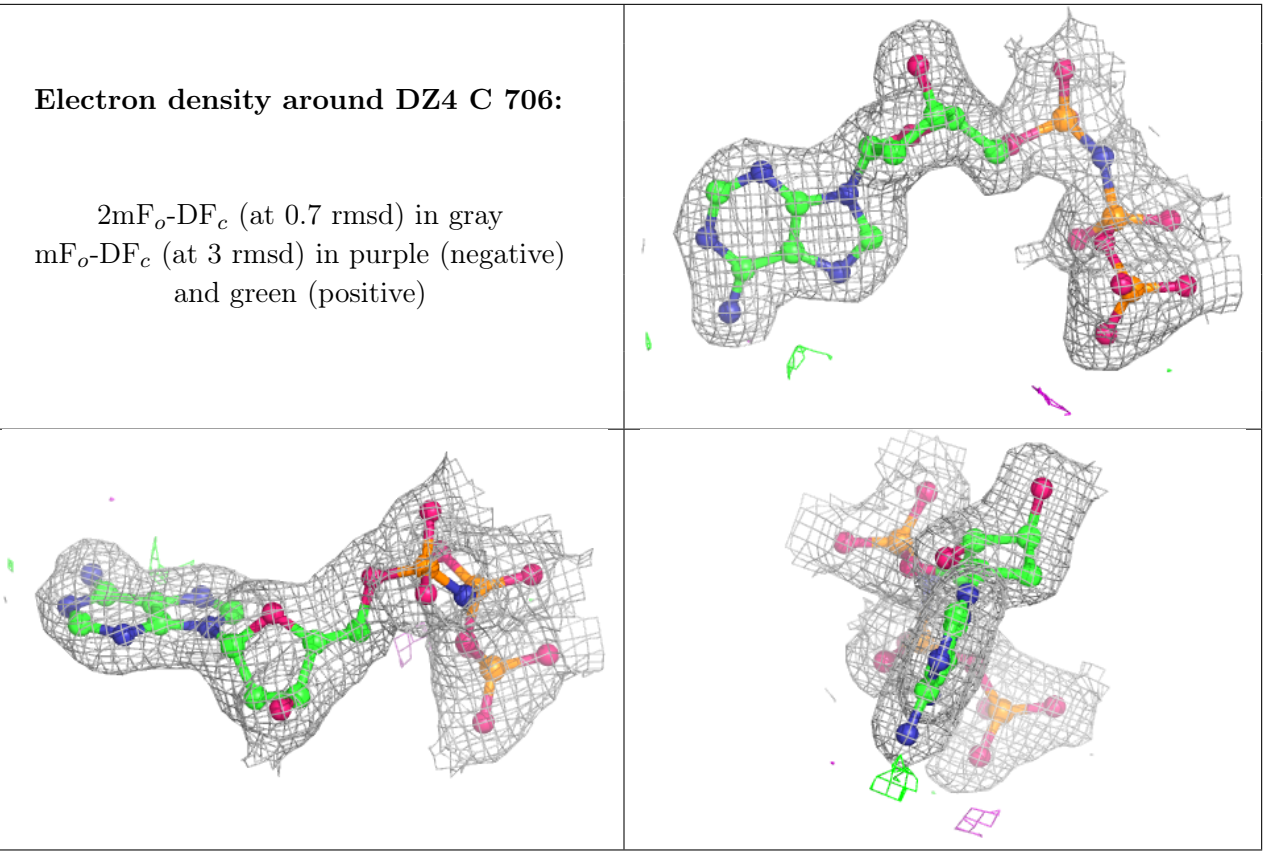
Electron density around MG E 704:

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



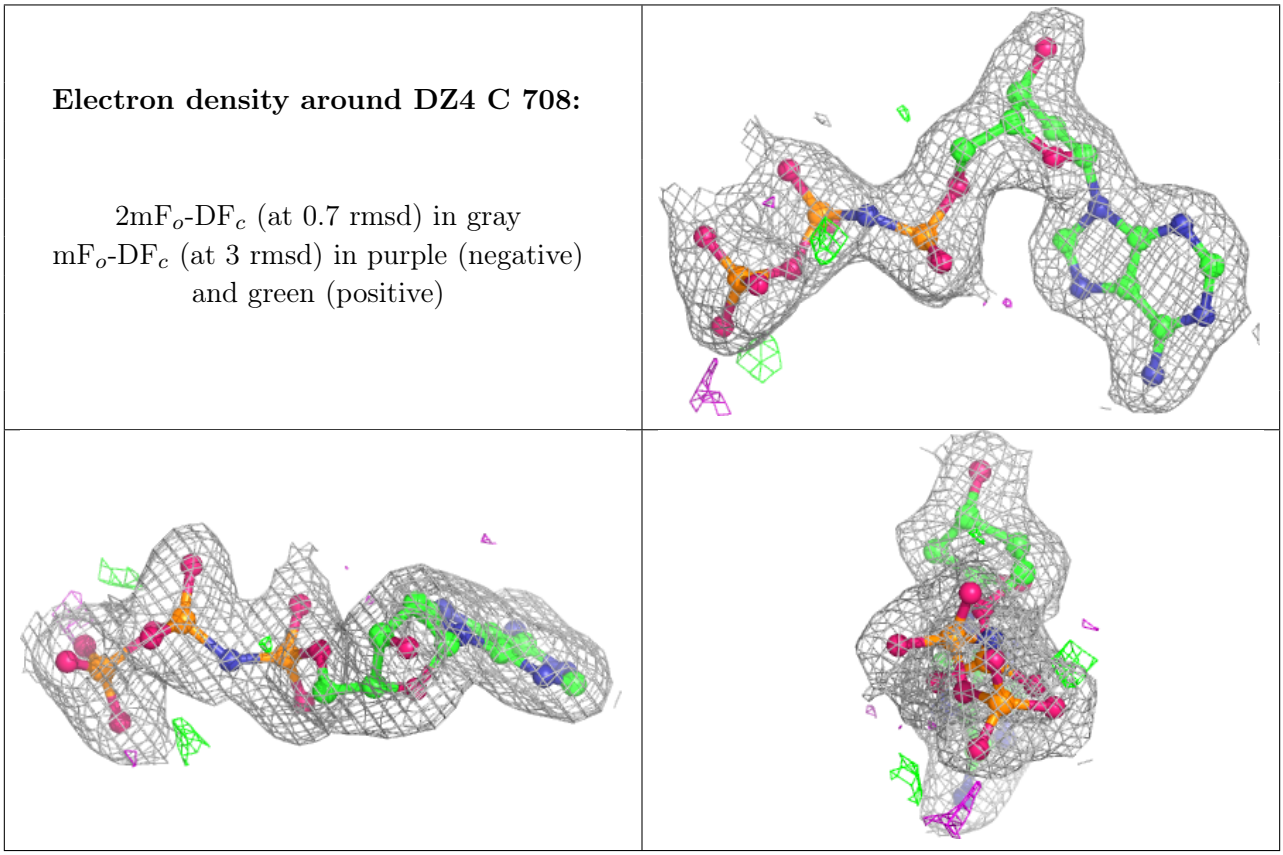
Electron density around DZ4 C 706:

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



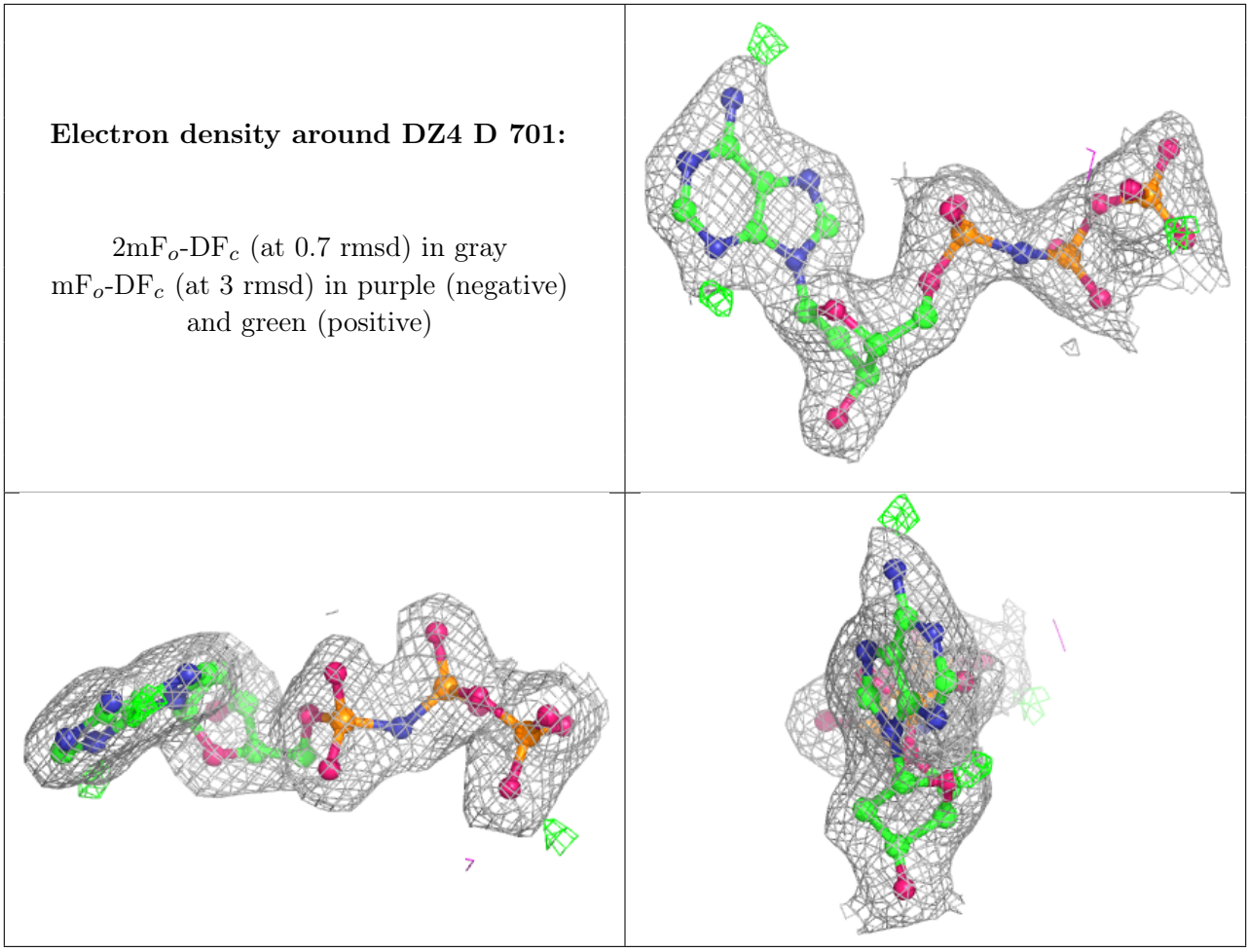
Electron density around DZ4 C 708:

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



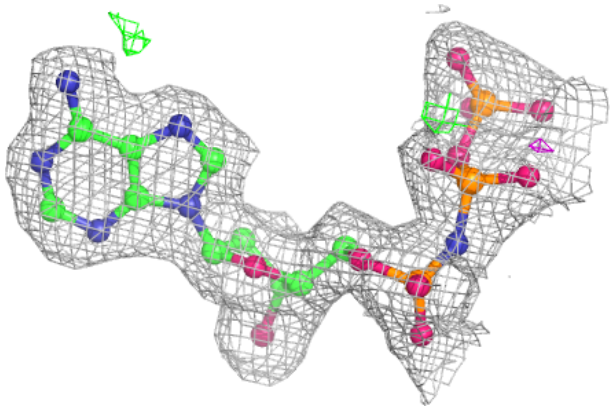
Electron density around DZ4 D 701:

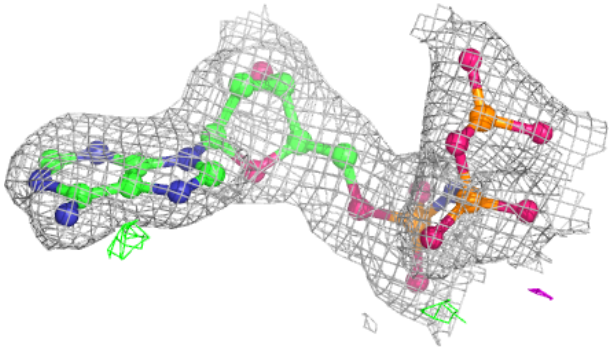
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

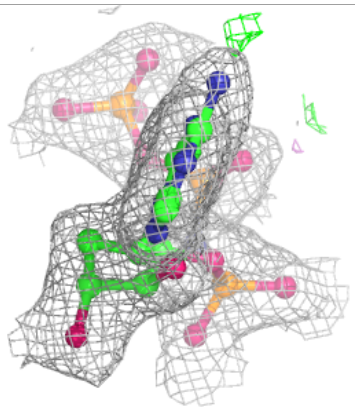


Electron density around DZ4 D 706:

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

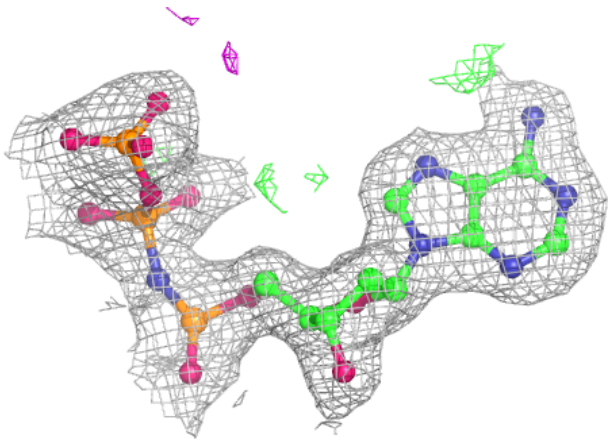


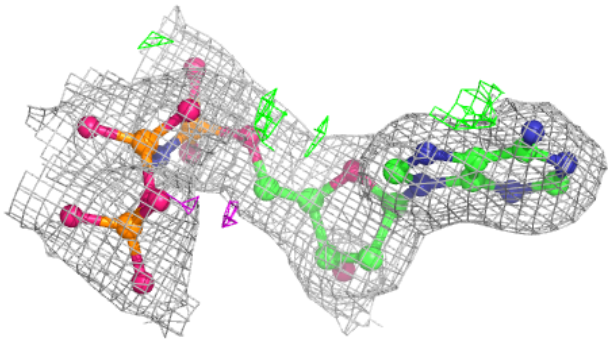


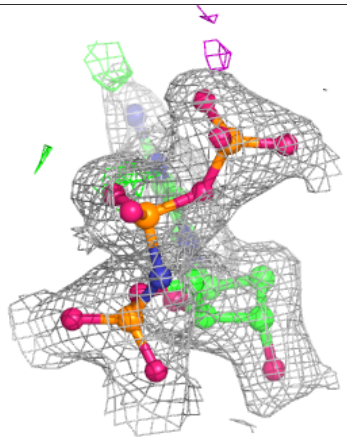


Electron density around DZ4 E 705:

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

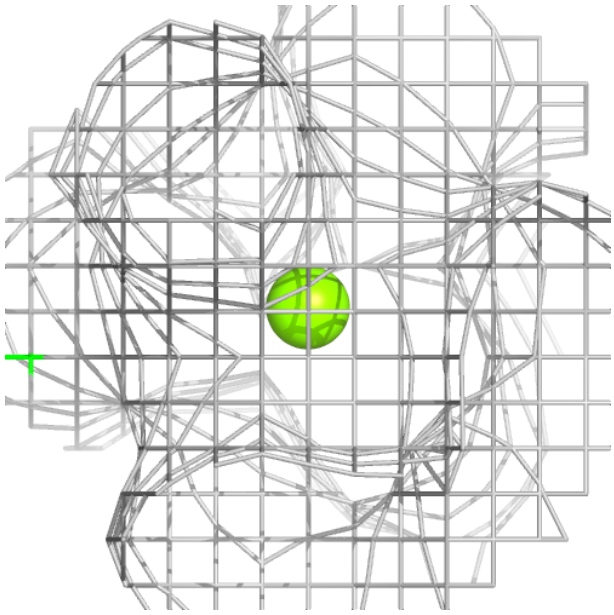


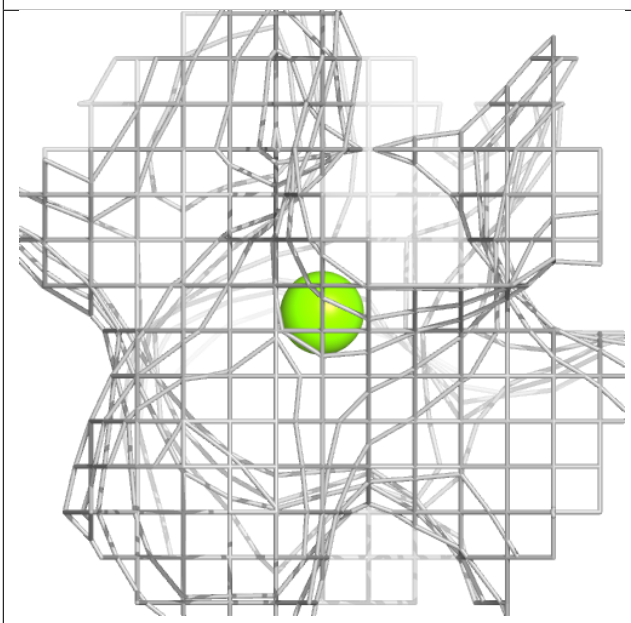




Electron density around MG A 704:

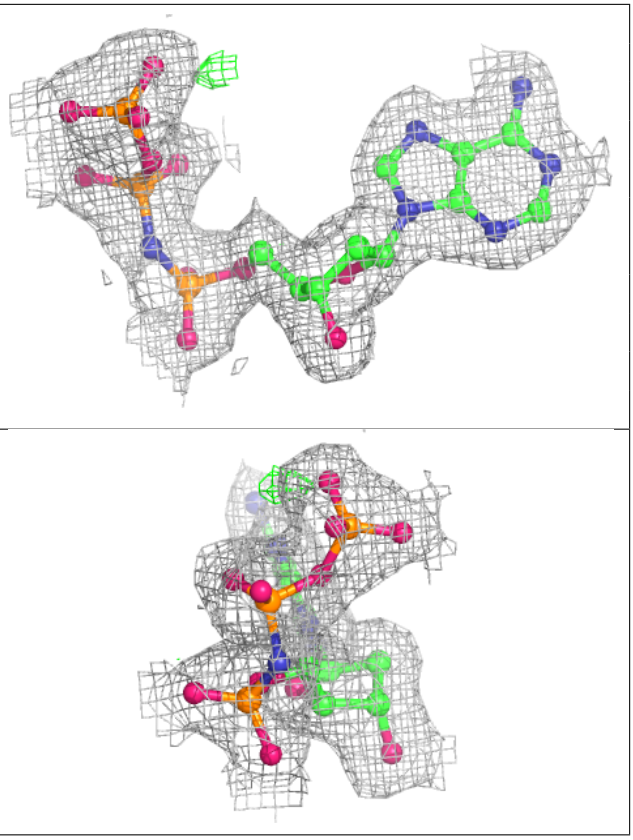
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





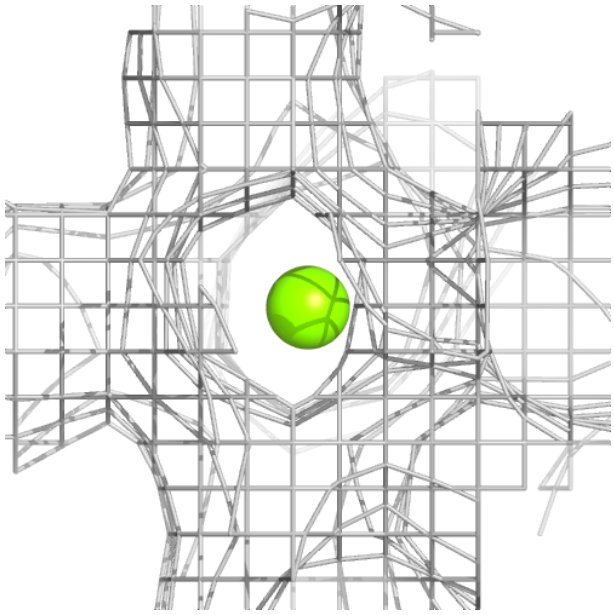
Electron density around DZ4 F 705:

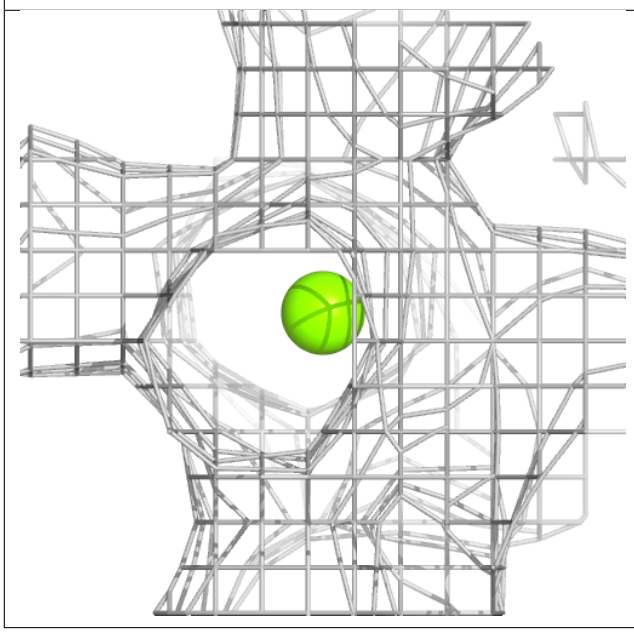
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

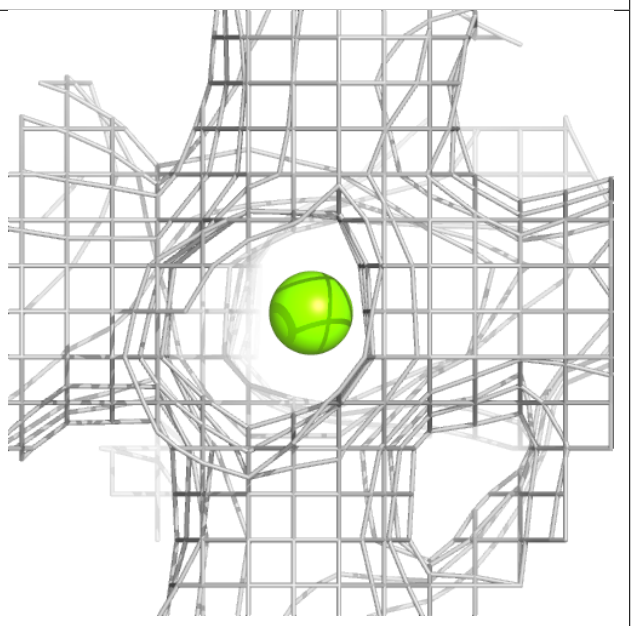


Electron density around MG D 703:

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

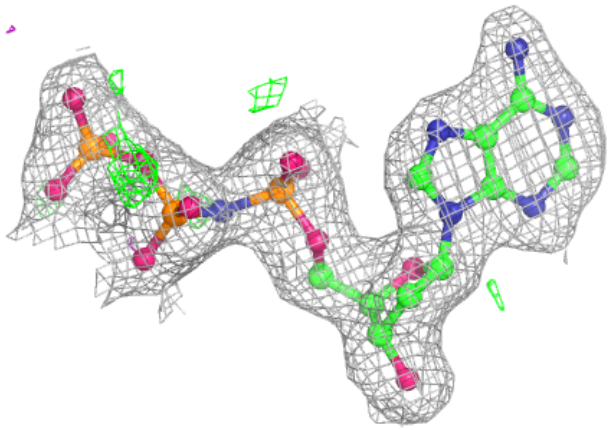


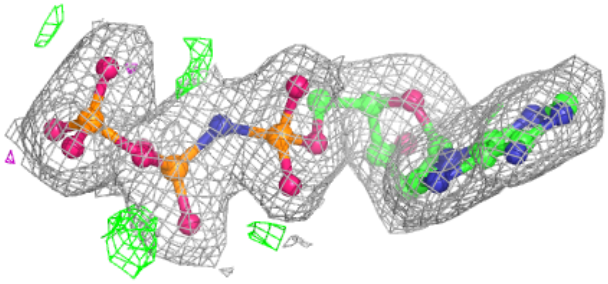


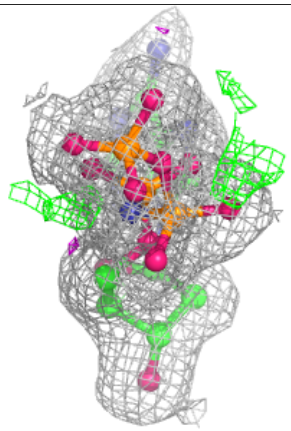


Electron density around DZ4 G 701:

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

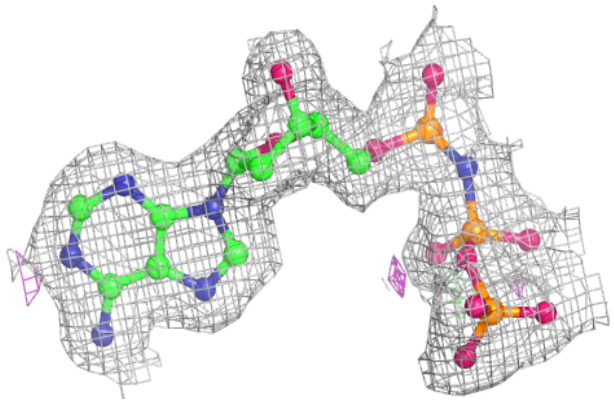


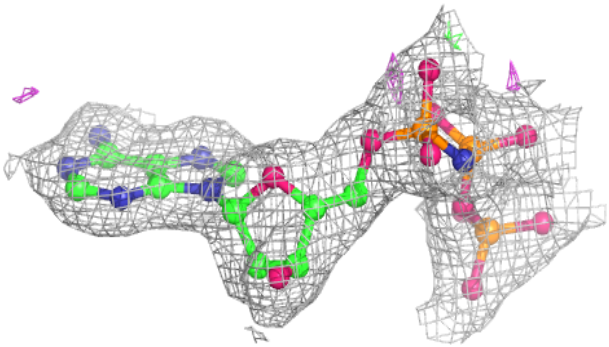




Electron density around DZ4 G 706:

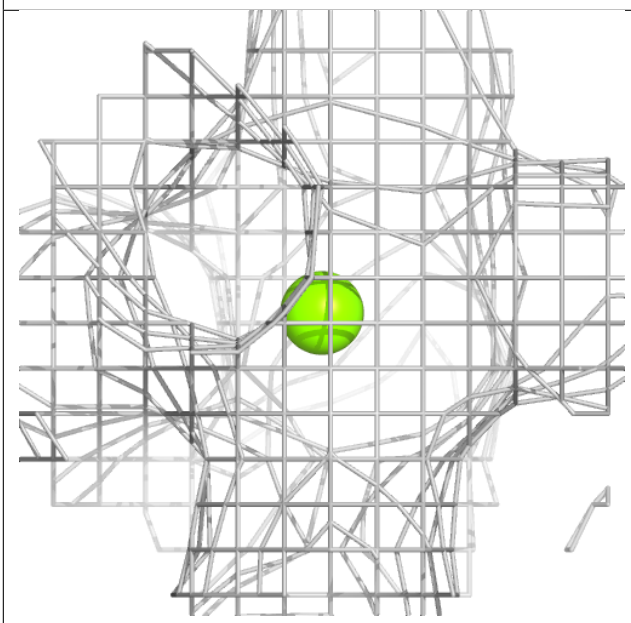
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

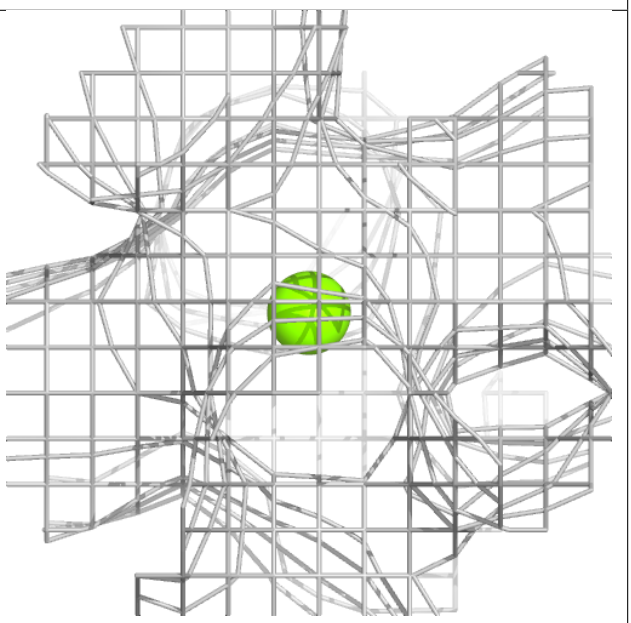




Electron density around MG G 703:

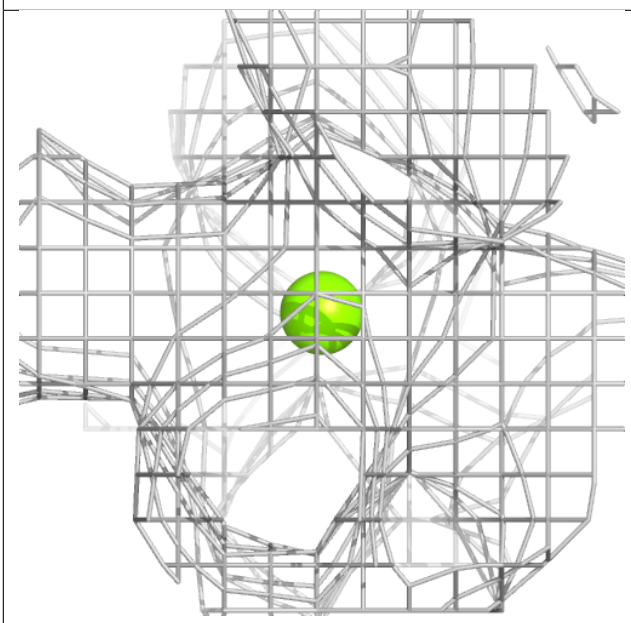
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

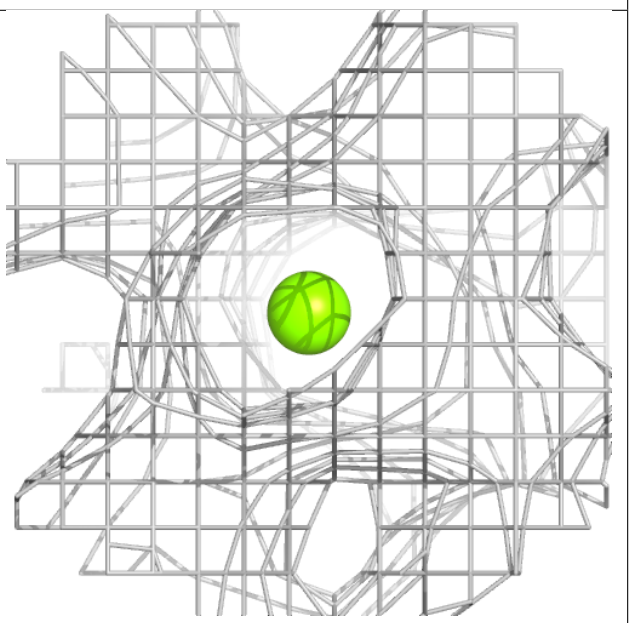




Electron density around MG A 702:

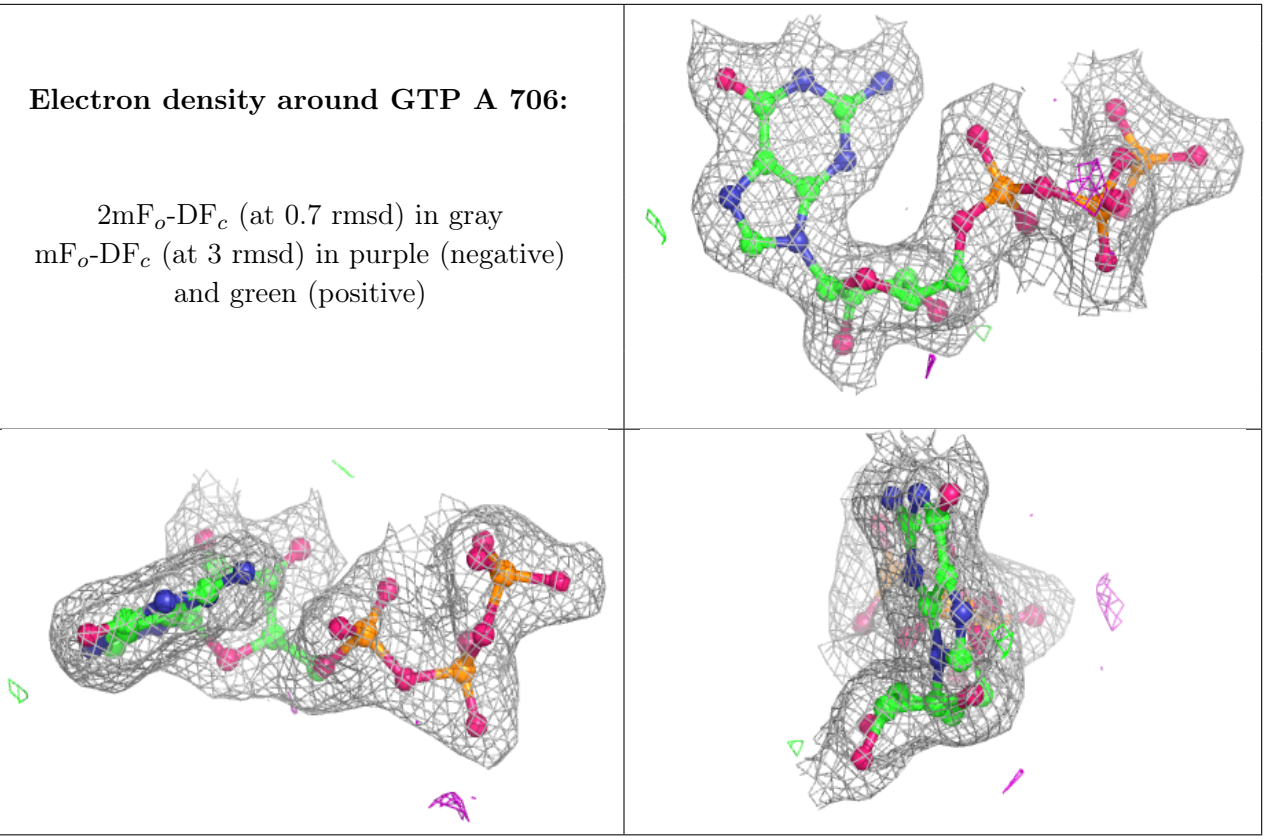
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





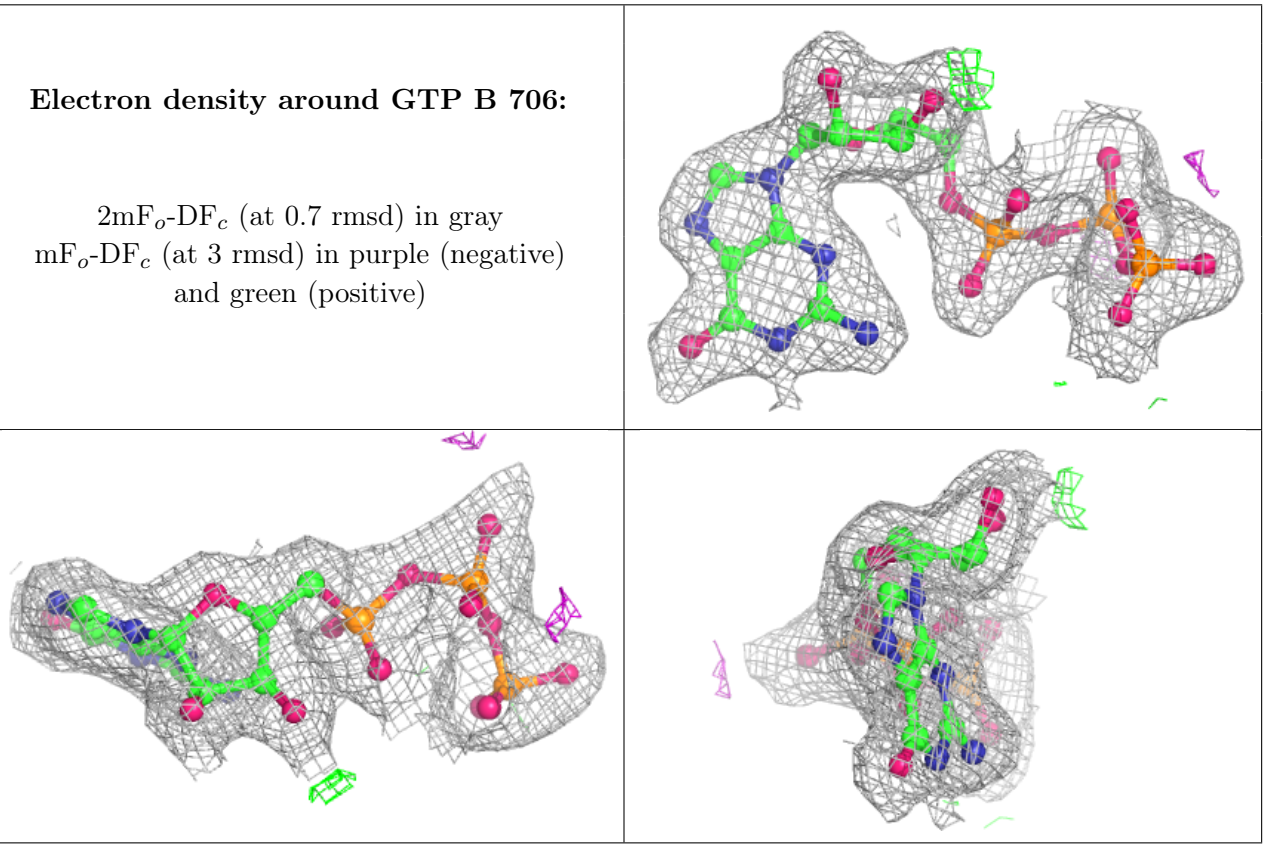
Electron density around GTP A 706:

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



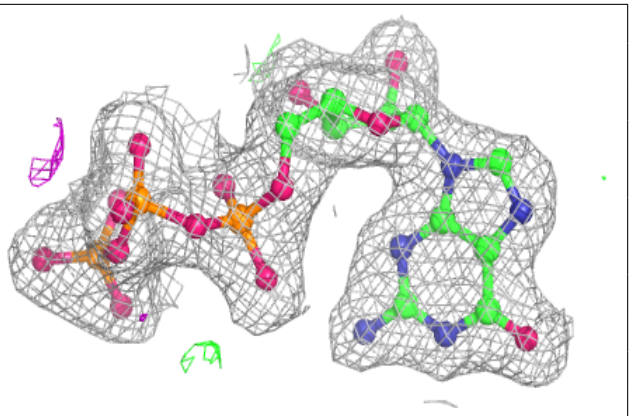
Electron density around GTP B 706:

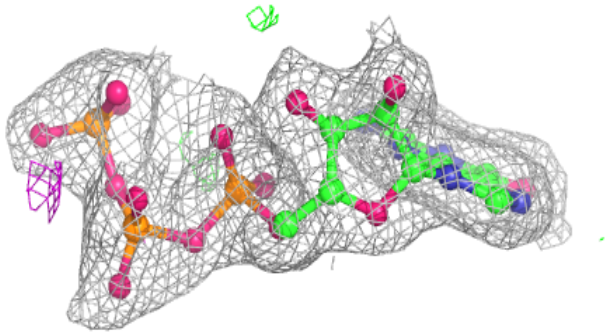
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

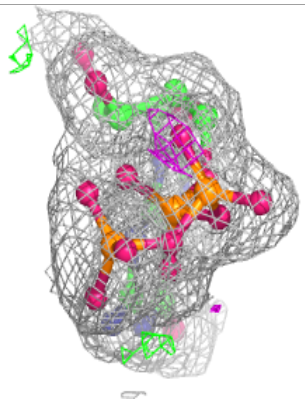


Electron density around GTP C 707:

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

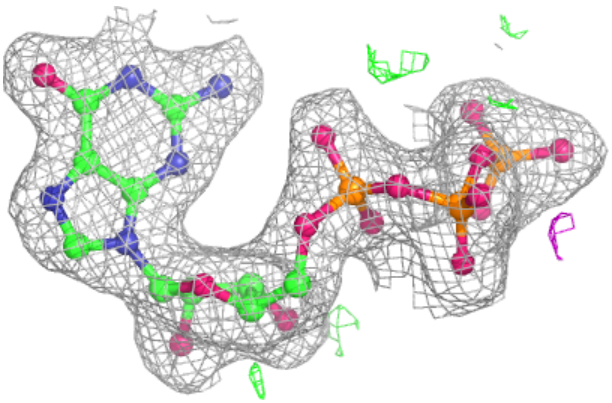


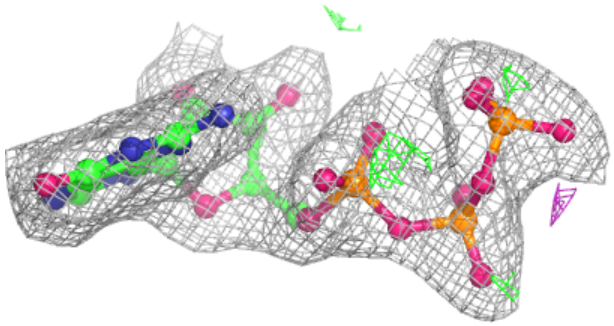


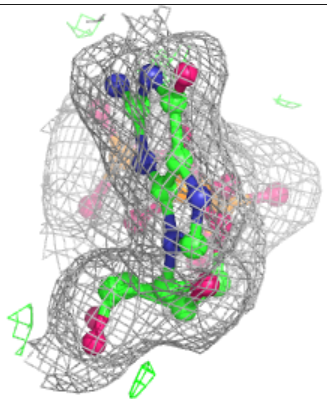


Electron density around GTP D 707:

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

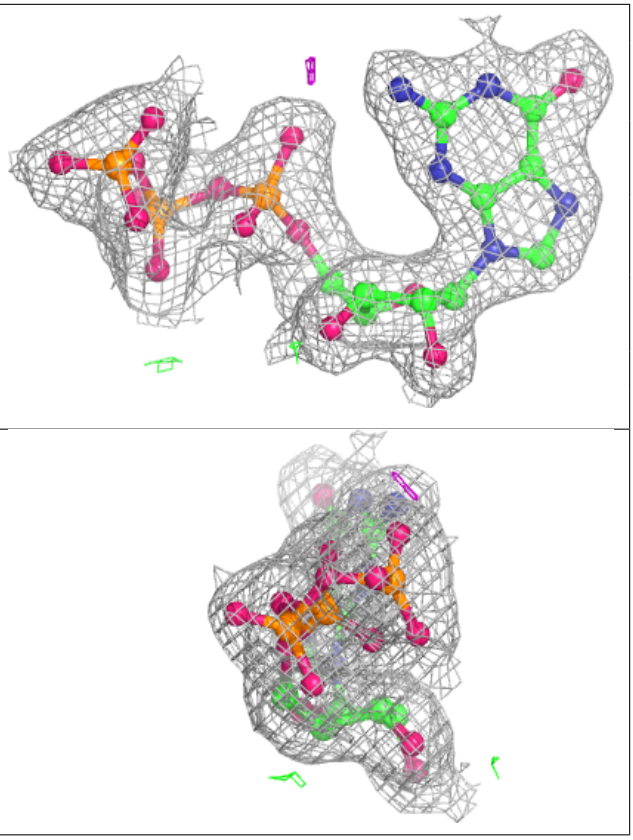






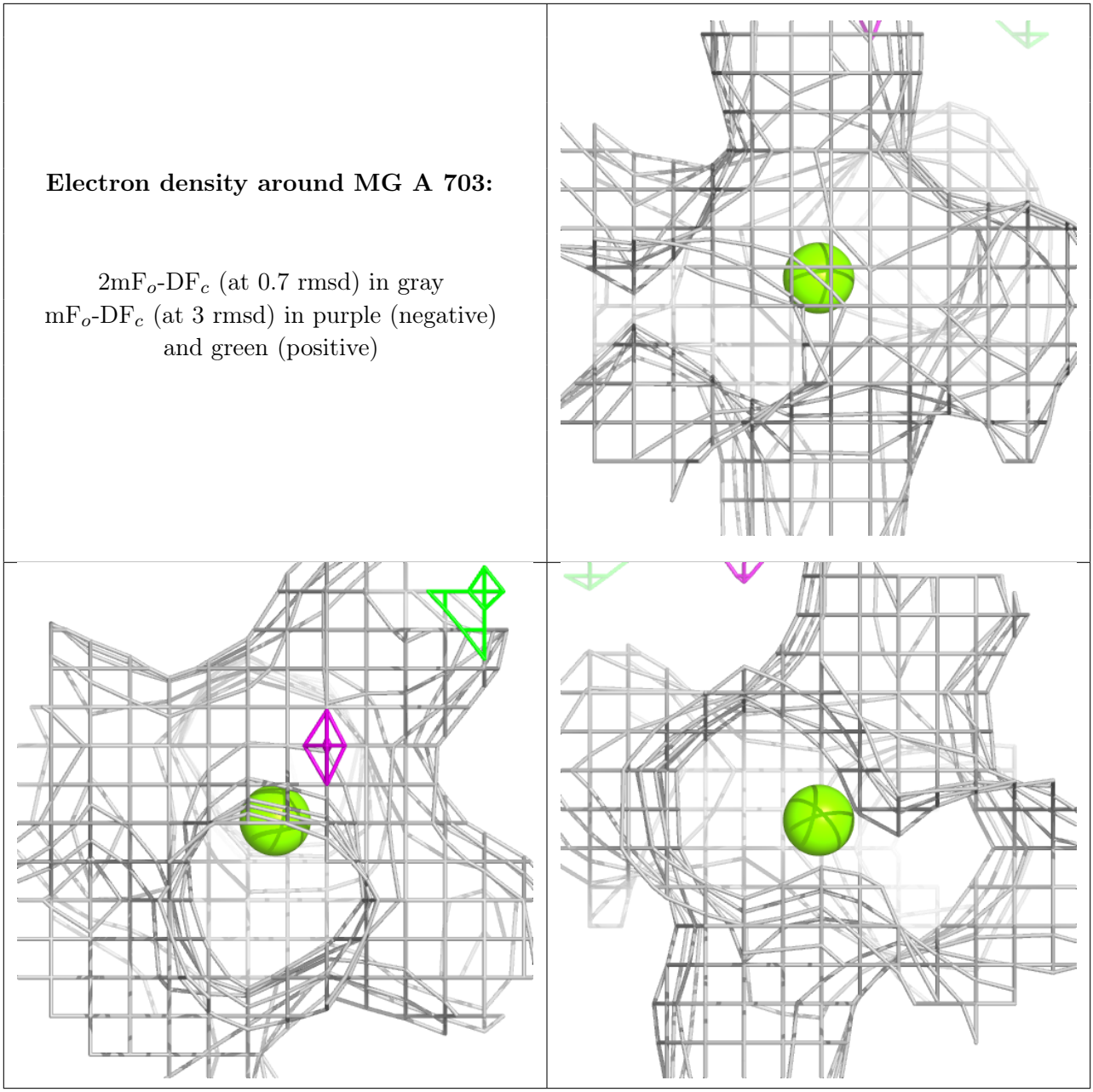
Electron density around GTP E 706:

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



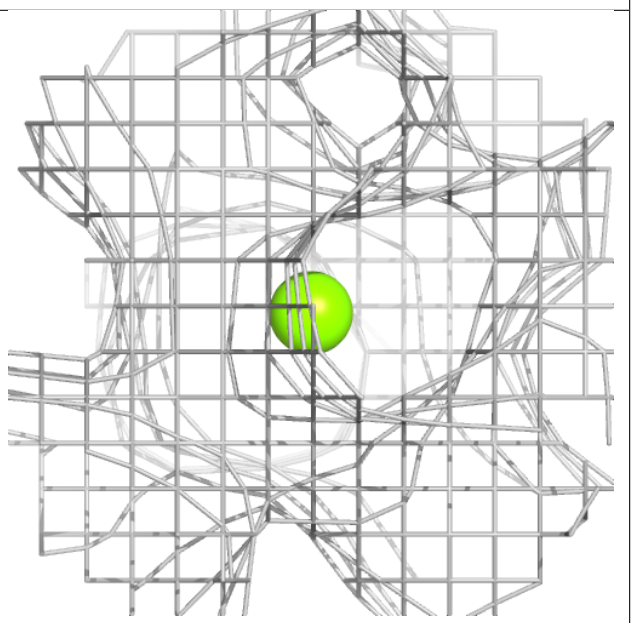
Electron density around MG A 703:

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



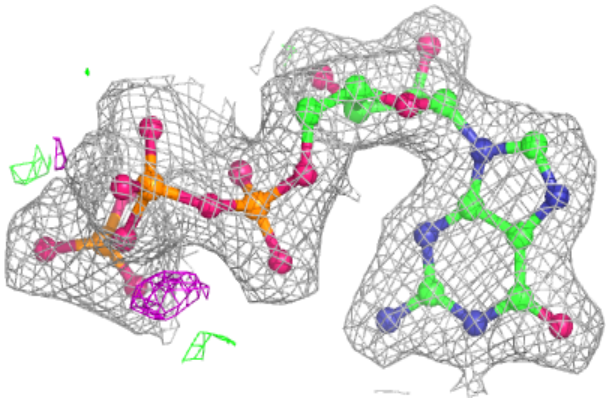
Electron density around MG C 703:

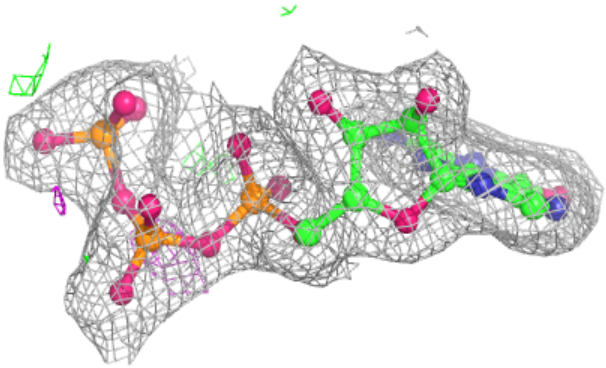
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

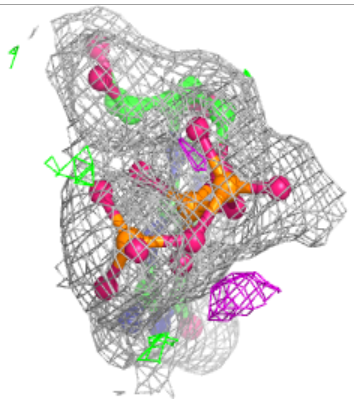


Electron density around GTP H 707:

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

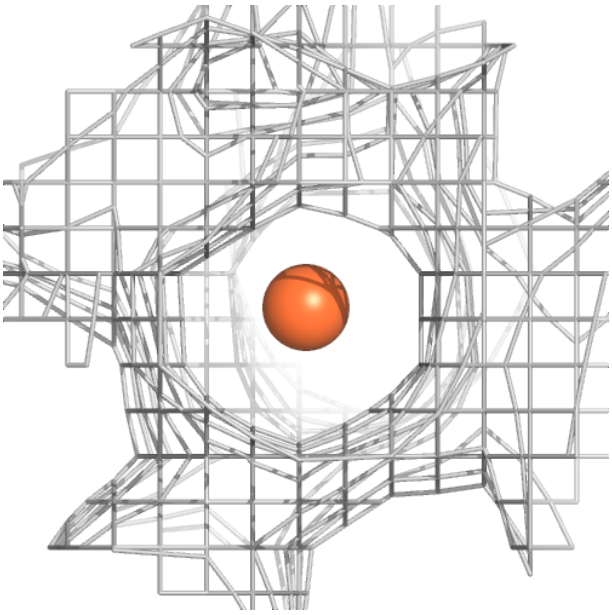


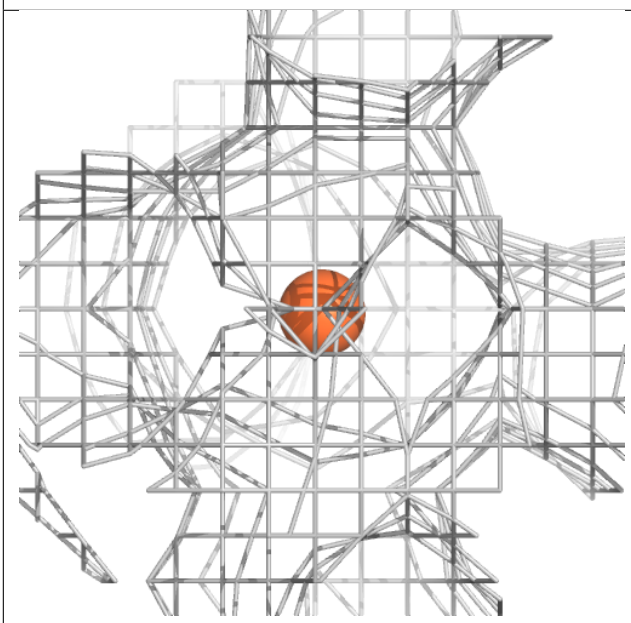


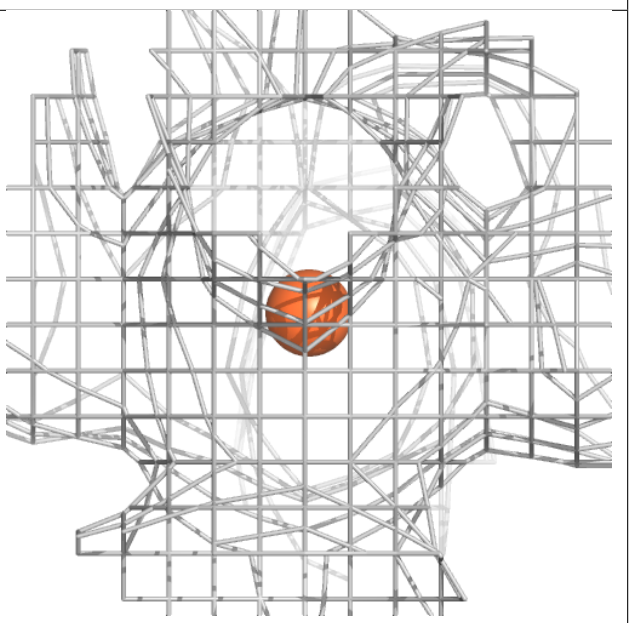


Electron density around FE A 701:

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

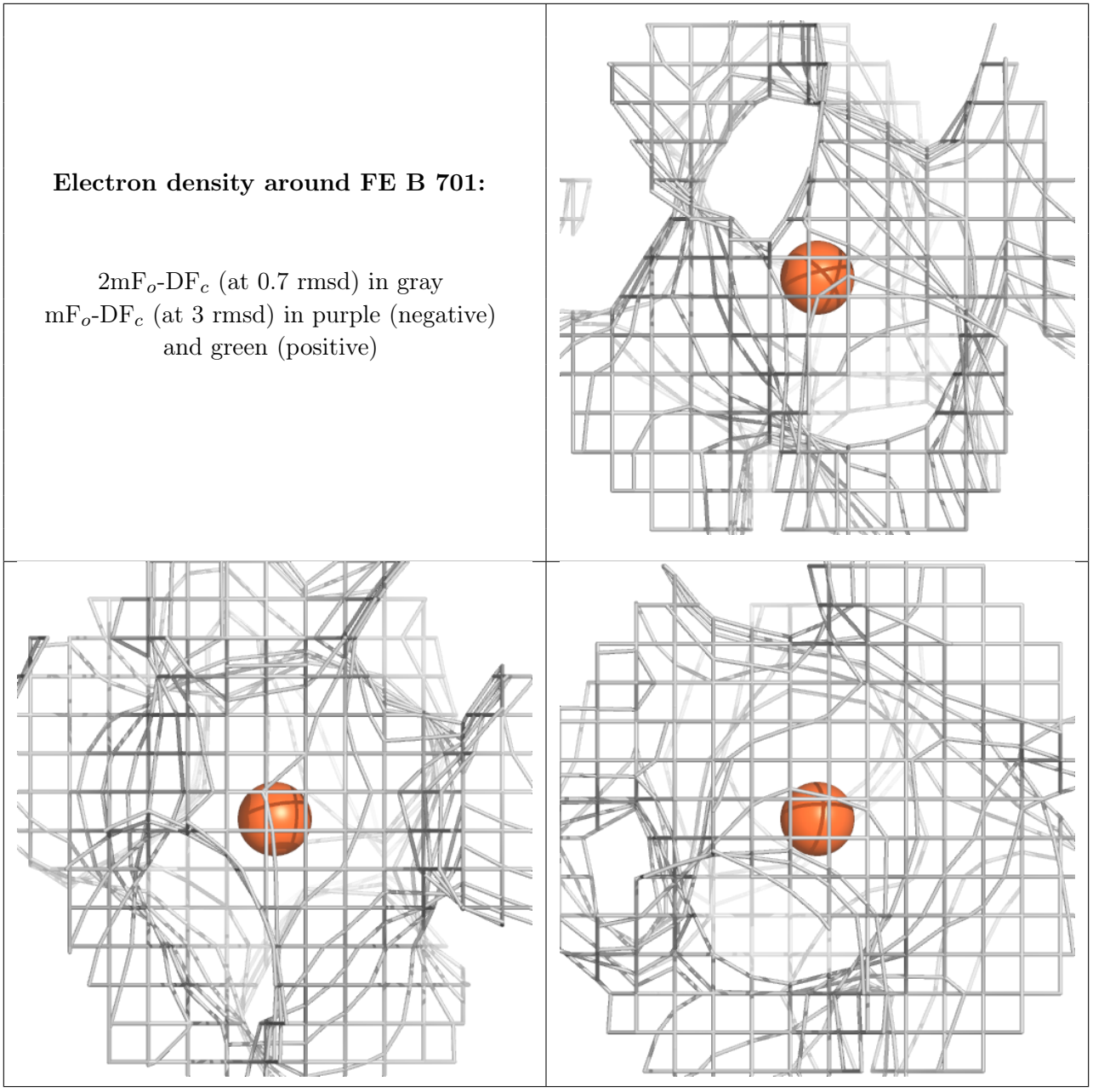






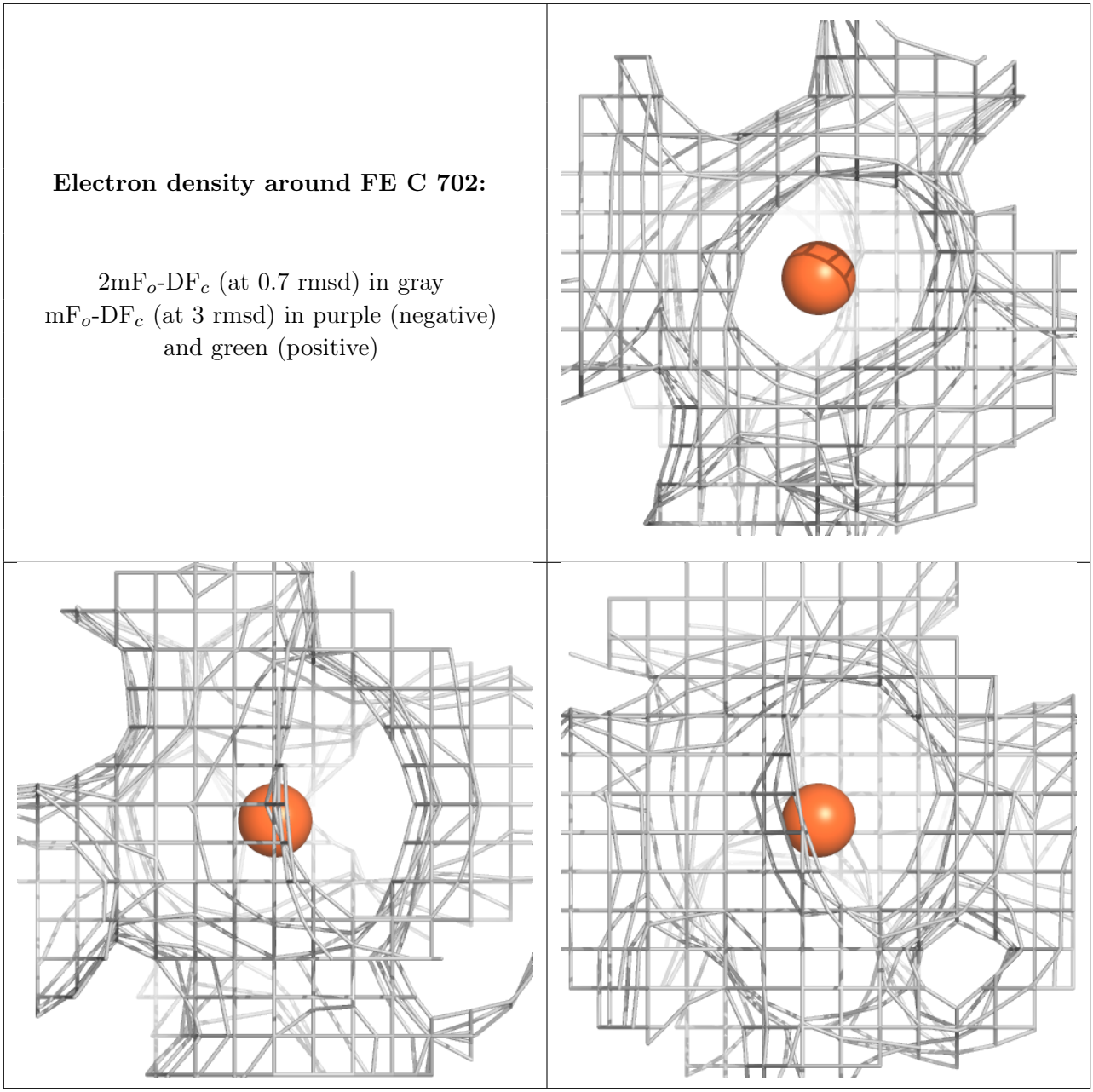
Electron density around FE B 701:

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



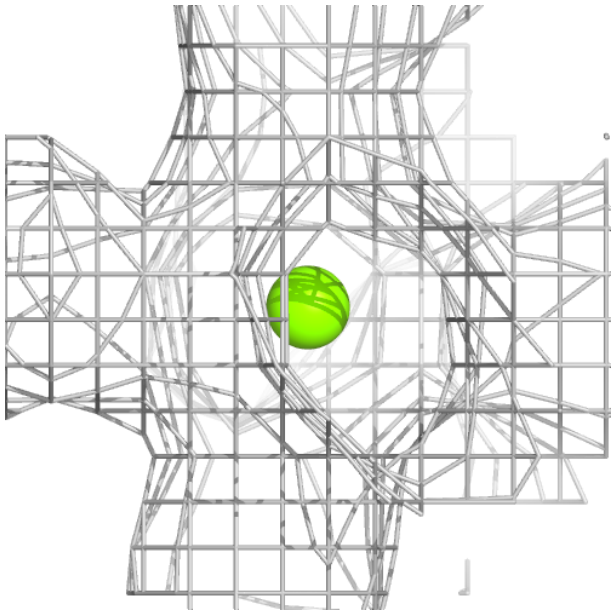
Electron density around FE C 702:

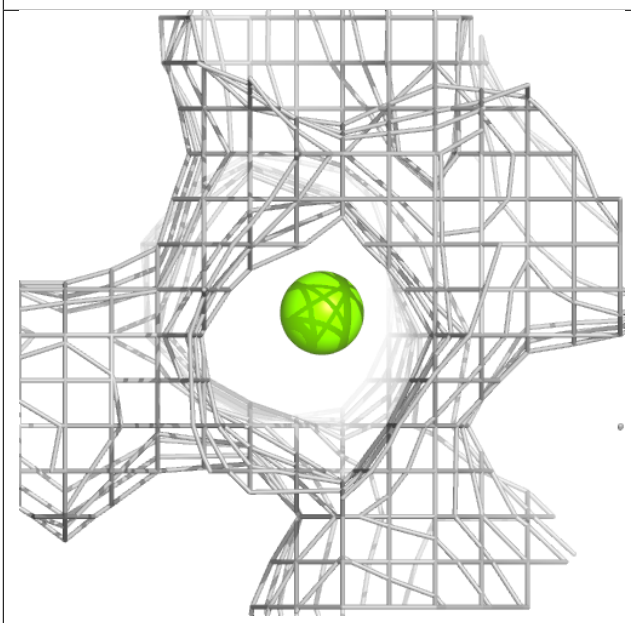
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

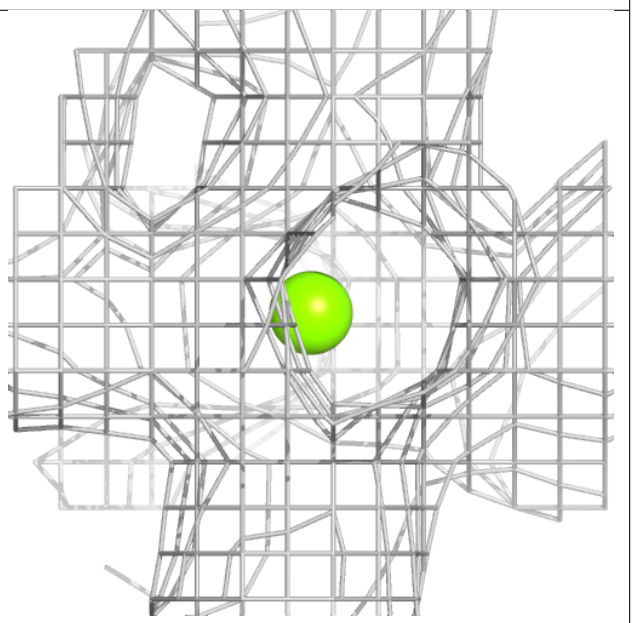


Electron density around MG B 702:

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

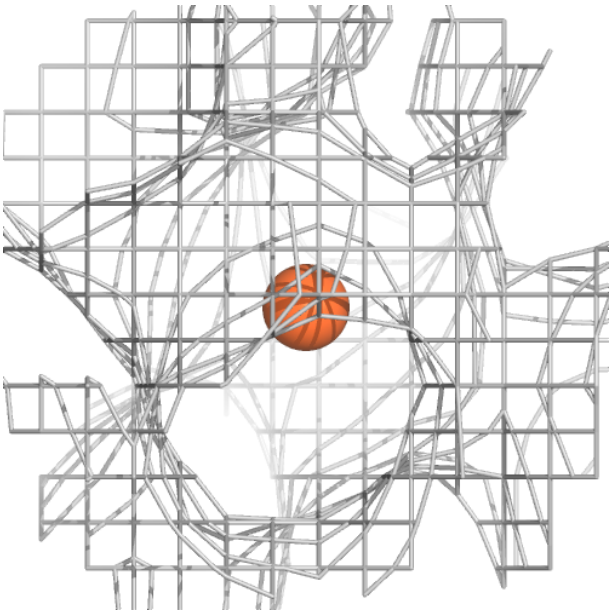


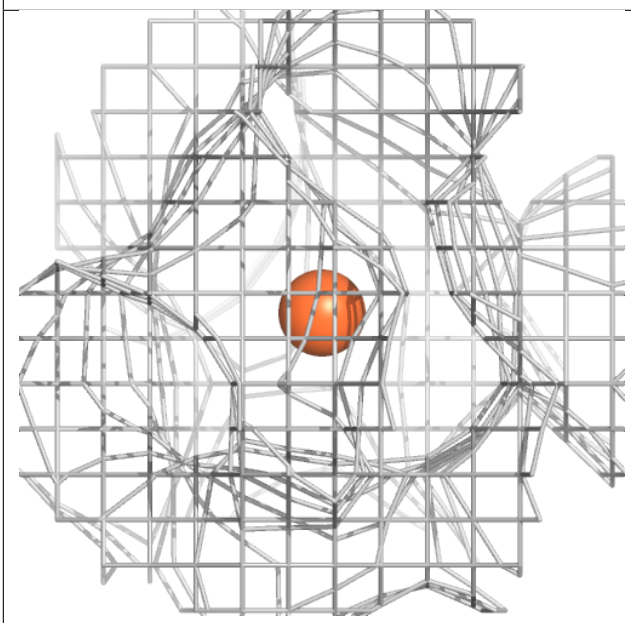


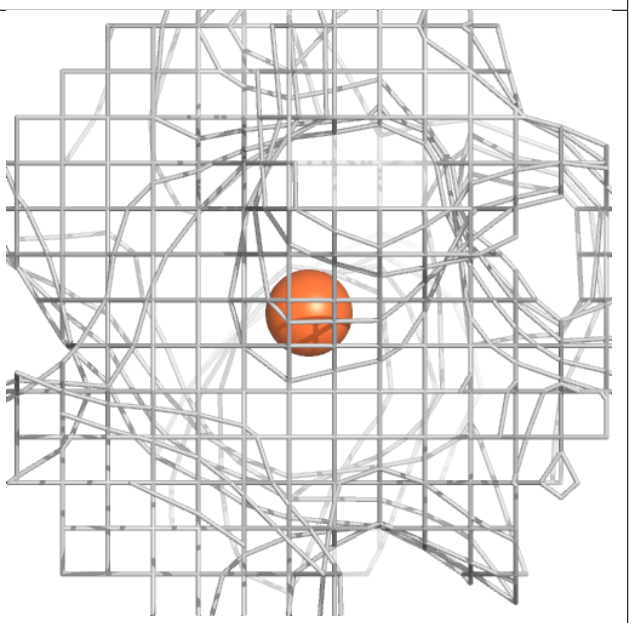


Electron density around FE D 702:

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

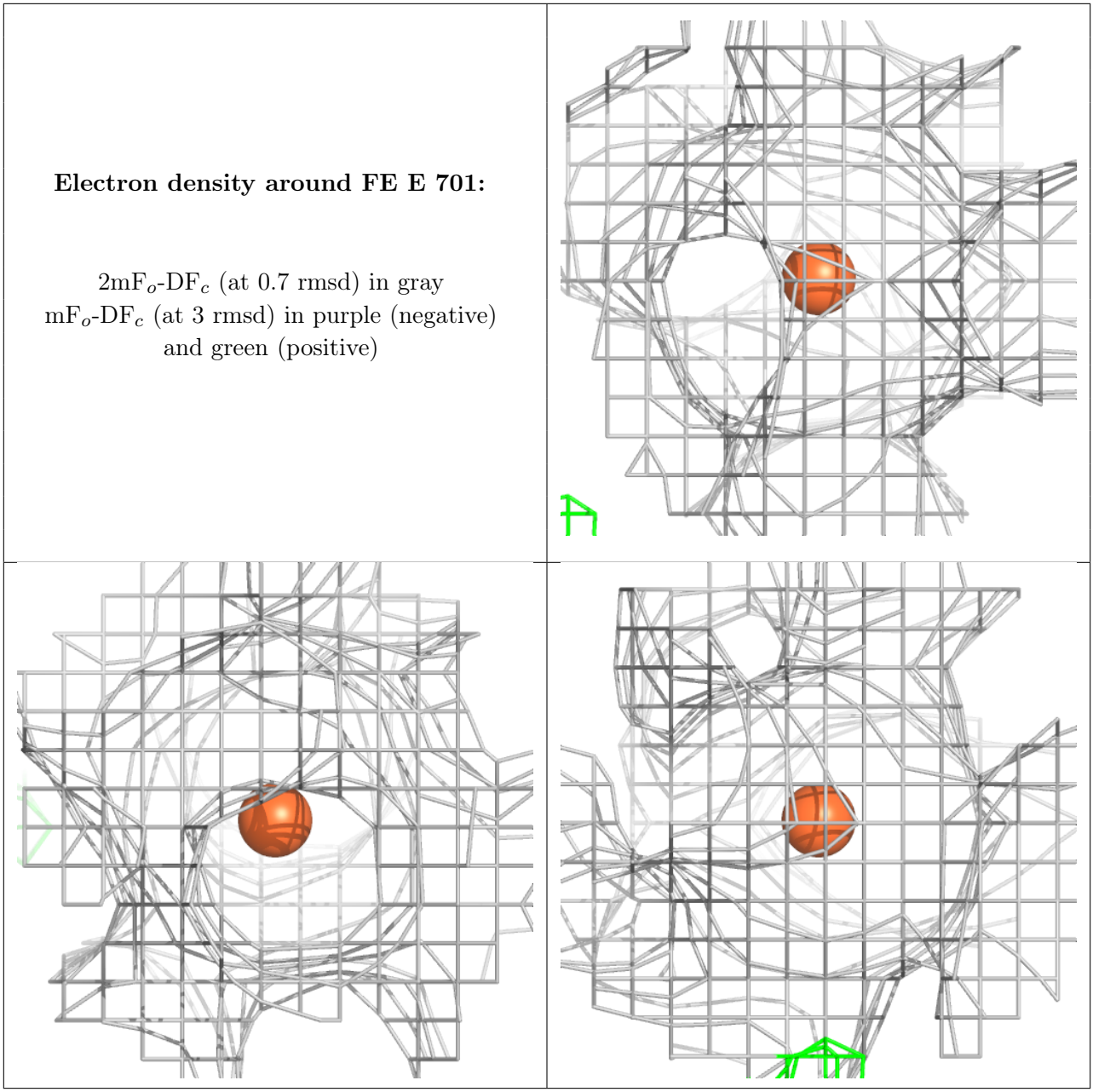






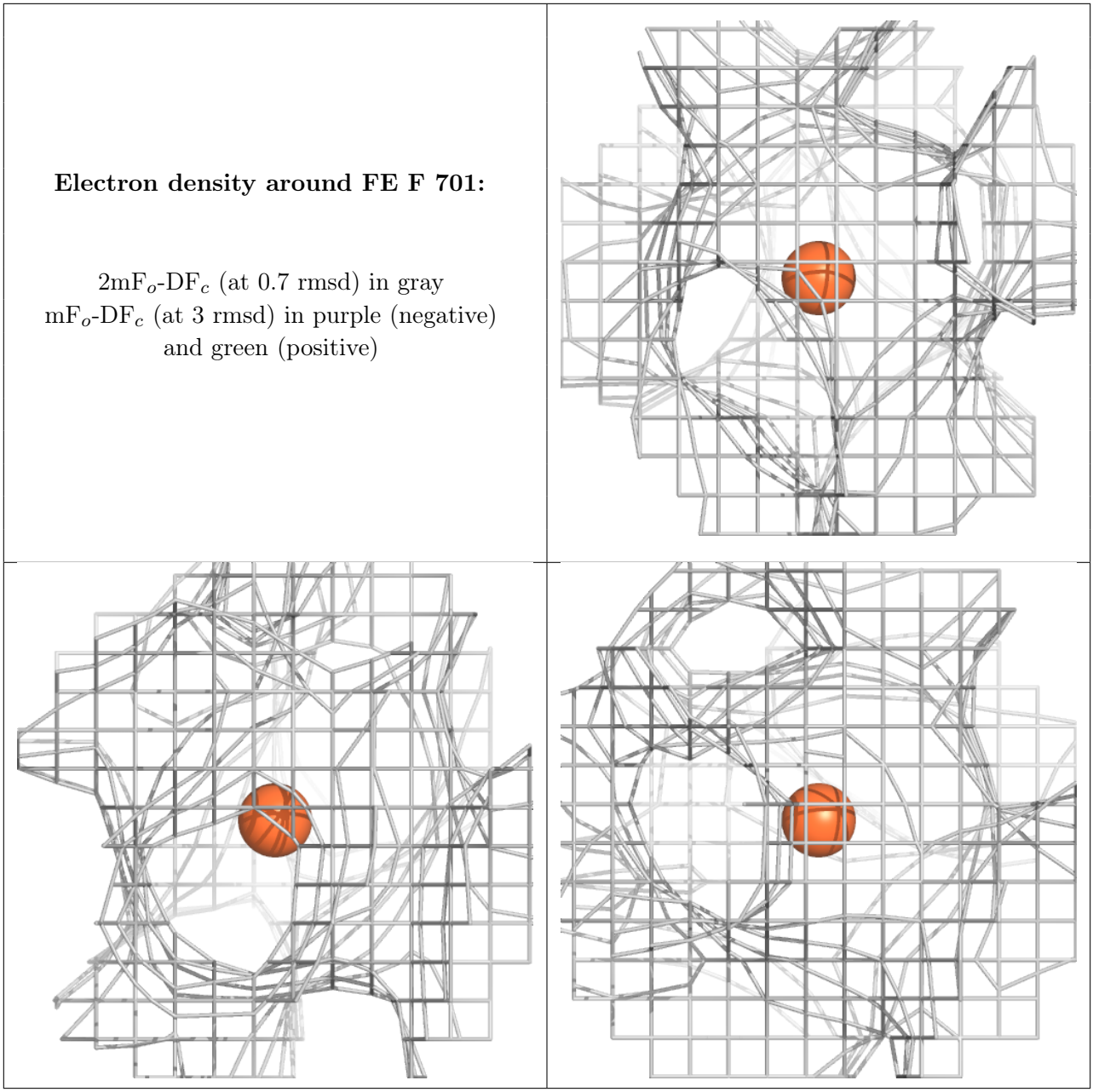
Electron density around FE E 701:

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



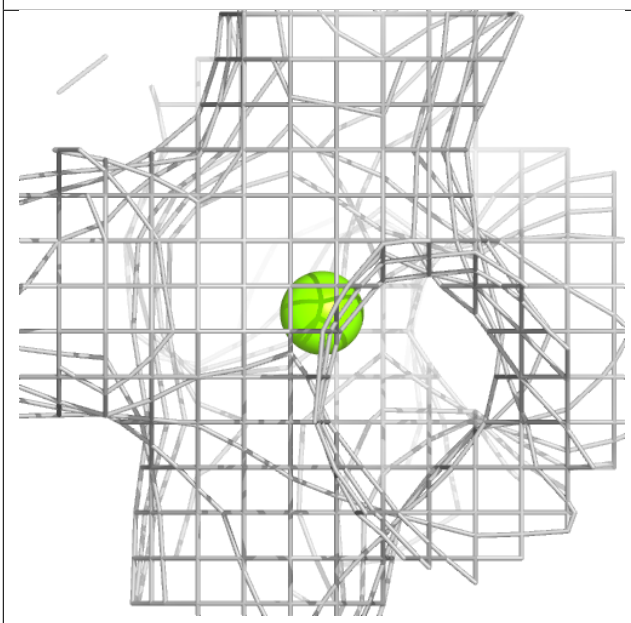
Electron density around FE F 701:

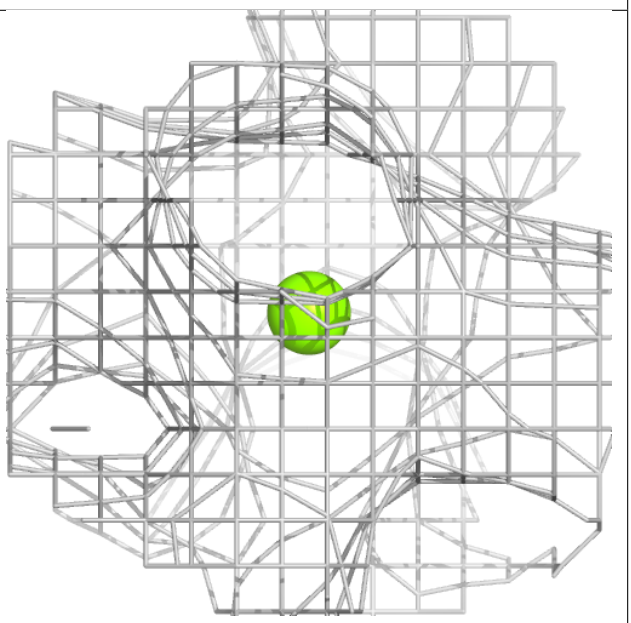
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around MG F 702:

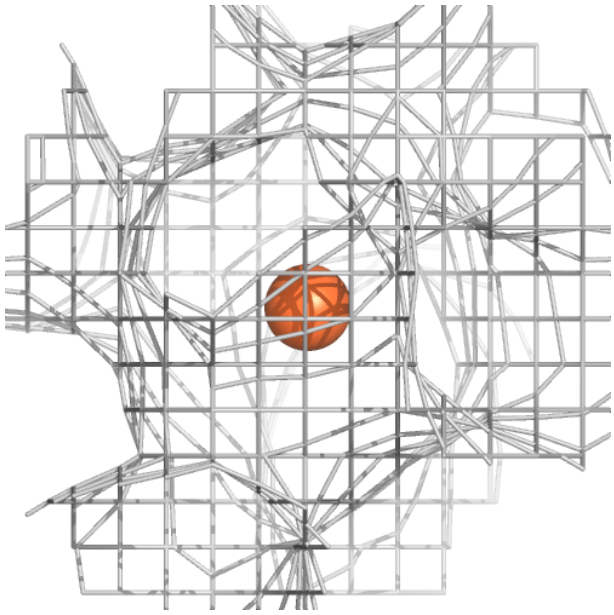
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

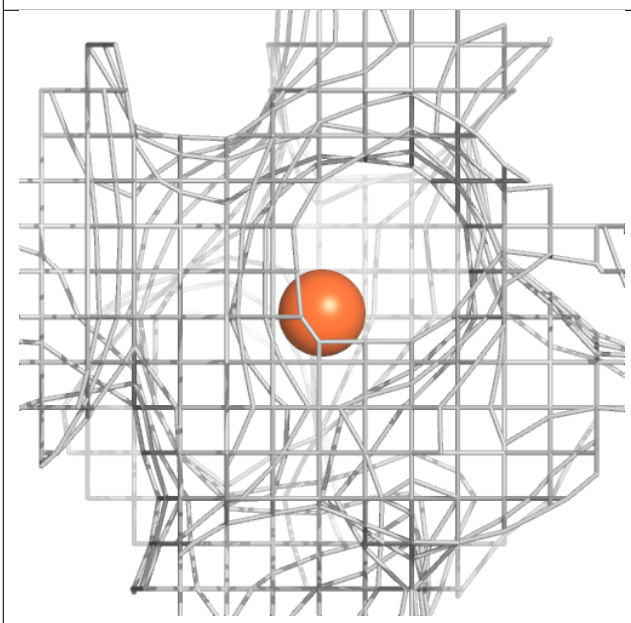


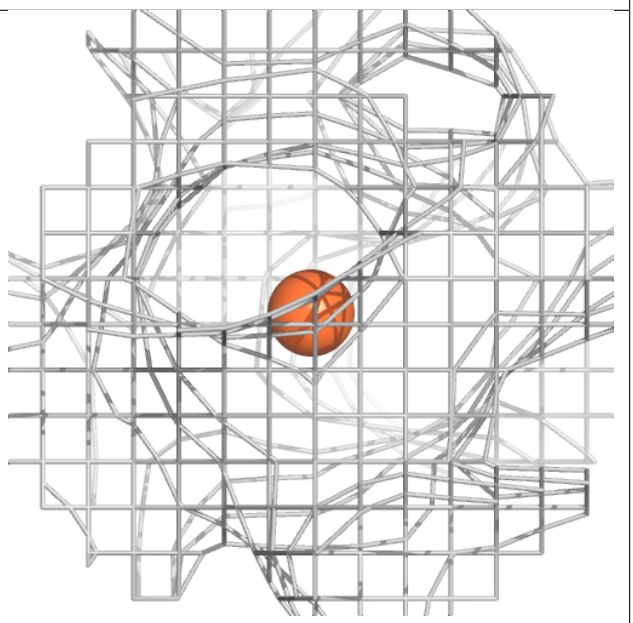


Electron density around FE G 702:

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

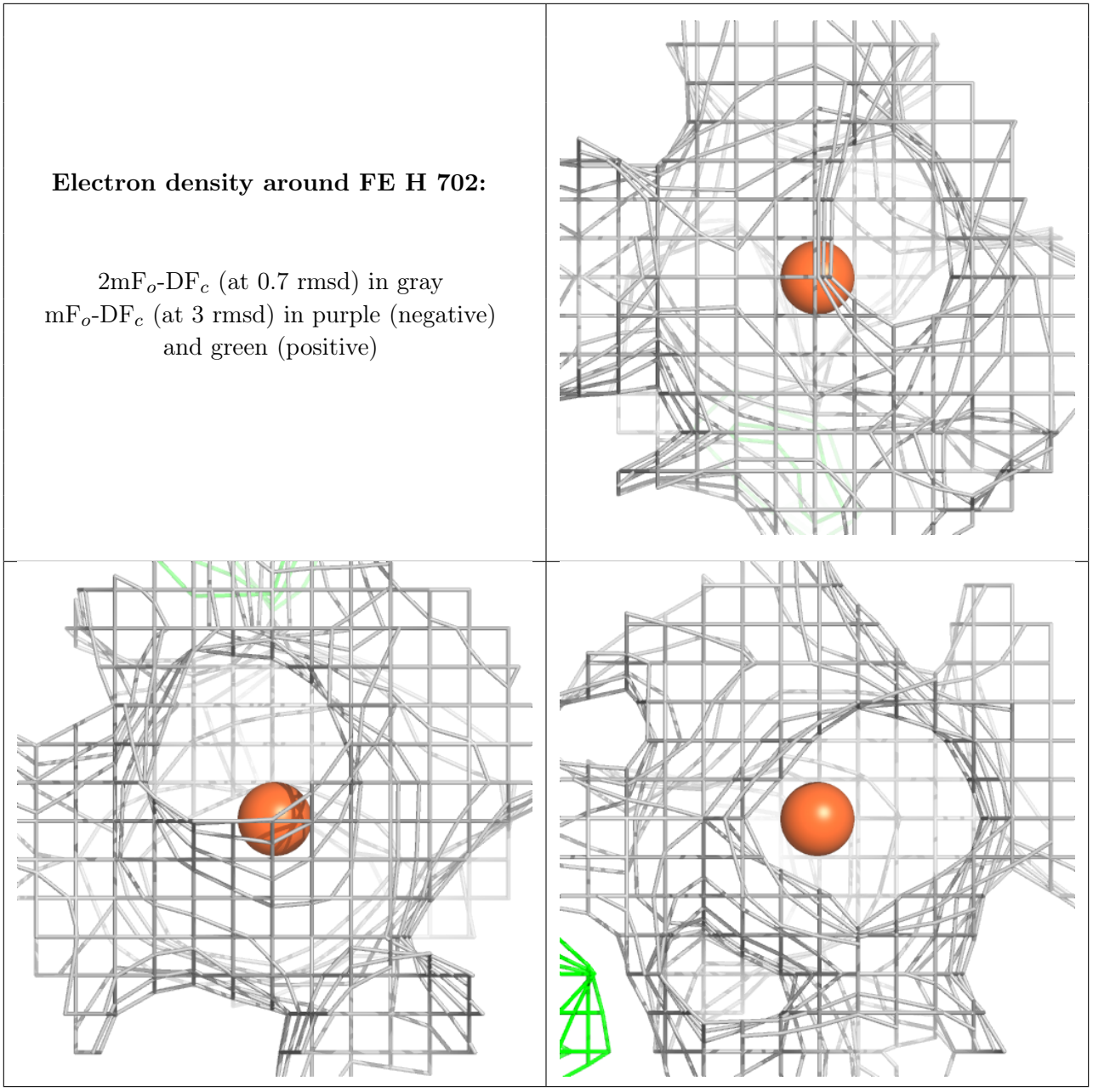






Electron density around FE H 702:

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



6.5 Other polymers

There are no such residues in this entry.