



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:35 AM UTC

PDB ID : 8Q5W / pdb_00008q5w
Title : MgADP-bound Fe protein of the molybdenum nitrogenase from *Methanocaldococcus infernus*
Authors : Maslac, N.; Wagner, T.
Deposited on : 2023-08-09
Resolution : 2.49 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

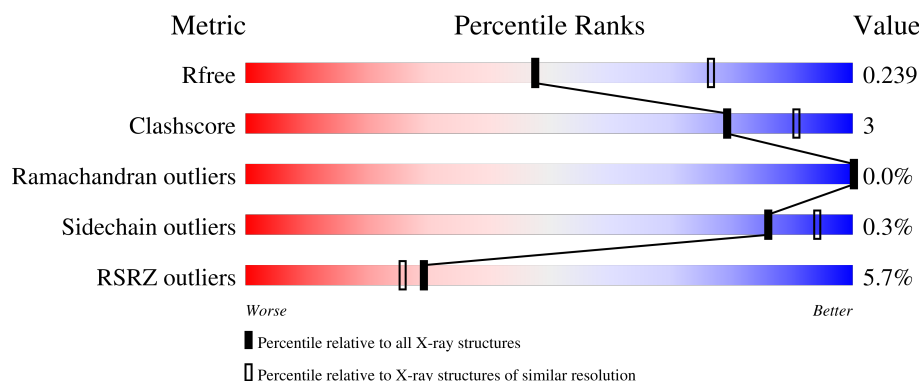
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	284	4% 95% ..
1	B	284	5% 92% 7% .
1	C	284	6% 93% 5% .
1	D	284	13% 89% 8% .
1	E	284	14% 89% 10% .

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Mol	Chain	Length	Quality of chain
1	F	284	
1	G	284	
1	H	284	
1	I	284	
1	J	284	
1	K	284	
1	L	284	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MG	B	303	-	-	-	X
3	MG	C	303	-	-	-	X
3	MG	D	402	-	-	-	X
3	MG	I	303	-	-	-	X
3	MG	K	303	-	-	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 26165 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.

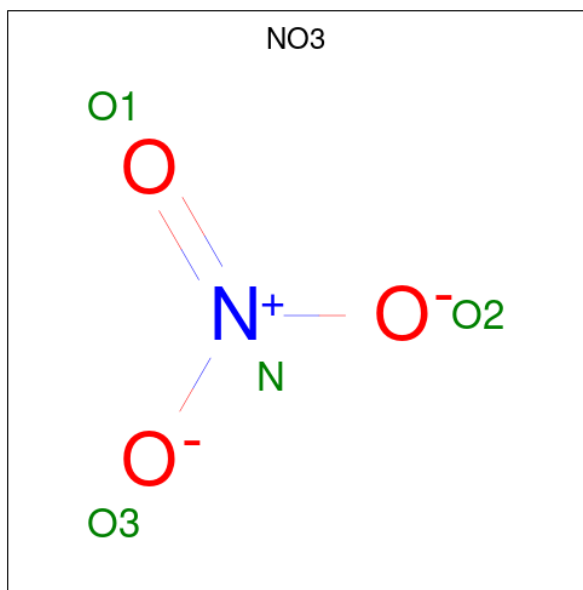
- Molecule 1 is a protein called Nitrogenase iron protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	280	Total	C	N	O	S	0	0	0
			2138	1358	354	408	18			
1	B	280	Total	C	N	O	S	0	0	0
			2144	1364	354	408	18			
1	C	279	Total	C	N	O	S	0	0	0
			2130	1352	353	407	18			
1	D	277	Total	C	N	O	S	0	0	0
			2113	1340	351	404	18			
1	E	279	Total	C	N	O	S	0	0	0
			2133	1355	353	407	18			
1	F	280	Total	C	N	O	S	0	0	0
			2144	1364	354	408	18			
1	G	281	Total	C	N	O	S	0	0	0
			2150	1367	355	410	18			
1	H	280	Total	C	N	O	S	0	0	0
			2144	1364	354	408	18			
1	I	280	Total	C	N	O	S	0	0	0
			2138	1358	354	408	18			
1	J	279	Total	C	N	O	S	0	0	0
			2132	1355	353	406	18			
1	K	281	Total	C	N	O	S	0	0	0
			2150	1367	355	410	18			
1	L	280	Total	C	N	O	S	0	0	0
			2144	1364	354	408	18			

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).

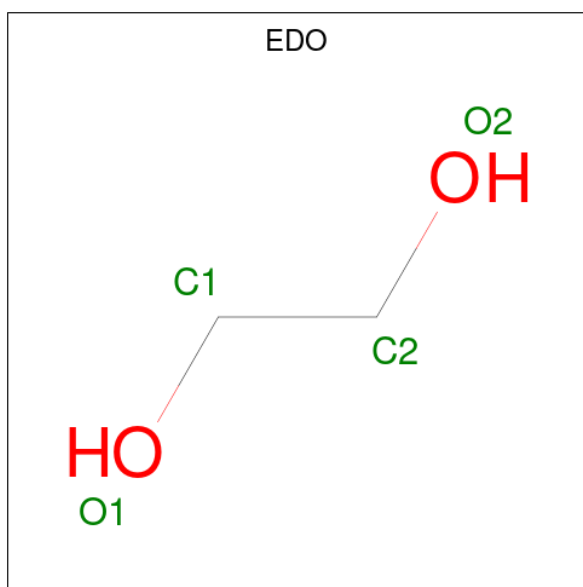
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0
3	B	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0
3	E	1	Total Mg 1 1	0	0
3	F	1	Total Mg 1 1	0	0
3	G	1	Total Mg 1 1	0	0
3	H	1	Total Mg 1 1	0	0
3	I	1	Total Mg 1 1	0	0
3	J	1	Total Mg 1 1	0	0
3	K	1	Total Mg 1 1	0	0
3	L	1	Total Mg 1 1	0	0

- Molecule 4 is NITRATE ION (CCD ID: NO3) (formula: NO₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total N O 4 1 3	0	0
4	A	1	Total N O 4 1 3	0	0
4	A	1	Total N O 4 1 3	0	0
4	F	1	Total N O 4 1 3	0	0
4	F	1	Total N O 4 1 3	0	0
4	H	1	Total N O 4 1 3	0	0
4	I	1	Total N O 4 1 3	0	0
4	I	1	Total N O 4 1 3	0	0
4	K	1	Total N O 4 1 3	0	0
4	L	1	Total N O 4 1 3	0	0

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



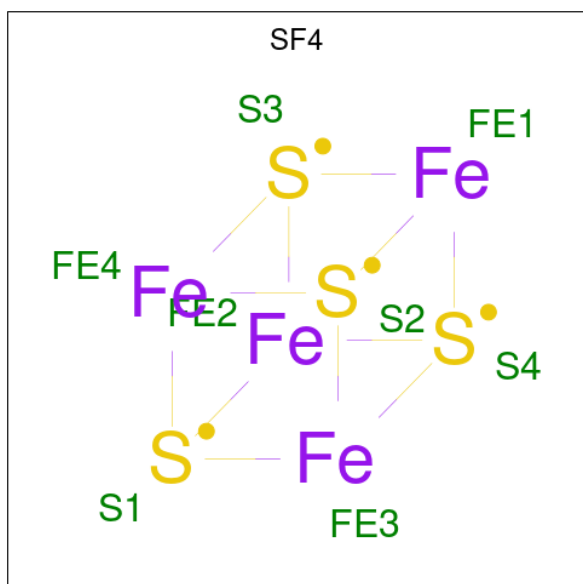
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	G	1	Total C O 4 2 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	G	1	Total	C	O	0	0
			4	2	2		
5	H	1	Total	C	O	0	0
			4	2	2		
5	I	1	Total	C	O	0	0
			4	2	2		
5	I	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄) (labeled as "Ligand of Interest" by depositor).

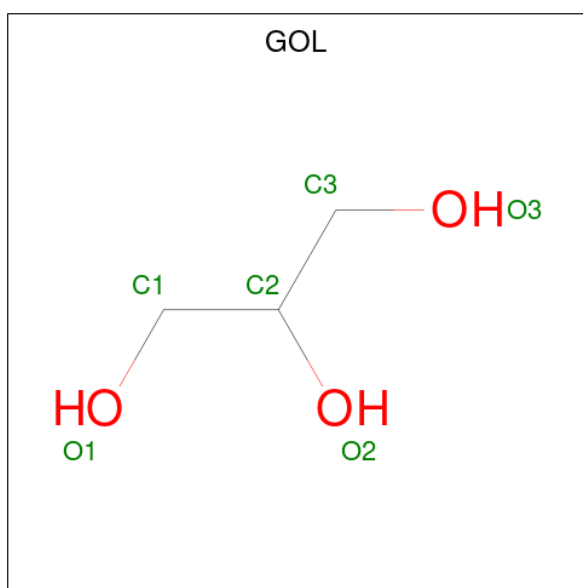


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	Fe	S	0	0
			8	4	4		
6	C	1	Total	Fe	S	0	0
			8	4	4		
6	E	1	Total	Fe	S	0	0
			8	4	4		
6	H	1	Total	Fe	S	0	0
			8	4	4		
6	I	1	Total	Fe	S	0	0
			8	4	4		
6	K	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	E	1	Total Cl 1 1	0	0
7	G	1	Total Cl 1 1	0	0
7	J	1	Total Cl 1 1	0	0
7	L	1	Total Cl 1 1	0	0

- Molecule 8 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	I	1	Total C O 6 3 3	0	0
8	K	1	Total C O 6 3 3	0	0

- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	11	Total O 11 11	0	0
9	B	1	Total O 1 1	0	0
9	C	2	Total O 2 2	0	0
9	D	2	Total O 2 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	E	1	Total	O	0	0
			1	1		
9	F	1	Total	O	0	0
			1	1		
9	G	5	Total	O	0	0
			5	5		
9	H	2	Total	O	0	0
			2	2		
9	I	5	Total	O	0	0
			5	5		
9	J	1	Total	O	0	0
			1	1		
9	K	2	Total	O	0	0
			2	2		
9	L	8	Total	O	0	0
			8	8		

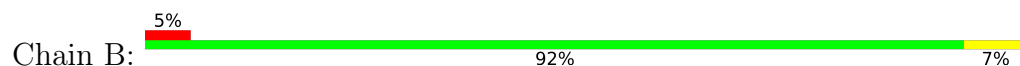
3 Residue-property plots [i](#)

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.

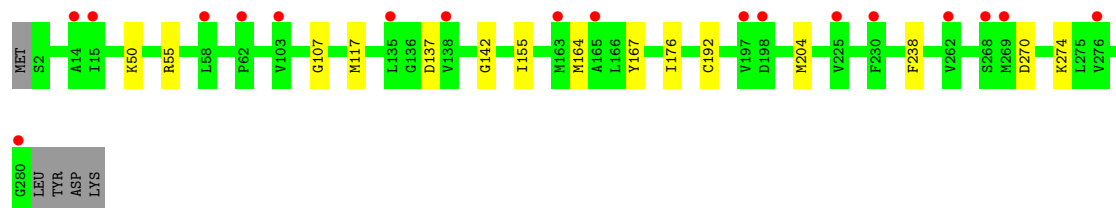
- Molecule 1: Nitrogenase iron protein



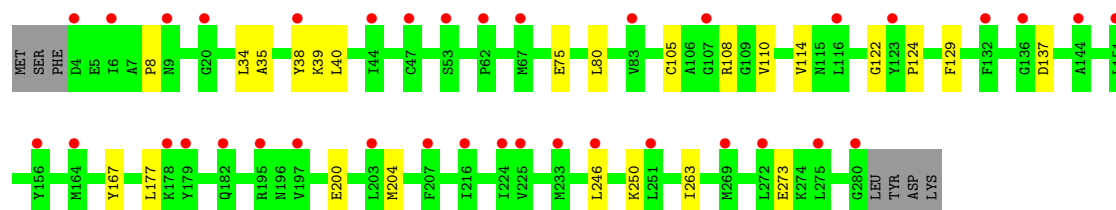
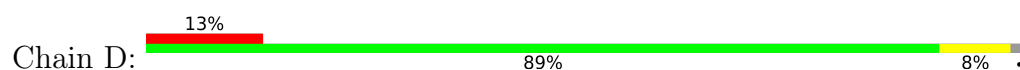
- Molecule 1: Nitrogenase iron protein



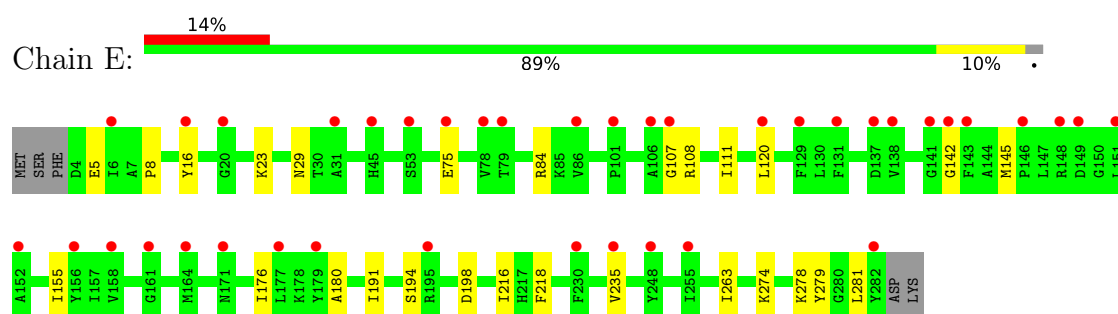
- Molecule 1: Nitrogenase iron protein



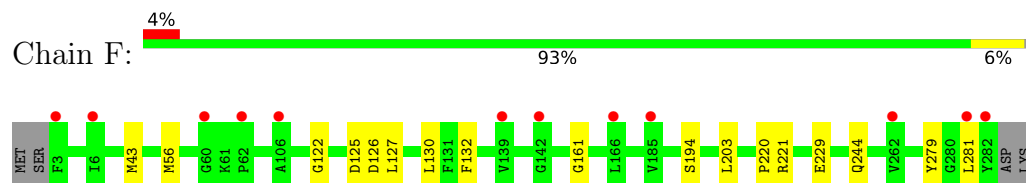
- Molecule 1: Nitrogenase iron protein



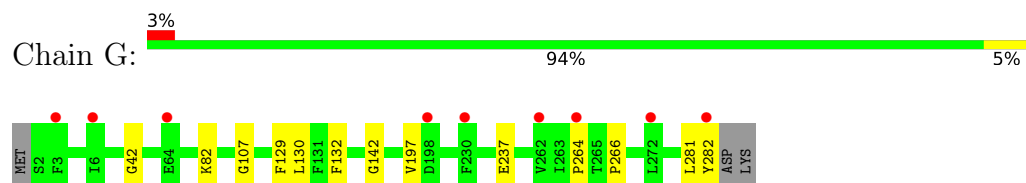
- Molecule 1: Nitrogenase iron protein



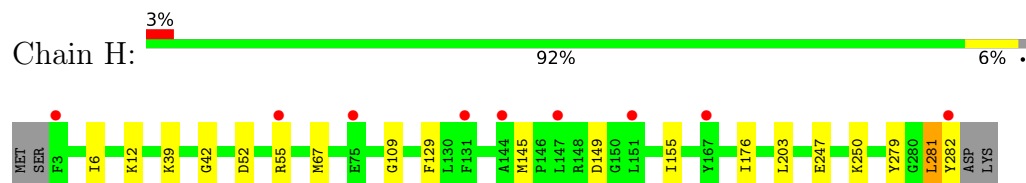
- Molecule 1: Nitrogenase iron protein



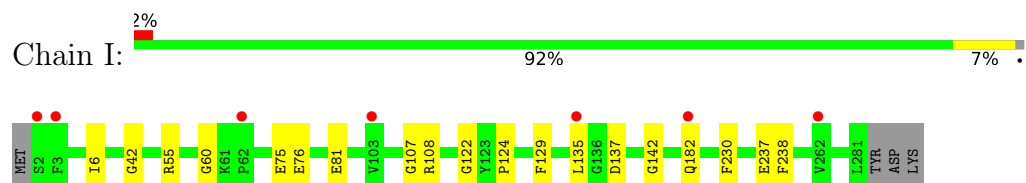
- Molecule 1: Nitrogenase iron protein



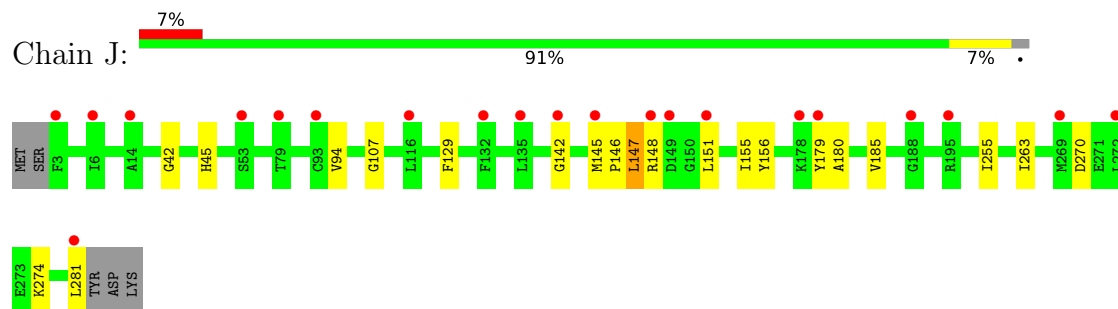
- Molecule 1: Nitrogenase iron protein



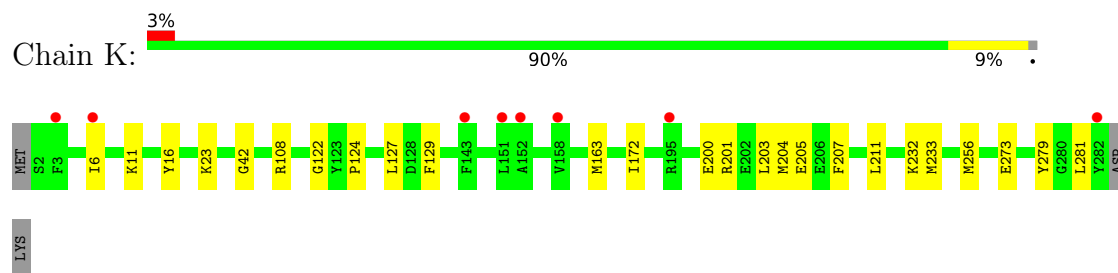
- Molecule 1: Nitrogenase iron protein



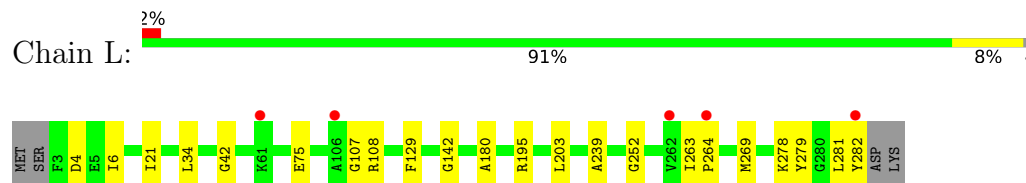
- Molecule 1: Nitrogenase iron protein



● Molecule 1: Nitrogenase iron protein



● Molecule 1: Nitrogenase iron protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	147.95Å 156.73Å 206.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.26 – 2.49 49.26 – 2.49	Depositor EDS
% Data completeness (in resolution range)	54.4 (49.26-2.49) 54.4 (49.26-2.49)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.55 (at 2.48Å)	Xtrriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.221 , 0.242 0.220 , 0.239	Depositor DCC
R_{free} test set	4422 reflections (2.64%)	wwPDB-VP
Wilson B-factor (Å ²)	66.9	Xtrriage
Anisotropy	0.064	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 21.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	26165	wwPDB-VP
Average B, all atoms (Å ²)	79.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 35.83 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.4891e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, ADP, GOL, MG, NO3, EDO, CL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.59	0/2174	0.88	1/2925 (0.0%)
1	B	0.61	0/2181	0.89	0/2935
1	C	0.57	0/2166	0.86	0/2914
1	D	0.62	0/2148	0.90	1/2890 (0.0%)
1	E	0.63	0/2169	0.92	0/2919
1	F	0.60	0/2181	0.88	0/2935
1	G	0.58	0/2187	0.86	0/2943
1	H	0.56	0/2181	0.86	0/2935
1	I	0.58	0/2174	0.87	1/2925 (0.0%)
1	J	0.59	0/2168	0.88	1/2917 (0.0%)
1	K	0.61	0/2187	0.88	0/2943
1	L	0.57	0/2181	0.88	2/2935 (0.1%)
All	All	0.59	0/26097	0.88	6/35116 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	4	ASP	N-CA-C	-6.92	104.72	113.02
1	I	230	PHE	CA-CB-CG	6.70	120.50	113.80
1	L	264	PRO	N-CA-C	6.47	121.50	111.21
1	A	259	ASP	N-CA-C	-5.53	107.78	114.75
1	D	8	PRO	N-CA-C	5.52	121.11	113.65
1	J	147	LEU	CB-CA-C	-5.39	101.69	110.85

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2138	0	2153	6	0
1	B	2144	0	2157	14	0
1	C	2130	0	2142	10	0
1	D	2113	0	2128	16	0
1	E	2133	0	2147	15	0
1	F	2144	0	2157	9	0
1	G	2150	0	2162	11	0
1	H	2144	0	2157	12	0
1	I	2138	0	2153	13	0
1	J	2132	0	2148	12	0
1	K	2150	0	2162	17	0
1	L	2144	0	2157	13	0
2	A	27	0	12	0	0
2	B	27	0	12	0	0
2	C	27	0	12	0	0
2	D	27	0	12	0	0
2	E	27	0	12	0	0
2	F	27	0	12	0	0
2	G	27	0	12	0	0
2	H	27	0	12	0	0
2	I	27	0	12	0	0
2	J	27	0	12	0	0
2	K	27	0	12	1	0
2	L	27	0	12	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
3	K	1	0	0	0	0
3	L	1	0	0	0	0
4	A	12	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	8	0	0	0	0
4	H	4	0	0	0	0
4	I	8	0	0	1	0
4	K	4	0	0	0	0
4	L	4	0	0	0	0
5	A	4	0	6	0	0
5	G	8	0	12	0	0
5	H	4	0	6	0	0
5	I	8	0	12	0	0
6	B	8	0	0	0	0
6	C	8	0	0	0	0
6	E	8	0	0	0	0
6	H	8	0	0	0	0
6	I	8	0	0	0	0
6	K	8	0	0	0	0
7	E	1	0	0	1	0
7	G	1	0	0	0	0
7	J	1	0	0	0	0
7	L	1	0	0	0	0
8	I	6	0	8	0	0
8	K	6	0	8	0	0
9	A	11	0	0	0	0
9	B	1	0	0	0	0
9	C	2	0	0	0	0
9	D	2	0	0	0	0
9	E	1	0	0	0	0
9	F	1	0	0	0	0
9	G	5	0	0	0	0
9	H	2	0	0	0	0
9	I	5	0	0	0	0
9	J	1	0	0	0	0
9	K	2	0	0	0	0
9	L	8	0	0	0	0
All	All	26165	0	26019	138	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (138) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:203:LEU:O	1:H:203:LEU:HD23	2.21	0.41
1:I:238:PHE:CZ	1:K:108:ARG:HB2	2.56	0.40
1:J:148:ARG:HA	1:J:179:TYR:CD2	2.57	0.40
1:J:156:TYR:CE2	1:J:255:ILE:HG12	2.56	0.40
1:E:274:LYS:O	1:E:278:LYS:HG2	2.22	0.40
1:B:281:LEU:N	1:B:281:LEU:HD23	2.36	0.40
1:D:122:GLY:O	1:D:124:PRO:HD3	2.22	0.40
1:G:130:LEU:CD2	1:G:132:PHE:CE2	3.04	0.40
1:I:135:LEU:HD11	1:I:137:ASP:OD2	2.22	0.40
1:K:201:ARG:O	1:K:205:GLU:HG3	2.22	0.40
1:J:42:GLY:HA3	1:J:129:PHE:CZ	2.56	0.40
1:J:45:HIS:CD2	1:J:94:VAL:HG23	2.57	0.40
1:J:107:GLY:O	1:J:142:GLY:HA3	2.21	0.40
1:K:163:MET:HE1	1:K:273:GLU:HA	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	278/284 (98%)	274 (99%)	4 (1%)	0	100	100
1	B	278/284 (98%)	274 (99%)	4 (1%)	0	100	100
1	C	277/284 (98%)	274 (99%)	3 (1%)	0	100	100
1	D	275/284 (97%)	269 (98%)	6 (2%)	0	100	100
1	E	277/284 (98%)	275 (99%)	2 (1%)	0	100	100
1	F	278/284 (98%)	272 (98%)	5 (2%)	1 (0%)	30	49
1	G	279/284 (98%)	274 (98%)	5 (2%)	0	100	100
1	H	278/284 (98%)	274 (99%)	4 (1%)	0	100	100
1	I	278/284 (98%)	274 (99%)	4 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	J	277/284 (98%)	271 (98%)	6 (2%)	0	100	100
1	K	279/284 (98%)	275 (99%)	4 (1%)	0	100	100
1	L	278/284 (98%)	273 (98%)	5 (2%)	0	100	100
All	All	3332/3408 (98%)	3279 (98%)	52 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	126	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	228/232 (98%)	227 (100%)	1 (0%)	84	93
1	B	228/232 (98%)	227 (100%)	1 (0%)	84	93
1	C	227/232 (98%)	227 (100%)	0	100	100
1	D	225/232 (97%)	225 (100%)	0	100	100
1	E	227/232 (98%)	225 (99%)	2 (1%)	70	87
1	F	228/232 (98%)	228 (100%)	0	100	100
1	G	229/232 (99%)	229 (100%)	0	100	100
1	H	228/232 (98%)	227 (100%)	1 (0%)	84	93
1	I	228/232 (98%)	227 (100%)	1 (0%)	84	93
1	J	227/232 (98%)	227 (100%)	0	100	100
1	K	229/232 (99%)	229 (100%)	0	100	100
1	L	228/232 (98%)	227 (100%)	1 (0%)	84	93
All	All	2732/2784 (98%)	2725 (100%)	7 (0%)	86	94

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	281	LEU
1	B	81	GLU
1	E	84	ARG
1	E	120	LEU
1	H	281	LEU
1	I	81	GLU
1	L	269	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	59	HIS
1	D	59	HIS
1	E	231	ASN
1	G	182	GLN
1	G	231	ASN
1	H	182	GLN
1	H	231	ASN
1	I	196	ASN
1	K	9	ASN
1	L	231	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 52 ligands modelled in this entry, 16 are monoatomic - leaving 36 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

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	302	ADP	C2-N1-C6	2.14	122.24	118.73
2	E	303	ADP	C2-N1-C6	2.12	122.21	118.73
2	A	501	ADP	C2-N1-C6	2.11	122.20	118.73
2	G	501	ADP	C2-N1-C6	2.09	122.17	118.73
2	L	401	ADP	C2-N1-C6	2.09	122.16	118.73
2	D	401	ADP	C2-N1-C6	2.06	122.11	118.73

There are no chirality outliers.

All (9) torsion outliers are listed below:

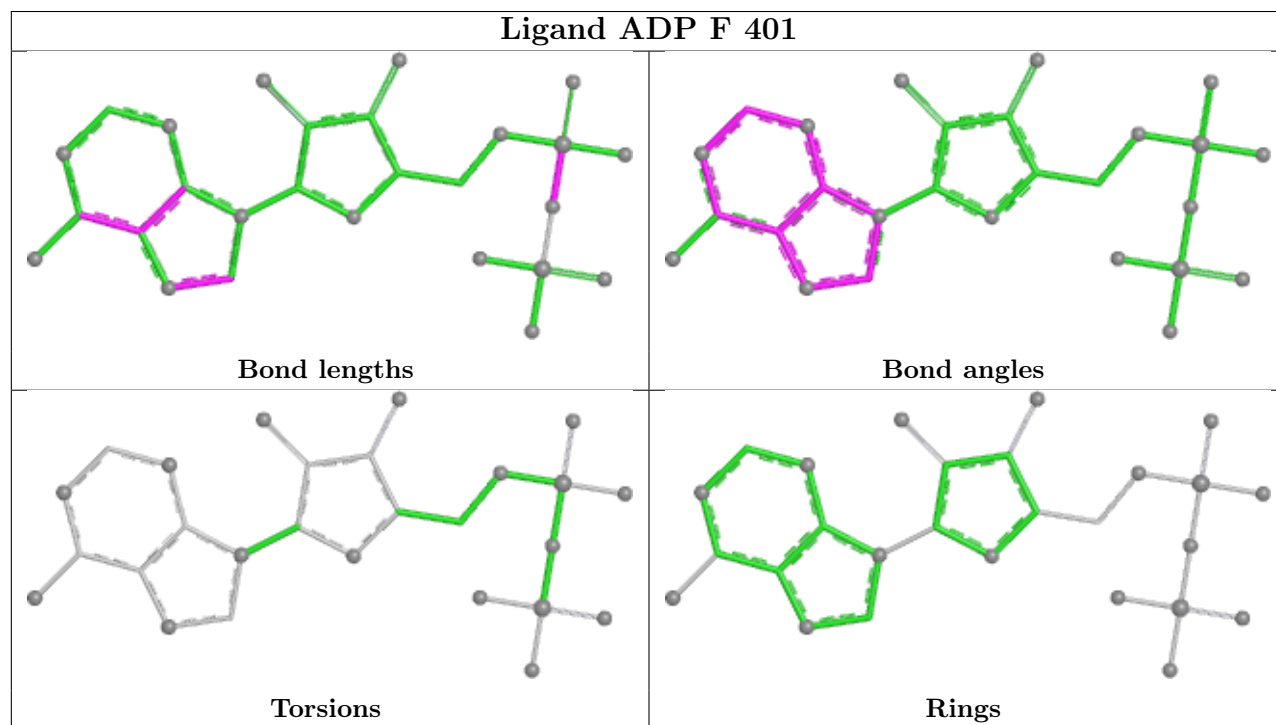
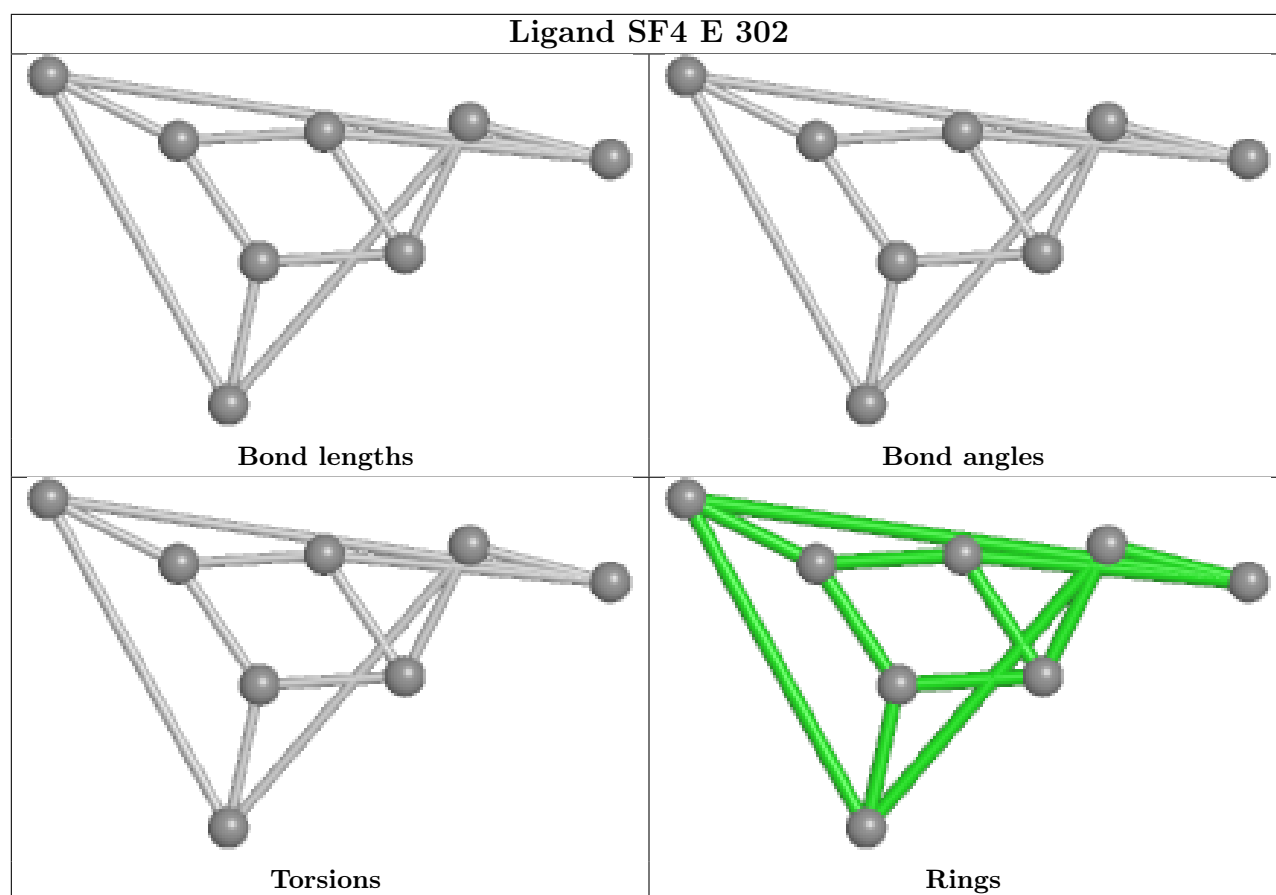
Mol	Chain	Res	Type	Atoms
8	K	305	GOL	O1-C1-C2-C3
8	K	305	GOL	O1-C1-C2-O2
8	I	306	GOL	O1-C1-C2-C3
5	I	308	EDO	O1-C1-C2-O2
5	G	503	EDO	O1-C1-C2-O2
8	I	306	GOL	O2-C2-C3-O3
5	I	304	EDO	O1-C1-C2-O2
5	G	504	EDO	O1-C1-C2-O2
2	A	501	ADP	PA-O3A-PB-O1B

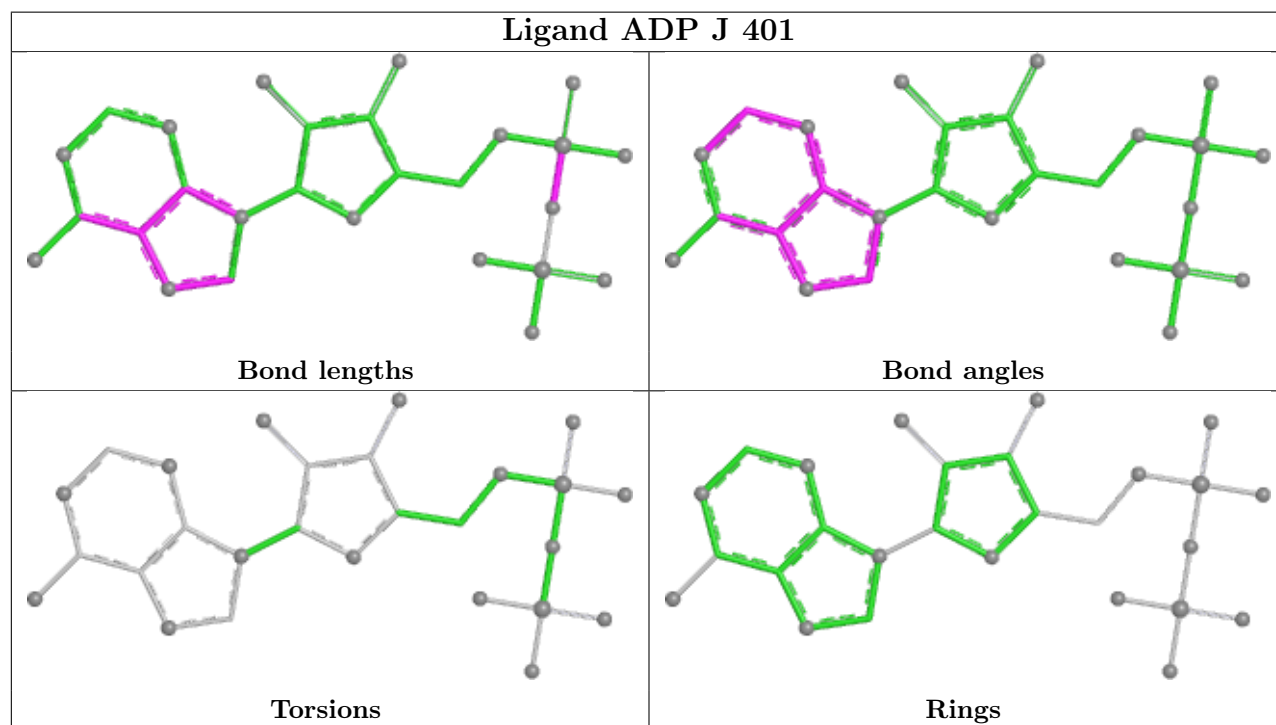
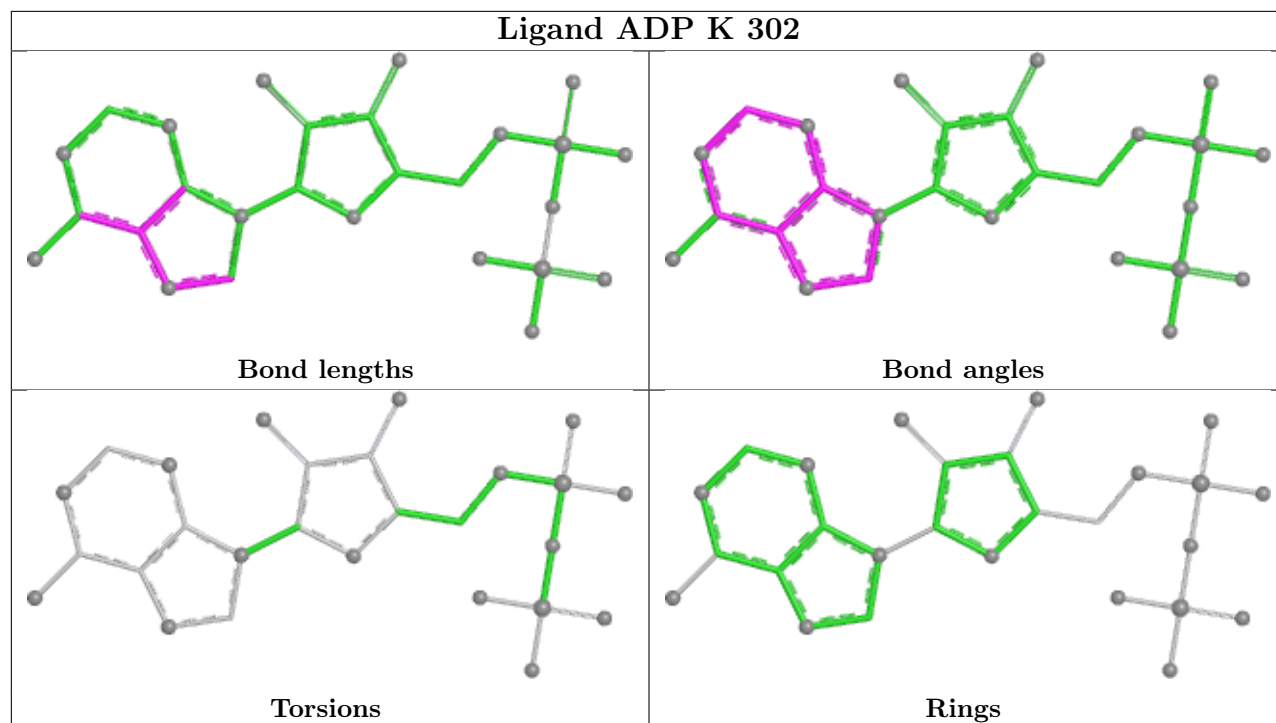
There are no ring outliers.

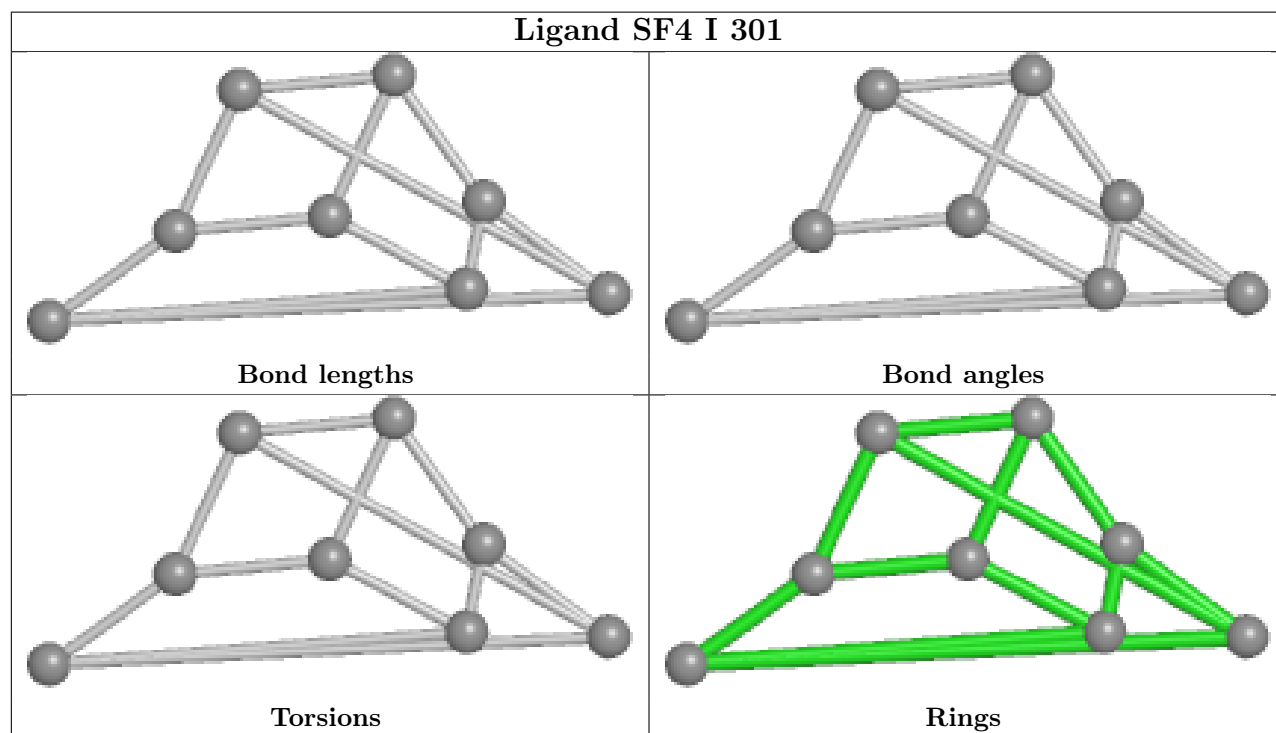
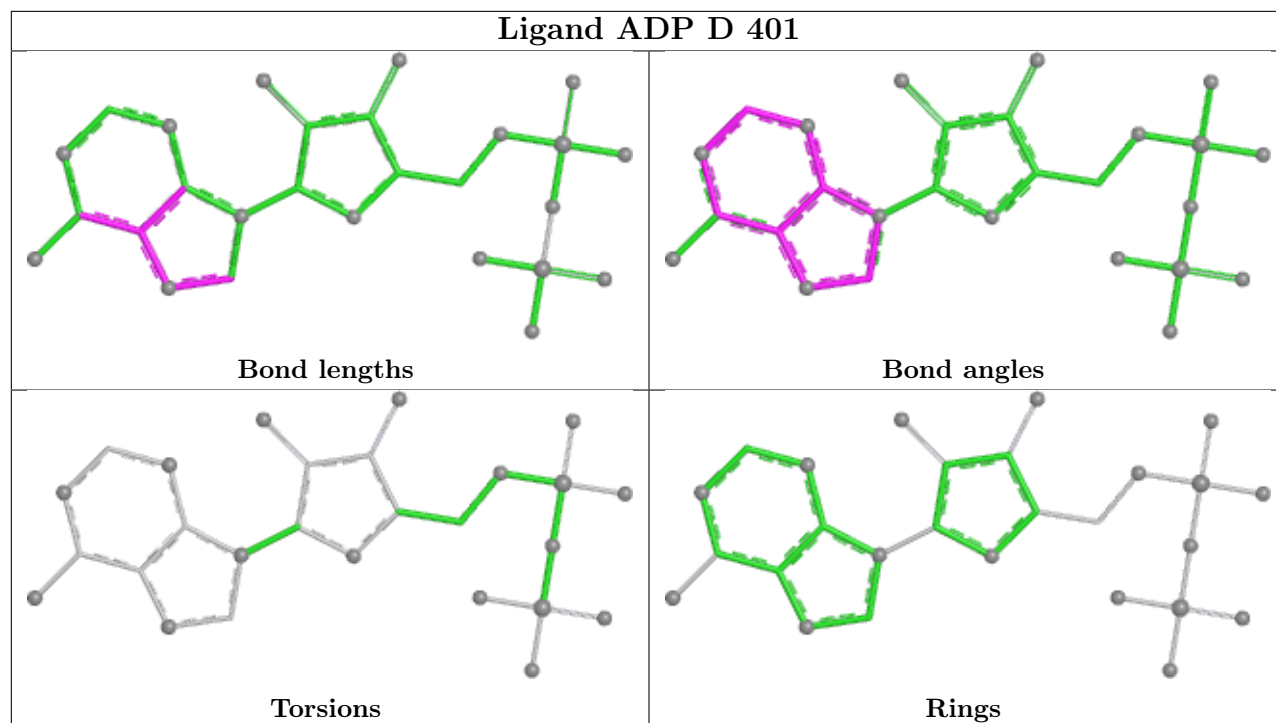
2 monomers are involved in 2 short contacts:

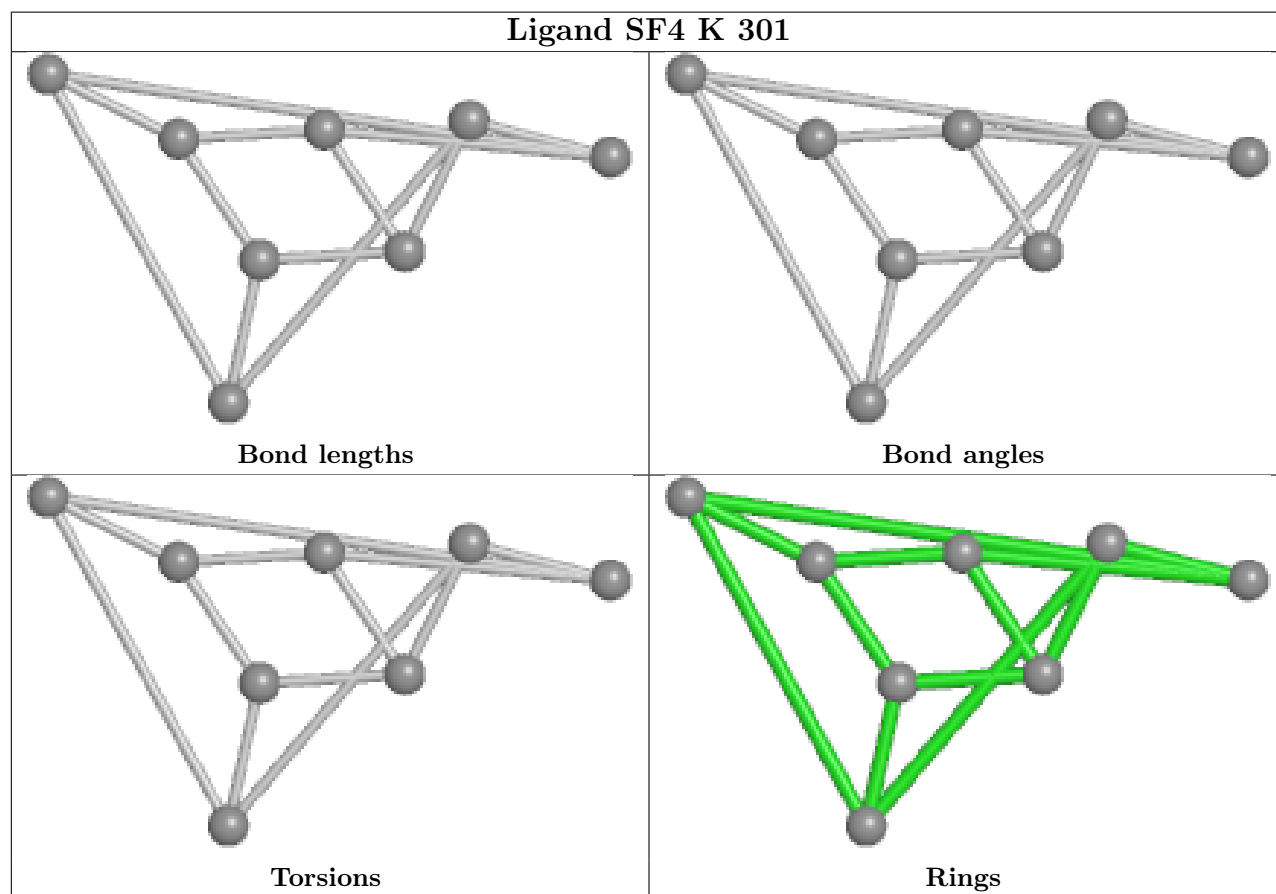
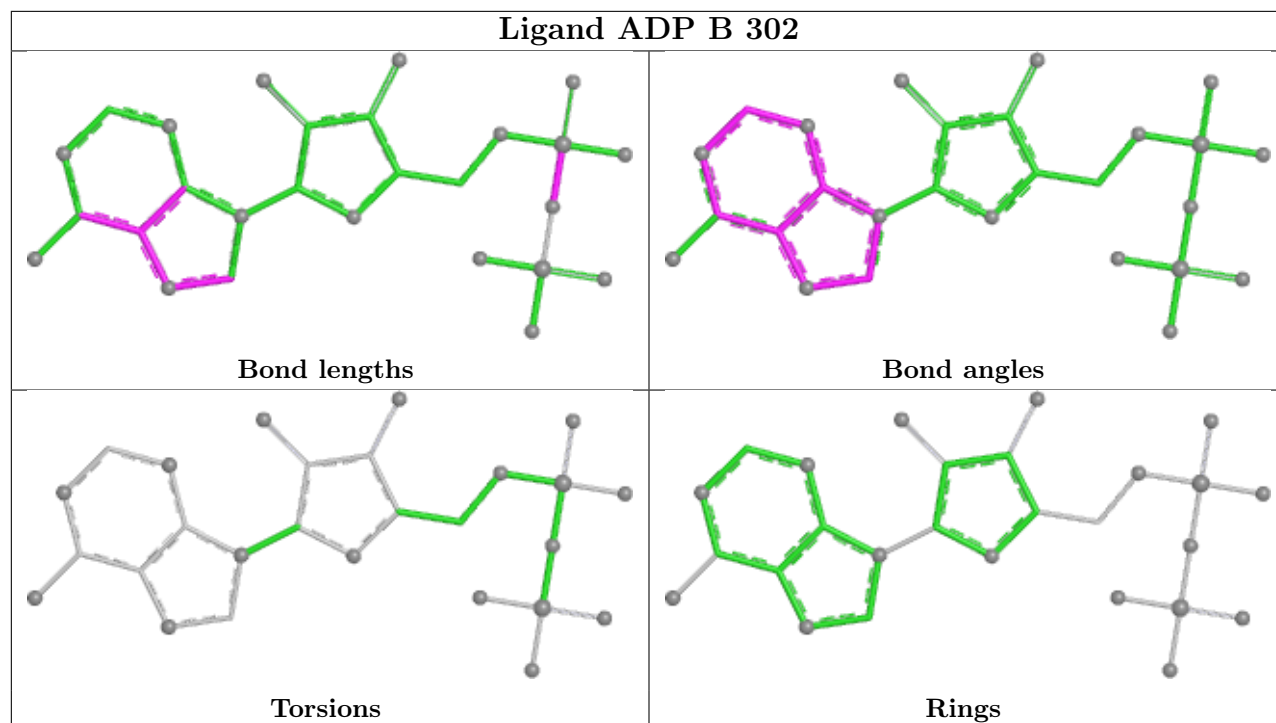
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	K	302	ADP	1	0
4	I	305	NO3	1	0

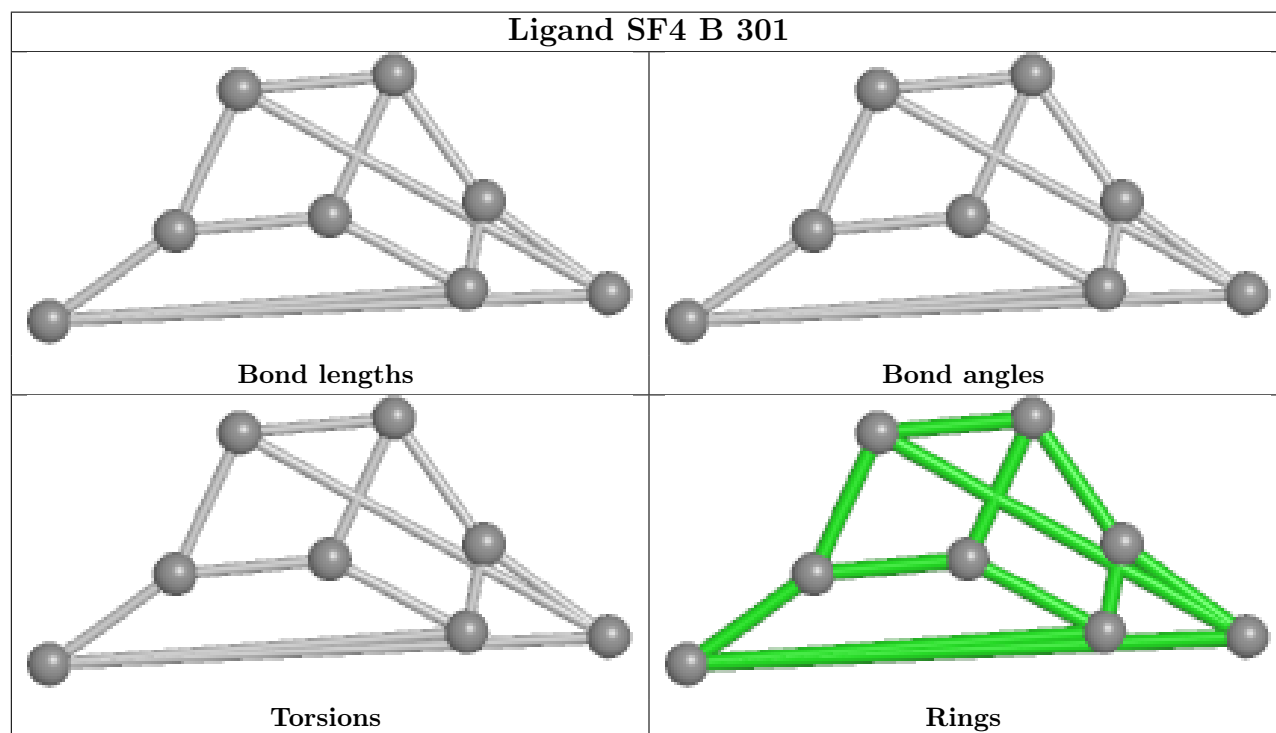
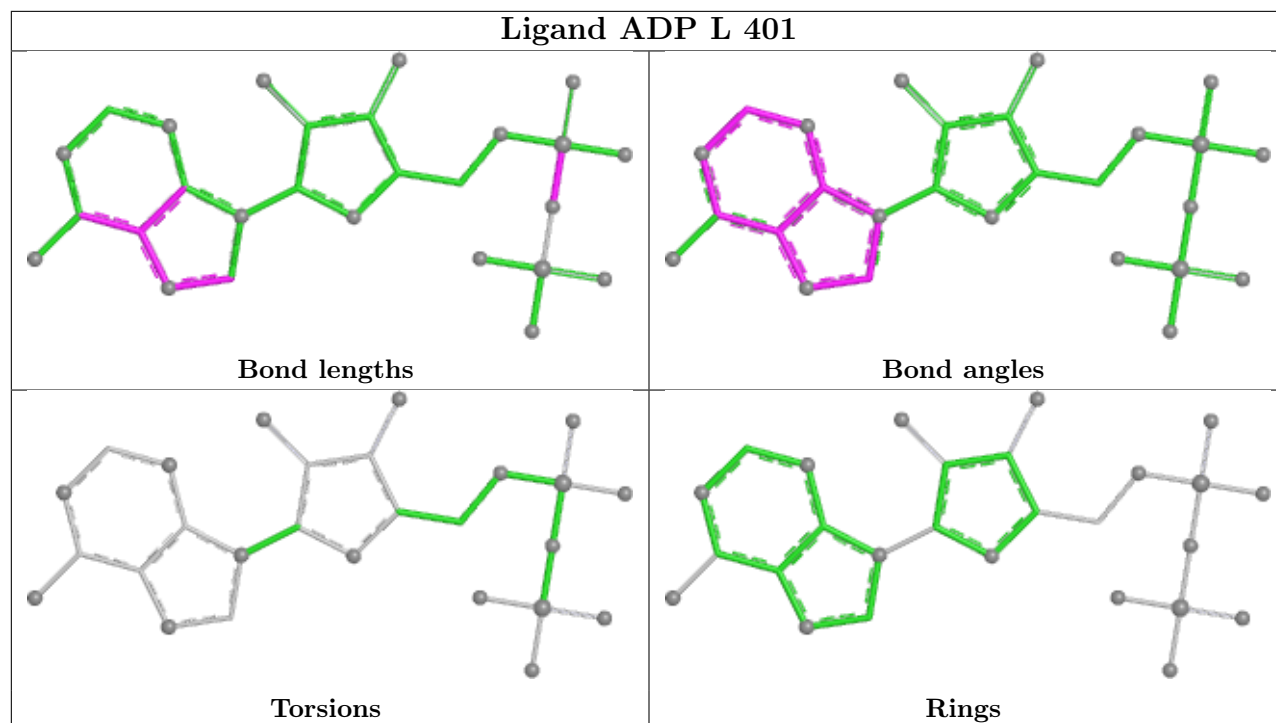
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

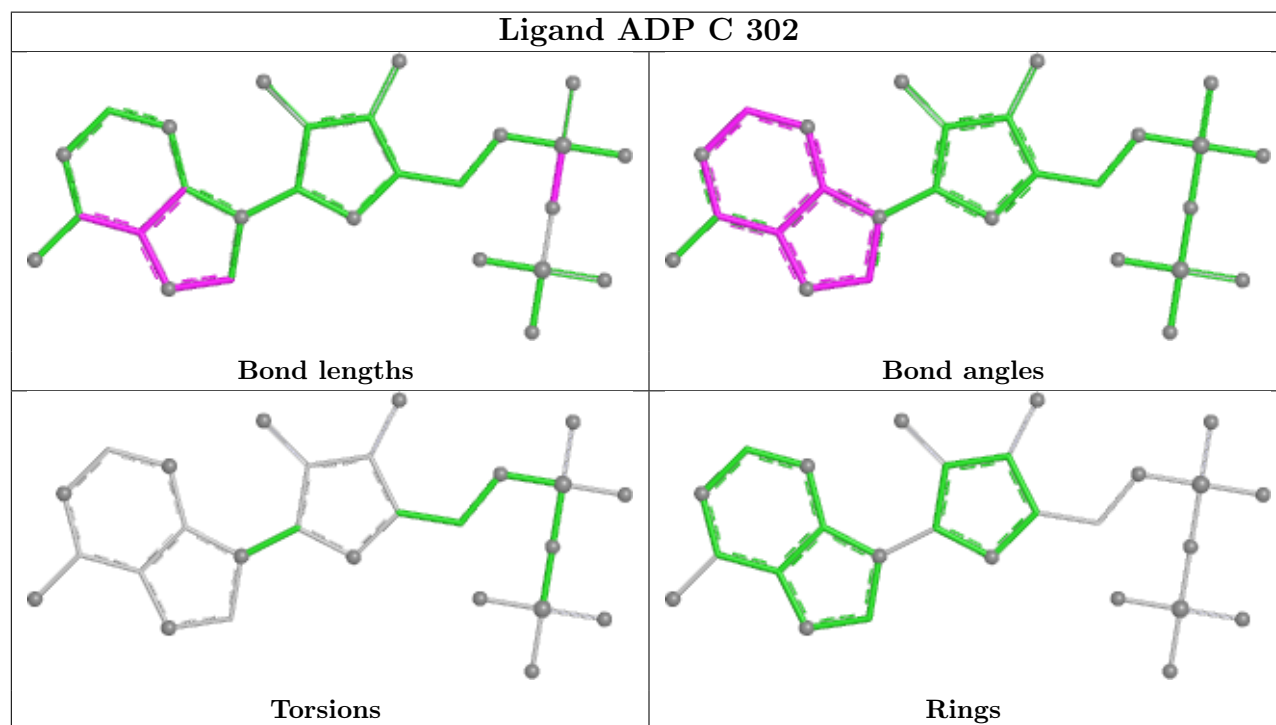
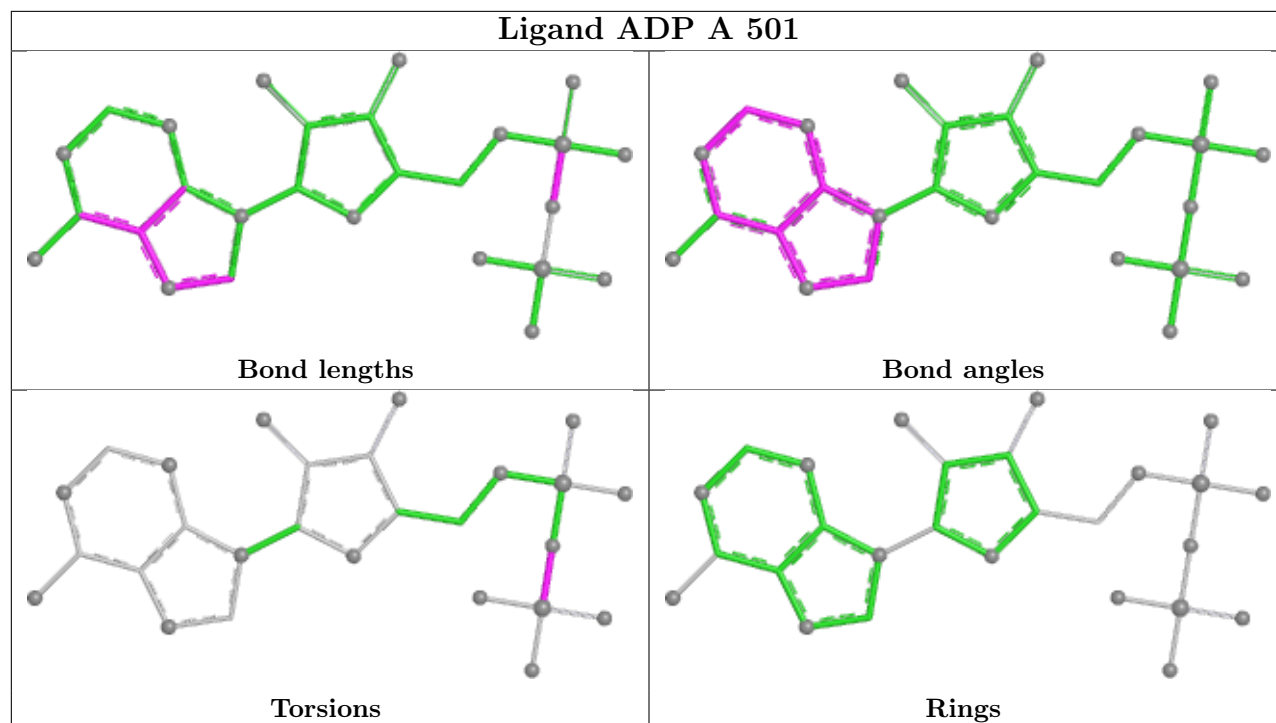




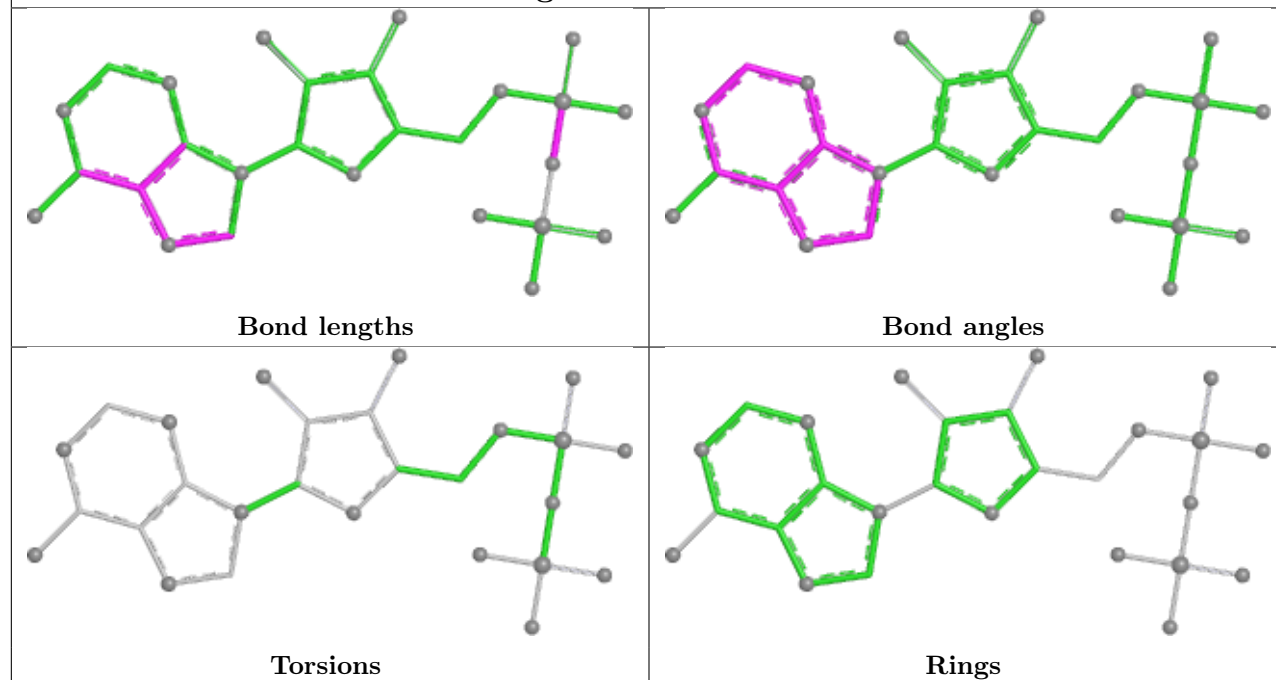




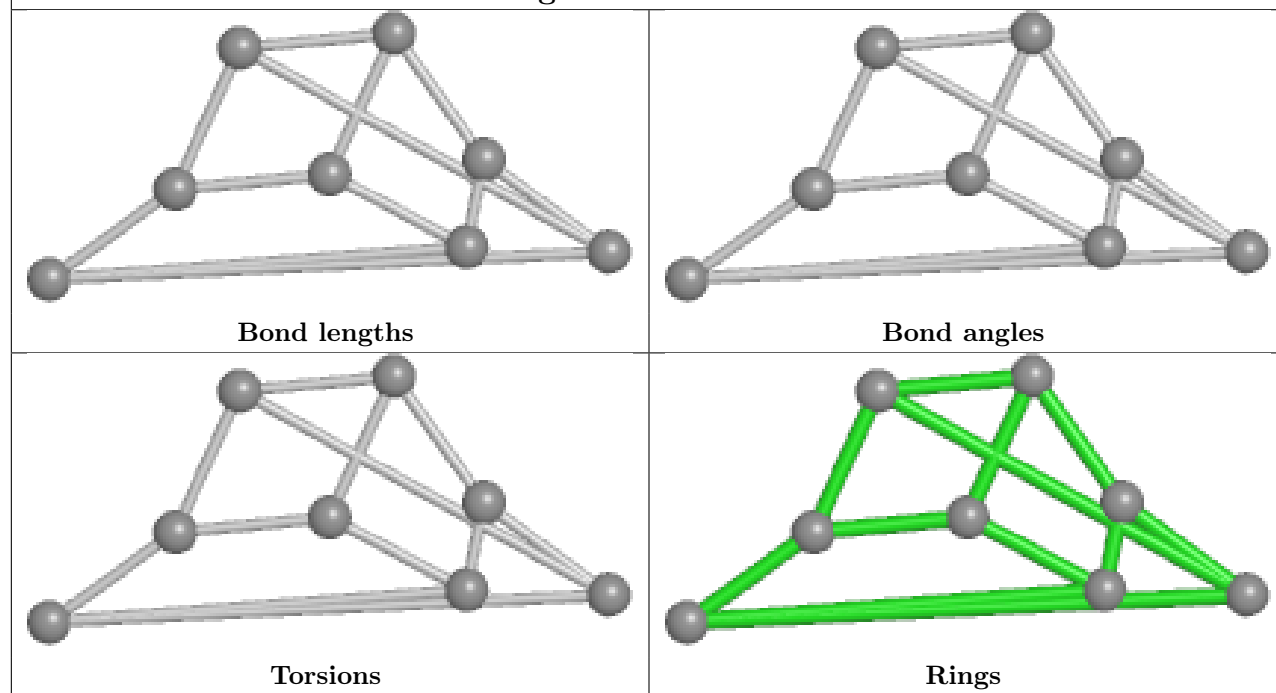


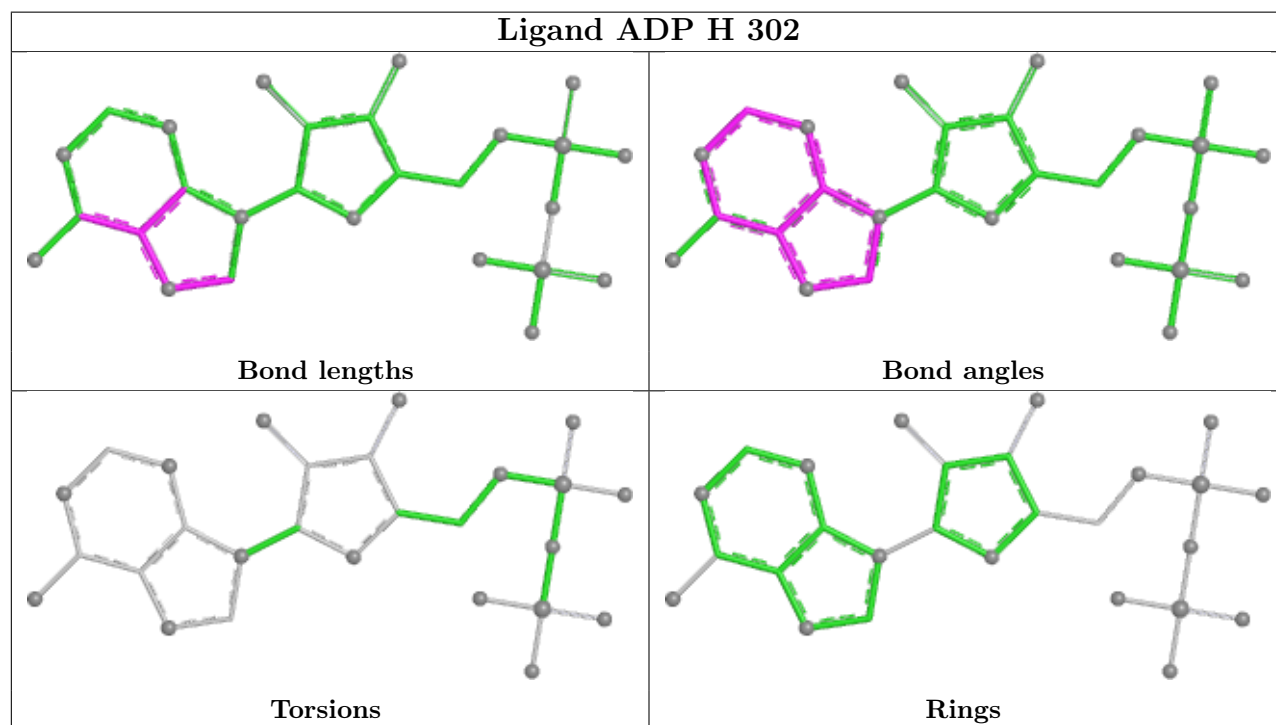
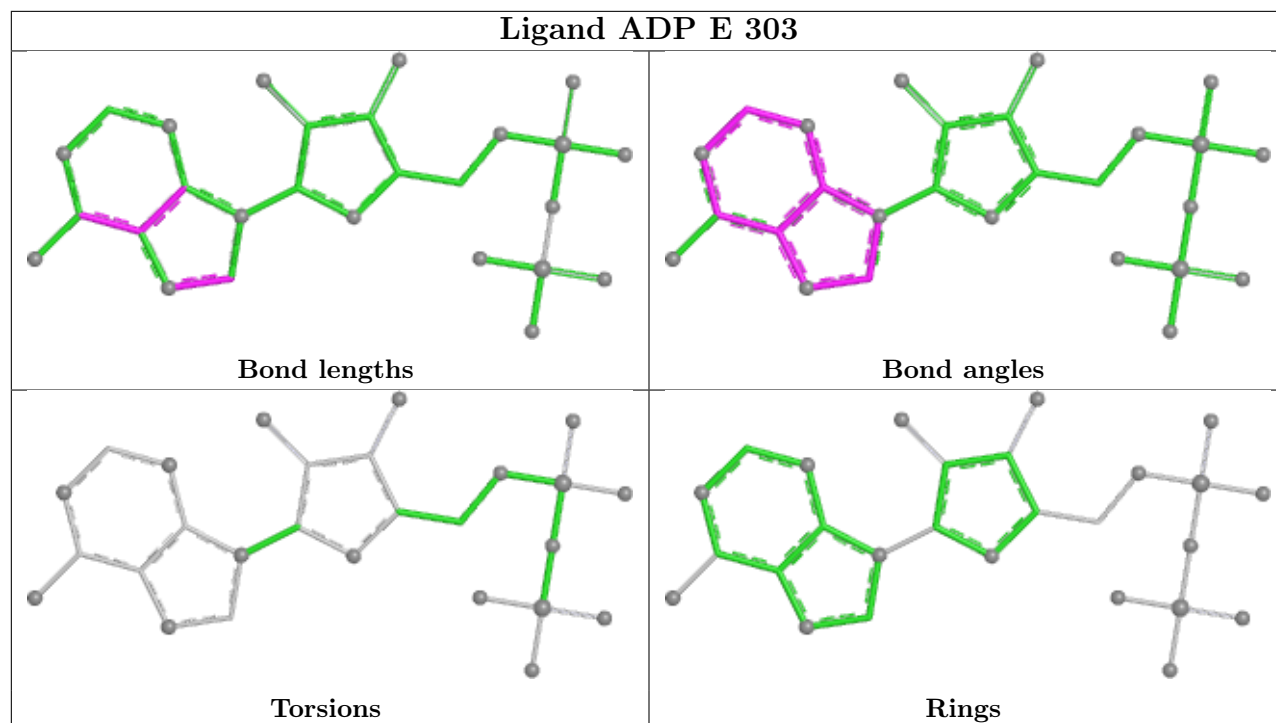


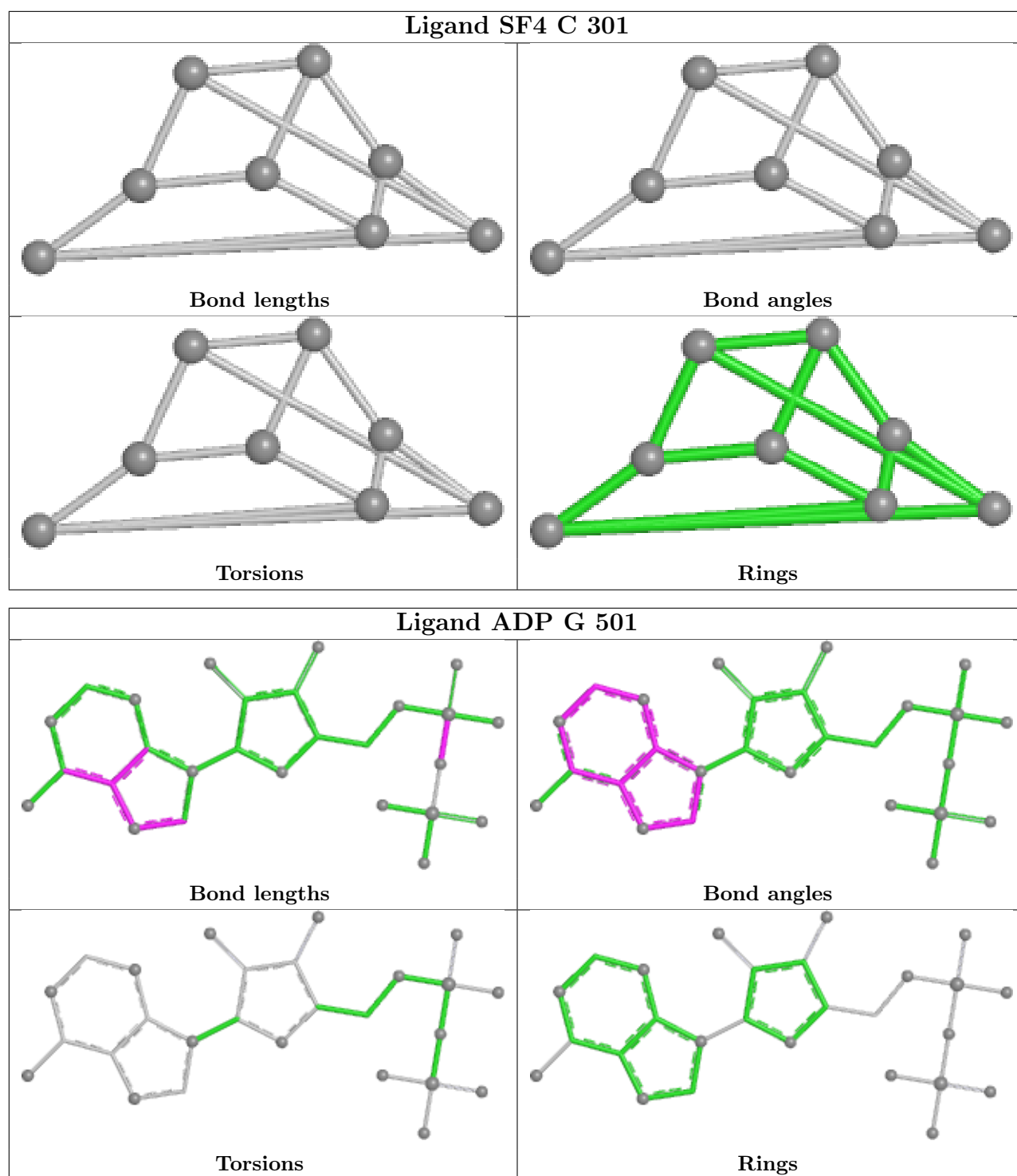
Ligand ADP I 302



Ligand SF4 H 301







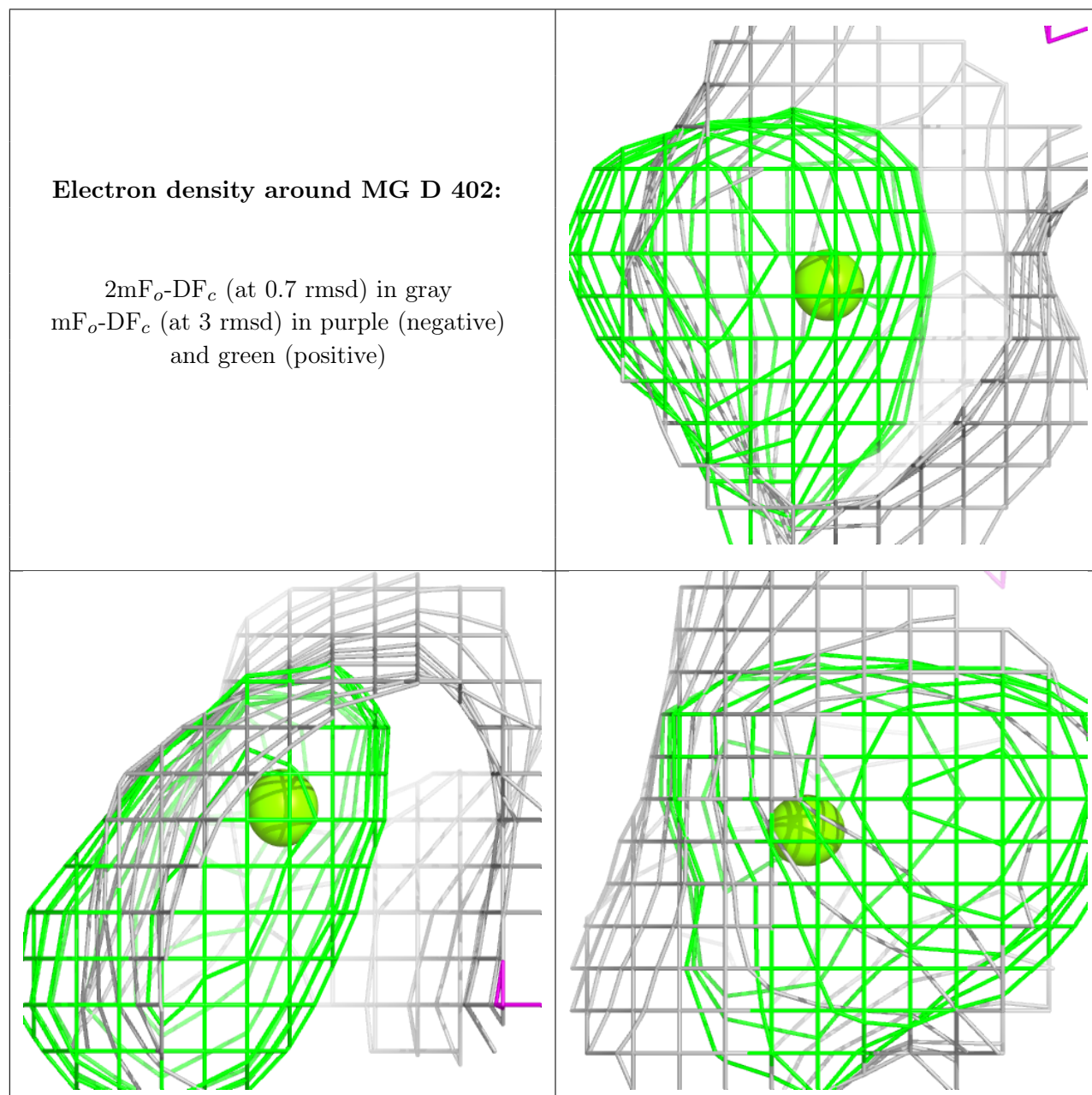
5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

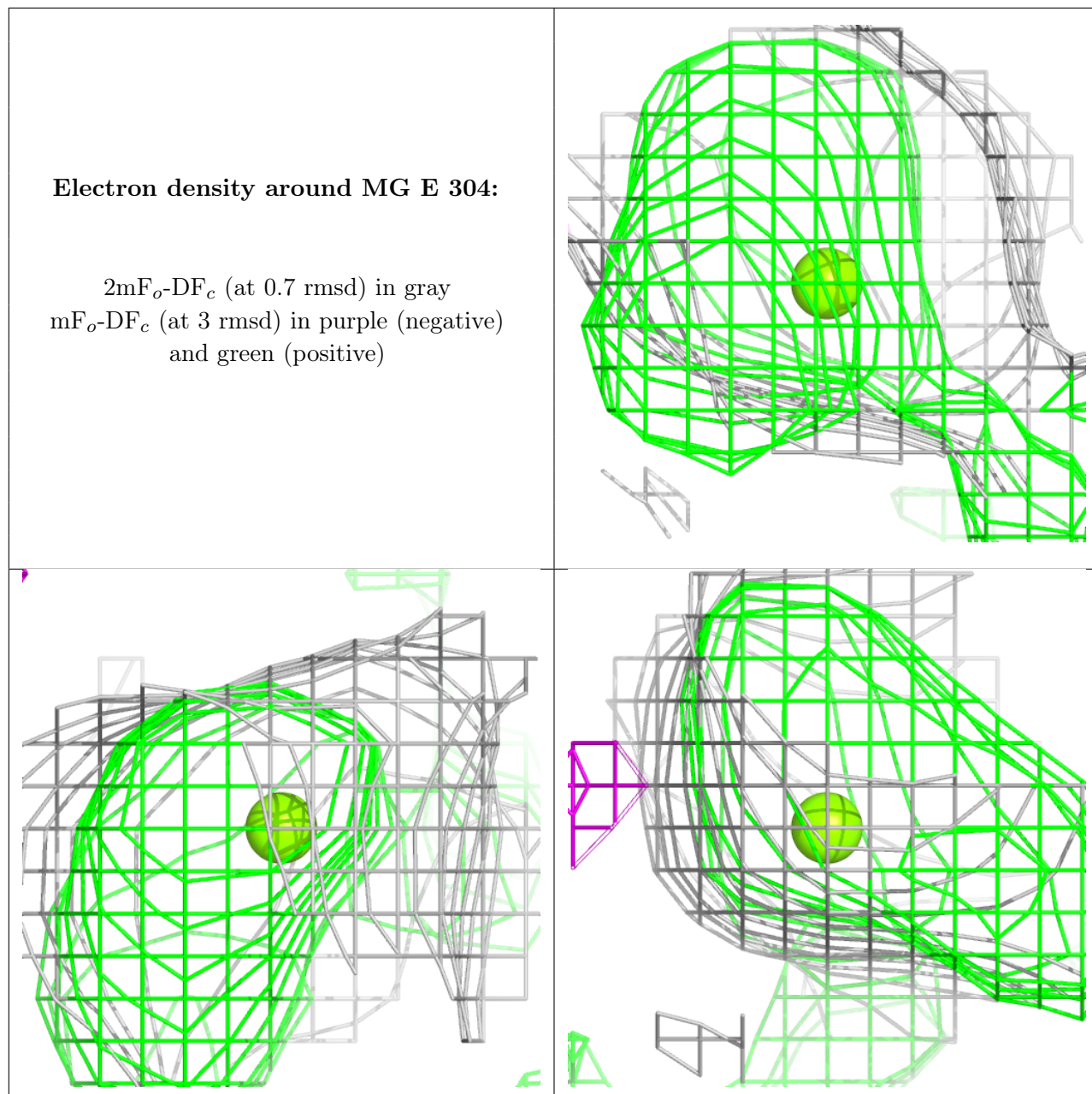
There are no chain breaks in this entry.

as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



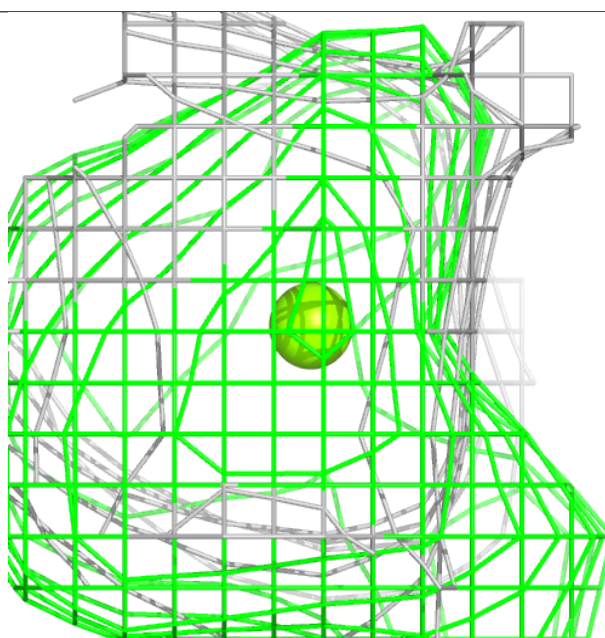
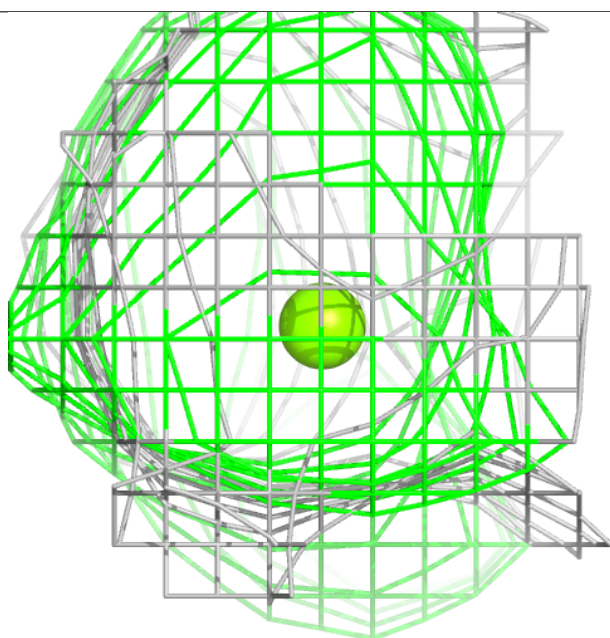
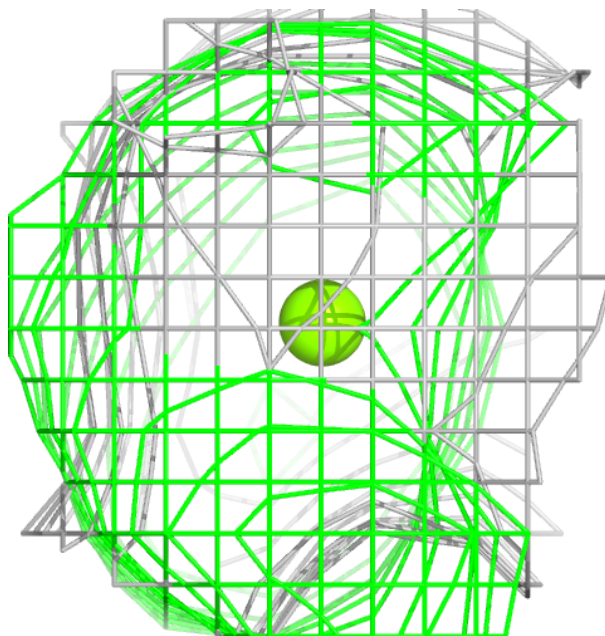
Electron density around MG E 304:

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



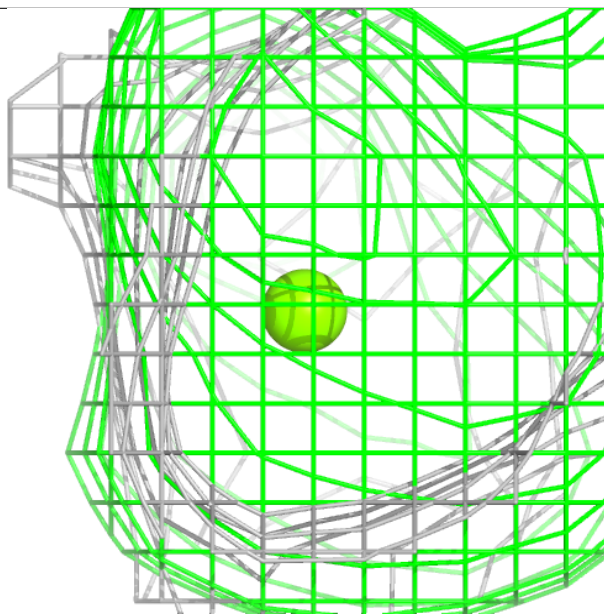
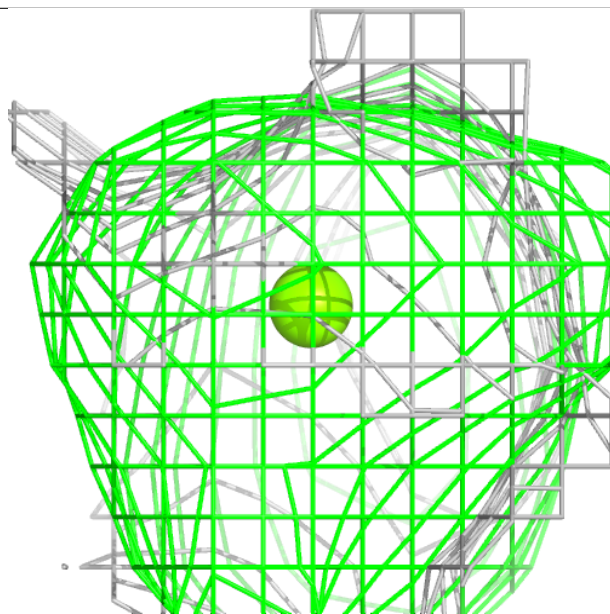
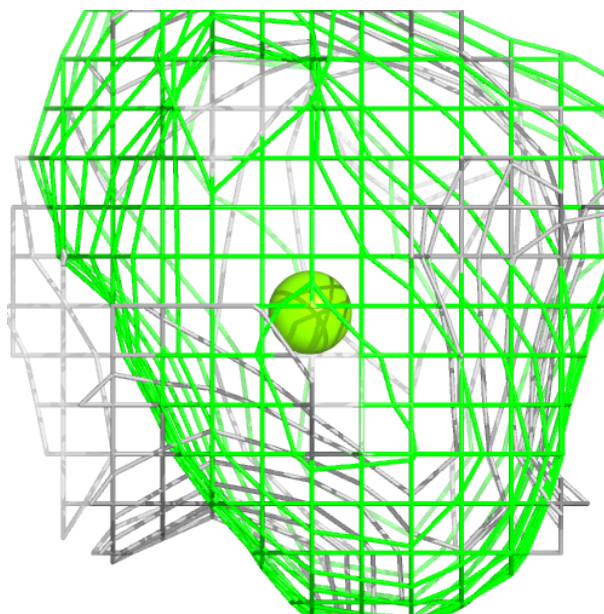
Electron density around MG C 303:

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



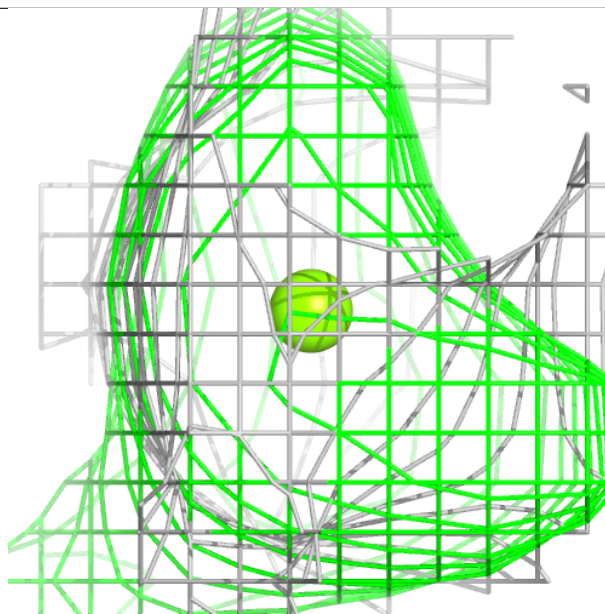
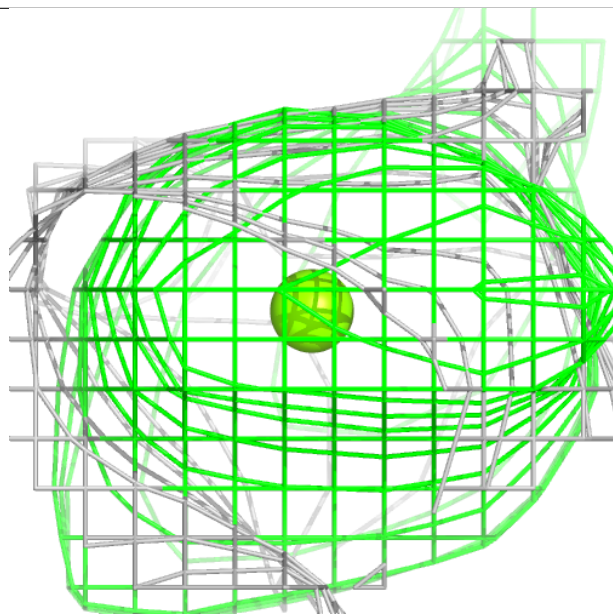
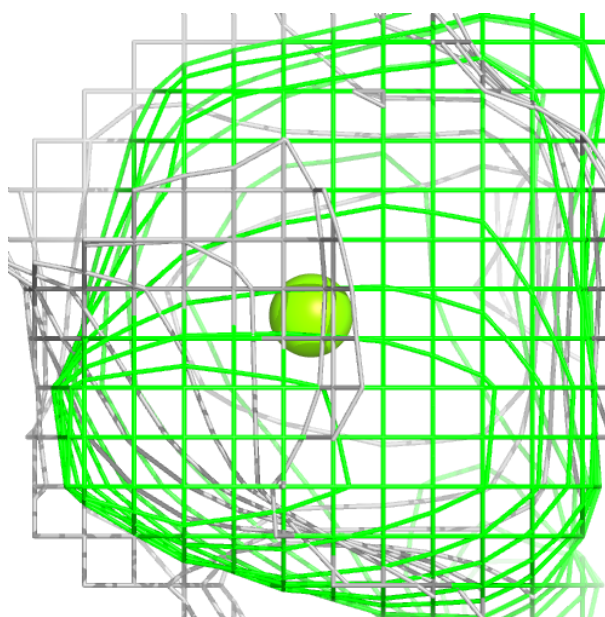
Electron density around MG I 303:

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



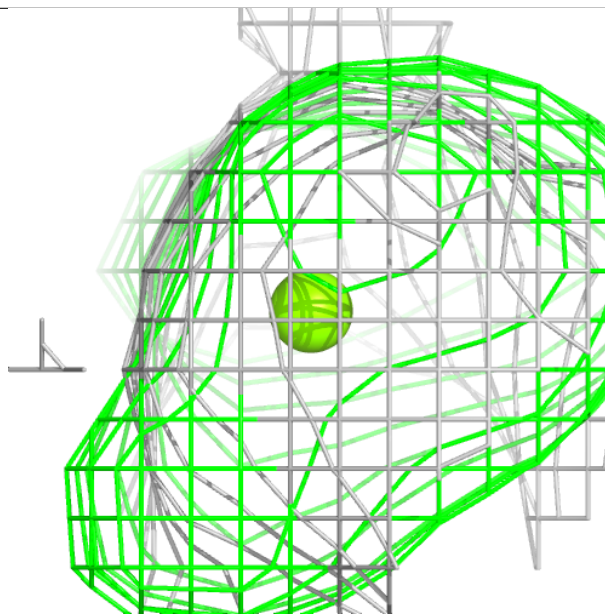
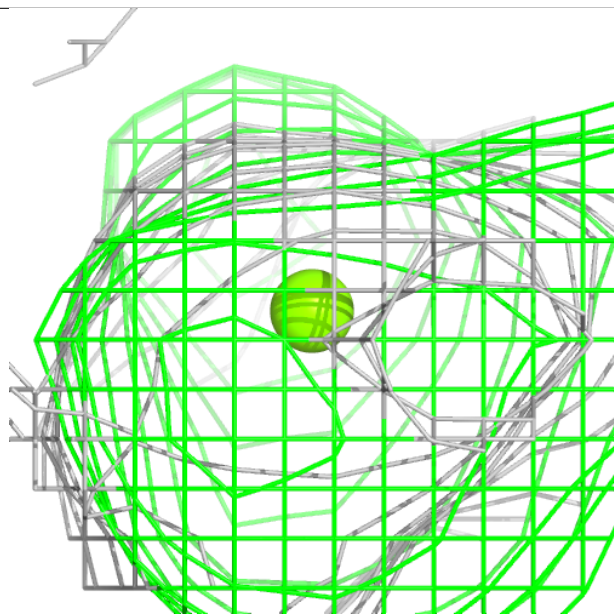
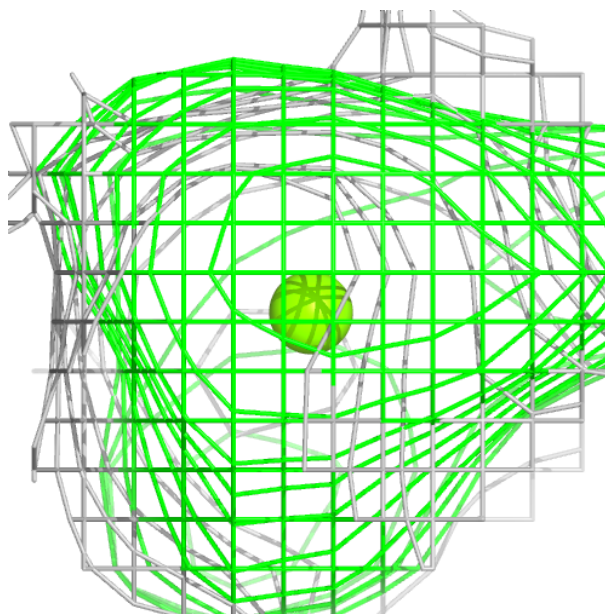
Electron density around MG K 303:

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



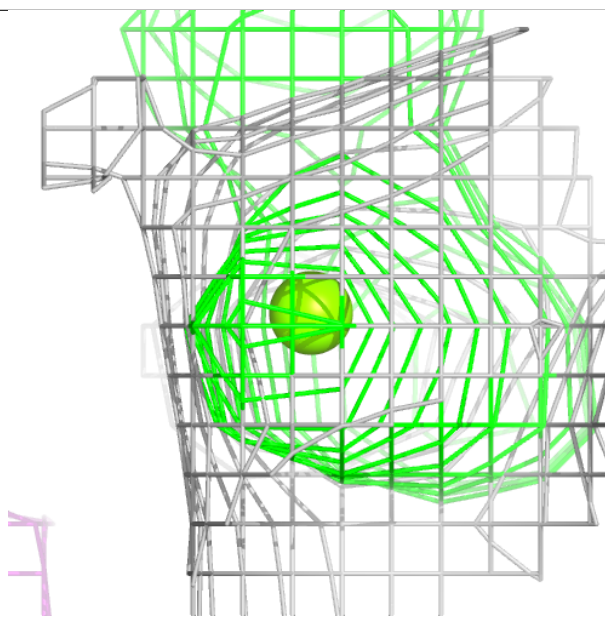
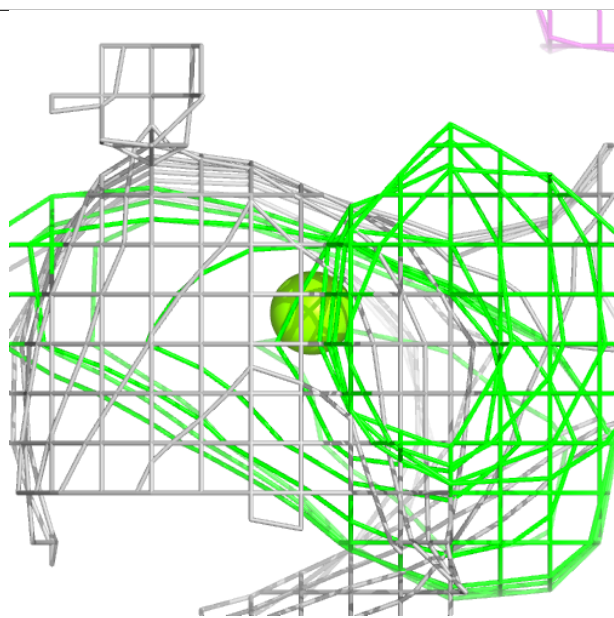
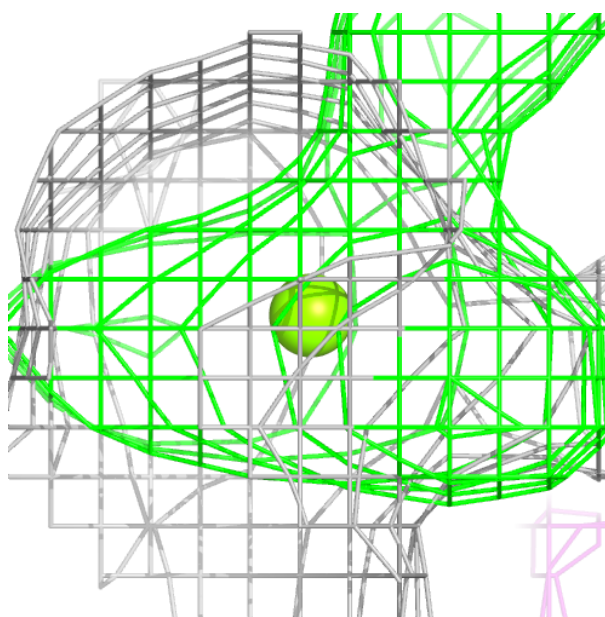
Electron density around MG L 402:

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



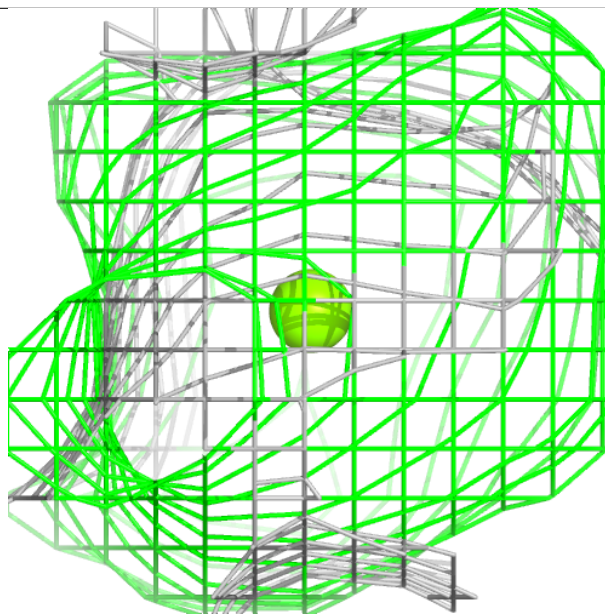
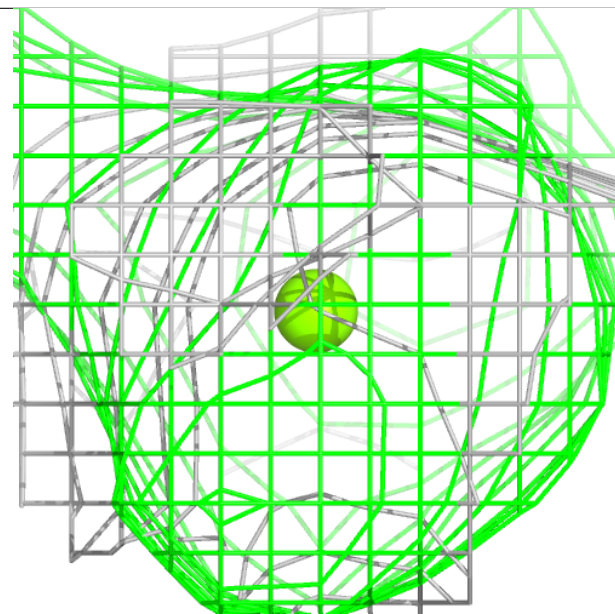
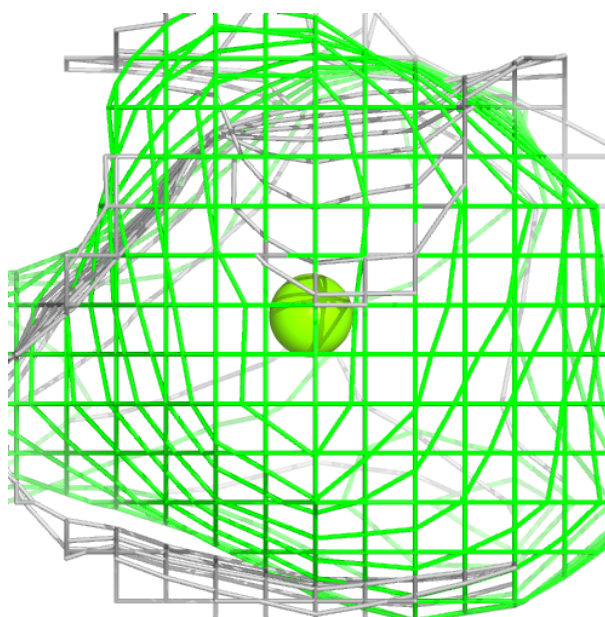
Electron density around MG J 402:

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



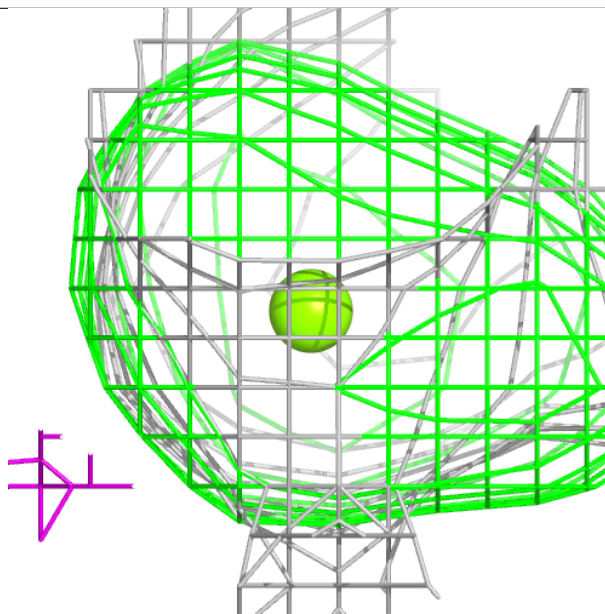
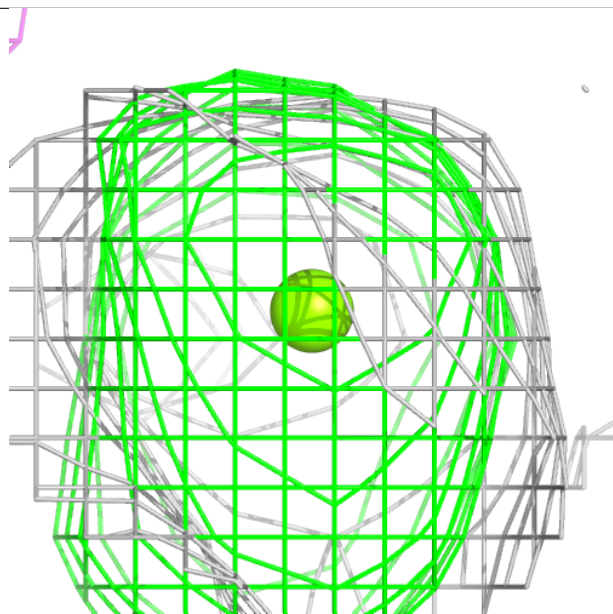
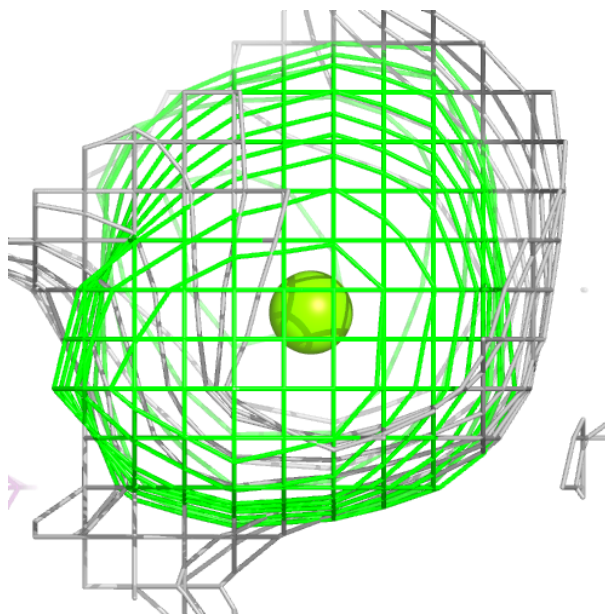
Electron density around MG B 303:

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



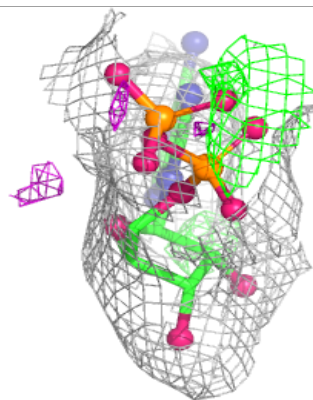
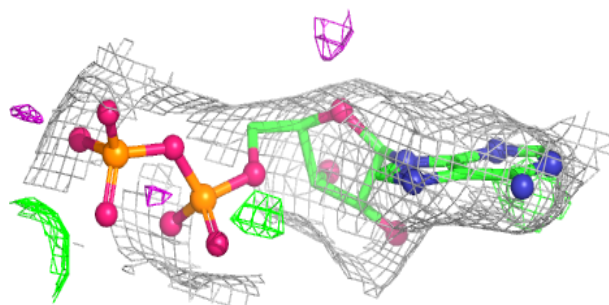
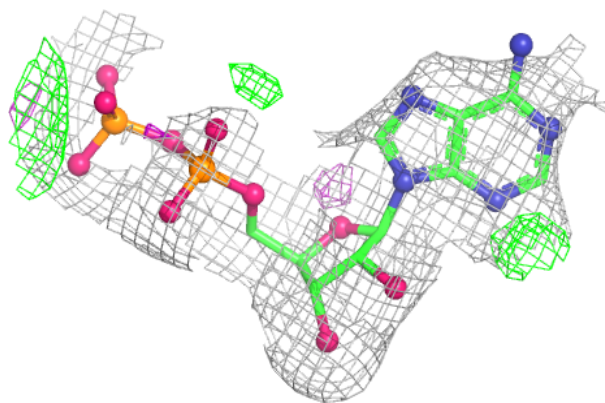
Electron density around MG F 402:

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



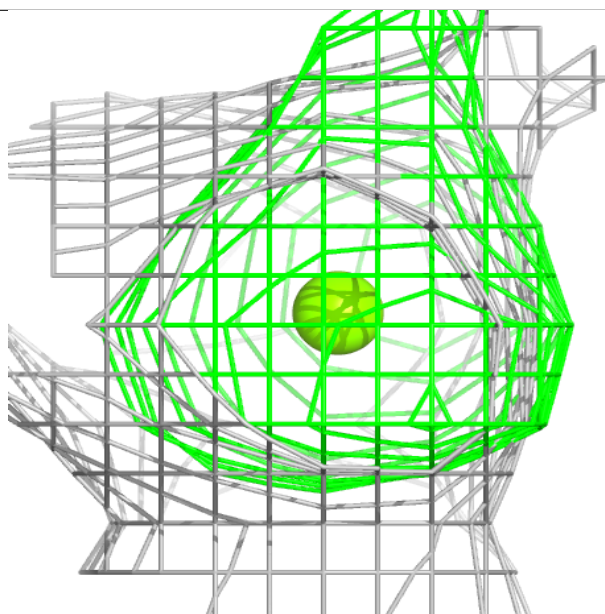
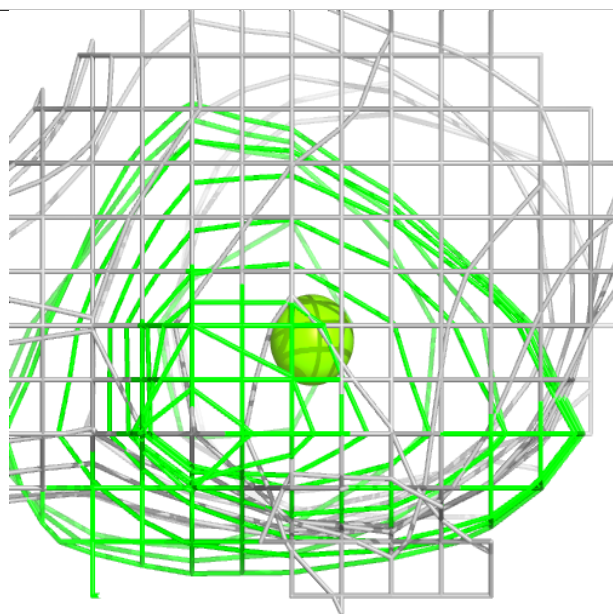
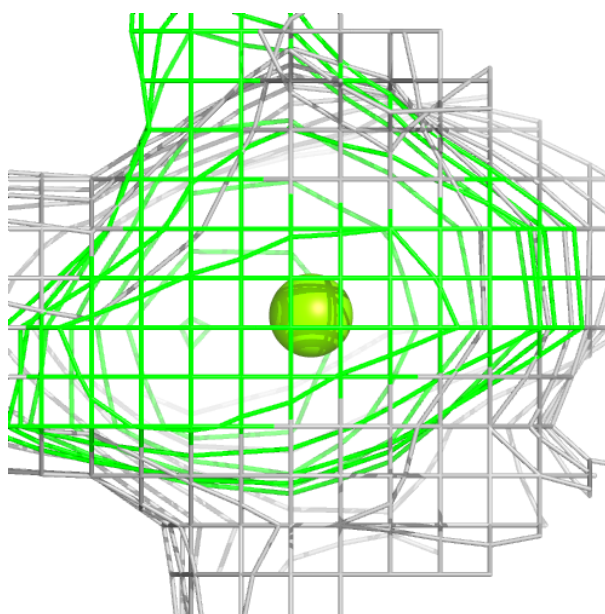
Electron density around ADP D 401:

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



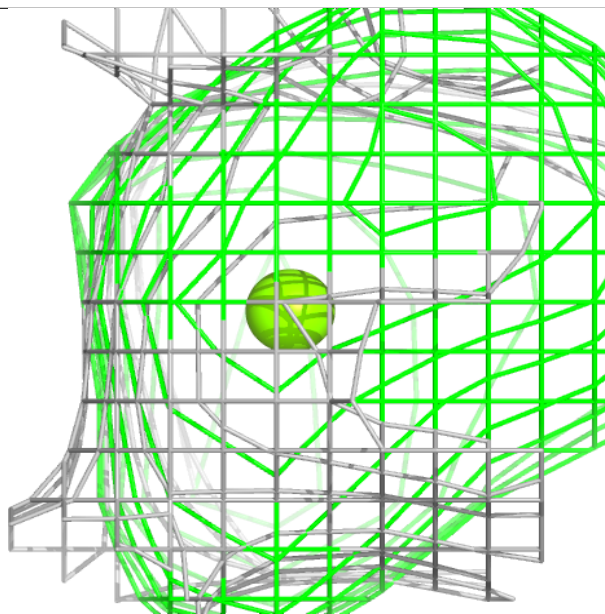
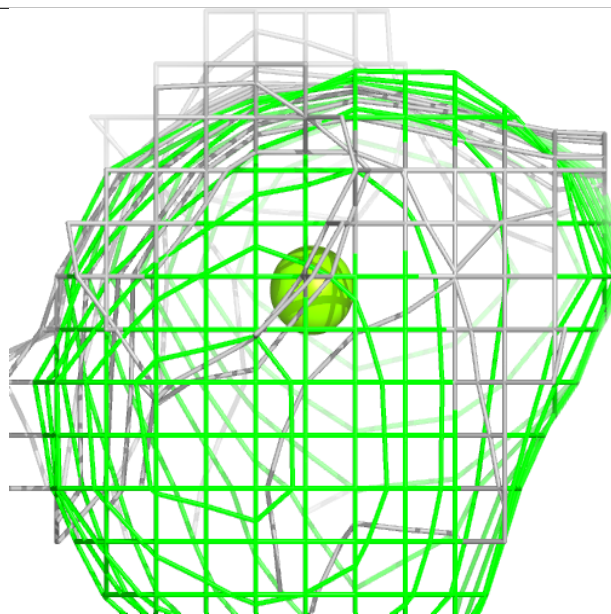
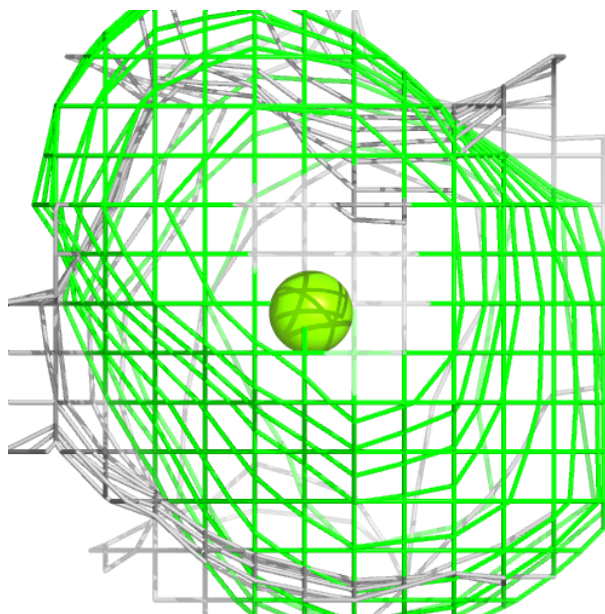
Electron density around MG A 502:

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



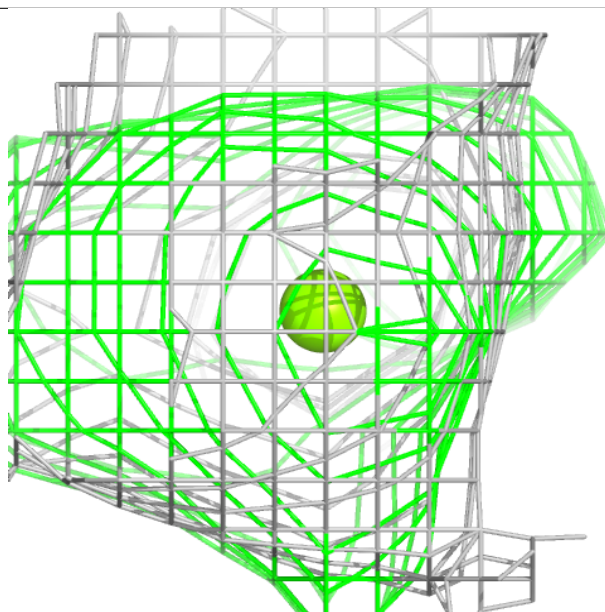
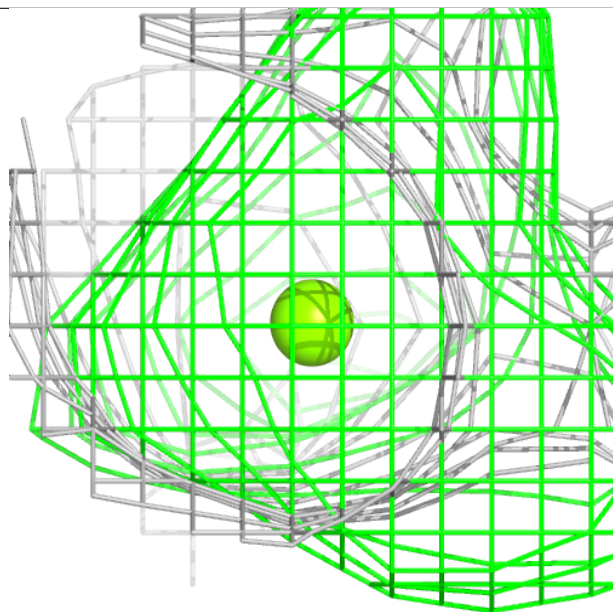
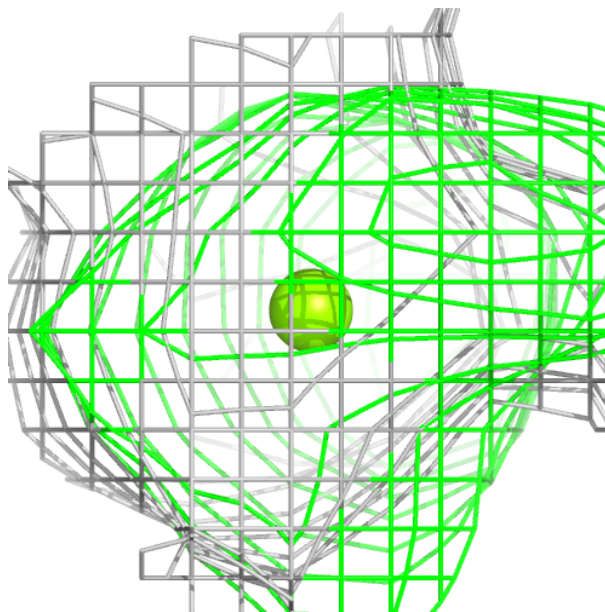
Electron density around MG H 303:

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



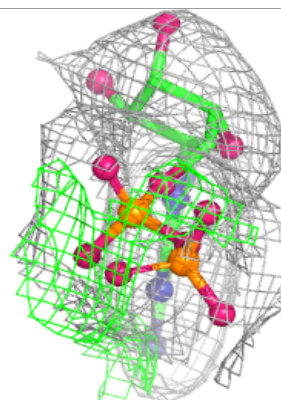
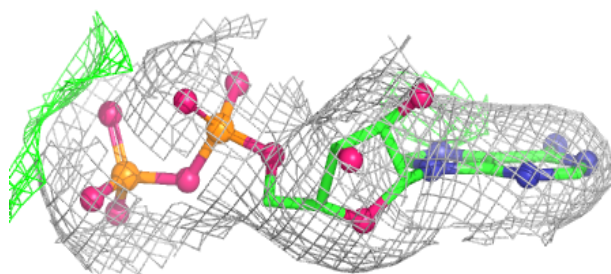
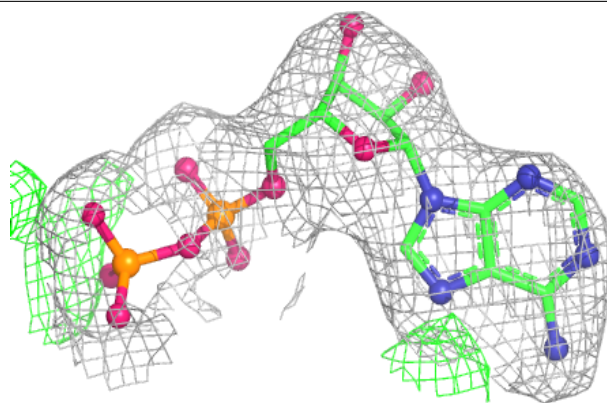
Electron density around MG G 502:

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

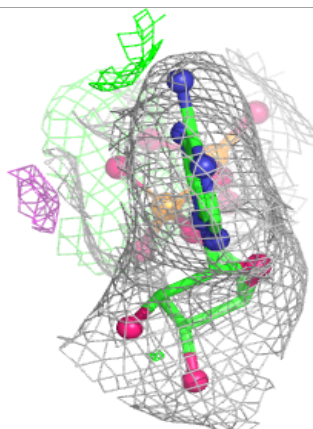
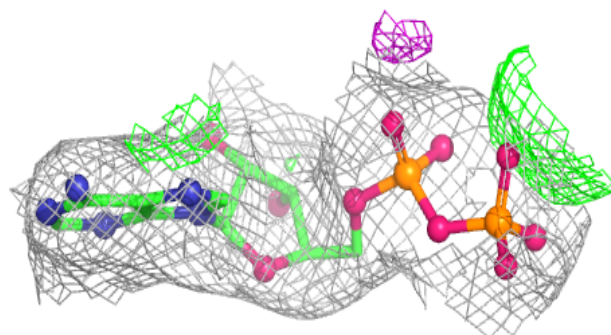
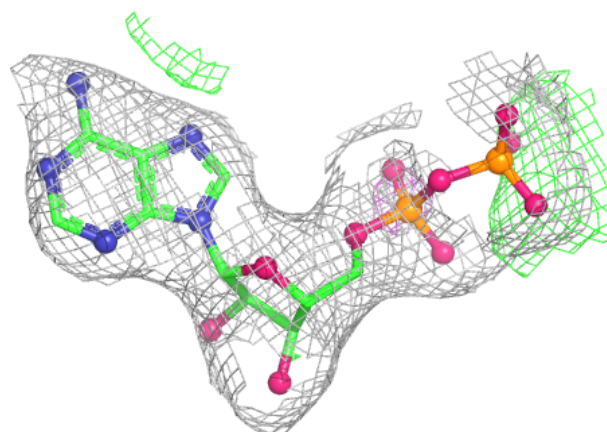


Electron density around ADP C 302:

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

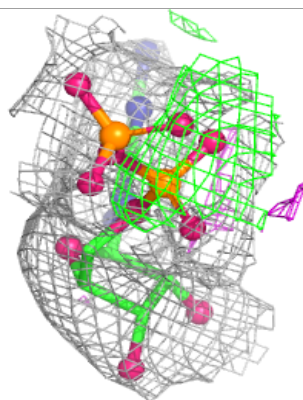
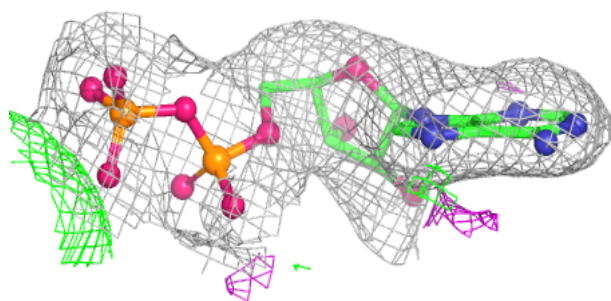
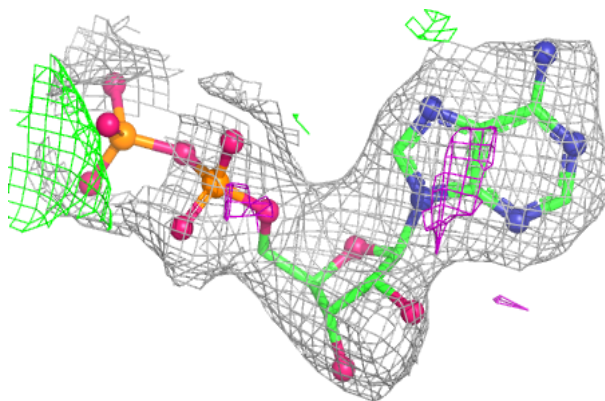
**Electron density around ADP H 302:**

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

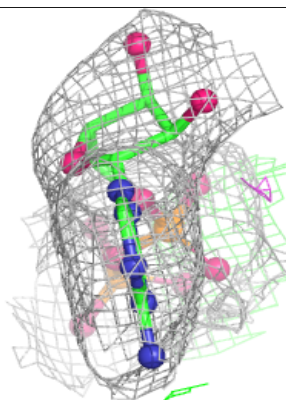
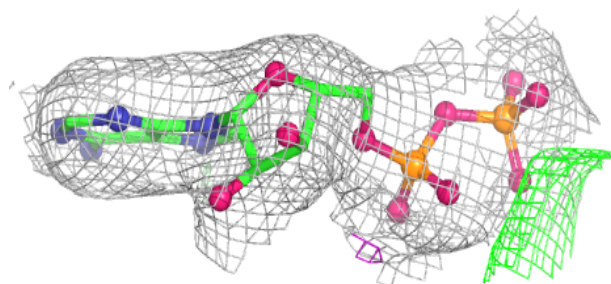
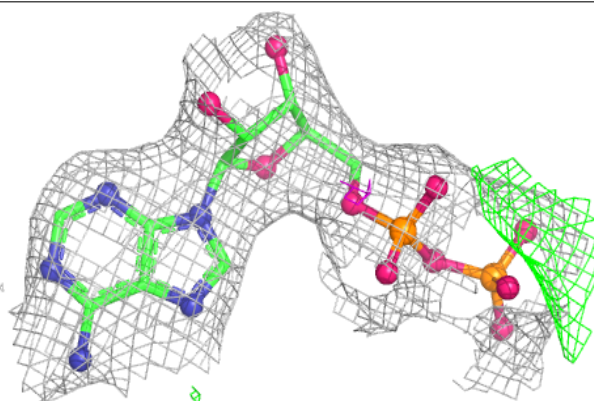


Electron density around ADP G 501:

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

**Electron density around ADP K 302:**

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



Electron density around ADP I 302:

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

