



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 30, 2020 – 02:20 PM EDT

PDB ID : 6X5K
Title : Crystal structure of CODH/ACS with carbon monoxide bound to the A-cluster
Authors : Cohen, S.E.; Wittenborn, E.C.; Hendrickson, R.; Drennan, C.L.
Deposited on : 2020-05-26
Resolution : 2.47 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.14.6
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) : 2.14.6

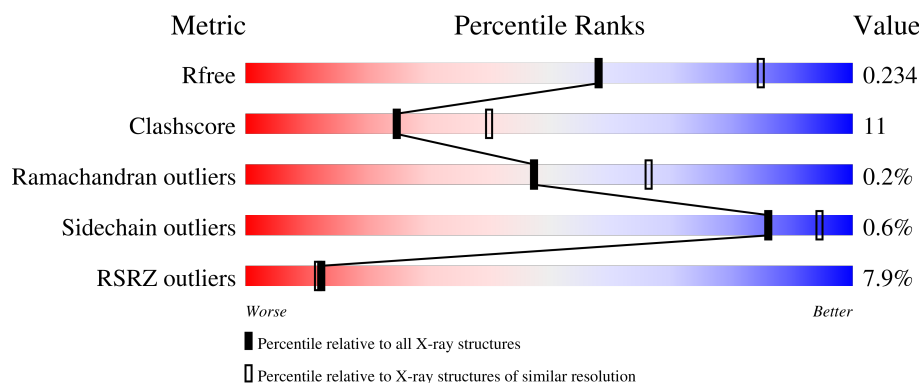
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.47 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.



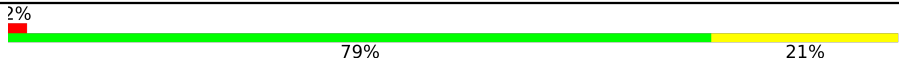
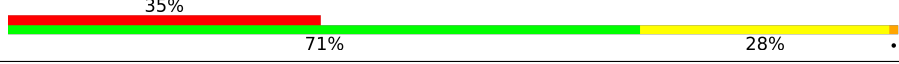
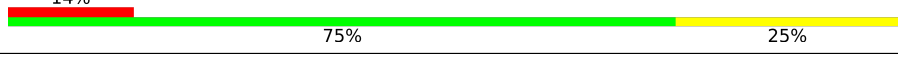
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5857 (2.50-2.46)
Clashscore	141614	6594 (2.50-2.46)
Ramachandran outliers	138981	6469 (2.50-2.46)
Sidechain outliers	138945	6471 (2.50-2.46)
RSRZ outliers	127900	5738 (2.50-2.46)

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 on 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	674	<div> <div>2%</div> <div>77%</div> <div>22%</div> </div>
1	B	674	<div> <div>78%</div> <div>21%</div> </div>
1	C	674	<div> <div>3%</div> <div>79%</div> <div>20%</div> </div>
1	D	674	<div> <div>3%</div> <div>77%</div> <div>22%</div> </div>
2	M	729	<div> <div>2%</div> <div>79%</div> <div>21%</div> </div>

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Mol	Chain	Length	Quality of chain
2	N	729	
2	O	729	
2	P	729	

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
4	XCC	A	703	-	-	X	-
4	XCC	B	702	-	-	X	-
4	XCC	C	703	-	-	X	-
4	XCC	D	702	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 44026 atoms, of which 32 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 Carbon monoxide dehydrogenase/acetyl-CoA synthase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	672	Total	C	N	O	S	0	3	0
			5109	3209	895	961	44			
1	B	672	Total	C	N	O	S	0	3	0
			5109	3209	895	961	44			
1	C	672	Total	C	N	O	S	0	3	0
			5109	3209	895	961	44			
1	D	672	Total	C	N	O	S	0	2	0
			5103	3206	894	960	43			

- Molecule 2 is a protein called Carbon monoxide dehydrogenase/acetyl-CoA synthase subunit alpha.

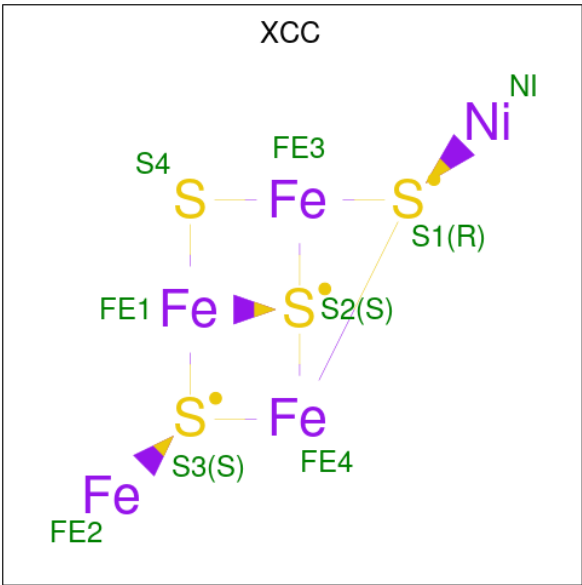
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	728	Total	C	N	O	S	0	0	0
			5740	3681	956	1068	35			
2	N	728	Total	C	N	O	S	0	0	0
			5740	3681	956	1068	35			
2	O	726	Total	C	N	O	S	0	0	0
			5723	3670	954	1065	34			
2	P	728	Total	C	N	O	S	0	0	0
			5740	3681	956	1068	35			

- Molecule 3 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄) (labeled as "Ligand of Interest" by author).



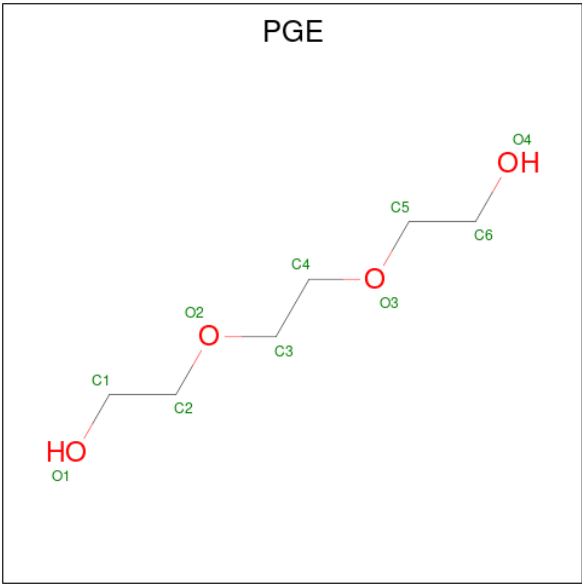
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Fe	S	0	0
			8	4	4		
3	A	1	Total	Fe	S	0	0
			8	4	4		
3	B	1	Total	Fe	S	0	0
			8	4	4		
3	C	1	Total	Fe	S	0	0
			8	4	4		
3	C	1	Total	Fe	S	0	0
			8	4	4		
3	D	1	Total	Fe	S	0	0
			8	4	4		
3	M	1	Total	Fe	S	0	0
			8	4	4		
3	N	1	Total	Fe	S	0	0
			8	4	4		
3	O	1	Total	Fe	S	0	0
			8	4	4		
3	P	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 4 is FE(4)-NI(1)-S(4) CLUSTER (three-letter code: XCC) (formula: Fe₄NiS₄).



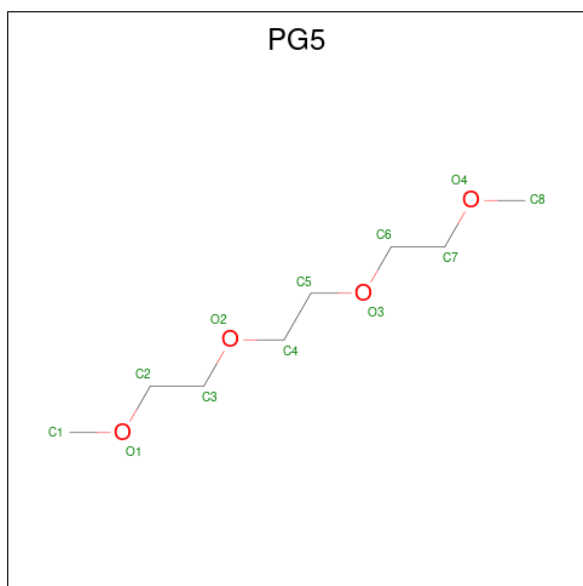
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	Fe	Ni	S	0	0
			9	4	1	4		
4	B	1	Total	Fe	Ni	S	0	0
			9	4	1	4		
4	C	1	Total	Fe	Ni	S	0	0
			9	4	1	4		
4	D	1	Total	Fe	Ni	S	0	0
			9	4	1	4		

- Molecule 5 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			24	6	14	4		

- Molecule 6 is 1-METHOXY-2-[2-(2-METHOXY-ETHOXY)]-ETHANE (three-letter code: PG5) (formula: C₈H₁₈O₄).

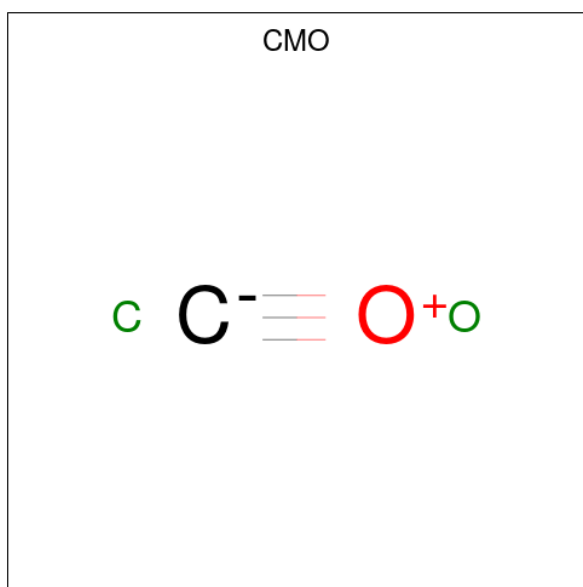


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	C	1	Total	C	H	O	0	0
			30	8	18	4		

- Molecule 7 is NICKEL (II) ION (three-letter code: NI) (formula: Ni) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	P	2	Total	Ni	0	0
			2	2		
7	O	2	Total	Ni	0	0
			2	2		
7	N	2	Total	Ni	0	0
			2	2		
7	M	2	Total	Ni	0	0
			2	2		

- Molecule 8 is CARBON MONOXIDE (three-letter code: CMO) (formula: CO) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	M	1	Total	C	O	0	0
			2	1	1		
8	N	1	Total	C	O	0	0
			2	1	1		
8	P	1	Total	C	O	0	0
			2	1	1		

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	N	1	Total	Mg	0	0
			1	1		

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	84	Total	O	0	0
			84	84		
10	B	77	Total	O	0	0
			77	77		
10	C	44	Total	O	0	0
			44	44		
10	D	51	Total	O	0	0
			51	51		
10	M	76	Total	O	0	0
			76	76		

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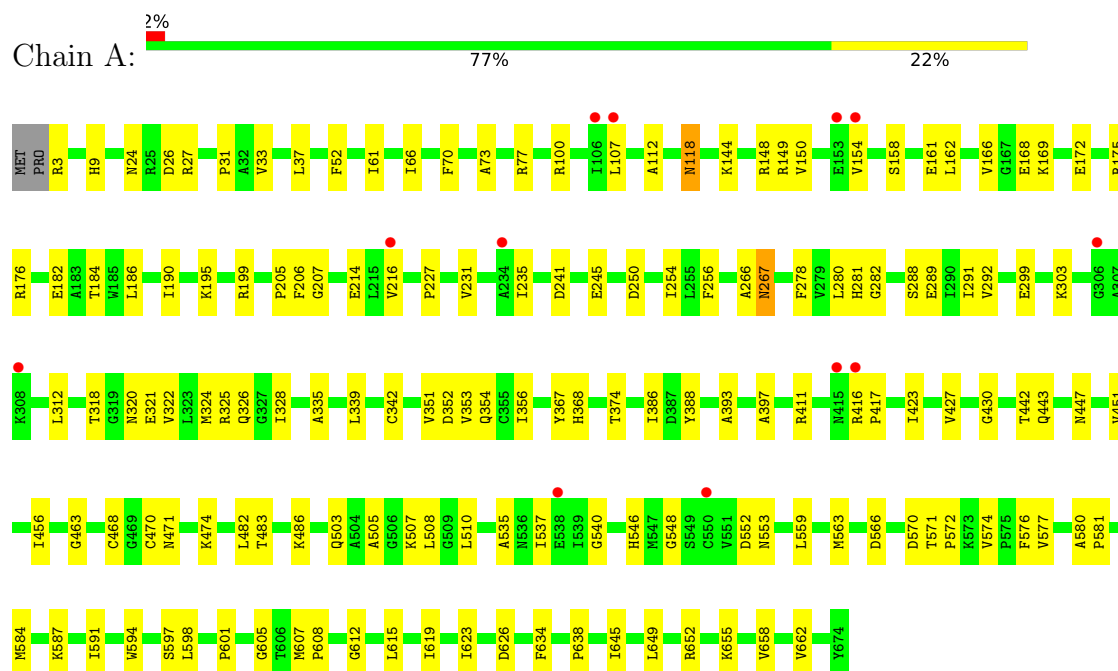
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	N	79	Total 79	O 79	0	0
10	O	12	Total 12	O 12	0	0
10	P	45	Total 45	O 45	0	0

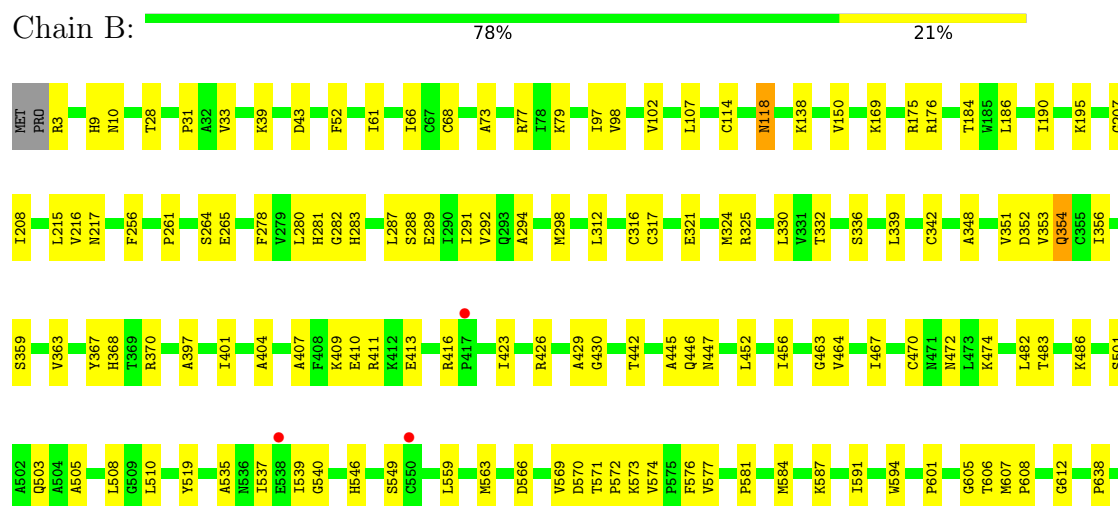
3 Residue-property plots

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

- Molecule 1: Carbon monoxide dehydrogenase/acetyl-CoA synthase subunit beta

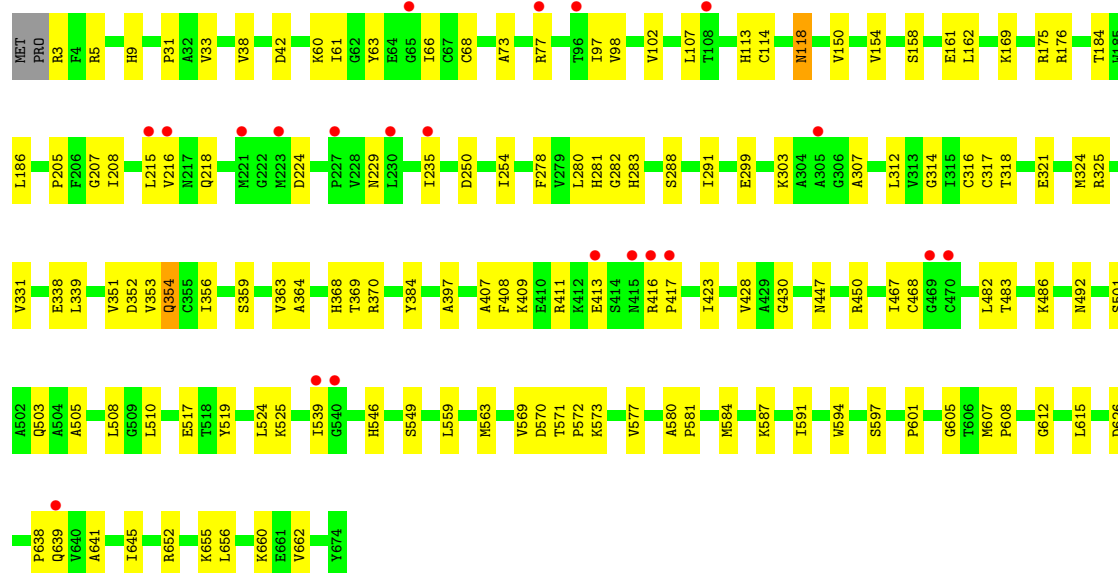
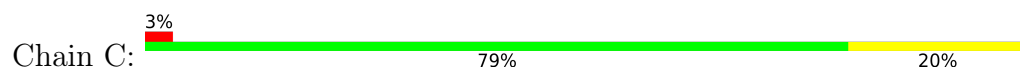


- Molecule 1: Carbon monoxide dehydrogenase/acetyl-CoA synthase subunit beta

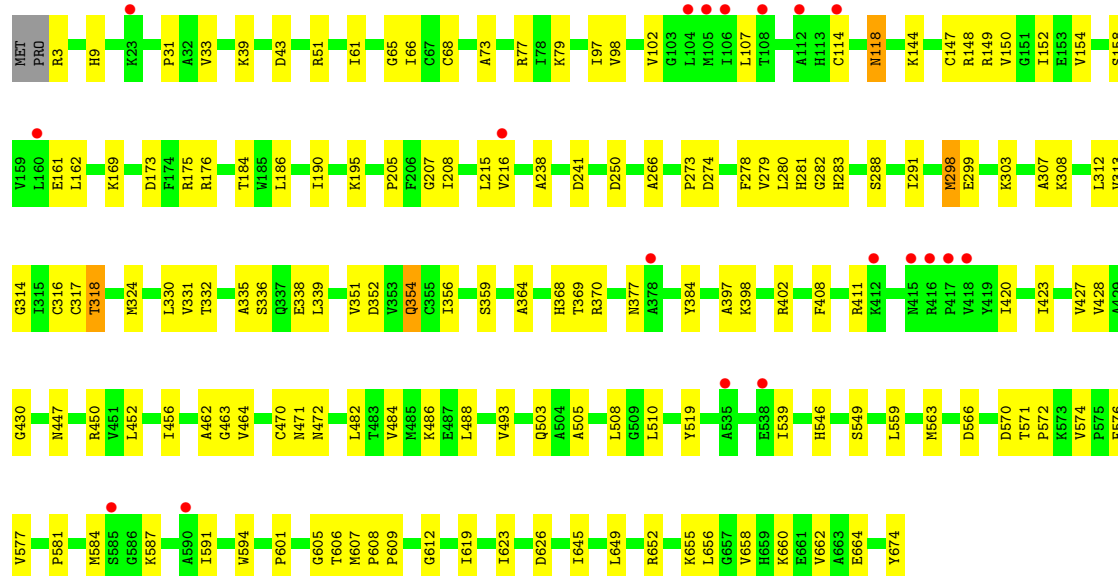
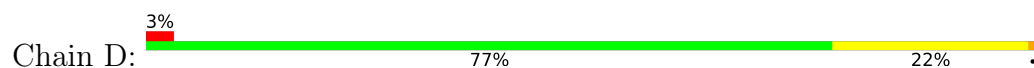




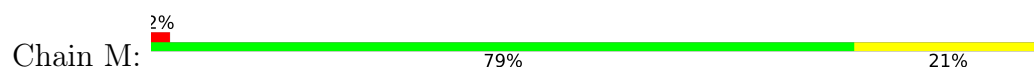
- Molecule 1: Carbon monoxide dehydrogenase/acetyl-CoA synthase subunit beta

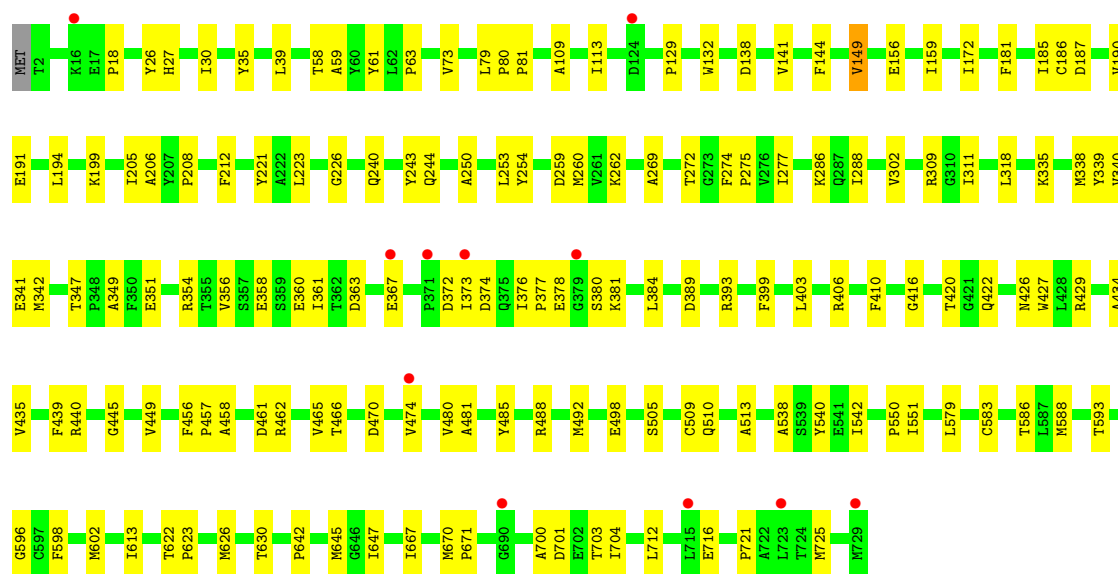


- Molecule 1: Carbon monoxide dehydrogenase/acetyl-CoA synthase subunit beta

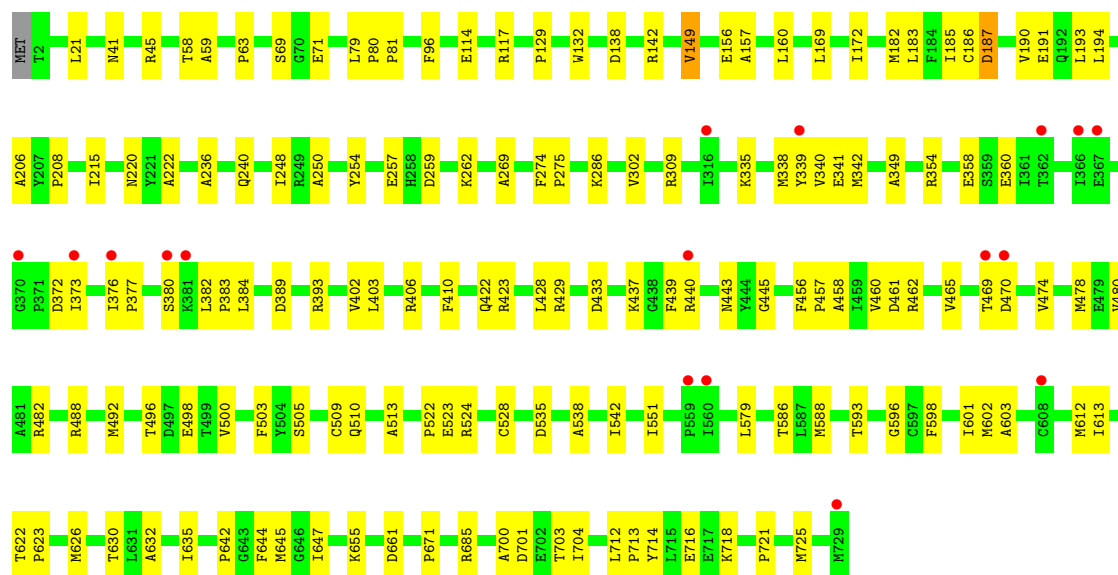
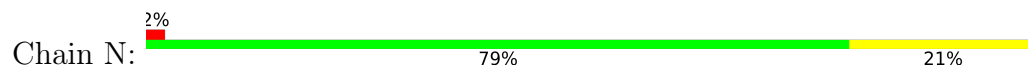


- Molecule 2: Carbon monoxide dehydrogenase/acetyl-CoA synthase subunit alpha

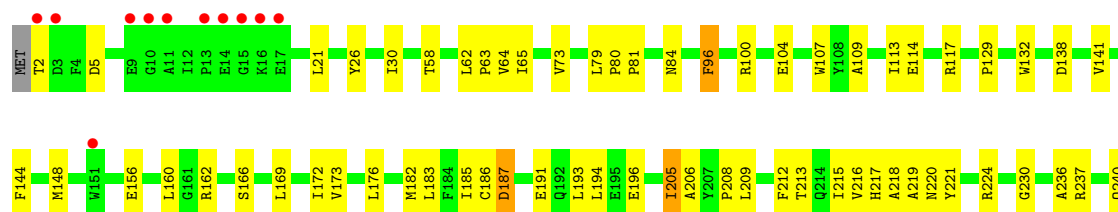


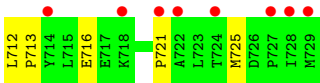


• Molecule 2: Carbon monoxide dehydrogenase/acetyl-CoA synthase subunit alpha



• Molecule 2: Carbon monoxide dehydrogenase/acetyl-CoA synthase subunit alpha





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	99.73Å 137.38Å 141.87Å 101.82° 109.08° 103.66°	Depositor
Resolution (Å)	49.63 – 2.47 49.63 – 2.47	Depositor EDS
% Data completeness (in resolution range)	86.9 (49.63-2.47) 79.3 (49.63-2.47)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.48Å)	Xtriage
Refinement program	PHENIX 1.17.1 _3660	Depositor
R, R_{free}	0.203 , 0.234 0.204 , 0.234	Depositor DCC
R_{free} test set	10245 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	34.7	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 49.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	44026	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.45% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CMO, XCC, MG, PGE, NI, SF4, PG5

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	0.24	0/5202	0.41	0/7048
1	B	0.24	0/5202	0.41	0/7048
1	C	0.24	0/5202	0.41	0/7048
1	D	0.24	0/5196	0.40	0/7040
2	M	0.24	0/5874	0.40	0/7954
2	N	0.24	0/5874	0.41	0/7954
2	O	0.24	0/5857	0.40	0/7933
2	P	0.24	0/5874	0.40	0/7954
All	All	0.24	0/44281	0.40	0/59979

There are no bond length outliers.

There are no bond angle outliers.

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	5109	0	5103	118	0
1	B	5109	0	5103	114	0
1	C	5109	0	5103	111	0
1	D	5103	0	5099	121	0
2	M	5740	0	5701	115	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	N	5740	0	5701	101	0
2	O	5723	0	5681	153	0
2	P	5740	0	5701	138	0
3	A	16	0	0	0	0
3	B	8	0	0	0	0
3	C	16	0	0	0	0
3	D	8	0	0	0	0
3	M	8	0	0	0	0
3	N	8	0	0	1	0
3	O	8	0	0	0	0
3	P	8	0	0	1	0
4	A	9	0	0	2	0
4	B	9	0	0	2	0
4	C	9	0	0	2	0
4	D	9	0	0	3	0
5	A	10	14	14	0	0
6	C	12	18	18	1	0
7	M	2	0	0	0	0
7	N	2	0	0	0	0
7	O	2	0	0	0	0
7	P	2	0	0	0	0
8	M	2	0	0	0	0
8	N	2	0	0	0	0
8	P	2	0	0	0	0
9	N	1	0	0	0	0
10	A	84	0	0	2	0
10	B	77	0	0	0	0
10	C	44	0	0	1	0
10	D	51	0	0	1	0
10	M	76	0	0	1	0
10	N	79	0	0	1	0
10	O	12	0	0	0	0
10	P	45	0	0	0	0
All	All	43994	32	43224	939	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 11.

The worst 5 of 939 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:D:482:LEU:HD21	1:D:508:LEU:HD12	1.53	0.90
1:A:281:HIS:HB3	1:A:351:VAL:HG12	1.51	0.90
1:A:150:VAL:HG11	1:A:169:LYS:HG2	1.56	0.87
2:P:497:ASP:O	2:P:553:LYS:NZ	2.07	0.86
1:B:535:ALA:HB3	1:B:537:ILE:HD11	1.58	0.85

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	673/674 (100%)	647 (96%)	25 (4%)	1 (0%)	51	71
1	B	673/674 (100%)	648 (96%)	24 (4%)	1 (0%)	51	71
1	C	673/674 (100%)	650 (97%)	22 (3%)	1 (0%)	51	71
1	D	672/674 (100%)	648 (96%)	23 (3%)	1 (0%)	51	71
2	M	726/729 (100%)	702 (97%)	23 (3%)	1 (0%)	51	71
2	N	726/729 (100%)	699 (96%)	25 (3%)	2 (0%)	41	59
2	O	724/729 (99%)	696 (96%)	24 (3%)	4 (1%)	25	40
2	P	726/729 (100%)	700 (96%)	24 (3%)	2 (0%)	41	59
All	All	5593/5612 (100%)	5390 (96%)	190 (3%)	13 (0%)	47	66

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	N	187	ASP
2	O	187	ASP
1	A	267	ASN
2	M	596	GLY
2	N	596	GLY

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	544/543 (100%)	540 (99%)	4 (1%)	84	93
1	B	544/543 (100%)	541 (99%)	3 (1%)	86	94
1	C	544/543 (100%)	540 (99%)	4 (1%)	84	93
1	D	543/543 (100%)	538 (99%)	5 (1%)	78	91
2	M	610/611 (100%)	607 (100%)	3 (0%)	88	95
2	N	610/611 (100%)	606 (99%)	4 (1%)	84	93
2	O	608/611 (100%)	605 (100%)	3 (0%)	88	95
2	P	610/611 (100%)	607 (100%)	3 (0%)	88	95
All	All	4613/4616 (100%)	4584 (99%)	29 (1%)	86	94

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	298	MET
2	M	149	VAL
2	P	96	PHE
1	D	318	THR
2	M	254	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	503	GLN
1	C	503	GLN
2	P	426	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 28 ligands modelled in this entry, 9 are monoatomic - leaving 19 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	XCC	C	703	1,10	0,11,11	0.00	-	-		
8	CMO	M	804	-	0,1,1	0.00	-	-		
8	CMO	N	804	7	0,1,1	0.00	-	-		
5	PGE	A	704	-	9,9,9	0.35	0	8,8,8	0.20	0
3	SF4	D	701	1	0,12,12	0.00	-	-		
3	SF4	O	900	2	0,12,12	0.00	-	-		
3	SF4	P	801	2	0,12,12	0.00	-	-		
3	SF4	B	701	1	0,12,12	0.00	-	-		
3	SF4	N	801	2	0,12,12	0.00	-	-		
3	SF4	C	701	1	0,12,12	0.00	-	-		
3	SF4	M	801	2	0,12,12	0.00	-	-		
3	SF4	A	702	1	0,12,12	0.00	-	-		
8	CMO	P	804	7	0,1,1	0.00	-	-		
6	PG5	C	704	-	11,11,11	0.20	0	10,10,10	0.28	0
4	XCC	D	702	1	0,11,11	0.00	-	-		
3	SF4	A	701	1	0,12,12	0.00	-	-		
3	SF4	C	702	1	0,12,12	0.00	-	-		
4	XCC	A	703	1,10	0,11,11	0.00	-	-		
4	XCC	B	702	1,10	0,11,11	0.00	-	-		

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	XCC	C	703	1,10	-	-	0/3/3/3
3	SF4	C	701	1	-	-	0/6/5/5
3	SF4	D	701	1	-	-	0/6/5/5
3	SF4	O	900	2	-	-	0/6/5/5
3	SF4	P	801	2	-	-	0/6/5/5
3	SF4	B	701	1	-	-	0/6/5/5
3	SF4	N	801	2	-	-	0/6/5/5
5	PGE	A	704	-	-	3/7/7/7	-
3	SF4	A	701	1	-	-	0/6/5/5
3	SF4	M	801	2	-	-	0/6/5/5
3	SF4	A	702	1	-	-	0/6/5/5
4	XCC	B	702	1,10	-	-	0/3/3/3
4	XCC	D	702	1	-	-	0/3/3/3
6	PG5	C	704	-	-	4/9/9/9	-
3	SF4	C	702	1	-	-	0/6/5/5
4	XCC	A	703	1,10	-	-	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	704	PGE	O3-C5-C6-O4
5	A	704	PGE	O1-C1-C2-O2
6	C	704	PG5	C3-C2-O1-C1
6	C	704	PG5	O1-C2-C3-O2
6	C	704	PG5	O2-C4-C5-O3

There are no ring outliers.

7 monomers are involved in 12 short contacts:

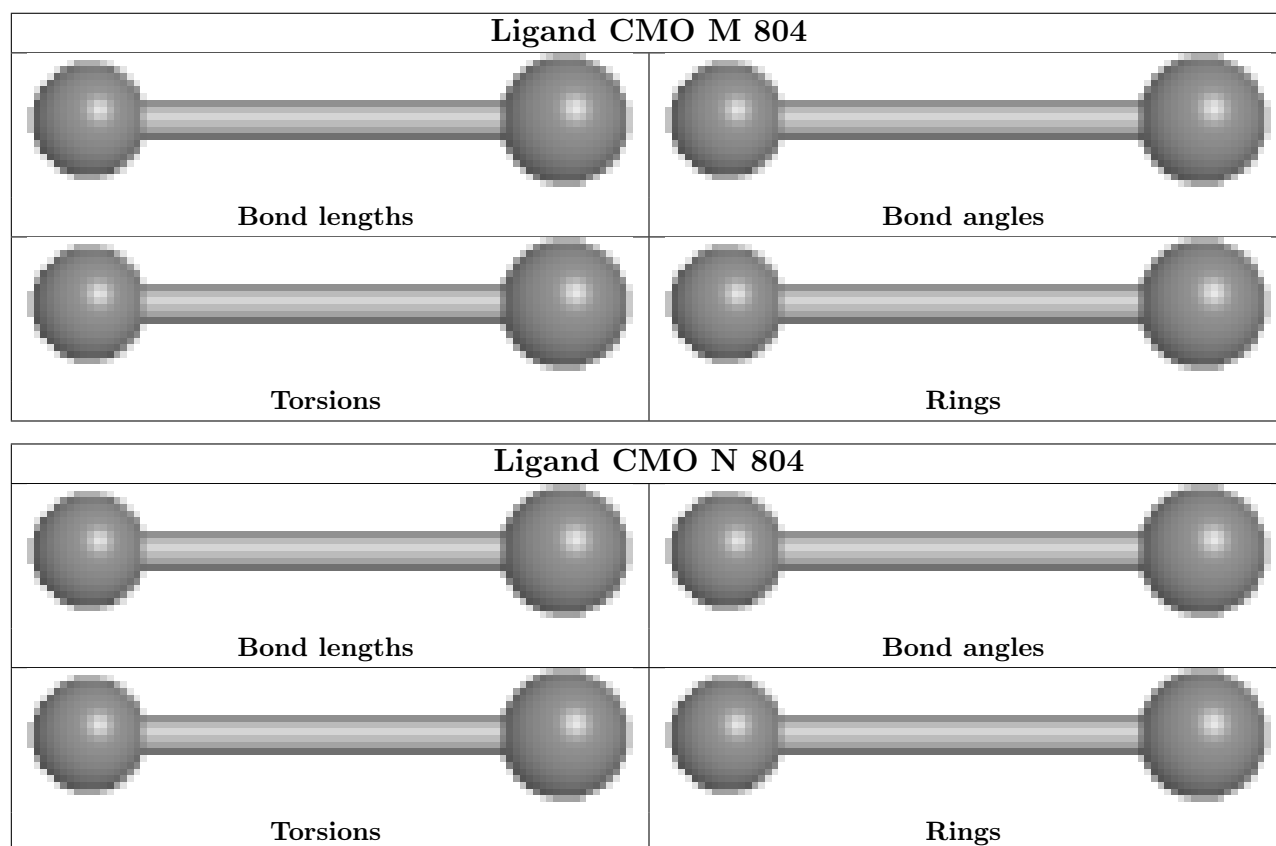
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	703	XCC	2	0
3	P	801	SF4	1	0
3	N	801	SF4	1	0
6	C	704	PG5	1	0
4	D	702	XCC	3	0

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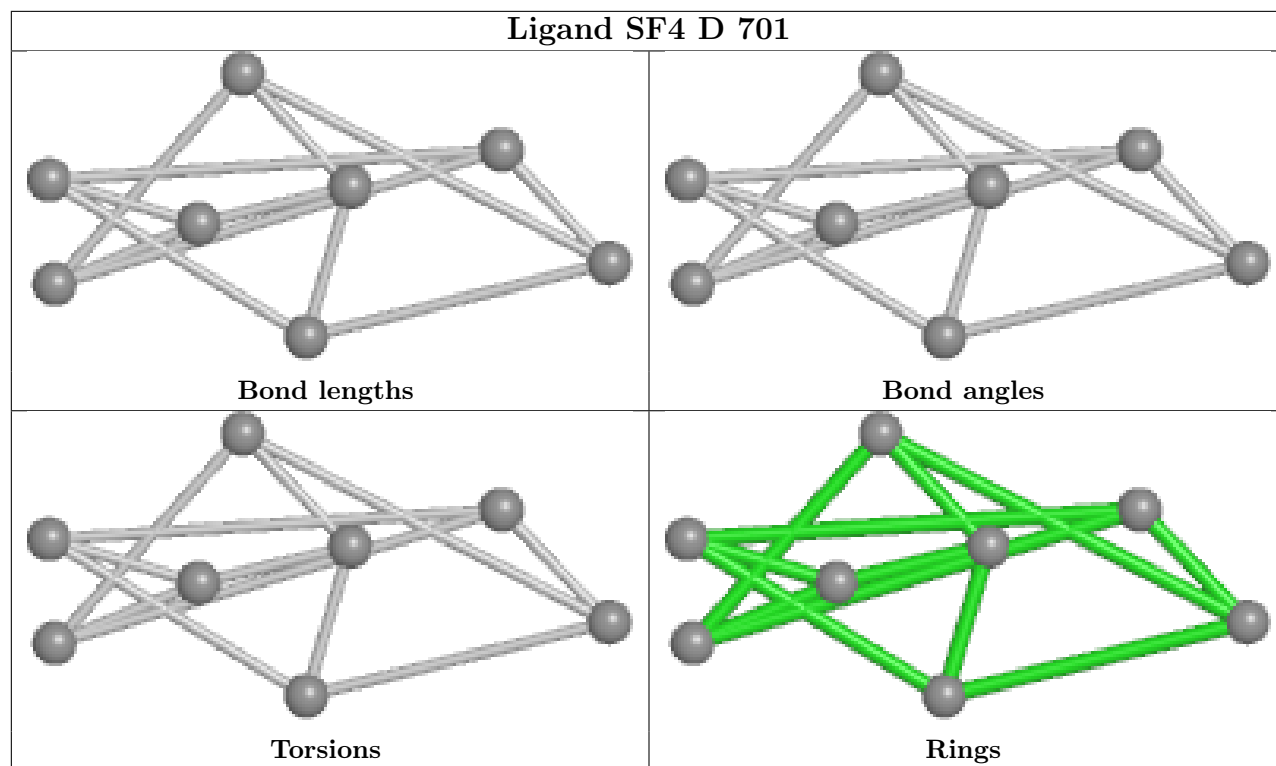
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	703	XCC	2	0
4	B	702	XCC	2	0

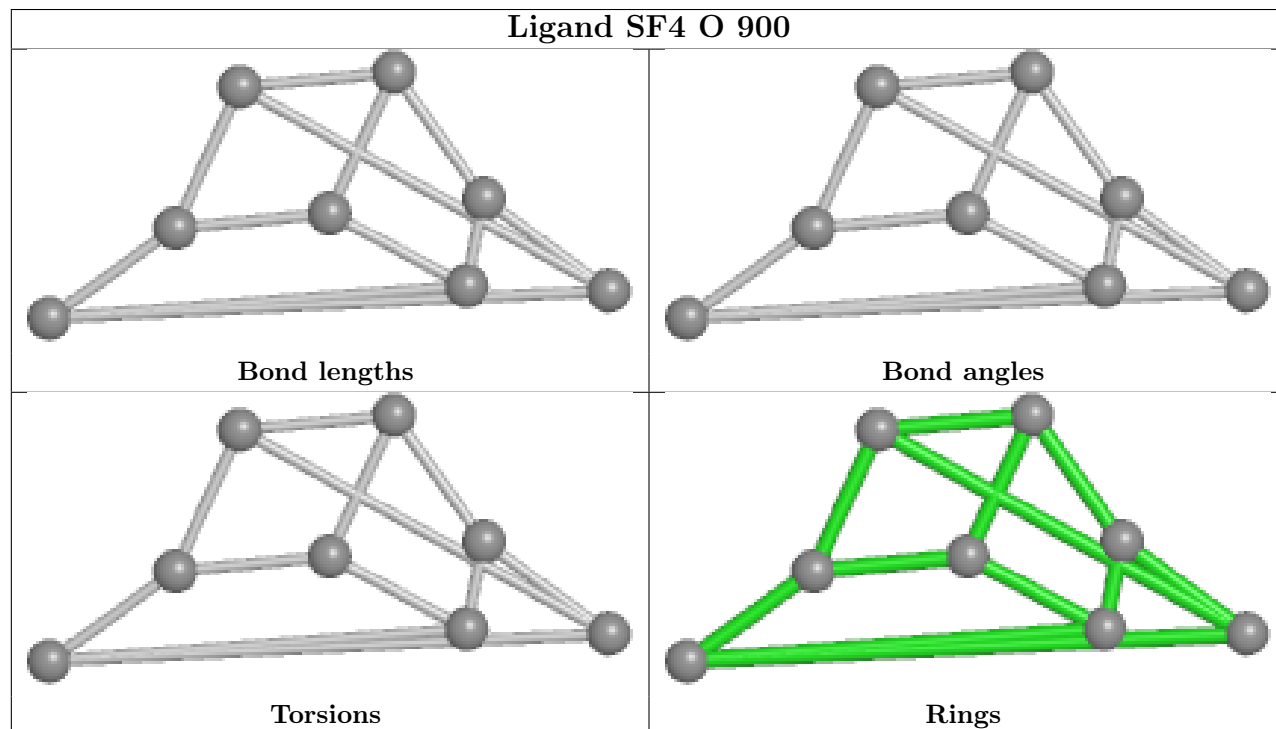
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

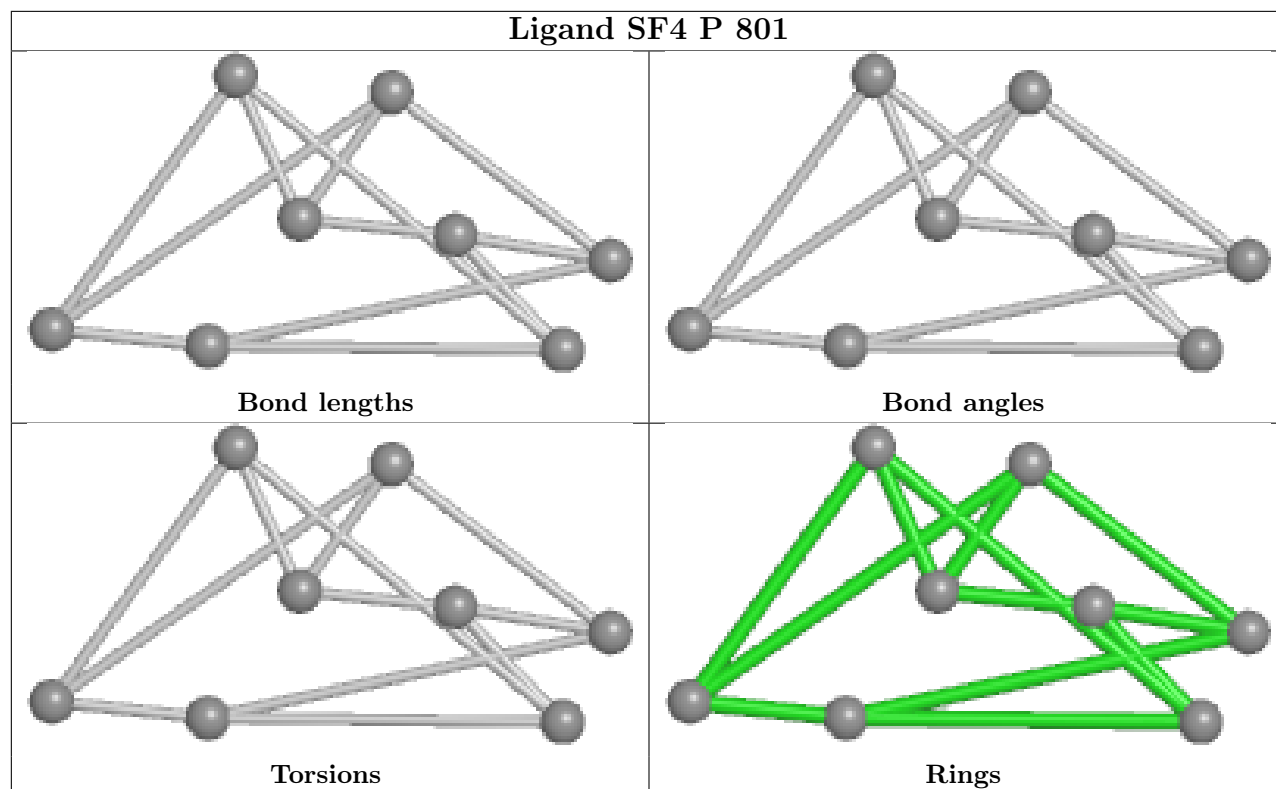


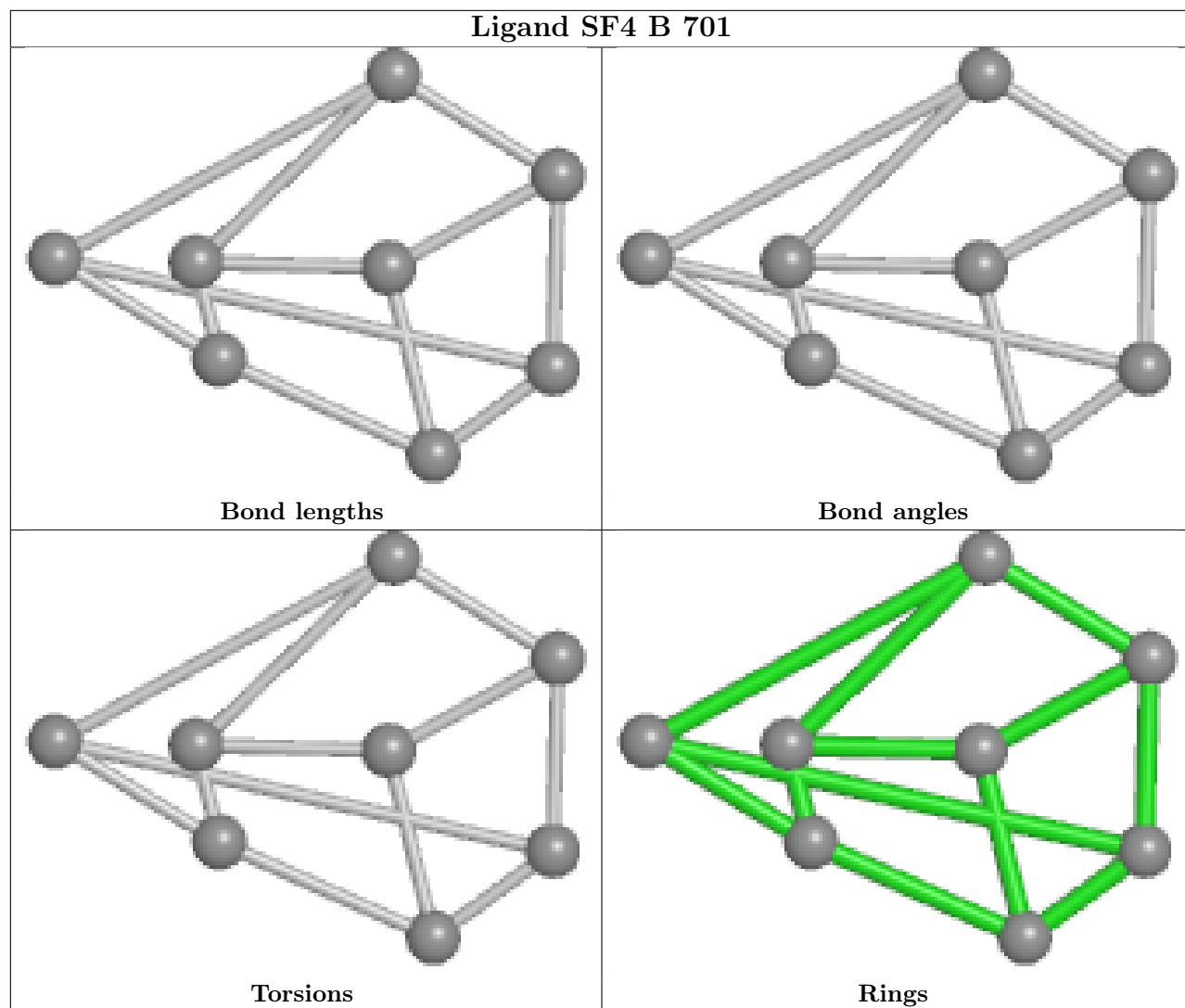
Ligand SF4 D 701

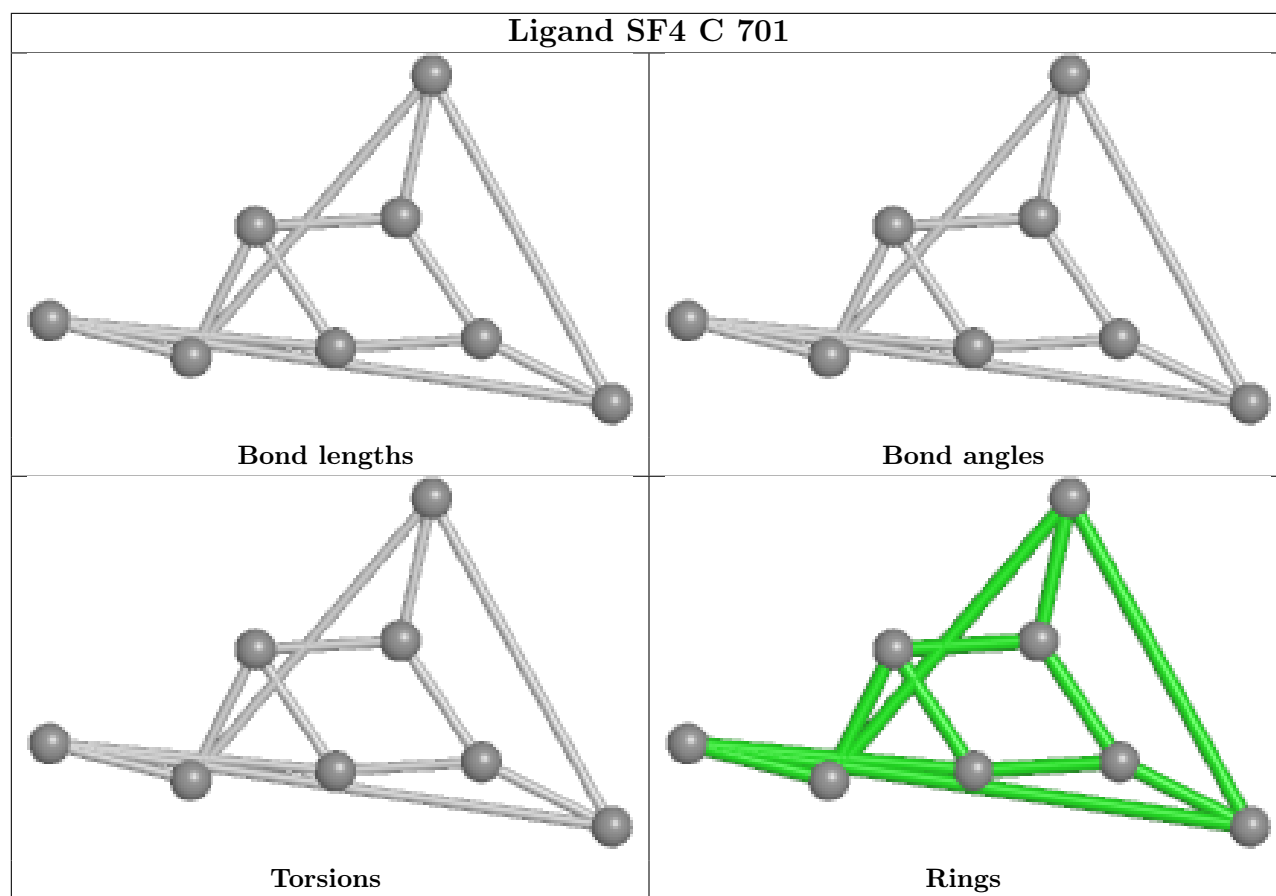
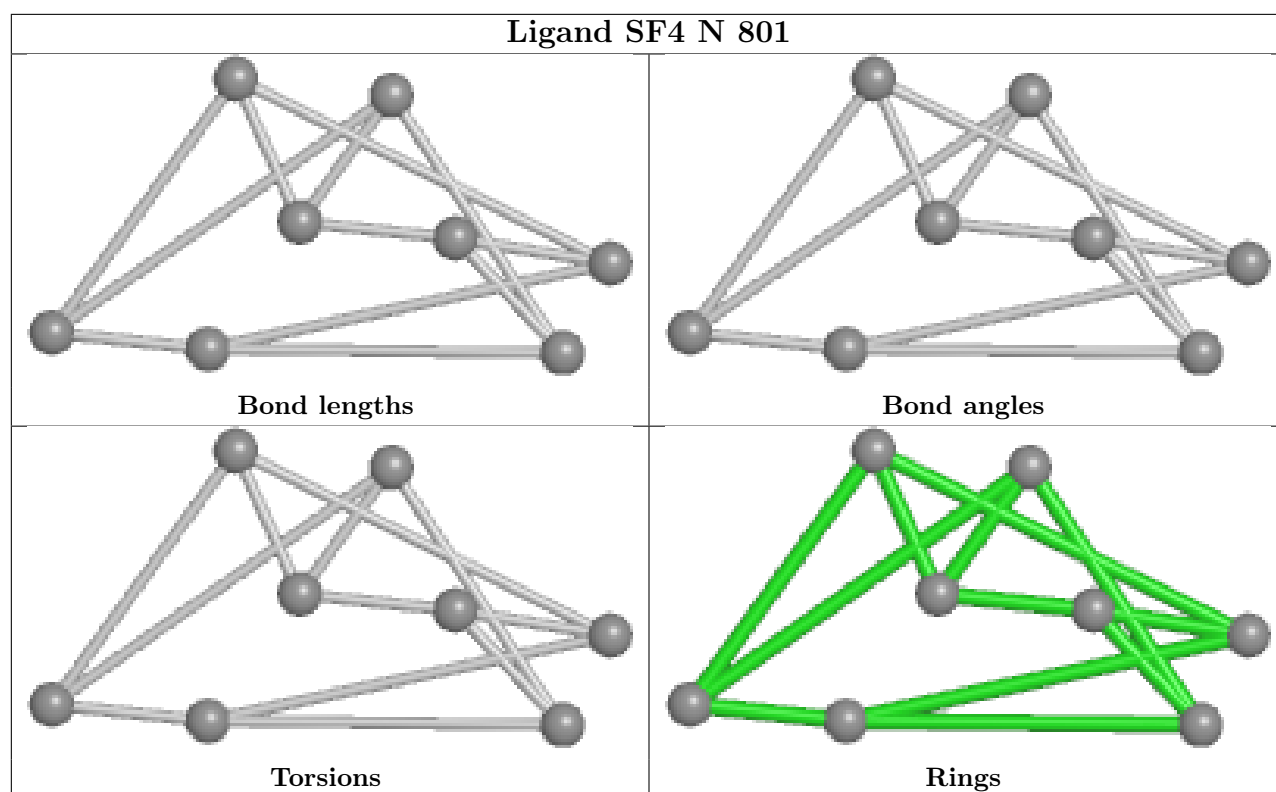


Ligand SF4 O 900

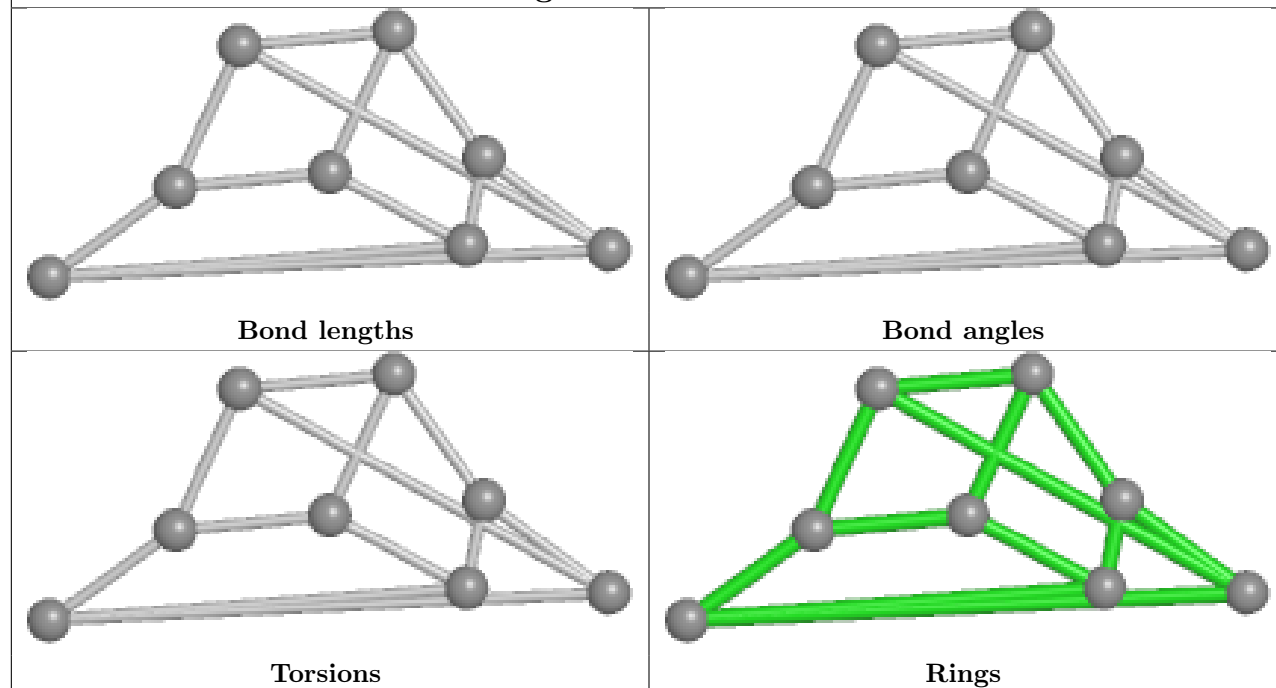




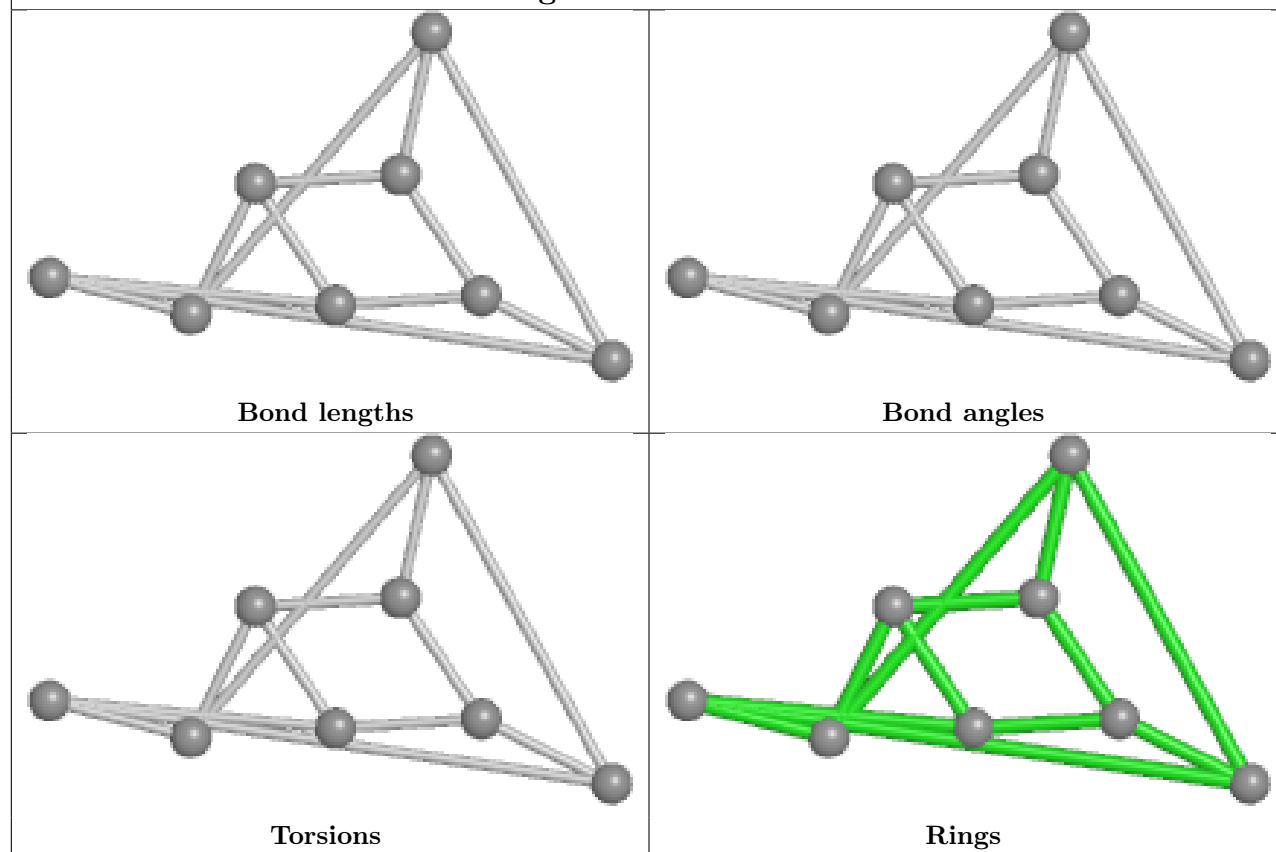


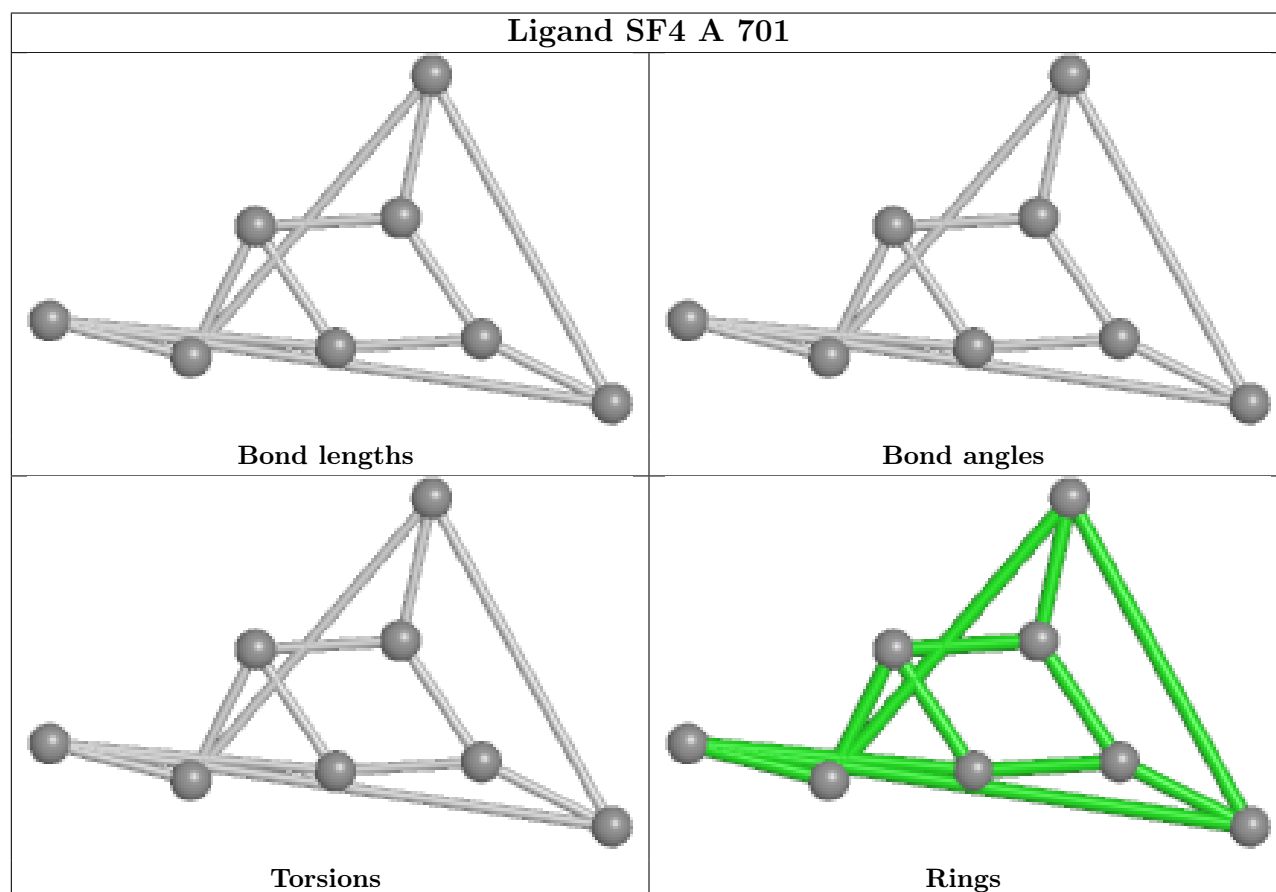
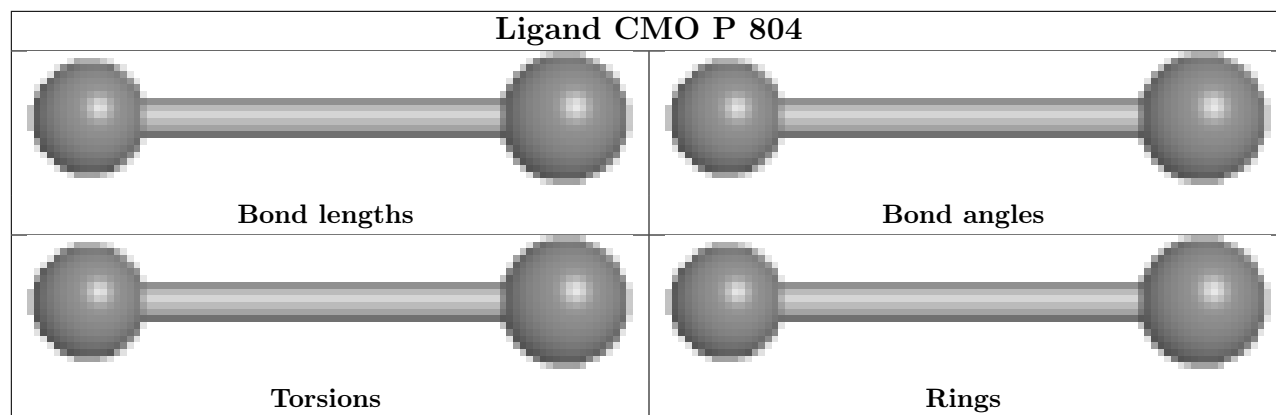


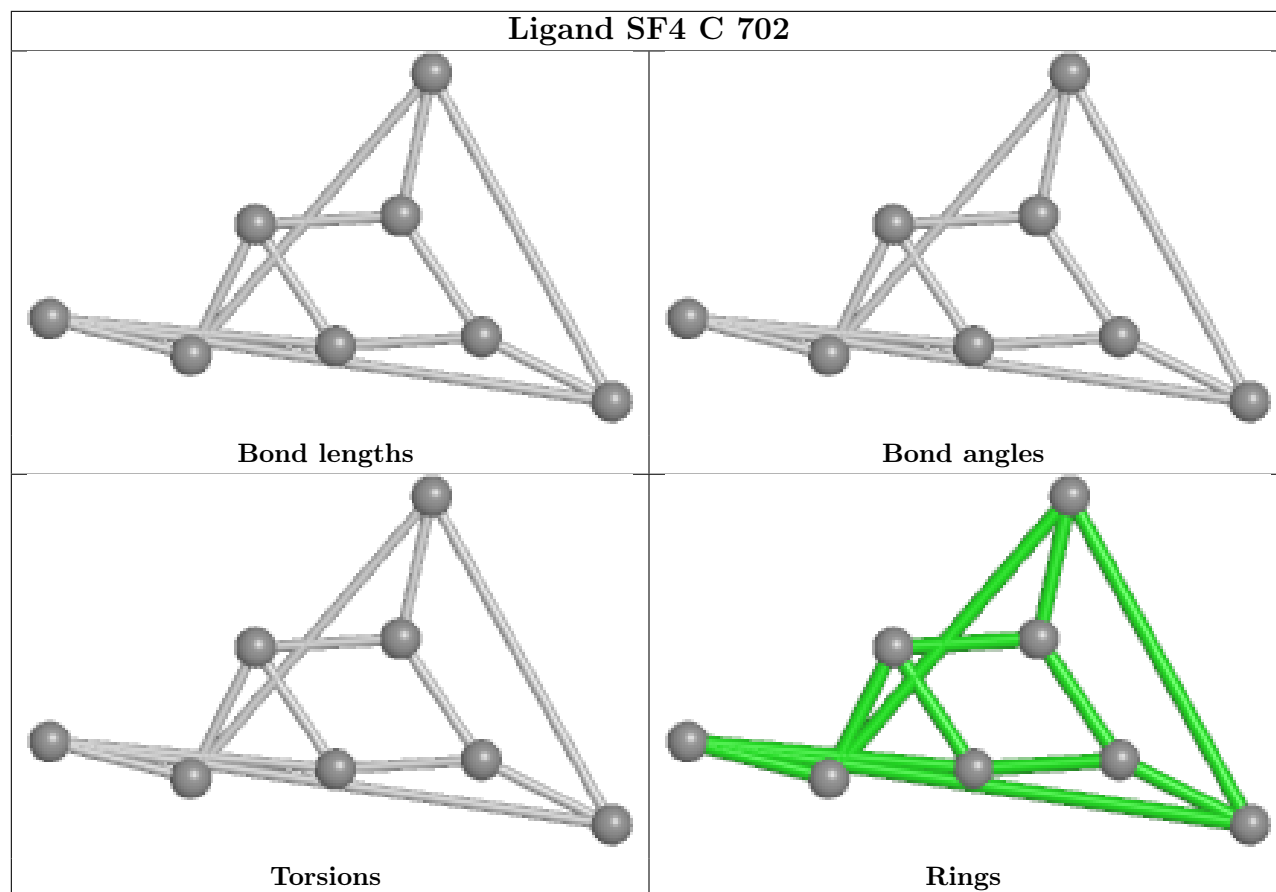
Ligand SF4 M 801



Ligand SF4 A 702







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	672/674 (99%)	-0.08	12 (1%) 68 70	21, 36, 55, 127	0
1	B	672/674 (99%)	-0.15	3 (0%) 92 93	21, 35, 54, 121	0
1	C	672/674 (99%)	0.00	21 (3%) 49 51	26, 40, 61, 109	0
1	D	672/674 (99%)	0.10	19 (2%) 53 55	26, 44, 67, 116	0
2	M	728/729 (99%)	-0.08	11 (1%) 73 75	23, 43, 71, 124	0
2	N	728/729 (99%)	-0.02	17 (2%) 60 62	20, 41, 72, 107	0
2	O	726/729 (99%)	1.59	258 (35%) 0 0	37, 87, 163, 238	0
2	P	728/729 (99%)	0.57	103 (14%) 2 2	28, 57, 117, 194	0
All	All	5598/5612 (99%)	0.25	444 (7%) 12 12	20, 43, 112, 238	0

The worst 5 of 444 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	O	474	VAL	13.1
2	O	485	TYR	11.6
2	O	356	VAL	10.8
2	O	354	ARG	10.5
2	O	460	VAL	9.5

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

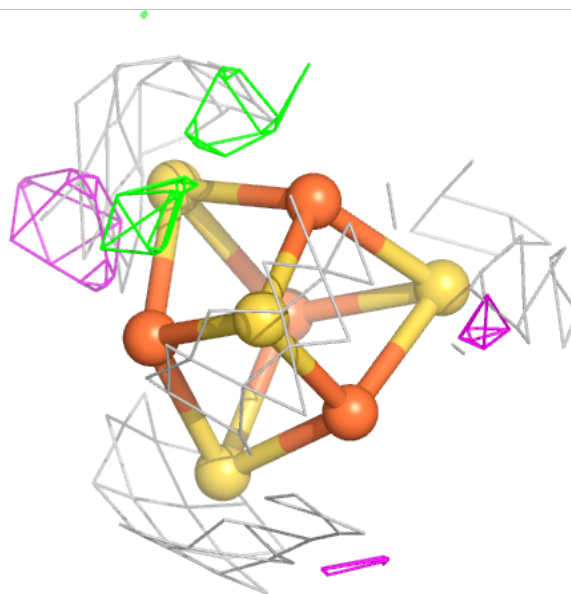
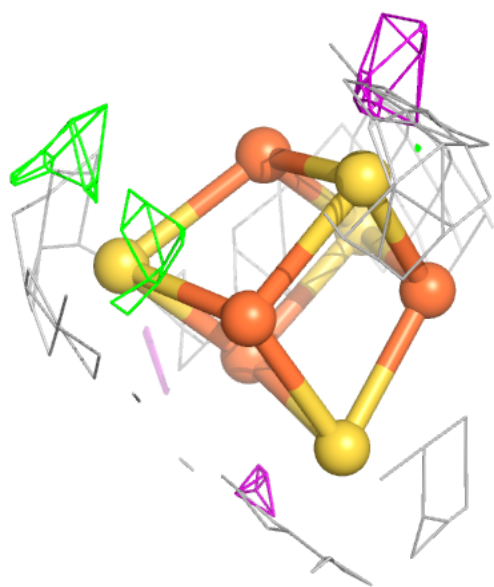
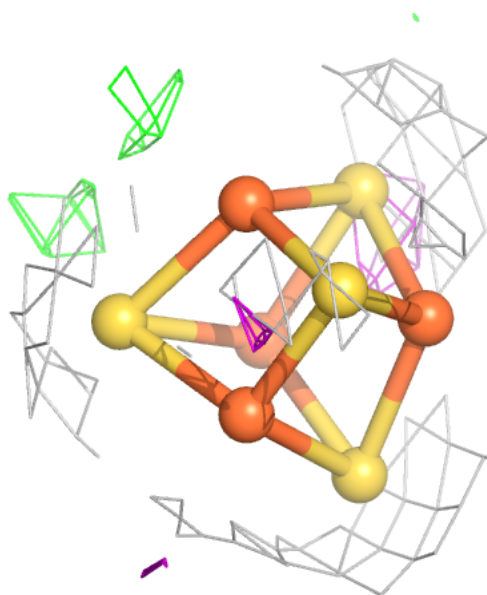
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	PGE	A	704	10/10	0.77	0.21	19,42,52,54	0
6	PG5	C	704	12/12	0.83	0.17	44,58,71,73	0
4	XCC	B	702	9/9	0.97	0.16	41,53,70,82	0
3	SF4	O	900	8/8	0.97	0.11	58,74,80,88	0
7	NI	M	802	1/1	0.97	0.14	48,48,48,48	0
9	MG	N	805	1/1	0.97	0.07	43,43,43,43	0
4	XCC	C	703	9/9	0.97	0.16	45,58,73,104	0
7	NI	O	902	1/1	0.97	0.15	90,90,90,90	0
4	XCC	A	703	9/9	0.97	0.14	43,52,63,69	0
8	CMO	N	804	2/2	0.98	0.21	40,40,40,42	0
7	NI	O	901	1/1	0.98	0.18	75,75,75,75	0
4	XCC	D	702	9/9	0.98	0.16	50,58,74,84	0
3	SF4	D	701	8/8	0.98	0.20	36,38,44,45	0
8	CMO	M	804	2/2	0.98	0.25	43,43,43,44	0
3	SF4	M	801	8/8	0.99	0.15	28,30,34,36	0
3	SF4	B	701	8/8	0.99	0.18	24,27,32,34	0
7	NI	N	802	1/1	0.99	0.12	43,43,43,43	0
7	NI	P	802	1/1	0.99	0.14	61,61,61,61	0
7	NI	M	803	1/1	0.99	0.12	31,31,31,31	0
3	SF4	C	702	8/8	0.99	0.18	35,38,41,43	0
8	CMO	P	804	2/2	0.99	0.19	61,61,61,63	0
3	SF4	P	801	8/8	0.99	0.13	45,49,53,55	0
3	SF4	A	701	8/8	0.99	0.12	21,26,27,29	0
3	SF4	C	701	8/8	0.99	0.14	35,40,42,44	0
3	SF4	A	702	8/8	0.99	0.18	24,26,28,31	0
3	SF4	N	801	8/8	0.99	0.17	27,32,33,35	0
7	NI	P	803	1/1	0.99	0.14	44,44,44,44	0
7	NI	N	803	1/1	1.00	0.18	31,31,31,31	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.

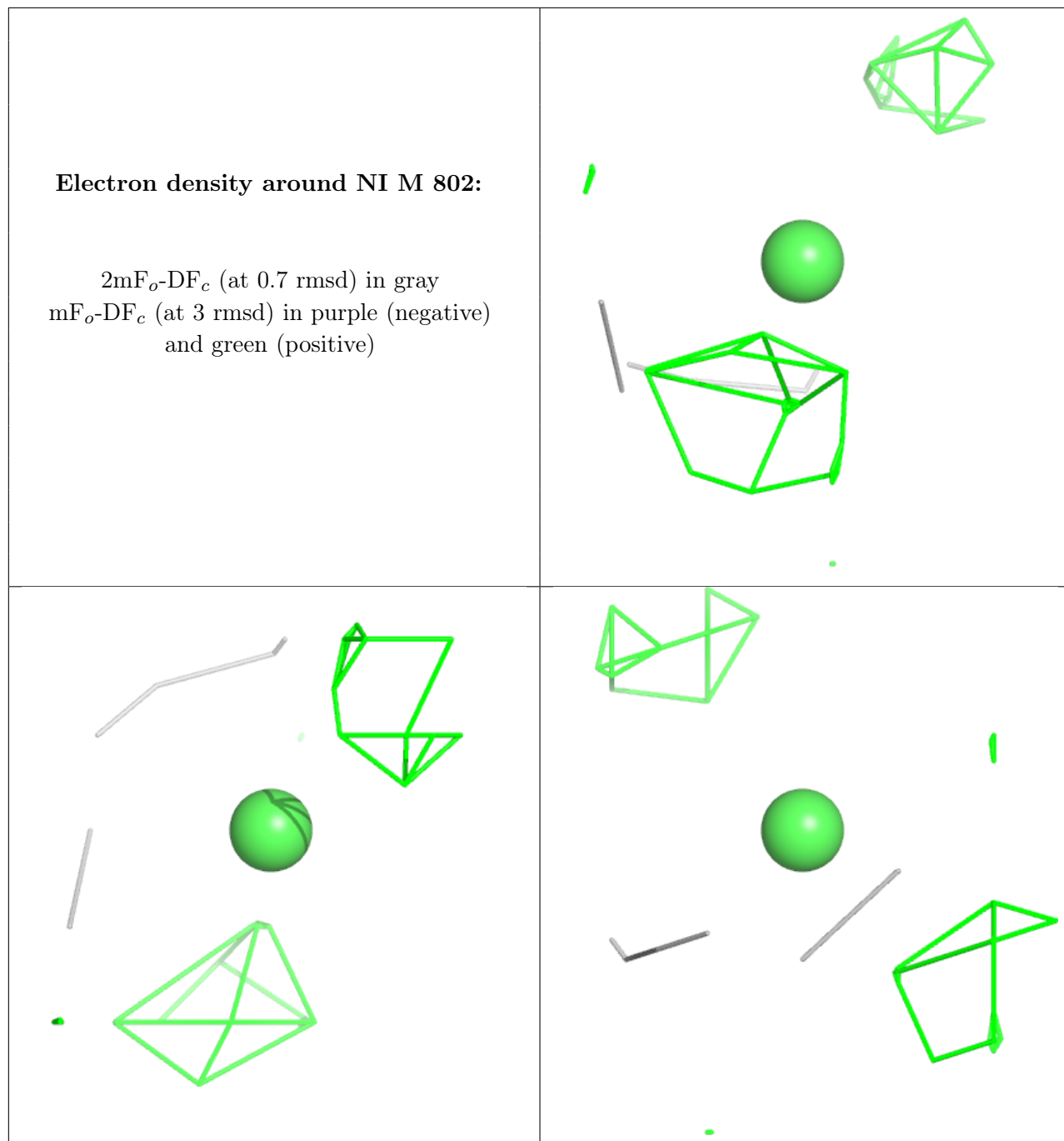
Electron density around SF4 O 900:

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



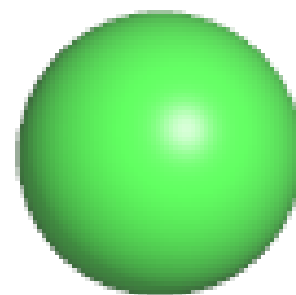
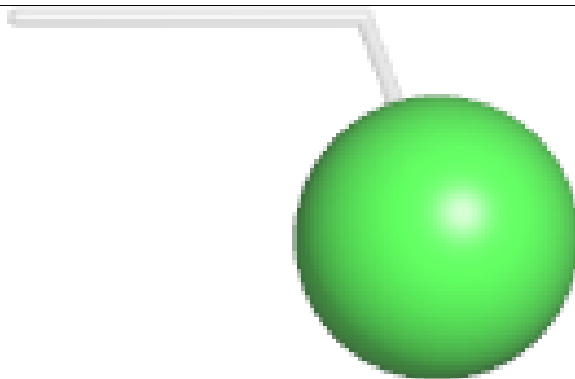
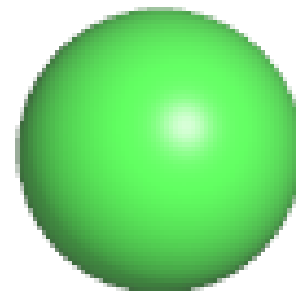
Electron density around NI M 802:

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



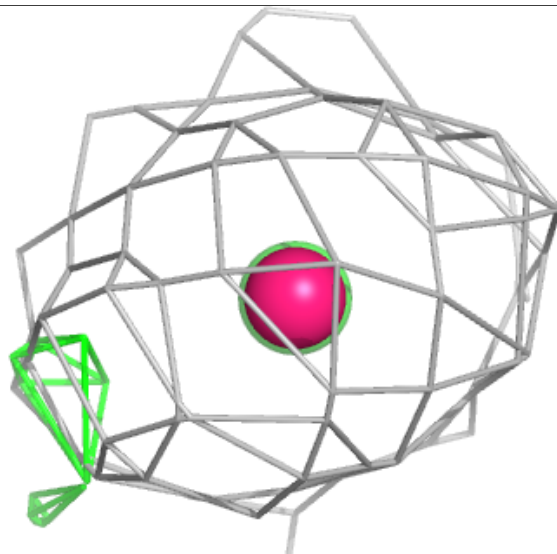
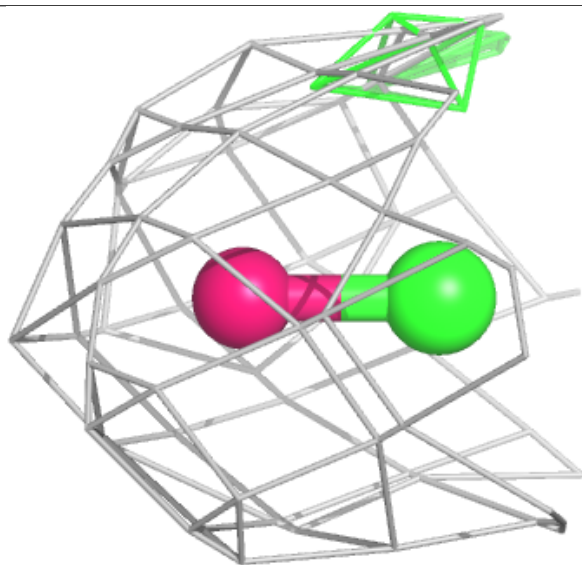
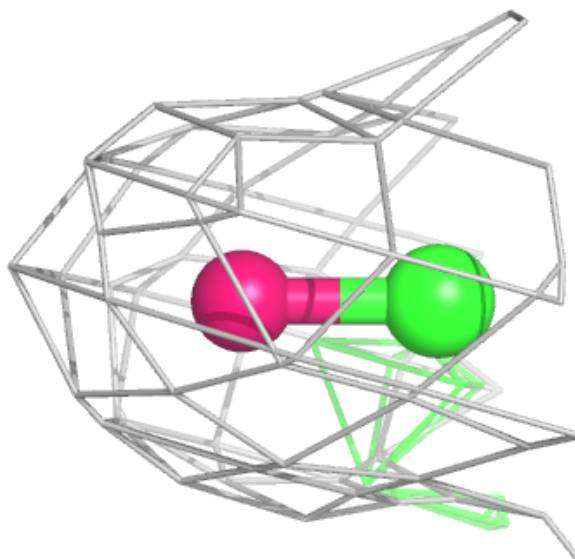
Electron density around NI O 902:

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



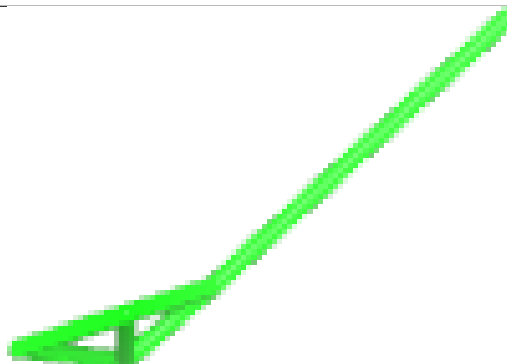
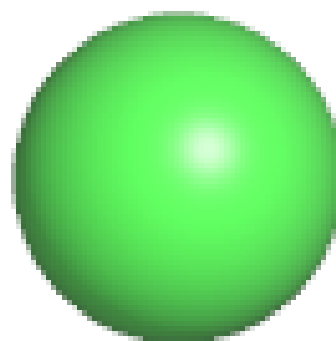
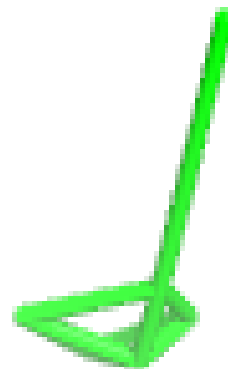
Electron density around CMO N 804:

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



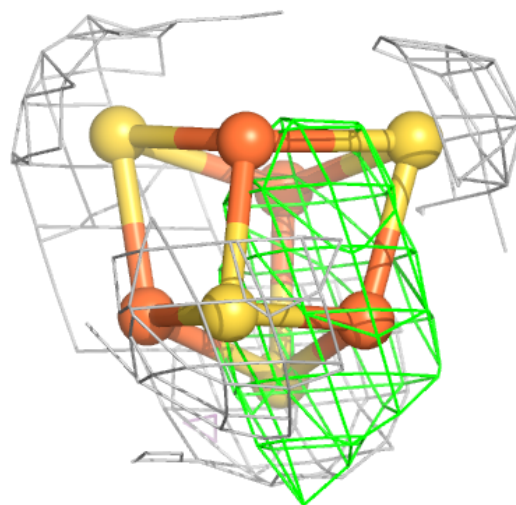
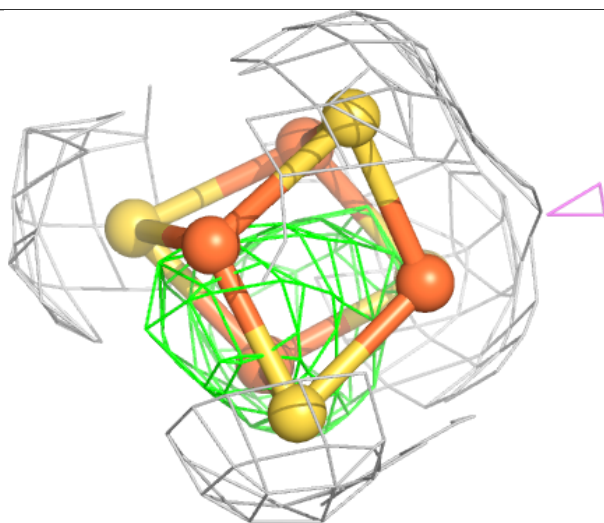
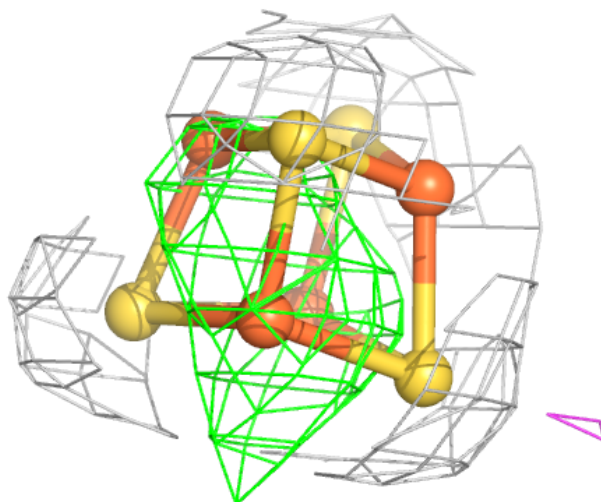
Electron density around NI O 901:

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and green (positive)



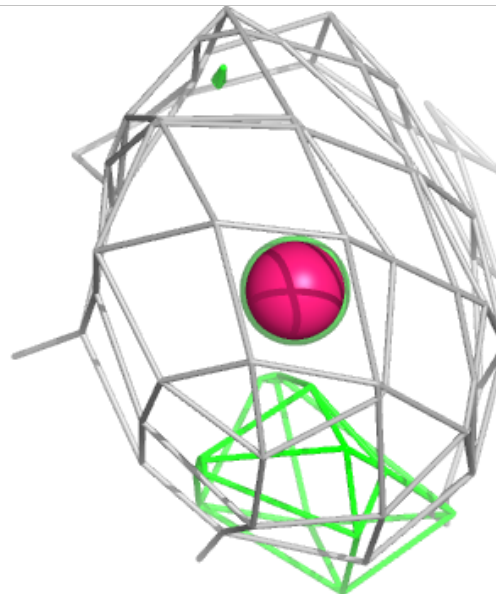
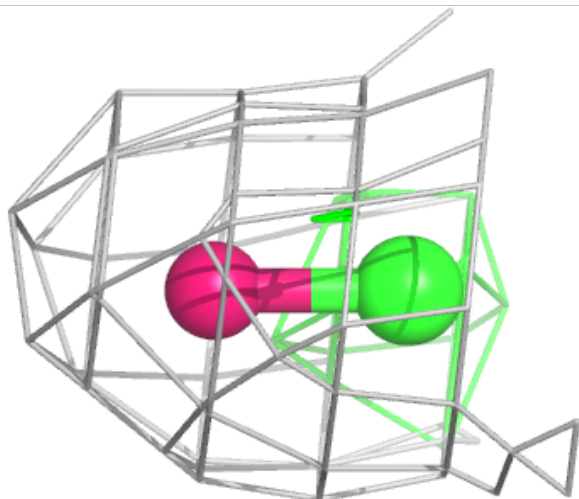
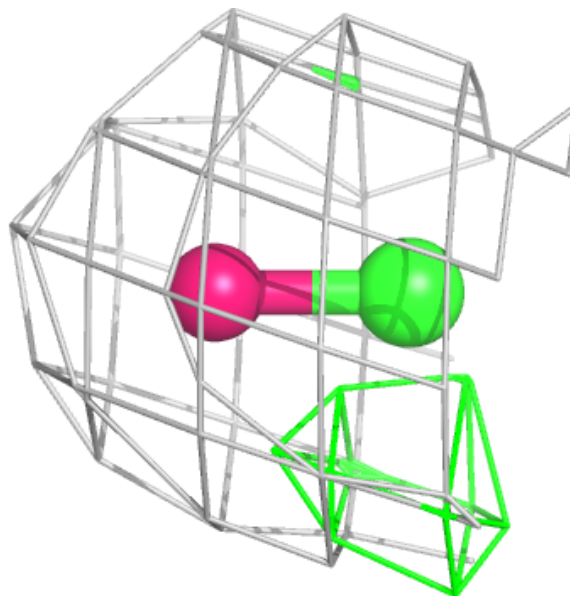
Electron density around SF4 D 701:

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



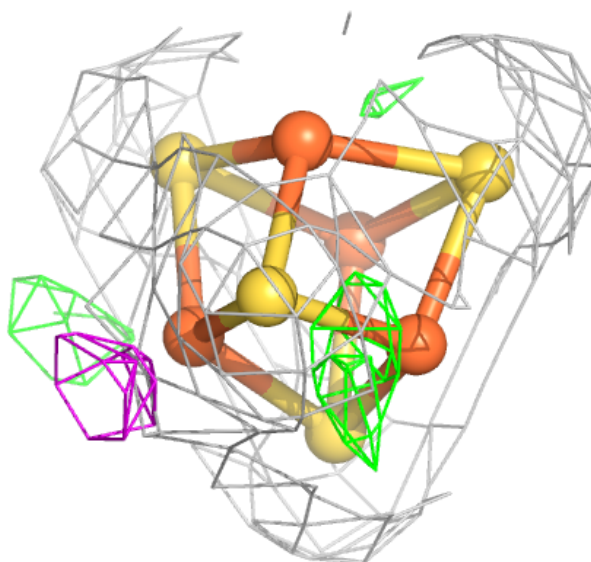
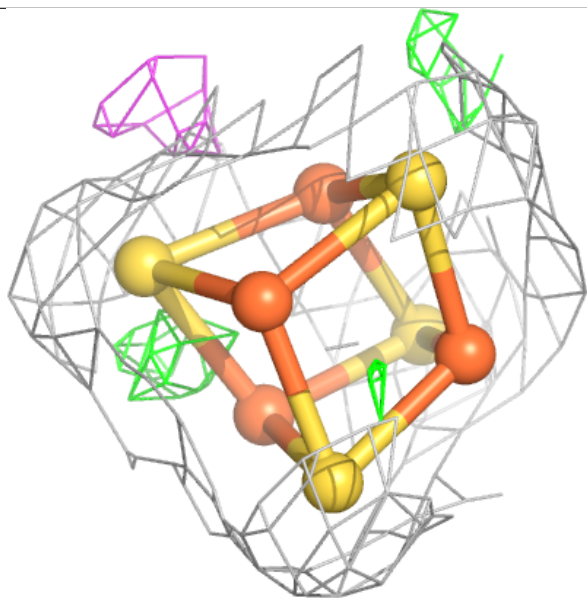
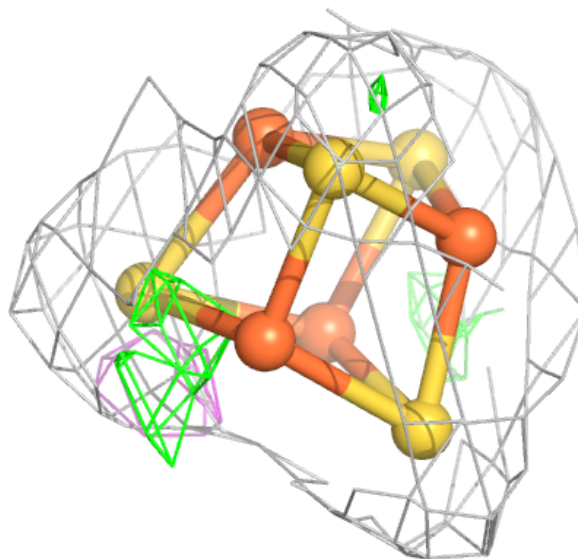
Electron density around CMO M 804:

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



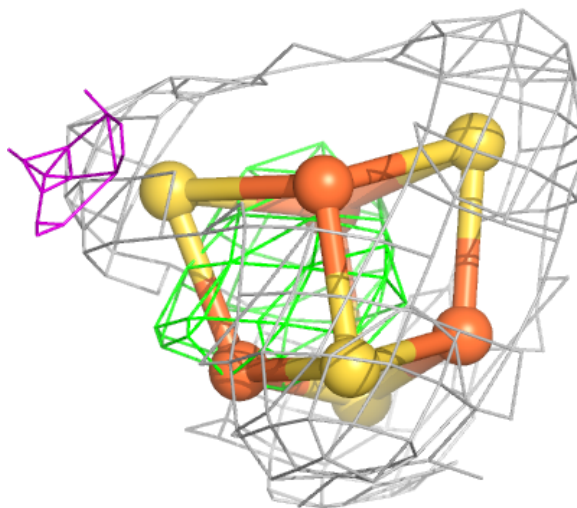
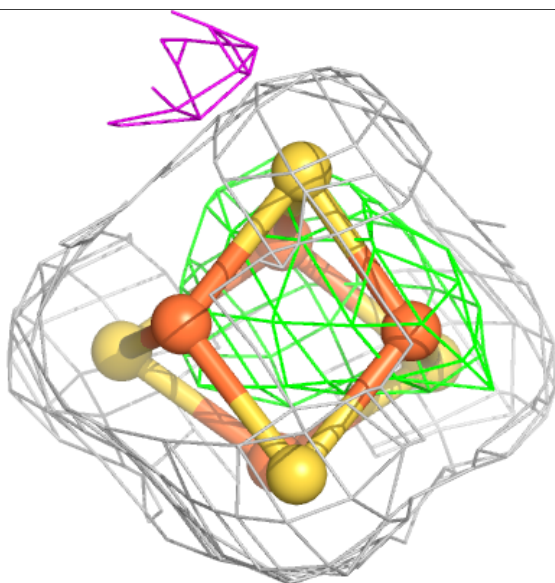
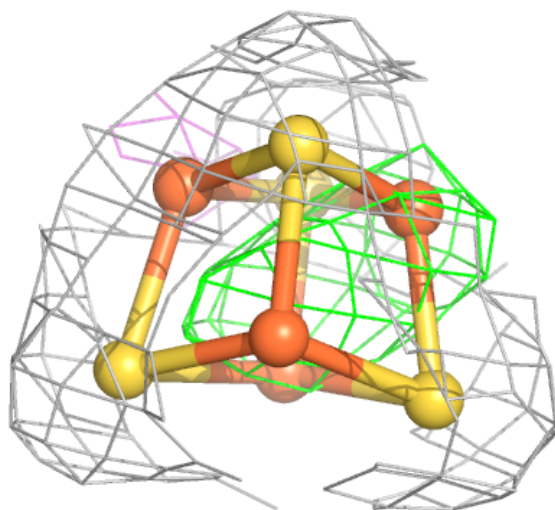
Electron density around SF4 M 801:

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



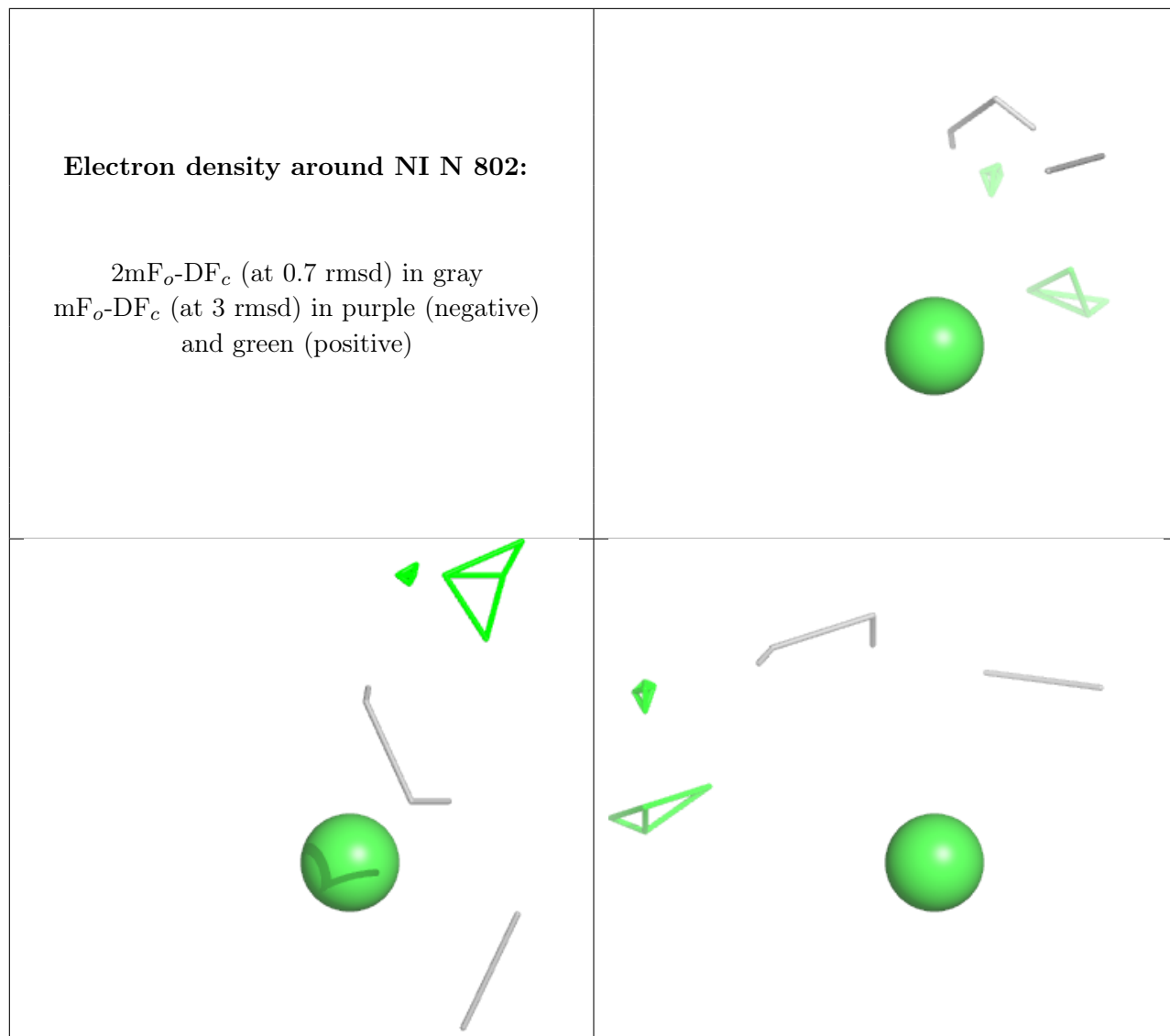
Electron density around SF4 B 701:

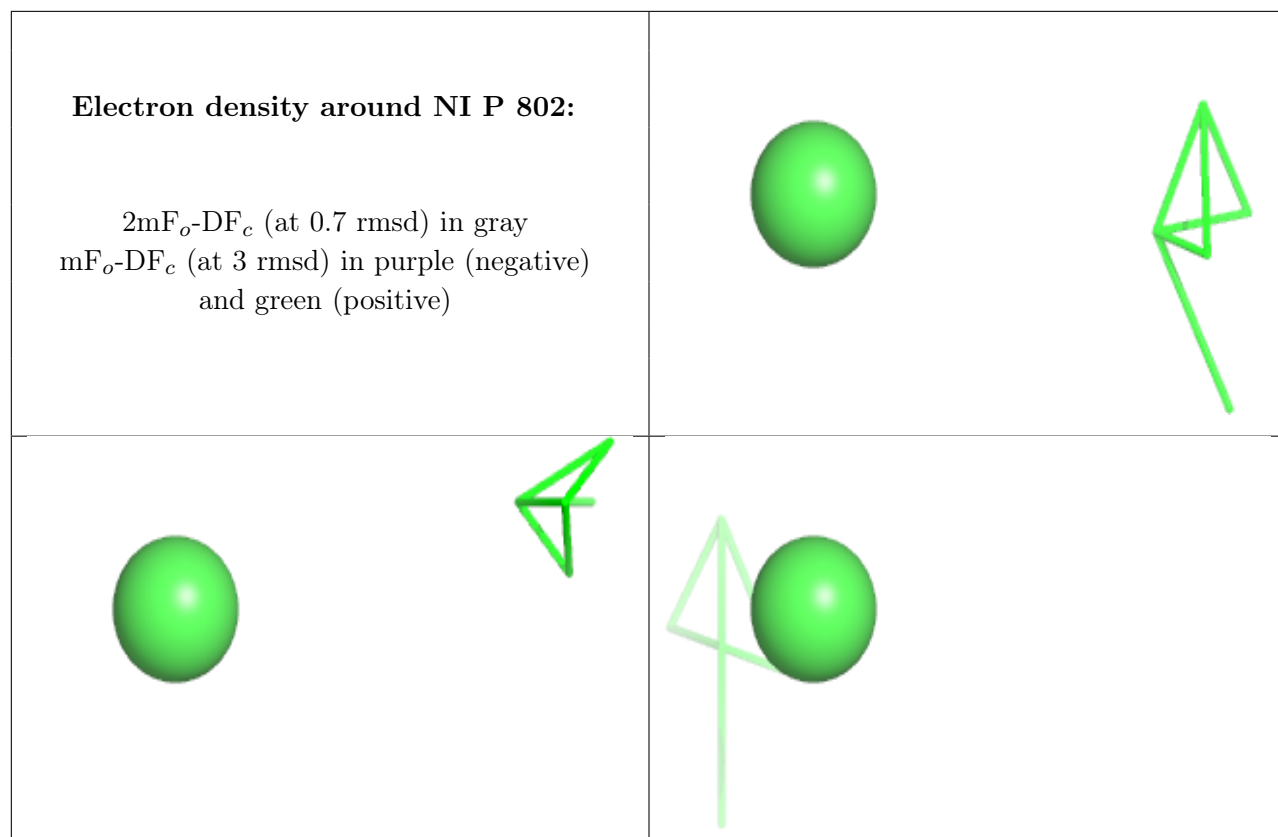
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around NI N 802:

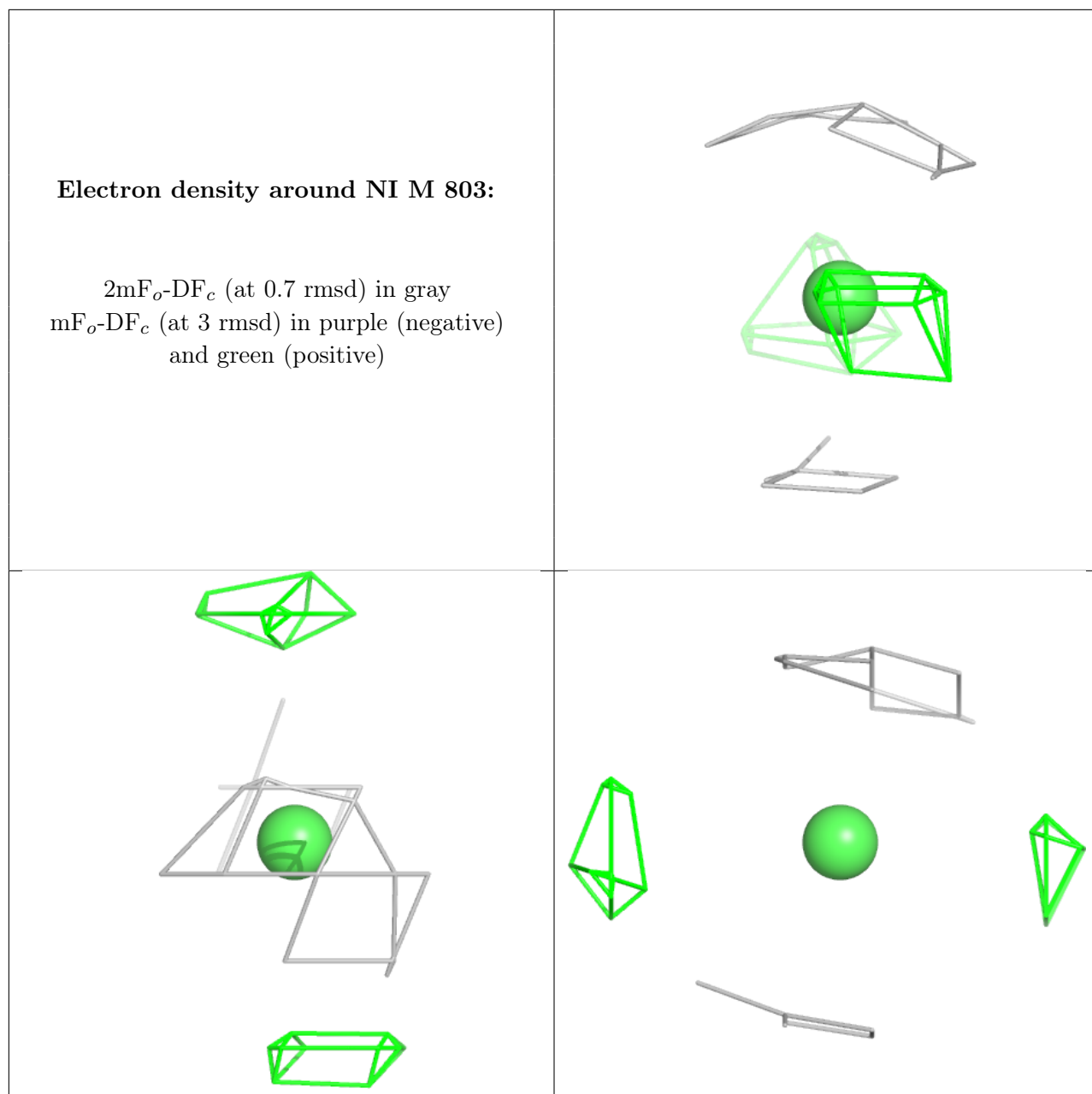
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





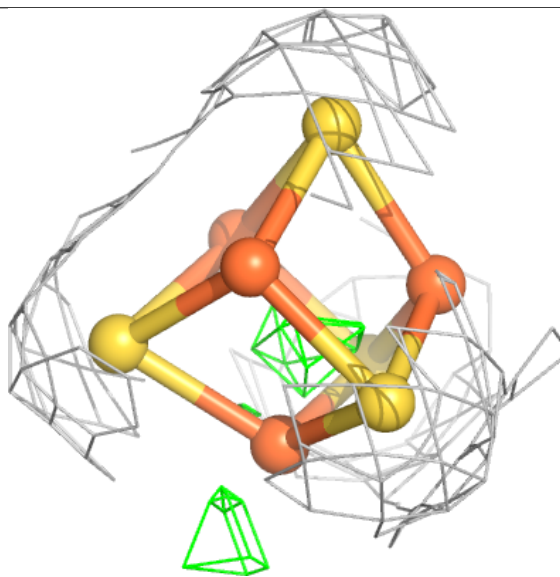
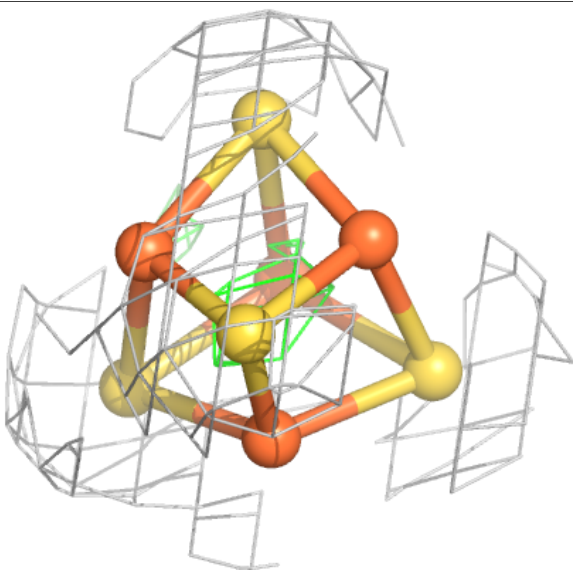
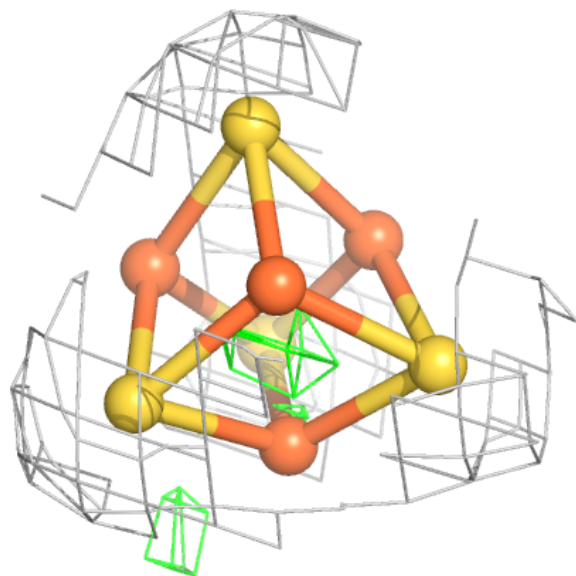
Electron density around NI M 803:

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



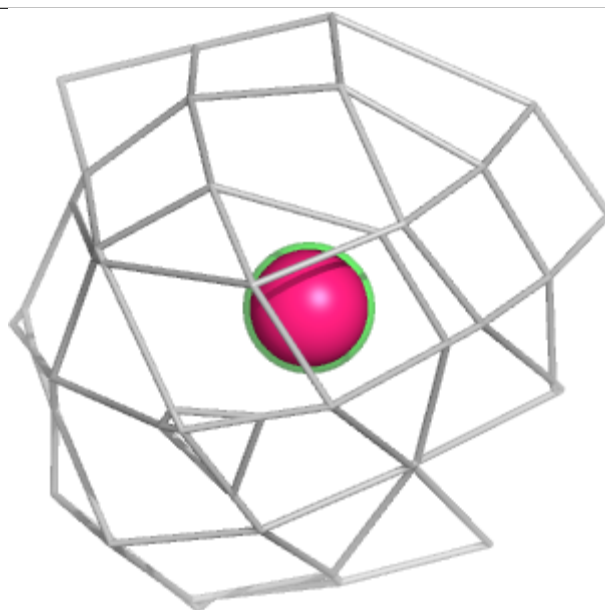
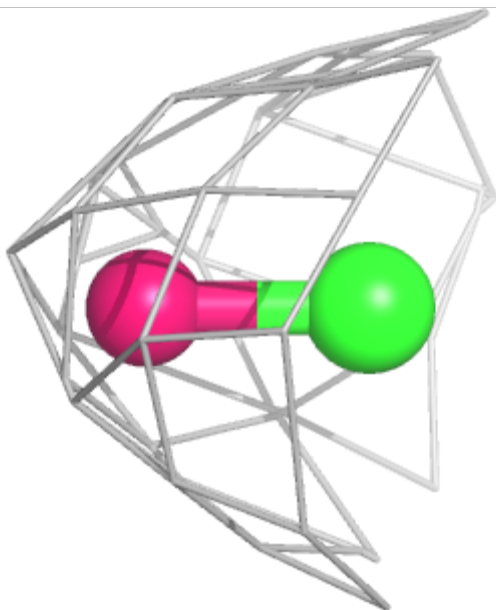
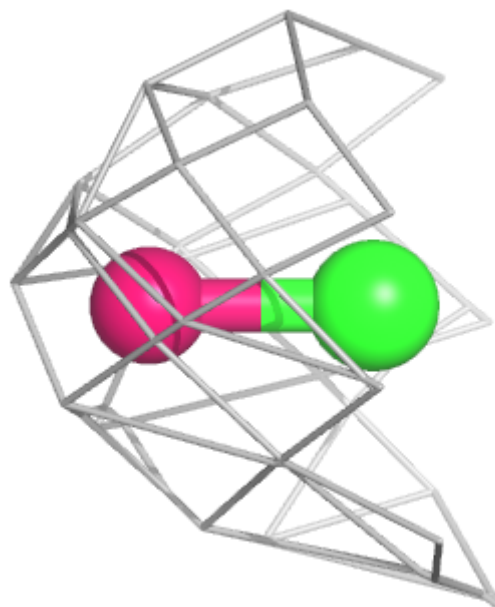
Electron density around SF4 C 702:

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



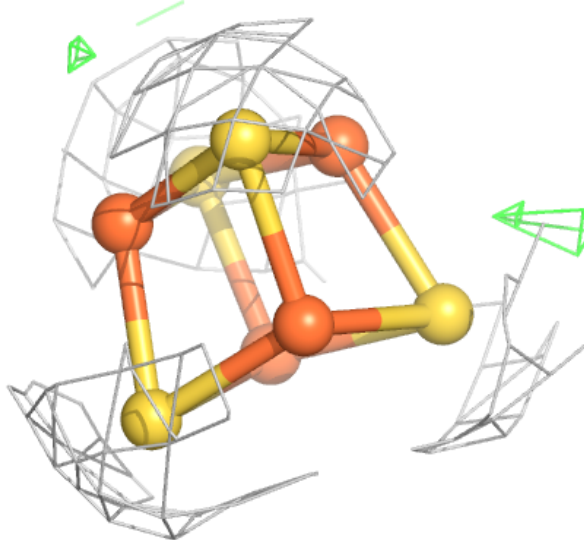
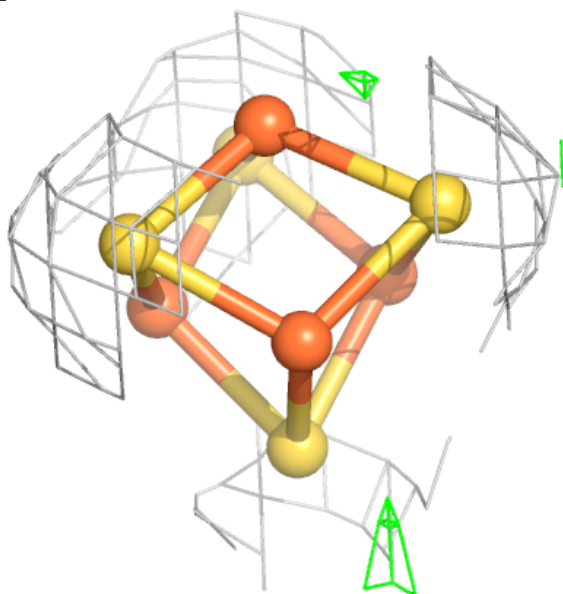
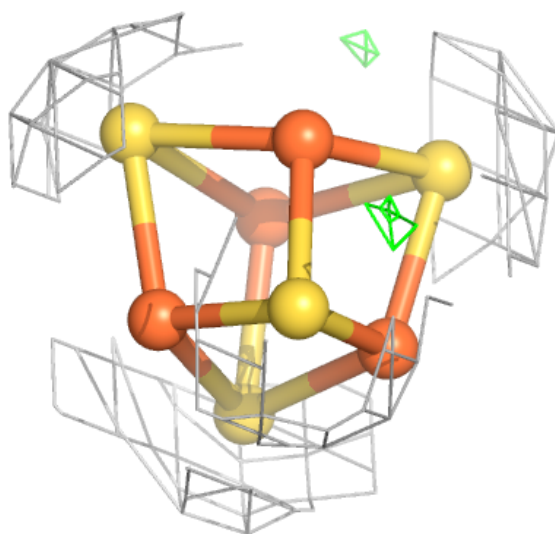
Electron density around CMO P 804:

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



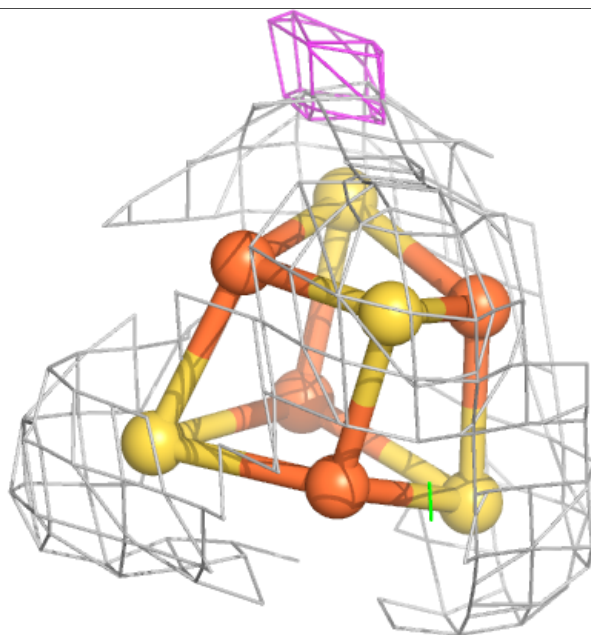
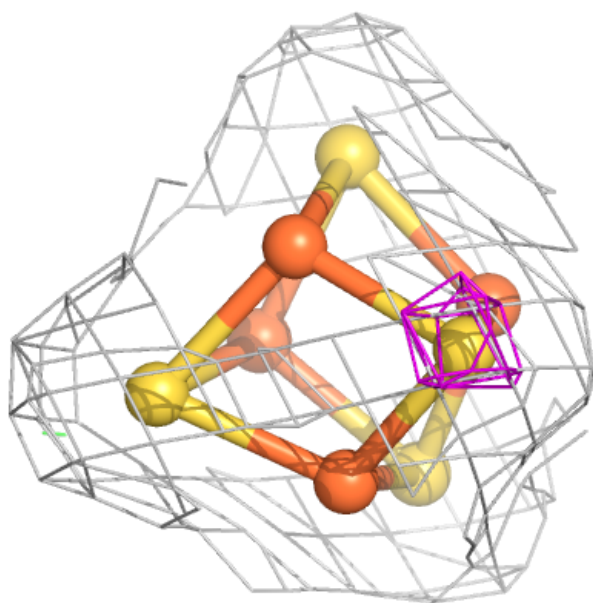
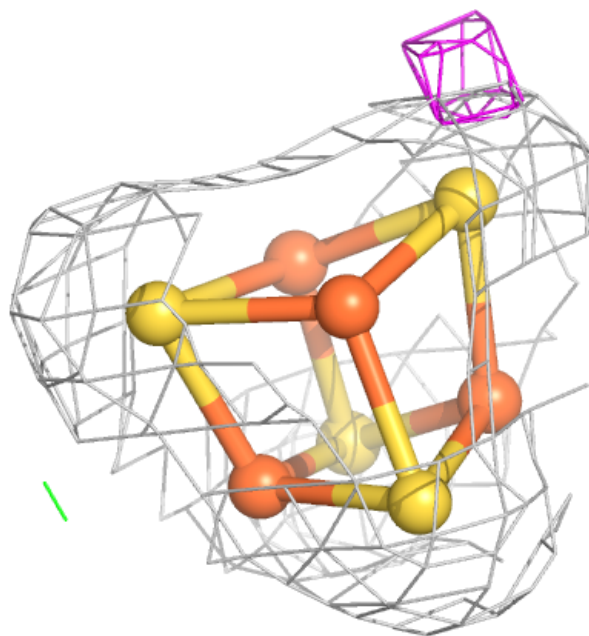
Electron density around SF4 P 801:

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



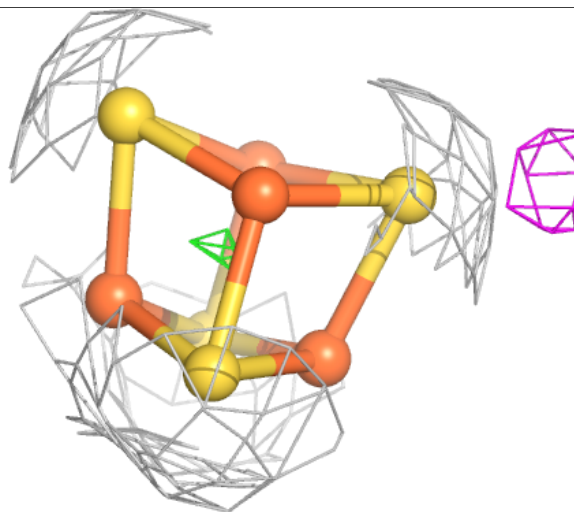
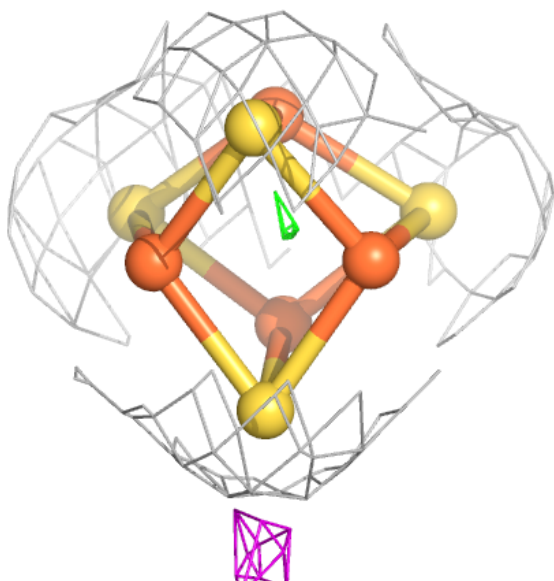
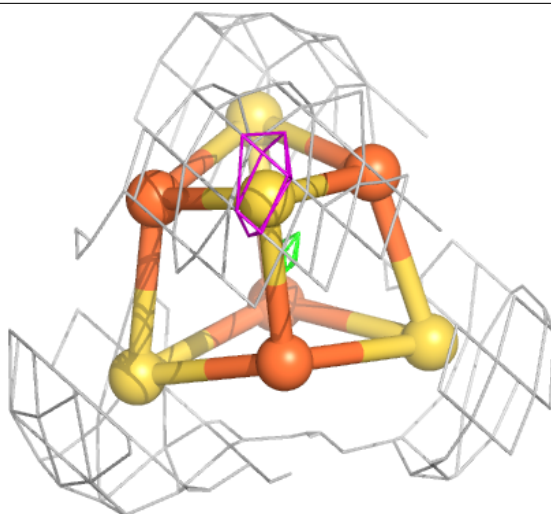
Electron density around SF4 A 701:

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



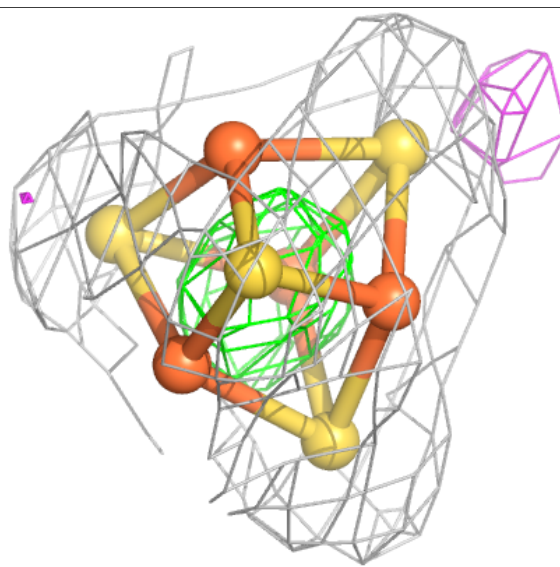
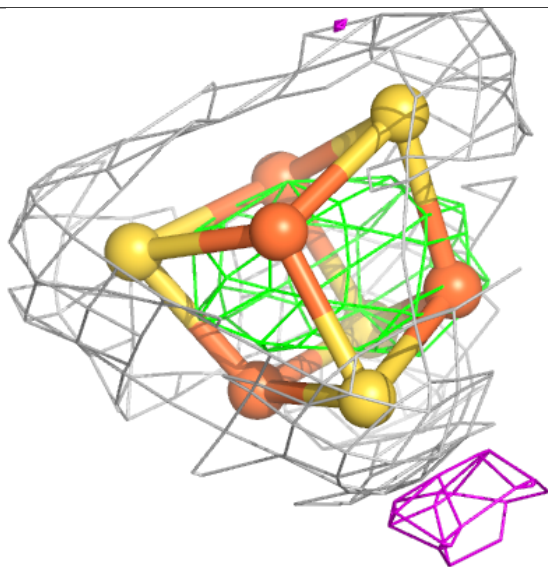
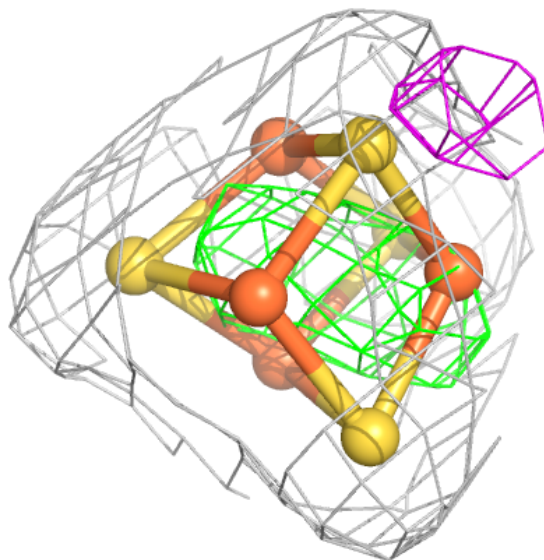
Electron density around SF4 C 701:

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



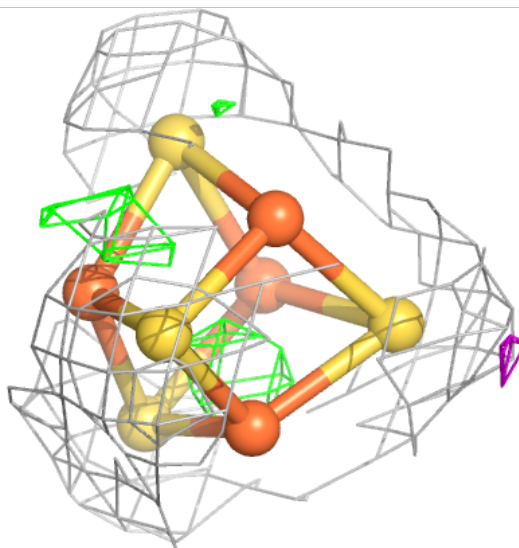
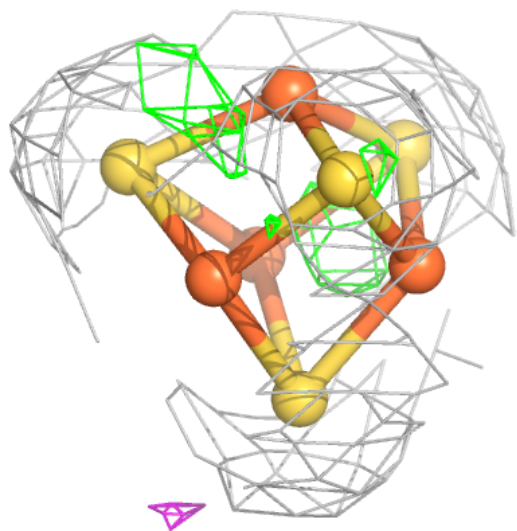
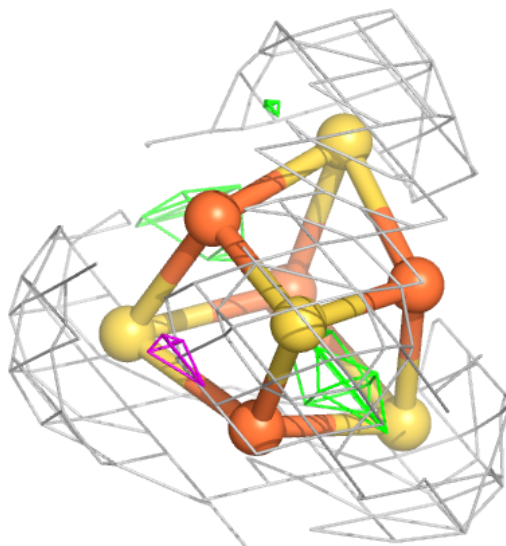
Electron density around SF4 A 702:

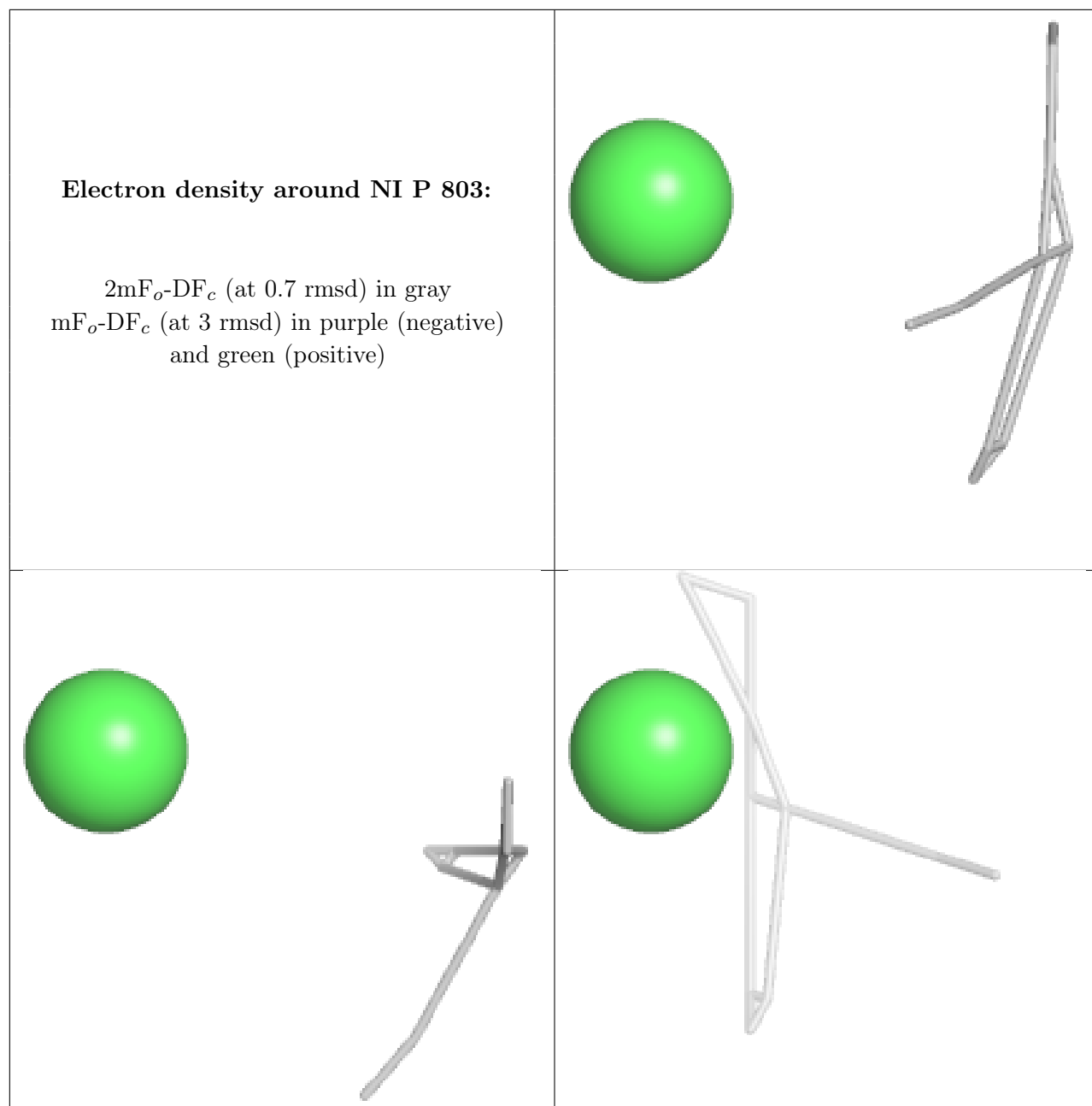
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

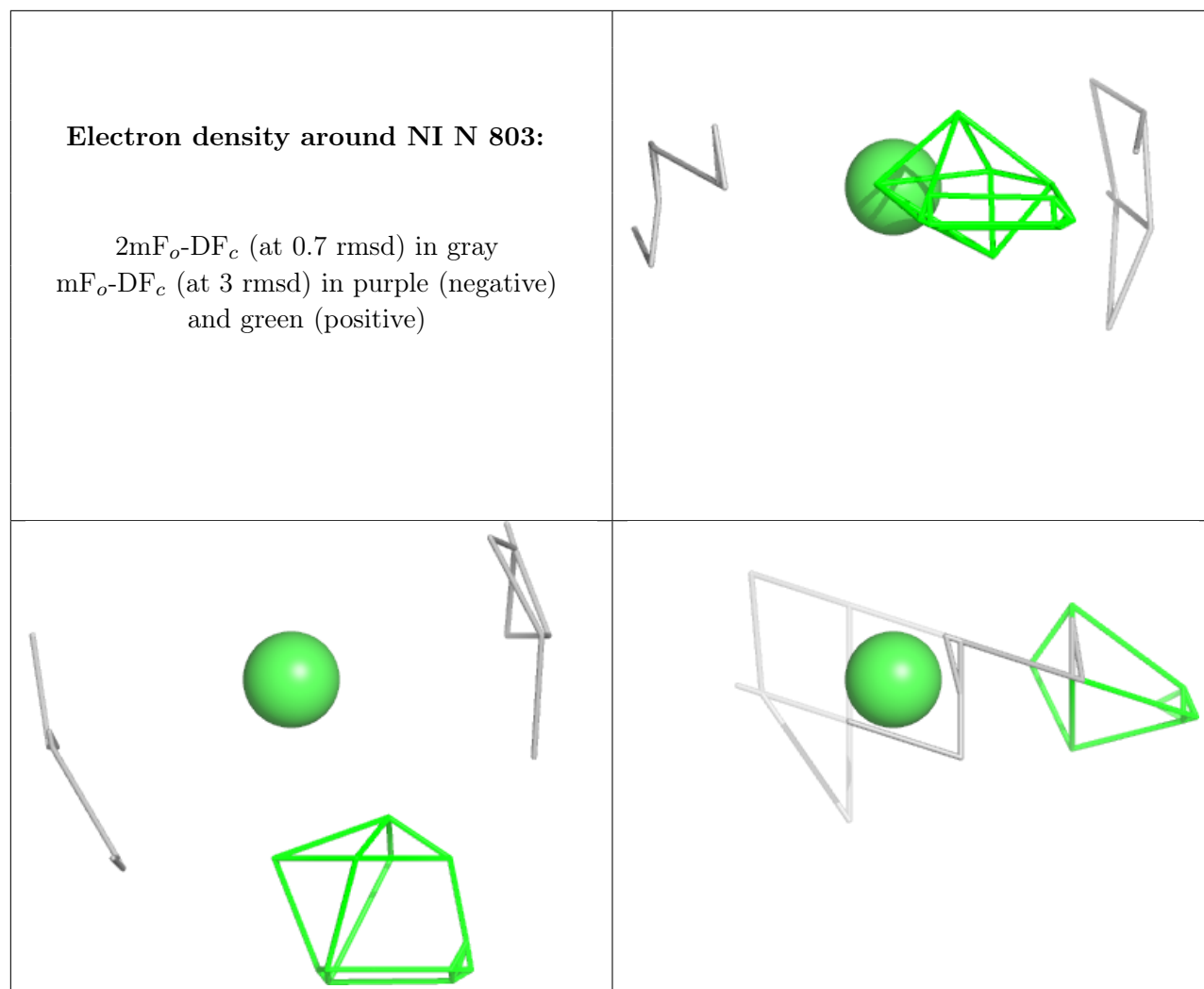


Electron density around SF4 N 801:

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







6.5 Other polymers [i](#)

There are no such residues in this entry.