WORLDWIDE PDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 13, 2024 – 07:18 pm GMT

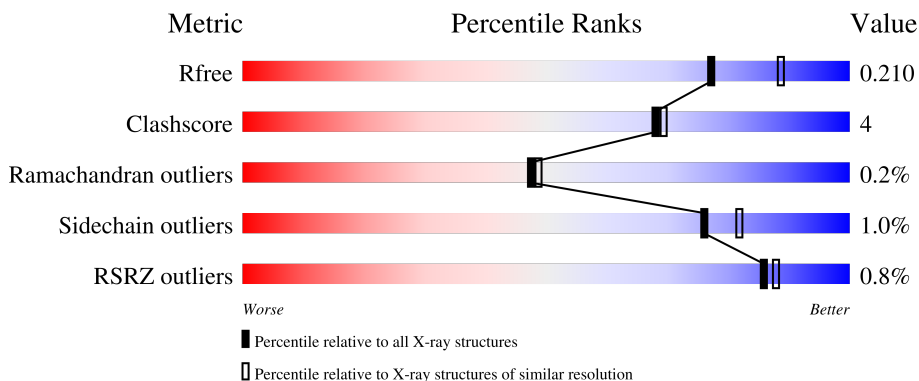|		
PDB ID	:	8CJA
Title	:	A225L/F231A variant of the CODH/ACS complex of C. hydrogenoformans
Authors	:	Ruickoldt, J.; Jeoung, J.; Lennartz, F.; Dobbek, H.
Deposited on	:	2023-02-13
Resolution	:	2.10 Å(reported)

1 Overall quality at a glance ⓘ

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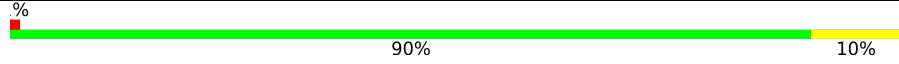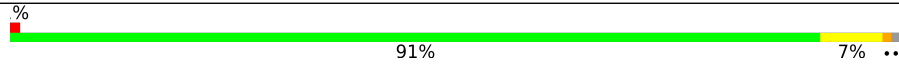*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	Percentile Ranks	Value
Rfree		0.210
Clashscore		4
Ramachandran outliers		0.2%
Sidechain outliers		1.0%
RSRZ outliers		0.8%

Worse *Better*

▮ Percentile relative to all X-ray structures

⬚ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	669	90% 10%
2	B	738	91% 7% ··

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
7	ACT	B	804	-	-	X	-

2 Entry composition ⓘ

There are 9 unique types of molecules in this entry. The entry contains 11761 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 Carbon monoxide dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	669	5146	3261	888	961	36	0	4	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	ASP	GLU	conflict	UNP A0A1L8D0M5
A	29	ILE	THR	conflict	UNP A0A1L8D0M5
A	73	GLN	MET	conflict	UNP A0A1L8D0M5
A	120	ALA	THR	conflict	UNP A0A1L8D0M5
A	153	THR	ILE	conflict	UNP A0A1L8D0M5
A	159	MET	LEU	conflict	UNP A0A1L8D0M5
A	199	GLU	ASP	conflict	UNP A0A1L8D0M5
A	205	SER	ALA	conflict	UNP A0A1L8D0M5
A	220	ILE	MET	conflict	UNP A0A1L8D0M5
A	231	ALA	PHE	engineered mutation	UNP A0A1L8D0M5
A	389	ILE	VAL	conflict	UNP A0A1L8D0M5
A	393	LEU	PHE	conflict	UNP A0A1L8D0M5
A	494	THR	ALA	conflict	UNP A0A1L8D0M5
A	602	THR	SER	conflict	UNP A0A1L8D0M5

- Molecule 2 is a protein called CO-methylating acetyl-CoA synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	731	5819	3733	979	1078	29	0	4	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	ILE	-	expression tag	UNP Q3ACS4
B	-1	ASN	-	expression tag	UNP Q3ACS4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	expression tag	UNP Q3ACS4
B	1	PYL	-	expression tag	UNP Q3ACS4
B	2	ASP	-	expression tag	UNP Q3ACS4
B	3	GLU	-	expression tag	UNP Q3ACS4
B	4	LEU	-	expression tag	UNP Q3ACS4
B	225	LEU	ALA	engineered mutation	UNP Q3ACS4
B	733	ARG	-	expression tag	UNP Q3ACS4
B	734	SER	-	expression tag	UNP Q3ACS4
B	735	HIS	-	expression tag	UNP Q3ACS4

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).
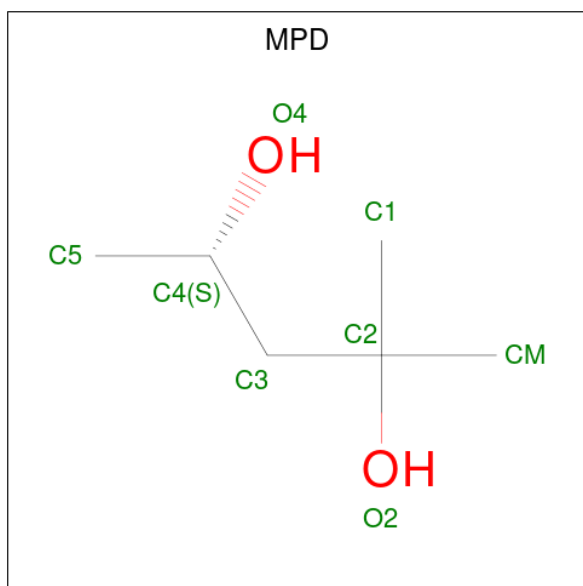
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 8	C 6	O 2	0	0
3	A	1	Total 8	C 6	O 2	0	0

- Molecule 4 is Fe(3)-Ni(1)-S(4) cluster (three-letter code: RQM) (formula: Fe_4NiS_4) (labeled as "Ligand of Interest" by depositor).

RQM
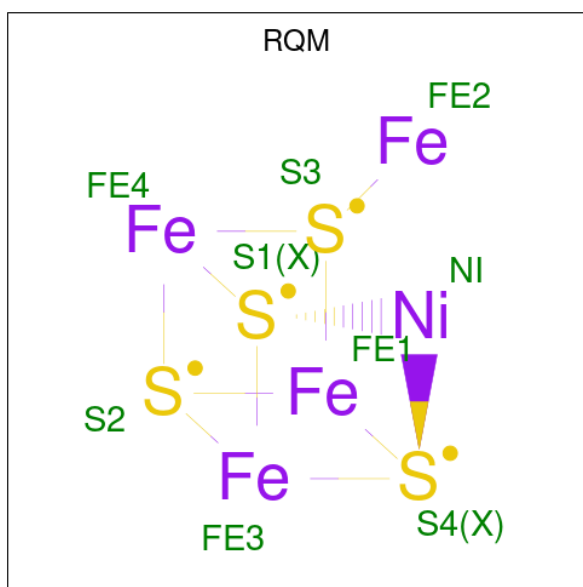
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	Fe	Ni	S		
4	A	1	9	4	1	4	0	0

- Molecule 5 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4) (labeled as "Ligand of Interest" by depositor).
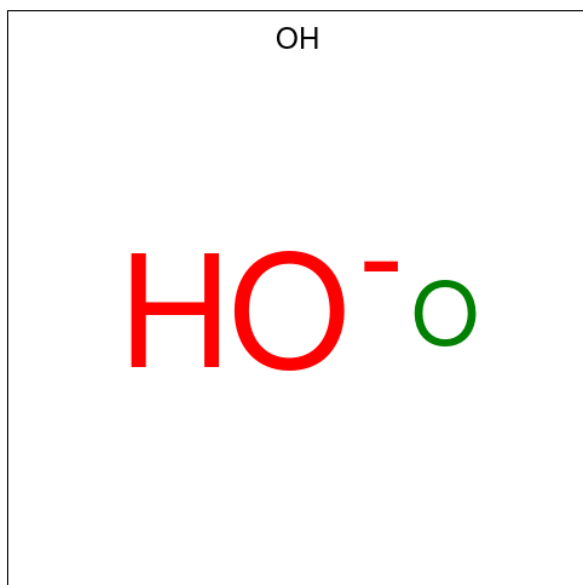

SF4
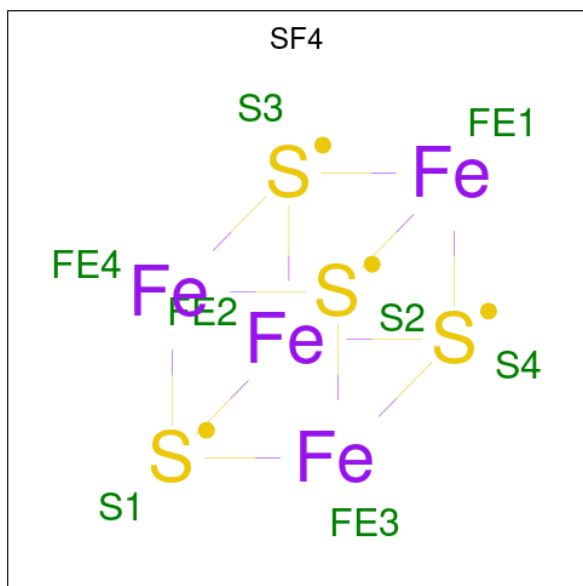
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
5	A	1	8	4	4	0	0
5	A	1	4	2	2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
5	B	1	8	4	4	0	0

- Molecule 6 is HYDROXIDE ION (three-letter code: OH) (formula: HO) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	1	1	1	0	0
6	A	1	Total	O	0	0
			1	1		

- Molecule 7 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total 4	C 2	O 2	0	0

- Molecule 8 is NICKEL (II) ION (three-letter code: NI) (formula: Ni) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	2	Total 2	Ni 2	0	0

- Molecule 9 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	308	Total 308	O 308	0	0
9	B	435	Total 435	O 435	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

Chain A:
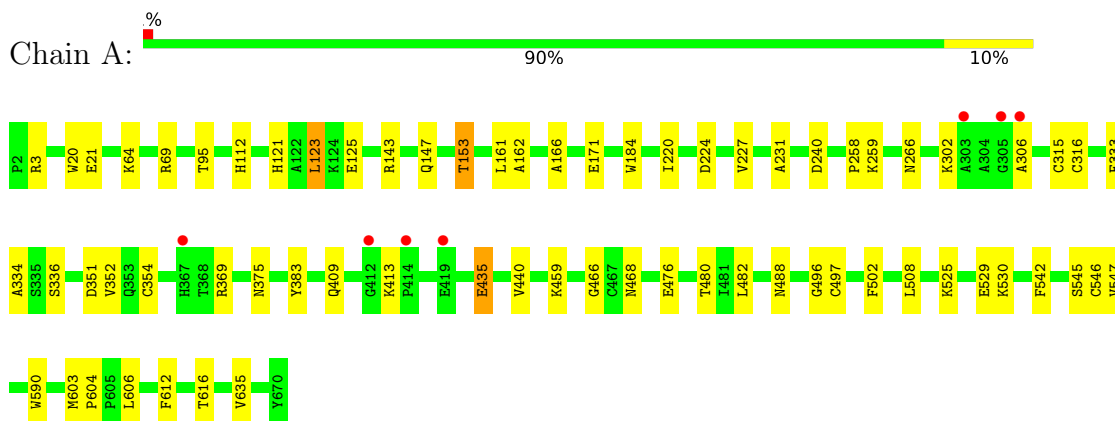
• Molecule 2: CO-methylating acetyl-CoA synthase

Chain B:
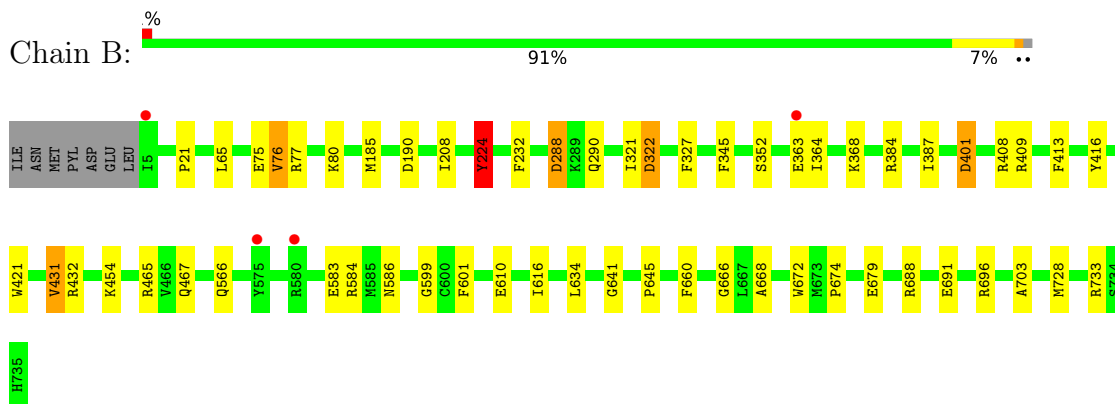
4   Data and refinement statistics   ⓘ

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α, β, γ	142.22Å 142.22Å 290.77Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.55 – 2.10 48.46 – 1.92	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.55-2.10) 99.8 (48.46-1.92)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.33 (at 1.92Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.178 , 0.209 0.179 , 0.210	Depositor DCC
R_{free} test set	1392 reflections (1.05%)	wwPDB-VP
Wilson B-factor (Å^2)	38.6	Xtriage
Anisotropy	0.241	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 38.2	EDS
L-test for twinning[2]	$< |L| > = 0.51, < L^2 > = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	11761	wwPDB-VP
Average B, all atoms (Å^2)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.22% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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: RQM, OH, NI, ACT, SF4, MPD

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	0.43	2/5257 (0.0%)	0.64	1/7117 (0.0%)
2	B	0.43	0/5963	0.68	6/8070 (0.1%)
All	All	0.43	2/11220 (0.0%)	0.66	7/15187 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	354	CYS	CB-SG	5.20	1.91	1.82
1	A	497	CYS	CB-SG	5.03	1.90	1.82

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	224	TYR	CB-CG-CD2	-7.51	116.50	121.00
2	B	322	ASP	CB-CG-OD1	6.67	124.30	118.30
1	A	590	TRP	CA-CB-CG	5.51	124.16	113.70
2	B	634	LEU	CA-CB-CG	5.30	127.48	115.30
2	B	288	ASP	CB-CG-OD1	-5.16	113.66	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	466	GLY	Peptide
2	B	224	TYR	Sidechain

5.2　Too-close contacts　ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5146	0	5168	47	0
2	B	5819	0	5801	37	2
3	A	16	0	28	8	0
4	A	9	0	0	0	0
5	A	12	0	0	1	0
5	B	8	0	0	0	0
6	A	2	0	0	1	0
7	B	4	0	3	2	0
8	B	2	0	0	0	0
9	A	308	0	0	8	1
9	B	435	0	0	9	1
All	All	11761	0	11000	84	3

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 4.

The worst 5 of 84 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:546[A]:CYS:SG	9:A:785:HOH:O	2.16	1.04
2:B:21:PRO:HA	2:B:288:ASP:HB2	1.47	0.96
1:A:525:LYS:NZ	9:A:1014:HOH:O	2.03	0.85
1:A:171:GLU:OE1	9:A:948:HOH:O	1.95	0.84
2:B:688:ARG:NH1	2:B:691:GLU:OE2	2.11	0.84

All (3) 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)
9:A:902:HOH:O	9:B:1225:HOH:O[6_455]	1.66	0.54
2:B:288:ASP:OD1	2:B:696:ARG:NH2[6_555]	2.10	0.10
2:B:288:ASP:OD2	2:B:696:ARG:NH1[6_555]	2.18	0.02

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	672/669 (100%)	645 (96%)	26 (4%)	1 (0%)	51	54
2	B	733/738 (99%)	713 (97%)	18 (2%)	2 (0%)	41	41
All	All	1405/1407 (100%)	1358 (97%)	44 (3%)	3 (0%)	47	49

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	266	ASN
2	B	190	ASP
2	B	599	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	552/547 (101%)	546 (99%)	6 (1%)	73	79
2	B	618/620 (100%)	611 (99%)	7 (1%)	73	79
All	All	1170/1167 (100%)	1157 (99%)	13 (1%)	76	79

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	80	LYS
2	B	224	TYR
2	B	601	PHE
2	B	401[B]	ASP
2	B	431	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 11 ligands modelled in this entry, 2 are modelled with single atom and 2 are monoatomic - leaving 7 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	$\#|Z| > 2$
5	SF4	A	701	1	0,4,12	-	-	-		
3	MPD	A	706	-	7,7,7	0.53	0	9,10,10	1.33	1 (11%)
5	SF4	B	802	2	0,12,12	-	-	-		
4	RQM	A	700	6,1	0,12,12	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	MPD	A	707	-	7,7,7	0.32	0	9,10,10	1.09	1 (11%)
7	ACT	B	804	8	3,3,3	1.34	1 (33%)	3,3,3	1.38	0
5	SF4	A	702	1	0,12,12	-	-	-		

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
5	SF4	A	701	1	-	-	0/1/1/5
3	MPD	A	706	-	-	1/5/5/5	-
5	SF4	B	802	2	-	-	0/6/5/5
4	RQM	A	700	6,1	-	-	0/4/4/4
3	MPD	A	707	-	-	1/5/5/5	-
5	SF4	A	702	1	-	-	0/6/5/5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	804	ACT	CH3-C	2.05	1.57	1.49

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	706	MPD	CM-C2-C1	-2.48	105.40	110.57
3	A	707	MPD	CM-C2-C1	-2.27	105.84	110.57

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	707	MPD	C2-C3-C4-O4
3	A	706	MPD	O2-C2-C3-C4

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	706	MPD	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	707	MPD	5	0
7	B	804	ACT	2	0
5	A	702	SF4	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 SF4 A 701

Bond lengths

Bond angles

Torsions

Rings

Ligand SF4 B 802

Bond lengths

Bond angles

Torsions

Rings

Ligand RQM A 700

Bond lengths

Bond angles

Torsions

Rings

Ligand SF4 A 702

Bond lengths

Bond angles

Torsions

Rings
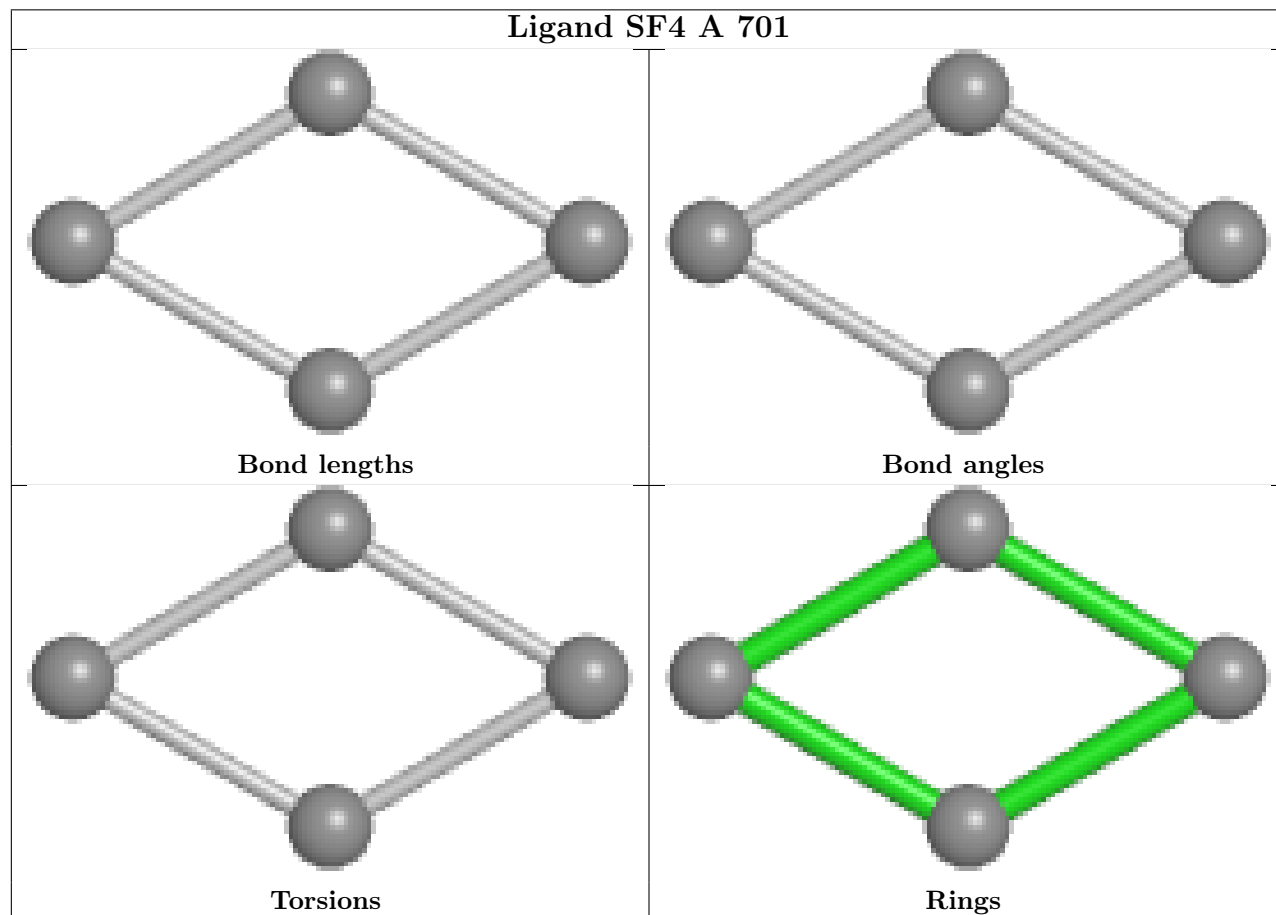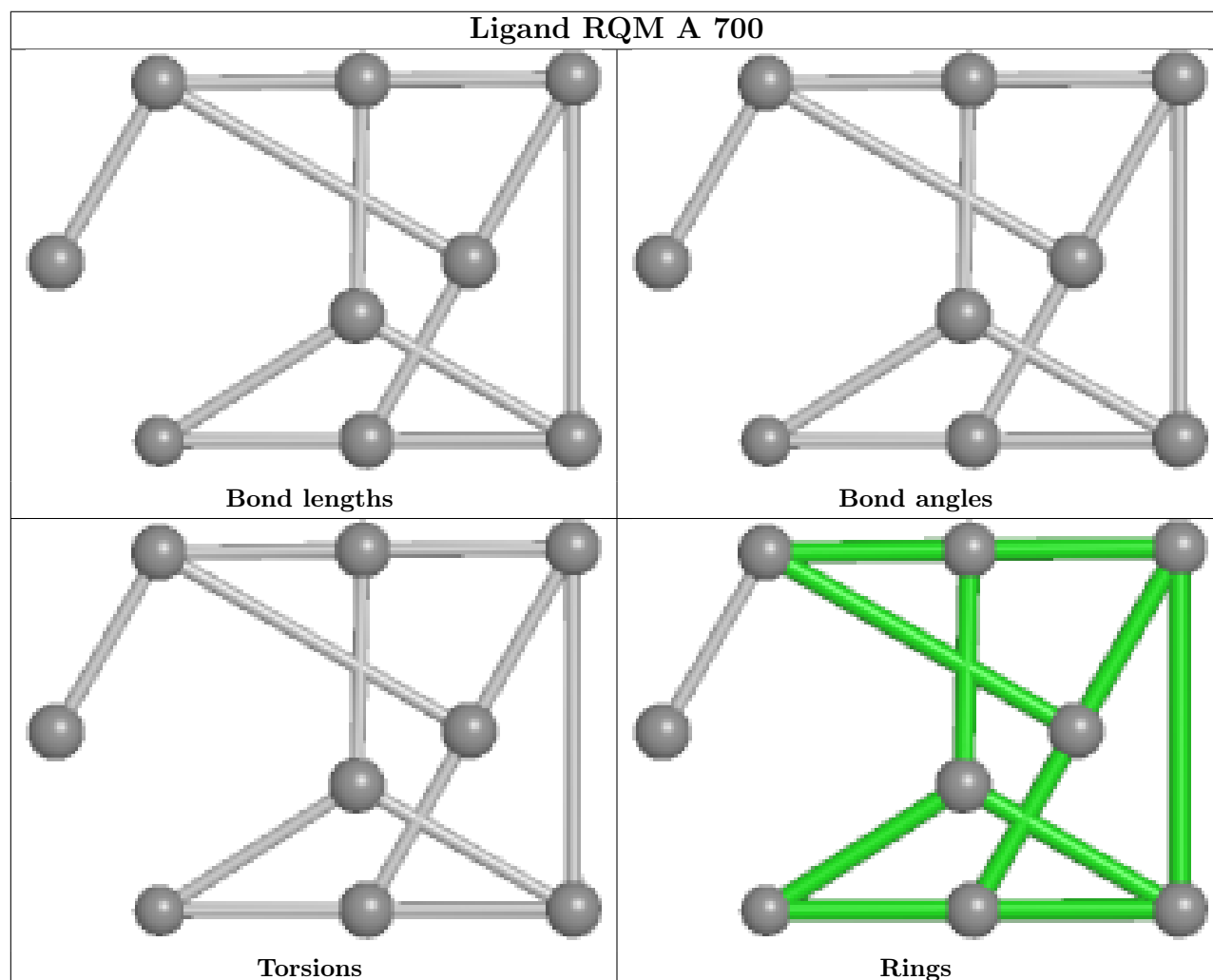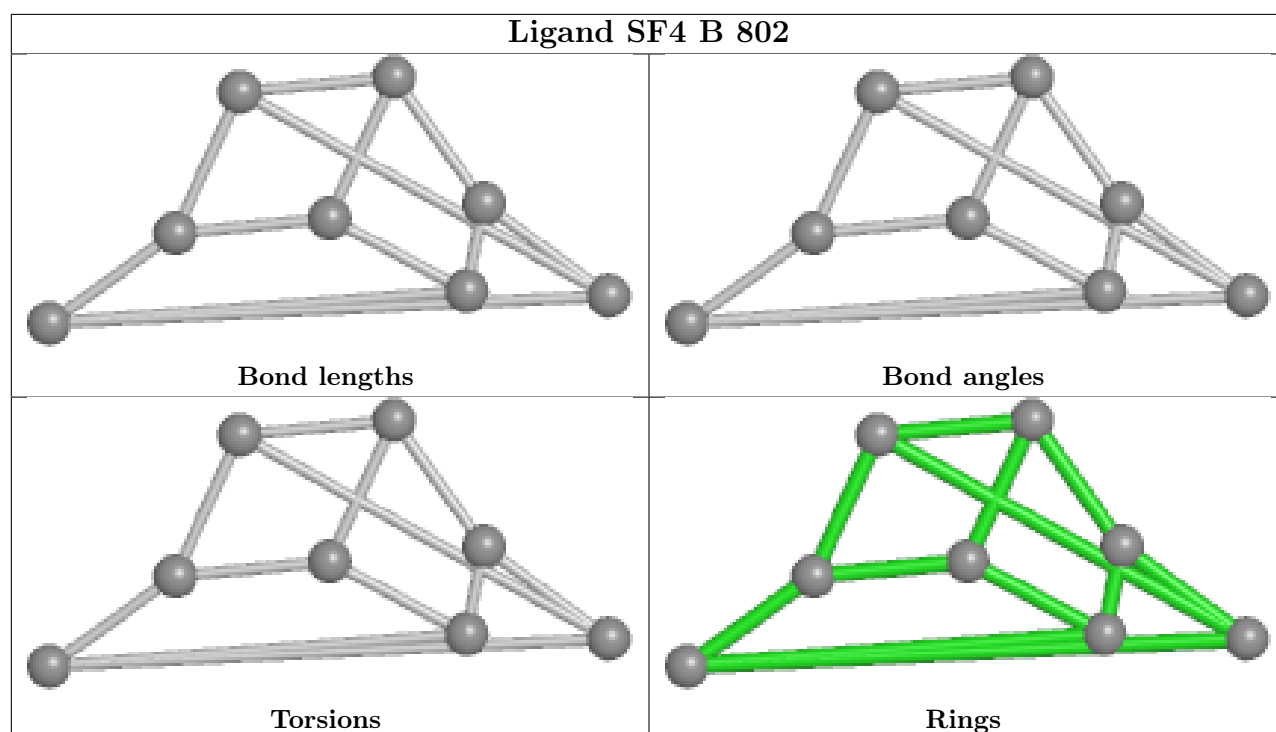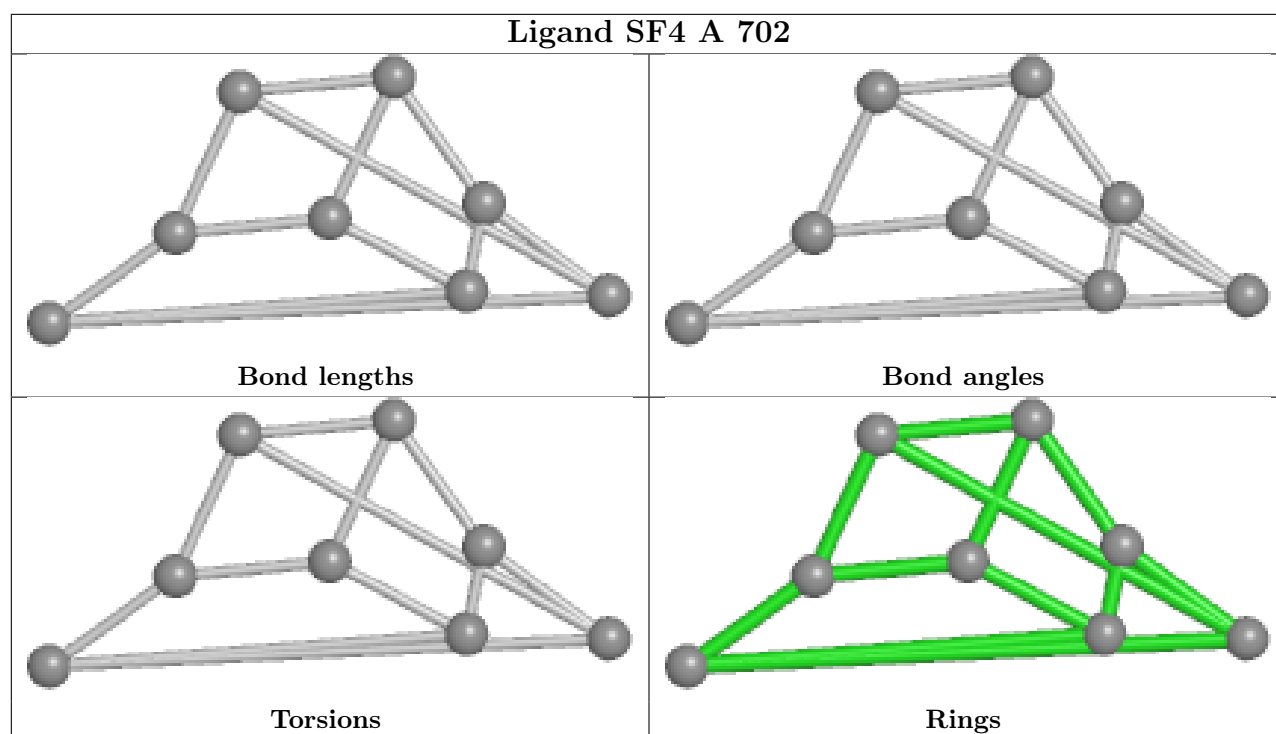
5.7   Other polymers ⓘ

There are no such residues in this entry.

5.8   Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6   Fit of model and data ⓘ

6.1   Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	669/669 (100%)	-0.40	7 (1%)	82	85	29, 42, 61, 80	0
2	B	731/738 (99%)	-0.70	4 (0%)	91	92	29, 40, 57, 85	0
All	All	1400/1407 (99%)	-0.56	11 (0%)	86	88	29, 41, 60, 85	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	363	GLU	4.4
1	A	306	ALA	3.2
2	B	5	ILE	2.9
1	A	305	GLY	2.9
1	A	367	HIS	2.8

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 ⓘ

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(Å²)	Q<0.9
3	MPD	A	706	8/8	0.90	0.23	30,36,44,45	0
3	MPD	A	707	8/8	0.93	0.18	36,40,42,46	0
6	OH	A	704	1/1	0.96	0.11	49,49,49,49	0
6	OH	A	705	1/1	0.96	0.12	47,47,47,47	0
4	RQM	A	700	9/9	0.97	0.11	43,50,58,64	8
5	SF4	A	701	4/8	0.98	0.06	35,37,37,38	0
5	SF4	A	702	8/8	0.99	0.08	32,33,33,34	0
5	SF4	B	802	8/8	0.99	0.06	34,36,37,38	0
7	ACT	B	804	4/4	0.99	0.08	37,38,39,39	0
8	NI	B	801	1/1	0.99	0.08	35,35,35,35	0
8	NI	B	803	1/1	0.99	0.07	28,28,28,28	1

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.
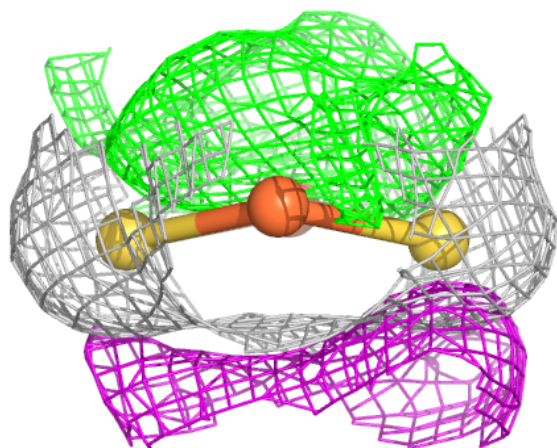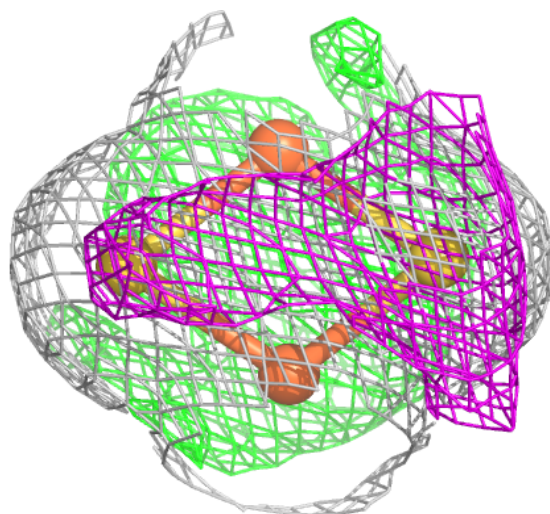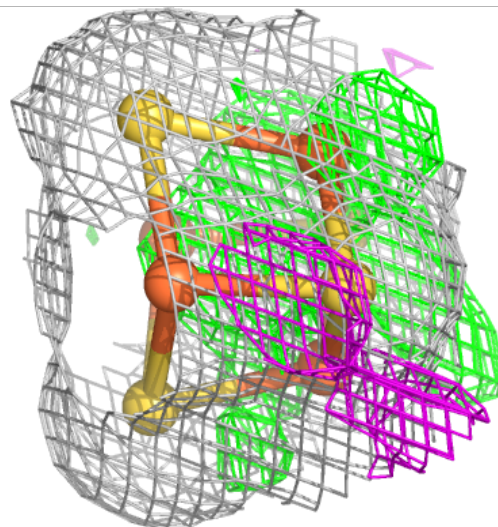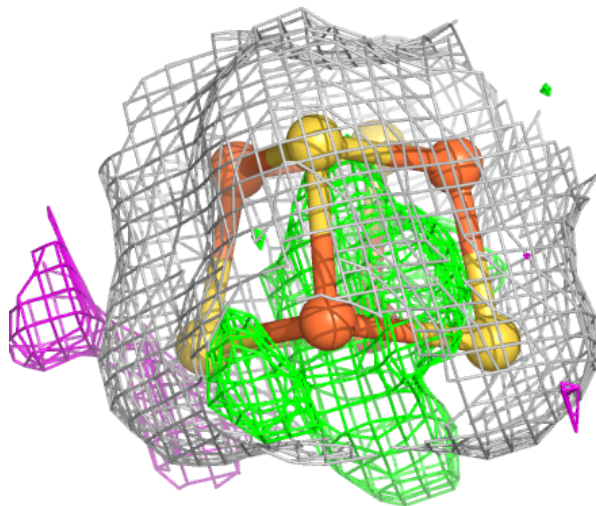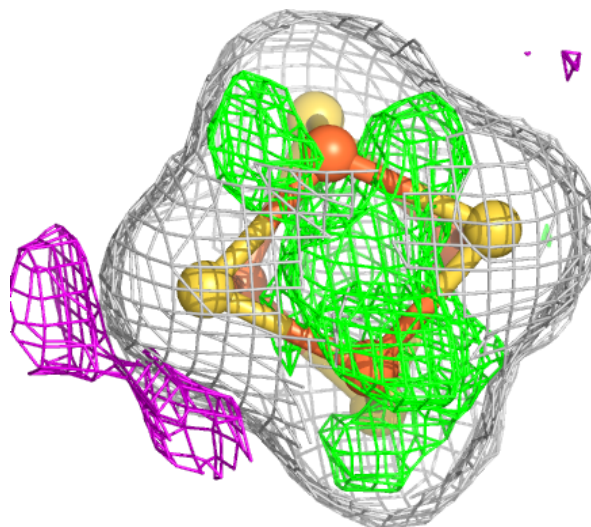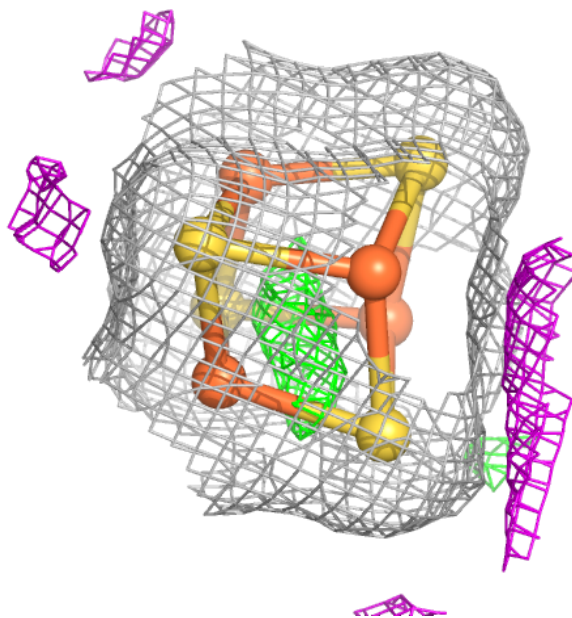
Electron density around OH A 704:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
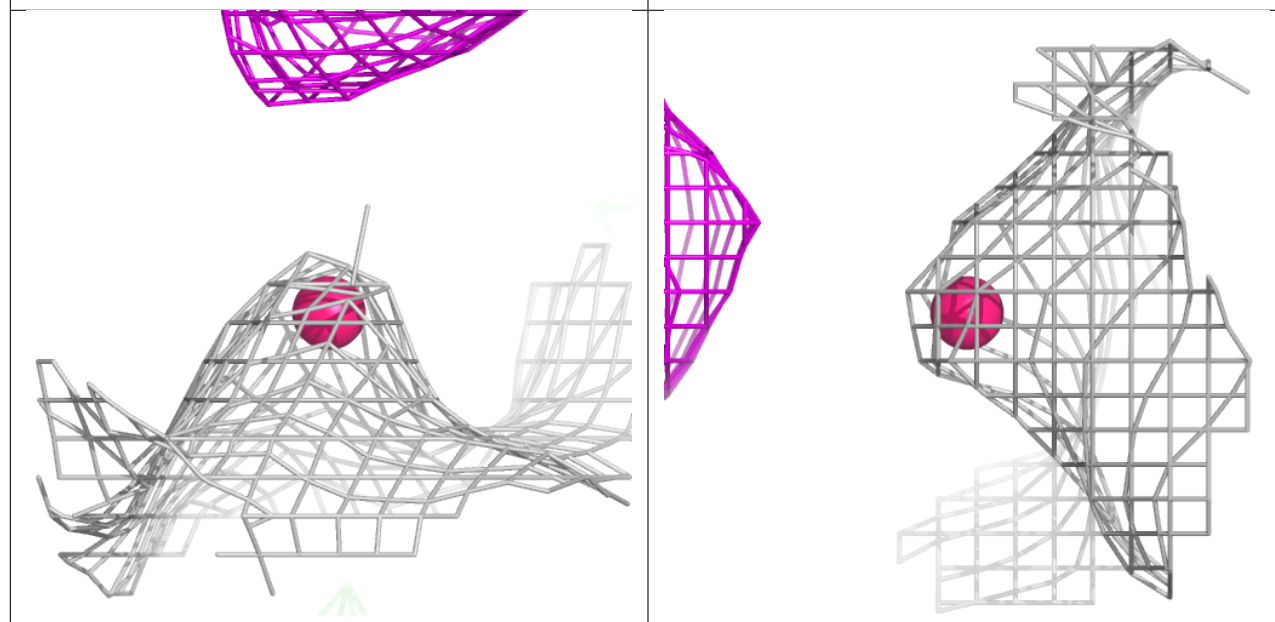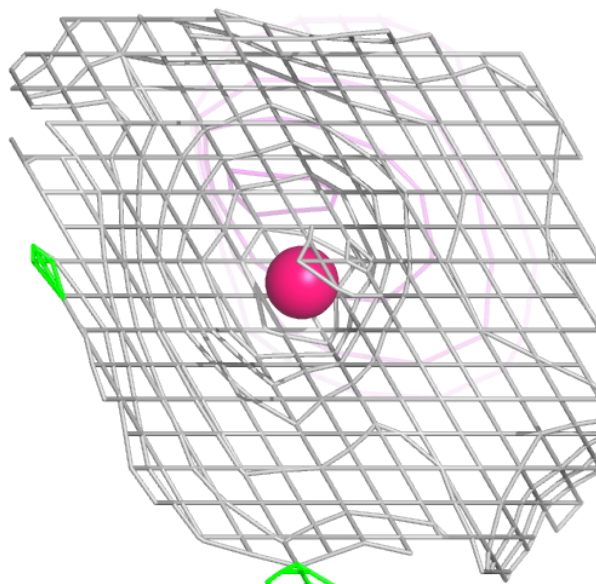
Electron density around OH A 705:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)
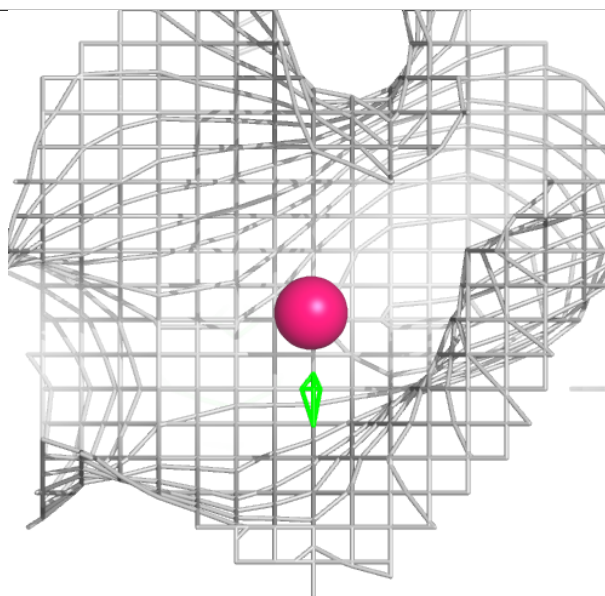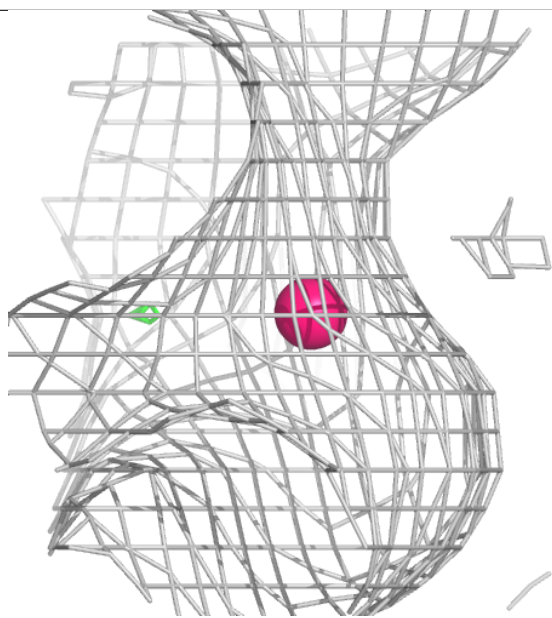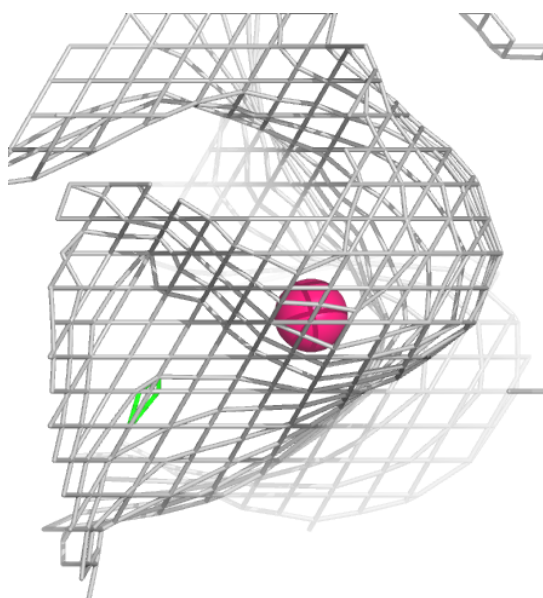
Electron density around RQM A 700:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
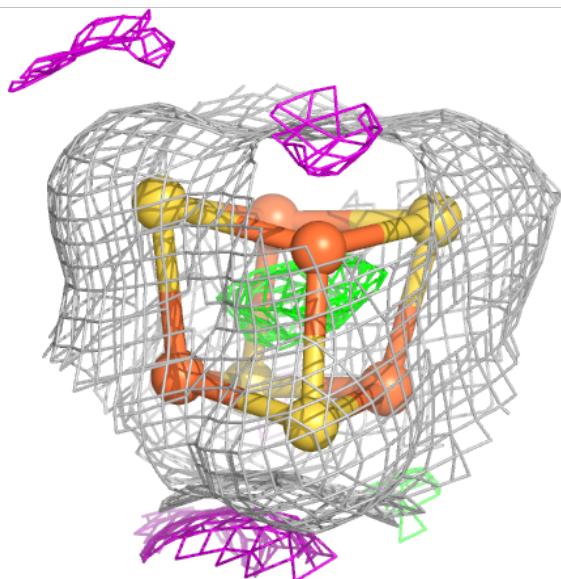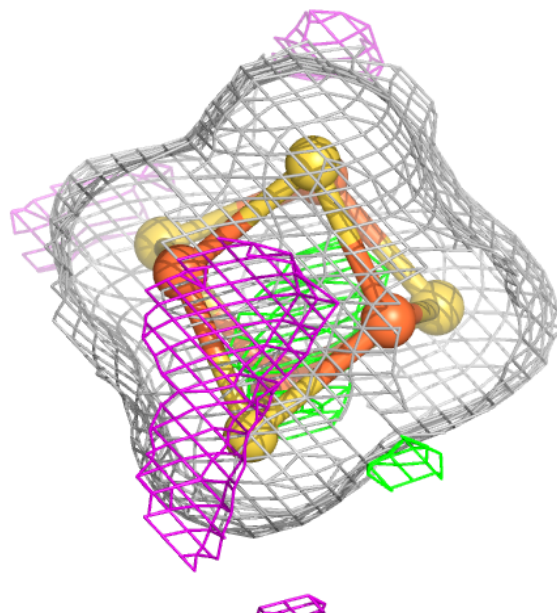and green (positive)
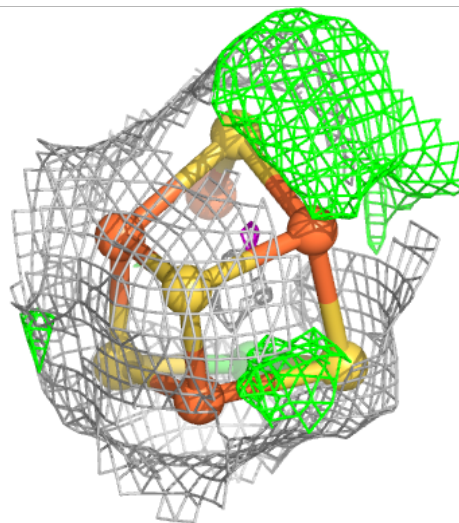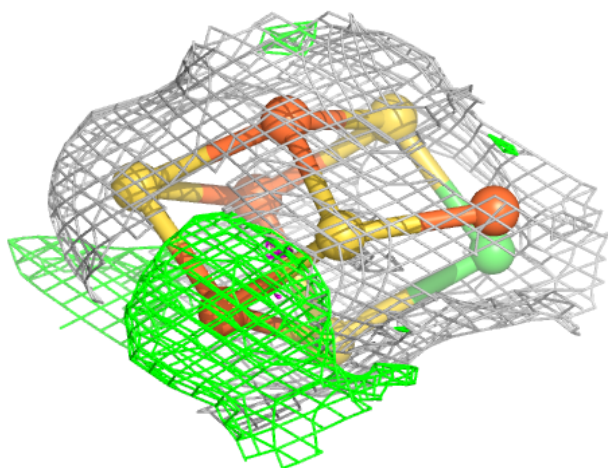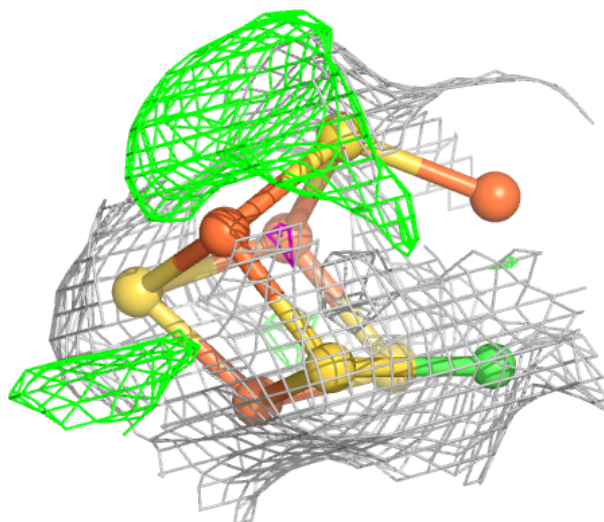
Electron density around SF4 A 701:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
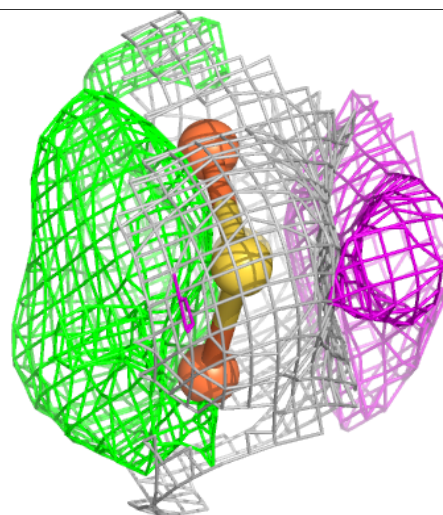
Electron density around SF4 A 702:
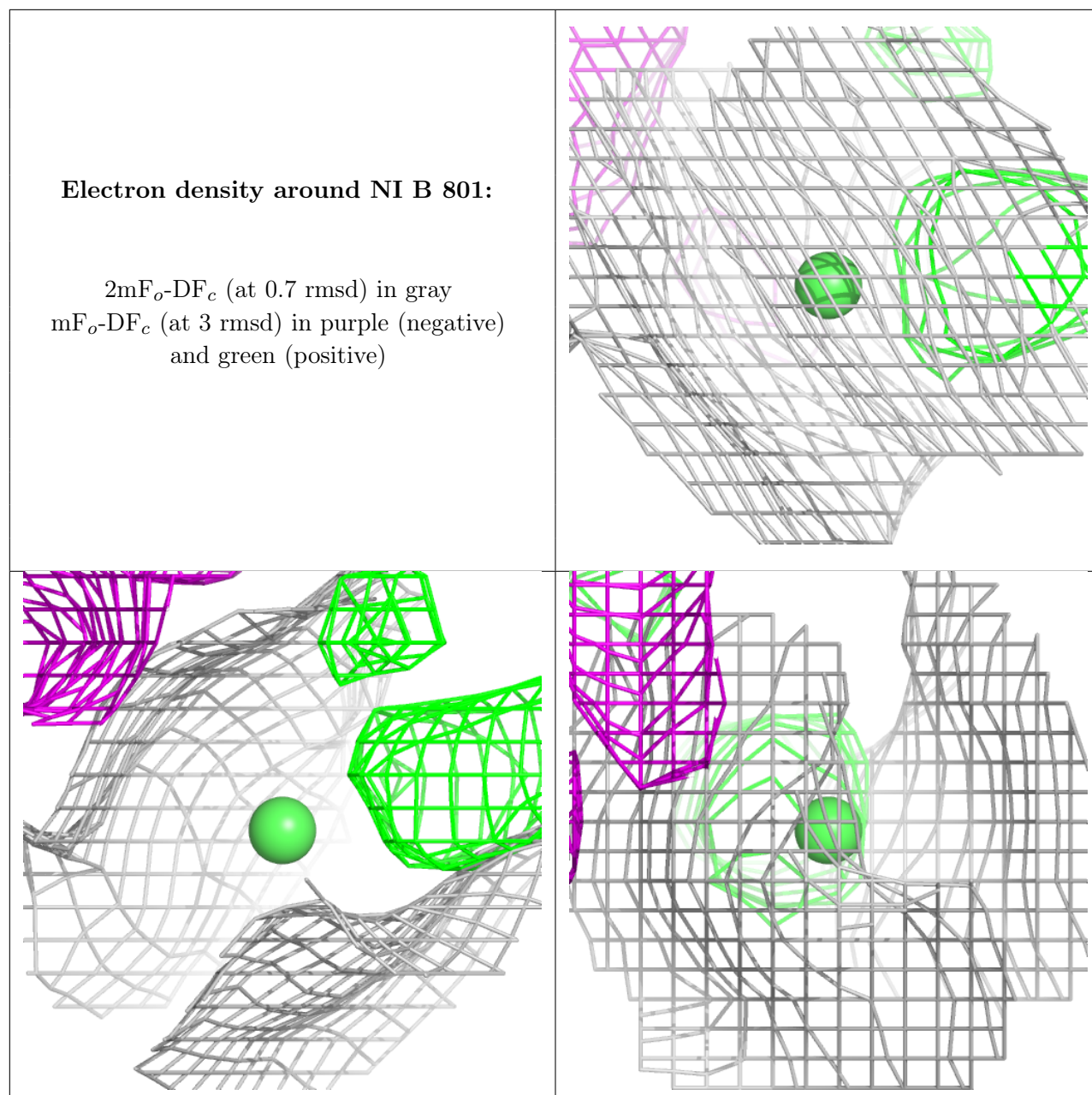
$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around SF4 B 802:

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

Electron density around NI B 801:

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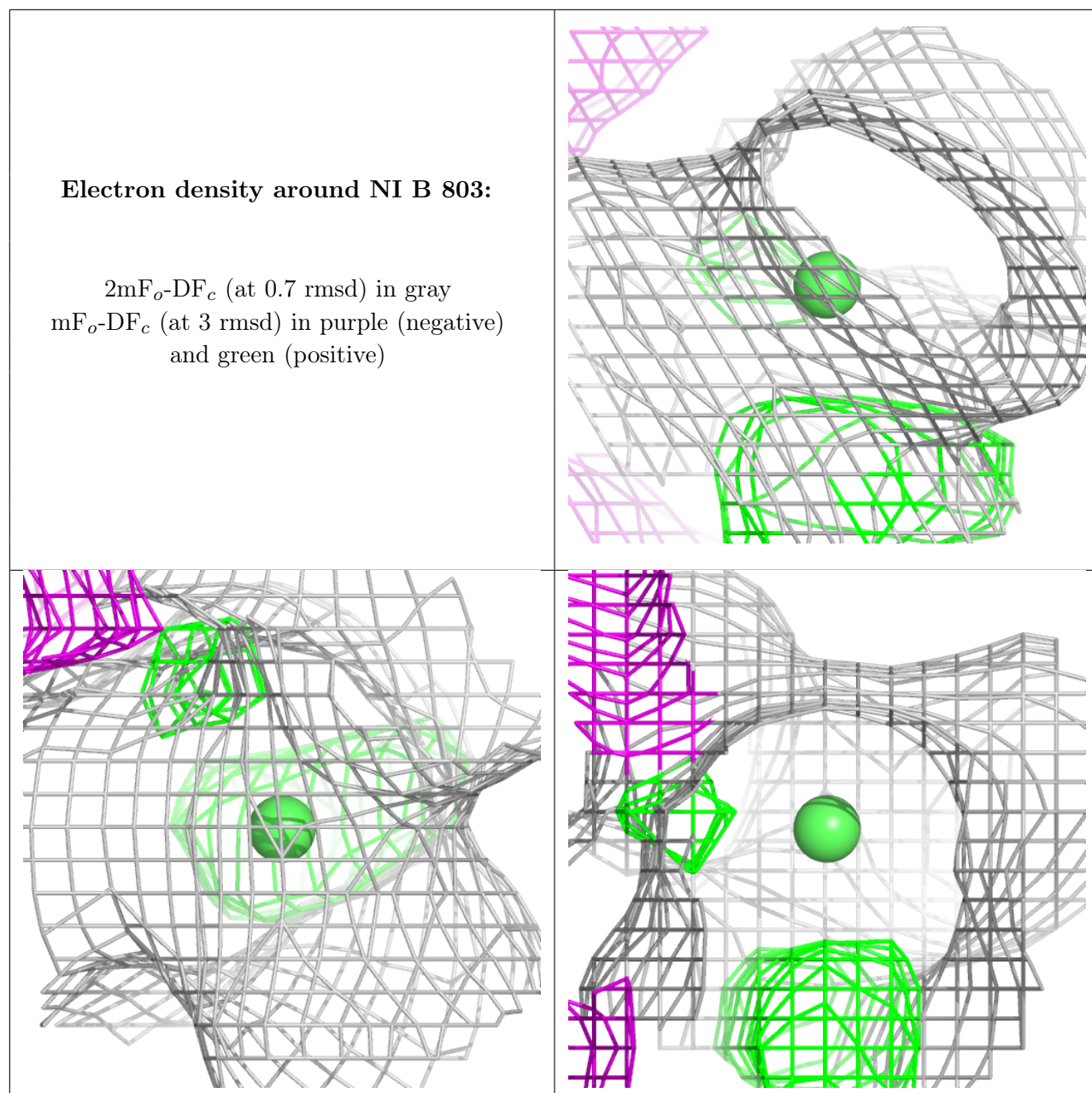mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

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Electron density around NI B 803:

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

6.5 Other polymers ⓘ

There are no such residues in this entry.