



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 25, 2024 – 04:20 pm GMT

PDB ID : 8QH4
Title : Crystal structure of reduced respiratory Complex I subunits NuoEF from Aquifex aeolicus bound to oxidized 3-acetylpyridine adenine dinucleotide
Authors : Wohlwend, D.; Friedrich, T.
Deposited on : 2023-09-06
Resolution : 1.96 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

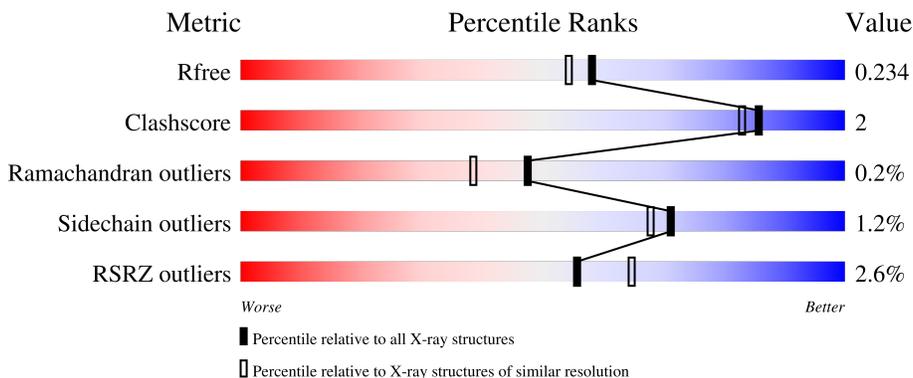
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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	160	 8% (red), 91% (green), 7% (yellow), 4% (grey)
1	C	160	 6% (red), 89% (green), 6% (yellow), 1% (grey)
2	B	434	 91% (green), 9% (yellow), 0% (red), 0% (grey)
2	D	434	 2% (red), 91% (green), 5% (yellow), 2% (grey)

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 10209 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 NADH-quinone oxidoreductase subunit E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	156	1268	821	204	234	9	0	0	0
1	C	155	1259	816	203	231	9	0	0	0

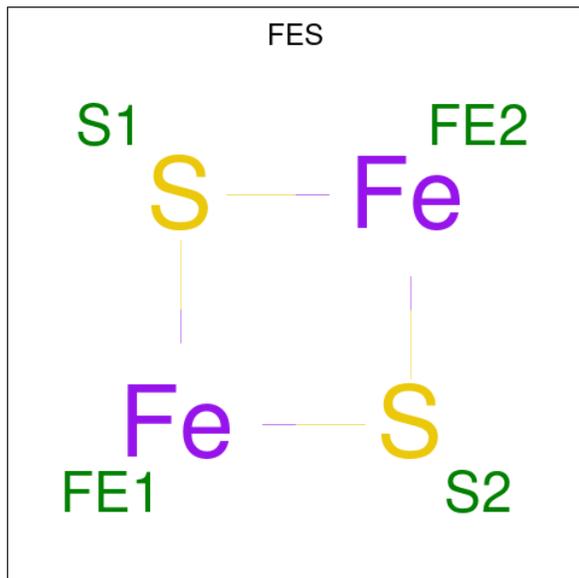
- Molecule 2 is a protein called NADH-quinone oxidoreductase subunit F.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	417	3290	2113	551	613	13	0	1	0
2	D	418	3305	2124	548	620	13	0	3	0

There are 16 discrepancies between the modelled and reference sequences:

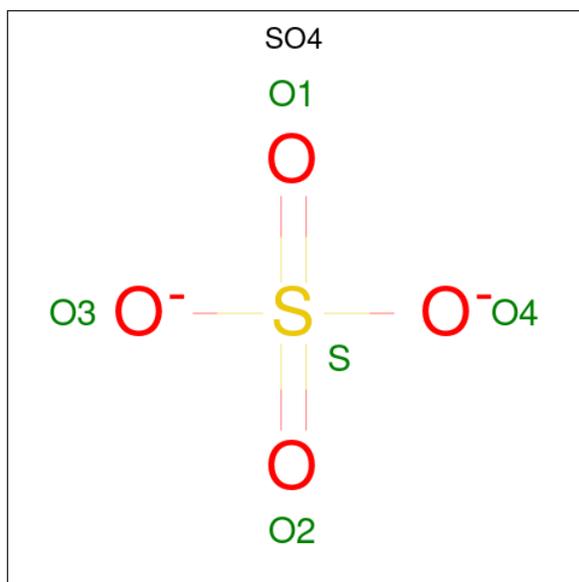
Chain	Residue	Modelled	Actual	Comment	Reference
B	427	ALA	-	expression tag	UNP O66841
B	428	GLY	-	expression tag	UNP O66841
B	429	HIS	-	expression tag	UNP O66841
B	430	HIS	-	expression tag	UNP O66841
B	431	HIS	-	expression tag	UNP O66841
B	432	HIS	-	expression tag	UNP O66841
B	433	HIS	-	expression tag	UNP O66841
B	434	HIS	-	expression tag	UNP O66841
D	427	ALA	-	expression tag	UNP O66841
D	428	GLY	-	expression tag	UNP O66841
D	429	HIS	-	expression tag	UNP O66841
D	430	HIS	-	expression tag	UNP O66841
D	431	HIS	-	expression tag	UNP O66841
D	432	HIS	-	expression tag	UNP O66841
D	433	HIS	-	expression tag	UNP O66841
D	434	HIS	-	expression tag	UNP O66841

- Molecule 3 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂) (labeled as "Ligand of Interest" by depositor).



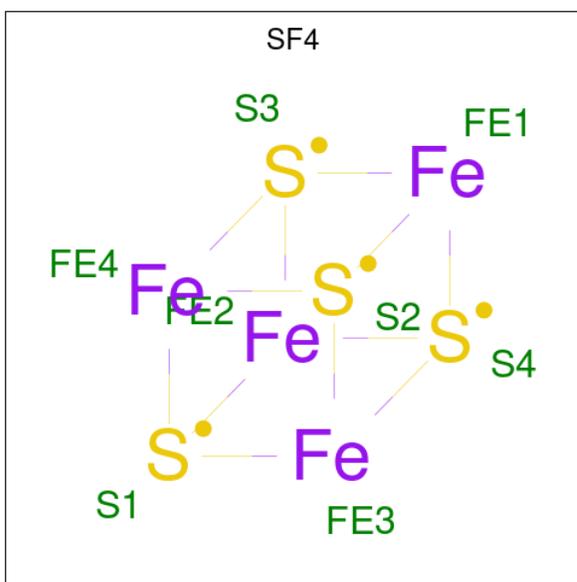
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Fe	S	0	0
			4	2	2		
3	C	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



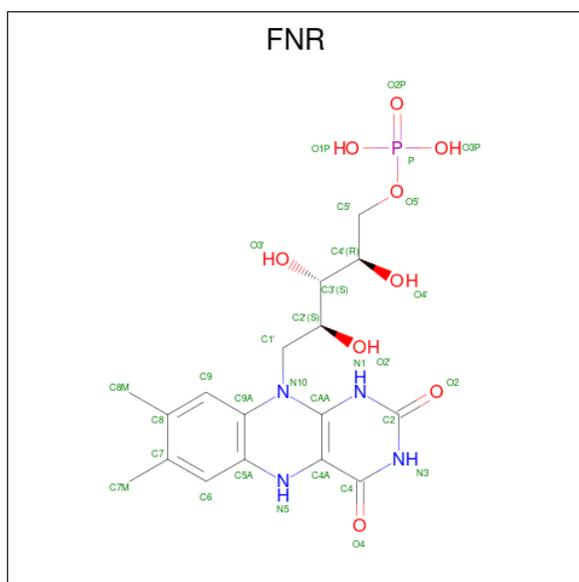
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	C	1	Total O S 5 4 1	0	0
4	C	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0

- Molecule 5 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄) (labeled as "Ligand of Interest" by depositor).



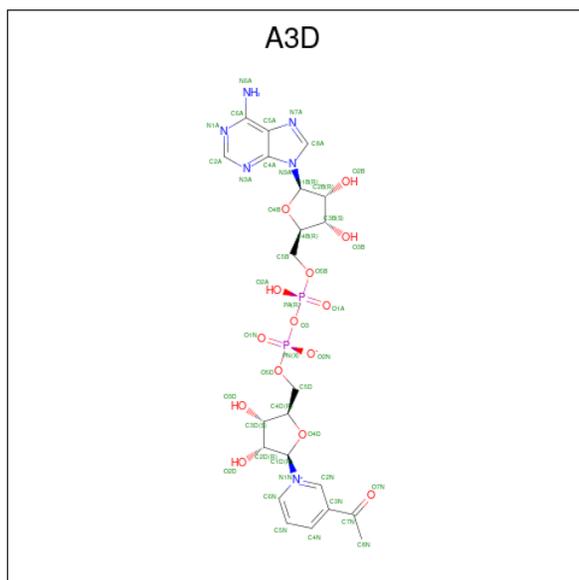
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Fe S 8 4 4	0	0
5	D	1	Total Fe S 8 4 4	0	0

- Molecule 6 is 1-DEOXY-1-(7,8-DIMETHYL-2,4-DIOXO-3,4-DIHYDRO-2H-BENZO[G]P TERIDIN-1-ID-10(5H)-YL)-5-O-PHOSPHONATO-D-RIBITOL (three-letter code: FNR) (formula: C₁₇H₂₃N₄O₉P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
6	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
6	D	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 7 is 3-ACETILPYRIDINE ADENINE DINUCLEOTIDE (three-letter code: A3D) (formula: $C_{22}H_{28}N_6O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).



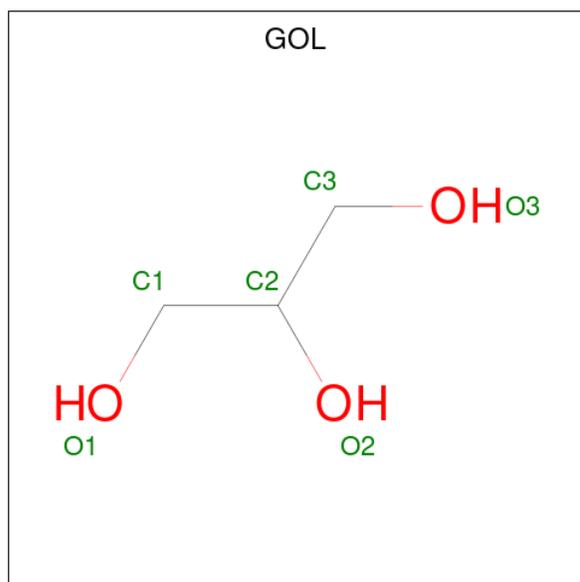
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
7	B	1	Total	C	N	O	P	0	0
			36	15	6	13	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
7	D	1	36	15	6	13	2	0	0

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
8	B	1	6	3	3	0	0
8	D	1	6	3	3	0	0

- Molecule 9 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
9	B	5	5	5	0	0
9	C	1	1	1	0	0
9	D	2	2	2	0	0

- Molecule 10 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	K		
10	D	1	1	1	0	0

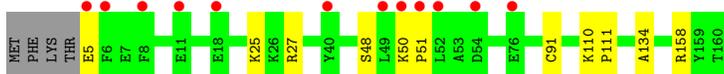
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	119	Total 119	O 119	0	0
11	B	326	Total 326	O 326	0	0
11	C	110	Total 110	O 110	0	0
11	D	317	Total 318	O 318	0	1

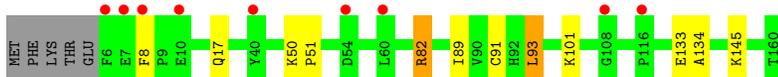
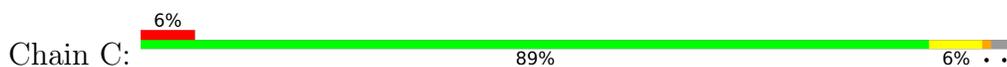
3 Residue-property plots [i](#)

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

- Molecule 1: NADH-quinone oxidoreductase subunit E



- Molecule 1: NADH-quinone oxidoreductase subunit E



- Molecule 2: NADH-quinone oxidoreductase subunit F



- Molecule 2: NADH-quinone oxidoreductase subunit F



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	63.53Å 116.62Å 190.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.15 – 1.96 48.11 – 1.96	Depositor EDS
% Data completeness (in resolution range)	99.2 (48.15-1.96) 99.2 (48.11-1.96)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.77 (at 1.97Å)	Xtrriage
Refinement program	REFMAC 5.8.0352	Depositor
R, R_{free}	0.192 , 0.224 0.201 , 0.234	Depositor DCC
R_{free} test set	5246 reflections (5.18%)	wwPDB-VP
Wilson B-factor (Å ²)	22.0	Xtrriage
Anisotropy	0.296	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10209	wwPDB-VP
Average B, all atoms (Å ²)	28.0	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 50.88 % 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 6.0705e-05. 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: A3D, FES, SF4, FNR, NA, K, GOL, SO4

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	0.31	0/1297	0.56	0/1752
1	C	0.30	0/1288	0.54	0/1740
2	B	0.33	0/3370	0.57	0/4558
2	D	0.34	0/3385	0.56	0/4582
All	All	0.33	0/9340	0.56	0/12632

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

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	27	ARG	Sidechain
1	C	82	ARG	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	1268	0	1269	7	1
1	C	1259	0	1263	9	0
2	B	3290	0	3264	13	0
2	D	3305	0	3242	15	1
3	A	4	0	0	0	0
3	C	4	0	0	0	0
4	A	10	0	0	0	0
4	B	5	0	0	0	0
4	C	10	0	0	0	0
4	D	10	0	0	0	0
5	B	8	0	0	1	0
5	D	8	0	0	0	0
6	B	31	0	22	0	0
6	D	31	0	22	0	0
7	B	36	0	19	0	0
7	D	36	0	19	0	0
8	B	6	0	8	0	0
8	D	6	0	8	0	0
9	B	5	0	0	0	0
9	C	1	0	0	0	0
9	D	2	0	0	0	0
10	D	1	0	0	0	0
11	A	119	0	0	1	0
11	B	326	0	0	2	1
11	C	110	0	0	3	0
11	D	318	0	0	2	1
All	All	10209	0	9136	41	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (41) 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)
2:D:33:GLU:OE1	11:D:601:HOH:O	2.12	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:360:GLN:NE2	2:B:384:ASN:HD22	1.91	0.67
1:A:48:SER:O	1:A:51:PRO:HD2	1.97	0.64
2:D:377:TRP:HB3	2:D:418:ARG:NH1	2.14	0.62
2:D:360:GLN:NE2	2:D:384:ASN:HD22	2.00	0.60
1:C:133:GLU:HG3	2:D:8:PRO:HB2	1.84	0.60
2:B:196:ARG:HH21	2:B:198:HIS:HE1	1.51	0.57
1:A:158:ARG:NH1	11:A:301:HOH:O	2.18	0.55
1:C:8:PHE:CE2	1:C:51:PRO:HB2	2.41	0.55
1:C:17:GLN:CG	11:C:399:HOH:O	2.55	0.54
2:D:60:LYS:O	2:D:239:ARG:HD2	2.08	0.53
2:D:77:TRP:HE1	2:D:219:ASN:HD21	1.56	0.53
2:B:388:GLN:HG3	11:B:742:HOH:O	2.08	0.53
1:C:17:GLN:HG3	11:C:399:HOH:O	2.07	0.53
1:C:82:ARG:NE	11:C:303:HOH:O	2.42	0.53
1:C:50:LYS:HB3	1:C:51:PRO:HD3	1.92	0.52
2:D:229:PHE:O	2:D:233:MET:HG2	2.11	0.51
2:B:412:GLU:H	2:B:412:GLU:CD	2.13	0.51
1:A:50:LYS:HB3	1:A:51:PRO:HD3	1.91	0.51
2:B:79:PHE:O	2:B:82:GLN:HG2	2.14	0.48
2:D:360:GLN:HE21	2:D:384:ASN:HD22	1.60	0.47
2:D:77:TRP:HE1	2:D:219:ASN:ND2	2.12	0.47
1:A:48:SER:C	1:A:51:PRO:HD2	2.35	0.46
1:A:91:CYS:HA	1:A:134:ALA:HB1	1.98	0.46
1:C:91:CYS:HA	1:C:134:ALA:HB1	1.98	0.45
2:B:94:ASP:O	2:B:95:GLU:C	2.55	0.45
1:A:25:LYS:HD2	2:B:212:TRP:CZ2	2.51	0.45
1:C:93:LEU:HD21	2:D:325:LEU:HG	1.98	0.44
2:D:418:ARG:O	2:D:419:LYS:HB2	2.17	0.44
2:B:360:GLN:HE22	2:B:384:ASN:HD22	1.63	0.44
2:D:377:TRP:HB3	2:D:418:ARG:HH11	1.82	0.43
1:A:110:LYS:HB3	1:A:111:PRO:HD2	1.99	0.43
2:B:388:GLN:N	2:B:389:PRO:CD	2.82	0.42
2:B:294:SER:HA	2:B:321:THR:O	2.20	0.41
2:D:394:GLY:O	2:D:398:VAL:HG22	2.20	0.41
2:B:252:PHE:CE1	2:B:309:MET:HB3	2.55	0.41
1:C:133:GLU:HB3	1:C:145:LYS:HB2	2.02	0.41
2:D:377:TRP:CE3	2:D:418:ARG:NH2	2.88	0.41
2:D:412:GLU:HB3	11:D:902:HOH:O	2.21	0.41
2:B:412:GLU:HG3	11:B:821:HOH:O	2.21	0.40
2:B:391:SER:HB2	5:B:501:SF4:S1	2.61	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:ARG:NH2	2:D:41[A]:GLN:OE1[1_655]	2.02	0.18
11:B:917:HOH:O	11:D:894:HOH:O[2_554]	2.06	0.14

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	154/160 (96%)	148 (96%)	6 (4%)	0	100	100
1	C	153/160 (96%)	149 (97%)	4 (3%)	0	100	100
2	B	416/434 (96%)	408 (98%)	7 (2%)	1 (0%)	47	38
2	D	419/434 (96%)	412 (98%)	6 (1%)	1 (0%)	47	38
All	All	1142/1188 (96%)	1117 (98%)	23 (2%)	2 (0%)	47	38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	95	GLU
2	D	95	GLU

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	142/146 (97%)	141 (99%)	1 (1%)	84	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	141/146 (97%)	138 (98%)	3 (2%)	53	46
2	B	344/357 (96%)	340 (99%)	4 (1%)	71	68
2	D	340/357 (95%)	336 (99%)	4 (1%)	71	68
All	All	967/1006 (96%)	955 (99%)	12 (1%)	71	68

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	GLU
2	B	36	LYS
2	B	240	TYR
2	B	393	CYS
2	B	412	GLU
1	C	89	ILE
1	C	93	LEU
1	C	101	LYS
2	D	3	SER
2	D	25	LYS
2	D	305	LEU
2	D	393	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	97	ASN
2	B	198	HIS
2	B	360	GLN
1	C	97	ASN
2	D	208	GLN
2	D	219	ASN
2	D	360	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 9 are monoatomic - leaving 17 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
8	GOL	B	504	-	5,5,5	0.07	0	5,5,5	0.20	0
6	FNR	D	502	-	32,33,33	0.49	0	40,50,50	0.66	0
7	A3D	D	503	10	33,39,48	0.63	0	38,60,73	0.71	1 (2%)
5	SF4	D	501	2	0,12,12	-	-	-		
4	SO4	B	505	-	4,4,4	0.36	0	6,6,6	0.06	0
4	SO4	C	202	-	4,4,4	0.30	0	6,6,6	0.09	0
7	A3D	B	503	9	33,39,48	0.62	0	38,60,73	0.69	1 (2%)
4	SO4	D	505	-	4,4,4	0.31	0	6,6,6	0.10	0
3	FES	A	201	1	0,4,4	-	-	-		
4	SO4	D	506	-	4,4,4	0.28	0	6,6,6	0.12	0
4	SO4	A	203	-	4,4,4	0.35	0	6,6,6	0.06	0
8	GOL	D	504	-	5,5,5	0.08	0	5,5,5	0.22	0
3	FES	C	201	1	0,4,4	-	-	-		
4	SO4	A	202	-	4,4,4	0.35	0	6,6,6	0.09	0
6	FNR	B	502	-	32,33,33	0.47	0	40,50,50	0.58	0
5	SF4	B	501	2	0,12,12	-	-	-		
4	SO4	C	203	-	4,4,4	0.35	0	6,6,6	0.07	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	GOL	B	504	-	-	0/4/4/4	-
6	FNR	D	502	-	-	2/18/18/18	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	A3D	D	503	10	-	1/18/54/62	0/4/4/5
5	SF4	D	501	2	-	-	0/6/5/5
7	A3D	B	503	9	-	0/18/54/62	0/4/4/5
3	FES	A	201	1	-	-	0/1/1/1
3	FES	C	201	1	-	-	0/1/1/1
6	FNR	B	502	-	-	2/18/18/18	0/3/3/3
8	GOL	D	504	-	-	2/4/4/4	-
5	SF4	B	501	2	-	-	0/6/5/5

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	503	A3D	C5A-C6A-N6A	2.38	123.97	120.35
7	D	503	A3D	C5A-C6A-N6A	2.31	123.86	120.35

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	D	504	GOL	O1-C1-C2-C3
6	D	502	FNR	C4'-C5'-O5'-P
6	B	502	FNR	C4'-C5'-O5'-P
8	D	504	GOL	C1-C2-C3-O3
7	D	503	A3D	C5B-O5B-PA-O1A
6	B	502	FNR	N10-C1'-C2'-O2'
6	D	502	FNR	N10-C1'-C2'-O2'

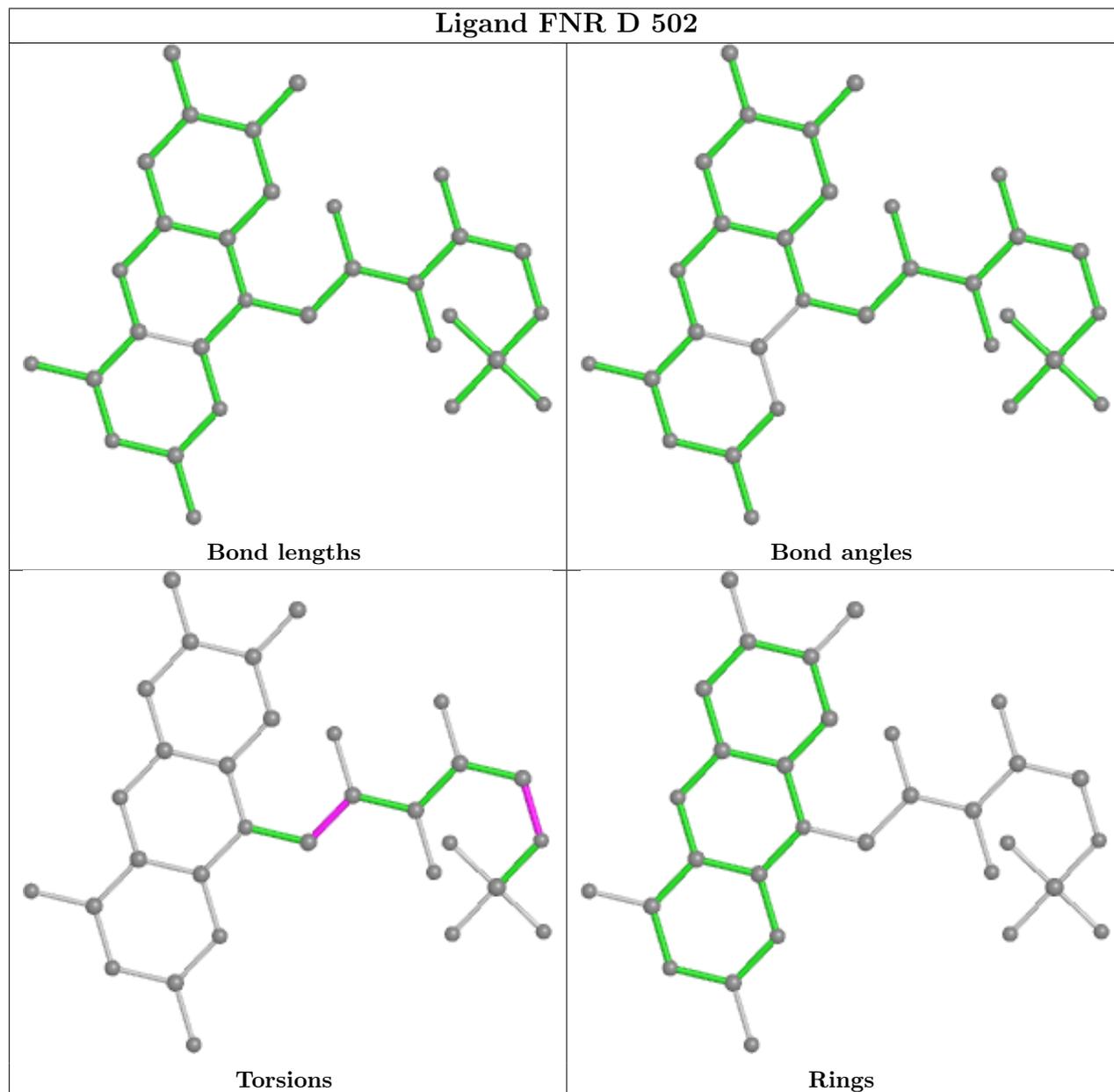
There are no ring outliers.

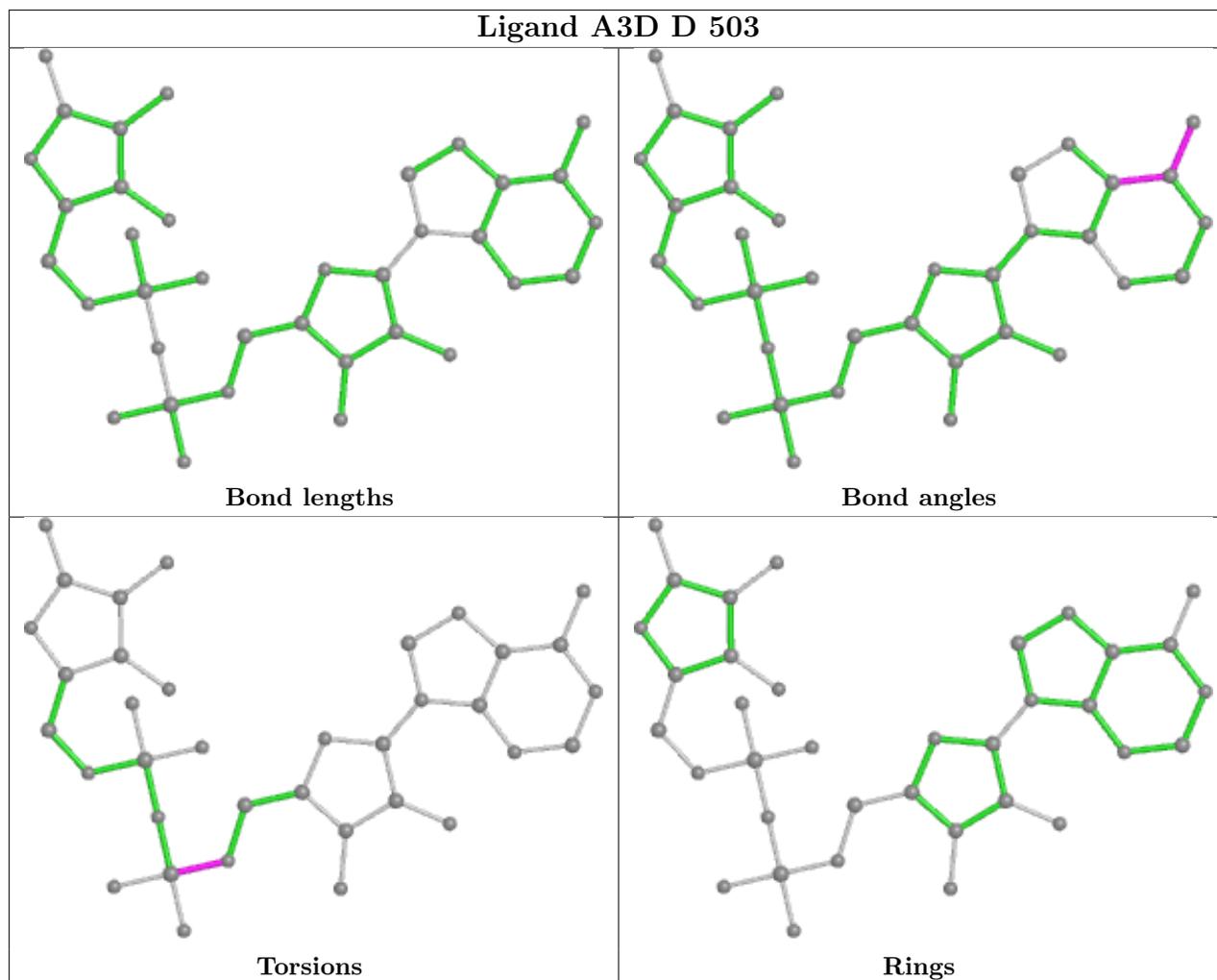
1 monomer is involved in 1 short contact:

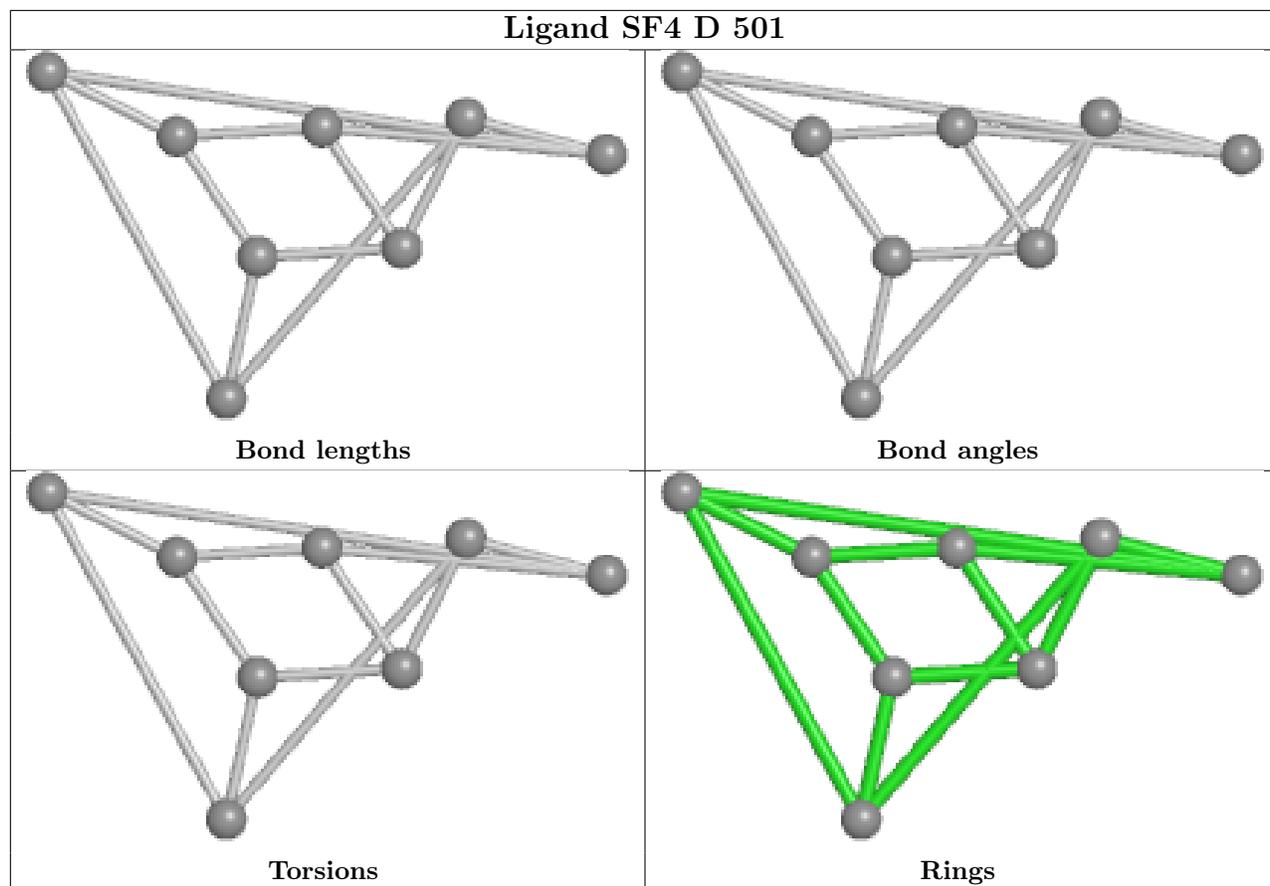
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	501	SF4	1	0

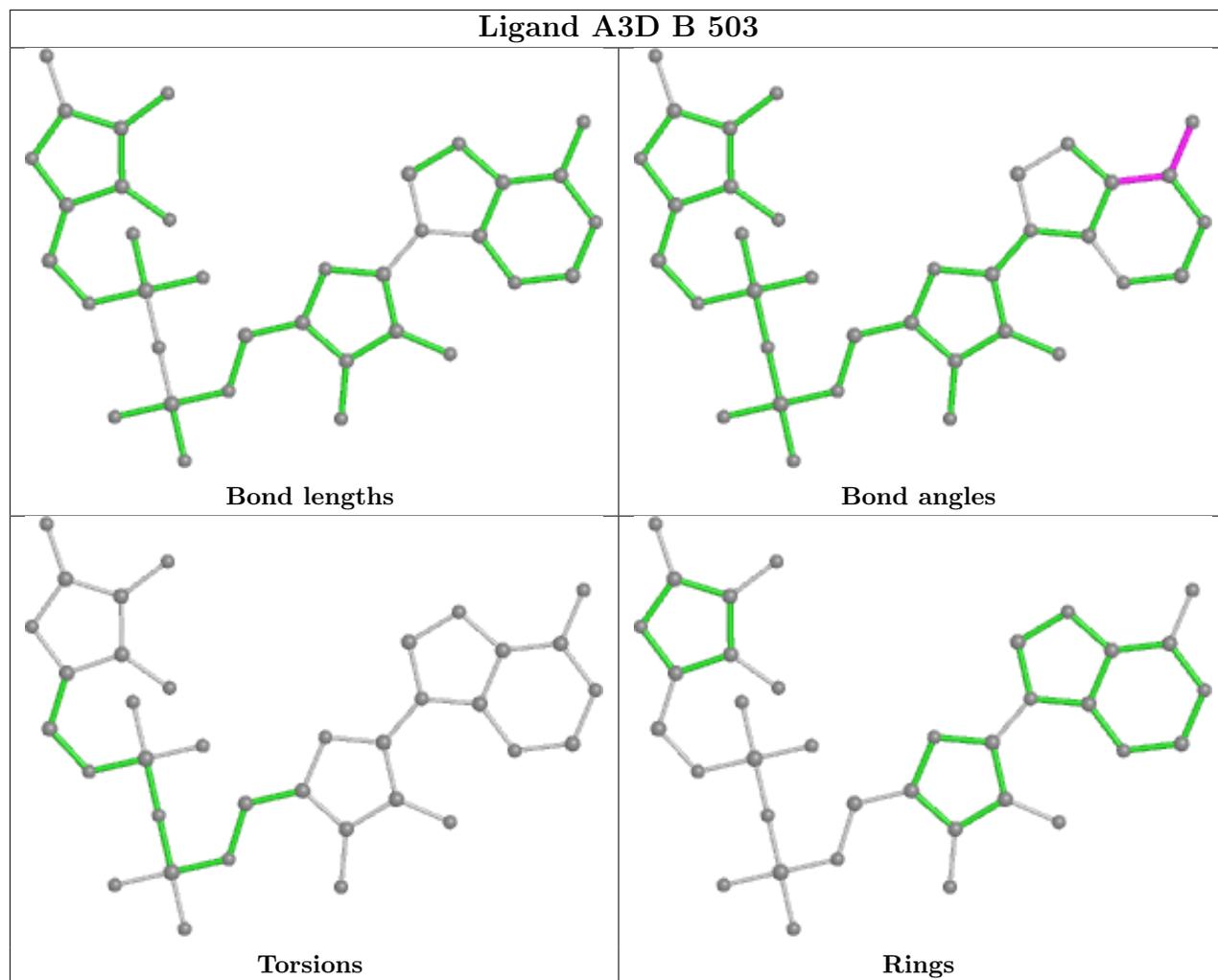
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

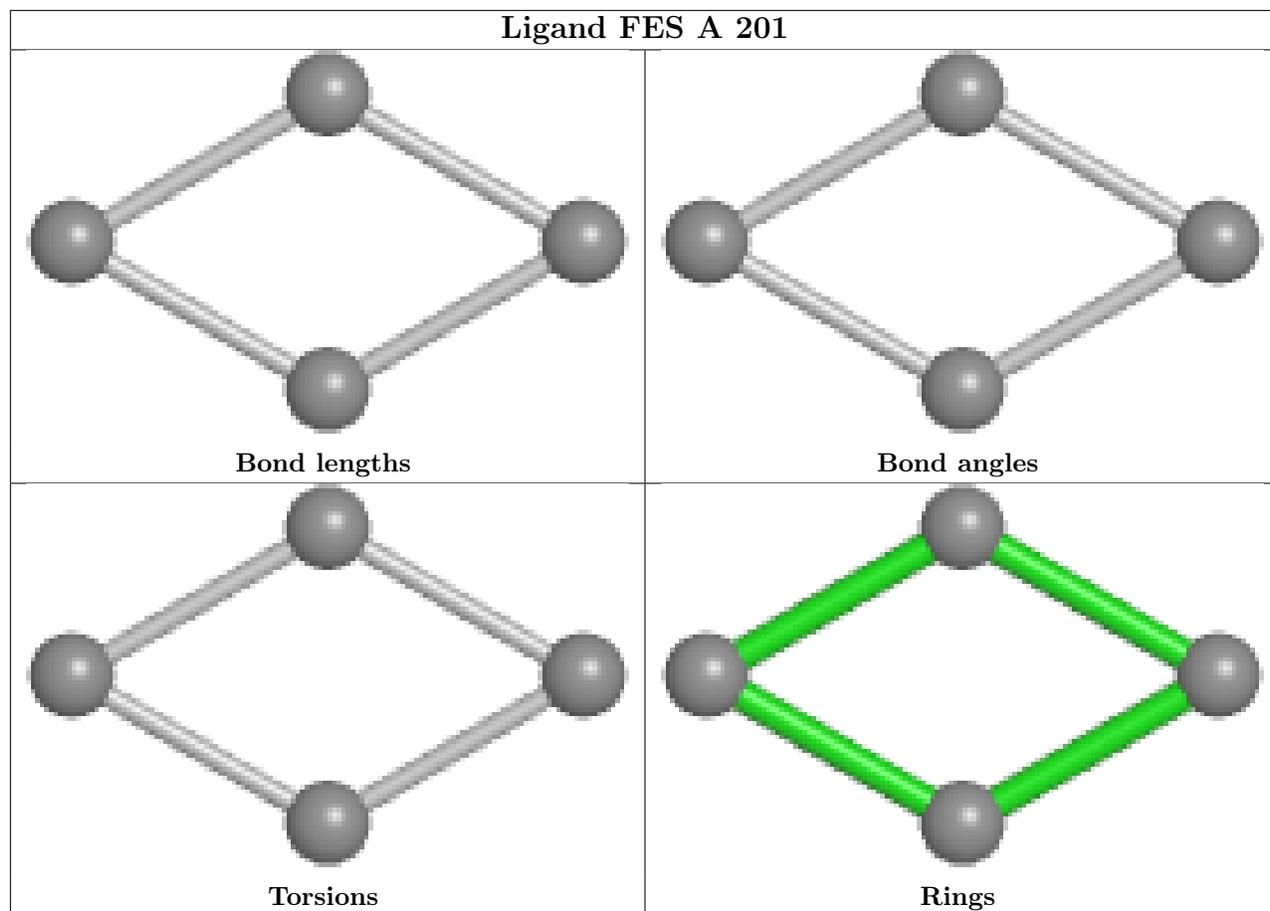
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

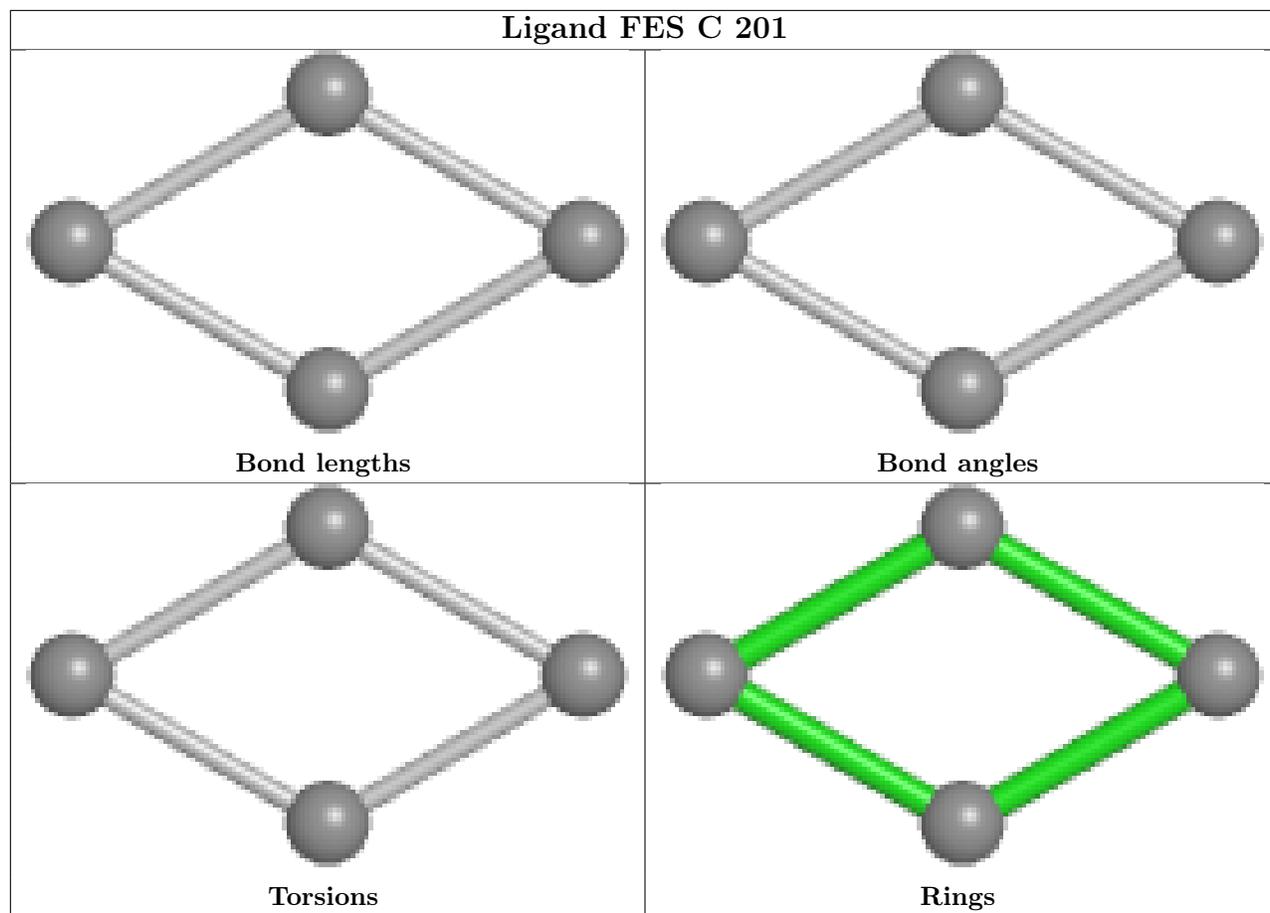


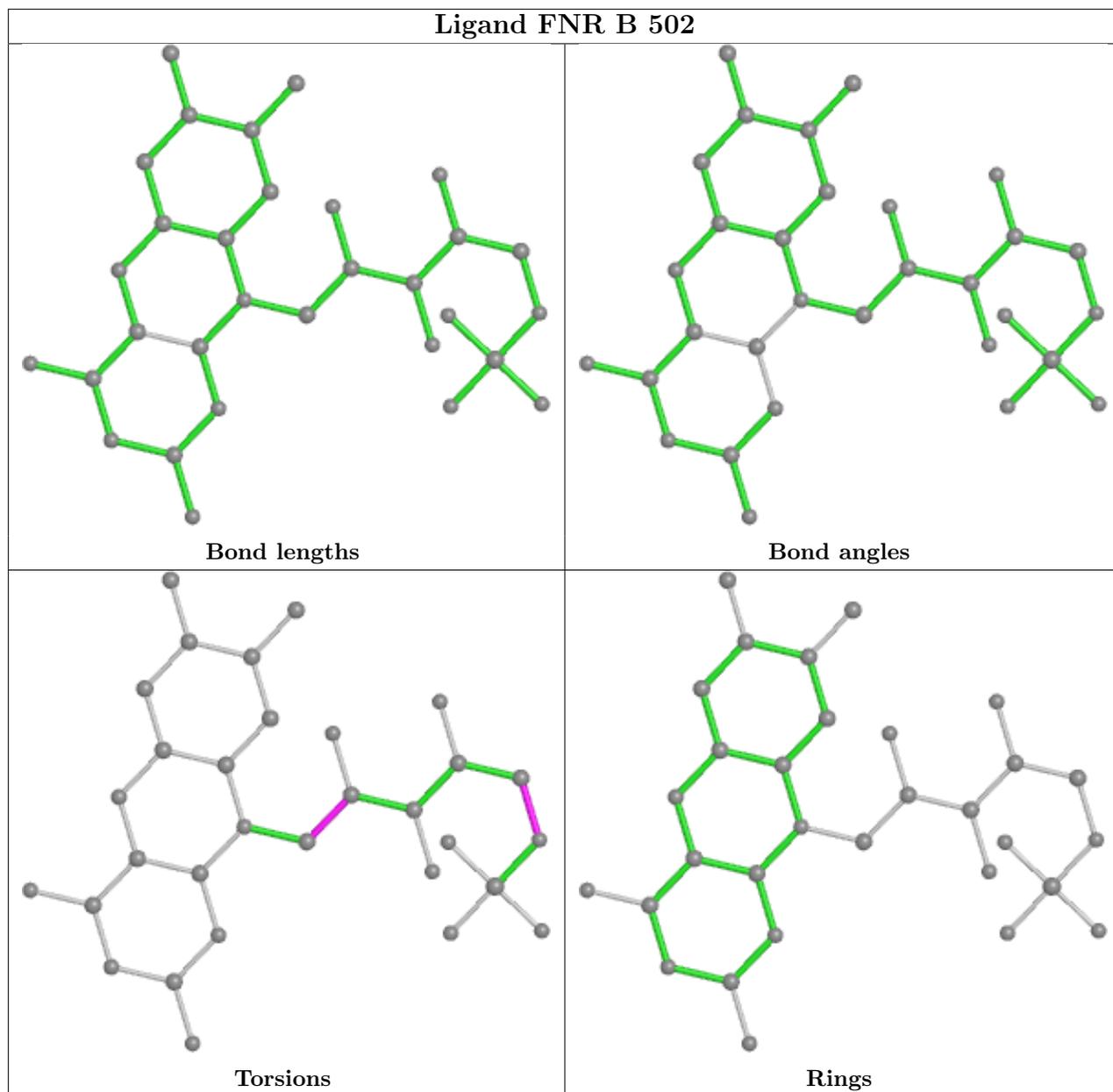


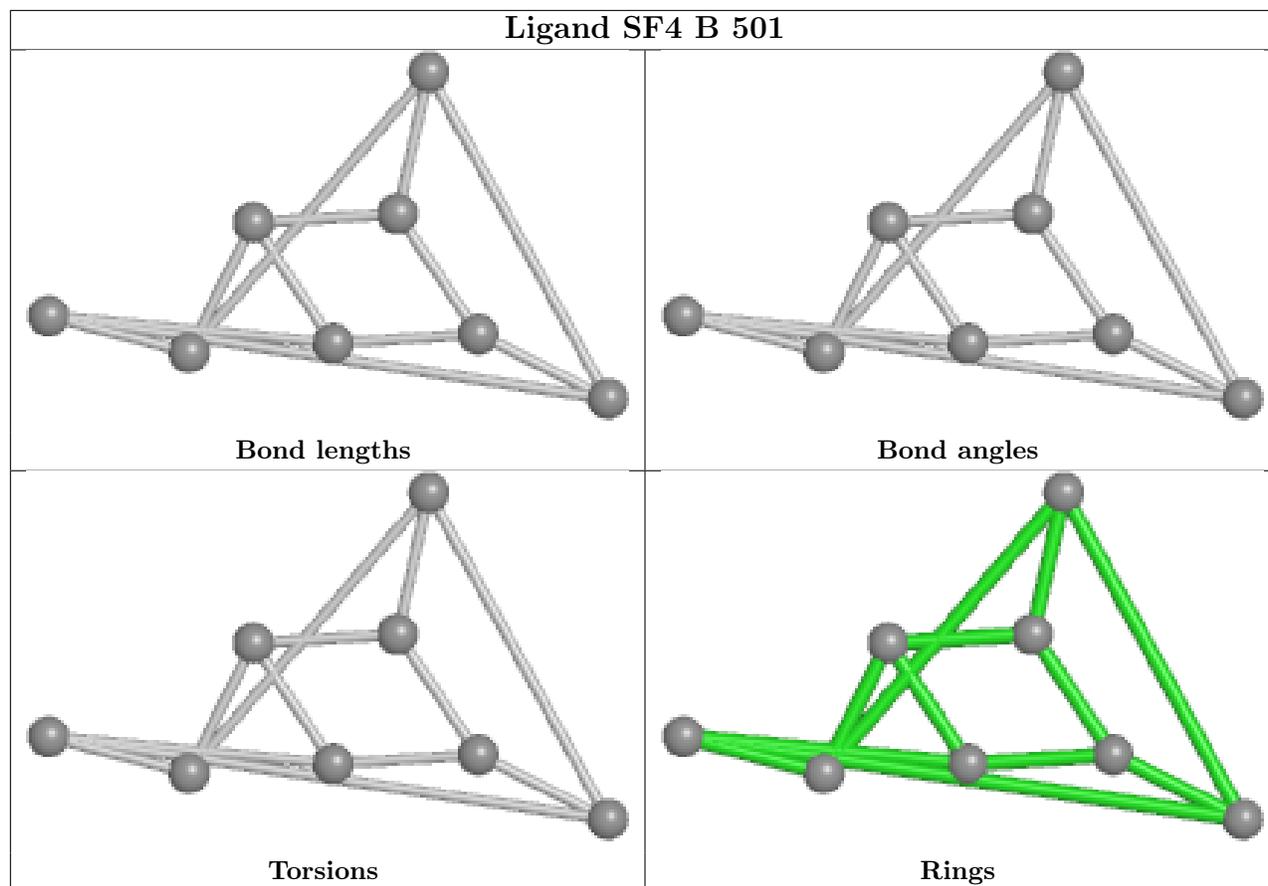












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	156/160 (97%)	0.42	12 (7%) 13 21	16, 32, 53, 86	0
1	C	155/160 (96%)	0.38	9 (5%) 23 31	16, 32, 51, 70	0
2	B	417/434 (96%)	-0.00	2 (0%) 91 94	15, 23, 37, 67	0
2	D	418/434 (96%)	0.09	7 (1%) 70 77	15, 24, 39, 66	0
All	All	1146/1188 (96%)	0.14	30 (2%) 56 65	15, 25, 45, 86	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	6	PHE	5.2
1	A	8	PHE	4.9
1	A	6	PHE	4.2
1	A	5	GLU	4.2
2	D	377	TRP	4.0
1	A	11	GLU	2.9
1	C	8	PHE	2.9
1	C	108	GLY	2.9
1	C	10	GLU	2.8
2	B	377	TRP	2.8
2	B	2	ARG	2.8
1	C	116	PRO	2.7
2	D	240	TYR	2.5
2	D	415	GLU	2.4
1	A	49	LEU	2.4
1	A	52	LEU	2.4
1	C	40	TYR	2.4
2	D	416	LYS	2.3
1	A	76	GLU	2.3
1	A	51	PRO	2.2
1	A	40	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	7	GLU	2.2
1	A	50	LYS	2.2
2	D	245	ASP	2.2
1	A	18	GLU	2.2
1	C	54	ASP	2.1
2	D	2	ARG	2.1
2	D	106	ILE	2.1
1	C	60	LEU	2.1
1	A	54	ASP	2.0

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 [\(i\)](#)

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

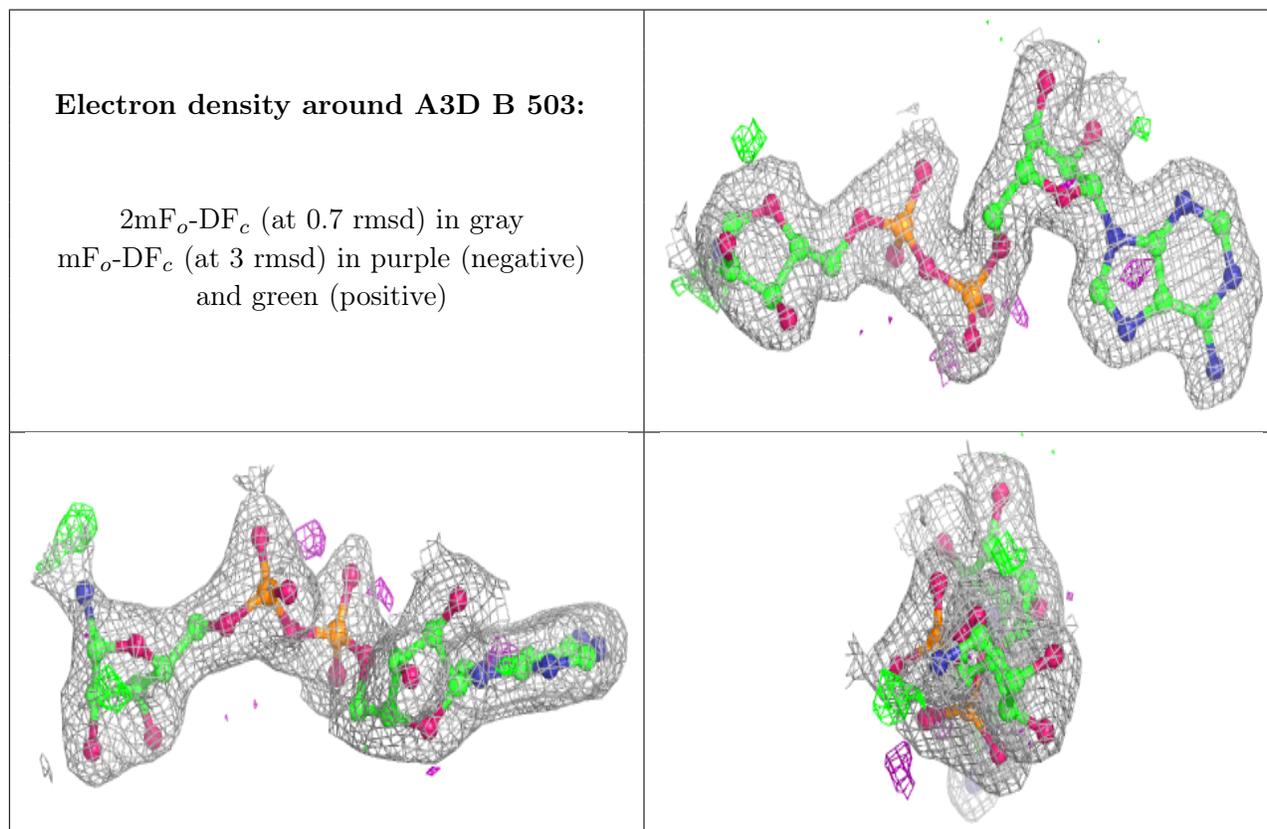
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
10	K	D	509	1/1	0.62	0.32	100,100,100,100	0
9	NA	D	508	1/1	0.69	0.40	59,59,59,59	0
4	SO4	B	505	5/5	0.71	0.25	84,86,89,93	0
9	NA	B	508	1/1	0.72	0.29	51,51,51,51	0
9	NA	B	506	1/1	0.85	0.18	49,49,49,49	0
4	SO4	D	506	5/5	0.86	0.19	45,55,57,59	0
9	NA	B	510	1/1	0.89	0.30	39,39,39,39	0
4	SO4	A	203	5/5	0.90	0.25	65,71,73,80	0
8	GOL	D	504	6/6	0.91	0.17	26,27,28,30	0
4	SO4	C	202	5/5	0.91	0.23	48,51,56,65	0
9	NA	B	507	1/1	0.92	0.36	48,48,48,48	0
9	NA	C	204	1/1	0.92	0.15	36,36,36,36	0
8	GOL	B	504	6/6	0.93	0.11	28,29,30,30	0
4	SO4	C	203	5/5	0.93	0.22	66,67,73,74	0

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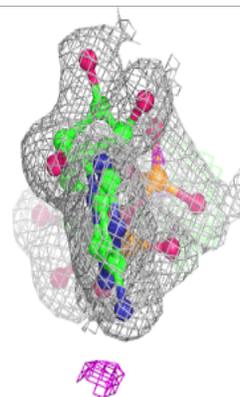
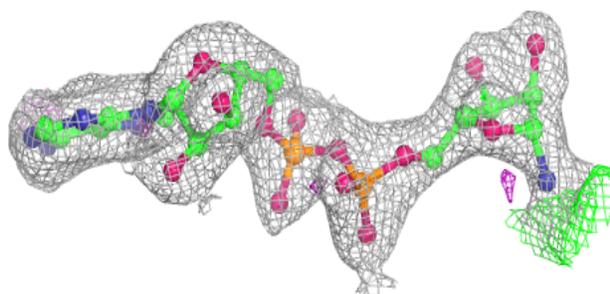
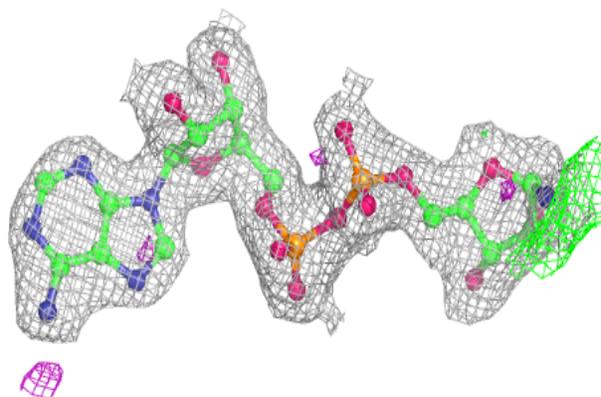
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	SO4	A	202	5/5	0.93	0.27	63,65,65,67	0
4	SO4	D	505	5/5	0.95	0.13	38,44,48,50	0
9	NA	D	507	1/1	0.95	0.13	41,41,41,41	0
7	A3D	B	503	36/44	0.96	0.09	22,28,44,45	0
7	A3D	D	503	36/44	0.96	0.10	23,30,43,46	0
6	FNR	B	502	31/31	0.97	0.10	16,17,19,20	0
9	NA	B	509	1/1	0.98	0.05	28,28,28,28	0
6	FNR	D	502	31/31	0.98	0.08	16,18,19,20	0
5	SF4	D	501	8/8	0.99	0.04	19,20,21,21	0
5	SF4	B	501	8/8	0.99	0.06	20,21,21,22	0
3	FES	A	201	4/4	1.00	0.08	16,17,18,18	0
3	FES	C	201	4/4	1.00	0.08	17,18,19,19	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.

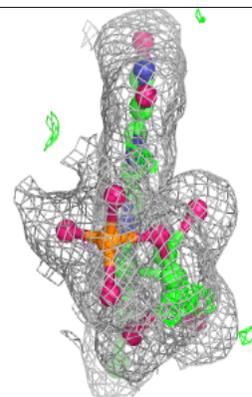
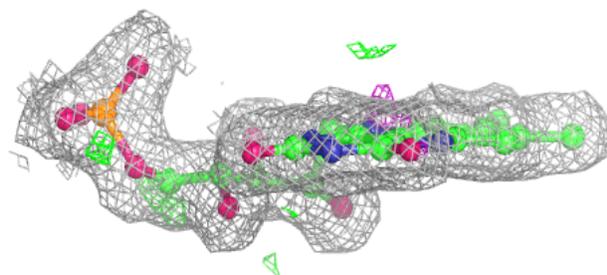
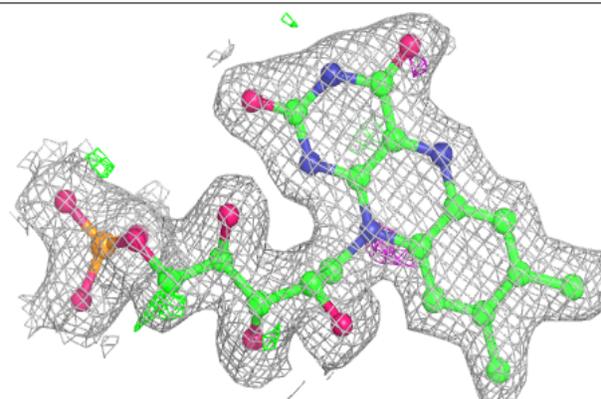


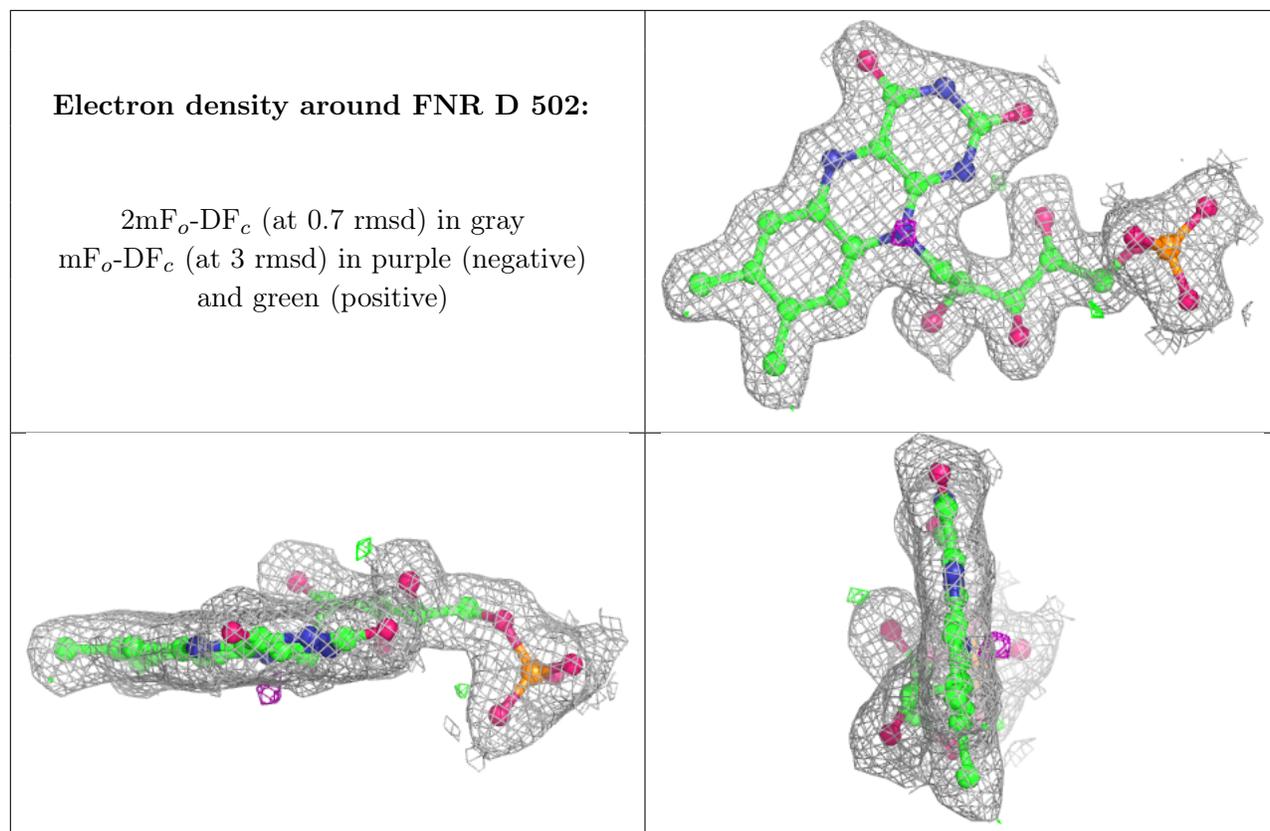
Electron density around A3D D 503:

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

**Electron density around FNR B 502:**

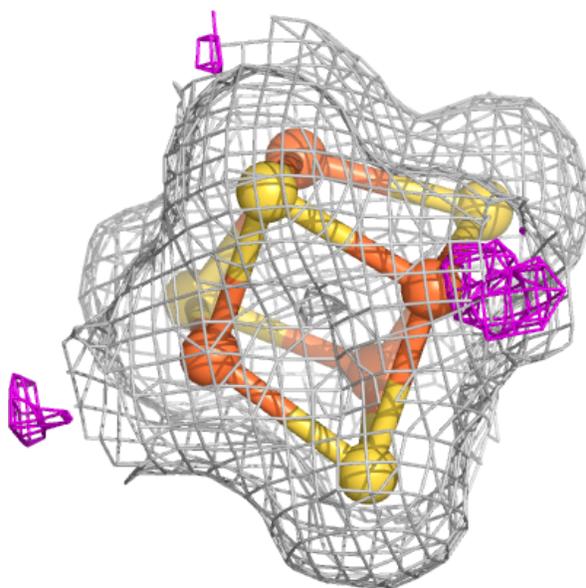
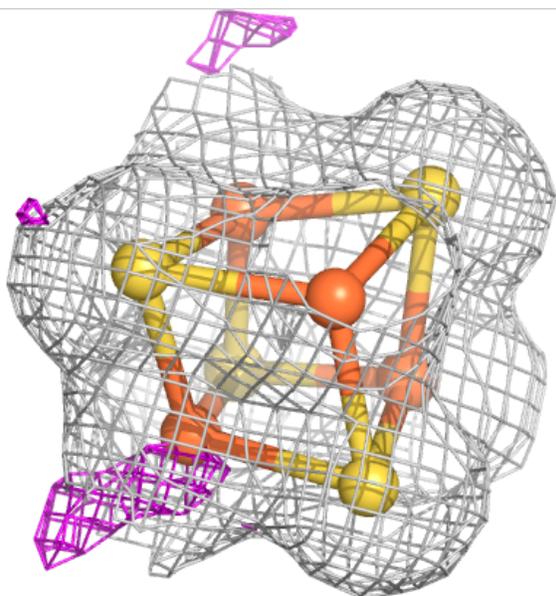
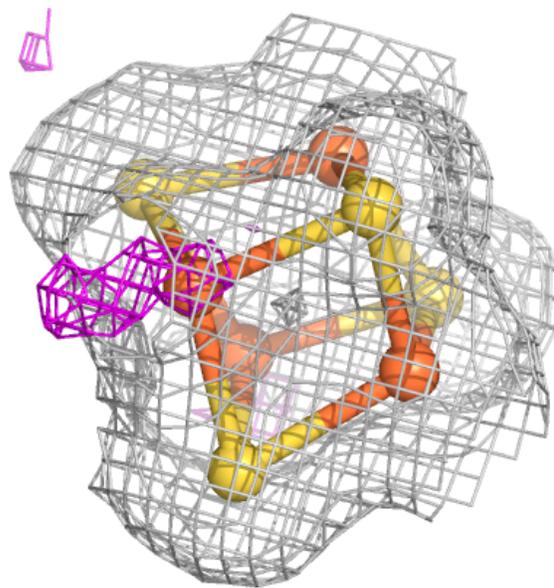
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





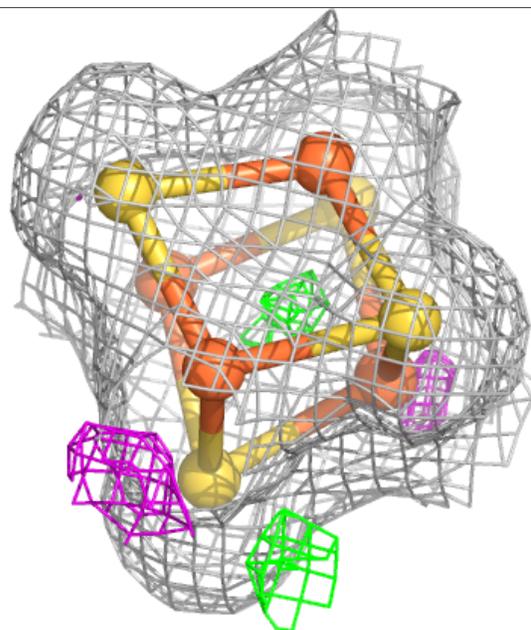
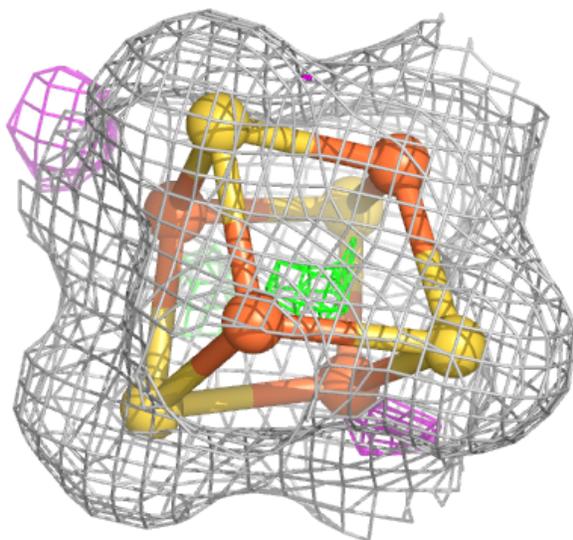
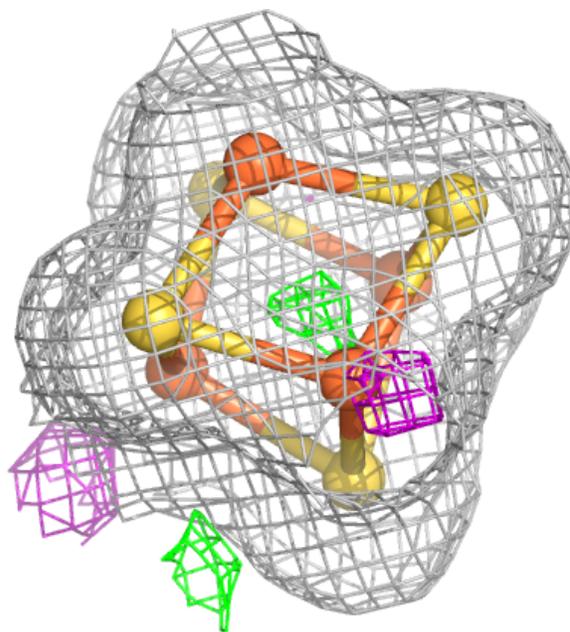
Electron density around SF4 D 501:

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



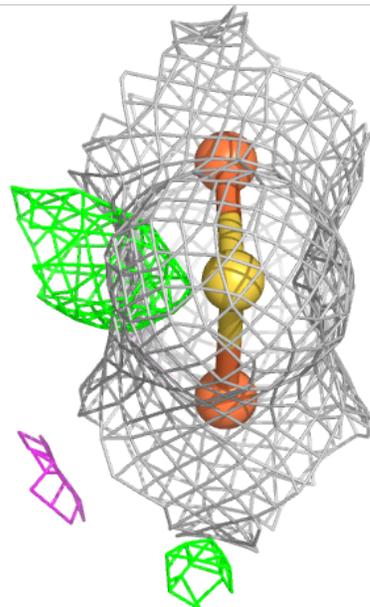
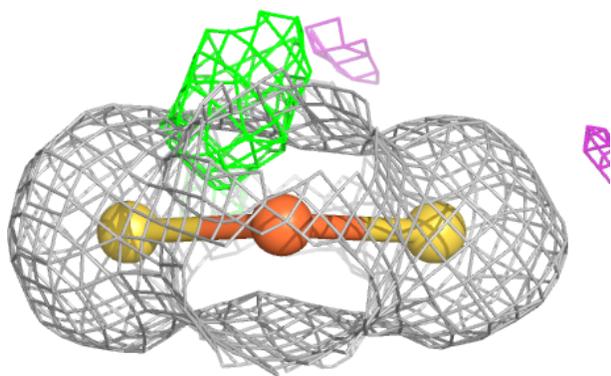
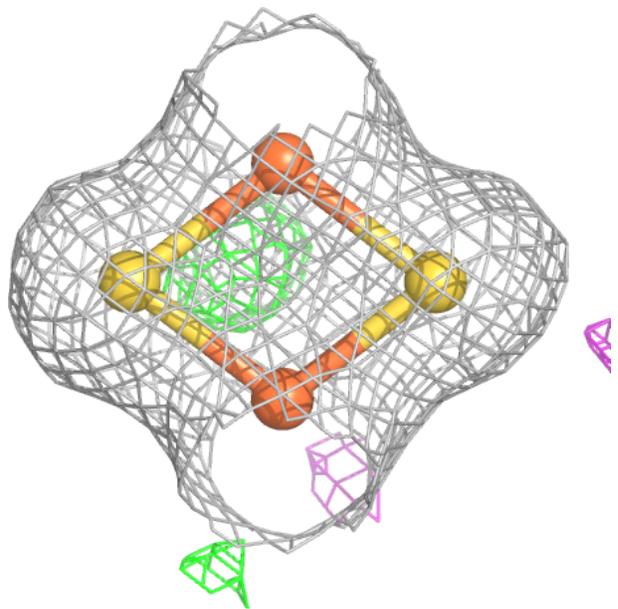
Electron density around SF4 B 501:

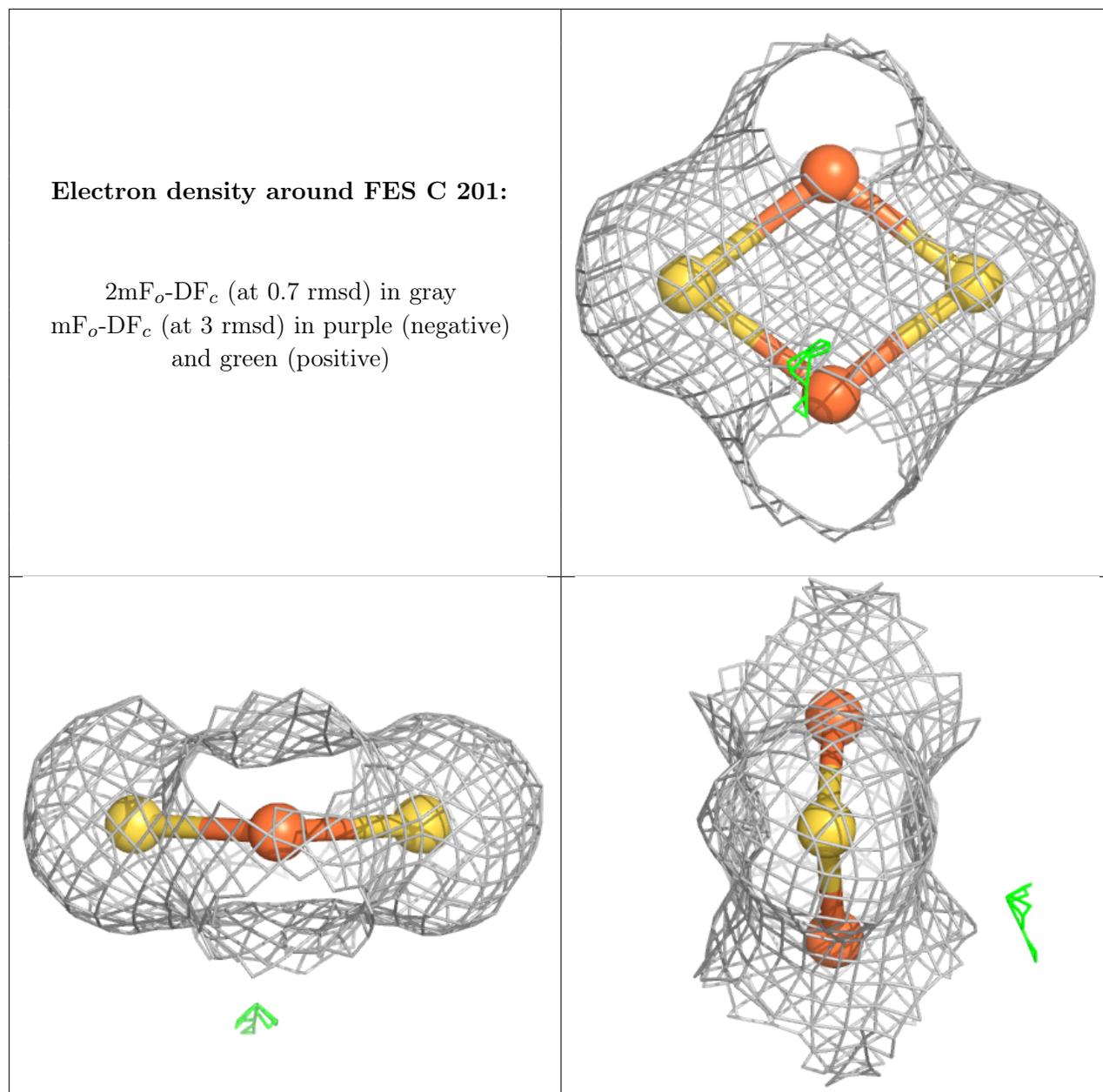
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around FES A 201:

$2mF_o-DF_c$ (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.