



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 06:43 AM UTC

PDB ID : 8I09 / pdb_00008i09
Title : Crystal structure of serine acetyltransferase from Salmonella typhimurium complexed with butyl gallate
Authors : Toyomoto, T.; Ono, K.; Shiba, T.; Momitani, K.; Zhang, T.; Tsutsuki, H.; Ishikawa, T.; Hosono, K.; Hamada, K.; Rahman, A.; Zhong, H.; Akaike, T.; Yamamoto, K.; Matsuoka, M.; Hanaoka, K.; Niidome, T.; Sawa, T.
Deposited on : 2023-01-10
Resolution : 1.80 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 types of validation reports are described at

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

The following versions of software and data (see [references](#) ①) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

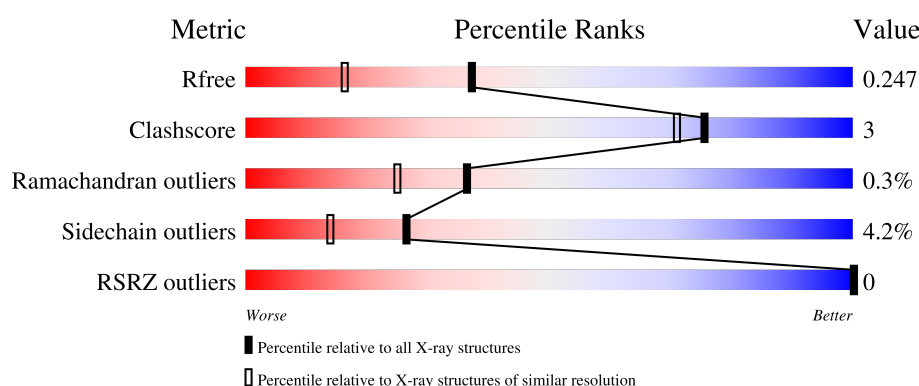
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	280	
1	B	280	
1	C	280	
1	D	280	
1	E	280	

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Mol	Chain	Length	Quality of chain
1	F	280	 79% 8% • 12%
1	G	280	 78% 8% • 12%
1	H	280	 81% 6% • 12%
1	I	280	 80% 6% • 12%
1	J	280	 82% 5% • 12%
1	K	280	 79% 6% • 12%
1	L	280	 78% 10% 12%

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
2	CYS	J	401	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 23191 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 Serine acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	246	Total	C	N	O	S	0	1	0
			1852	1178	328	336	10			
1	B	246	Total	C	N	O	S	0	0	0
			1844	1173	327	335	9			
1	C	246	Total	C	N	O	S	0	1	0
			1852	1178	328	336	10			
1	D	246	Total	C	N	O	S	0	0	0
			1842	1171	327	335	9			
1	E	245	Total	C	N	O	S	0	0	0
			1837	1168	326	334	9			
1	F	245	Total	C	N	O	S	0	0	0
			1837	1168	326	334	9			
1	G	246	Total	C	N	O	S	0	1	0
			1850	1176	328	336	10			
1	H	247	Total	C	N	O	S	0	1	0
			1857	1181	329	337	10			
1	I	246	Total	C	N	O	S	0	1	0
			1850	1176	328	336	10			
1	J	246	Total	C	N	O	S	0	0	0
			1844	1173	327	335	9			
1	K	246	Total	C	N	O	S	0	0	0
			1844	1173	327	335	9			
1	L	246	Total	C	N	O	S	0	1	0
			1852	1178	328	336	10			

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP A0A0D6I3Y9
A	-6	HIS	-	expression tag	UNP A0A0D6I3Y9
A	-5	HIS	-	expression tag	UNP A0A0D6I3Y9
A	-4	HIS	-	expression tag	UNP A0A0D6I3Y9
A	-3	HIS	-	expression tag	UNP A0A0D6I3Y9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	HIS	-	expression tag	UNP A0A0D6I3Y9
A	-1	HIS	-	expression tag	UNP A0A0D6I3Y9
A	0	ASP	-	expression tag	UNP A0A0D6I3Y9
A	1	PRO	-	expression tag	UNP A0A0D6I3Y9
B	-7	MET	-	initiating methionine	UNP A0A0D6I3Y9
B	-6	HIS	-	expression tag	UNP A0A0D6I3Y9
B	-5	HIS	-	expression tag	UNP A0A0D6I3Y9
B	-4	HIS	-	expression tag	UNP A0A0D6I3Y9
B	-3	HIS	-	expression tag	UNP A0A0D6I3Y9
B	-2	HIS	-	expression tag	UNP A0A0D6I3Y9
B	-1	HIS	-	expression tag	UNP A0A0D6I3Y9
B	0	ASP	-	expression tag	UNP A0A0D6I3Y9
B	1	PRO	-	expression tag	UNP A0A0D6I3Y9
C	-7	MET	-	initiating methionine	UNP A0A0D6I3Y9
C	-6	HIS	-	expression tag	UNP A0A0D6I3Y9
C	-5	HIS	-	expression tag	UNP A0A0D6I3Y9
C	-4	HIS	-	expression tag	UNP A0A0D6I3Y9
C	-3	HIS	-	expression tag	UNP A0A0D6I3Y9
C	-2	HIS	-	expression tag	UNP A0A0D6I3Y9
C	-1	HIS	-	expression tag	UNP A0A0D6I3Y9
C	0	ASP	-	expression tag	UNP A0A0D6I3Y9
C	1	PRO	-	expression tag	UNP A0A0D6I3Y9
D	-7	MET	-	initiating methionine	UNP A0A0D6I3Y9
D	-6	HIS	-	expression tag	UNP A0A0D6I3Y9
D	-5	HIS	-	expression tag	UNP A0A0D6I3Y9
D	-4	HIS	-	expression tag	UNP A0A0D6I3Y9
D	-3	HIS	-	expression tag	UNP A0A0D6I3Y9
D	-2	HIS	-	expression tag	UNP A0A0D6I3Y9
D	-1	HIS	-	expression tag	UNP A0A0D6I3Y9
D	0	ASP	-	expression tag	UNP A0A0D6I3Y9
D	1	PRO	-	expression tag	UNP A0A0D6I3Y9
E	-7	MET	-	initiating methionine	UNP A0A0D6I3Y9
E	-6	HIS	-	expression tag	UNP A0A0D6I3Y9
E	-5	HIS	-	expression tag	UNP A0A0D6I3Y9
E	-4	HIS	-	expression tag	UNP A0A0D6I3Y9
E	-3	HIS	-	expression tag	UNP A0A0D6I3Y9
E	-2	HIS	-	expression tag	UNP A0A0D6I3Y9
E	-1	HIS	-	expression tag	UNP A0A0D6I3Y9
E	0	ASP	-	expression tag	UNP A0A0D6I3Y9
E	1	PRO	-	expression tag	UNP A0A0D6I3Y9
F	-7	MET	-	initiating methionine	UNP A0A0D6I3Y9
F	-6	HIS	-	expression tag	UNP A0A0D6I3Y9

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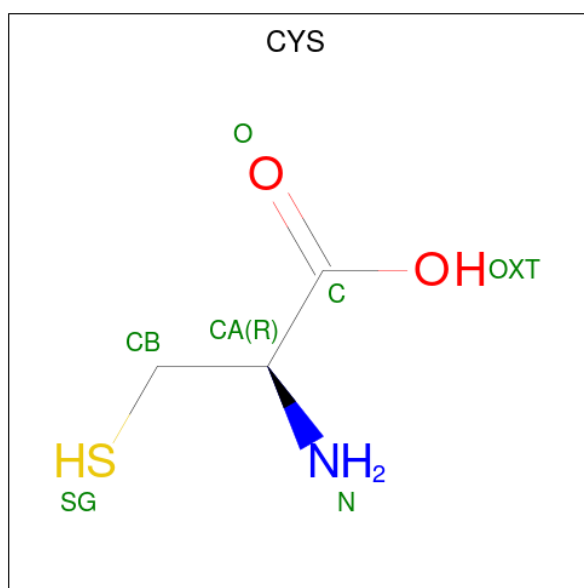
Chain	Residue	Modelled	Actual	Comment	Reference
F	-5	HIS	-	expression tag	UNP A0A0D6I3Y9
F	-4	HIS	-	expression tag	UNP A0A0D6I3Y9
F	-3	HIS	-	expression tag	UNP A0A0D6I3Y9
F	-2	HIS	-	expression tag	UNP A0A0D6I3Y9
F	-1	HIS	-	expression tag	UNP A0A0D6I3Y9
F	0	ASP	-	expression tag	UNP A0A0D6I3Y9
F	1	PRO	-	expression tag	UNP A0A0D6I3Y9
G	-7	MET	-	initiating methionine	UNP A0A0D6I3Y9
G	-6	HIS	-	expression tag	UNP A0A0D6I3Y9
G	-5	HIS	-	expression tag	UNP A0A0D6I3Y9
G	-4	HIS	-	expression tag	UNP A0A0D6I3Y9
G	-3	HIS	-	expression tag	UNP A0A0D6I3Y9
G	-2	HIS	-	expression tag	UNP A0A0D6I3Y9
G	-1	HIS	-	expression tag	UNP A0A0D6I3Y9
G	0	ASP	-	expression tag	UNP A0A0D6I3Y9
G	1	PRO	-	expression tag	UNP A0A0D6I3Y9
H	-7	MET	-	initiating methionine	UNP A0A0D6I3Y9
H	-6	HIS	-	expression tag	UNP A0A0D6I3Y9
H	-5	HIS	-	expression tag	UNP A0A0D6I3Y9
H	-4	HIS	-	expression tag	UNP A0A0D6I3Y9
H	-3	HIS	-	expression tag	UNP A0A0D6I3Y9
H	-2	HIS	-	expression tag	UNP A0A0D6I3Y9
H	-1	HIS	-	expression tag	UNP A0A0D6I3Y9
H	0	ASP	-	expression tag	UNP A0A0D6I3Y9
H	1	PRO	-	expression tag	UNP A0A0D6I3Y9
I	-7	MET	-	initiating methionine	UNP A0A0D6I3Y9
I	-6	HIS	-	expression tag	UNP A0A0D6I3Y9
I	-5	HIS	-	expression tag	UNP A0A0D6I3Y9
I	-4	HIS	-	expression tag	UNP A0A0D6I3Y9
I	-3	HIS	-	expression tag	UNP A0A0D6I3Y9
I	-2	HIS	-	expression tag	UNP A0A0D6I3Y9
I	-1	HIS	-	expression tag	UNP A0A0D6I3Y9
I	0	ASP	-	expression tag	UNP A0A0D6I3Y9
I	1	PRO	-	expression tag	UNP A0A0D6I3Y9
J	-7	MET	-	initiating methionine	UNP A0A0D6I3Y9
J	-6	HIS	-	expression tag	UNP A0A0D6I3Y9
J	-5	HIS	-	expression tag	UNP A0A0D6I3Y9
J	-4	HIS	-	expression tag	UNP A0A0D6I3Y9
J	-3	HIS	-	expression tag	UNP A0A0D6I3Y9
J	-2	HIS	-	expression tag	UNP A0A0D6I3Y9
J	-1	HIS	-	expression tag	UNP A0A0D6I3Y9
J	0	ASP	-	expression tag	UNP A0A0D6I3Y9

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Chain	Residue	Modelled	Actual	Comment	Reference
J	1	PRO	-	expression tag	UNP A0A0D6I3Y9
K	-7	MET	-	initiating methionine	UNP A0A0D6I3Y9
K	-6	HIS	-	expression tag	UNP A0A0D6I3Y9
K	-5	HIS	-	expression tag	UNP A0A0D6I3Y9
K	-4	HIS	-	expression tag	UNP A0A0D6I3Y9
K	-3	HIS	-	expression tag	UNP A0A0D6I3Y9
K	-2	HIS	-	expression tag	UNP A0A0D6I3Y9
K	-1	HIS	-	expression tag	UNP A0A0D6I3Y9
K	0	ASP	-	expression tag	UNP A0A0D6I3Y9
K	1	PRO	-	expression tag	UNP A0A0D6I3Y9
L	-7	MET	-	initiating methionine	UNP A0A0D6I3Y9
L	-6	HIS	-	expression tag	UNP A0A0D6I3Y9
L	-5	HIS	-	expression tag	UNP A0A0D6I3Y9
L	-4	HIS	-	expression tag	UNP A0A0D6I3Y9
L	-3	HIS	-	expression tag	UNP A0A0D6I3Y9
L	-2	HIS	-	expression tag	UNP A0A0D6I3Y9
L	-1	HIS	-	expression tag	UNP A0A0D6I3Y9
L	0	ASP	-	expression tag	UNP A0A0D6I3Y9
L	1	PRO	-	expression tag	UNP A0A0D6I3Y9

- Molecule 2 is CYSTEINE (CCD ID: CYS) (formula: $C_3H_7NO_2S$).



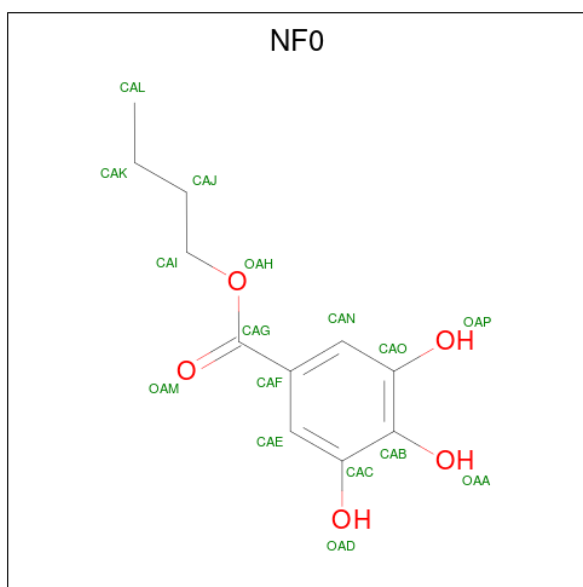
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			7	3	1	2	1		
2	A	1	Total	C	N	O	S	0	0
			7	3	1	2	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			7	3	1	2	1		
2	D	1	Total	C	N	O	S	0	0
			7	3	1	2	1		
2	E	1	Total	C	N	O	S	0	0
			7	3	1	2	1		
2	F	1	Total	C	N	O	S	0	0
			7	3	1	2	1		
2	G	1	Total	C	N	O	S	0	0
			7	3	1	2	1		
2	H	1	Total	C	N	O	S	0	0
			7	3	1	2	1		
2	I	1	Total	C	N	O	S	0	0
			7	3	1	2	1		
2	J	1	Total	C	N	O	S	0	0
			7	3	1	2	1		
2	J	1	Total	C	N	O	S	0	0
			7	3	1	2	1		
2	K	1	Total	C	N	O	S	0	0
			7	3	1	2	1		

- Molecule 3 is butyl 3,4,5-tris(oxidanyl)benzoate (CCD ID: NF0) (formula: $C_{11}H_{14}O_5$) (labeled as "Ligand of Interest" by depositor).



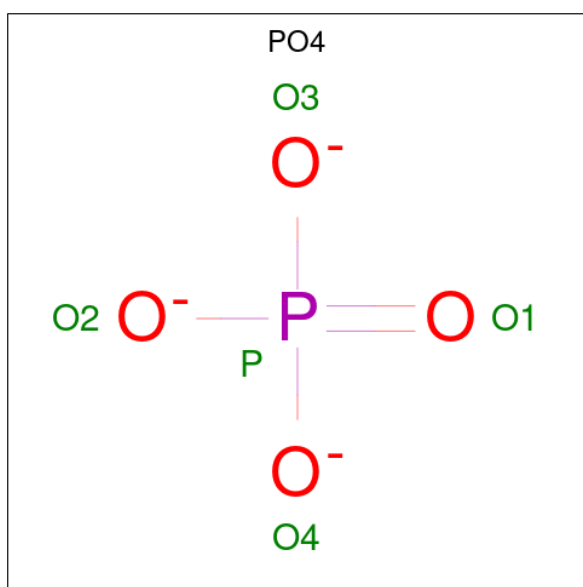
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			16	11	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			16	11	5		
3	C	1	Total	C	O	0	0
			16	11	5		
3	E	1	Total	C	O	0	0
			16	11	5		
3	E	1	Total	C	O	0	0
			16	11	5		
3	F	1	Total	C	O	0	0
			16	11	5		
3	G	1	Total	C	O	0	0
			16	11	5		
3	H	1	Total	C	O	0	0
			16	11	5		
3	I	1	Total	C	O	0	0
			16	11	5		
3	J	1	Total	C	O	0	0
			16	11	5		
3	L	1	Total	C	O	0	0
			16	11	5		
3	L	1	Total	C	O	0	0
			16	11	5		

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O P 5 4 1	0	0
4	F	1	Total O P 5 4 1	0	0
4	G	1	Total O P 5 4 1	0	0
4	K	1	Total O P 5 4 1	0	0

- Molecule 5 is water.

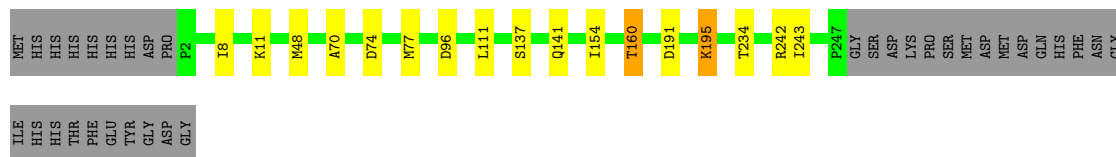
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	71	Total O 71 71	0	0
5	B	67	Total O 67 67	0	0
5	C	67	Total O 67 67	0	0
5	D	52	Total O 52 52	0	0
5	E	54	Total O 54 54	0	0
5	F	51	Total O 51 51	0	0
5	G	62	Total O 62 62	0	0
5	H	62	Total O 62 62	0	0
5	I	60	Total O 60 60	0	0
5	J	63	Total O 63 63	0	0
5	K	61	Total O 61 61	0	0
5	L	64	Total O 64 64	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.

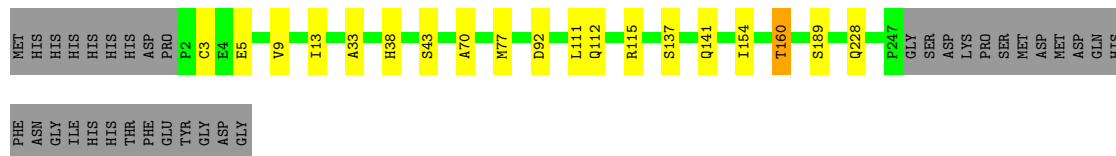
• Molecule 1: Serine acetyltransferase

Chain A: 



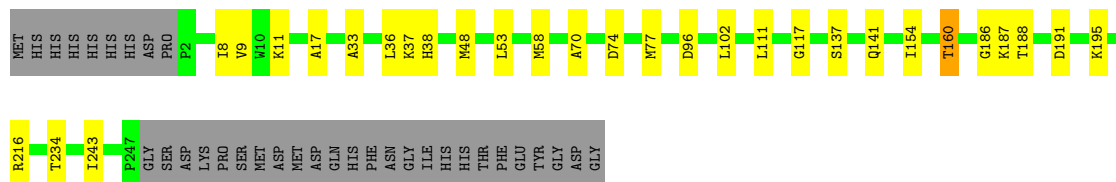
• Molecule 1: Serine acetyltransferase

Chain B: 



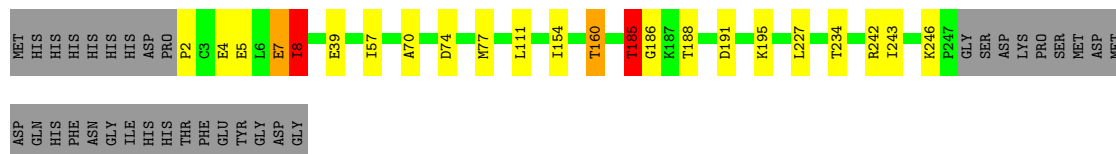
• Molecule 1: Serine acetyltransferase

Chain C: 

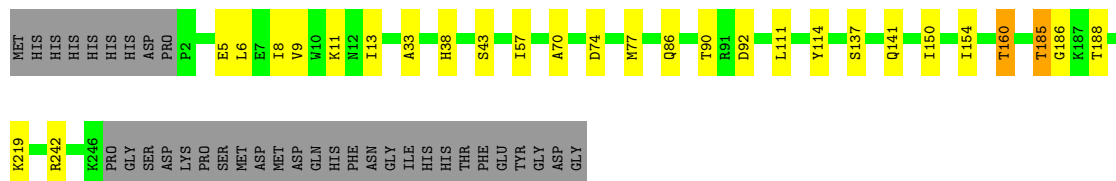


• Molecule 1: Serine acetyltransferase

Chain D: 



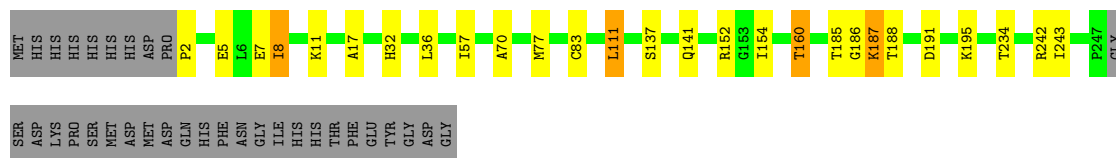
• Molecule 1: Serine acetyltransferase

Chain E:  78% 9% • 12%

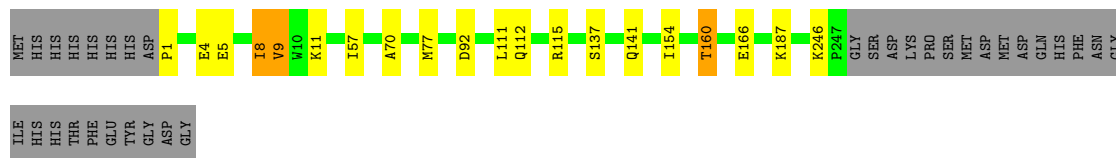
• Molecule 1: Serine acetyltransferase

Chain F:  79% 8% • 12%

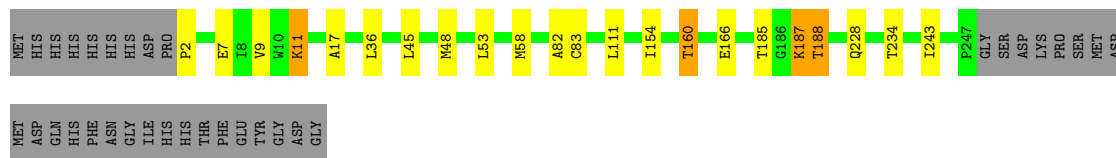
• Molecule 1: Serine acetyltransferase

Chain G:  78% 8% • 12%

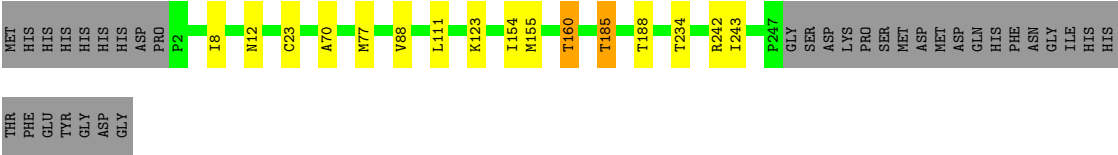
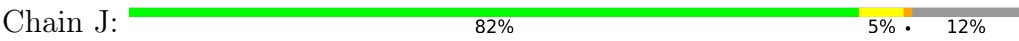
• Molecule 1: Serine acetyltransferase

Chain H:  81% 6% • 12%

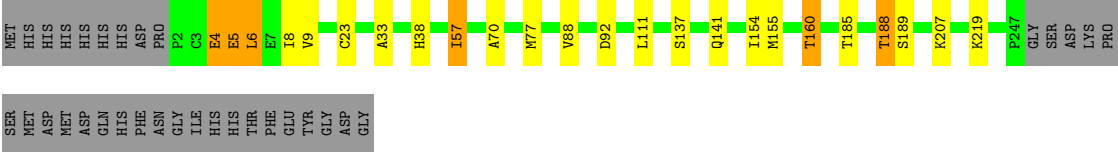
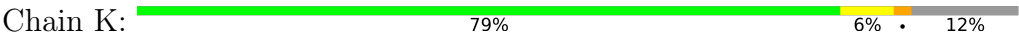
• Molecule 1: Serine acetyltransferase

Chain I:  80% 6% • 12%

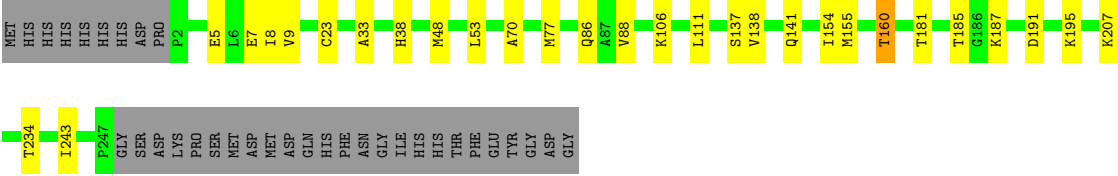
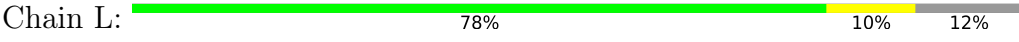
• Molecule 1: Serine acetyltransferase



• Molecule 1: Serine acetyltransferase



• Molecule 1: Serine acetyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	177.36Å 102.65Å 158.72Å 90.00° 111.85° 90.00°	Depositor
Resolution (Å)	19.96 – 1.80 19.96 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.3 (19.96-1.80) 99.1 (19.96-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.204 , 0.241 0.213 , 0.247	Depositor DCC
R_{free} test set	12032 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	34.1	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 29.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.438 for $1/2^*h+3/2^*k, 1/2^*h-1/2^*k, -1/2^*h-1/2^*k-l$ 0.438 for $1/2^*h-3/2^*k, -1/2^*h-1/2^*k, -1/2^*h+1/2^*k-l$	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	23191	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 47.80 % 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 9.4291e-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: PO4, NF0

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	0.78	0/1889	0.92	0/2564
1	B	0.81	1/1881 (0.1%)	0.95	0/2554
1	C	0.76	0/1889	0.95	0/2564
1	D	0.75	0/1878	0.95	4/2550 (0.2%)
1	E	0.80	1/1873 (0.1%)	0.94	1/2542 (0.0%)
1	F	0.77	0/1873	0.93	0/2543
1	G	0.75	0/1886	0.98	2/2560 (0.1%)
1	H	0.77	1/1894 (0.1%)	0.96	2/2572 (0.1%)
1	I	0.72	0/1886	0.95	2/2560 (0.1%)
1	J	0.74	0/1881	0.92	0/2554
1	K	0.77	0/1881	0.94	2/2554 (0.1%)
1	L	0.76	0/1889	0.95	1/2564 (0.0%)
All	All	0.77	3/22600 (0.0%)	0.94	14/30681 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	13	ILE	C-O	-5.68	1.17	1.24
1	B	13	ILE	C-O	-5.68	1.17	1.24
1	H	9	VAL	C-O	-5.17	1.18	1.24

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	185	THR	N-CA-C	8.00	123.04	113.28
1	L	185	THR	N-CA-C	7.92	122.95	113.28
1	D	185	THR	N-CA-C	7.75	123.79	113.72
1	H	1	PRO	N-CA-CB	7.36	111.09	103.00
1	G	2	PRO	N-CA-CB	6.78	110.46	103.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1852	0	1898	10	0
1	B	1844	0	1890	7	0
1	C	1852	0	1898	16	0
1	D	1842	0	1884	16	0
1	E	1837	0	1883	10	0
1	F	1837	0	1882	14	0
1	G	1850	0	1892	12	0
1	H	1857	0	1899	7	0
1	I	1850	0	1892	11	0
1	J	1844	0	1890	8	0
1	K	1844	0	1890	11	0
1	L	1852	0	1898	13	0
2	A	14	0	8	0	0
2	B	7	0	4	0	0
2	D	7	0	4	0	0
2	E	7	0	4	0	0
2	F	7	0	4	0	0
2	G	7	0	4	0	0
2	H	7	0	4	0	0
2	I	7	0	4	0	0
2	J	14	0	8	1	0
2	K	7	0	4	0	0
3	A	16	0	0	0	0
3	B	16	0	0	0	0
3	C	16	0	0	0	0
3	E	32	0	0	0	0
3	F	16	0	0	1	0
3	G	16	0	0	0	0
3	H	16	0	0	0	0
3	I	16	0	0	0	0
3	J	16	0	0	0	0
3	L	32	0	0	0	0
4	A	5	0	0	0	0
4	F	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	G	5	0	0	0	0
4	K	5	0	0	0	0
5	A	71	0	0	1	0
5	B	67	0	0	2	0
5	C	67	0	0	2	0
5	D	52	0	0	0	0
5	E	54	0	0	2	0
5	F	51	0	0	2	0
5	G	62	0	0	2	0
5	H	62	0	0	2	0
5	I	60	0	0	2	0
5	J	63	0	0	2	0
5	K	61	0	0	2	0
5	L	64	0	0	1	0
All	All	23191	0	22744	136	0

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

The worst 5 of 136 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:4:GLU:OE2	1:D:8:ILE:HG12	1.80	0.81
1:J:111:LEU:HD21	1:J:154:ILE:HB	1.70	0.71
1:K:111:LEU:HD21	1:K:154:ILE:HB	1.76	0.67
1:F:3:CYS:SG	1:F:4:GLU:N	2.69	0.66
1:E:92:ASP:O	5:E:601:HOH:O	2.14	0.64

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	245/280 (88%)	239 (98%)	6 (2%)	0	100	100
1	B	244/280 (87%)	240 (98%)	4 (2%)	0	100	100
1	C	245/280 (88%)	240 (98%)	5 (2%)	0	100	100
1	D	244/280 (87%)	240 (98%)	4 (2%)	0	100	100
1	E	243/280 (87%)	237 (98%)	3 (1%)	3 (1%)	10	3
1	F	243/280 (87%)	237 (98%)	6 (2%)	0	100	100
1	G	245/280 (88%)	238 (97%)	5 (2%)	2 (1%)	16	6
1	H	246/280 (88%)	238 (97%)	8 (3%)	0	100	100
1	I	245/280 (88%)	237 (97%)	7 (3%)	1 (0%)	30	19
1	J	244/280 (87%)	238 (98%)	6 (2%)	0	100	100
1	K	244/280 (87%)	235 (96%)	6 (2%)	3 (1%)	10	3
1	L	245/280 (88%)	237 (97%)	8 (3%)	0	100	100
All	All	2933/3360 (87%)	2856 (97%)	68 (2%)	9 (0%)	36	25

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	6	LEU
1	G	188	THR
1	I	188	THR
1	K	5	GLU
1	K	6	LEU

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	191/220 (87%)	185 (97%)	6 (3%)	35	23
1	B	190/220 (86%)	183 (96%)	7 (4%)	30	18
1	C	191/220 (87%)	181 (95%)	10 (5%)	21	9
1	D	189/220 (86%)	181 (96%)	8 (4%)	26	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	189/220 (86%)	181 (96%)	8 (4%)	26	14
1	F	189/220 (86%)	180 (95%)	9 (5%)	23	11
1	G	190/220 (86%)	183 (96%)	7 (4%)	30	18
1	H	191/220 (87%)	183 (96%)	8 (4%)	26	14
1	I	190/220 (86%)	183 (96%)	7 (4%)	30	18
1	J	190/220 (86%)	184 (97%)	6 (3%)	34	22
1	K	190/220 (86%)	181 (95%)	9 (5%)	23	11
1	L	191/220 (87%)	181 (95%)	10 (5%)	21	9
All	All	2281/2640 (86%)	2186 (96%)	95 (4%)	26	14

5 of 95 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	9	VAL
1	J	23	CYS
1	H	57	ILE
1	I	58	MET
1	J	242	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	38	HIS
1	L	38	HIS
1	H	135	GLN
1	K	133	GLN
1	H	133	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

28 ligands are modelled in this entry.

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
2	CYS	A	401	-	5,6,6	1.27	1 (20%)	3,7,7	1.94	1 (33%)
3	NF0	E	501	-	16,16,16	1.41	2 (12%)	21,21,21	2.01	4 (19%)
3	NF0	C	501	-	16,16,16	1.43	1 (6%)	21,21,21	1.35	1 (4%)
3	NF0	L	501	-	16,16,16	1.51	3 (18%)	21,21,21	2.24	6 (28%)
2	CYS	J	402	-	5,6,6	1.21	1 (20%)	3,7,7	1.68	1 (33%)
4	PO4	A	404	-	4,4,4	0.89	0	6,6,6	0.58	0
3	NF0	B	402	-	16,16,16	1.38	1 (6%)	21,21,21	2.14	4 (19%)
2	CYS	K	401	-	5,6,6	1.26	0	3,7,7	1.77	1 (33%)
3	NF0	A	403	-	16,16,16	1.45	2 (12%)	21,21,21	1.78	3 (14%)
3	NF0	L	502	-	16,16,16	1.41	2 (12%)	21,21,21	1.76	3 (14%)
2	CYS	H	502	-	5,6,6	1.04	1 (20%)	3,7,7	1.56	1 (33%)
4	PO4	F	503	-	4,4,4	0.84	0	6,6,6	0.63	0
3	NF0	J	403	-	16,16,16	1.39	2 (12%)	21,21,21	1.51	2 (9%)
2	CYS	A	402	-	5,6,6	1.14	1 (20%)	3,7,7	1.55	1 (33%)
2	CYS	I	502	-	5,6,6	1.14	1 (20%)	3,7,7	1.69	1 (33%)
2	CYS	B	401	-	5,6,6	1.32	0	3,7,7	1.64	1 (33%)
2	CYS	D	401	-	5,6,6	1.04	1 (20%)	3,7,7	1.65	1 (33%)
2	CYS	J	401	-	5,6,6	1.32	0	3,7,7	2.56	2 (66%)
3	NF0	F	501	-	16,16,16	1.37	1 (6%)	21,21,21	1.30	2 (9%)
2	CYS	F	502	-	5,6,6	1.08	1 (20%)	3,7,7	1.56	1 (33%)
3	NF0	H	501	-	16,16,16	1.51	2 (12%)	21,21,21	2.21	5 (23%)
4	PO4	K	402	-	4,4,4	0.88	0	6,6,6	0.49	0
3	NF0	E	503	-	16,16,16	1.33	1 (6%)	21,21,21	1.10	2 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PO4	G	403	-	4,4,4	0.95	0	6,6,6	0.48	0
2	CYS	G	401	-	5,6,6	1.04	1 (20%)	3,7,7	1.66	1 (33%)
2	CYS	E	502	-	5,6,6	1.09	0	3,7,7	1.46	1 (33%)
3	NF0	I	501	-	16,16,16	1.52	2 (12%)	21,21,21	1.53	3 (14%)
3	NF0	G	402	-	16,16,16	1.46	1 (6%)	21,21,21	1.43	3 (14%)

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
2	CYS	A	401	-	-	5/6/6/6	-
3	NF0	E	501	-	-	4/9/9/9	0/1/1/1
3	NF0	C	501	-	-	5/9/9/9	0/1/1/1
3	NF0	L	501	-	-	4/9/9/9	0/1/1/1
2	CYS	J	402	-	-	1/6/6/6	-
3	NF0	B	402	-	-	4/9/9/9	0/1/1/1
2	CYS	K	401	-	-	2/6/6/6	-
3	NF0	A	403	-	-	5/9/9/9	0/1/1/1
3	NF0	L	502	-	-	5/9/9/9	0/1/1/1
2	CYS	H	502	-	-	0/6/6/6	-
3	NF0	J	403	-	-	5/9/9/9	0/1/1/1
2	CYS	A	402	-	-	0/6/6/6	-
2	CYS	I	502	-	-	0/6/6/6	-
2	CYS	B	401	-	-	0/6/6/6	-
2	CYS	D	401	-	-	0/6/6/6	-
2	CYS	J	401	-	-	6/6/6/6	-
3	NF0	F	501	-	-	5/9/9/9	0/1/1/1
2	CYS	F	502	-	-	1/6/6/6	-
3	NF0	H	501	-	-	4/9/9/9	0/1/1/1
3	NF0	E	503	-	-	5/9/9/9	0/1/1/1
2	CYS	G	401	-	-	4/6/6/6	-
2	CYS	E	502	-	-	1/6/6/6	-
3	NF0	I	501	-	-	5/9/9/9	0/1/1/1
3	NF0	G	402	-	-	6/9/9/9	0/1/1/1

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	501	NF0	CAF-CAG	-4.92	1.39	1.50
3	F	501	NF0	CAF-CAG	-4.78	1.39	1.50
3	I	501	NF0	CAF-CAG	-4.59	1.39	1.50
3	G	402	NF0	CAF-CAG	-4.57	1.39	1.50
3	H	501	NF0	CAF-CAG	-4.49	1.39	1.50

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	402	NF0	OAH-CAG-CAF	7.00	123.88	112.15
3	A	403	NF0	OAH-CAG-CAF	6.47	122.98	112.15
3	E	501	NF0	OAH-CAG-CAF	6.44	122.94	112.15
3	L	501	NF0	OAH-CAG-CAF	6.09	122.35	112.15
3	H	501	NF0	OAH-CAG-CAF	6.07	122.32	112.15

There are no chirality outliers.

5 of 77 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	CYS	O-C-CA-N
2	A	401	CYS	C-CA-CB-SG
2	G	401	CYS	O-C-CA-N
2	G	401	CYS	N-CA-CB-SG
2	G	401	CYS	C-CA-CB-SG

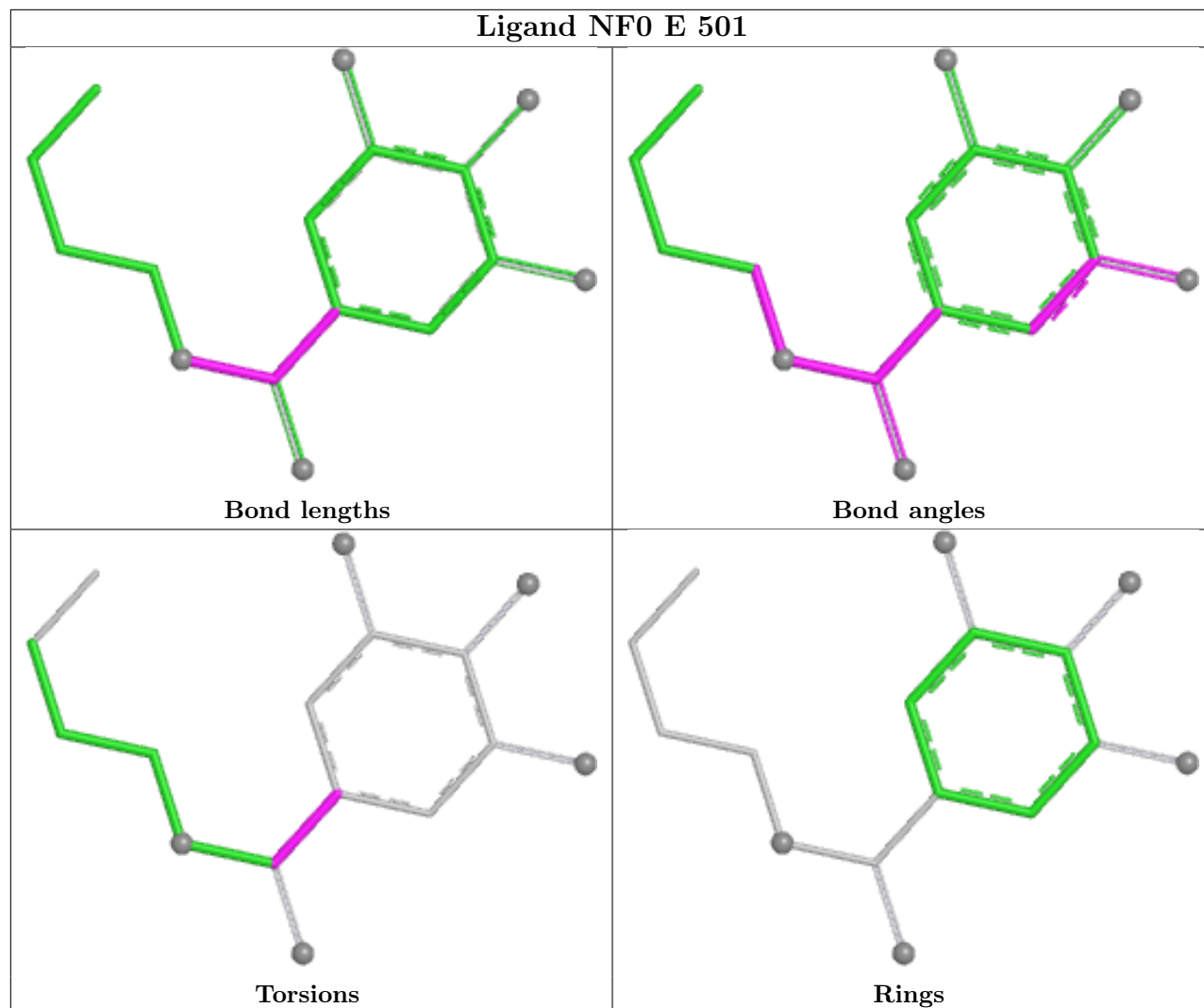
There are no ring outliers.

2 monomers are involved in 2 short contacts:

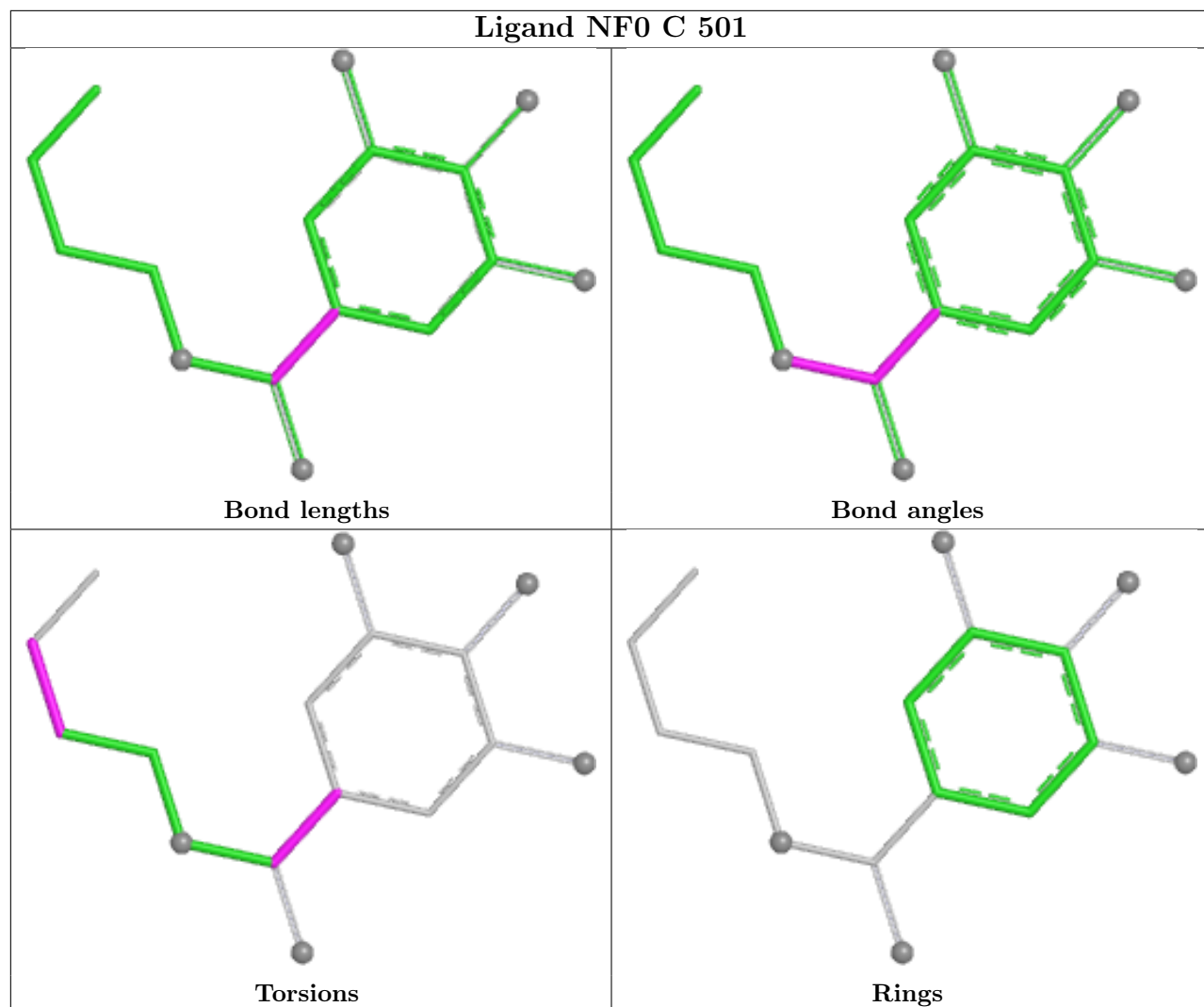
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	J	401	CYS	1	0
3	F	501	NF0	1	0

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

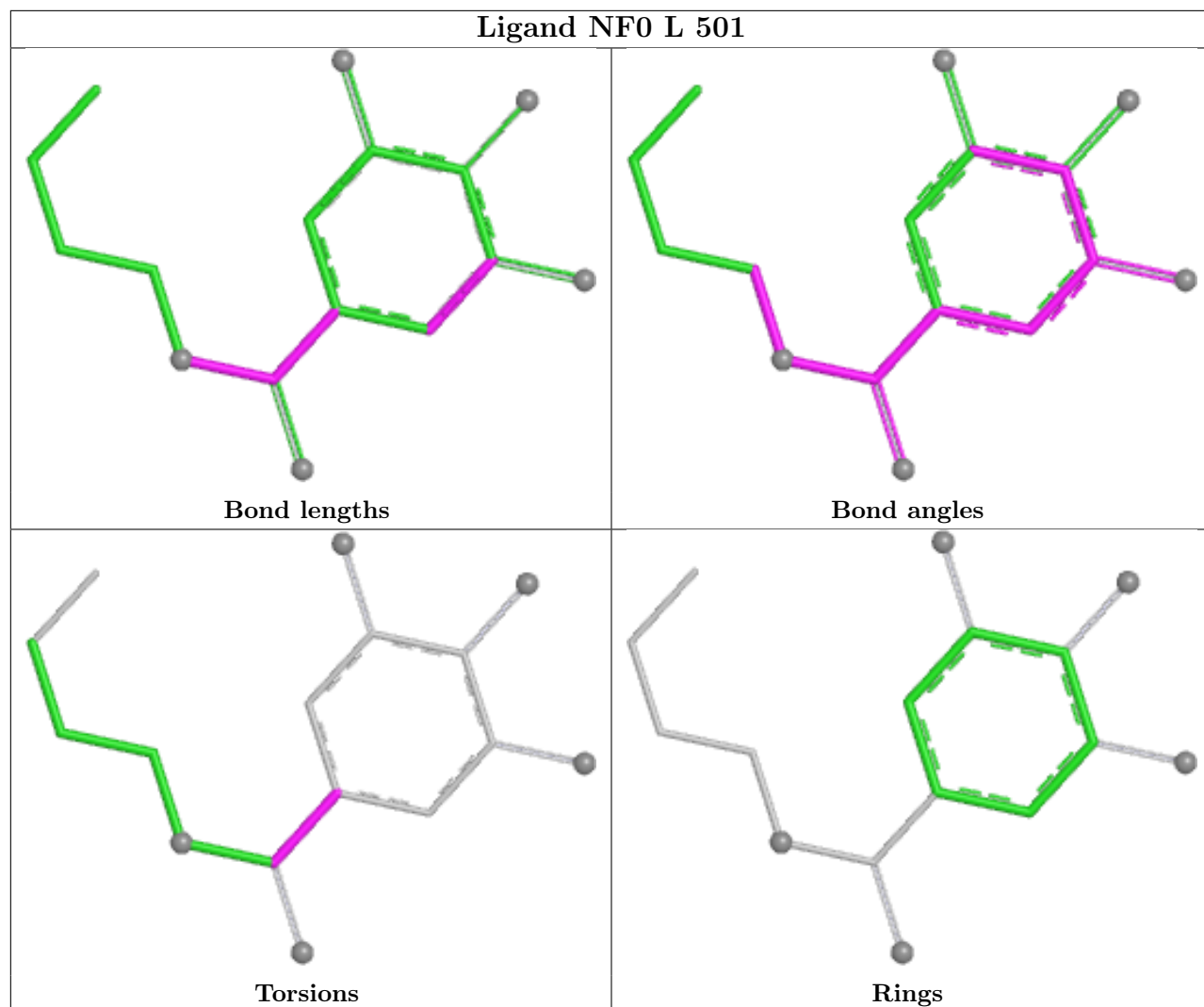
equivalents in the CSD to analyse the geometry.



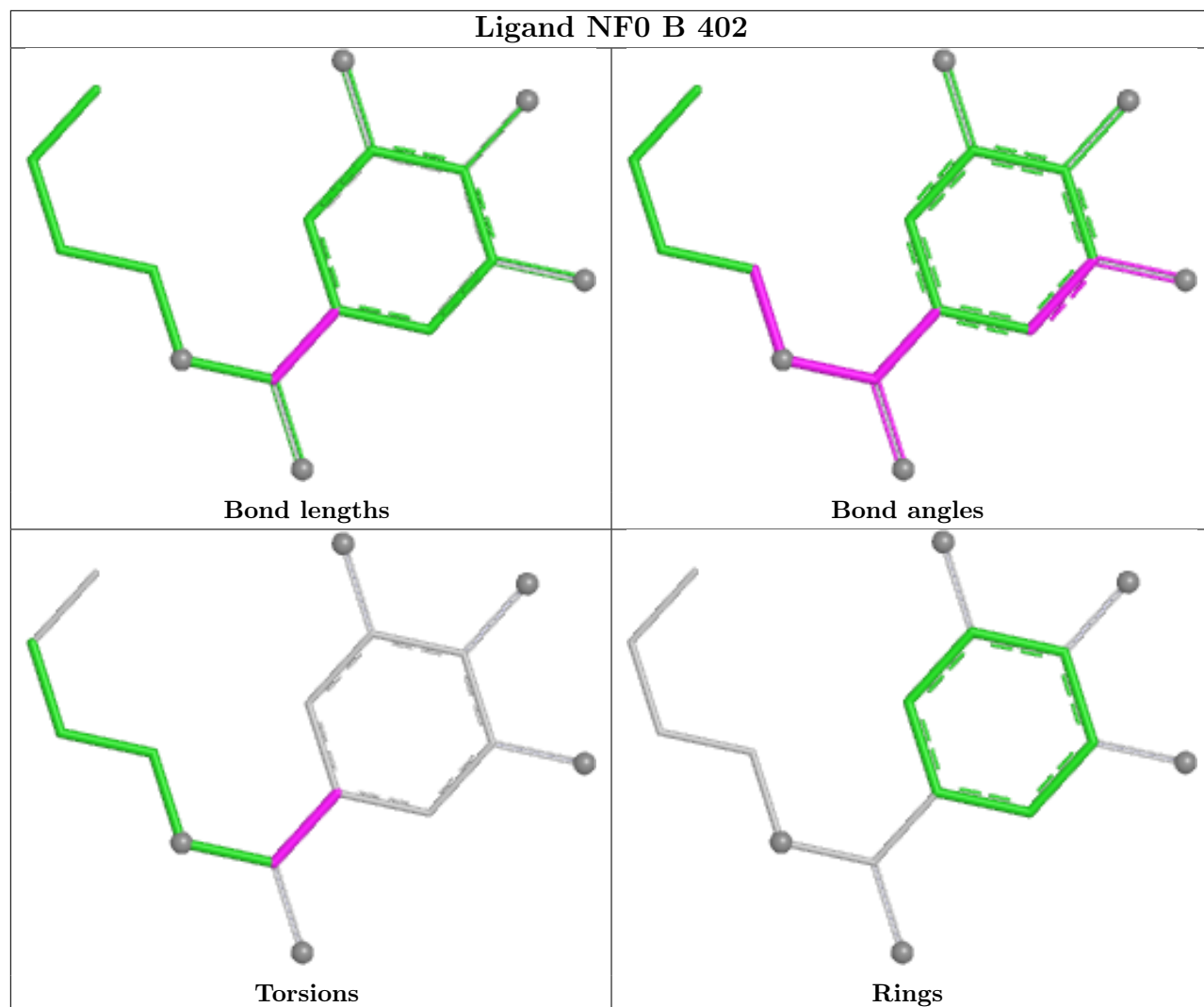
Ligand NF0 C 501



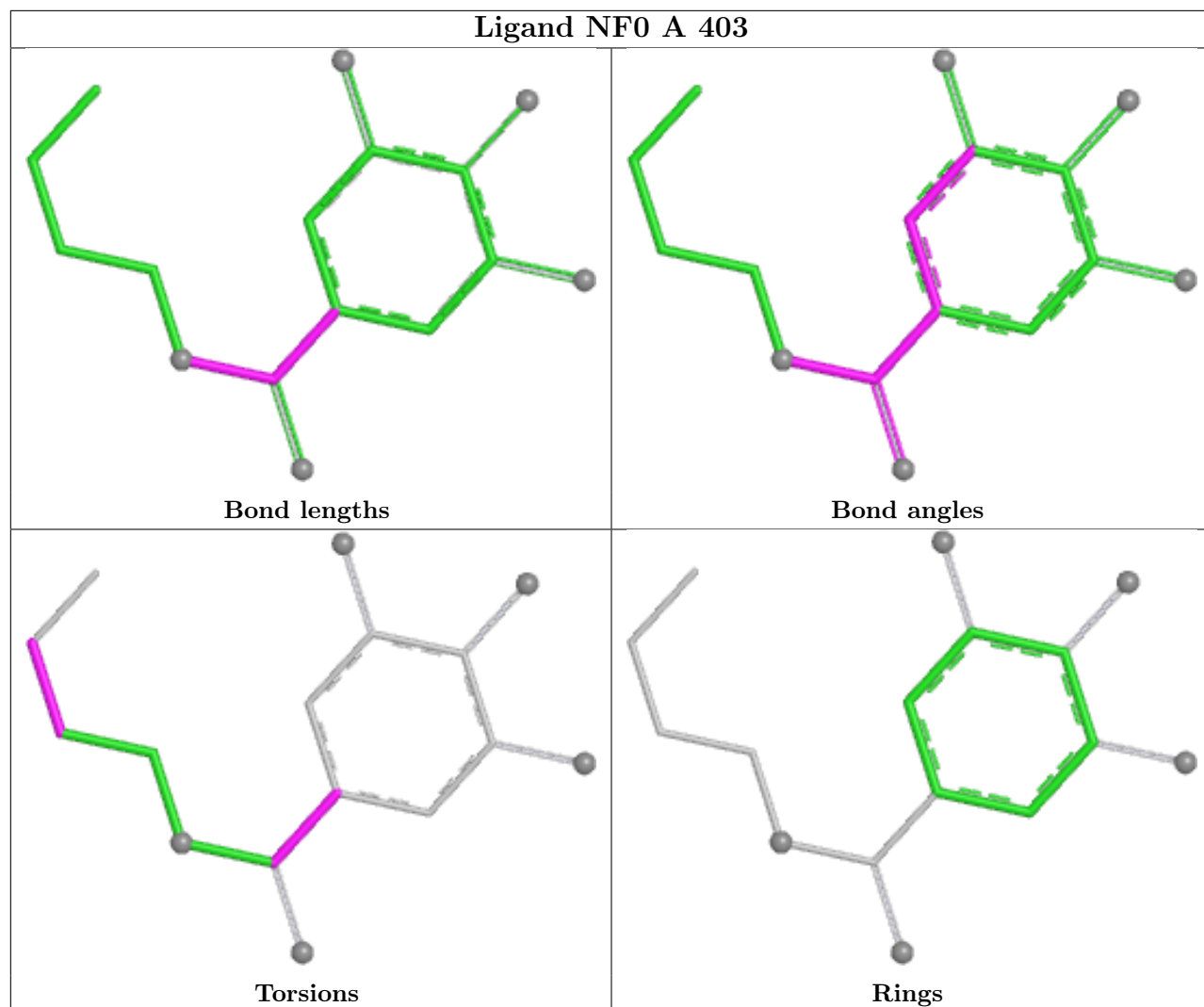
Ligand NF0 L 501



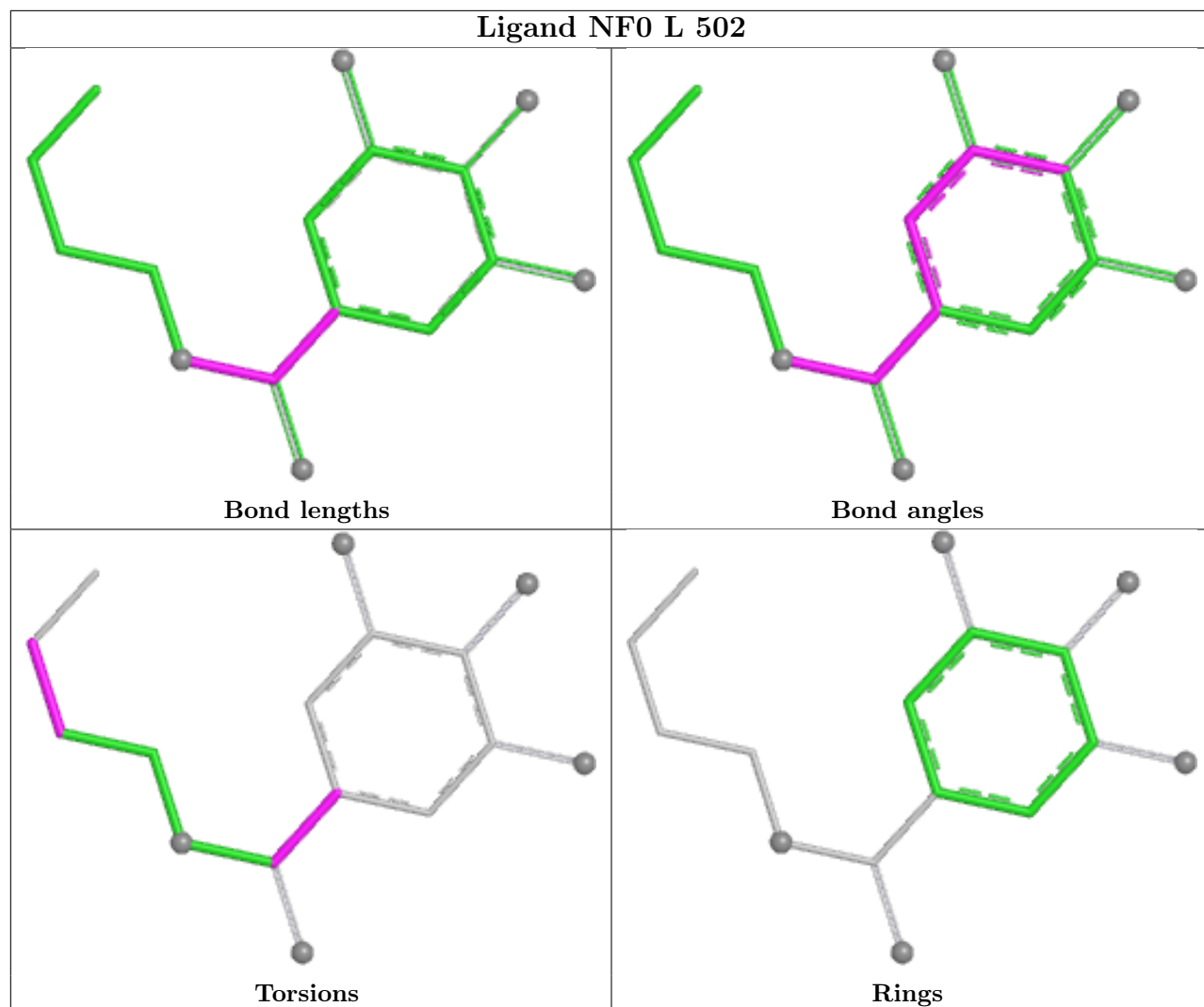
Ligand NF0 B 402



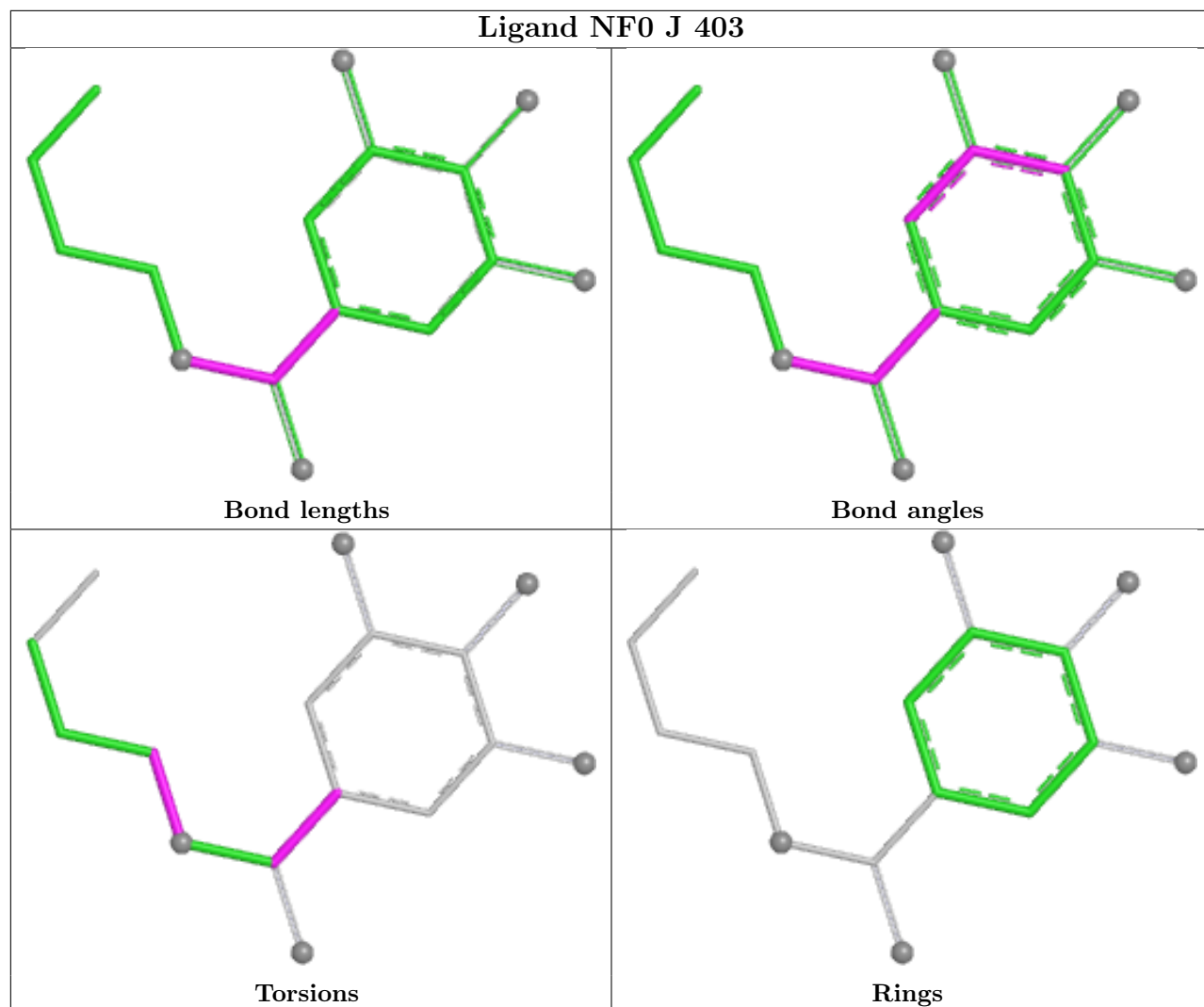
Ligand NF0 A 403



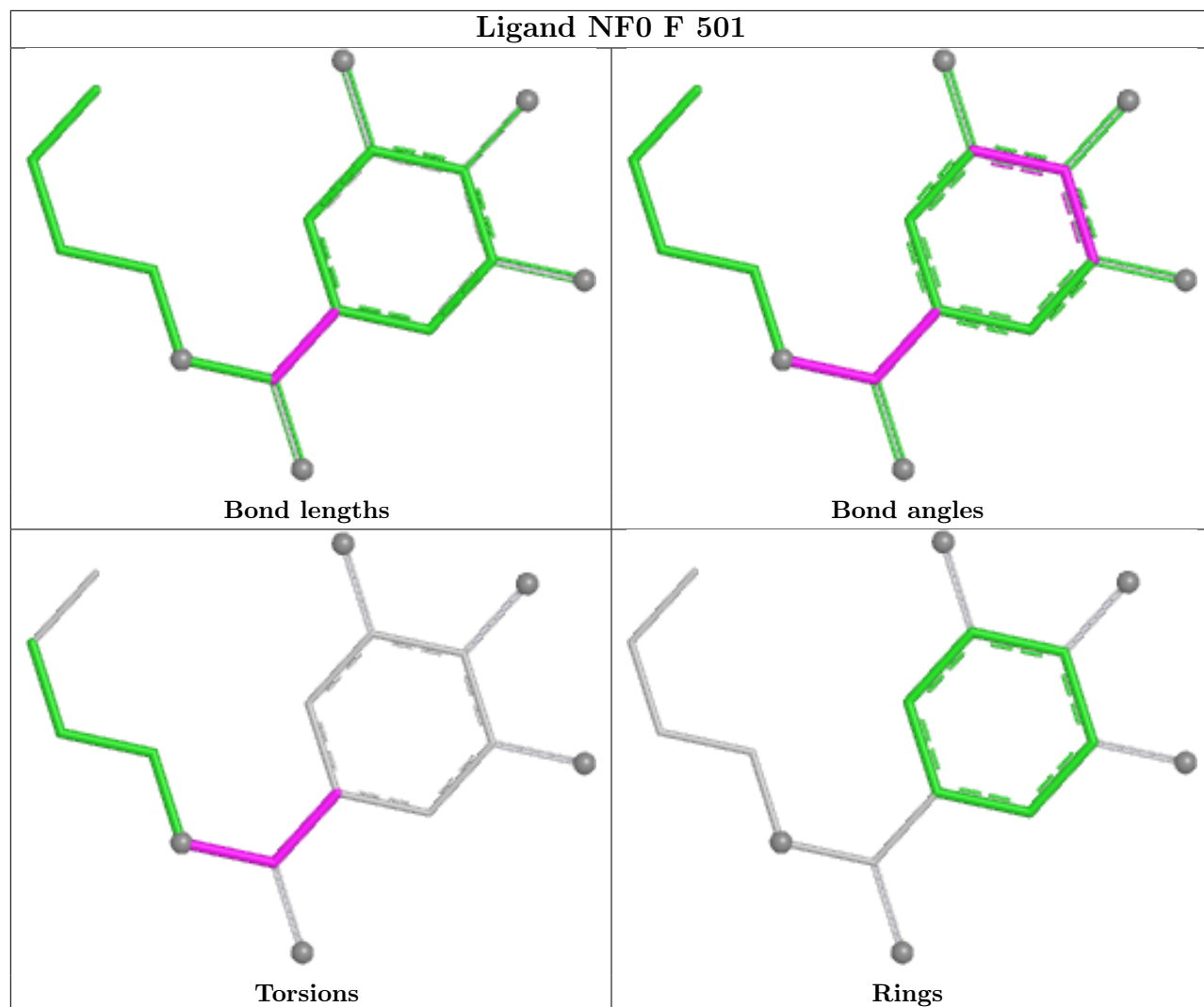
Ligand NF0 L 502



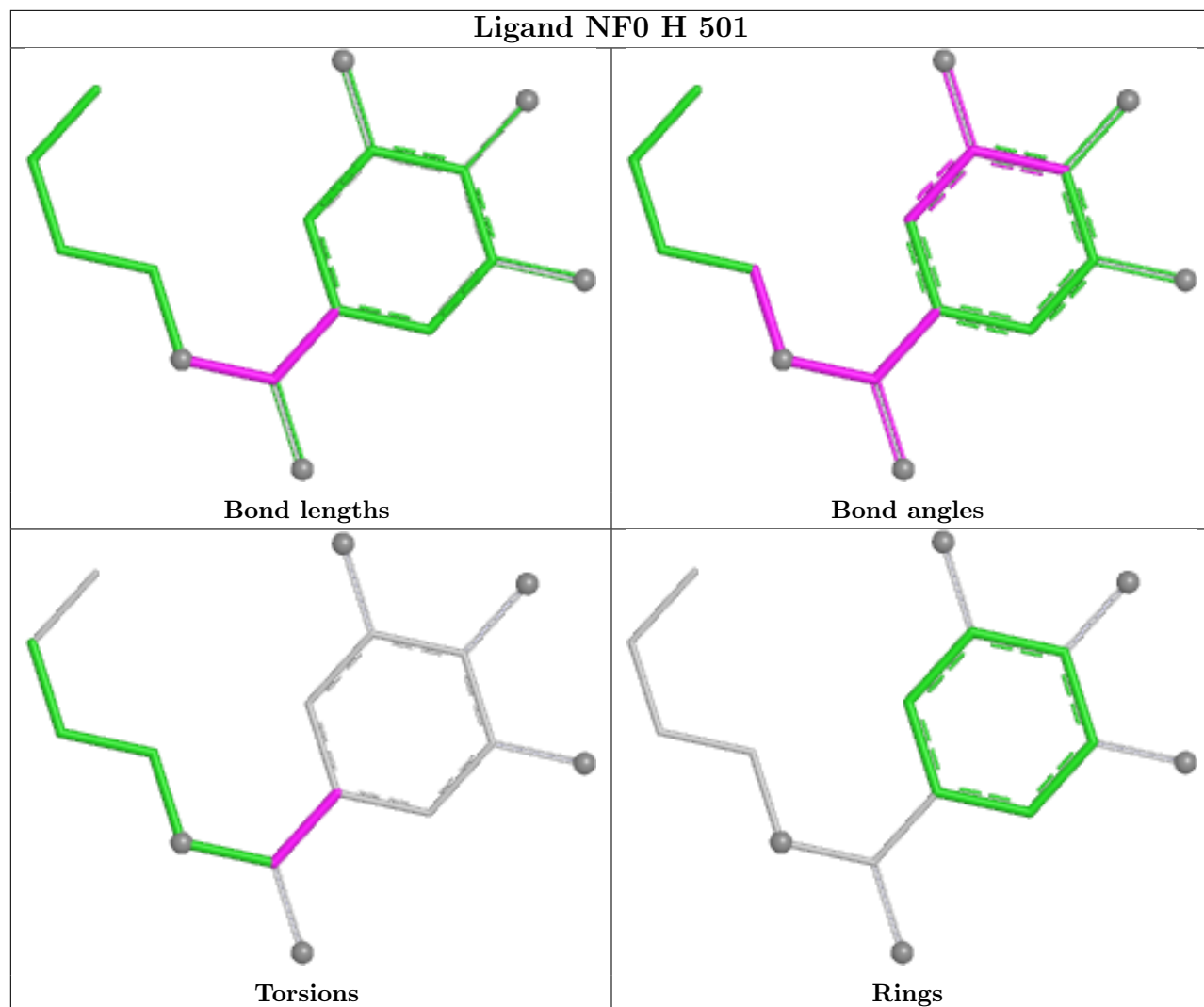
Ligand NF0 J 403



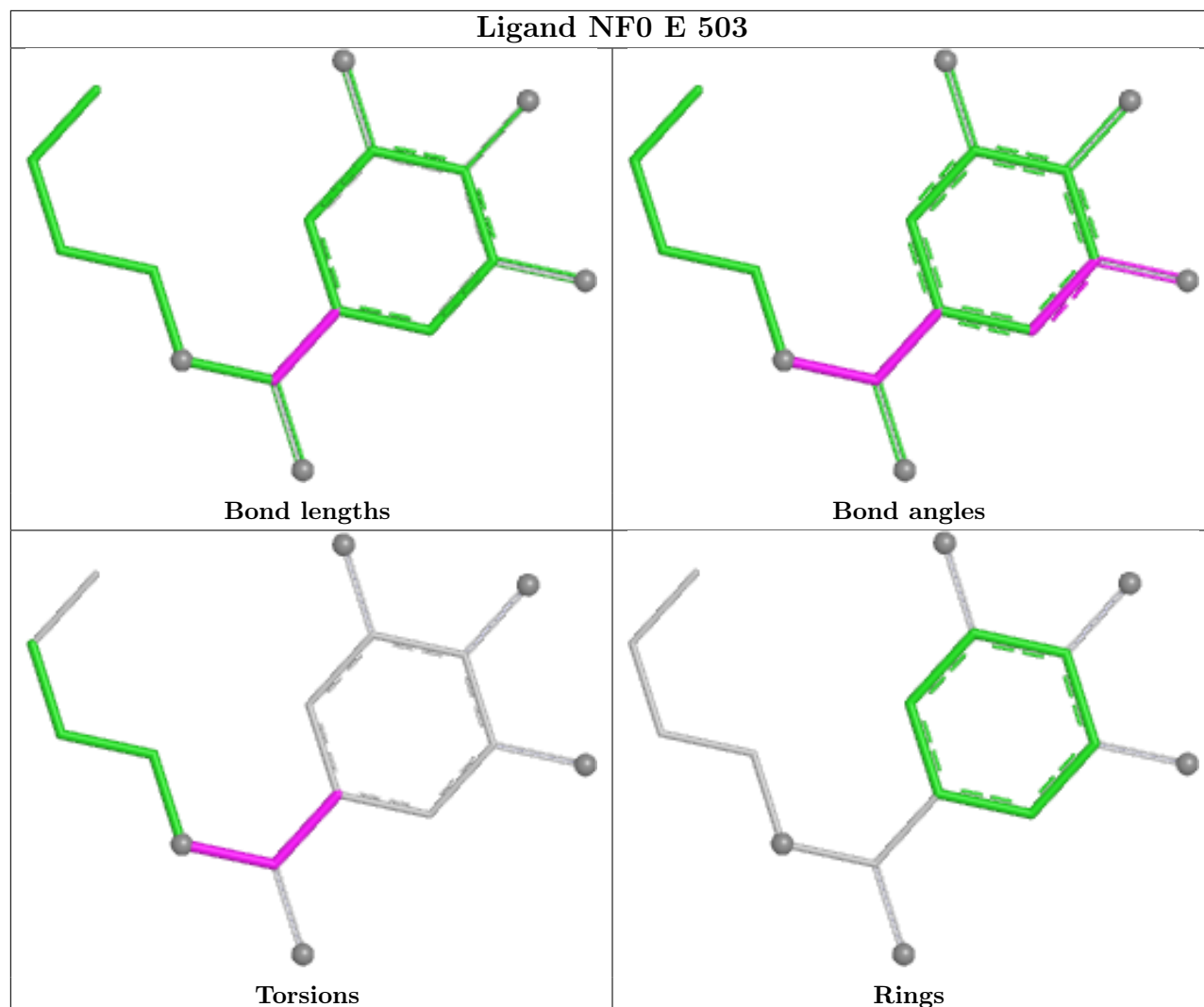
Ligand NF0 F 501



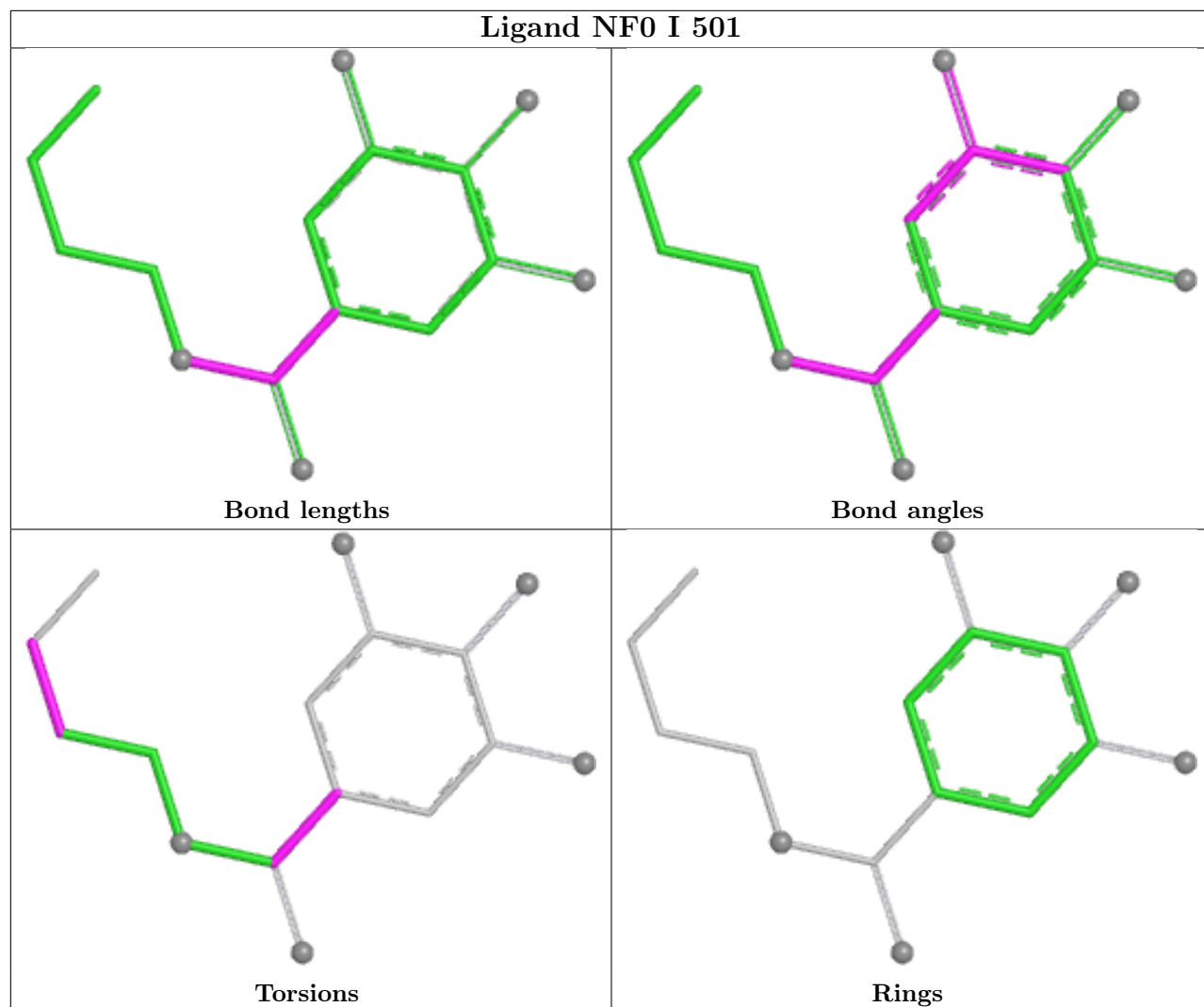
Ligand NF0 H 501

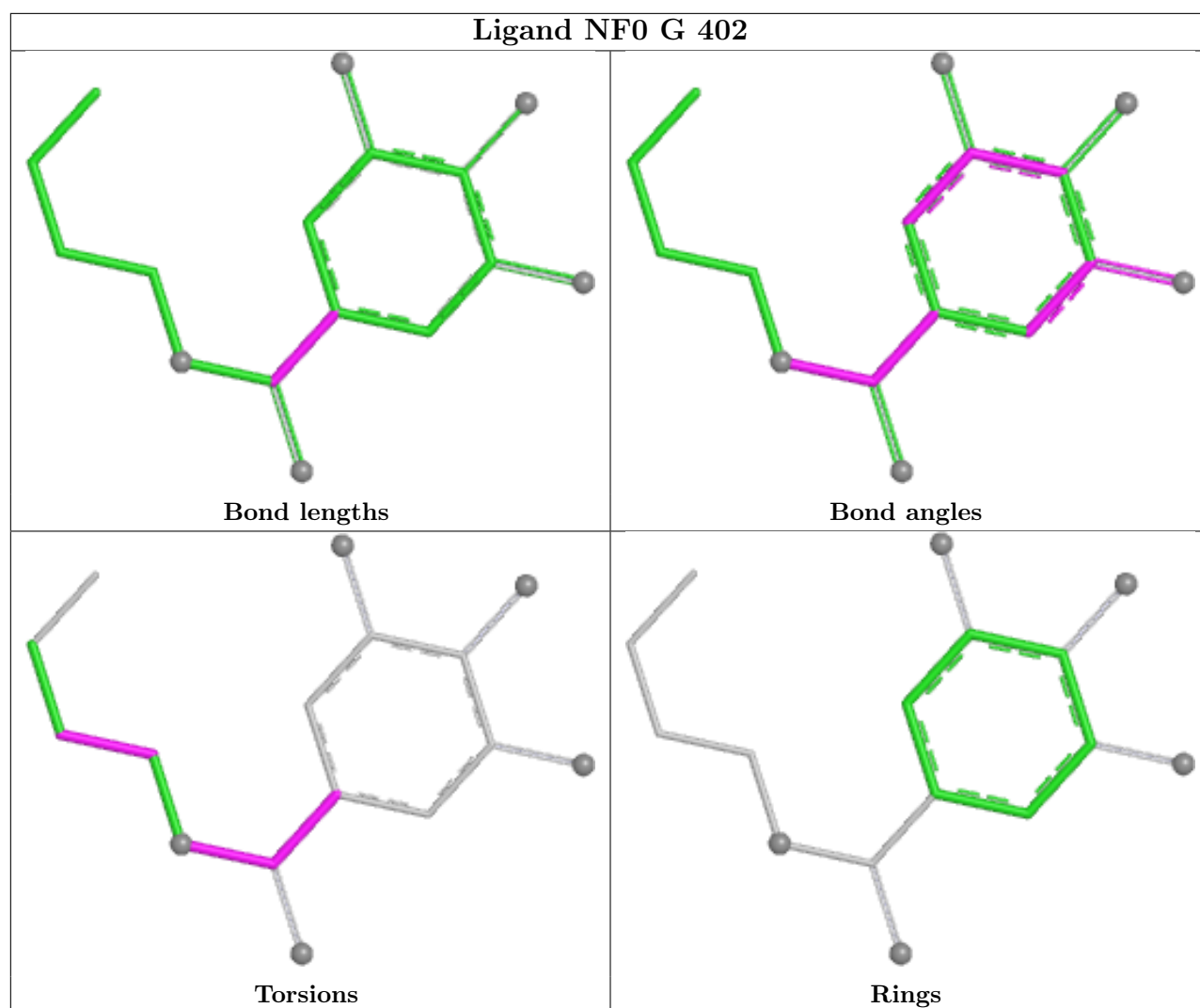


Ligand NF0 E 503



Ligand NF0 I 501





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	246/280 (87%)	-1.05	0 100 100	15, 33, 59, 83	1 (0%)
1	B	246/280 (87%)	-1.06	0 100 100	22, 32, 58, 79	0
1	C	246/280 (87%)	-1.09	0 100 100	15, 33, 60, 85	1 (0%)
1	D	246/280 (87%)	-1.01	0 100 100	26, 39, 68, 100	0
1	E	245/280 (87%)	-1.02	0 100 100	25, 39, 65, 84	0
1	F	245/280 (87%)	-1.05	0 100 100	25, 39, 65, 92	0
1	G	246/280 (87%)	-0.97	0 100 100	16, 35, 62, 86	1 (0%)
1	H	247/280 (88%)	-1.00	0 100 100	15, 34, 64, 81	1 (0%)
1	I	246/280 (87%)	-0.98	0 100 100	16, 35, 64, 81	1 (0%)
1	J	246/280 (87%)	-0.96	0 100 100	24, 35, 61, 82	0
1	K	246/280 (87%)	-0.98	0 100 100	24, 35, 62, 82	0
1	L	246/280 (87%)	-0.99	0 100 100	16, 35, 61, 86	1 (0%)
All	All	2951/3360 (87%)	-1.01	0 100 100	15, 36, 63, 100	6 (0%)

There are no RSRZ outliers to report.

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 oligosaccharides in this entry.

6.4 Ligands ⓘ

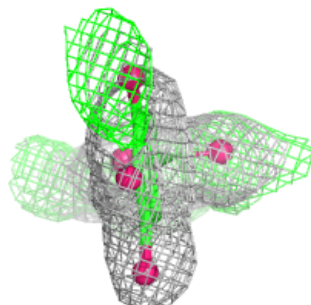
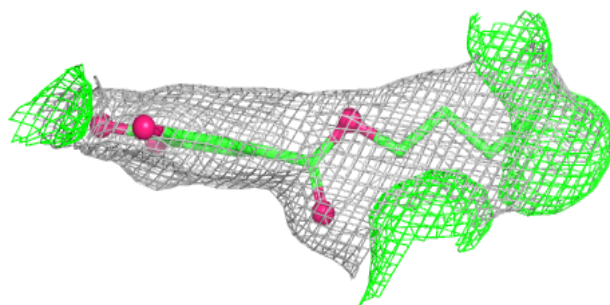
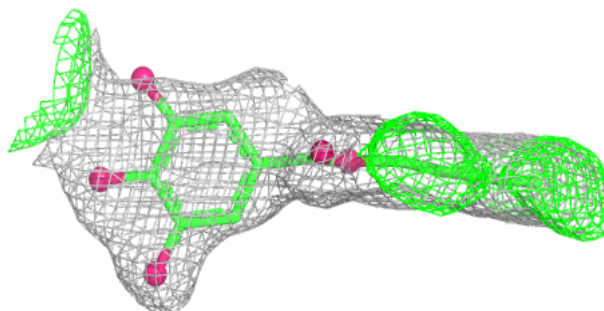
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NF0	H	501	16/16	0.91	0.07	41,48,51,51	0
3	NF0	E	501	16/16	0.93	0.08	52,55,57,57	0
2	CYS	F	502	7/7	0.93	0.08	94,95,96,96	0
3	NF0	B	402	16/16	0.94	0.07	40,48,53,53	0
2	CYS	E	502	7/7	0.94	0.09	77,83,84,85	0
2	CYS	I	502	7/7	0.94	0.10	72,80,82,82	0
3	NF0	I	501	16/16	0.94	0.07	40,46,49,50	0
4	PO4	G	403	5/5	0.94	0.15	111,113,115,115	0
2	CYS	J	402	7/7	0.95	0.10	91,95,97,97	0
3	NF0	J	403	16/16	0.95	0.06	41,48,50,53	0
3	NF0	L	501	16/16	0.95	0.07	41,47,53,53	0
3	NF0	L	502	16/16	0.95	0.07	39,46,51,51	0
2	CYS	A	402	7/7	0.95	0.09	70,78,78,80	0
2	CYS	A	401	7/7	0.96	0.08	65,71,74,77	0
3	NF0	C	501	16/16	0.96	0.07	42,48,54,55	0
2	CYS	D	401	7/7	0.96	0.08	87,92,96,97	0
3	NF0	E	503	16/16	0.96	0.05	50,55,58,58	0
3	NF0	F	501	16/16	0.96	0.06	52,56,58,59	0
4	PO4	A	404	5/5	0.96	0.08	114,116,117,118	0
3	NF0	G	402	16/16	0.96	0.06	45,51,54,54	0
2	CYS	B	401	7/7	0.97	0.07	56,64,65,68	0
2	CYS	J	401	7/7	0.97	0.08	77,84,85,85	0
2	CYS	G	401	7/7	0.97	0.08	82,90,95,99	0
2	CYS	K	401	7/7	0.97	0.07	69,78,82,86	0
3	NF0	A	403	16/16	0.97	0.06	42,51,55,56	0
4	PO4	F	503	5/5	0.97	0.08	107,107,109,110	0
2	CYS	H	502	7/7	0.97	0.06	69,74,77,77	0
4	PO4	K	402	5/5	0.98	0.07	86,86,86,92	0

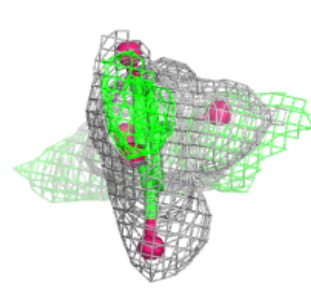
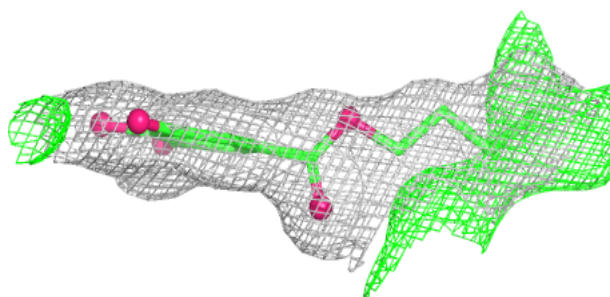
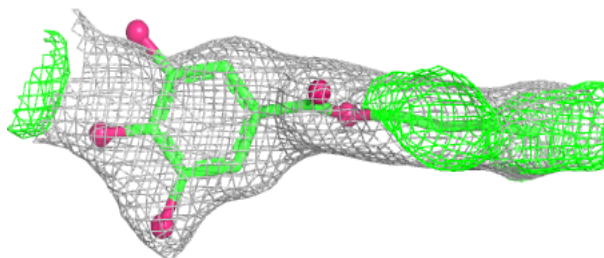
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NF0 H 501:

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

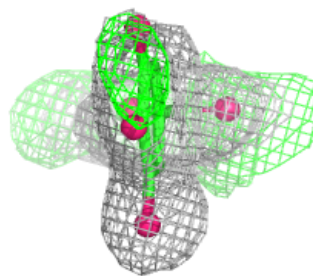
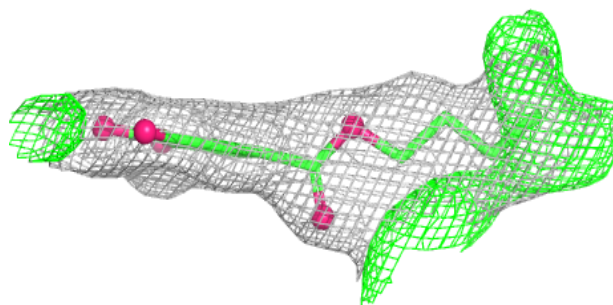
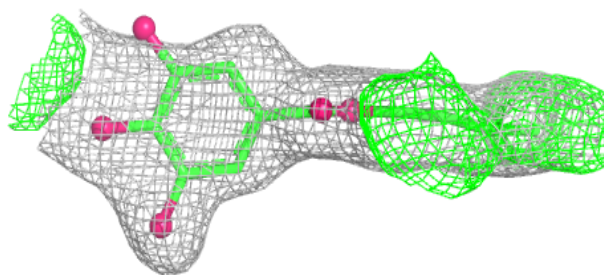
**Electron density around NF0 E 501:**

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

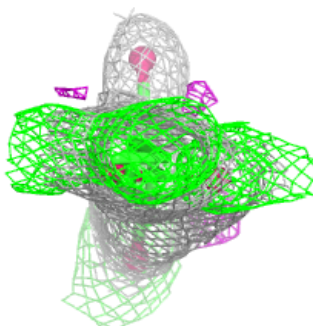
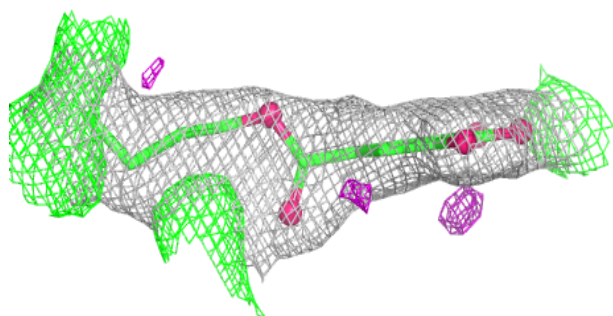
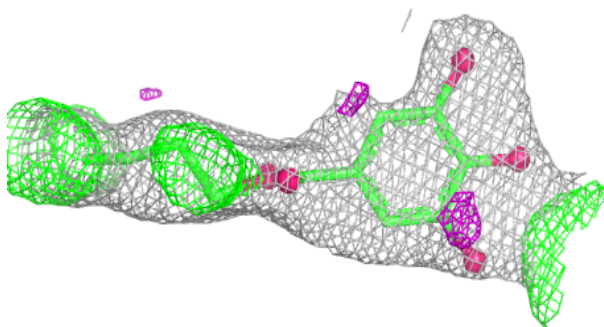


Electron density around NF0 B 402:

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

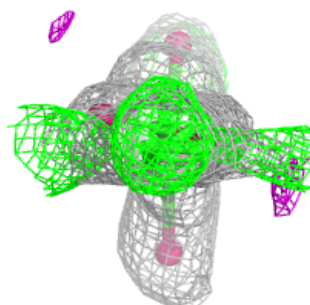
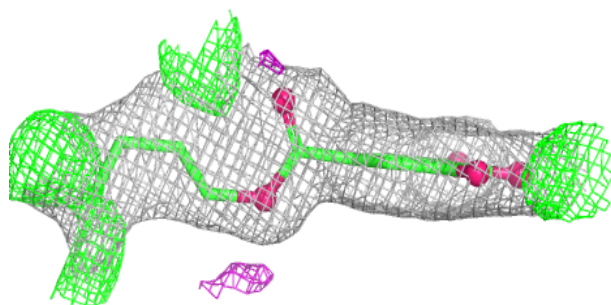
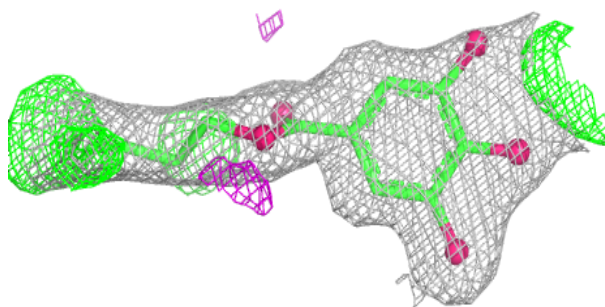
**Electron density around NF0 I 501:**

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

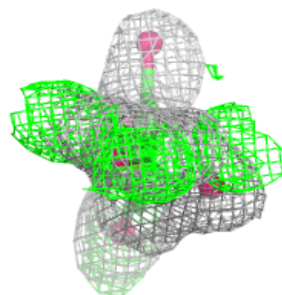
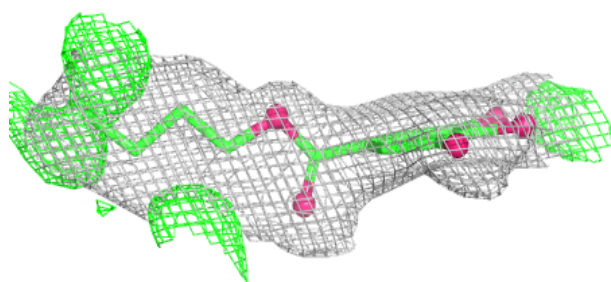
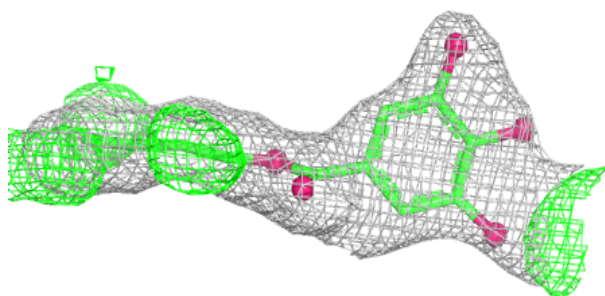


Electron density around NF0 J 403:

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

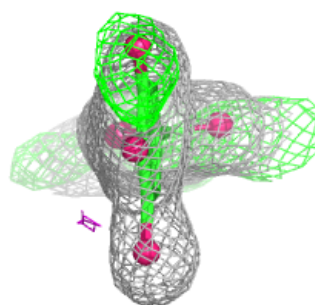
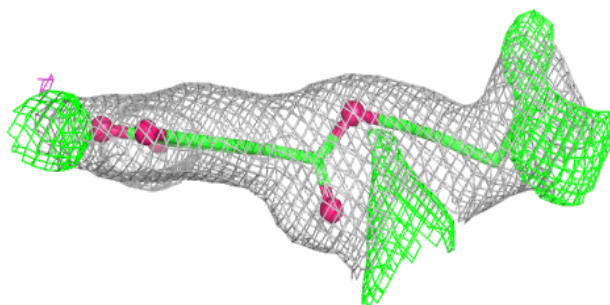
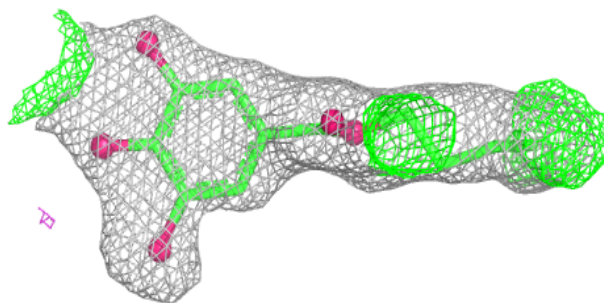
**Electron density around NF0 L 501:**

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

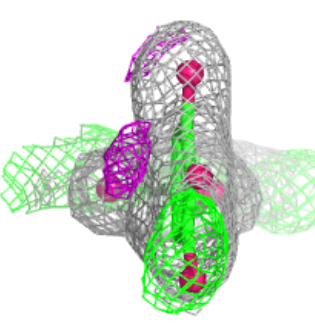
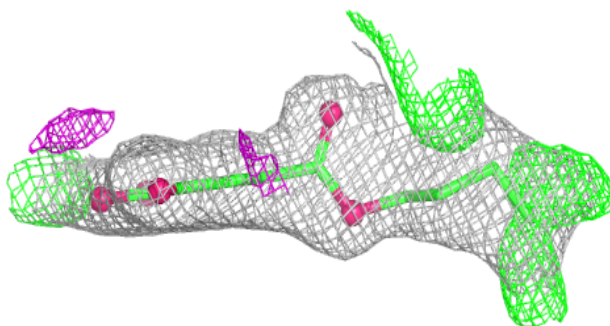
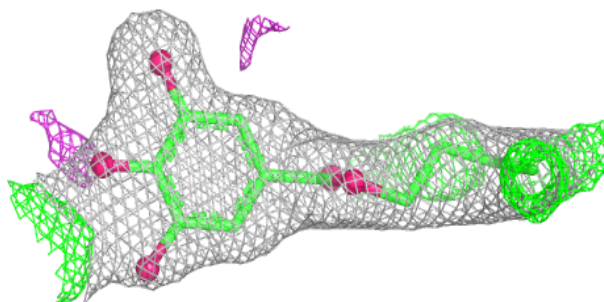


Electron density around NF0 L 502:

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

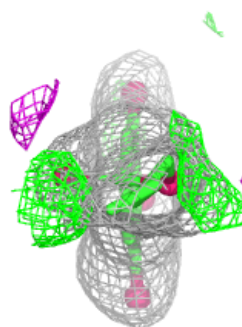
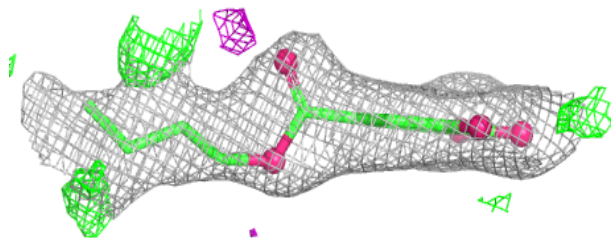
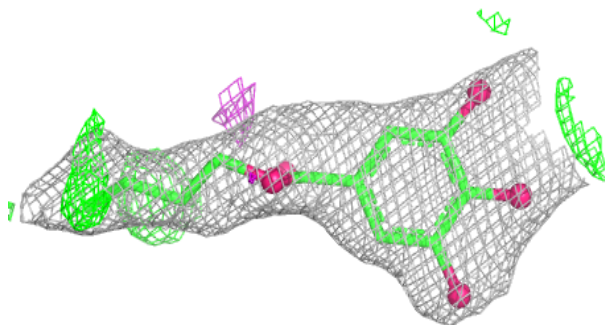
**Electron density around NF0 C 501:**

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

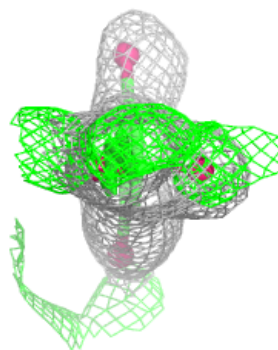
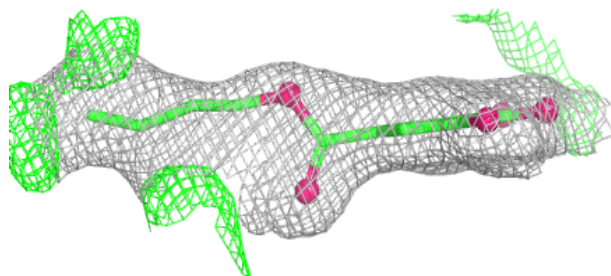
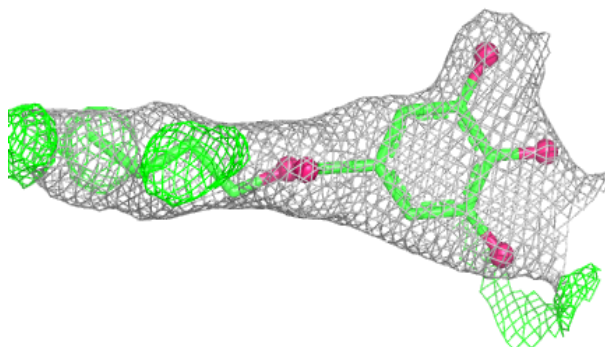


Electron density around NF0 E 503:

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

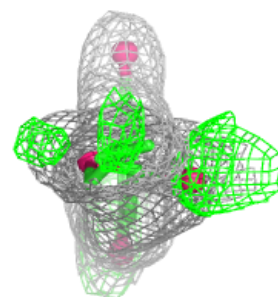
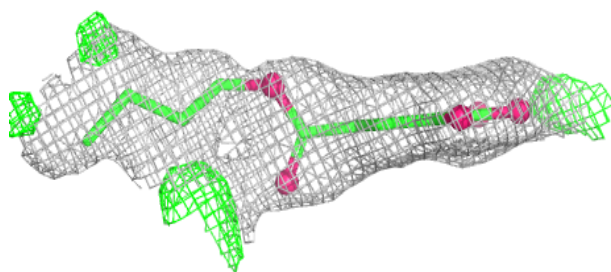
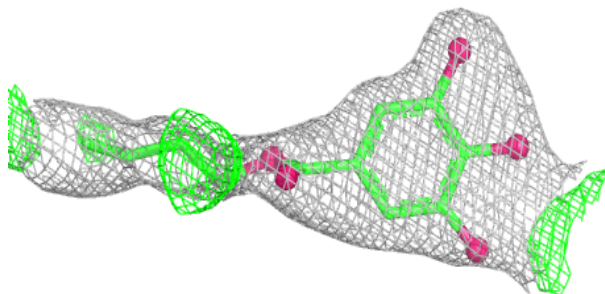
**Electron density around NF0 F 501:**

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

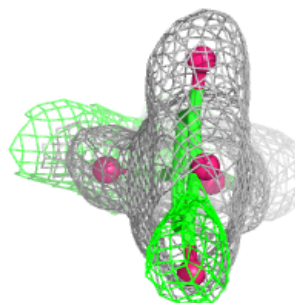
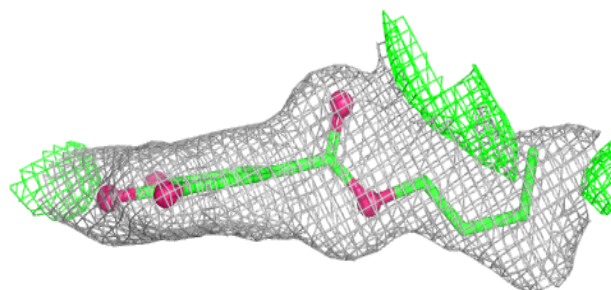
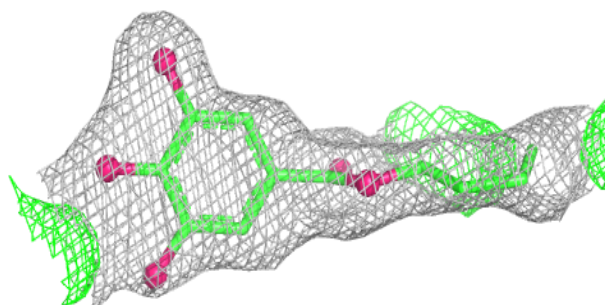


Electron density around NF0 G 402:

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

**Electron density around NF0 A 403:**

$2mF_o-DF_c$ (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.