



wwPDB X-ray Structure Validation Summary Report ⓘ

May 18, 2020 – 12:58 am BST

PDB ID : 1ZMC
Title : Crystal Structure of Human dihydrolipoamide dehydrogenase complexed to NAD+
Authors : Brautigam, C.A.; Chuang, J.L.; Tomchick, D.R.; Machius, M.; Chuang, D.T.
Deposited on : 2005-05-10
Resolution : 2.53 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

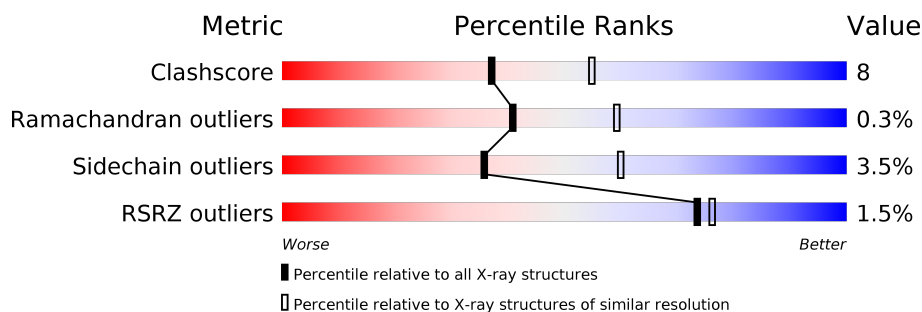
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.53 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))
Clashscore	141614	6463 (2.54-2.50)
Ramachandran outliers	138981	6335 (2.54-2.50)
Sidechain outliers	138945	6337 (2.54-2.50)
RSRZ outliers	127900	5630 (2.54-2.50)

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

Mol	Chain	Length	Quality of chain
1	A	474	<div> <div>2%</div> <div>76%</div> <div>21%</div> <div>.</div> </div>
1	B	474	<div> <div>2%</div> <div>79%</div> <div>20%</div> <div>..</div> </div>
1	C	474	<div> <div>2%</div> <div>77%</div> <div>22%</div> <div>..</div> </div>
1	D	474	<div> <div>2%</div> <div>75%</div> <div>24%</div> <div>.</div> </div>
1	E	474	<div> <div>%</div> <div>81%</div> <div>17%</div> <div>.</div> </div>
1	F	474	<div> <div>%</div> <div>82%</div> <div>16%</div> <div>..</div> </div>
1	G	474	<div> <div>%</div> <div>82%</div> <div>16%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	H	474	<div> <div>%</div> <div> </div> <div>82%17%..</div> </div>

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	SO4	A	2003	-	-	X	-
2	SO4	B	2007	-	-	X	-
2	SO4	D	2014	-	-	X	-
2	SO4	D	2016	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 30312 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 Dihydrolipoyl dehydrogenase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	472	Total	C	N	O	S	0	1	0
			3515	2214	609	673	19			
1	B	471	Total	C	N	O	S	0	0	0
			3496	2203	604	670	19			
1	C	471	Total	C	N	O	S	6	0	0
			3496	2203	604	670	19			
1	D	474	Total	C	N	O	S	0	1	0
			3528	2221	611	677	19			
1	E	472	Total	C	N	O	S	0	0	0
			3505	2208	606	672	19			
1	F	471	Total	C	N	O	S	4	1	0
			3506	2209	607	671	19			
1	G	472	Total	C	N	O	S	0	1	0
			3515	2214	609	673	19			
1	H	471	Total	C	N	O	S	0	0	0
			3496	2203	604	670	19			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	69	THR	LYS	conflict	UNP P09622
B	69	THR	LYS	conflict	UNP P09622
C	69	THR	LYS	conflict	UNP P09622
D	69	THR	LYS	conflict	UNP P09622
E	69	THR	LYS	conflict	UNP P09622
F	69	THR	LYS	conflict	UNP P09622
G	69	THR	LYS	conflict	UNP P09622
H	69	THR	LYS	conflict	UNP P09622

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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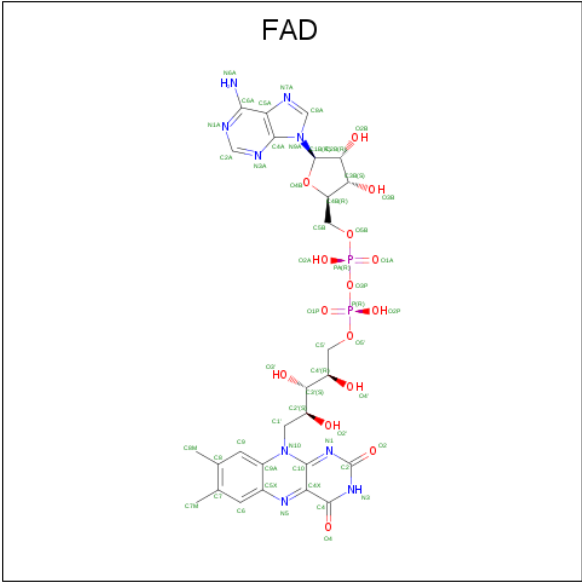
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	G	1	Total	O	S	0	0
			5	4	1		
2	G	1	Total	O	S	0	0
			5	4	1		
2	G	1	Total	O	S	0	0
			5	4	1		
2	G	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	0
			5	4	1		

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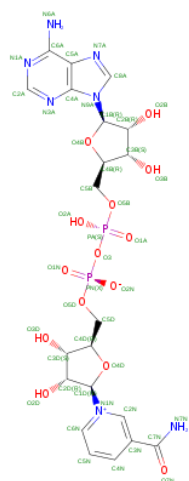
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	E	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	F	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	G	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	H	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



- Molecule 5 is water.

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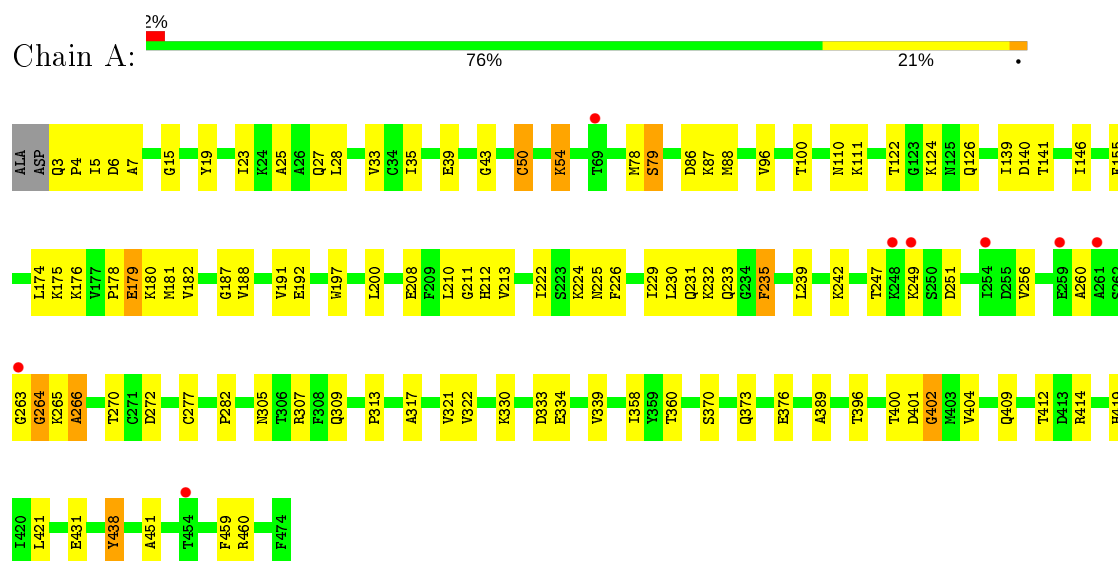
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	E	175	Total 175	O 175	0	0
5	F	229	Total 229	O 229	0	0
5	G	247	Total 247	O 247	0	0
5	H	173	Total 173	O 173	0	0

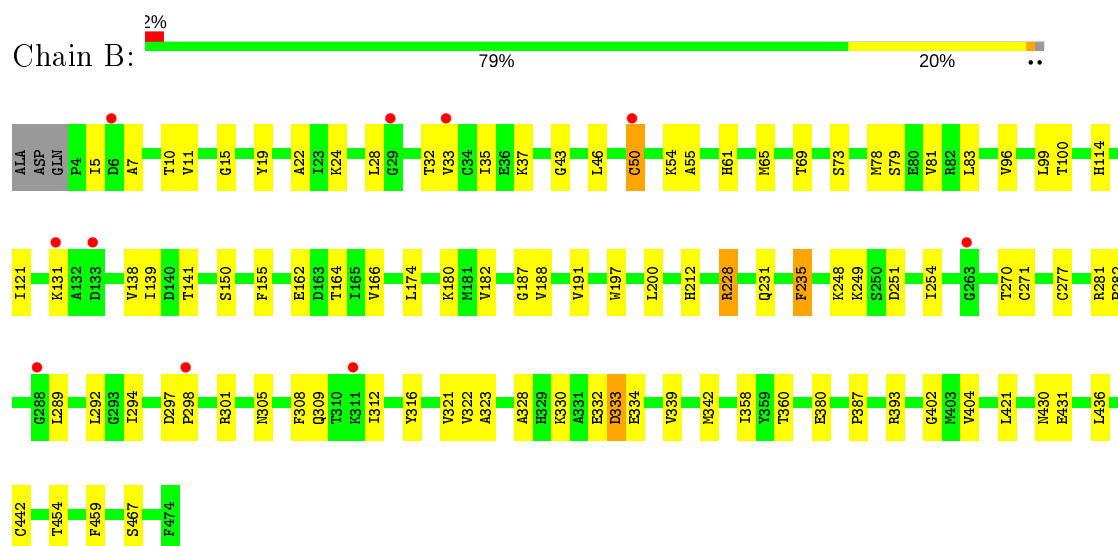
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

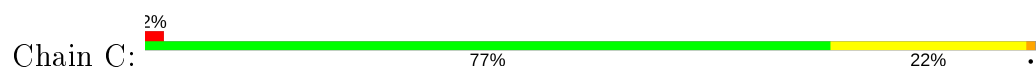
- Molecule 1: Dihydrolipoyl dehydrogenase, mitochondrial

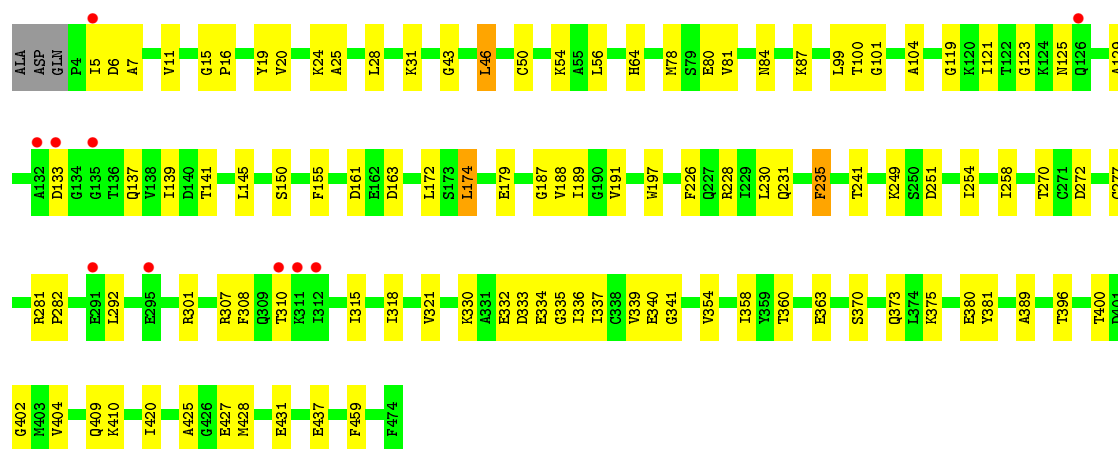


- Molecule 1: Dihydrolipoyl dehydrogenase, mitochondrial

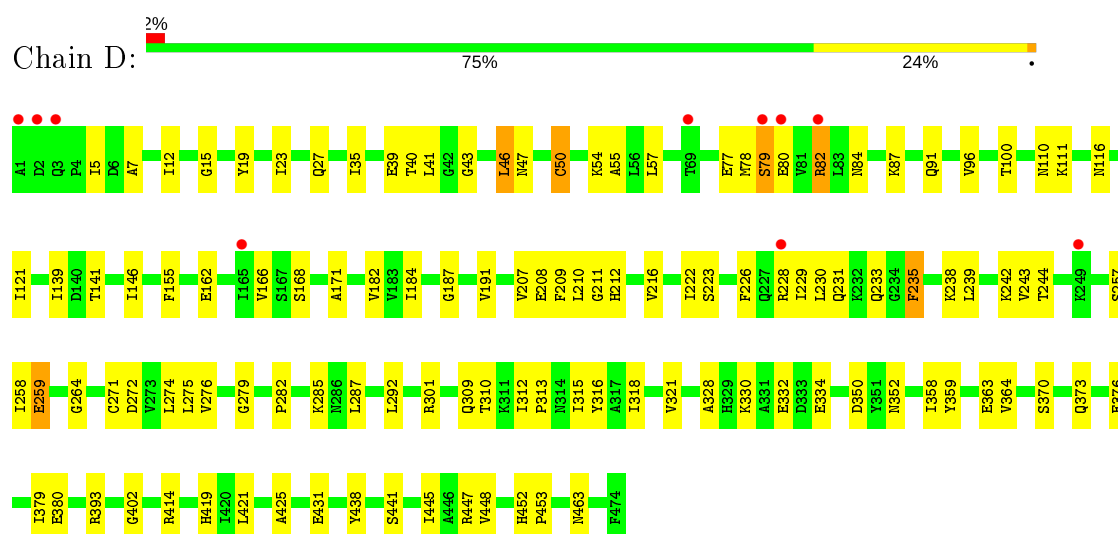


- Molecule 1: Dihydrolipoyl dehydrogenase, mitochondrial

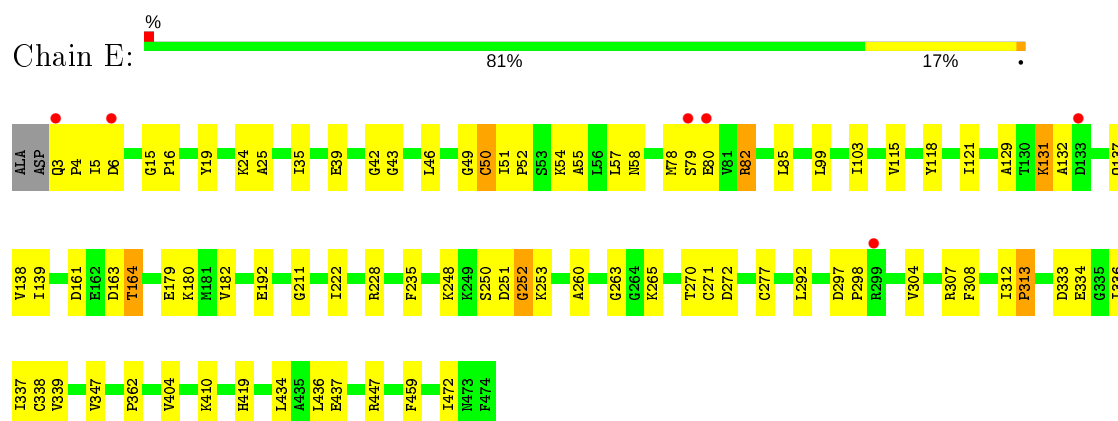




- Molecule 1: Dihydrolipoyl dehydrogenase, mitochondrial

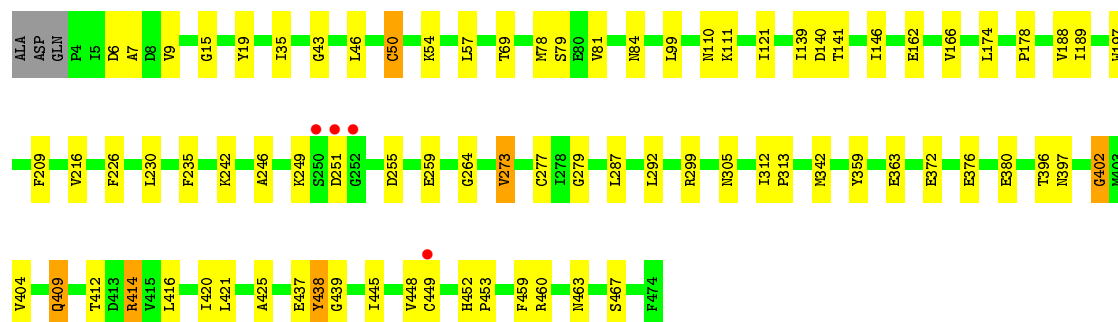


- Molecule 1: Dihydrolipoyl dehydrogenase, mitochondrial

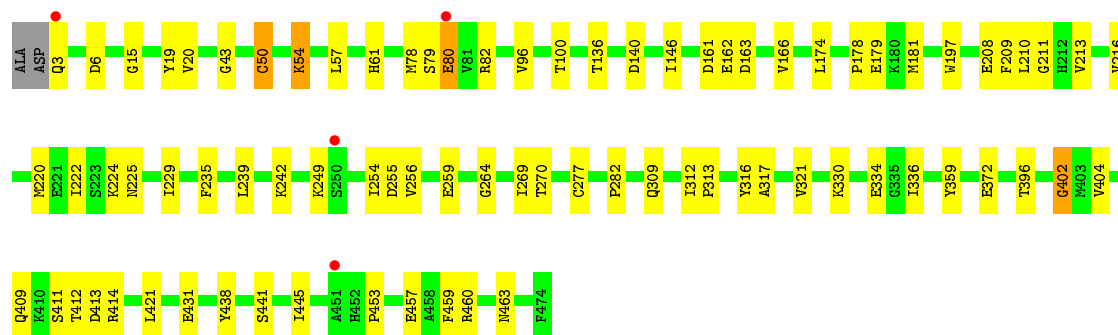
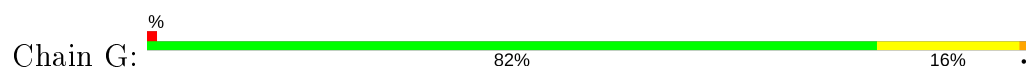


- Molecule 1: Dihydrolipoyl dehydrogenase, mitochondrial

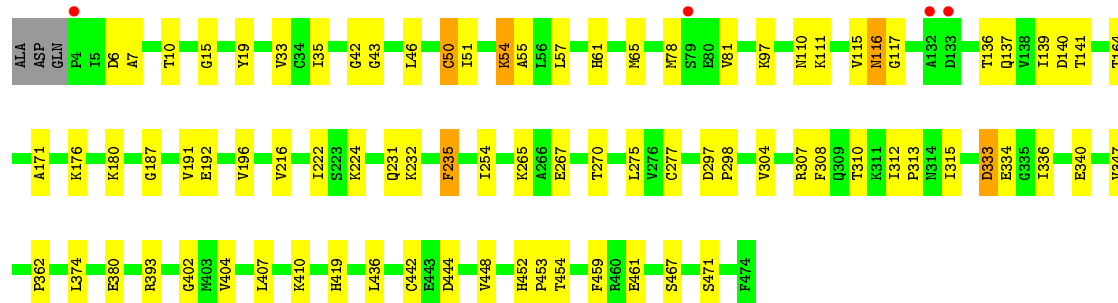
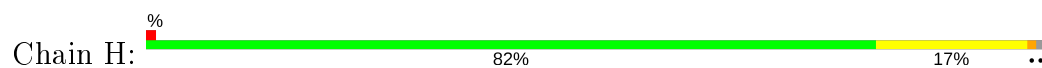




- Molecule 1: Dihydrolipoyl dehydrogenase, mitochondrial



- Molecule 1: Dihydrolipoyl dehydrogenase, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	176.12Å 210.76Å 126.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.09 – 2.53 43.09 – 2.53	Depositor EDS
% Data completeness (in resolution range)	99.2 (43.09-2.53) 99.4 (43.09-2.53)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.91 (at 2.54Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.211 , 0.267 0.203 , (Not available)	Depositor DCC
R_{free} test set	942 reflections (0.60%)	wwPDB-VP
Wilson B-factor (Å ²)	34.6	Xtriage
Anisotropy	0.404	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 41.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	30312	wwPDB-VP
Average B, all atoms (Å ²)	37.0	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 53.36 % 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 4.2598e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: SO4, NAD, FAD

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	0.51	0/3571	0.76	3/4824 (0.1%)
1	B	0.52	0/3551	0.75	1/4796 (0.0%)
1	C	0.51	0/3551	0.73	2/4796 (0.0%)
1	D	0.50	0/3584	0.75	1/4842 (0.0%)
1	E	0.53	0/3560	0.76	2/4809 (0.0%)
1	F	0.57	0/3562	0.79	3/4811 (0.1%)
1	G	0.57	0/3571	0.78	1/4824 (0.0%)
1	H	0.57	1/3551 (0.0%)	0.76	2/4796 (0.0%)
All	All	0.54	1/28501 (0.0%)	0.76	15/38498 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	176	LYS	CD-CE	5.25	1.64	1.51

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	50	CYS	CA-CB-SG	7.18	126.92	114.00
1	C	50	CYS	CA-CB-SG	6.52	125.74	114.00
1	A	264	GLY	N-CA-C	6.15	128.48	113.10
1	A	50	CYS	CA-CB-SG	6.01	124.83	114.00
1	E	50	CYS	CA-CB-SG	5.92	124.65	114.00

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	3515	0	3562	68	0
1	B	3496	0	3549	60	0
1	C	3496	0	3549	61	0
1	D	3528	0	3574	73	0
1	E	3505	0	3556	56	0
1	F	3506	0	3555	64	0
1	G	3515	0	3562	49	0
1	H	3496	0	3549	53	0
2	A	20	0	0	3	0
2	B	20	0	0	3	0
2	C	20	0	0	1	0
2	D	25	0	0	4	0
2	E	25	0	0	1	0
2	F	20	0	0	1	0
2	G	25	0	0	1	0
2	H	25	0	0	0	0
3	A	53	0	31	2	0
3	B	53	0	31	4	0
3	C	53	0	31	3	0
3	D	53	0	31	3	0
3	E	53	0	31	3	0
3	F	53	0	31	2	0
3	G	53	0	31	3	0
3	H	53	0	31	2	0
4	A	44	0	26	0	0
4	B	27	0	12	0	0
4	C	27	0	12	0	0
4	D	44	0	26	2	0
4	E	27	0	12	0	0
4	F	27	0	12	2	0
4	G	27	0	12	0	0
4	H	27	0	12	1	0
5	A	158	0	0	3	0
5	B	137	0	0	1	0
5	C	138	0	0	1	0
5	D	144	0	0	2	0
5	E	175	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	F	229	0	0	2	0
5	G	247	0	0	4	0
5	H	173	0	0	2	1
All	All	30312	0	28828	449	1

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 8.

The worst 5 of 449 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:C:437:GLU:HG3	1:D:448:VAL:HG22	1.37	1.05
1:B:228:ARG:HG2	1:B:228:ARG:HH11	1.27	0.98
1:C:78:MET:HG2	1:D:78:MET:HG2	1.53	0.88
1:B:228:ARG:HG2	1:B:228:ARG:NH1	1.94	0.79
1:E:297:ASP:HB2	1:E:298:PRO:HD2	1.65	0.79

All (1) 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)
5:H:2166:HOH:O	5:H:2166:HOH:O[2_675]	2.00	0.20

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	471/474 (99%)	447 (95%)	21 (4%)	3 (1%)	25	41
1	B	469/474 (99%)	444 (95%)	23 (5%)	2 (0%)	34	53
1	C	469/474 (99%)	441 (94%)	26 (6%)	2 (0%)	34	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	473/474 (100%)	448 (95%)	24 (5%)	1 (0%)	47	67
1	E	470/474 (99%)	448 (95%)	19 (4%)	3 (1%)	25	41
1	F	470/474 (99%)	453 (96%)	17 (4%)	0	100	100
1	G	471/474 (99%)	451 (96%)	19 (4%)	1 (0%)	47	67
1	H	469/474 (99%)	448 (96%)	21 (4%)	0	100	100
All	All	3762/3792 (99%)	3580 (95%)	170 (4%)	12 (0%)	41	59

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	79	SER
1	G	79	SER
1	A	266	ALA
1	E	131	LYS
1	B	131	LYS

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	373/373 (100%)	354 (95%)	19 (5%)	24	43
1	B	371/373 (100%)	359 (97%)	12 (3%)	39	63
1	C	371/373 (100%)	361 (97%)	10 (3%)	44	69
1	D	374/373 (100%)	357 (96%)	17 (4%)	27	48
1	E	372/373 (100%)	358 (96%)	14 (4%)	33	56
1	F	372/373 (100%)	361 (97%)	11 (3%)	41	66
1	G	373/373 (100%)	362 (97%)	11 (3%)	42	67
1	H	371/373 (100%)	361 (97%)	10 (3%)	44	69
All	All	2977/2984 (100%)	2873 (96%)	104 (4%)	36	60

5 of 104 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	82	ARG
1	E	6	ASP
1	H	54	LYS
1	D	116	ASN
1	D	285	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	125	ASN
1	E	137	GLN
1	H	114	HIS
1	E	58	ASN
1	G	361	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

52 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	SO4	G	2027	-	4,4,4	0.62	0	6,6,6	0.06	0
2	SO4	G	2028	-	4,4,4	0.63	0	6,6,6	0.06	0
3	FAD	C	480	-	51,58,58	2.03	10 (19%)	60,89,89	2.19	9 (15%)
3	FAD	B	480	-	51,58,58	1.86	11 (21%)	60,89,89	2.16	10 (16%)
2	SO4	A	2002	-	4,4,4	0.62	0	6,6,6	0.05	0
2	SO4	H	2031	-	4,4,4	0.62	0	6,6,6	0.04	0
2	SO4	D	2015	-	4,4,4	0.62	0	6,6,6	0.06	0
2	SO4	F	2024	-	4,4,4	0.62	0	6,6,6	0.05	0
2	SO4	A	2003	-	4,4,4	0.63	0	6,6,6	0.09	0
2	SO4	G	2026	-	4,4,4	0.62	0	6,6,6	0.07	0
4	NAD	D	481	-	42,48,48	1.14	4 (9%)	50,73,73	1.25	4 (8%)
4	NAD	C	481	-	24,29,48	1.23	3 (12%)	29,45,73	1.57	4 (13%)
2	SO4	A	2000	-	4,4,4	0.63	0	6,6,6	0.06	0
2	SO4	D	2013	-	4,4,4	0.61	0	6,6,6	0.08	0
2	SO4	C	2011	-	4,4,4	0.62	0	6,6,6	0.08	0
2	SO4	G	2029	-	4,4,4	0.62	0	6,6,6	0.06	0
2	SO4	H	2034	-	4,4,4	0.62	0	6,6,6	0.06	0
2	SO4	E	2019	-	4,4,4	0.62	0	6,6,6	0.07	0
3	FAD	F	480	-	51,58,58	1.81	10 (19%)	60,89,89	2.05	11 (18%)
3	FAD	H	480	-	51,58,58	1.61	9 (17%)	60,89,89	2.12	11 (18%)
2	SO4	B	2006	-	4,4,4	0.63	0	6,6,6	0.06	0
2	SO4	E	2018	-	4,4,4	0.63	0	6,6,6	0.05	0
4	NAD	B	481	-	24,29,48	1.13	1 (4%)	29,45,73	1.53	4 (13%)
4	NAD	A	481	-	42,48,48	1.13	4 (9%)	50,73,73	1.31	4 (8%)
2	SO4	D	2012	-	4,4,4	0.62	0	6,6,6	0.06	0
2	SO4	F	2022	-	4,4,4	0.62	0	6,6,6	0.07	0
2	SO4	F	2025	-	4,4,4	0.62	0	6,6,6	0.04	0
3	FAD	A	480	-	51,58,58	1.63	8 (15%)	60,89,89	2.09	9 (15%)
2	SO4	H	2032	-	4,4,4	0.62	0	6,6,6	0.06	0
3	FAD	E	480	-	51,58,58	1.71	9 (17%)	60,89,89	2.07	8 (13%)
3	FAD	D	480	-	51,58,58	1.76	12 (23%)	60,89,89	2.05	9 (15%)
2	SO4	B	2005	-	4,4,4	0.63	0	6,6,6	0.06	0
2	SO4	E	2017	-	4,4,4	0.62	0	6,6,6	0.06	0
2	SO4	F	2023	-	4,4,4	0.63	0	6,6,6	0.06	0
2	SO4	H	2035	-	4,4,4	0.63	0	6,6,6	0.06	0
2	SO4	B	2004	-	4,4,4	0.61	0	6,6,6	0.07	0
4	NAD	F	481	-	24,29,48	1.22	3 (12%)	29,45,73	1.46	4 (13%)
2	SO4	C	2009	-	4,4,4	0.62	0	6,6,6	0.06	0
2	SO4	B	2007	-	4,4,4	0.63	0	6,6,6	0.11	0
2	SO4	G	2030	-	4,4,4	0.63	0	6,6,6	0.08	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	D	2014	-	4,4,4	0.62	0	6,6,6	0.06	0
2	SO4	E	2020	-	4,4,4	0.63	0	6,6,6	0.06	0
4	NAD	G	481	-	24,29,48	1.15	2 (8%)	29,45,73	1.52	4 (13%)
2	SO4	H	2033	-	4,4,4	0.62	0	6,6,6	0.07	0
2	SO4	C	2008	-	4,4,4	0.62	0	6,6,6	0.04	0
2	SO4	C	2010	-	4,4,4	0.62	0	6,6,6	0.07	0
2	SO4	E	2021	-	4,4,4	0.63	0	6,6,6	0.10	0
2	SO4	D	2016	-	4,4,4	0.64	0	6,6,6	0.09	0
4	NAD	E	481	-	24,29,48	1.14	2 (8%)	29,45,73	1.62	4 (13%)
4	NAD	H	481	-	24,29,48	1.14	2 (8%)	29,45,73	1.58	4 (13%)
3	FAD	G	480	-	51,58,58	1.76	11 (21%)	60,89,89	2.06	8 (13%)
2	SO4	A	2001	-	4,4,4	0.63	0	6,6,6	0.05	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
3	FAD	A	480	-	-	4/30/50/50	0/6/6/6
3	FAD	C	480	-	-	3/30/50/50	0/6/6/6
3	FAD	E	480	-	-	3/30/50/50	0/6/6/6
3	FAD	B	480	-	-	4/30/50/50	0/6/6/6
3	FAD	G	480	-	-	4/30/50/50	0/6/6/6
3	FAD	D	480	-	-	4/30/50/50	0/6/6/6
3	FAD	F	480	-	-	4/30/50/50	0/6/6/6
3	FAD	H	480	-	-	4/30/50/50	0/6/6/6
4	NAD	B	481	-	-	1/12/32/62	0/3/3/5
4	NAD	A	481	-	-	4/26/62/62	0/5/5/5
4	NAD	D	481	-	-	5/26/62/62	0/5/5/5
4	NAD	C	481	-	-	4/12/32/62	0/3/3/5
4	NAD	F	481	-	-	5/12/32/62	0/3/3/5
4	NAD	E	481	-	-	3/12/32/62	0/3/3/5
4	NAD	H	481	-	-	1/12/32/62	0/3/3/5
4	NAD	G	481	-	-	1/12/32/62	0/3/3/5

The worst 5 of 101 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	480	FAD	C10-N1	5.72	1.40	1.33
3	D	480	FAD	C4X-C10	5.63	1.44	1.38
3	C	480	FAD	C4X-C10	5.63	1.44	1.38
3	F	480	FAD	C4X-C10	5.46	1.44	1.38
3	B	480	FAD	C4X-N5	5.37	1.41	1.33

The worst 5 of 107 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	480	FAD	C4-N3-C2	11.95	125.23	115.14
3	B	480	FAD	C4-N3-C2	11.70	125.02	115.14
3	A	480	FAD	C4-N3-C2	11.37	124.74	115.14
3	E	480	FAD	C4-N3-C2	11.01	124.44	115.14
3	H	480	FAD	C4-N3-C2	10.94	124.38	115.14

There are no chirality outliers.

5 of 54 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	481	NAD	C5B-O5B-PA-O1A
4	A	481	NAD	C5B-O5B-PA-O1A
4	F	481	NAD	C5B-O5B-PA-O1A
4	E	481	NAD	C5B-O5B-PA-O3
3	C	480	FAD	O4B-C4B-C5B-O5B

There are no ring outliers.

20 monomers are involved in 41 short contacts:

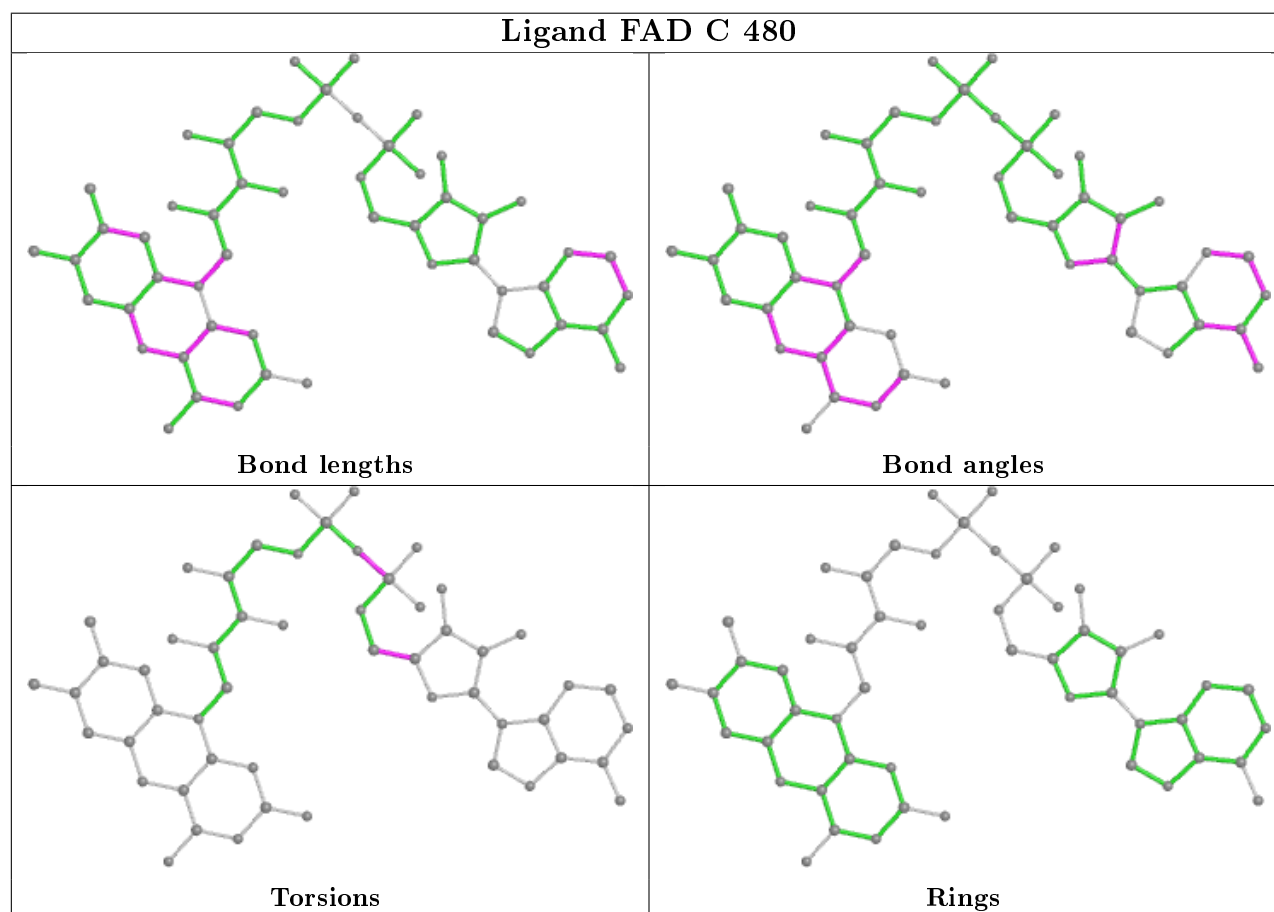
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	480	FAD	3	0
3	B	480	FAD	4	0
2	F	2024	SO4	1	0
2	A	2003	SO4	3	0
4	D	481	NAD	2	0
3	F	480	FAD	2	0
3	H	480	FAD	2	0
3	A	480	FAD	2	0
3	E	480	FAD	3	0
3	D	480	FAD	3	0
2	B	2004	SO4	1	0
4	F	481	NAD	2	0
2	C	2009	SO4	1	0

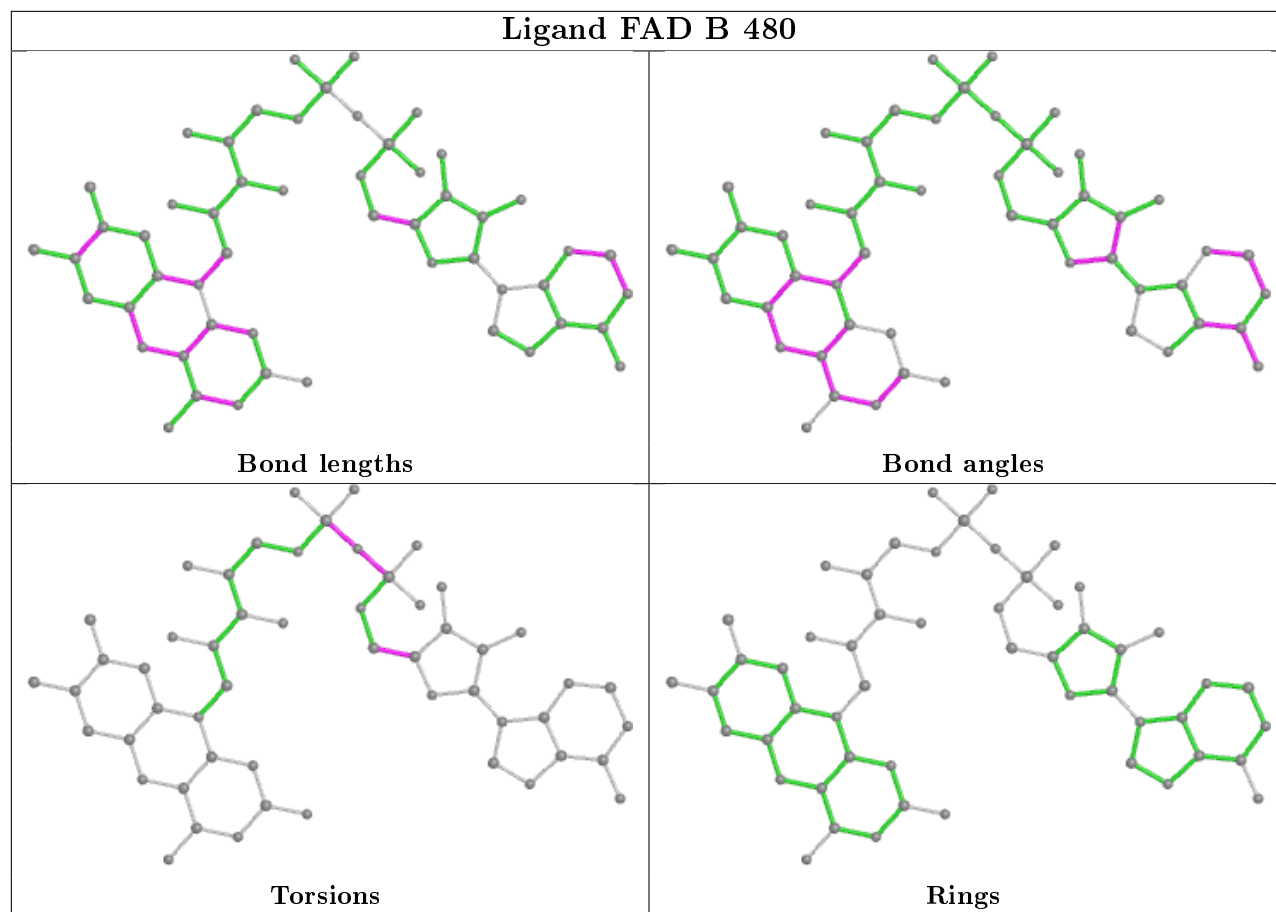
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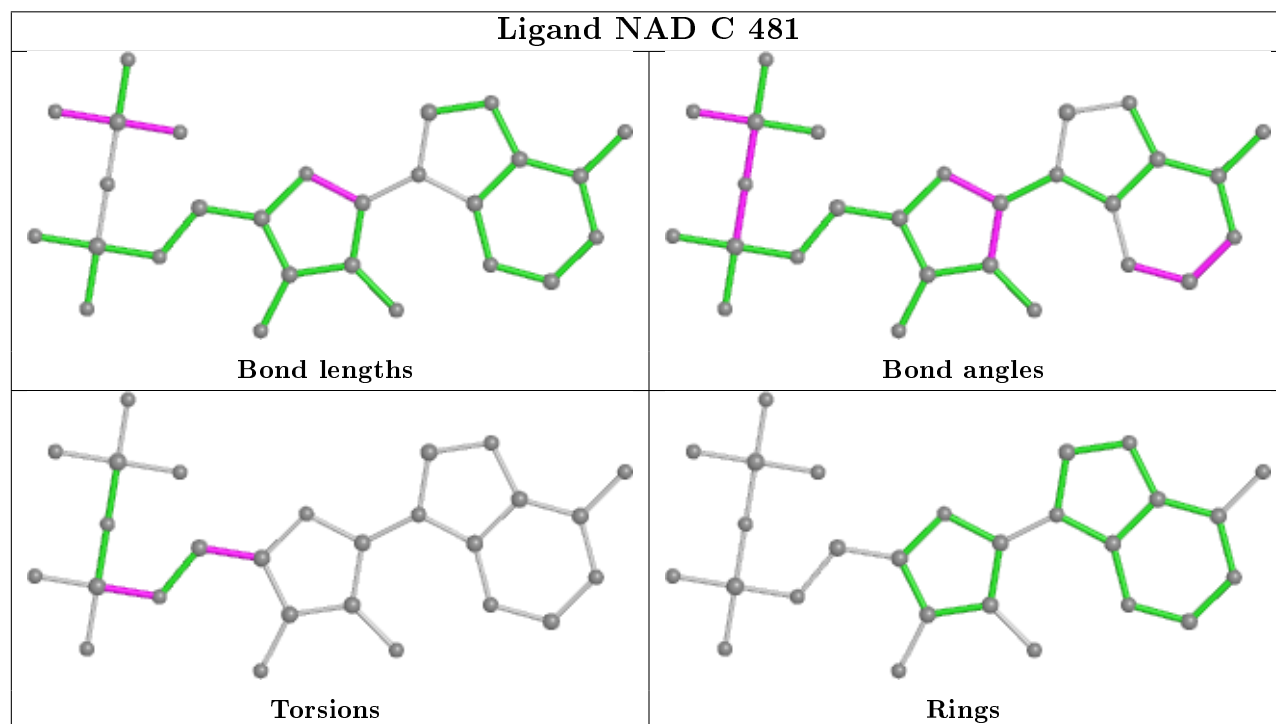
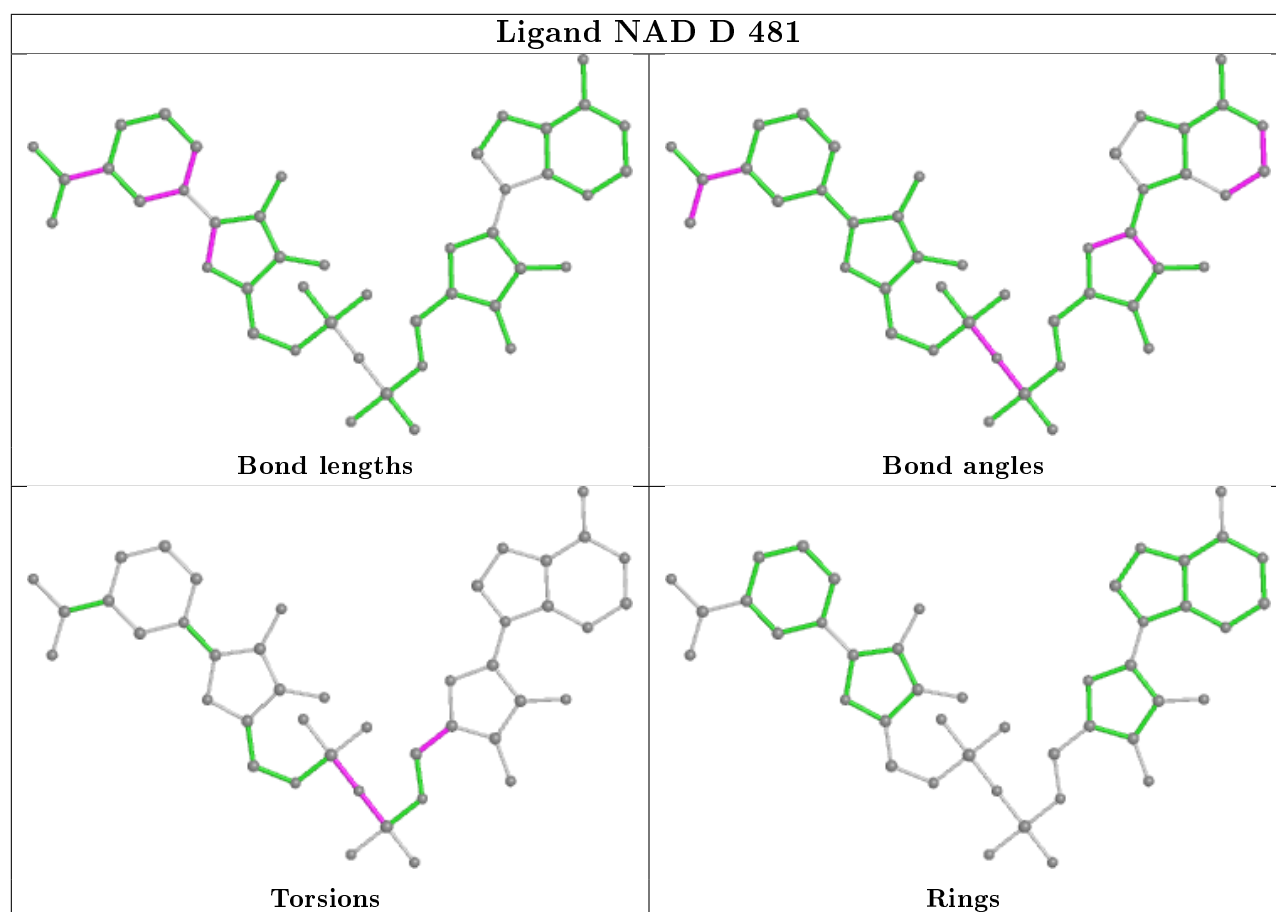
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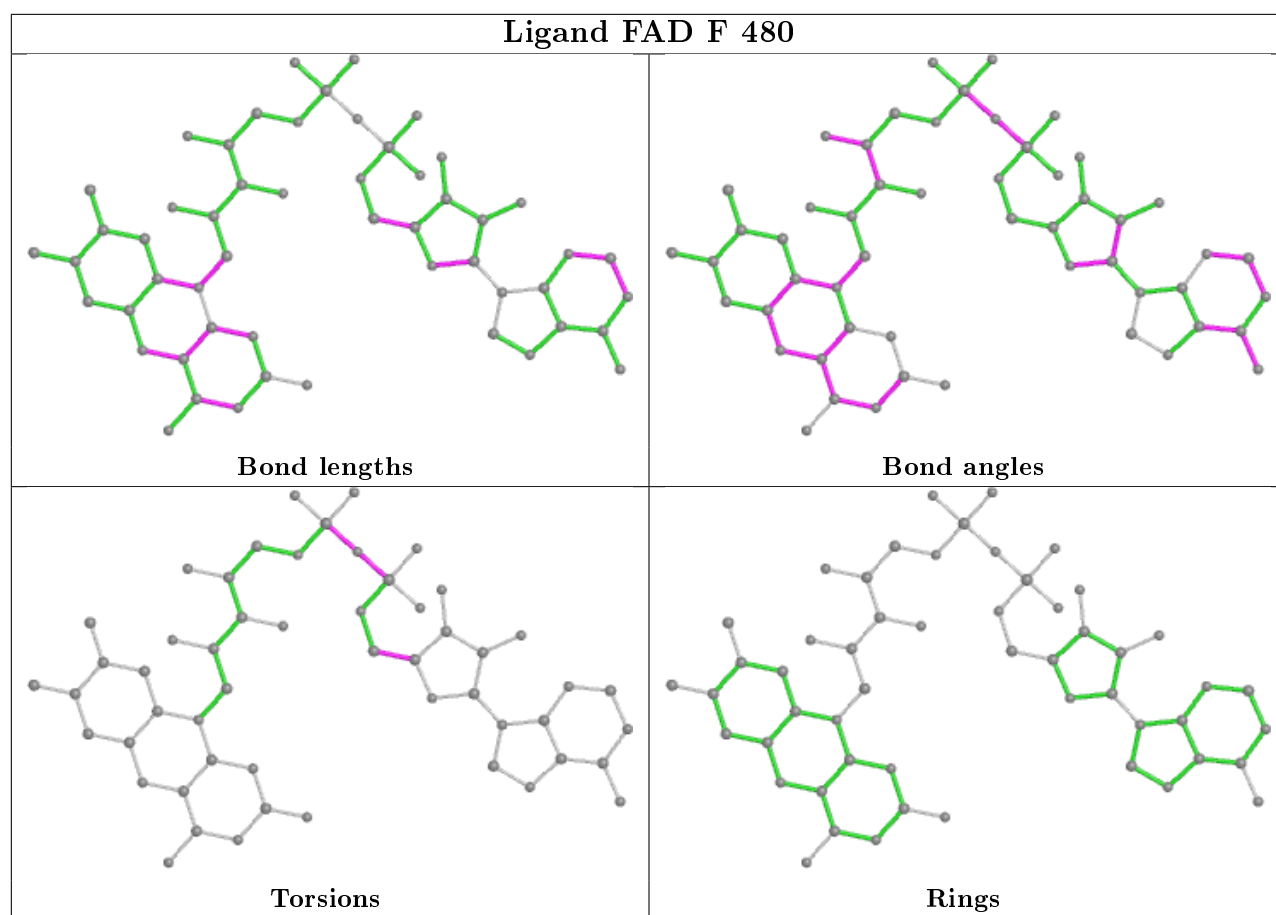
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2007	SO4	2	0
2	G	2030	SO4	1	0
2	D	2014	SO4	2	0
2	E	2021	SO4	1	0
2	D	2016	SO4	2	0
4	H	481	NAD	1	0
3	G	480	FAD	3	0

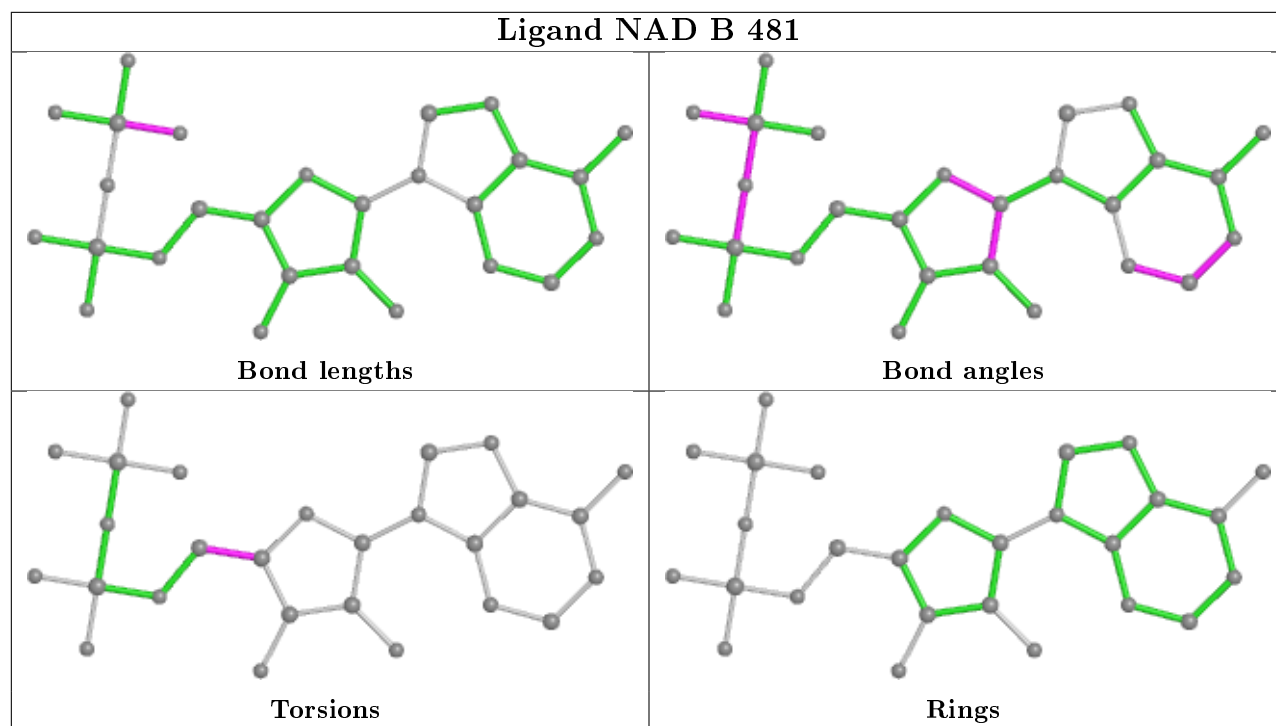
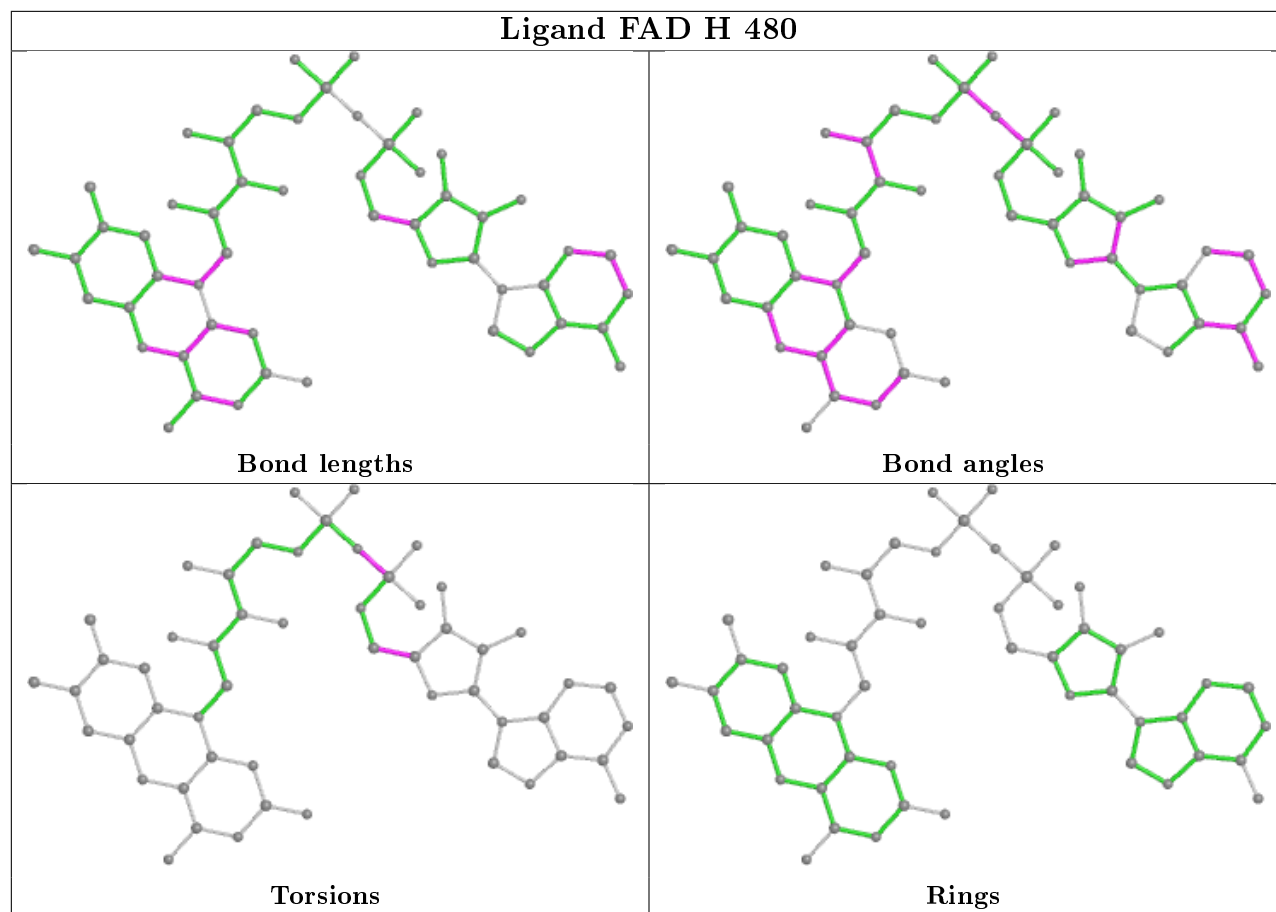
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

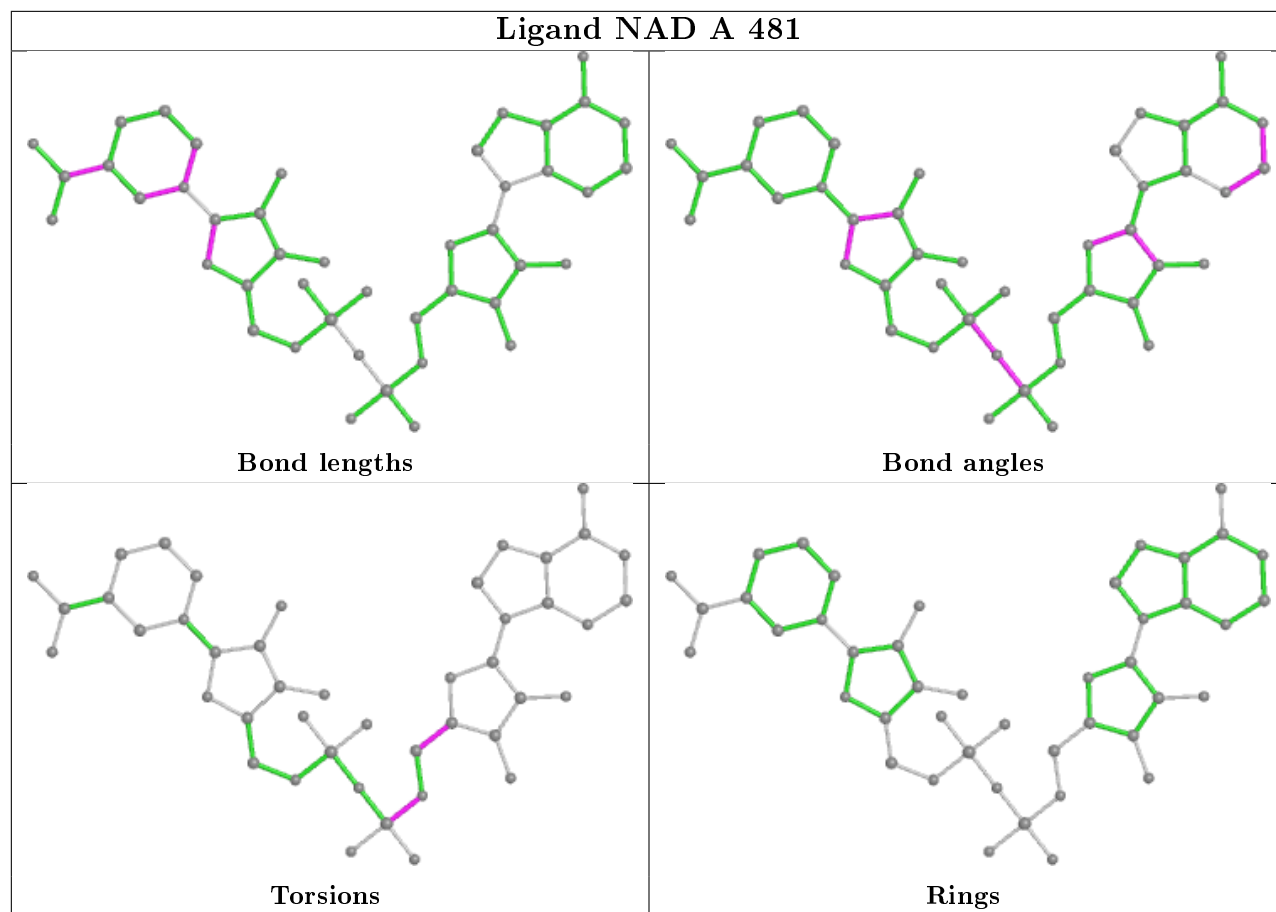


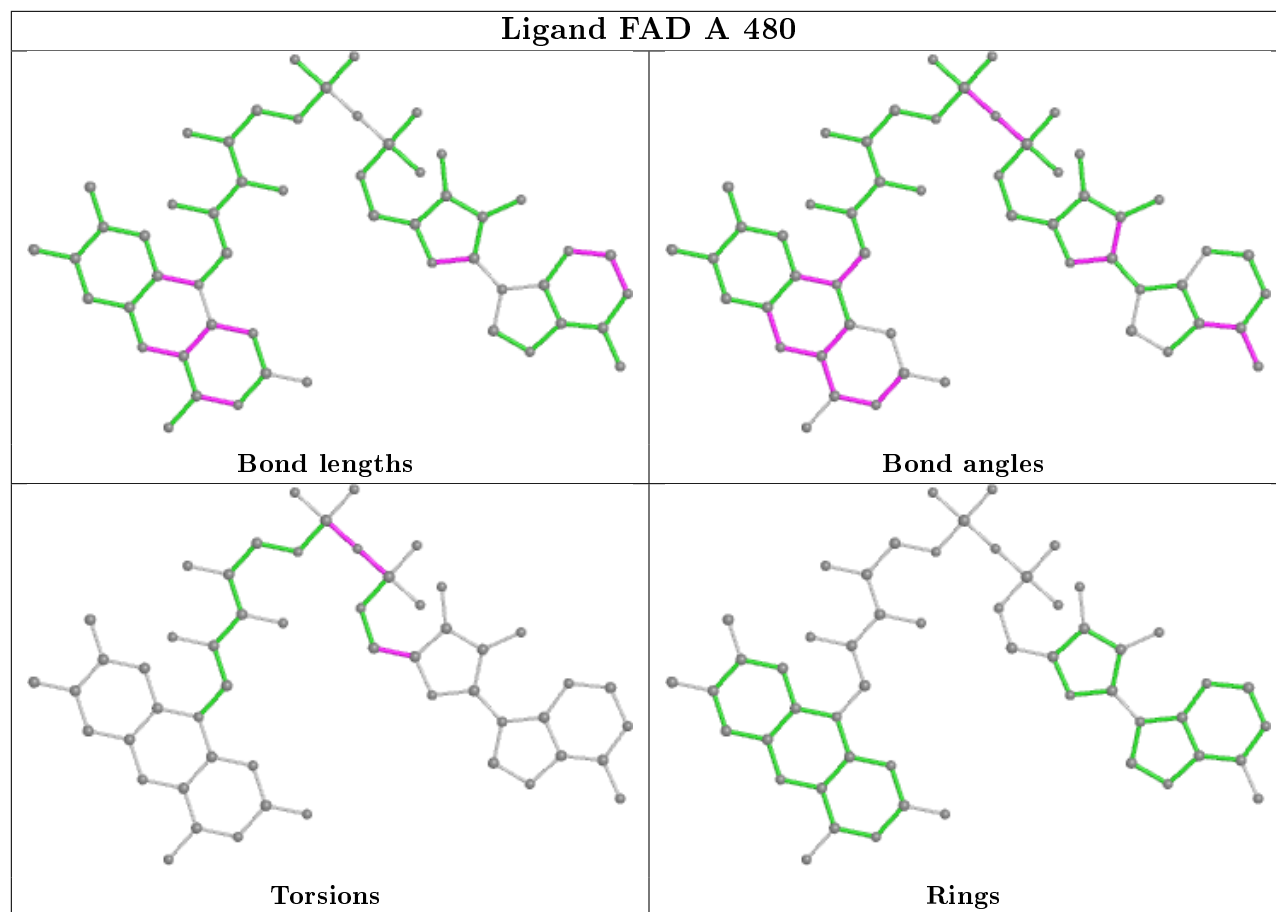


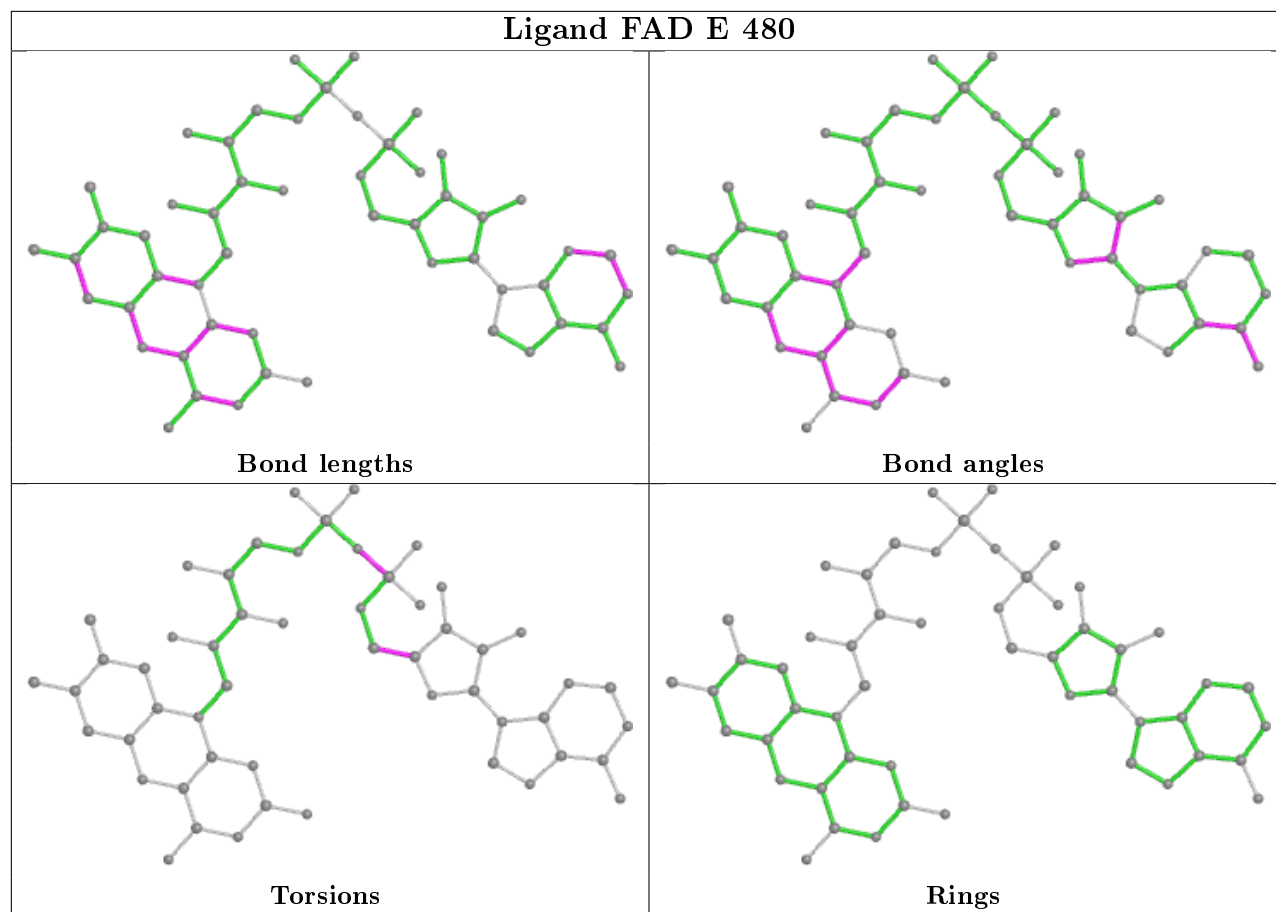


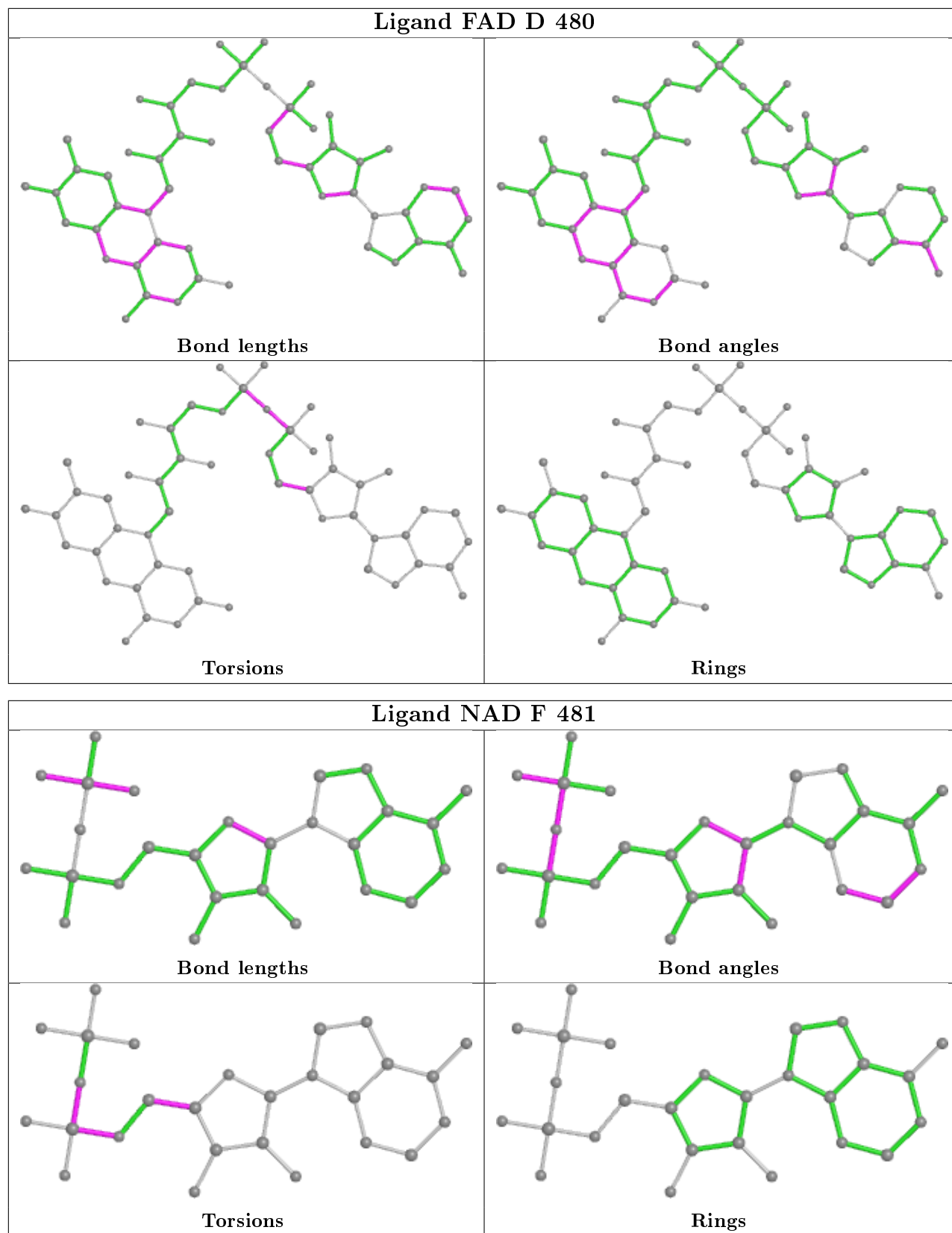


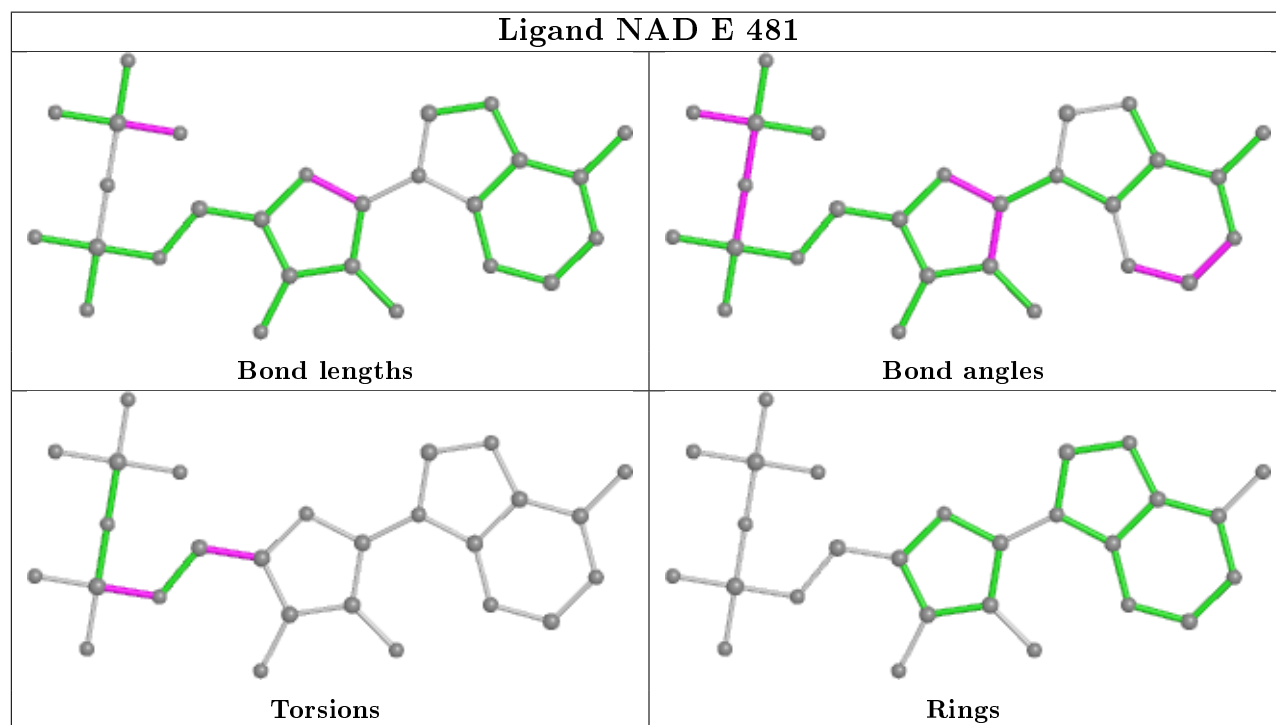
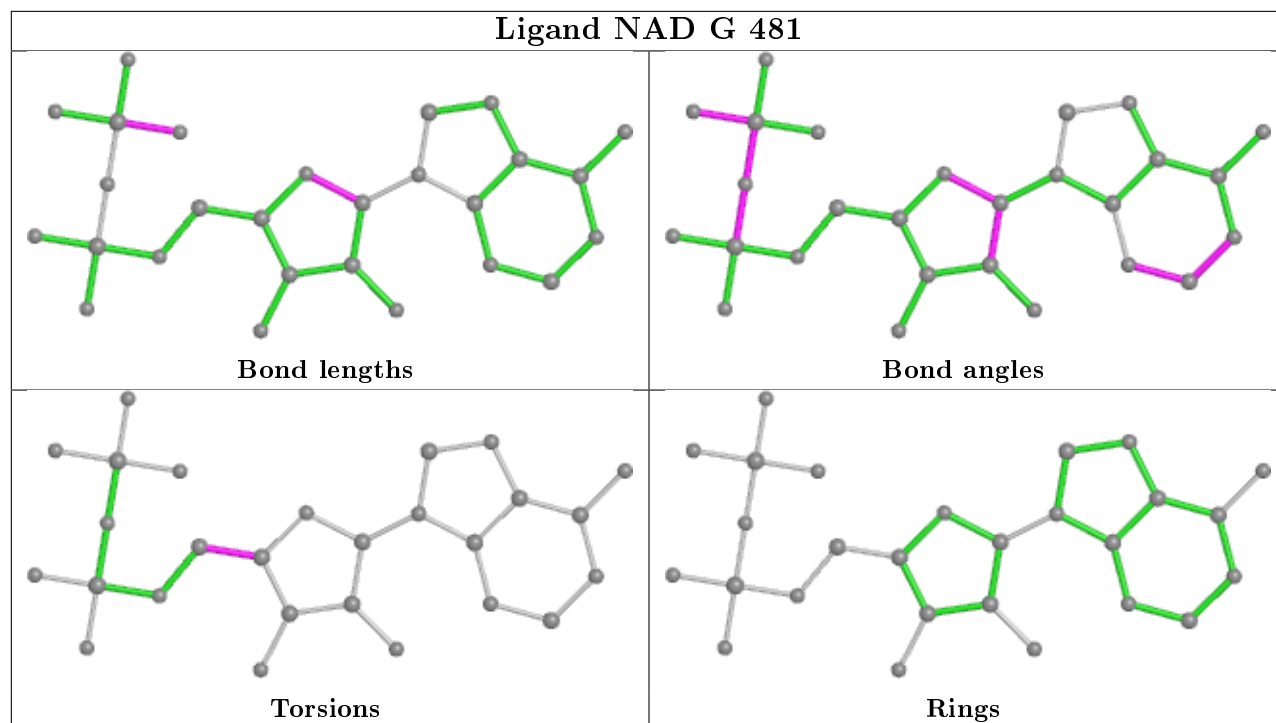


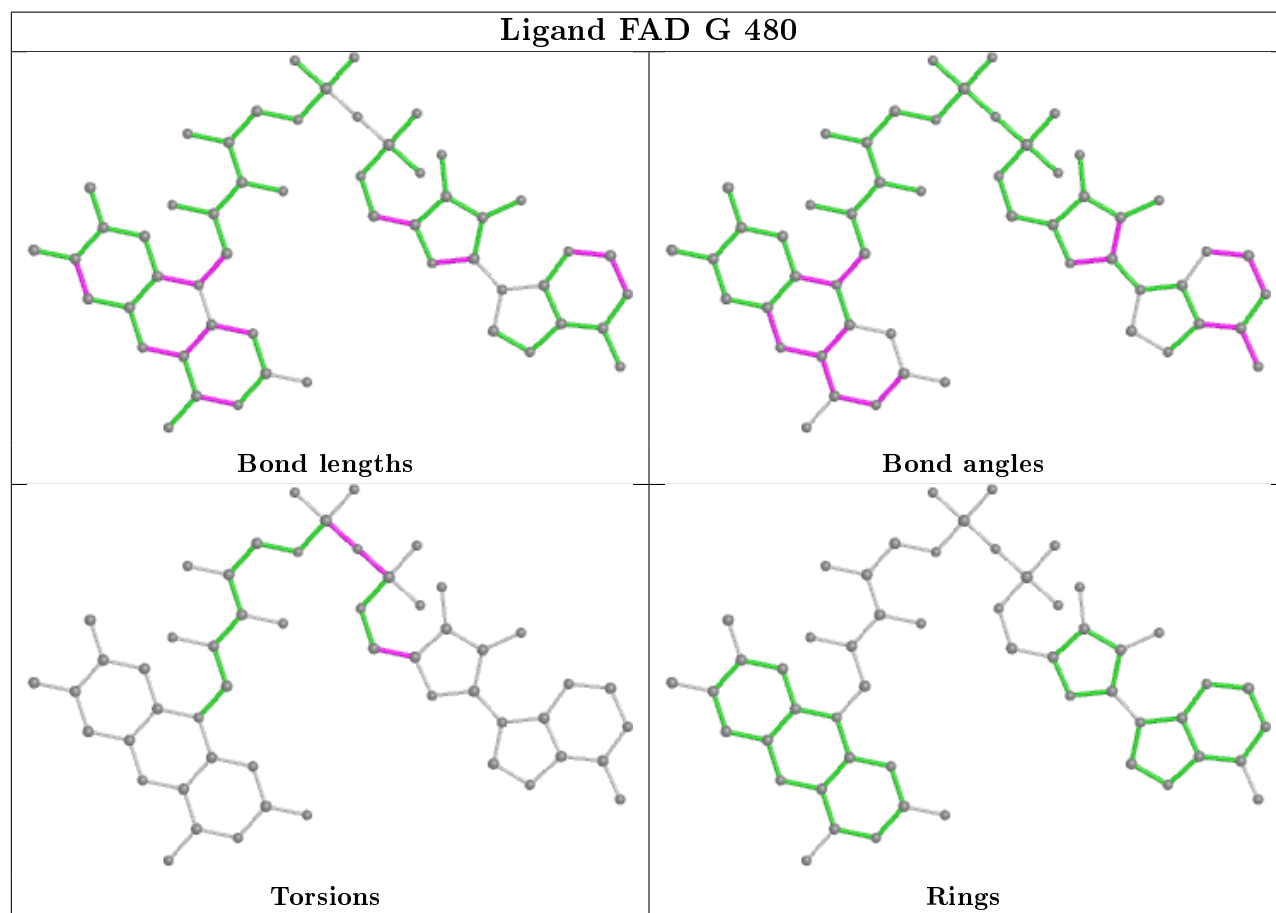
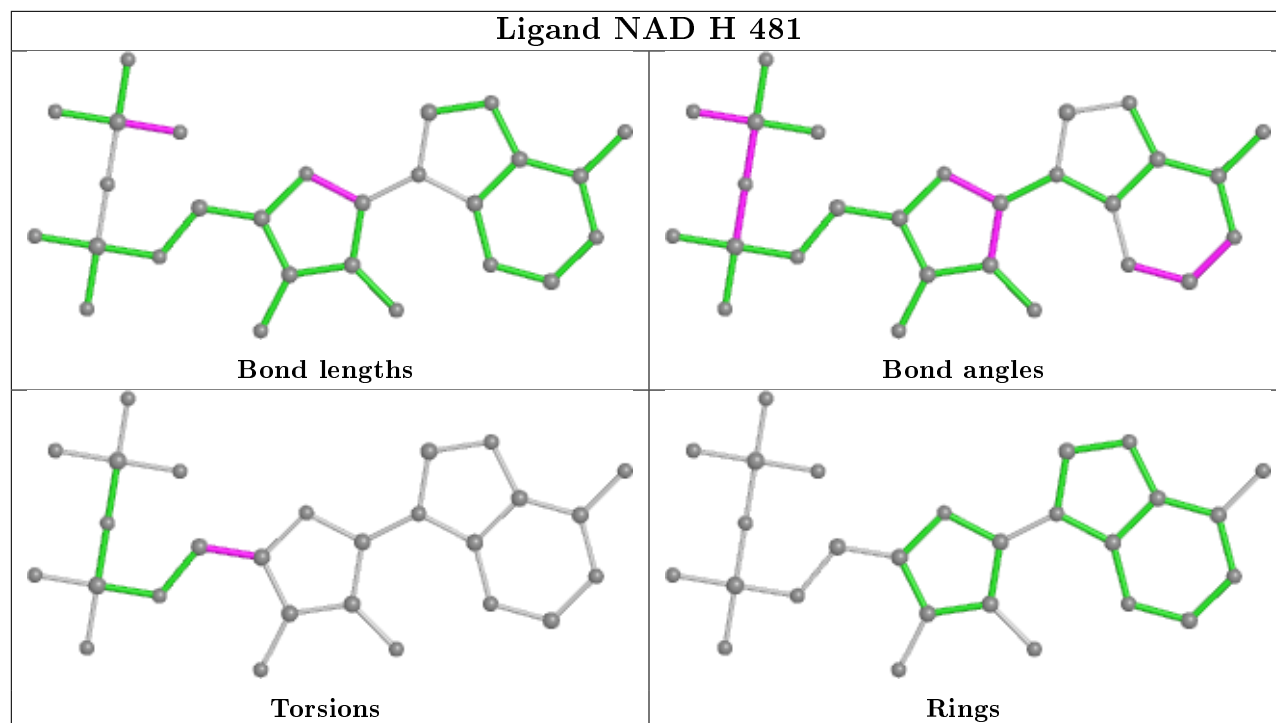












5.7 Other polymers [i](#)

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	472/474 (99%)	-0.03	8 (1%) 70 73	22, 37, 60, 82	0
1	B	471/474 (99%)	0.01	10 (2%) 63 67	18, 40, 70, 84	0
1	C	471/474 (99%)	0.03	10 (2%) 63 67	18, 41, 69, 83	1 (0%)
1	D	474/474 (100%)	0.03	10 (2%) 63 67	22, 37, 61, 84	0
1	E	472/474 (99%)	-0.02	6 (1%) 77 79	17, 35, 64, 85	0
1	F	471/474 (99%)	-0.18	4 (0%) 86 88	17, 29, 47, 68	1 (0%)
1	G	472/474 (99%)	-0.18	4 (0%) 86 88	18, 29, 46, 64	0
1	H	471/474 (99%)	-0.10	4 (0%) 86 88	15, 34, 56, 69	0
All	All	3774/3792 (99%)	-0.05	56 (1%) 73 76	15, 35, 62, 85	2 (0%)

The worst 5 of 56 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	1	ALA	6.7
1	D	3	GLN	5.7
1	G	250	SER	4.9
1	F	250	SER	4.2
1	D	249	LYS	4.1

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 carbohydrates 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
2	SO4	F	2025	5/5	0.60	0.23	107,108,109,109	0
2	SO4	G	2029	5/5	0.72	0.27	119,119,119,120	0
2	SO4	A	2002	5/5	0.76	0.24	123,124,124,124	0
2	SO4	E	2018	5/5	0.78	0.30	120,120,120,120	0
2	SO4	D	2015	5/5	0.79	0.24	115,115,115,115	0
2	SO4	H	2032	5/5	0.81	0.23	120,120,121,121	0
2	SO4	G	2028	5/5	0.82	0.48	127,127,128,128	0
2	SO4	D	2014	5/5	0.82	0.74	148,148,148,148	0
4	NAD	A	481	44/44	0.86	0.20	52,64,86,88	0
2	SO4	B	2006	5/5	0.87	0.18	104,104,104,104	0
4	NAD	C	481	27/44	0.87	0.20	70,73,87,87	0
4	NAD	F	481	27/44	0.87	0.20	50,57,80,81	0
2	SO4	H	2034	5/5	0.87	0.16	80,80,81,81	0
2	SO4	F	2024	5/5	0.88	0.35	121,121,121,121	0
4	NAD	E	481	27/44	0.89	0.20	58,64,71,72	0
2	SO4	C	2009	5/5	0.89	0.17	91,91,91,91	0
4	NAD	H	481	27/44	0.89	0.20	51,55,69,69	0
4	NAD	B	481	27/44	0.90	0.20	63,66,81,82	0
2	SO4	G	2027	5/5	0.90	0.17	80,80,81,81	0
2	SO4	C	2010	5/5	0.90	0.17	103,103,103,103	0
2	SO4	D	2016	5/5	0.90	0.37	83,83,84,84	0
2	SO4	C	2011	5/5	0.90	0.24	82,83,83,84	0
2	SO4	D	2013	5/5	0.91	0.23	87,88,88,88	0
2	SO4	A	2001	5/5	0.91	0.24	82,83,83,83	0
2	SO4	B	2005	5/5	0.92	0.25	88,88,89,89	0
2	SO4	E	2020	5/5	0.93	0.15	90,90,91,91	0
4	NAD	G	481	27/44	0.93	0.15	31,37,63,64	0
2	SO4	A	2003	5/5	0.93	0.46	87,87,87,88	0
2	SO4	B	2007	5/5	0.93	0.30	78,78,79,79	0
2	SO4	F	2023	5/5	0.93	0.17	76,76,77,77	0
3	FAD	B	480	53/53	0.93	0.17	32,37,45,46	0
3	FAD	A	480	53/53	0.94	0.17	22,30,34,36	0
3	FAD	H	480	53/53	0.94	0.17	24,31,43,44	0
3	FAD	E	480	53/53	0.94	0.16	26,32,44,44	0
4	NAD	D	481	44/44	0.94	0.16	55,59,64,64	0
2	SO4	G	2030	5/5	0.94	0.29	79,79,80,80	0
3	FAD	C	480	53/53	0.94	0.15	27,37,51,52	0

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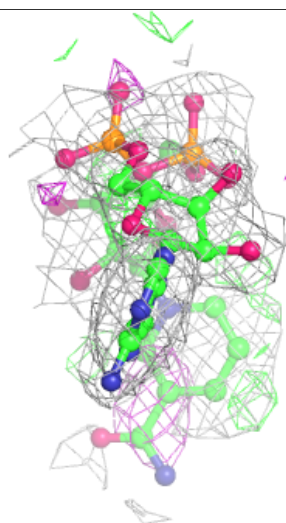
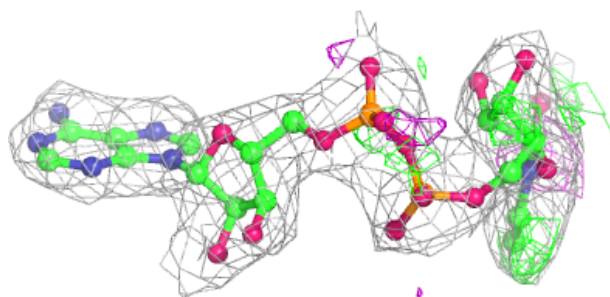
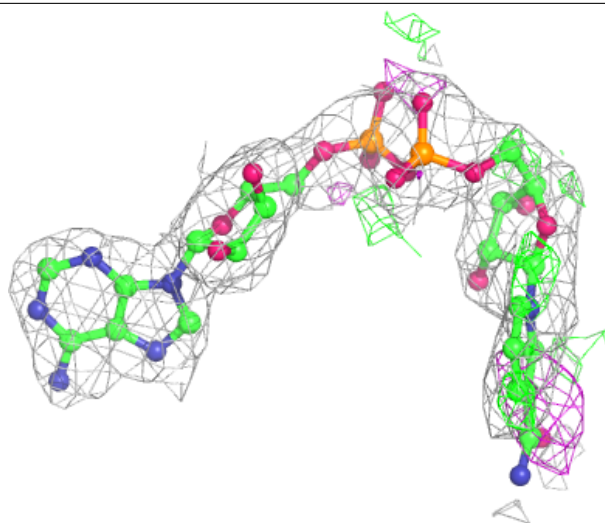
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SO4	E	2021	5/5	0.95	0.22	79,79,79,80	0
2	SO4	F	2022	5/5	0.95	0.19	62,62,64,66	0
2	SO4	H	2033	5/5	0.95	0.21	81,81,82,83	0
2	SO4	E	2019	5/5	0.95	0.17	78,79,80,80	0
2	SO4	G	2026	5/5	0.96	0.17	62,63,64,66	0
2	SO4	H	2035	5/5	0.96	0.31	78,78,78,78	0
3	FAD	D	480	53/53	0.96	0.15	21,29,33,35	0
3	FAD	G	480	53/53	0.96	0.16	18,23,28,31	0
2	SO4	D	2012	5/5	0.96	0.18	71,71,72,72	0
3	FAD	F	480	53/53	0.97	0.14	19,22,28,31	0
2	SO4	A	2000	5/5	0.97	0.14	67,68,69,69	0
2	SO4	E	2017	5/5	0.97	0.16	56,56,57,59	0
2	SO4	H	2031	5/5	0.97	0.15	57,58,59,60	0
2	SO4	B	2004	5/5	0.98	0.17	64,64,65,66	0
2	SO4	C	2008	5/5	0.99	0.20	64,65,66,66	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.

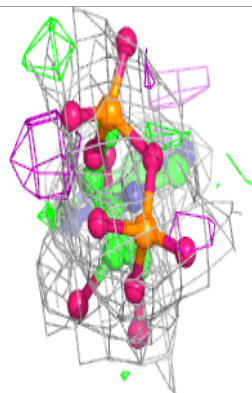
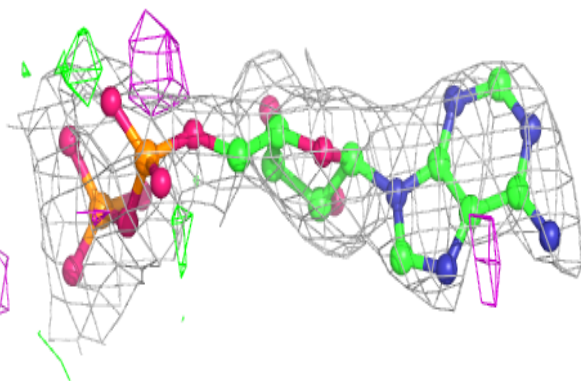
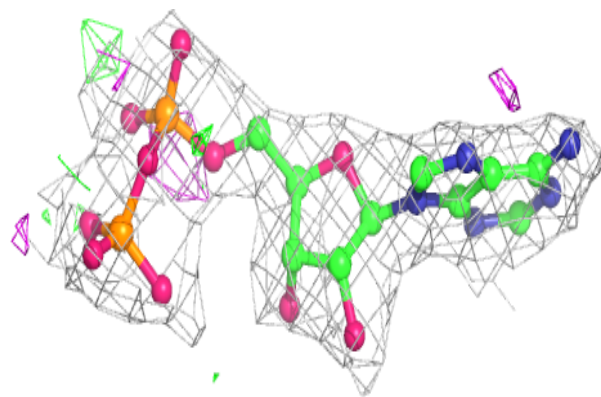
Electron density around NAD A 481:

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

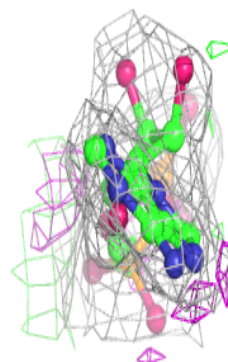
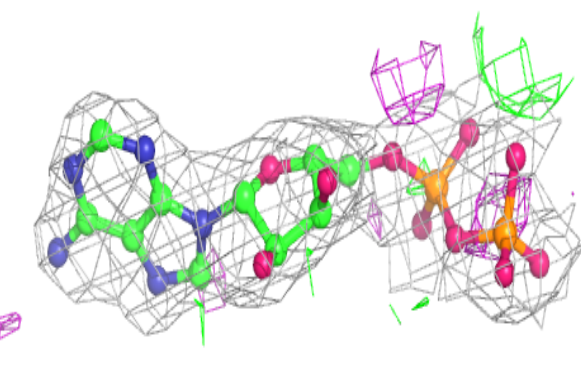
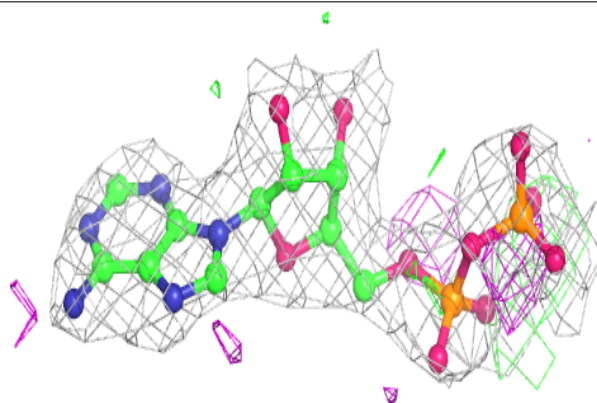


Electron density around NAD C 481:

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

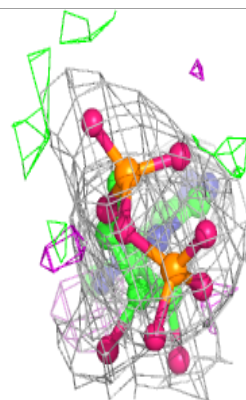
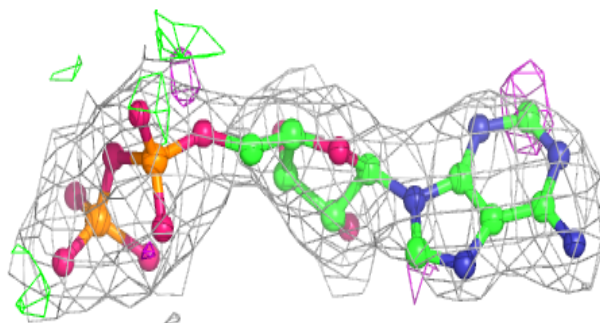
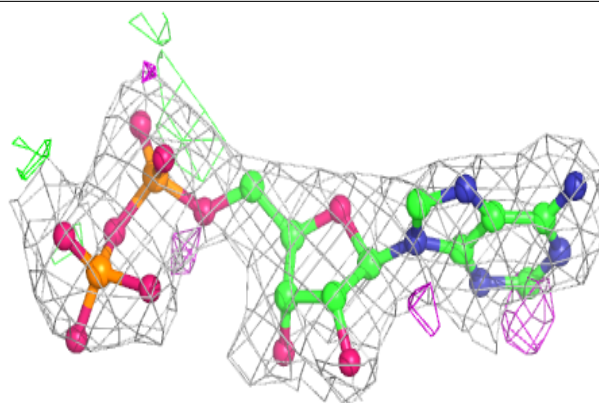
**Electron density around NAD F 481:**

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

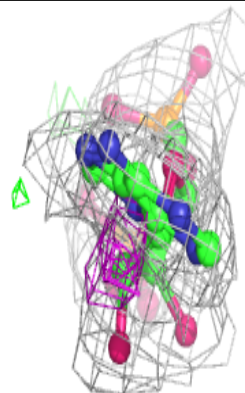
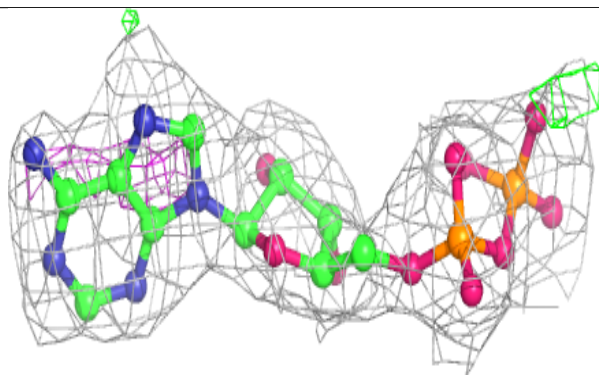
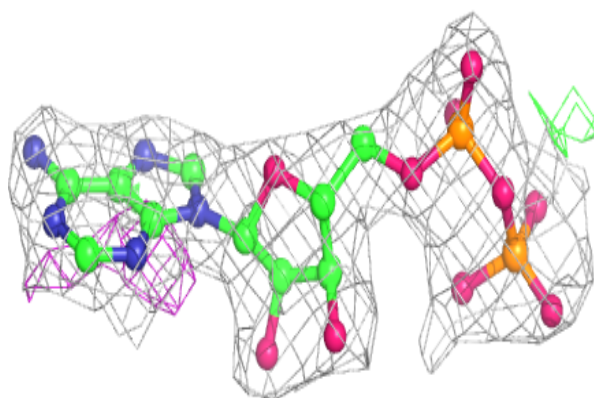


Electron density around NAD E 481:

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

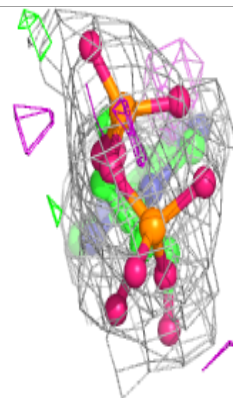
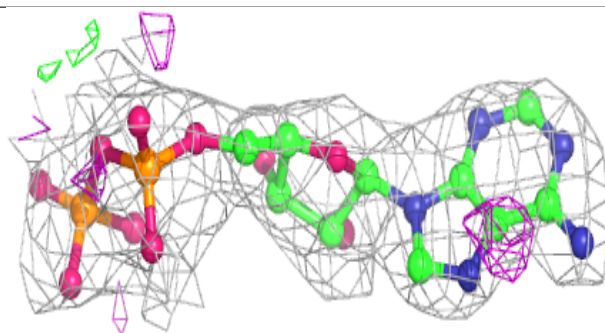
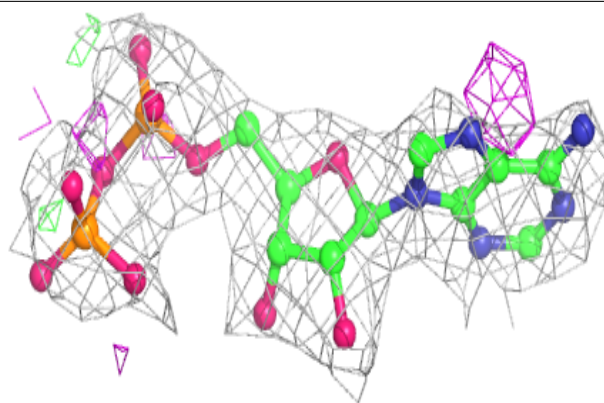
**Electron density around NAD H 481:**

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

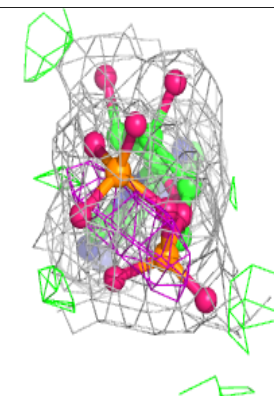
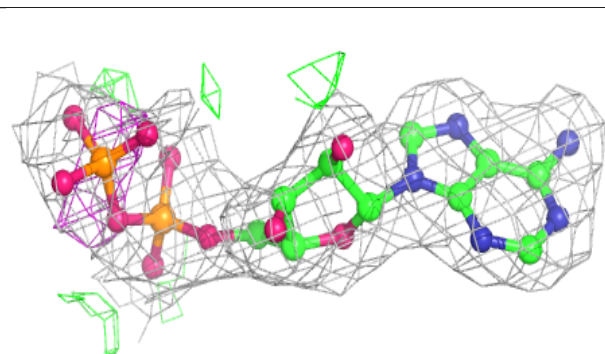
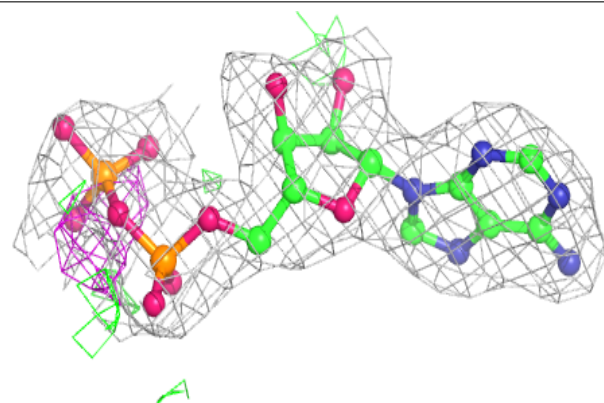


Electron density around NAD B 481:

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

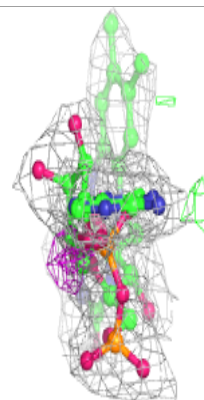
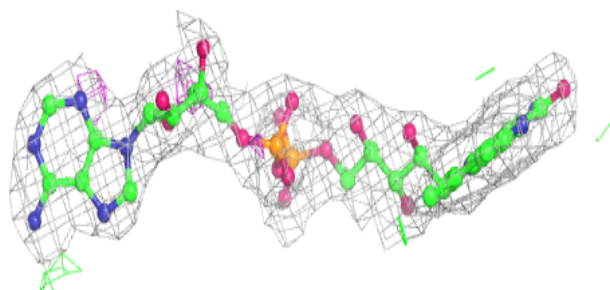
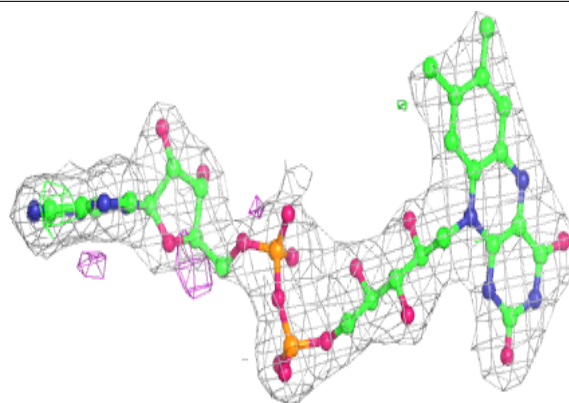
**Electron density around NAD G 481:**

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

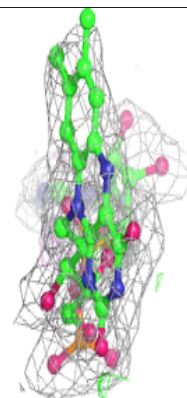
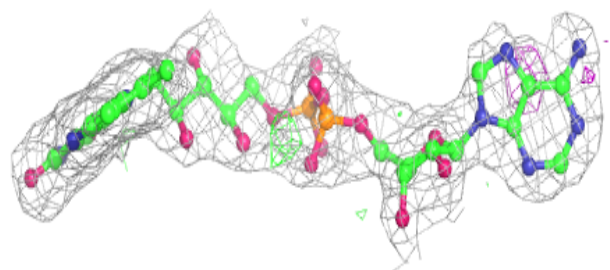
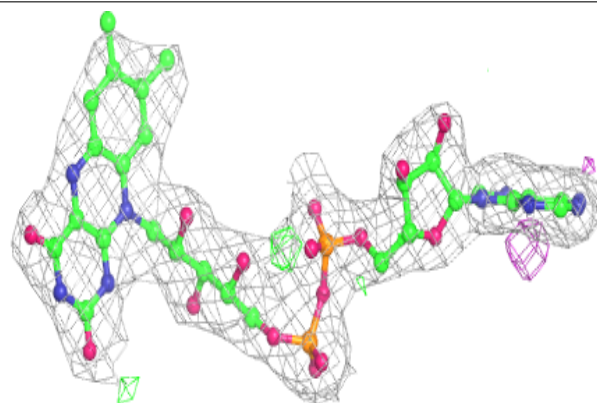


Electron density around FAD B 480:

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

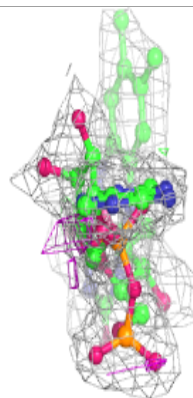
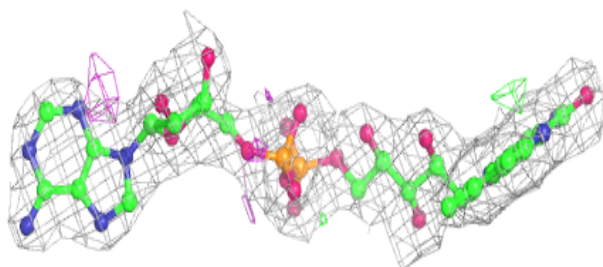
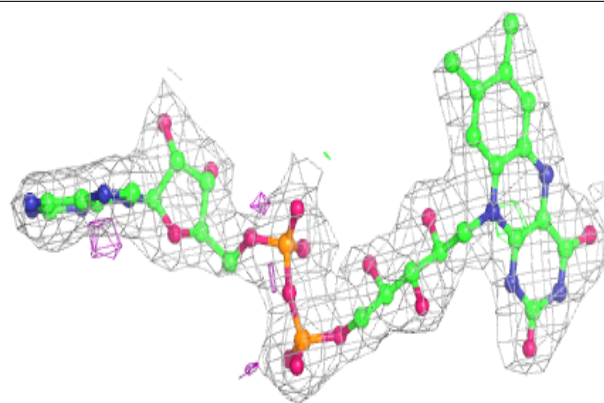
**Electron density around FAD A 480:**

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

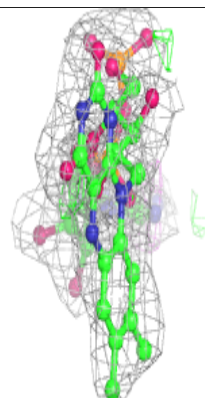
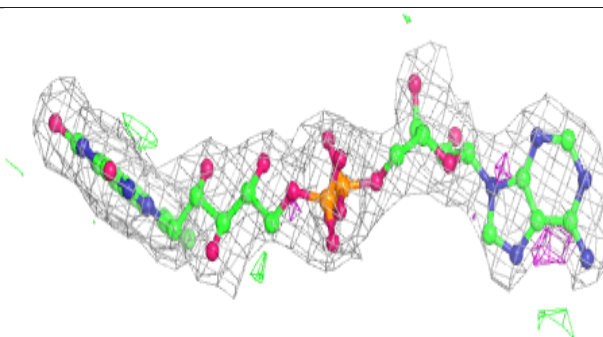
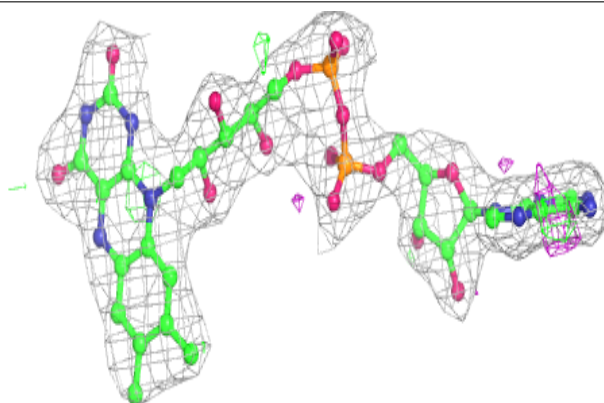


Electron density around FAD H 480:

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

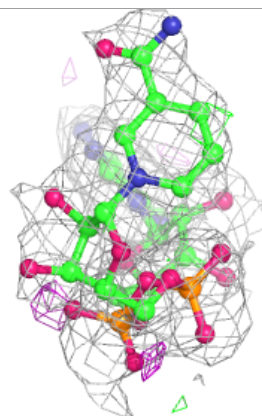
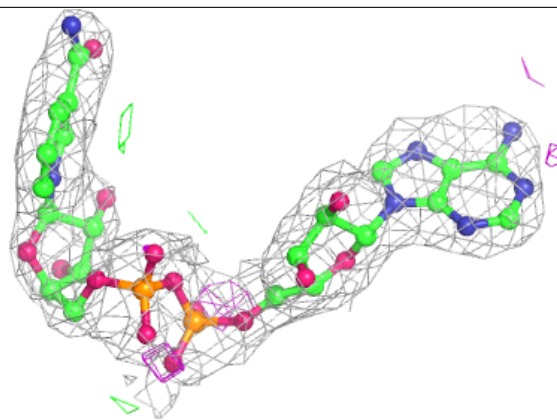
**Electron density around FAD E 480:**

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

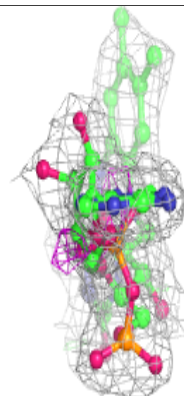
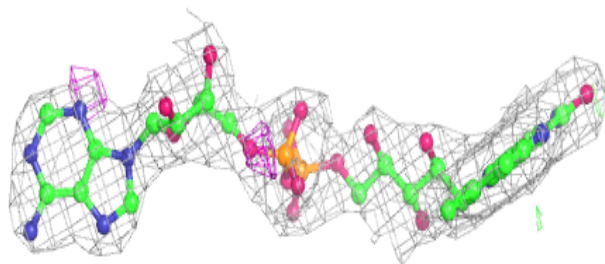
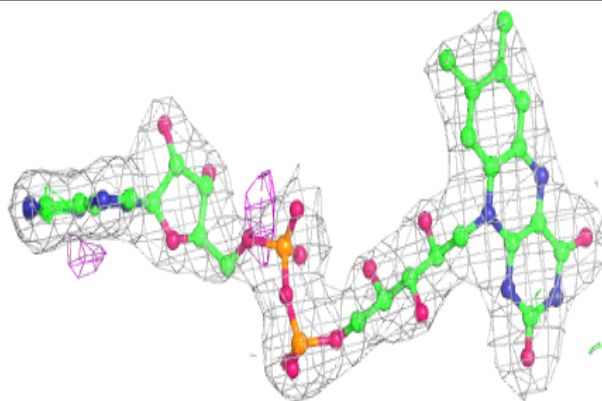


Electron density around NAD D 481:

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

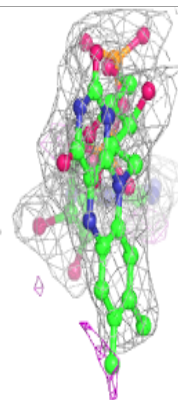
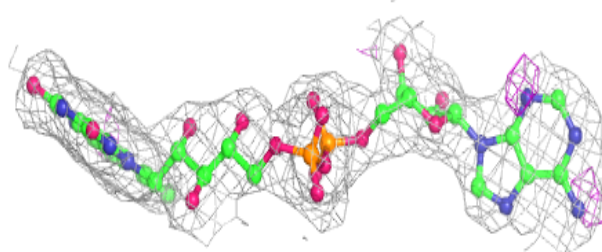
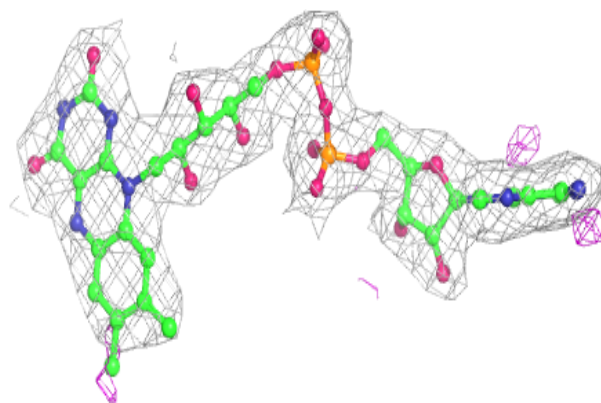
**Electron density around FAD C 480:**

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

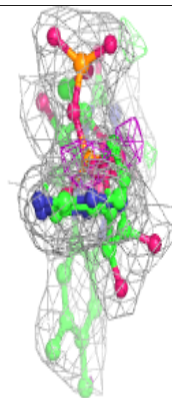
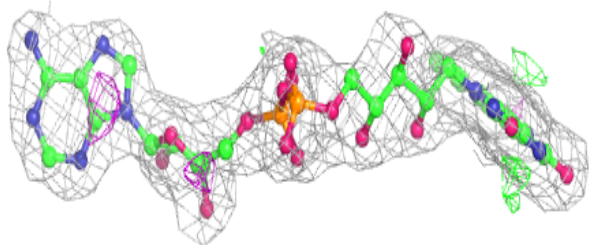
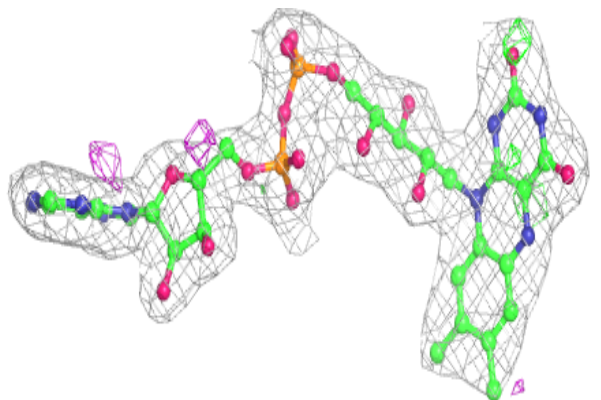


Electron density around FAD D 480:

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

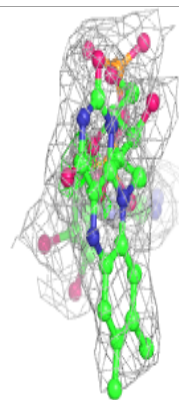
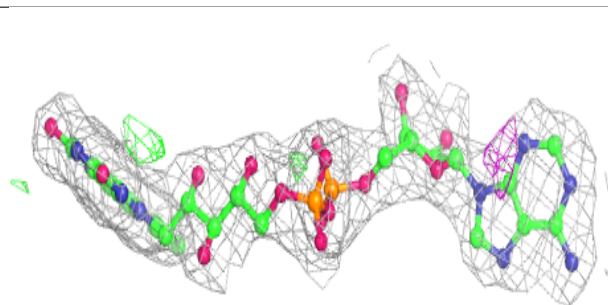
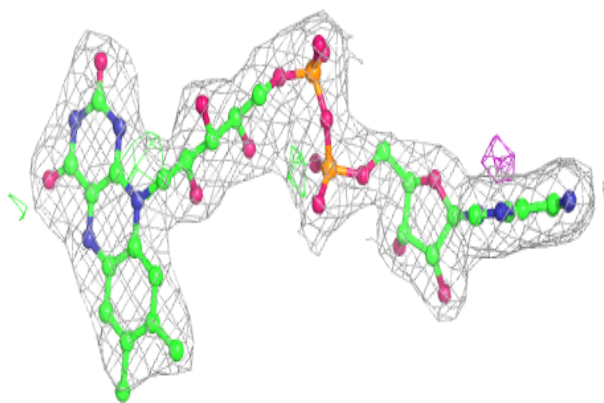
**Electron density around FAD G 480:**

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



Electron density around FAD F 480:

$2mF_o-DF_c$ (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.