



wwPDB X-ray Structure Validation Summary Report ⓘ

May 21, 2020 – 11:35 pm BST

PDB ID : 5VN0
Title : Water-forming NADH oxidase from *Lactobacillus brevis* (LbNOX) bound to NADH.
Authors : Cracan, V.; Grabarek, Z.
Deposited on : 2017-04-28
Resolution : 2.00 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

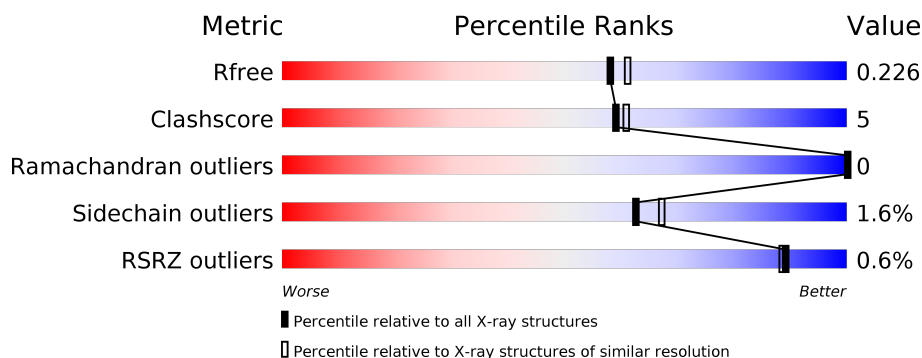
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	518	<div> <div style="width: 78%;"></div> <div style="width: 8%;"></div> <div style="width: 13%;"></div> </div>
1	B	518	<div> <div style="width: 76%;"></div> <div style="width: 10%;"></div> <div style="width: 13%;"></div> </div>
1	C	518	<div> <div style="width: 78%;"></div> <div style="width: 8%;"></div> <div style="width: 13%;"></div> </div>
1	D	518	<div> <div style="width: 77%;"></div> <div style="width: 9%;"></div> <div style="width: 13%;"></div> </div>
1	E	518	<div> <div style="width: 78%;"></div> <div style="width: 8%;"></div> <div style="width: 13%;"></div> </div>
1	F	518	<div> <div style="width: 74%;"></div> <div style="width: 12%;"></div> <div style="width: 14%;"></div> </div>

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Mol	Chain	Length	Quality of chain
1	G	518	 77% 10% 14%
1	H	518	 76% 10% 13%

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
3	OXY	A	502	-	X	-	-
3	OXY	B	502	-	X	-	-
3	OXY	C	502	-	X	-	-
3	OXY	D	502	-	X	-	-
3	OXY	E	502	-	X	-	-
3	OXY	F	502	-	X	-	-
3	OXY	G	502	-	X	-	-
3	OXY	H	502	-	X	-	-
5	EDO	H	504	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 31379 atoms, of which 534 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 NAD(FAD)-dependent dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	449	Total	C	N	O	S	0	0	0
			3426	2156	572	680	18			
1	B	450	Total	C	N	O	S	0	0	0
			3434	2160	574	682	18			
1	C	450	Total	C	N	O	S	0	0	0
			3434	2160	574	682	18			
1	D	450	Total	C	N	O	S	0	0	0
			3434	2160	574	682	18			
1	E	449	Total	C	N	O	S	0	0	0
			3426	2156	572	680	18			
1	F	448	Total	C	N	O	S	0	0	0
			3419	2151	571	679	18			
1	G	448	Total	C	N	O	S	0	0	0
			3419	2151	571	679	18			
1	H	449	Total	C	N	O	S	0	0	0
			3426	2156	572	680	18			

There are 544 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-49	MET	-	initiating methionine	UNP Q03Q85
A	-48	HIS	-	expression tag	UNP Q03Q85
A	-47	HIS	-	expression tag	UNP Q03Q85
A	-46	HIS	-	expression tag	UNP Q03Q85
A	-45	HIS	-	expression tag	UNP Q03Q85
A	-44	HIS	-	expression tag	UNP Q03Q85
A	-43	HIS	-	expression tag	UNP Q03Q85
A	-42	SER	-	expression tag	UNP Q03Q85
A	-41	SER	-	expression tag	UNP Q03Q85
A	-40	GLY	-	expression tag	UNP Q03Q85
A	-39	LEU	-	expression tag	UNP Q03Q85
A	-38	VAL	-	expression tag	UNP Q03Q85
A	-37	PRO	-	expression tag	UNP Q03Q85

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-36	ARG	-	expression tag	UNP Q03Q85
A	-35	GLY	-	expression tag	UNP Q03Q85
A	-34	SER	-	expression tag	UNP Q03Q85
A	-33	GLY	-	expression tag	UNP Q03Q85
A	-32	MET	-	expression tag	UNP Q03Q85
A	-31	LYS	-	expression tag	UNP Q03Q85
A	-30	GLU	-	expression tag	UNP Q03Q85
A	-29	THR	-	expression tag	UNP Q03Q85
A	-28	ALA	-	expression tag	UNP Q03Q85
A	-27	ALA	-	expression tag	UNP Q03Q85
A	-26	ALA	-	expression tag	UNP Q03Q85
A	-25	LYS	-	expression tag	UNP Q03Q85
A	-24	PHE	-	expression tag	UNP Q03Q85
A	-23	GLU	-	expression tag	UNP Q03Q85
A	-22	ARG	-	expression tag	UNP Q03Q85
A	-21	GLN	-	expression tag	UNP Q03Q85
A	-20	HIS	-	expression tag	UNP Q03Q85
A	-19	MET	-	expression tag	UNP Q03Q85
A	-18	ASP	-	expression tag	UNP Q03Q85
A	-17	SER	-	expression tag	UNP Q03Q85
A	-16	PRO	-	expression tag	UNP Q03Q85
A	-15	ASP	-	expression tag	UNP Q03Q85
A	-14	LEU	-	expression tag	UNP Q03Q85
A	-13	GLY	-	expression tag	UNP Q03Q85
A	-12	THR	-	expression tag	UNP Q03Q85
A	-11	ASP	-	expression tag	UNP Q03Q85
A	-10	ASP	-	expression tag	UNP Q03Q85
A	-9	ASP	-	expression tag	UNP Q03Q85
A	-8	ASP	-	expression tag	UNP Q03Q85
A	-7	LYS	-	expression tag	UNP Q03Q85
A	-6	ALA	-	expression tag	UNP Q03Q85
A	-5	MET	-	expression tag	UNP Q03Q85
A	-4	ALA	-	expression tag	UNP Q03Q85
A	-3	ASP	-	expression tag	UNP Q03Q85
A	-2	ILE	-	expression tag	UNP Q03Q85
A	-1	GLY	-	expression tag	UNP Q03Q85
A	0	SER	-	expression tag	UNP Q03Q85
A	451	GLY	-	expression tag	UNP Q03Q85
A	452	GLY	-	expression tag	UNP Q03Q85
A	453	SER	-	expression tag	UNP Q03Q85
A	454	GLY	-	expression tag	UNP Q03Q85
A	455	GLY	-	expression tag	UNP Q03Q85

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Chain	Residue	Modelled	Actual	Comment	Reference
A	456	SER	-	expression tag	UNP Q03Q85
A	457	GLY	-	expression tag	UNP Q03Q85
A	458	GLY	-	expression tag	UNP Q03Q85
A	459	SER	-	expression tag	UNP Q03Q85
A	460	MET	-	expression tag	UNP Q03Q85
A	461	ASP	-	expression tag	UNP Q03Q85
A	462	TYR	-	expression tag	UNP Q03Q85
A	463	LYS	-	expression tag	UNP Q03Q85
A	464	ASP	-	expression tag	UNP Q03Q85
A	465	ASP	-	expression tag	UNP Q03Q85
A	466	ASP	-	expression tag	UNP Q03Q85
A	467	ASP	-	expression tag	UNP Q03Q85
A	468	LYS	-	expression tag	UNP Q03Q85
B	-49	MET	-	initiating methionine	UNP Q03Q85
B	-48	HIS	-	expression tag	UNP Q03Q85
B	-47	HIS	-	expression tag	UNP Q03Q85
B	-46	HIS	-	expression tag	UNP Q03Q85
B	-45	HIS	-	expression tag	UNP Q03Q85
B	-44	HIS	-	expression tag	UNP Q03Q85
B	-43	HIS	-	expression tag	UNP Q03Q85
B	-42	SER	-	expression tag	UNP Q03Q85
B	-41	SER	-	expression tag	UNP Q03Q85
B	-40	GLY	-	expression tag	UNP Q03Q85
B	-39	LEU	-	expression tag	UNP Q03Q85
B	-38	VAL	-	expression tag	UNP Q03Q85
B	-37	PRO	-	expression tag	UNP Q03Q85
B	-36	ARG	-	expression tag	UNP Q03Q85
B	-35	GLY	-	expression tag	UNP Q03Q85
B	-34	SER	-	expression tag	UNP Q03Q85
B	-33	GLY	-	expression tag	UNP Q03Q85
B	-32	MET	-	expression tag	UNP Q03Q85
B	-31	LYS	-	expression tag	UNP Q03Q85
B	-30	GLU	-	expression tag	UNP Q03Q85
B	-29	THR	-	expression tag	UNP Q03Q85
B	-28	ALA	-	expression tag	UNP Q03Q85
B	-27	ALA	-	expression tag	UNP Q03Q85
B	-26	ALA	-	expression tag	UNP Q03Q85
B	-25	LYS	-	expression tag	UNP Q03Q85
B	-24	PHE	-	expression tag	UNP Q03Q85
B	-23	GLU	-	expression tag	UNP Q03Q85
B	-22	ARG	-	expression tag	UNP Q03Q85
B	-21	GLN	-	expression tag	UNP Q03Q85

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-20	HIS	-	expression tag	UNP Q03Q85
B	-19	MET	-	expression tag	UNP Q03Q85
B	-18	ASP	-	expression tag	UNP Q03Q85
B	-17	SER	-	expression tag	UNP Q03Q85
B	-16	PRO	-	expression tag	UNP Q03Q85
B	-15	ASP	-	expression tag	UNP Q03Q85
B	-14	LEU	-	expression tag	UNP Q03Q85
B	-13	GLY	-	expression tag	UNP Q03Q85
B	-12	THR	-	expression tag	UNP Q03Q85
B	-11	ASP	-	expression tag	UNP Q03Q85
B	-10	ASP	-	expression tag	UNP Q03Q85
B	-9	ASP	-	expression tag	UNP Q03Q85
B	-8	ASP	-	expression tag	UNP Q03Q85
B	-7	LYS	-	expression tag	UNP Q03Q85
B	-6	ALA	-	expression tag	UNP Q03Q85
B	-5	MET	-	expression tag	UNP Q03Q85
B	-4	ALA	-	expression tag	UNP Q03Q85
B	-3	ASP	-	expression tag	UNP Q03Q85
B	-2	ILE	-	expression tag	UNP Q03Q85
B	-1	GLY	-	expression tag	UNP Q03Q85
B	0	SER	-	expression tag	UNP Q03Q85
B	451	GLY	-	expression tag	UNP Q03Q85
B	452	GLY	-	expression tag	UNP Q03Q85
B	453	SER	-	expression tag	UNP Q03Q85
B	454	GLY	-	expression tag	UNP Q03Q85
B	455	GLY	-	expression tag	UNP Q03Q85
B	456	SER	-	expression tag	UNP Q03Q85
B	457	GLY	-	expression tag	UNP Q03Q85
B	458	GLY	-	expression tag	UNP Q03Q85
B	459	SER	-	expression tag	UNP Q03Q85
B	460	MET	-	expression tag	UNP Q03Q85
B	461	ASP	-	expression tag	UNP Q03Q85
B	462	TYR	-	expression tag	UNP Q03Q85
B	463	LYS	-	expression tag	UNP Q03Q85
B	464	ASP	-	expression tag	UNP Q03Q85
B	465	ASP	-	expression tag	UNP Q03Q85
B	466	ASP	-	expression tag	UNP Q03Q85
B	467	ASP	-	expression tag	UNP Q03Q85
B	468	LYS	-	expression tag	UNP Q03Q85
C	-49	MET	-	initiating methionine	UNP Q03Q85
C	-48	HIS	-	expression tag	UNP Q03Q85
C	-47	HIS	-	expression tag	UNP Q03Q85

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-46	HIS	-	expression tag	UNP Q03Q85
C	-45	HIS	-	expression tag	UNP Q03Q85
C	-44	HIS	-	expression tag	UNP Q03Q85
C	-43	HIS	-	expression tag	UNP Q03Q85
C	-42	SER	-	expression tag	UNP Q03Q85
C	-41	SER	-	expression tag	UNP Q03Q85
C	-40	GLY	-	expression tag	UNP Q03Q85
C	-39	LEU	-	expression tag	UNP Q03Q85
C	-38	VAL	-	expression tag	UNP Q03Q85
C	-37	PRO	-	expression tag	UNP Q03Q85
C	-36	ARG	-	expression tag	UNP Q03Q85
C	-35	GLY	-	expression tag	UNP Q03Q85
C	-34	SER	-	expression tag	UNP Q03Q85
C	-33	GLY	-	expression tag	UNP Q03Q85
C	-32	MET	-	expression tag	UNP Q03Q85
C	-31	LYS	-	expression tag	UNP Q03Q85
C	-30	GLU	-	expression tag	UNP Q03Q85
C	-29	THR	-	expression tag	UNP Q03Q85
C	-28	ALA	-	expression tag	UNP Q03Q85
C	-27	ALA	-	expression tag	UNP Q03Q85
C	-26	ALA	-	expression tag	UNP Q03Q85
C	-25	LYS	-	expression tag	UNP Q03Q85
C	-24	PHE	-	expression tag	UNP Q03Q85
C	-23	GLU	-	expression tag	UNP Q03Q85
C	-22	ARG	-	expression tag	UNP Q03Q85
C	-21	GLN	-	expression tag	UNP Q03Q85
C	-20	HIS	-	expression tag	UNP Q03Q85
C	-19	MET	-	expression tag	UNP Q03Q85
C	-18	ASP	-	expression tag	UNP Q03Q85
C	-17	SER	-	expression tag	UNP Q03Q85
C	-16	PRO	-	expression tag	UNP Q03Q85
C	-15	ASP	-	expression tag	UNP Q03Q85
C	-14	LEU	-	expression tag	UNP Q03Q85
C	-13	GLY	-	expression tag	UNP Q03Q85
C	-12	THR	-	expression tag	UNP Q03Q85
C	-11	ASP	-	expression tag	UNP Q03Q85
C	-10	ASP	-	expression tag	UNP Q03Q85
C	-9	ASP	-	expression tag	UNP Q03Q85
C	-8	ASP	-	expression tag	UNP Q03Q85
C	-7	LYS	-	expression tag	UNP Q03Q85
C	-6	ALA	-	expression tag	UNP Q03Q85
C	-5	MET	-	expression tag	UNP Q03Q85

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	ALA	-	expression tag	UNP Q03Q85
C	-3	ASP	-	expression tag	UNP Q03Q85
C	-2	ILE	-	expression tag	UNP Q03Q85
C	-1	GLY	-	expression tag	UNP Q03Q85
C	0	SER	-	expression tag	UNP Q03Q85
C	451	GLY	-	expression tag	UNP Q03Q85
C	452	GLY	-	expression tag	UNP Q03Q85
C	453	SER	-	expression tag	UNP Q03Q85
C	454	GLY	-	expression tag	UNP Q03Q85
C	455	GLY	-	expression tag	UNP Q03Q85
C	456	SER	-	expression tag	UNP Q03Q85
C	457	GLY	-	expression tag	UNP Q03Q85
C	458	GLY	-	expression tag	UNP Q03Q85
C	459	SER	-	expression tag	UNP Q03Q85
C	460	MET	-	expression tag	UNP Q03Q85
C	461	ASP	-	expression tag	UNP Q03Q85
C	462	TYR	-	expression tag	UNP Q03Q85
C	463	LYS	-	expression tag	UNP Q03Q85
C	464	ASP	-	expression tag	UNP Q03Q85
C	465	ASP	-	expression tag	UNP Q03Q85
C	466	ASP	-	expression tag	UNP Q03Q85
C	467	ASP	-	expression tag	UNP Q03Q85
C	468	LYS	-	expression tag	UNP Q03Q85
D	-49	MET	-	initiating methionine	UNP Q03Q85
D	-48	HIS	-	expression tag	UNP Q03Q85
D	-47	HIS	-	expression tag	UNP Q03Q85
D	-46	HIS	-	expression tag	UNP Q03Q85
D	-45	HIS	-	expression tag	UNP Q03Q85
D	-44	HIS	-	expression tag	UNP Q03Q85
D	-43	HIS	-	expression tag	UNP Q03Q85
D	-42	SER	-	expression tag	UNP Q03Q85
D	-41	SER	-	expression tag	UNP Q03Q85
D	-40	GLY	-	expression tag	UNP Q03Q85
D	-39	LEU	-	expression tag	UNP Q03Q85
D	-38	VAL	-	expression tag	UNP Q03Q85
D	-37	PRO	-	expression tag	UNP Q03Q85
D	-36	ARG	-	expression tag	UNP Q03Q85
D	-35	GLY	-	expression tag	UNP Q03Q85
D	-34	SER	-	expression tag	UNP Q03Q85
D	-33	GLY	-	expression tag	UNP Q03Q85
D	-32	MET	-	expression tag	UNP Q03Q85
D	-31	LYS	-	expression tag	UNP Q03Q85

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-30	GLU	-	expression tag	UNP Q03Q85
D	-29	THR	-	expression tag	UNP Q03Q85
D	-28	ALA	-	expression tag	UNP Q03Q85
D	-27	ALA	-	expression tag	UNP Q03Q85
D	-26	ALA	-	expression tag	UNP Q03Q85
D	-25	LYS	-	expression tag	UNP Q03Q85
D	-24	PHE	-	expression tag	UNP Q03Q85
D	-23	GLU	-	expression tag	UNP Q03Q85
D	-22	ARG	-	expression tag	UNP Q03Q85
D	-21	GLN	-	expression tag	UNP Q03Q85
D	-20	HIS	-	expression tag	UNP Q03Q85
D	-19	MET	-	expression tag	UNP Q03Q85
D	-18	ASP	-	expression tag	UNP Q03Q85
D	-17	SER	-	expression tag	UNP Q03Q85
D	-16	PRO	-	expression tag	UNP Q03Q85
D	-15	ASP	-	expression tag	UNP Q03Q85
D	-14	LEU	-	expression tag	UNP Q03Q85
D	-13	GLY	-	expression tag	UNP Q03Q85
D	-12	THR	-	expression tag	UNP Q03Q85
D	-11	ASP	-	expression tag	UNP Q03Q85
D	-10	ASP	-	expression tag	UNP Q03Q85
D	-9	ASP	-	expression tag	UNP Q03Q85
D	-8	ASP	-	expression tag	UNP Q03Q85
D	-7	LYS	-	expression tag	UNP Q03Q85
D	-6	ALA	-	expression tag	UNP Q03Q85
D	-5	MET	-	expression tag	UNP Q03Q85
D	-4	ALA	-	expression tag	UNP Q03Q85
D	-3	ASP	-	expression tag	UNP Q03Q85
D	-2	ILE	-	expression tag	UNP Q03Q85
D	-1	GLY	-	expression tag	UNP Q03Q85
D	0	SER	-	expression tag	UNP Q03Q85
D	451	GLY	-	expression tag	UNP Q03Q85
D	452	GLY	-	expression tag	UNP Q03Q85
D	453	SER	-	expression tag	UNP Q03Q85
D	454	GLY	-	expression tag	UNP Q03Q85
D	455	GLY	-	expression tag	UNP Q03Q85
D	456	SER	-	expression tag	UNP Q03Q85
D	457	GLY	-	expression tag	UNP Q03Q85
D	458	GLY	-	expression tag	UNP Q03Q85
D	459	SER	-	expression tag	UNP Q03Q85
D	460	MET	-	expression tag	UNP Q03Q85
D	461	ASP	-	expression tag	UNP Q03Q85

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Chain	Residue	Modelled	Actual	Comment	Reference
D	462	TYR	-	expression tag	UNP Q03Q85
D	463	LYS	-	expression tag	UNP Q03Q85
D	464	ASP	-	expression tag	UNP Q03Q85
D	465	ASP	-	expression tag	UNP Q03Q85
D	466	ASP	-	expression tag	UNP Q03Q85
D	467	ASP	-	expression tag	UNP Q03Q85
D	468	LYS	-	expression tag	UNP Q03Q85
E	-49	MET	-	initiating methionine	UNP Q03Q85
E	-48	HIS	-	expression tag	UNP Q03Q85
E	-47	HIS	-	expression tag	UNP Q03Q85
E	-46	HIS	-	expression tag	UNP Q03Q85
E	-45	HIS	-	expression tag	UNP Q03Q85
E	-44	HIS	-	expression tag	UNP Q03Q85
E	-43	HIS	-	expression tag	UNP Q03Q85
E	-42	SER	-	expression tag	UNP Q03Q85
E	-41	SER	-	expression tag	UNP Q03Q85
E	-40	GLY	-	expression tag	UNP Q03Q85
E	-39	LEU	-	expression tag	UNP Q03Q85
E	-38	VAL	-	expression tag	UNP Q03Q85
E	-37	PRO	-	expression tag	UNP Q03Q85
E	-36	ARG	-	expression tag	UNP Q03Q85
E	-35	GLY	-	expression tag	UNP Q03Q85
E	-34	SER	-	expression tag	UNP Q03Q85
E	-33	GLY	-	expression tag	UNP Q03Q85
E	-32	MET	-	expression tag	UNP Q03Q85
E	-31	LYS	-	expression tag	UNP Q03Q85
E	-30	GLU	-	expression tag	UNP Q03Q85
E	-29	THR	-	expression tag	UNP Q03Q85
E	-28	ALA	-	expression tag	UNP Q03Q85
E	-27	ALA	-	expression tag	UNP Q03Q85
E	-26	ALA	-	expression tag	UNP Q03Q85
E	-25	LYS	-	expression tag	UNP Q03Q85
E	-24	PHE	-	expression tag	UNP Q03Q85
E	-23	GLU	-	expression tag	UNP Q03Q85
E	-22	ARG	-	expression tag	UNP Q03Q85
E	-21	GLN	-	expression tag	UNP Q03Q85
E	-20	HIS	-	expression tag	UNP Q03Q85
E	-19	MET	-	expression tag	UNP Q03Q85
E	-18	ASP	-	expression tag	UNP Q03Q85
E	-17	SER	-	expression tag	UNP Q03Q85
E	-16	PRO	-	expression tag	UNP Q03Q85
E	-15	ASP	-	expression tag	UNP Q03Q85

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-14	LEU	-	expression tag	UNP Q03Q85
E	-13	GLY	-	expression tag	UNP Q03Q85
E	-12	THR	-	expression tag	UNP Q03Q85
E	-11	ASP	-	expression tag	UNP Q03Q85
E	-10	ASP	-	expression tag	UNP Q03Q85
E	-9	ASP	-	expression tag	UNP Q03Q85
E	-8	ASP	-	expression tag	UNP Q03Q85
E	-7	LYS	-	expression tag	UNP Q03Q85
E	-6	ALA	-	expression tag	UNP Q03Q85
E	-5	MET	-	expression tag	UNP Q03Q85
E	-4	ALA	-	expression tag	UNP Q03Q85
E	-3	ASP	-	expression tag	UNP Q03Q85
E	-2	ILE	-	expression tag	UNP Q03Q85
E	-1	GLY	-	expression tag	UNP Q03Q85
E	0	SER	-	expression tag	UNP Q03Q85
E	451	GLY	-	expression tag	UNP Q03Q85
E	452	GLY	-	expression tag	UNP Q03Q85
E	453	SER	-	expression tag	UNP Q03Q85
E	454	GLY	-	expression tag	UNP Q03Q85
E	455	GLY	-	expression tag	UNP Q03Q85
E	456	SER	-	expression tag	UNP Q03Q85
E	457	GLY	-	expression tag	UNP Q03Q85
E	458	GLY	-	expression tag	UNP Q03Q85
E	459	SER	-	expression tag	UNP Q03Q85
E	460	MET	-	expression tag	UNP Q03Q85
E	461	ASP	-	expression tag	UNP Q03Q85
E	462	TYR	-	expression tag	UNP Q03Q85
E	463	LYS	-	expression tag	UNP Q03Q85
E	464	ASP	-	expression tag	UNP Q03Q85
E	465	ASP	-	expression tag	UNP Q03Q85
E	466	ASP	-	expression tag	UNP Q03Q85
E	467	ASP	-	expression tag	UNP Q03Q85
E	468	LYS	-	expression tag	UNP Q03Q85
F	-49	MET	-	initiating methionine	UNP Q03Q85
F	-48	HIS	-	expression tag	UNP Q03Q85
F	-47	HIS	-	expression tag	UNP Q03Q85
F	-46	HIS	-	expression tag	UNP Q03Q85
F	-45	HIS	-	expression tag	UNP Q03Q85
F	-44	HIS	-	expression tag	UNP Q03Q85
F	-43	HIS	-	expression tag	UNP Q03Q85
F	-42	SER	-	expression tag	UNP Q03Q85
F	-41	SER	-	expression tag	UNP Q03Q85

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-40	GLY	-	expression tag	UNP Q03Q85
F	-39	LEU	-	expression tag	UNP Q03Q85
F	-38	VAL	-	expression tag	UNP Q03Q85
F	-37	PRO	-	expression tag	UNP Q03Q85
F	-36	ARG	-	expression tag	UNP Q03Q85
F	-35	GLY	-	expression tag	UNP Q03Q85
F	-34	SER	-	expression tag	UNP Q03Q85
F	-33	GLY	-	expression tag	UNP Q03Q85
F	-32	MET	-	expression tag	UNP Q03Q85
F	-31	LYS	-	expression tag	UNP Q03Q85
F	-30	GLU	-	expression tag	UNP Q03Q85
F	-29	THR	-	expression tag	UNP Q03Q85
F	-28	ALA	-	expression tag	UNP Q03Q85
F	-27	ALA	-	expression tag	UNP Q03Q85
F	-26	ALA	-	expression tag	UNP Q03Q85
F	-25	LYS	-	expression tag	UNP Q03Q85
F	-24	PHE	-	expression tag	UNP Q03Q85
F	-23	GLU	-	expression tag	UNP Q03Q85
F	-22	ARG	-	expression tag	UNP Q03Q85
F	-21	GLN	-	expression tag	UNP Q03Q85
F	-20	HIS	-	expression tag	UNP Q03Q85
F	-19	MET	-	expression tag	UNP Q03Q85
F	-18	ASP	-	expression tag	UNP Q03Q85
F	-17	SER	-	expression tag	UNP Q03Q85
F	-16	PRO	-	expression tag	UNP Q03Q85
F	-15	ASP	-	expression tag	UNP Q03Q85
F	-14	LEU	-	expression tag	UNP Q03Q85
F	-13	GLY	-	expression tag	UNP Q03Q85
F	-12	THR	-	expression tag	UNP Q03Q85
F	-11	ASP	-	expression tag	UNP Q03Q85
F	-10	ASP	-	expression tag	UNP Q03Q85
F	-9	ASP	-	expression tag	UNP Q03Q85
F	-8	ASP	-	expression tag	UNP Q03Q85
F	-7	LYS	-	expression tag	UNP Q03Q85
F	-6	ALA	-	expression tag	UNP Q03Q85
F	-5	MET	-	expression tag	UNP Q03Q85
F	-4	ALA	-	expression tag	UNP Q03Q85
F	-3	ASP	-	expression tag	UNP Q03Q85
F	-2	ILE	-	expression tag	UNP Q03Q85
F	-1	GLY	-	expression tag	UNP Q03Q85
F	0	SER	-	expression tag	UNP Q03Q85
F	451	GLY	-	expression tag	UNP Q03Q85

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Chain	Residue	Modelled	Actual	Comment	Reference
F	452	GLY	-	expression tag	UNP Q03Q85
F	453	SER	-	expression tag	UNP Q03Q85
F	454	GLY	-	expression tag	UNP Q03Q85
F	455	GLY	-	expression tag	UNP Q03Q85
F	456	SER	-	expression tag	UNP Q03Q85
F	457	GLY	-	expression tag	UNP Q03Q85
F	458	GLY	-	expression tag	UNP Q03Q85
F	459	SER	-	expression tag	UNP Q03Q85
F	460	MET	-	expression tag	UNP Q03Q85
F	461	ASP	-	expression tag	UNP Q03Q85
F	462	TYR	-	expression tag	UNP Q03Q85
F	463	LYS	-	expression tag	UNP Q03Q85
F	464	ASP	-	expression tag	UNP Q03Q85
F	465	ASP	-	expression tag	UNP Q03Q85
F	466	ASP	-	expression tag	UNP Q03Q85
F	467	ASP	-	expression tag	UNP Q03Q85
F	468	LYS	-	expression tag	UNP Q03Q85
G	-49	MET	-	initiating methionine	UNP Q03Q85
G	-48	HIS	-	expression tag	UNP Q03Q85
G	-47	HIS	-	expression tag	UNP Q03Q85
G	-46	HIS	-	expression tag	UNP Q03Q85
G	-45	HIS	-	expression tag	UNP Q03Q85
G	-44	HIS	-	expression tag	UNP Q03Q85
G	-43	HIS	-	expression tag	UNP Q03Q85
G	-42	SER	-	expression tag	UNP Q03Q85
G	-41	SER	-	expression tag	UNP Q03Q85
G	-40	GLY	-	expression tag	UNP Q03Q85
G	-39	LEU	-	expression tag	UNP Q03Q85
G	-38	VAL	-	expression tag	UNP Q03Q85
G	-37	PRO	-	expression tag	UNP Q03Q85
G	-36	ARG	-	expression tag	UNP Q03Q85
G	-35	GLY	-	expression tag	UNP Q03Q85
G	-34	SER	-	expression tag	UNP Q03Q85
G	-33	GLY	-	expression tag	UNP Q03Q85
G	-32	MET	-	expression tag	UNP Q03Q85
G	-31	LYS	-	expression tag	UNP Q03Q85
G	-30	GLU	-	expression tag	UNP Q03Q85
G	-29	THR	-	expression tag	UNP Q03Q85
G	-28	ALA	-	expression tag	UNP Q03Q85
G	-27	ALA	-	expression tag	UNP Q03Q85
G	-26	ALA	-	expression tag	UNP Q03Q85
G	-25	LYS	-	expression tag	UNP Q03Q85

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-24	PHE	-	expression tag	UNP Q03Q85
G	-23	GLU	-	expression tag	UNP Q03Q85
G	-22	ARG	-	expression tag	UNP Q03Q85
G	-21	GLN	-	expression tag	UNP Q03Q85
G	-20	HIS	-	expression tag	UNP Q03Q85
G	-19	MET	-	expression tag	UNP Q03Q85
G	-18	ASP	-	expression tag	UNP Q03Q85
G	-17	SER	-	expression tag	UNP Q03Q85
G	-16	PRO	-	expression tag	UNP Q03Q85
G	-15	ASP	-	expression tag	UNP Q03Q85
G	-14	LEU	-	expression tag	UNP Q03Q85
G	-13	GLY	-	expression tag	UNP Q03Q85
G	-12	THR	-	expression tag	UNP Q03Q85
G	-11	ASP	-	expression tag	UNP Q03Q85
G	-10	ASP	-	expression tag	UNP Q03Q85
G	-9	ASP	-	expression tag	UNP Q03Q85
G	-8	ASP	-	expression tag	UNP Q03Q85
G	-7	LYS	-	expression tag	UNP Q03Q85
G	-6	ALA	-	expression tag	UNP Q03Q85
G	-5	MET	-	expression tag	UNP Q03Q85
G	-4	ALA	-	expression tag	UNP Q03Q85
G	-3	ASP	-	expression tag	UNP Q03Q85
G	-2	ILE	-	expression tag	UNP Q03Q85
G	-1	GLY	-	expression tag	UNP Q03Q85
G	0	SER	-	expression tag	UNP Q03Q85
G	451	GLY	-	expression tag	UNP Q03Q85
G	452	GLY	-	expression tag	UNP Q03Q85
G	453	SER	-	expression tag	UNP Q03Q85
G	454	GLY	-	expression tag	UNP Q03Q85
G	455	GLY	-	expression tag	UNP Q03Q85
G	456	SER	-	expression tag	UNP Q03Q85
G	457	GLY	-	expression tag	UNP Q03Q85
G	458	GLY	-	expression tag	UNP Q03Q85
G	459	SER	-	expression tag	UNP Q03Q85
G	460	MET	-	expression tag	UNP Q03Q85
G	461	ASP	-	expression tag	UNP Q03Q85
G	462	TYR	-	expression tag	UNP Q03Q85
G	463	LYS	-	expression tag	UNP Q03Q85
G	464	ASP	-	expression tag	UNP Q03Q85
G	465	ASP	-	expression tag	UNP Q03Q85
G	466	ASP	-	expression tag	UNP Q03Q85
G	467	ASP	-	expression tag	UNP Q03Q85

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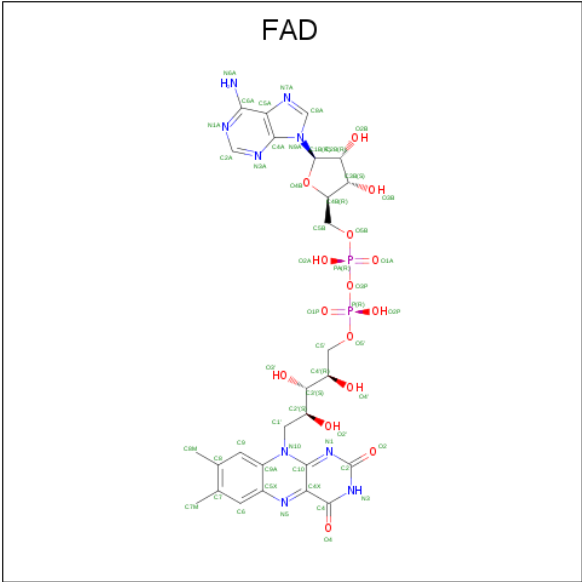
Chain	Residue	Modelled	Actual	Comment	Reference
G	468	LYS	-	expression tag	UNP Q03Q85
H	-49	MET	-	initiating methionine	UNP Q03Q85
H	-48	HIS	-	expression tag	UNP Q03Q85
H	-47	HIS	-	expression tag	UNP Q03Q85
H	-46	HIS	-	expression tag	UNP Q03Q85
H	-45	HIS	-	expression tag	UNP Q03Q85
H	-44	HIS	-	expression tag	UNP Q03Q85
H	-43	HIS	-	expression tag	UNP Q03Q85
H	-42	SER	-	expression tag	UNP Q03Q85
H	-41	SER	-	expression tag	UNP Q03Q85
H	-40	GLY	-	expression tag	UNP Q03Q85
H	-39	LEU	-	expression tag	UNP Q03Q85
H	-38	VAL	-	expression tag	UNP Q03Q85
H	-37	PRO	-	expression tag	UNP Q03Q85
H	-36	ARG	-	expression tag	UNP Q03Q85
H	-35	GLY	-	expression tag	UNP Q03Q85
H	-34	SER	-	expression tag	UNP Q03Q85
H	-33	GLY	-	expression tag	UNP Q03Q85
H	-32	MET	-	expression tag	UNP Q03Q85
H	-31	LYS	-	expression tag	UNP Q03Q85
H	-30	GLU	-	expression tag	UNP Q03Q85
H	-29	THR	-	expression tag	UNP Q03Q85
H	-28	ALA	-	expression tag	UNP Q03Q85
H	-27	ALA	-	expression tag	UNP Q03Q85
H	-26	ALA	-	expression tag	UNP Q03Q85
H	-25	LYS	-	expression tag	UNP Q03Q85
H	-24	PHE	-	expression tag	UNP Q03Q85
H	-23	GLU	-	expression tag	UNP Q03Q85
H	-22	ARG	-	expression tag	UNP Q03Q85
H	-21	GLN	-	expression tag	UNP Q03Q85
H	-20	HIS	-	expression tag	UNP Q03Q85
H	-19	MET	-	expression tag	UNP Q03Q85
H	-18	ASP	-	expression tag	UNP Q03Q85
H	-17	SER	-	expression tag	UNP Q03Q85
H	-16	PRO	-	expression tag	UNP Q03Q85
H	-15	ASP	-	expression tag	UNP Q03Q85
H	-14	LEU	-	expression tag	UNP Q03Q85
H	-13	GLY	-	expression tag	UNP Q03Q85
H	-12	THR	-	expression tag	UNP Q03Q85
H	-11	ASP	-	expression tag	UNP Q03Q85
H	-10	ASP	-	expression tag	UNP Q03Q85
H	-9	ASP	-	expression tag	UNP Q03Q85

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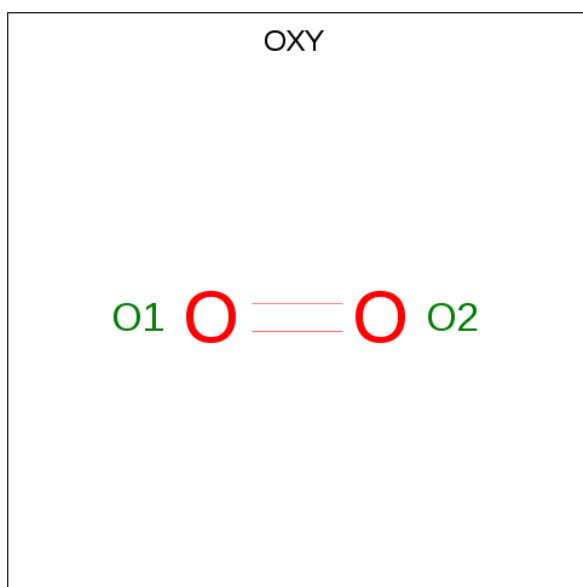
Chain	Residue	Modelled	Actual	Comment	Reference
H	-8	ASP	-	expression tag	UNP Q03Q85
H	-7	LYS	-	expression tag	UNP Q03Q85
H	-6	ALA	-	expression tag	UNP Q03Q85
H	-5	MET	-	expression tag	UNP Q03Q85
H	-4	ALA	-	expression tag	UNP Q03Q85
H	-3	ASP	-	expression tag	UNP Q03Q85
H	-2	ILE	-	expression tag	UNP Q03Q85
H	-1	GLY	-	expression tag	UNP Q03Q85
H	0	SER	-	expression tag	UNP Q03Q85
H	451	GLY	-	expression tag	UNP Q03Q85
H	452	GLY	-	expression tag	UNP Q03Q85
H	453	SER	-	expression tag	UNP Q03Q85
H	454	GLY	-	expression tag	UNP Q03Q85
H	455	GLY	-	expression tag	UNP Q03Q85
H	456	SER	-	expression tag	UNP Q03Q85
H	457	GLY	-	expression tag	UNP Q03Q85
H	458	GLY	-	expression tag	UNP Q03Q85
H	459	SER	-	expression tag	UNP Q03Q85
H	460	MET	-	expression tag	UNP Q03Q85
H	461	ASP	-	expression tag	UNP Q03Q85
H	462	TYR	-	expression tag	UNP Q03Q85
H	463	LYS	-	expression tag	UNP Q03Q85
H	464	ASP	-	expression tag	UNP Q03Q85
H	465	ASP	-	expression tag	UNP Q03Q85
H	466	ASP	-	expression tag	UNP Q03Q85
H	467	ASP	-	expression tag	UNP Q03Q85
H	468	LYS	-	expression tag	UNP Q03Q85

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



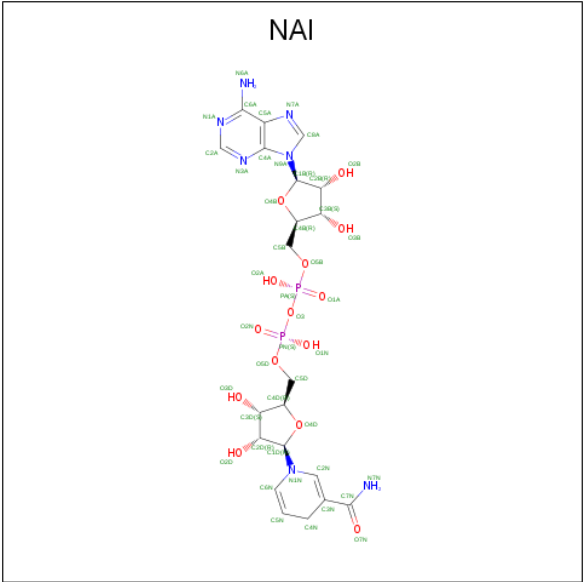
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	P	0	0
			83	27	30	9	15	2		
2	B	1	Total	C	H	N	O	P	0	0
			83	27	30	9	15	2		
2	C	1	Total	C	H	N	O	P	0	0
			83	27	30	9	15	2		
2	D	1	Total	C	H	N	O	P	0	0
			83	27	30	9	15	2		
2	E	1	Total	C	H	N	O	P	0	0
			83	27	30	9	15	2		
2	F	1	Total	C	H	N	O	P	0	0
			83	27	30	9	15	2		
2	G	1	Total	C	H	N	O	P	0	0
			83	27	30	9	15	2		
2	H	1	Total	C	H	N	O	P	0	0
			83	27	30	9	15	2		

- Molecule 3 is OXYGEN MOLECULE (three-letter code: OXY) (formula: O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O 2 2	0	0
3	B	1	Total O 2 2	0	0
3	C	1	Total O 2 2	0	0
3	D	1	Total O 2 2	0	0
3	E	1	Total O 2 2	0	0
3	F	1	Total O 2 2	0	0
3	G	1	Total O 2 2	0	0
3	H	1	Total O 2 2	0	0

- Molecule 4 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (three-letter code: NAI) (formula: $C_{21}H_{29}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	H	N	O	P	0	0
			71	21	27	7	14	2		
4	B	1	Total	C	H	N	O	P	0	0
			71	21	27	7	14	2		
4	C	1	Total	C	H	N	O	P	0	0
			71	21	27	7	14	2		
4	D	1	Total	C	H	N	O	P	0	0
			71	21	27	7	14	2		
4	E	1	Total	C	H	N	O	P	0	0
			71	21	27	7	14	2		
4	F	1	Total	C	H	N	O	P	0	0
			71	21	27	7	14	2		
4	G	1	Total	C	H	N	O	P	0	0
			71	21	27	7	14	2		
4	H	1	Total	C	H	N	O	P	0	0
			71	21	27	7	14	2		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			10	2	6	2		
5	A	1	Total	C	H	O	0	0
			10	2	6	2		
5	B	1	Total	C	H	O	0	0
			10	2	6	2		
5	C	1	Total	C	H	O	0	0
			10	2	6	2		
5	D	1	Total	C	H	O	0	0
			10	2	6	2		
5	D	1	Total	C	H	O	0	0
			10	2	6	2		
5	E	1	Total	C	H	O	0	0
			10	2	6	2		
5	F	1	Total	C	H	O	0	0
			10	2	6	2		
5	F	1	Total	C	H	O	0	0
			10	2	6	2		
5	F	1	Total	C	H	O	0	0
			10	2	6	2		
5	G	1	Total	C	H	O	0	0
			10	2	6	2		
5	H	1	Total	C	H	O	0	0
			10	2	6	2		
5	H	1	Total	C	H	O	0	0
			10	2	6	2		


- Molecule 6 is water.

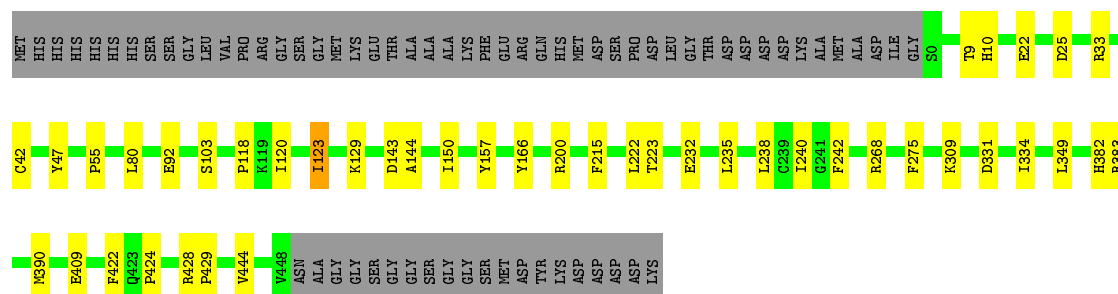
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	374	Total 374	O 374	0	0
6	B	317	Total 317	O 317	0	0
6	C	331	Total 331	O 331	0	0
6	D	362	Total 362	O 362	0	0
6	E	298	Total 298	O 298	0	0
6	F	289	Total 289	O 289	0	0
6	G	296	Total 296	O 296	0	0
6	H	316	Total 316	O 316	0	0

3 Residue-property plots


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.

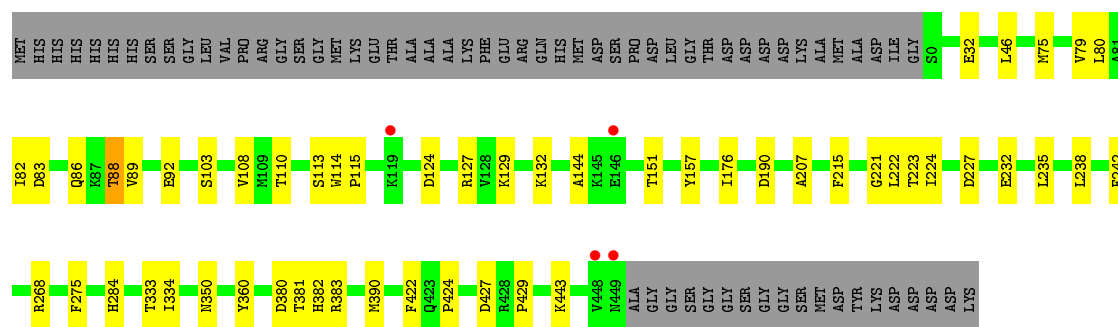
- Molecule 1: NAD(FAD)-dependent dehydrogenase

Chain A: 




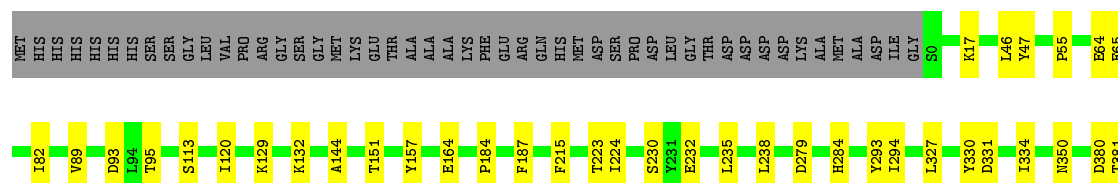
- Molecule 1: NAD(FAD)-dependent dehydrogenase

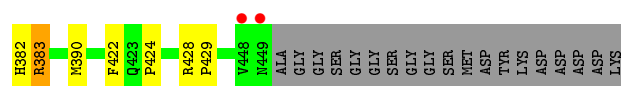
Chain B: 



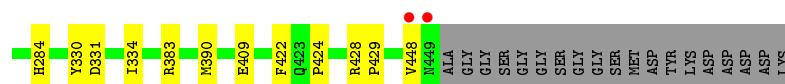
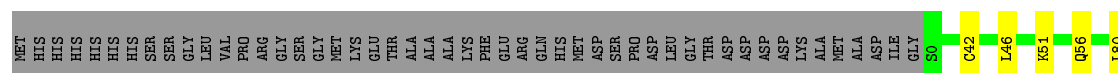
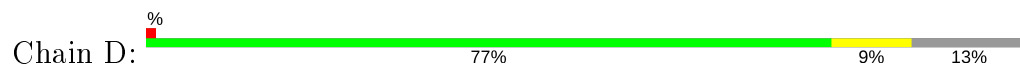
- Molecule 1: NAD(FAD)-dependent dehydrogenase

Chain C: 

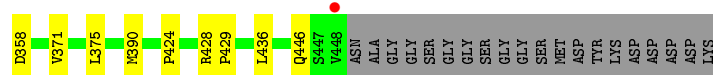
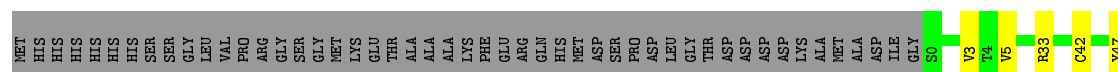
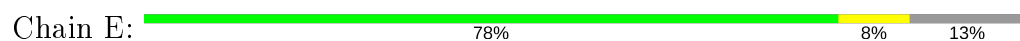




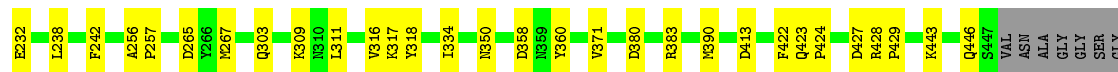
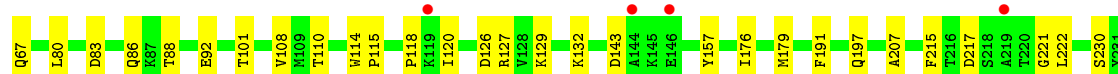
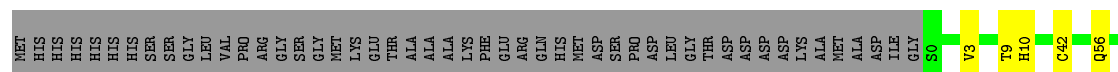
- Molecule 1: NAD(FAD)-dependent dehydrogenase



- Molecule 1: NAD(FAD)-dependent dehydrogenase



- Molecule 1: NAD(FAD)-dependent dehydrogenase



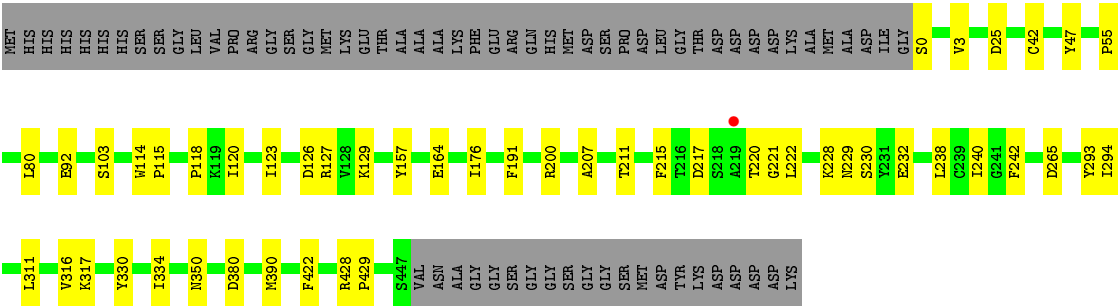
- Molecule 1: NAD(FAD)-dependent dehydrogenase

Chain G:

77%

10%

14%



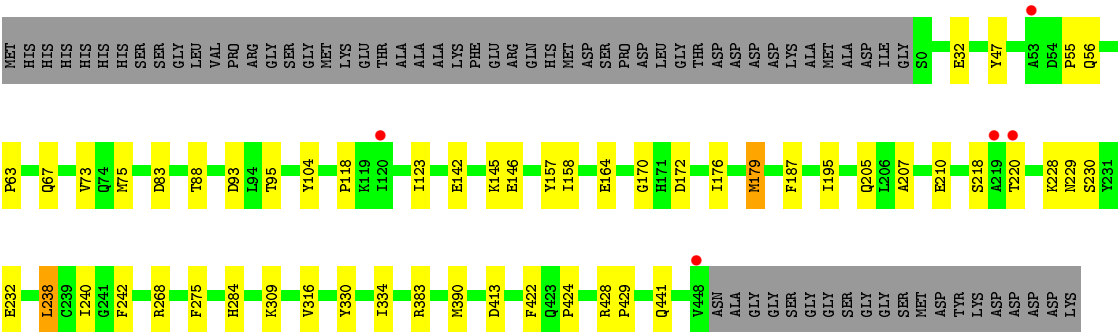
● Molecule 1: NAD(FAD)-dependent dehydrogenase

Chain H:

76%

10%

13%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	96.53Å 107.51Å 119.30Å 63.37° 90.04° 89.95°	Depositor
Resolution (Å)	42.95 – 2.00 42.95 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.6 (42.95-2.00) 97.7 (42.95-2.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.179 , 0.225 0.183 , 0.226	Depositor DCC
R_{free} test set	14447 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	22.5	Xtriage
Anisotropy	0.660	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 28.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.477 for h,-k,-l 0.036 for -h,k,k-l 0.036 for -h,-k,-k+l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	31379	wwPDB-VP
Average B, all atoms (Å ²)	29.0	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 48.68 % 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 8.3108e-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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAI, OXY, FAD, EDO

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	0.37	0/3489	0.55	0/4750
1	B	0.35	0/3497	0.54	0/4761
1	C	0.37	0/3497	0.55	0/4761
1	D	0.37	0/3497	0.55	0/4761
1	E	0.35	0/3489	0.54	0/4750
1	F	0.34	0/3482	0.53	0/4740
1	G	0.35	0/3482	0.53	0/4740
1	H	0.35	0/3489	0.54	0/4750
All	All	0.36	0/27922	0.54	0/38013

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3426	0	3383	31	0
1	B	3434	0	3389	34	0
1	C	3434	0	3389	30	0
1	D	3434	0	3389	33	0
1	E	3426	0	3383	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	3419	0	3374	46	0
1	G	3419	0	3374	31	0
1	H	3426	0	3383	38	0
2	A	53	30	31	2	0
2	B	53	30	31	1	0
2	C	53	30	31	0	0
2	D	53	30	31	1	0
2	E	53	30	31	3	0
2	F	53	30	31	2	0
2	G	53	30	31	1	0
2	H	53	30	31	1	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
3	G	2	0	0	0	0
3	H	2	0	0	0	0
4	A	44	27	26	2	0
4	B	44	27	26	2	0
4	C	44	27	26	2	0
4	D	44	27	26	1	0
4	E	44	27	26	2	0
4	F	44	27	26	2	0
4	G	44	27	27	2	0
4	H	44	27	26	2	0
5	A	8	12	12	0	0
5	B	4	6	6	0	0
5	C	4	6	6	0	0
5	D	8	12	12	0	0
5	E	4	6	6	0	0
5	F	12	18	18	4	0
5	G	4	6	6	0	0
5	H	8	12	12	5	0
6	A	374	0	0	6	0
6	B	317	0	0	5	0
6	C	331	0	0	5	0
6	D	362	0	0	8	0
6	E	298	0	0	2	0
6	F	289	0	0	4	0
6	G	296	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	H	316	0	0	6	0
All	All	30845	534	27599	264	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 5.

The worst 5 of 264 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:92:GLU:OE1	6:D:601:HOH:O	1.95	0.85
1:C:223:THR:OG1	1:C:232:GLU:OE2	1.96	0.83
1:D:83:ASP:HB3	1:D:88:THR:HG22	1.60	0.82
1:D:205:GLN:OE1	6:D:602:HOH:O	1.98	0.81
1:A:25:ASP:OD2	6:A:601:HOH:O	1.98	0.80

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	447/518 (86%)	433 (97%)	14 (3%)	0	100	100
1	B	448/518 (86%)	435 (97%)	13 (3%)	0	100	100
1	C	448/518 (86%)	434 (97%)	14 (3%)	0	100	100
1	D	448/518 (86%)	434 (97%)	14 (3%)	0	100	100
1	E	447/518 (86%)	434 (97%)	13 (3%)	0	100	100
1	F	446/518 (86%)	431 (97%)	15 (3%)	0	100	100
1	G	446/518 (86%)	434 (97%)	12 (3%)	0	100	100
1	H	447/518 (86%)	429 (96%)	18 (4%)	0	100	100
All	All	3577/4144 (86%)	3464 (97%)	113 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	375/427 (88%)	371 (99%)	4 (1%)	73	78
1	B	376/427 (88%)	371 (99%)	5 (1%)	69	74
1	C	376/427 (88%)	372 (99%)	4 (1%)	73	78
1	D	376/427 (88%)	370 (98%)	6 (2%)	62	67
1	E	375/427 (88%)	367 (98%)	8 (2%)	53	57
1	F	374/427 (88%)	367 (98%)	7 (2%)	57	61
1	G	374/427 (88%)	367 (98%)	7 (2%)	57	61
1	H	375/427 (88%)	367 (98%)	8 (2%)	53	57
All	All	3001/3416 (88%)	2952 (98%)	49 (2%)	62	67

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	145	LYS
1	F	56	GLN
1	H	220	THR
1	E	230	SER
1	F	67	GLN

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

Mol	Chain	Res	Type
1	F	72	ASN
1	F	74	GLN
1	H	441	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

37 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	$\# Z > 2$
5	EDO	H	504	-	3,3,3	0.59	0	2,2,2	0.37	0
4	NAI	D	503	-	42,48,48	4.83	20 (47%)	47,73,73	1.77	9 (19%)
5	EDO	B	504	-	3,3,3	0.45	0	2,2,2	0.42	0
4	NAI	F	503	-	42,48,48	4.93	21 (50%)	47,73,73	1.76	7 (14%)
2	FAD	C	501	-	51,58,58	4.09	21 (41%)	60,89,89	2.40	13 (21%)
4	NAI	E	503	-	42,48,48	4.83	20 (47%)	47,73,73	1.75	8 (17%)
2	FAD	A	501	-	51,58,58	3.99	21 (41%)	60,89,89	2.46	13 (21%)
2	FAD	B	501	-	51,58,58	4.13	19 (37%)	60,89,89	2.49	14 (23%)
5	EDO	D	504	-	3,3,3	0.45	0	2,2,2	0.40	0
4	NAI	C	503	-	42,48,48	4.85	22 (52%)	47,73,73	1.64	6 (12%)
5	EDO	A	505	-	3,3,3	0.48	0	2,2,2	0.43	0
5	EDO	H	505	-	3,3,3	0.40	0	2,2,2	0.56	0
3	OXY	D	502	-	1,1,1	2.05	1 (100%)	-		
5	EDO	D	505	-	3,3,3	0.47	0	2,2,2	0.38	0
2	FAD	G	501	-	51,58,58	4.12	21 (41%)	60,89,89	2.46	14 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	FAD	H	501	-	51,58,58	4.08	20 (39%)	60,89,89	2.51	14 (23%)
5	EDO	A	504	-	3,3,3	0.48	0	2,2,2	0.51	0
2	FAD	F	501	-	51,58,58	4.14	21 (41%)	60,89,89	2.46	14 (23%)
5	EDO	E	504	-	3,3,3	0.47	0	2,2,2	0.12	0
4	NAI	A	503	-	42,48,48	4.88	21 (50%)	47,73,73	1.77	7 (14%)
4	NAI	H	503	-	42,48,48	4.90	21 (50%)	47,73,73	1.73	8 (17%)
3	OXY	H	502	-	1,1,1	2.02	1 (100%)	-	-	-
5	EDO	F	506	-	3,3,3	0.50	0	2,2,2	0.41	0
3	OXY	G	502	-	1,1,1	2.03	1 (100%)	-	-	-
3	OXY	A	502	-	1,1,1	2.04	1 (100%)	-	-	-
2	FAD	E	501	-	51,58,58	4.11	21 (41%)	60,89,89	2.50	16 (26%)
2	FAD	D	501	-	51,58,58	4.02	18 (35%)	60,89,89	2.49	14 (23%)
5	EDO	G	504	-	3,3,3	0.44	0	2,2,2	0.14	0
4	NAI	G	503	-	42,48,48	4.89	21 (50%)	47,73,73	1.80	6 (12%)
3	OXY	B	502	-	1,1,1	2.02	1 (100%)	-	-	-
4	NAI	B	503	-	42,48,48	4.84	21 (50%)	47,73,73	1.69	7 (14%)
3	OXY	C	502	-	1,1,1	2.04	1 (100%)	-	-	-
5	EDO	F	505	-	3,3,3	0.61	0	2,2,2	0.30	0
5	EDO	F	504	-	3,3,3	0.41	0	2,2,2	0.18	0
5	EDO	C	504	-	3,3,3	0.47	0	2,2,2	0.59	0
3	OXY	E	502	-	1,1,1	2.04	1 (100%)	-	-	-
3	OXY	F	502	-	1,1,1	2.03	1 (100%)	-	-	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	H	504	-	-	1/1/1/1	-
4	NAI	D	503	-	-	4/25/72/72	0/5/5/5
5	EDO	B	504	-	-	0/1/1/1	-
4	NAI	F	503	-	-	5/25/72/72	0/5/5/5
2	FAD	C	501	-	-	1/30/50/50	0/6/6/6
4	NAI	E	503	-	-	4/25/72/72	0/5/5/5
2	FAD	A	501	-	-	3/30/50/50	0/6/6/6
2	FAD	B	501	-	-	1/30/50/50	0/6/6/6
5	EDO	D	504	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAI	C	503	-	-	3/25/72/72	0/5/5/5
5	EDO	A	505	-	-	0/1/1/1	-
5	EDO	H	505	-	-	1/1/1/1	-
5	EDO	D	505	-	-	0/1/1/1	-
2	FAD	G	501	-	-	1/30/50/50	0/6/6/6
2	FAD	H	501	-	-	1/30/50/50	0/6/6/6
5	EDO	A	504	-	-	0/1/1/1	-
2	FAD	F	501	-	-	2/30/50/50	0/6/6/6
5	EDO	E	504	-	-	0/1/1/1	-
4	NAI	A	503	-	-	3/25/72/72	0/5/5/5
4	NAI	H	503	-	-	5/25/72/72	0/5/5/5
5	EDO	F	506	-	-	1/1/1/1	-
2	FAD	E	501	-	-	1/30/50/50	0/6/6/6
2	FAD	D	501	-	-	1/30/50/50	0/6/6/6
5	EDO	G	504	-	-	1/1/1/1	-
4	NAI	G	503	-	-	4/25/72/72	0/5/5/5
4	NAI	B	503	-	-	4/25/72/72	0/5/5/5
5	EDO	F	505	-	-	1/1/1/1	-
5	EDO	F	504	-	-	0/1/1/1	-
5	EDO	C	504	-	-	0/1/1/1	-

The worst 5 of 337 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	503	NAI	C2B-C1B	-17.08	1.27	1.53
4	H	503	NAI	C2B-C1B	-17.07	1.27	1.53
4	D	503	NAI	C2B-C1B	-17.06	1.27	1.53
4	G	503	NAI	C2B-C1B	-17.03	1.27	1.53
4	F	503	NAI	C2B-C1B	-17.02	1.27	1.53

The worst 5 of 170 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	501	FAD	C5A-C6A-N6A	7.88	132.32	120.35
2	B	501	FAD	C5A-C6A-N6A	7.80	132.21	120.35
2	E	501	FAD	C5A-C6A-N6A	7.77	132.17	120.35
2	H	501	FAD	C5A-C6A-N6A	7.75	132.12	120.35
2	A	501	FAD	C5A-C6A-N6A	7.53	131.80	120.35

There are no chirality outliers.

5 of 48 torsion outliers are listed below:

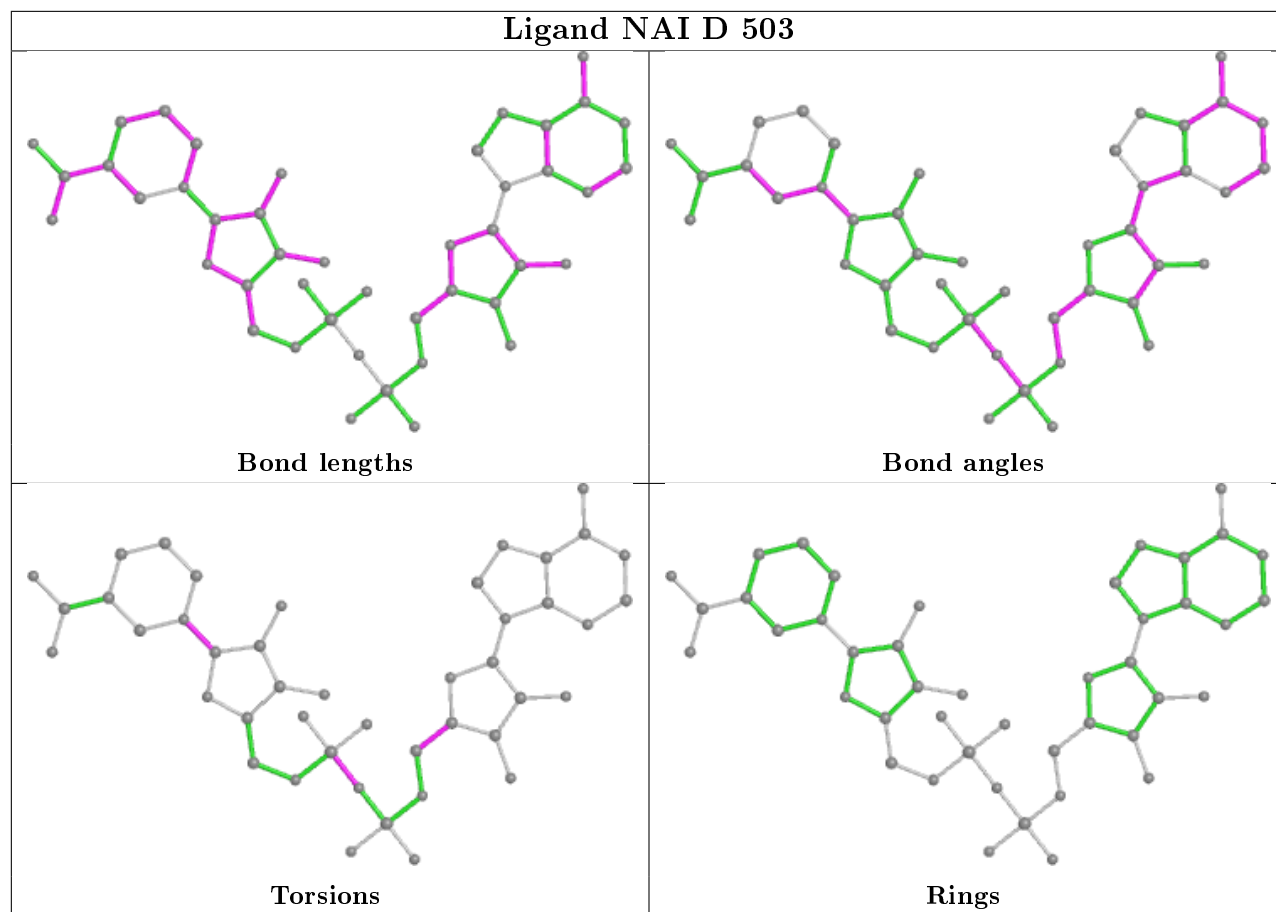
Mol	Chain	Res	Type	Atoms
4	D	503	NAI	O4D-C1D-N1N-C2N
4	F	503	NAI	O4D-C1D-N1N-C2N
4	E	503	NAI	O4D-C1D-N1N-C2N
4	C	503	NAI	O4D-C1D-N1N-C2N
4	A	503	NAI	O4D-C1D-N1N-C2N

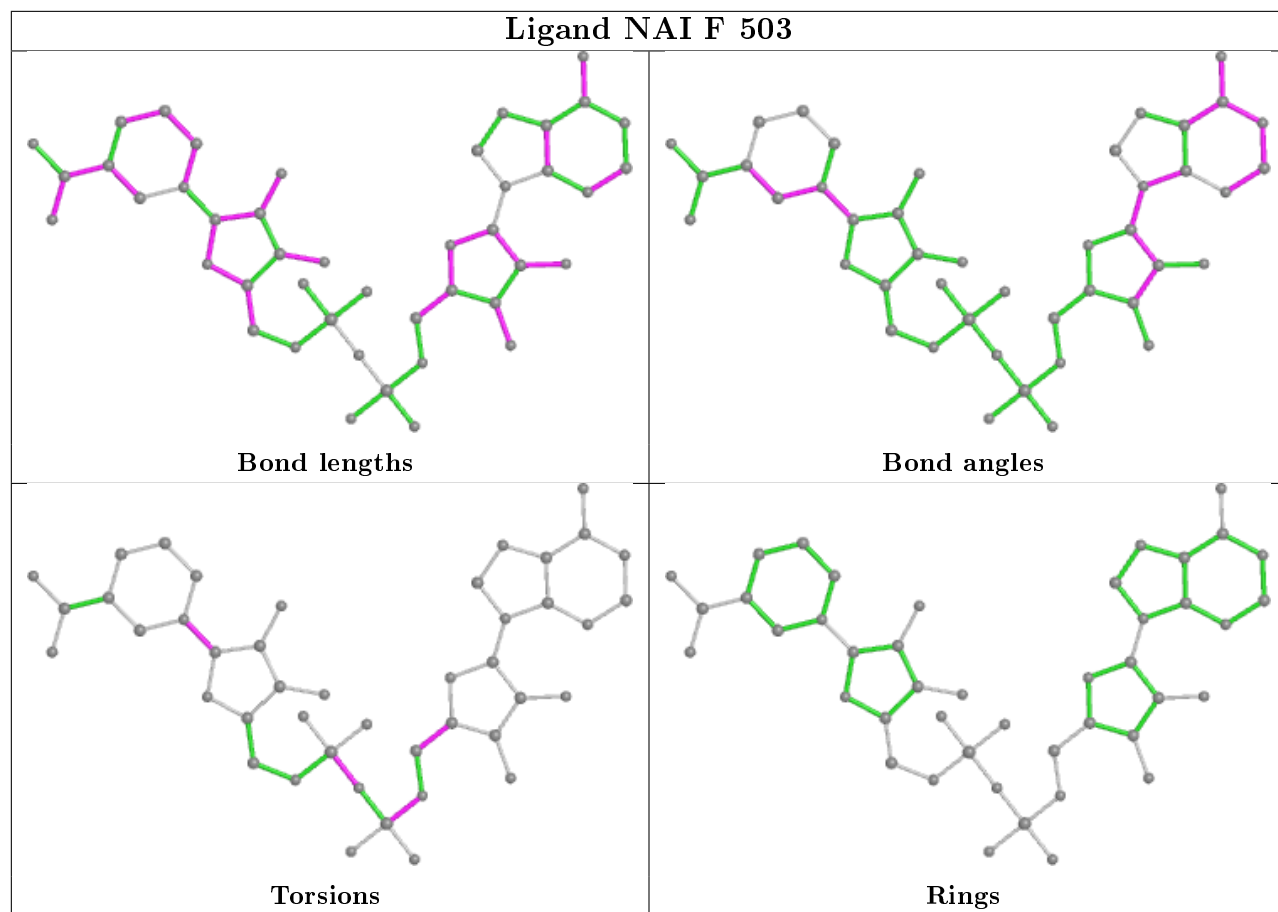
There are no ring outliers.

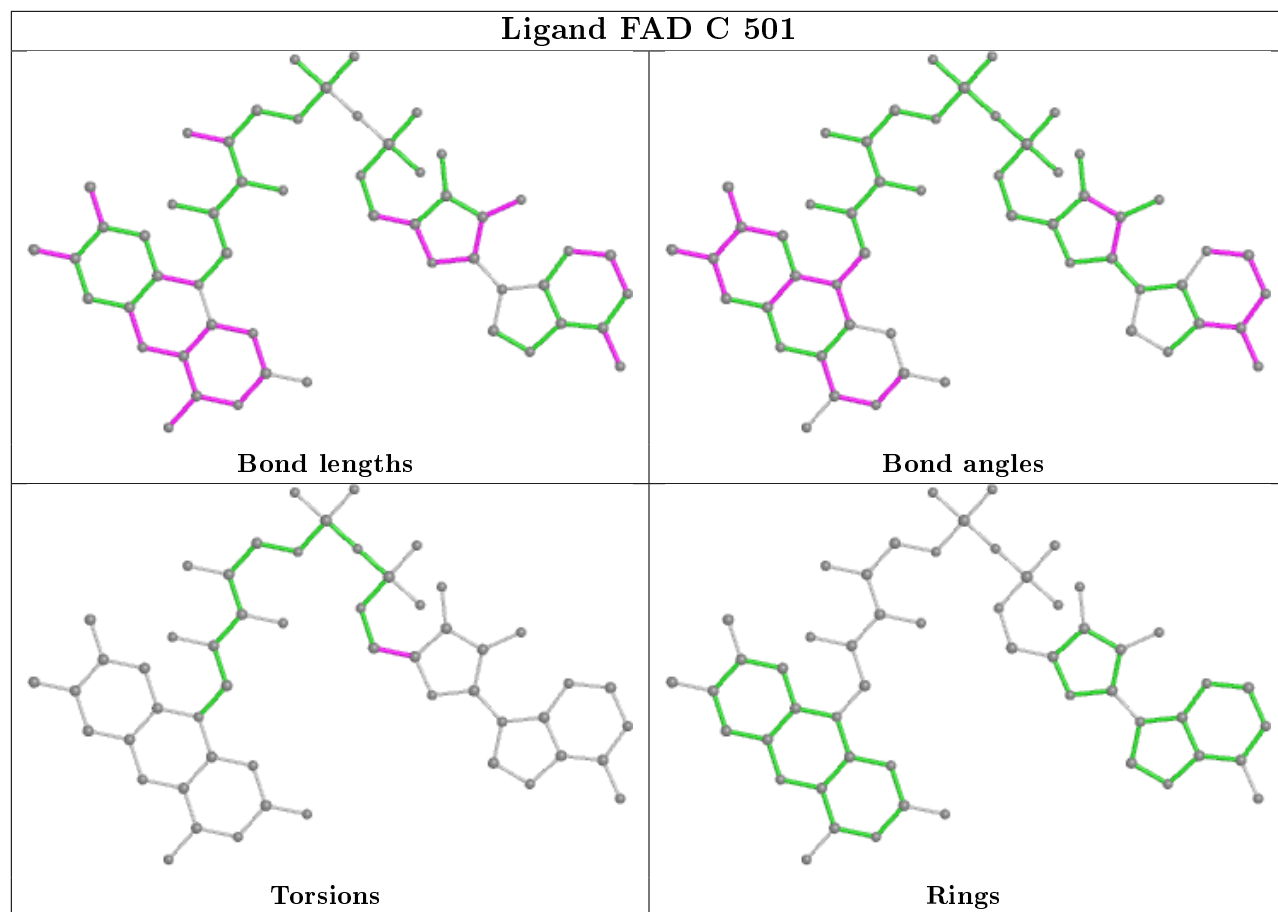
18 monomers are involved in 35 short contacts:

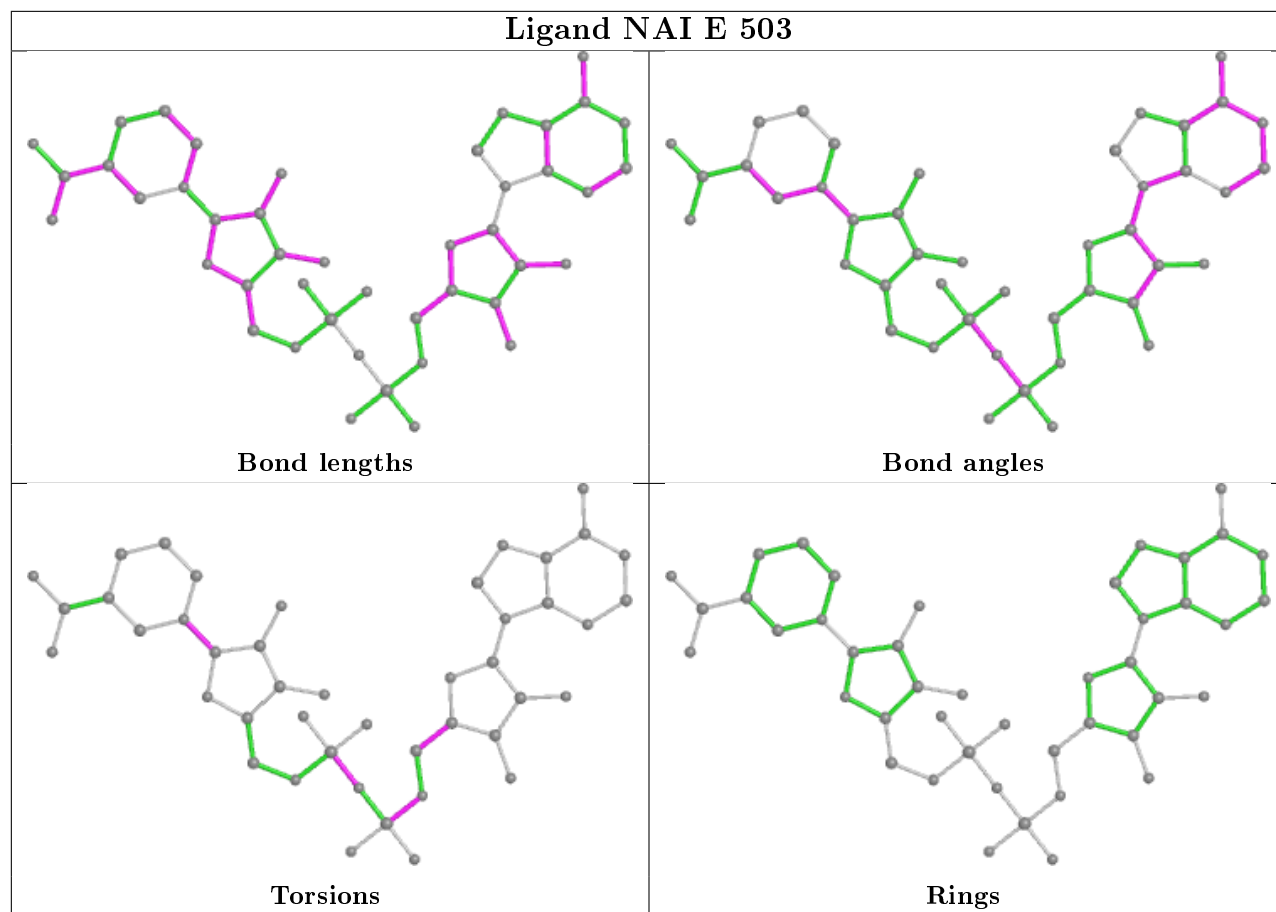
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	H	504	EDO	5	0
4	D	503	NAI	1	0
4	F	503	NAI	2	0
4	E	503	NAI	2	0
2	A	501	FAD	2	0
2	B	501	FAD	1	0
4	C	503	NAI	2	0
2	G	501	FAD	1	0
2	H	501	FAD	1	0
2	F	501	FAD	2	0
4	A	503	NAI	2	0
4	H	503	NAI	2	0
2	E	501	FAD	3	0
2	D	501	FAD	1	0
4	G	503	NAI	2	0
4	B	503	NAI	2	0
5	F	505	EDO	3	0
5	F	504	EDO	1	0

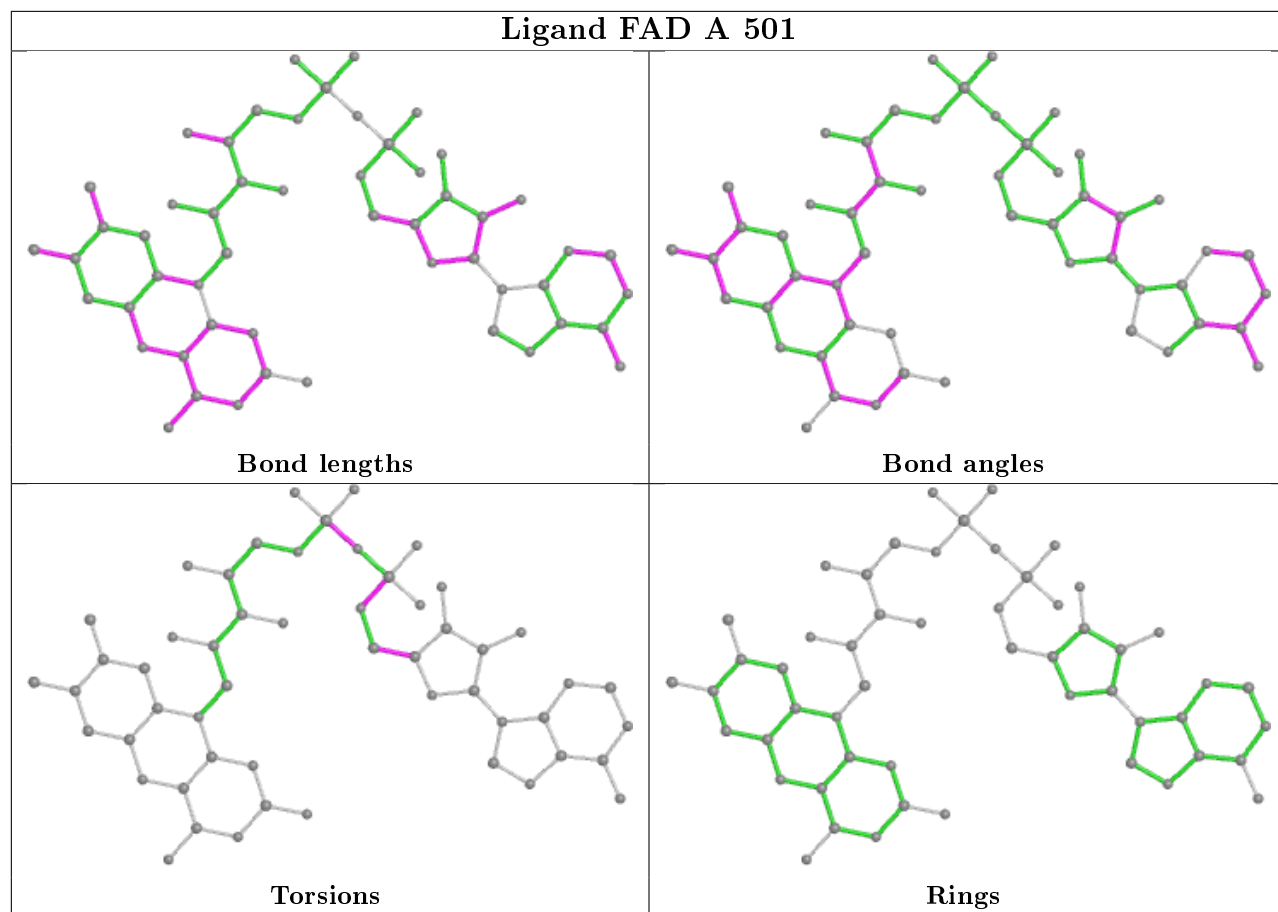
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

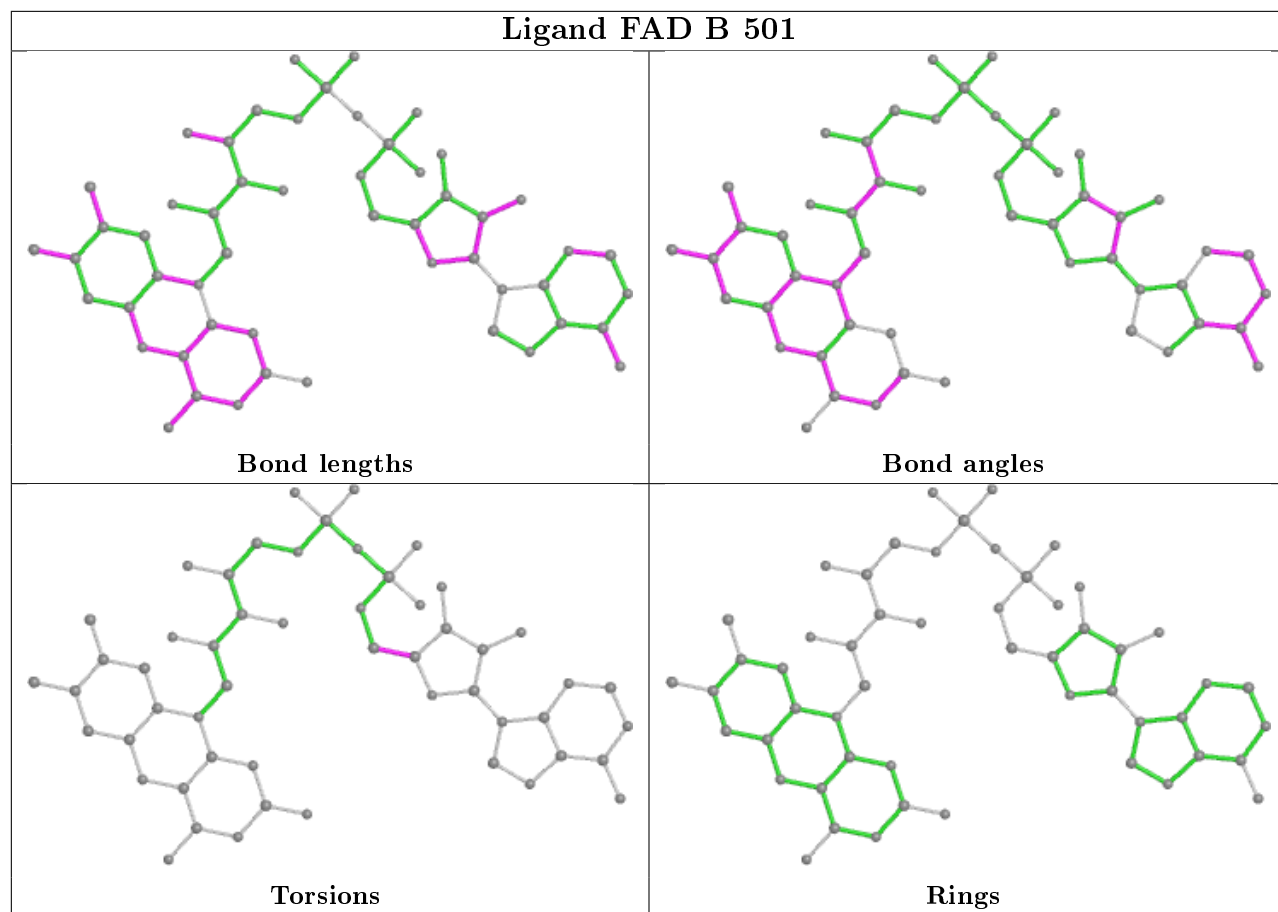


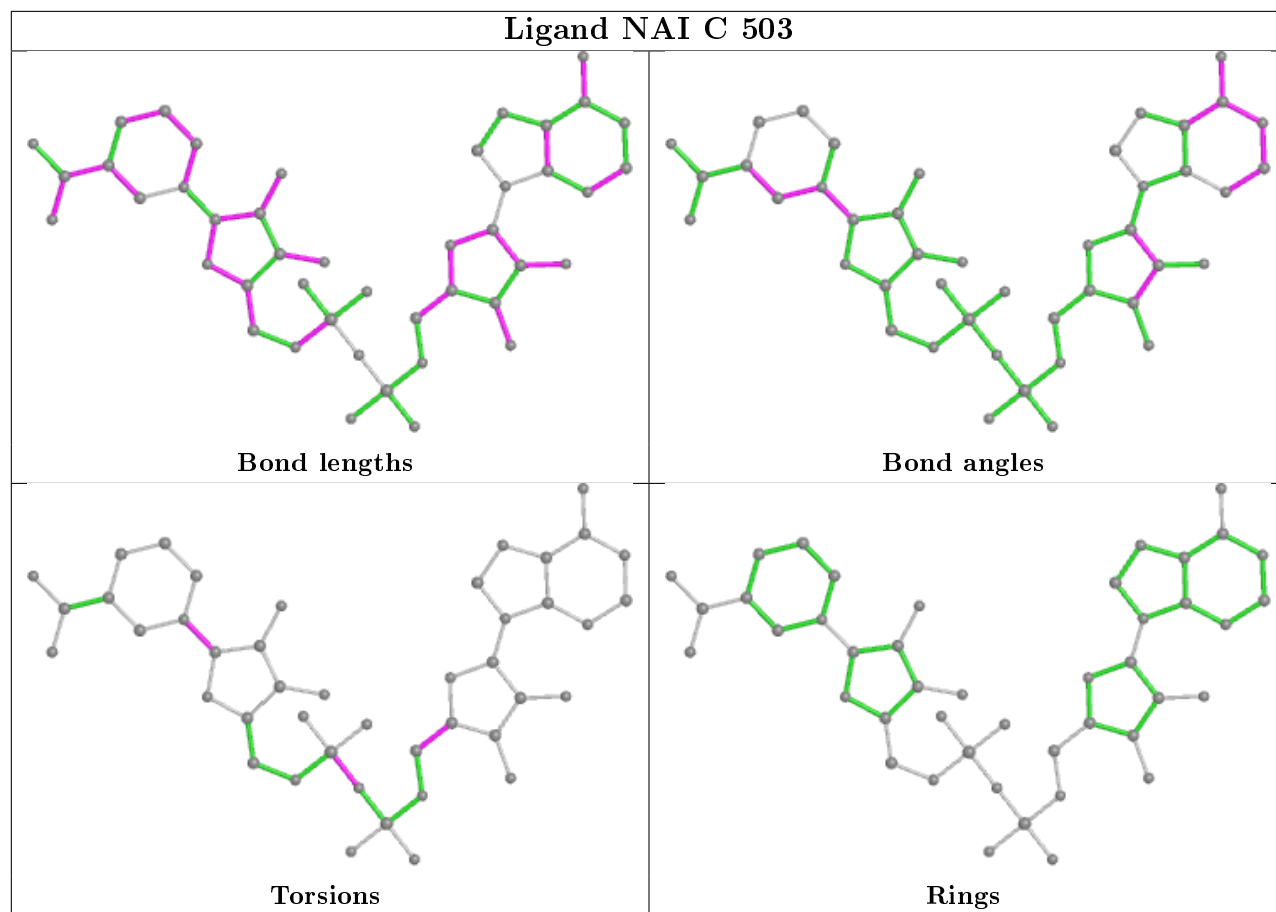


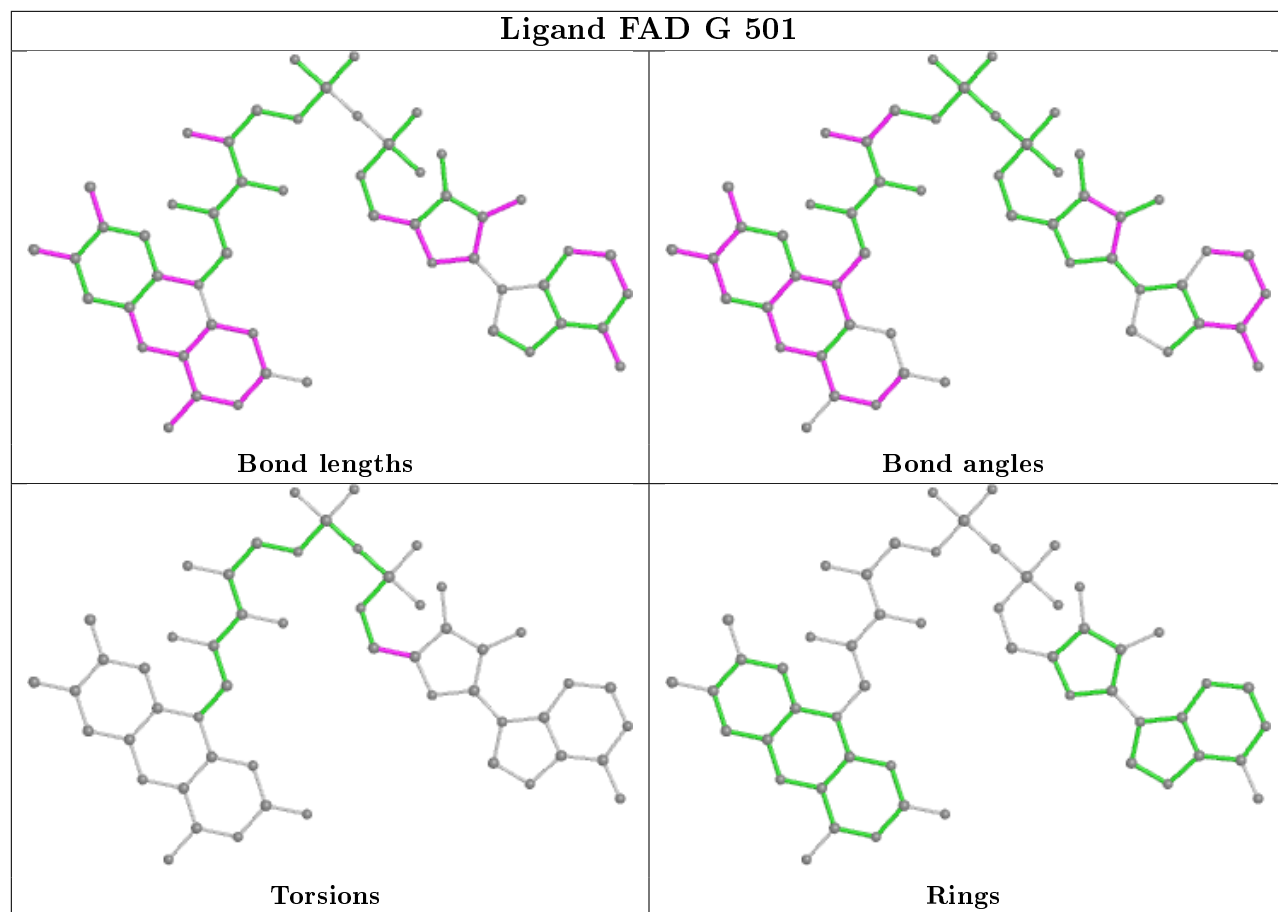


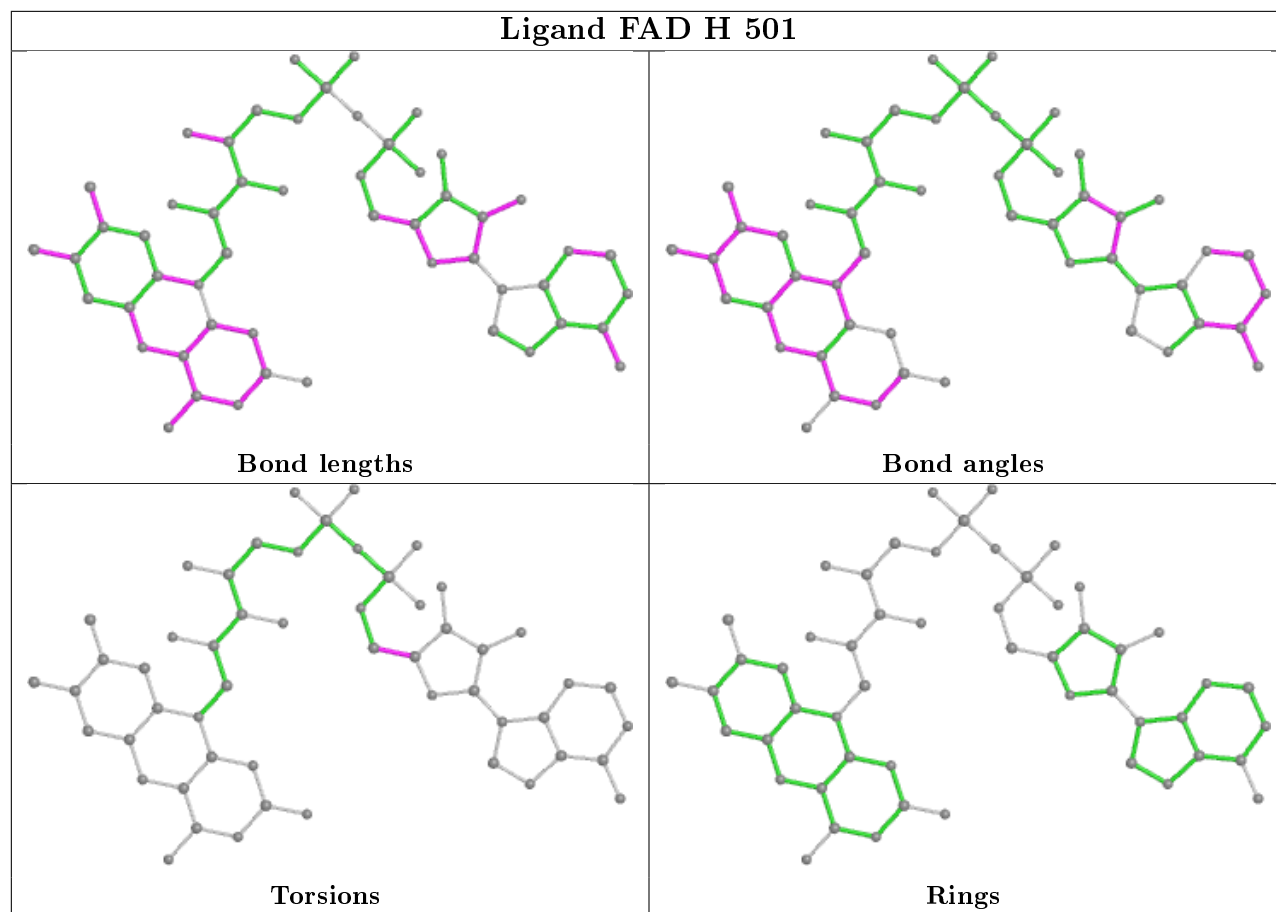


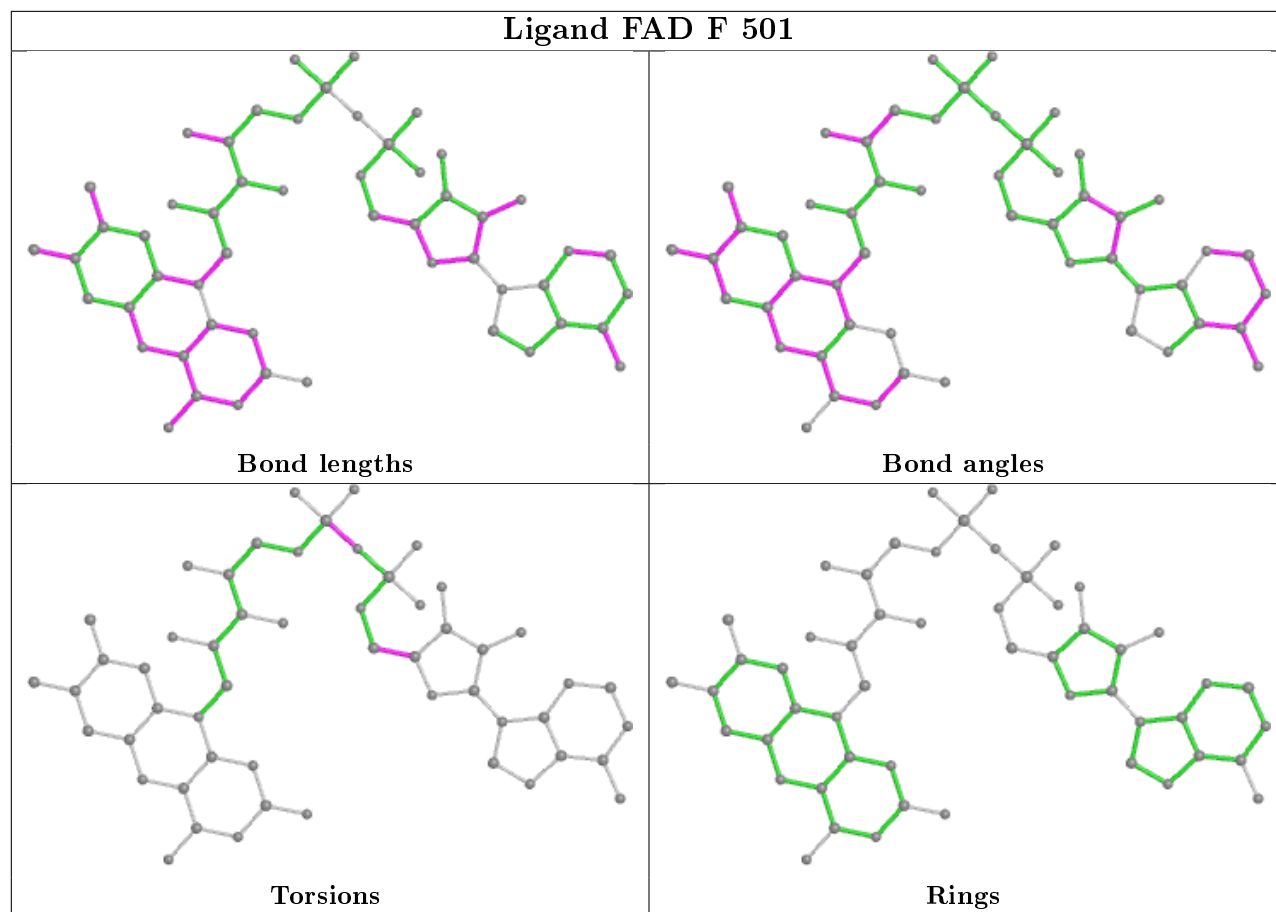


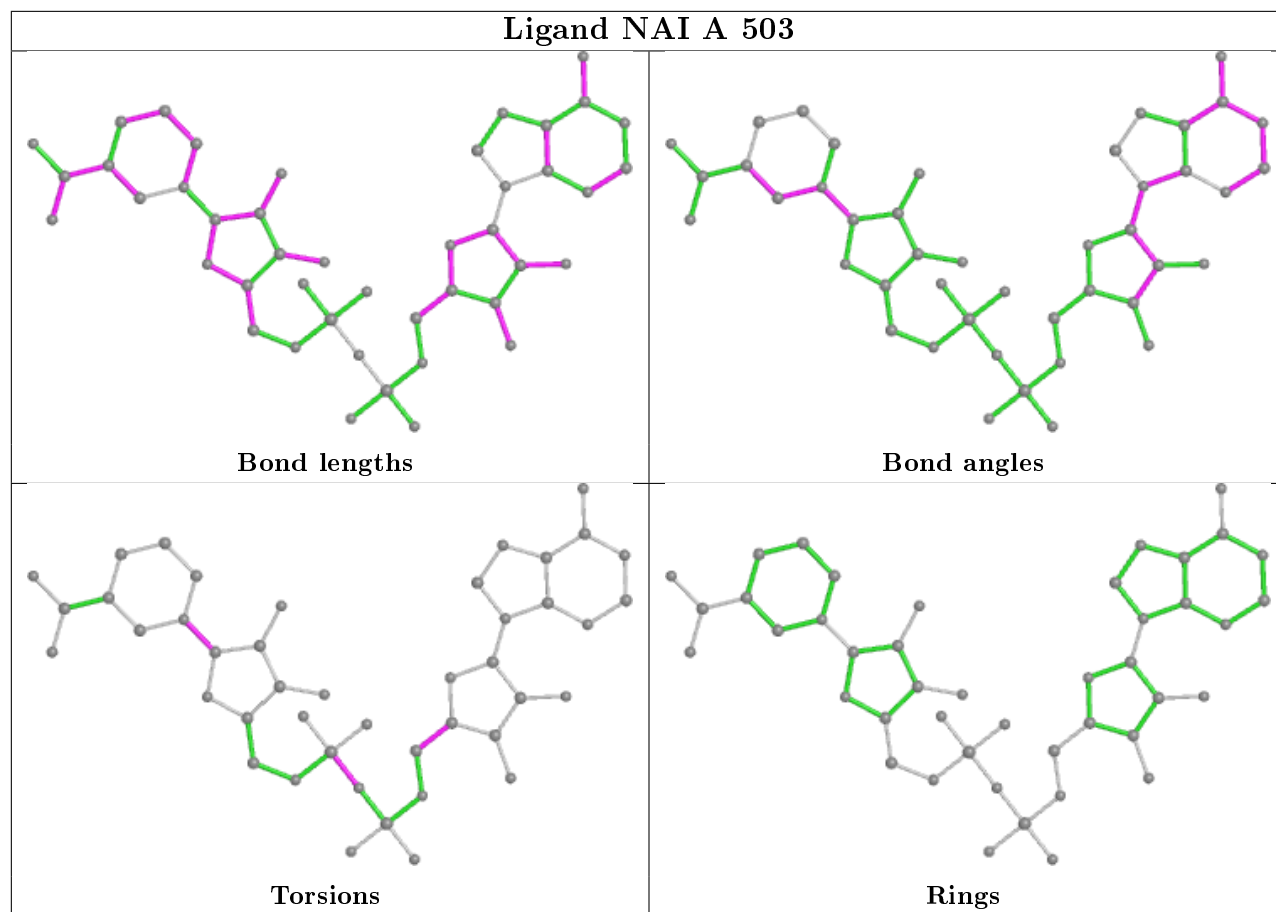


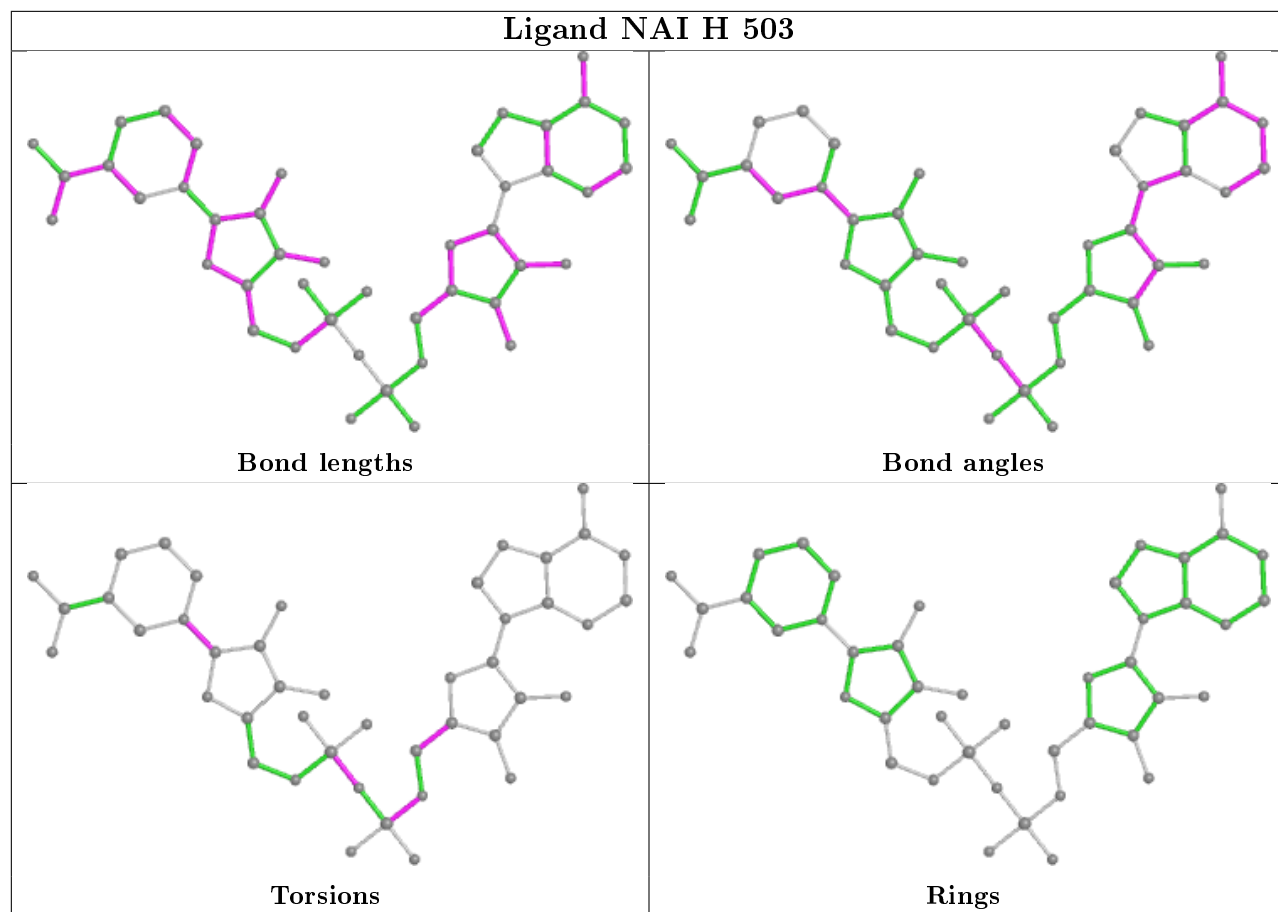


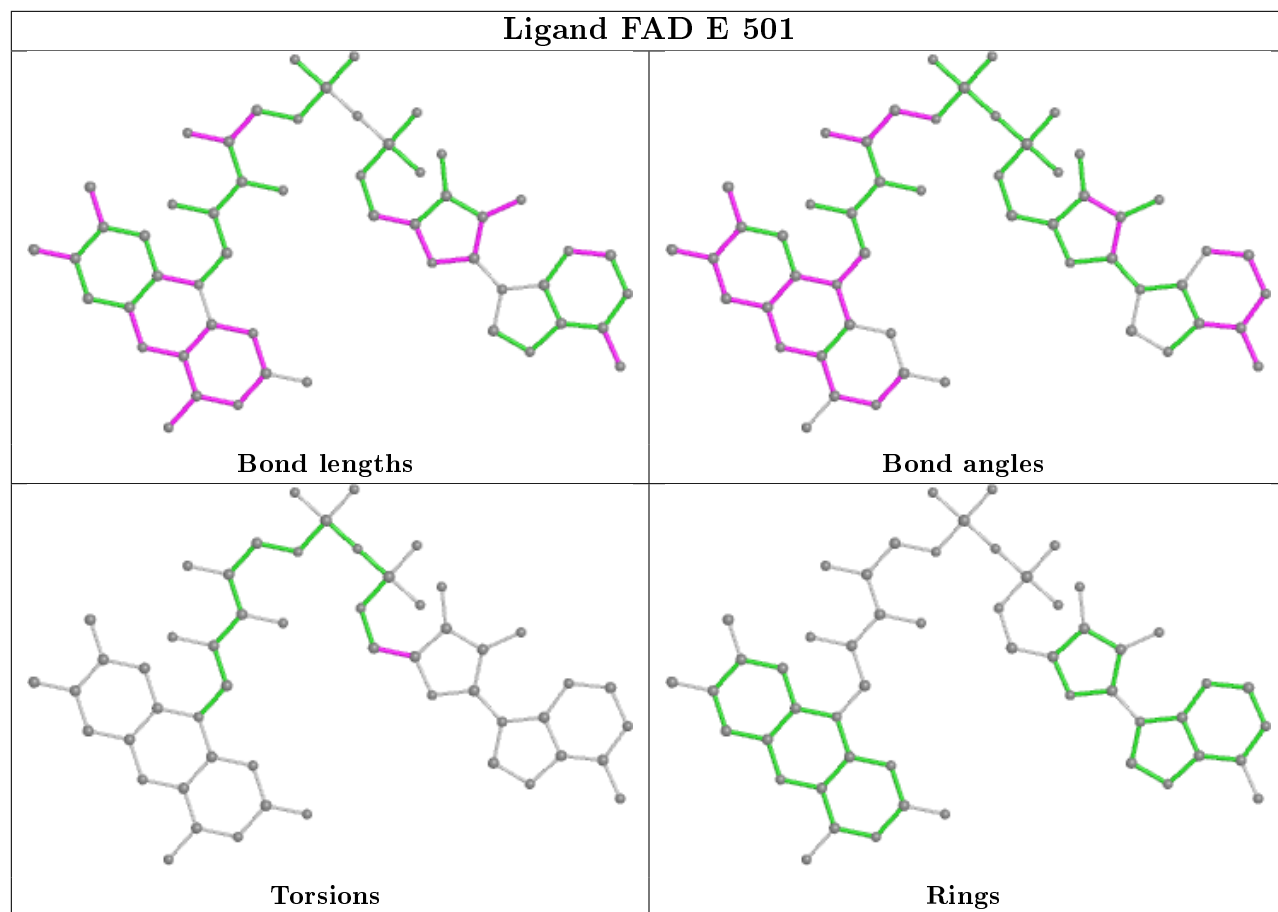


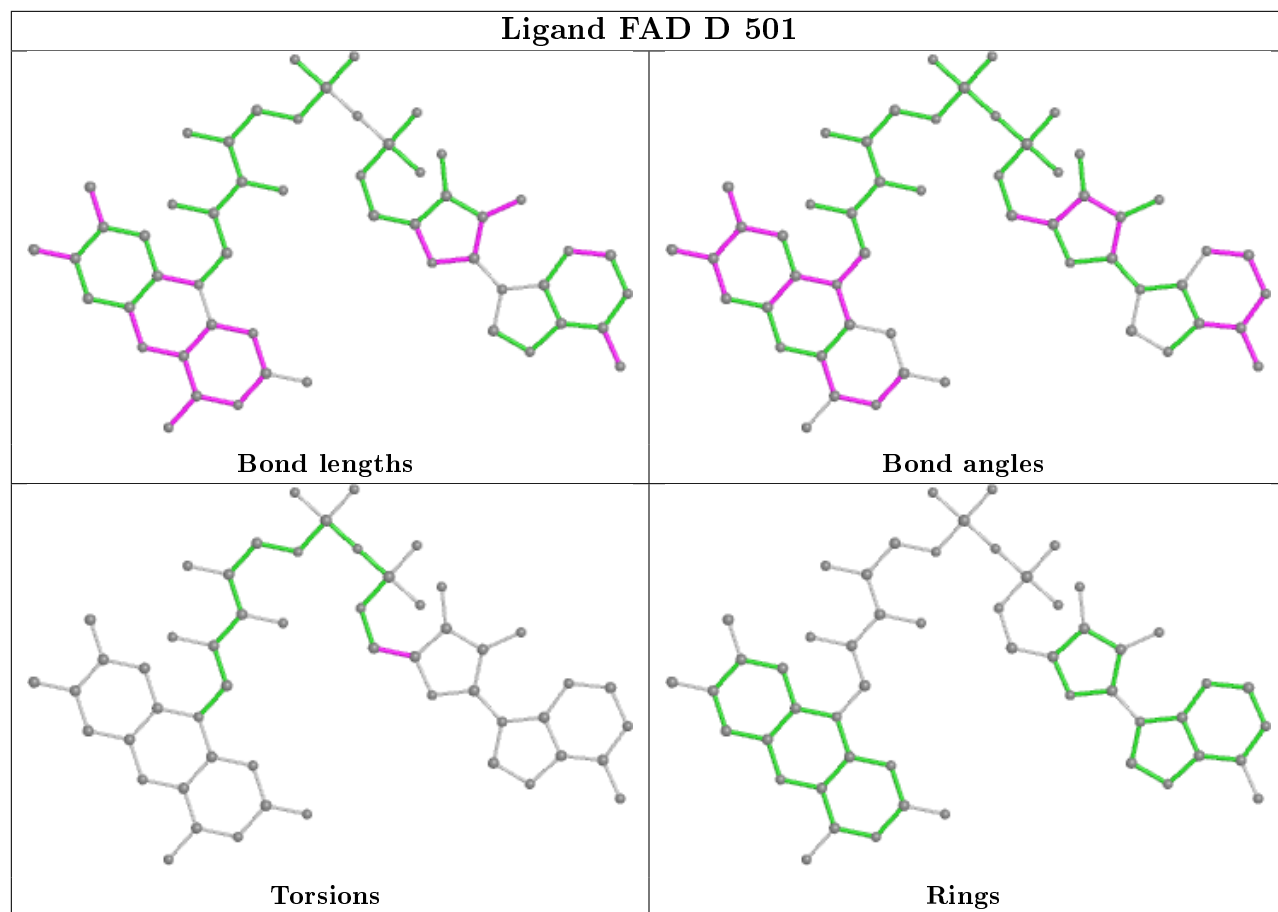


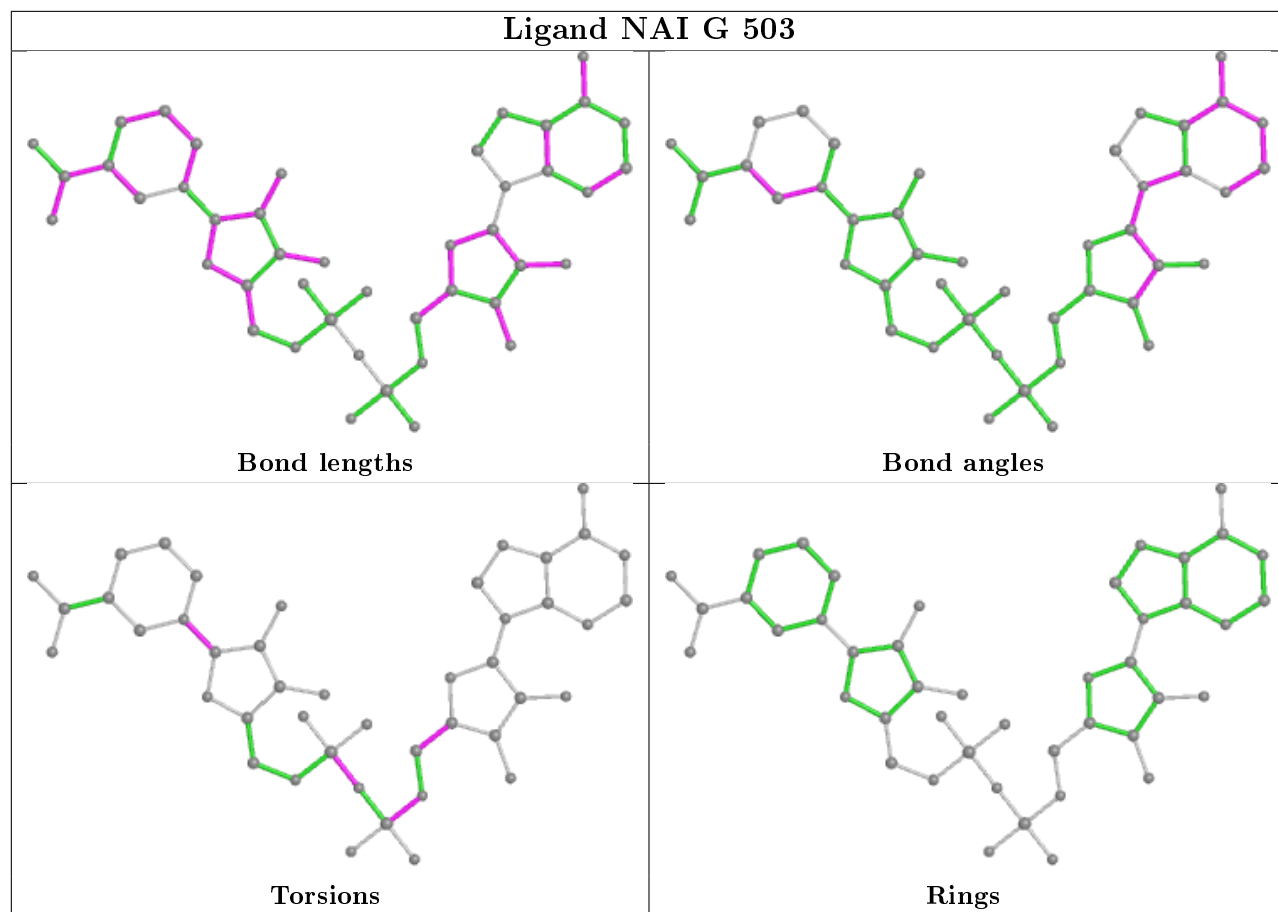


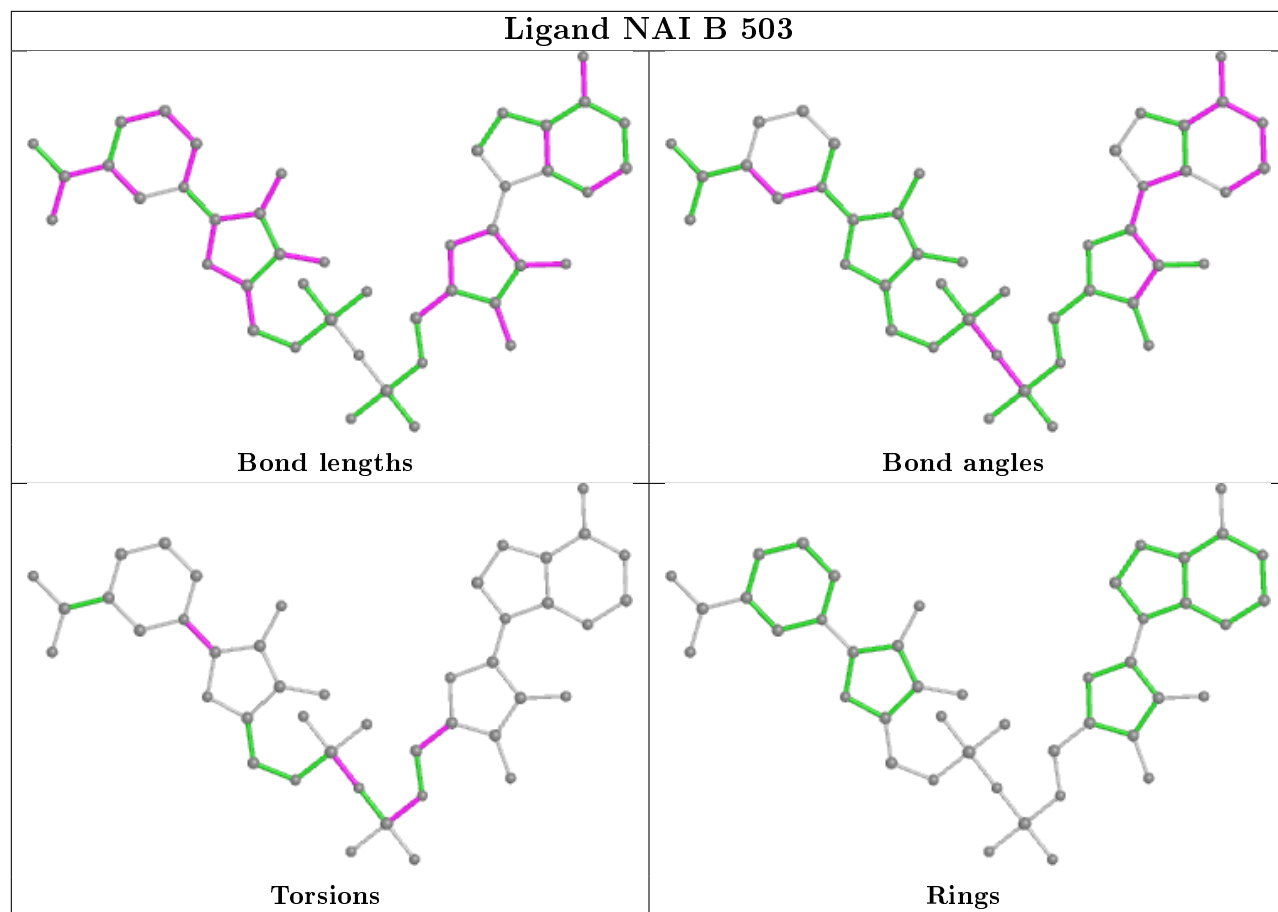












5.7 Other polymers [i](#)

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	449/518 (86%)	-0.70	0 100 100	13, 23, 42, 66	0
1	B	450/518 (86%)	-0.60	4 (0%) 84 83	14, 27, 49, 78	0
1	C	450/518 (86%)	-0.64	2 (0%) 92 92	14, 27, 49, 80	0
1	D	450/518 (86%)	-0.69	3 (0%) 87 87	13, 23, 42, 80	0
1	E	449/518 (86%)	-0.61	2 (0%) 92 92	15, 27, 53, 77	0
1	F	448/518 (86%)	-0.57	4 (0%) 84 83	14, 29, 55, 81	0
1	G	448/518 (86%)	-0.61	1 (0%) 95 94	14, 28, 53, 80	0
1	H	449/518 (86%)	-0.57	5 (1%) 80 79	14, 27, 53, 73	0
All	All	3593/4144 (86%)	-0.62	21 (0%) 89 88	13, 26, 51, 81	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	448	VAL	4.5
1	E	219	ALA	4.5
1	B	119	LYS	3.4
1	C	448	VAL	3.3
1	B	449	ASN	3.2

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 ⓘ

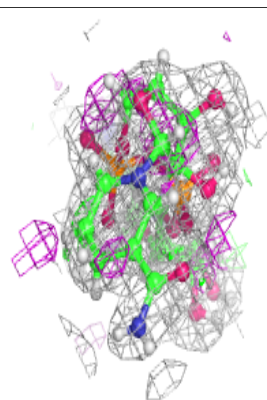
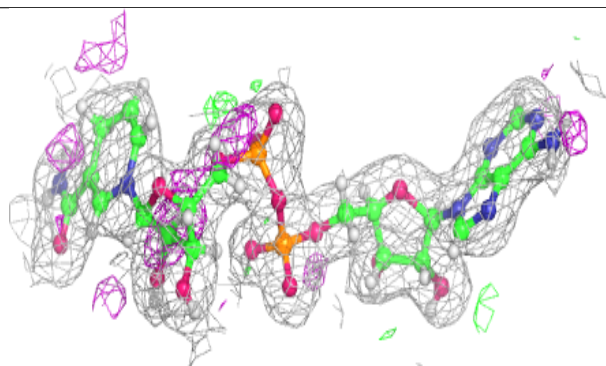
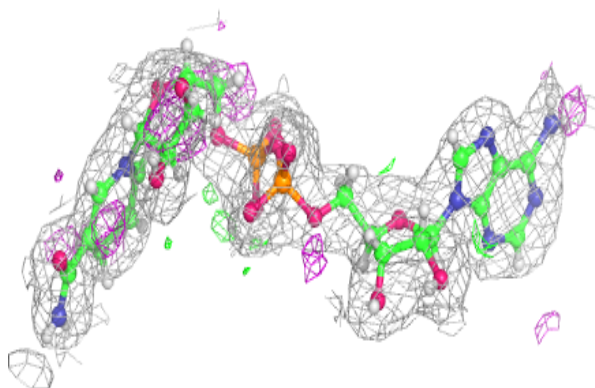
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	EDO	F	505	4/4	0.90	0.19	21,30,43,43	0
5	EDO	H	504	4/4	0.91	0.17	25,32,40,40	0
5	EDO	F	506	4/4	0.92	0.12	30,41,53,55	0
5	EDO	H	505	4/4	0.93	0.11	21,31,47,56	0
5	EDO	E	504	4/4	0.95	0.10	27,35,36,42	0
5	EDO	D	504	4/4	0.95	0.12	28,34,41,49	0
4	NAI	E	503	44/44	0.95	0.09	19,26,33,40	0
5	EDO	A	505	4/4	0.96	0.08	22,26,31,36	0
4	NAI	F	503	44/44	0.96	0.10	20,29,36,39	0
5	EDO	G	504	4/4	0.96	0.10	27,32,35,42	0
4	NAI	G	503	44/44	0.96	0.09	19,28,36,38	0
5	EDO	A	504	4/4	0.96	0.06	27,33,46,56	0
5	EDO	F	504	4/4	0.96	0.15	27,34,39,47	0
2	FAD	H	501	53/53	0.97	0.07	16,23,31,37	0
2	FAD	B	501	53/53	0.97	0.08	15,24,32,38	0
2	FAD	F	501	53/53	0.97	0.08	18,27,32,36	0
2	FAD	C	501	53/53	0.97	0.08	15,24,32,37	0
4	NAI	A	503	44/44	0.97	0.09	16,23,29,38	0
4	NAI	H	503	44/44	0.97	0.09	18,28,36,38	0
4	NAI	C	503	44/44	0.97	0.09	18,26,34,37	0
2	FAD	E	501	53/53	0.97	0.09	16,23,33,40	0
4	NAI	D	503	44/44	0.97	0.09	16,23,31,38	0
2	FAD	A	501	53/53	0.97	0.08	16,20,26,31	0
4	NAI	B	503	44/44	0.97	0.09	19,26,34,39	0
5	EDO	D	505	4/4	0.97	0.13	29,37,46,55	0
2	FAD	G	501	53/53	0.97	0.09	16,24,30,37	0
2	FAD	D	501	53/53	0.98	0.09	14,20,27,31	0
5	EDO	B	504	4/4	0.98	0.10	25,30,37,44	0
5	EDO	C	504	4/4	0.98	0.09	25,31,45,55	0
3	OXY	F	502	2/2	0.98	0.05	27,27,27,27	0
3	OXY	H	502	2/2	0.99	0.04	25,25,25,25	0
3	OXY	C	502	2/2	0.99	0.04	25,25,25,26	0
3	OXY	D	502	2/2	0.99	0.07	23,23,23,24	0
3	OXY	G	502	2/2	0.99	0.06	25,25,25,26	0
3	OXY	A	502	2/2	0.99	0.06	24,24,24,26	0
3	OXY	E	502	2/2	0.99	0.10	23,23,23,26	0
3	OXY	B	502	2/2	0.99	0.04	26,26,26,26	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.

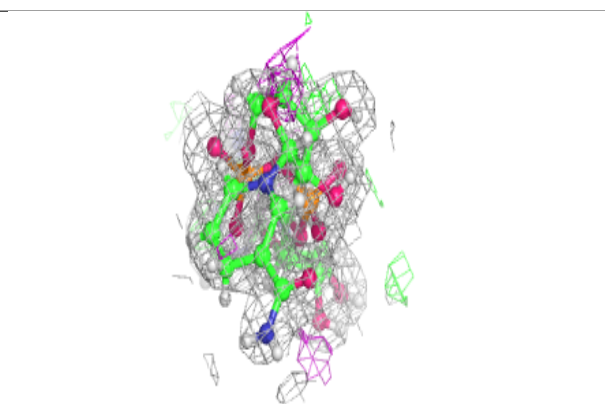
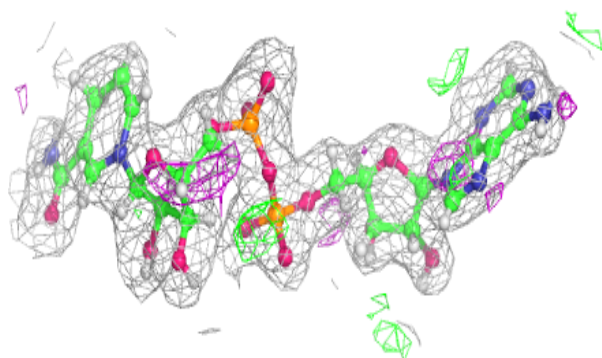
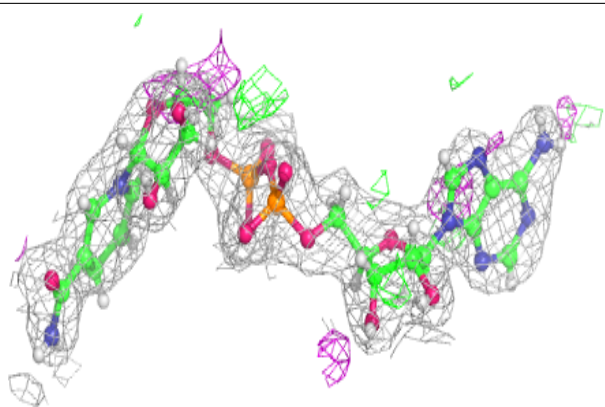
Electron density around NAI E 503:

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

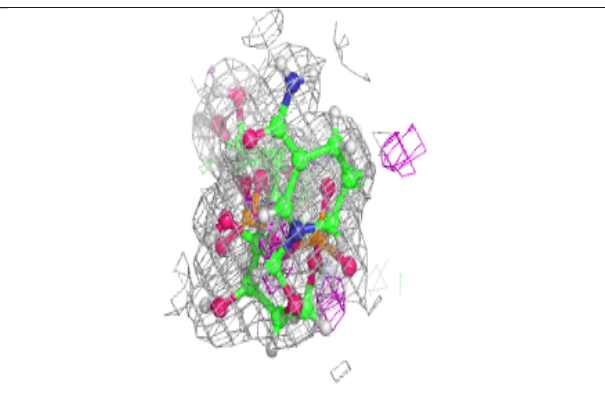
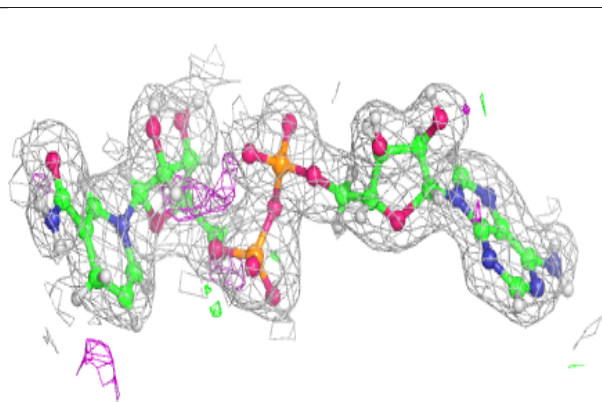
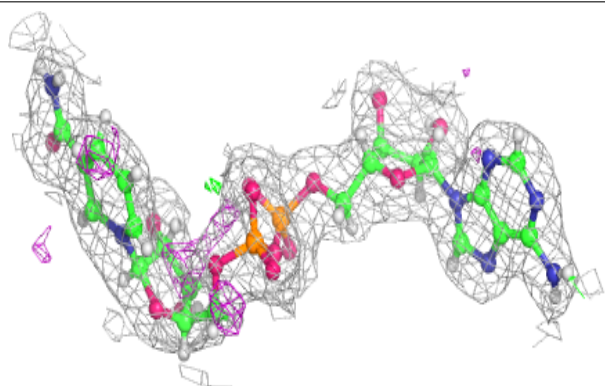


Electron density around NAI F 503:

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

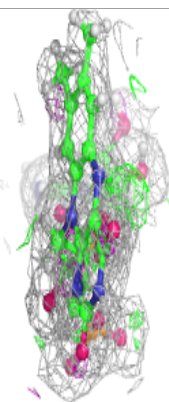
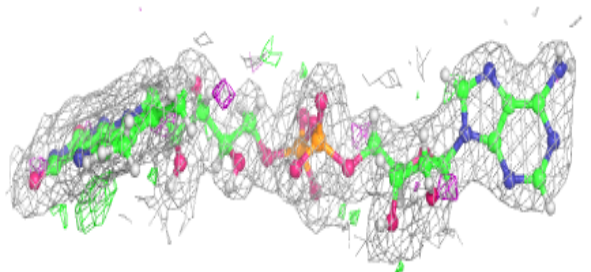
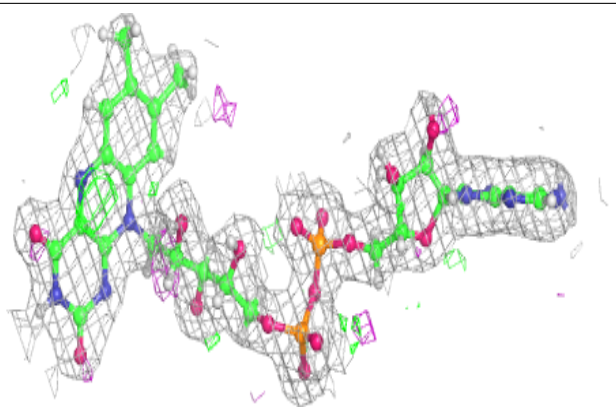
**Electron density around NAI G 503:**

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

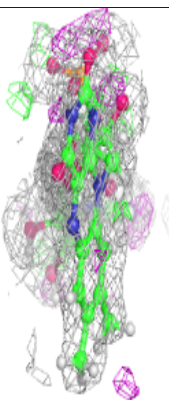
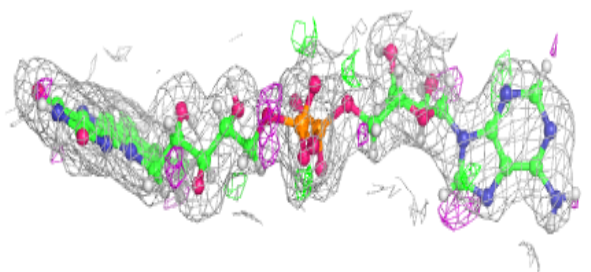
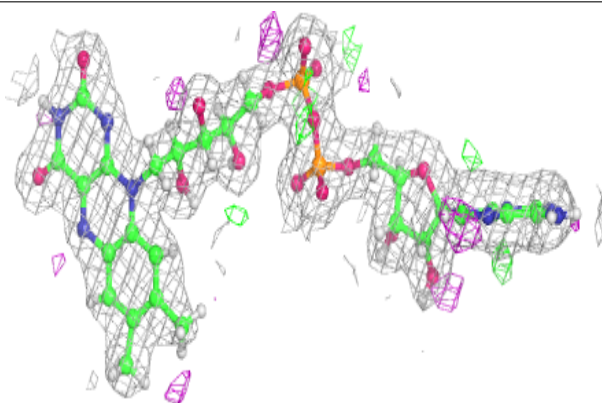


Electron density around FAD H 501:

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

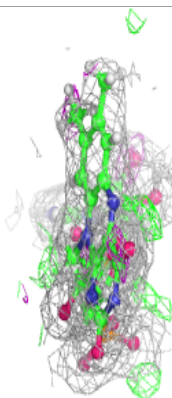
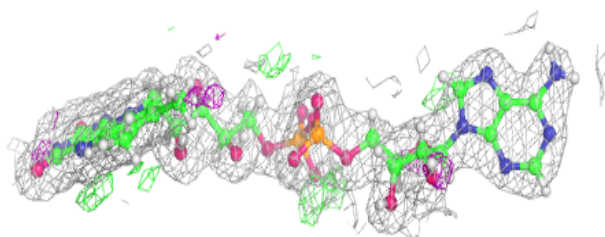
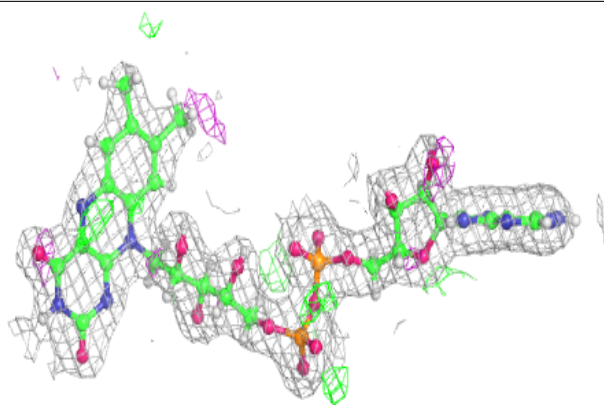
**Electron density around FAD B 501:**

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

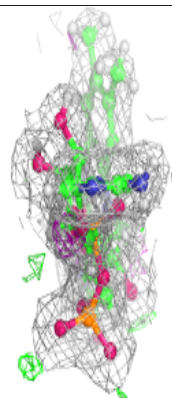
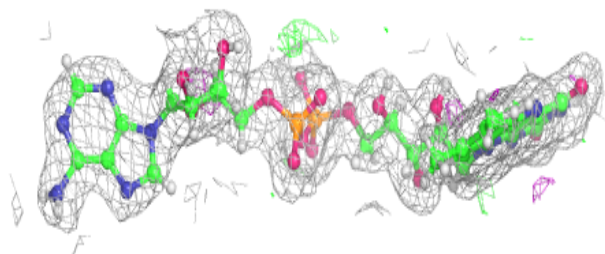
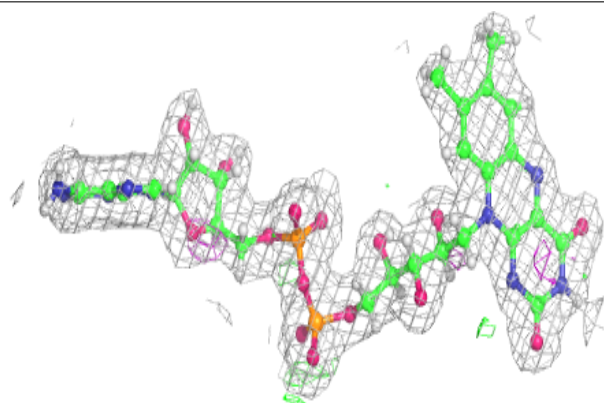


Electron density around FAD F 501:

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

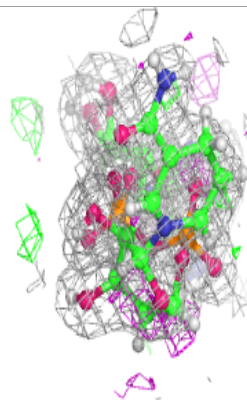
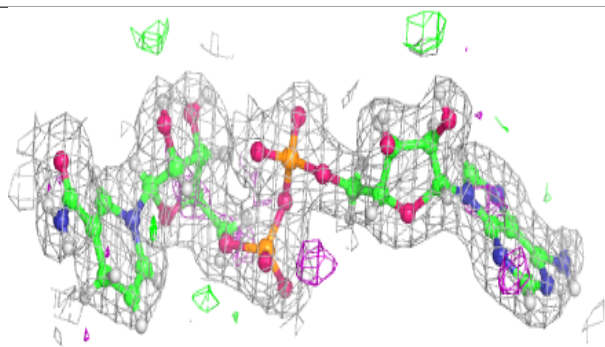
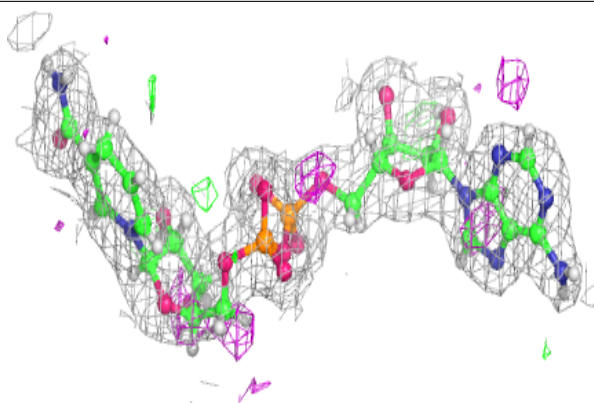
**Electron density around FAD C 501:**

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

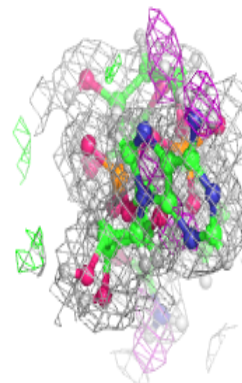
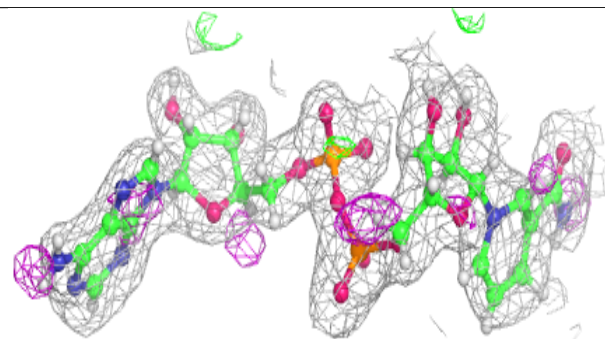
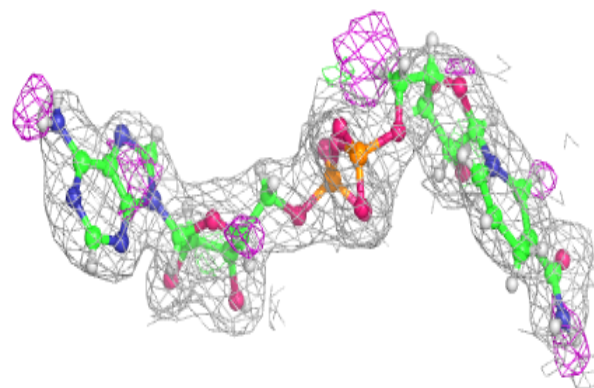


Electron density around NAI A 503:

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

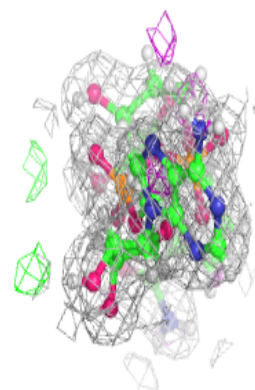
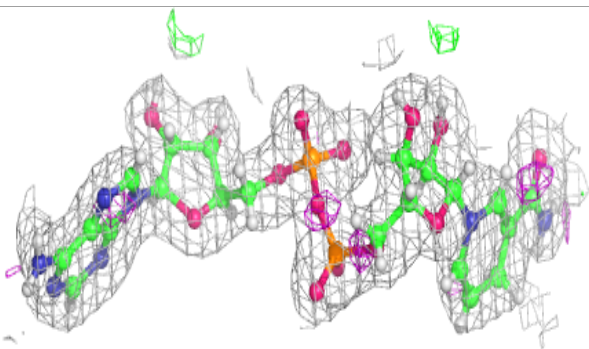
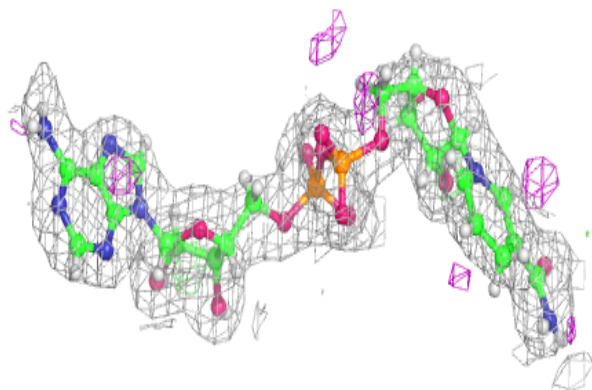
**Electron density around NAI H 503:**

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

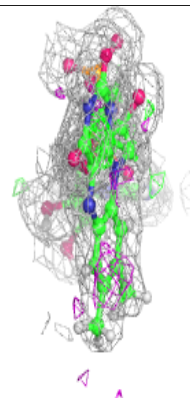
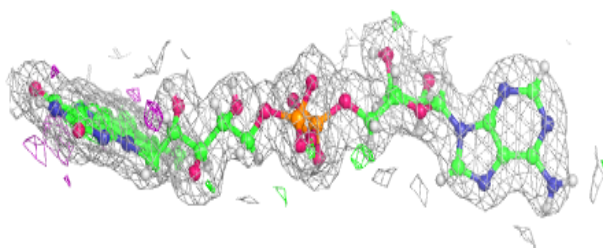
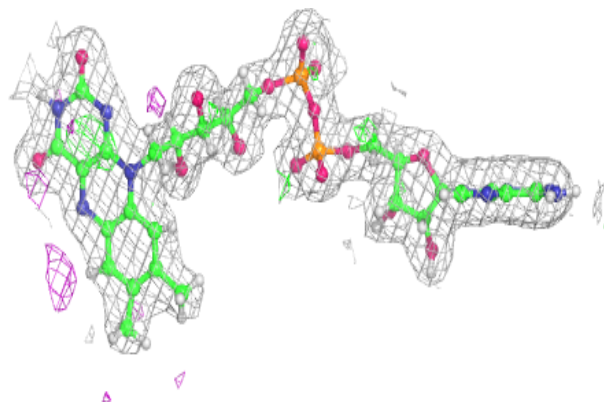


Electron density around NAI C 503:

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

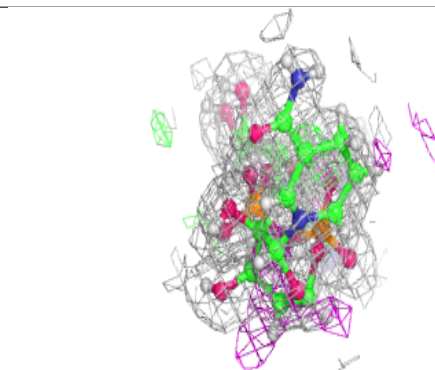
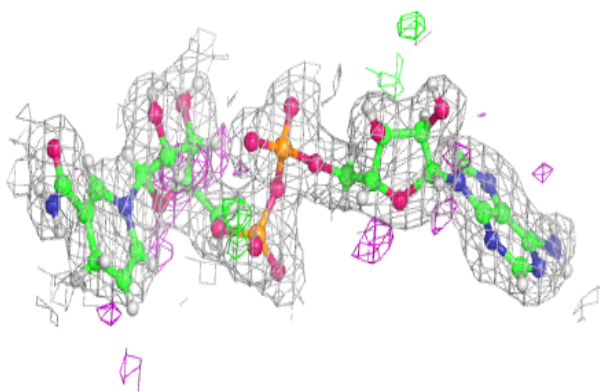
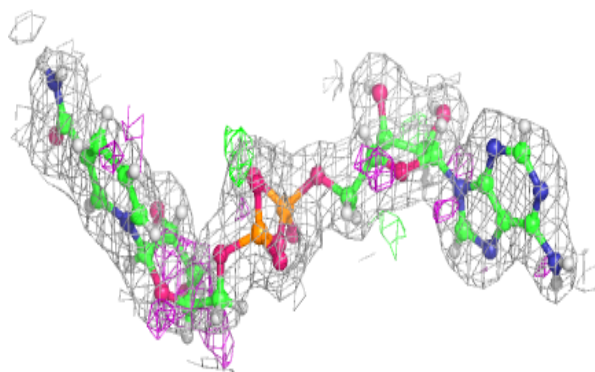
**Electron density around FAD E 501:**

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

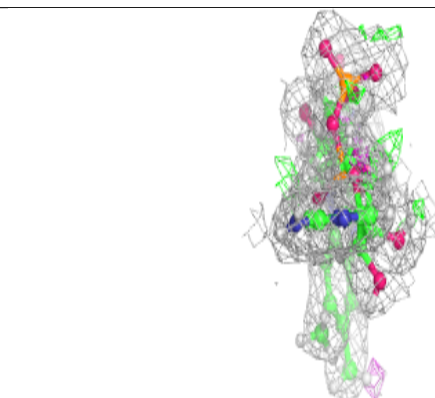
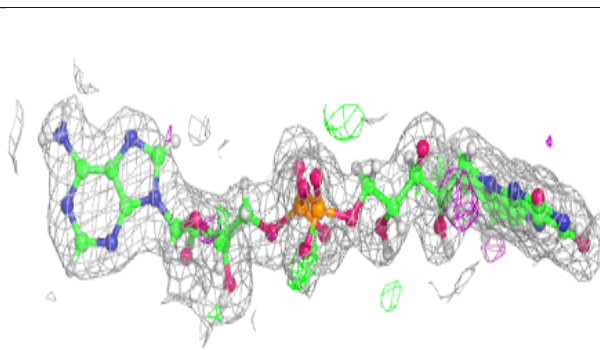
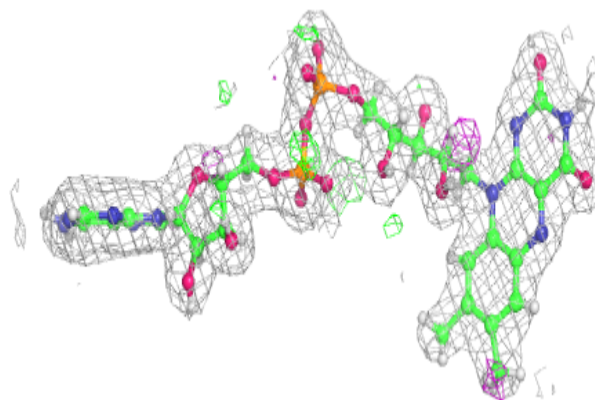


Electron density around NAI D 503:

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

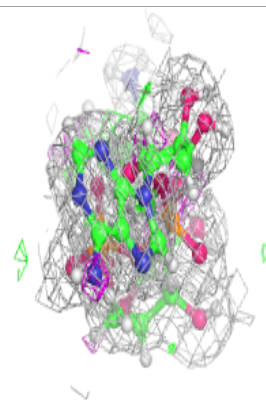
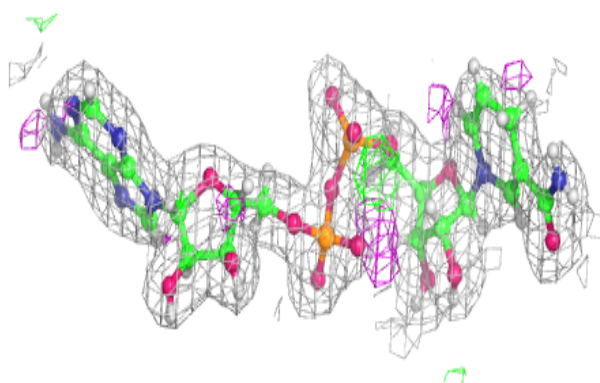
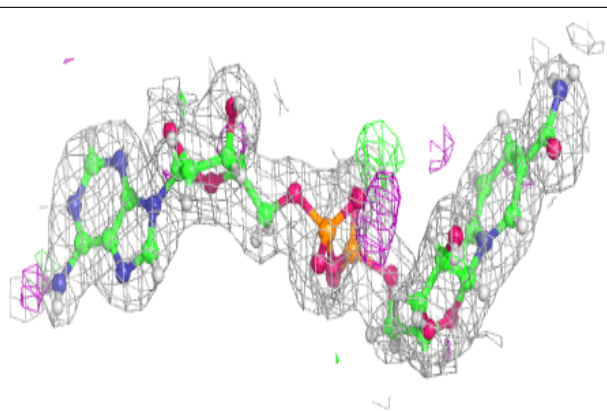
**Electron density around FAD A 501:**

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

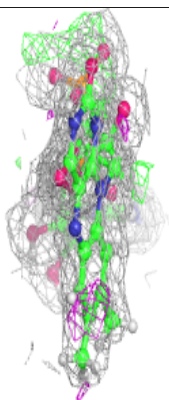
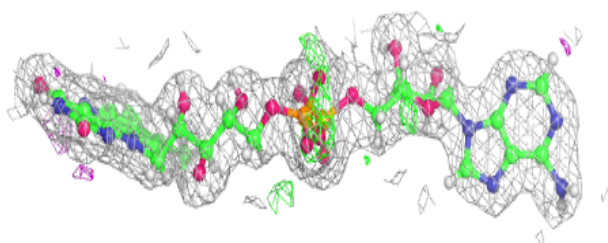
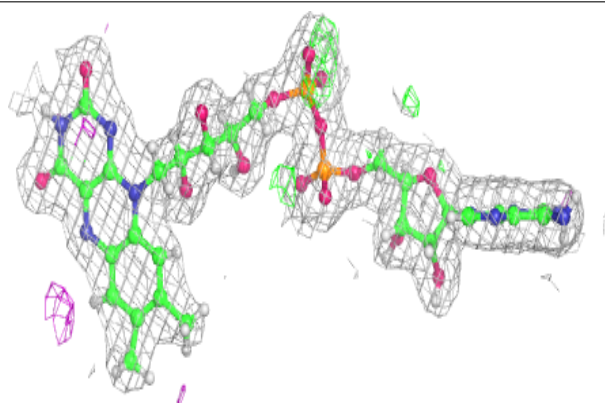


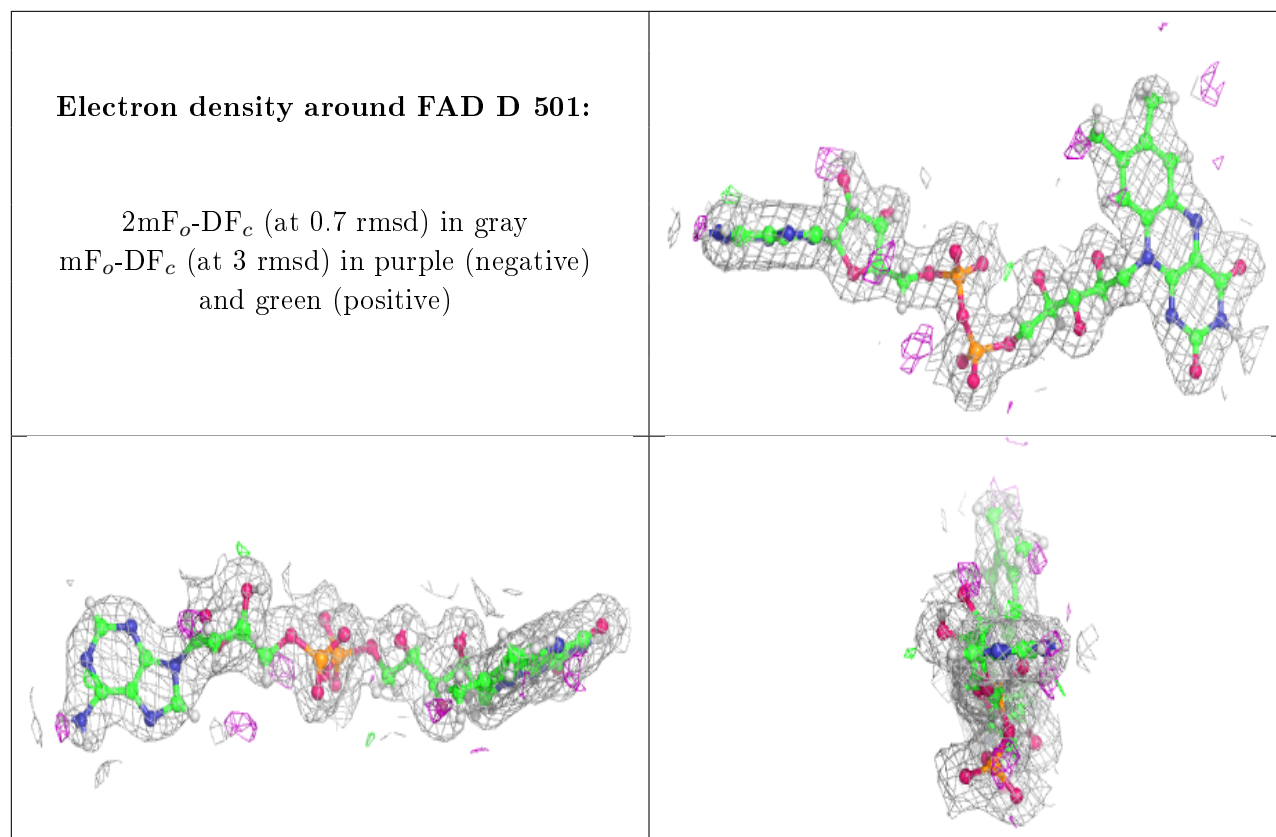
Electron density around NAI B 503:

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

**Electron density around FAD G 501:**

$2mF_o-DF_c$ (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.