



# Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 05:52 am BST

PDB ID : 2XLT  
Title : Joint-functions of protein residues and NADP(H) in oxygen-activation by flavin-containing monooxygenase: complex with 3-Acetylpyridine adenine dinucleotide phosphate (APADP)  
Authors : Orru, R.; Fraaije, M.W.; Mattevi, A.  
Deposited on : 2010-07-21  
Resolution : 2.20 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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

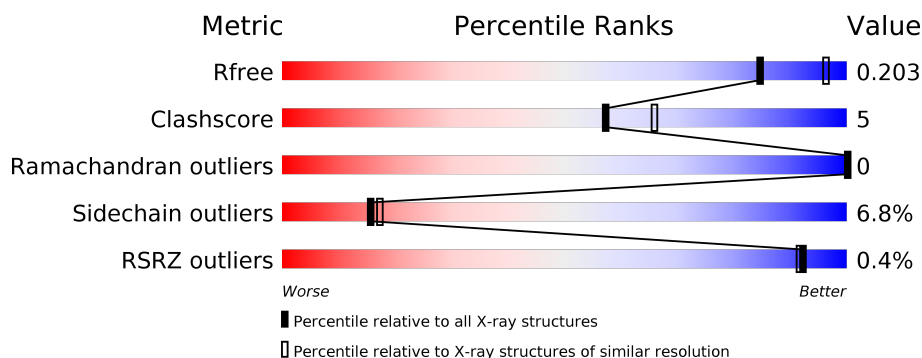
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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  $\geq 3$ , 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	461	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>84%</span> <span>10%</span> </div> </div>
1	B	461	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>82%</span> <span>11%</span> </div> </div>
1	C	461	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>81%</span> <span>11%</span> </div> </div>
1	D	461	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>85%</span> <span>10%</span> </div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 16288 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 FLAVIN-CONTAINING MONOOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	446	Total	C	N	O	S	0	0	0
			3660	2348	607	685	20			
1	B	446	Total	C	N	O	S	0	0	0
			3660	2348	607	685	20			
1	C	446	Total	C	N	O	S	0	0	0
			3660	2348	607	685	20			
1	D	446	Total	C	N	O	S	0	0	0
			3660	2348	607	685	20			

There are 28 discrepancies between the modelled and reference sequences:

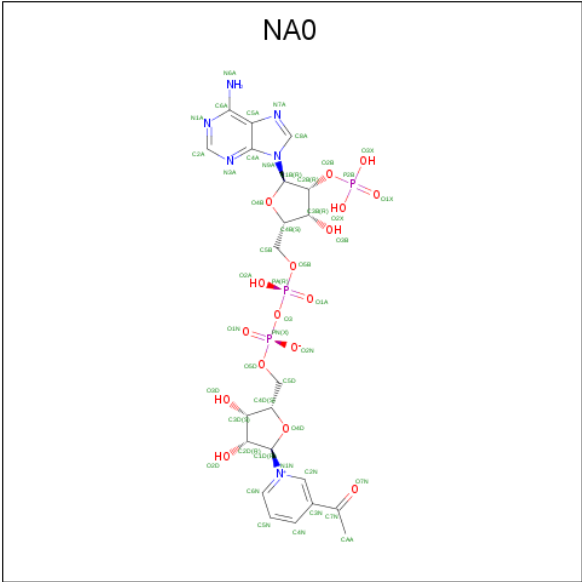
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q83XK4
A	2	ALA	-	expression tag	UNP Q83XK4
A	3	MET	-	expression tag	UNP Q83XK4
A	4	GLY	-	expression tag	UNP Q83XK4
A	5	SER	-	expression tag	UNP Q83XK4
A	158	ALA	GLU	conflict	UNP Q83XK4
A	159	ALA	GLU	conflict	UNP Q83XK4
B	1	GLY	-	expression tag	UNP Q83XK4
B	2	ALA	-	expression tag	UNP Q83XK4
B	3	MET	-	expression tag	UNP Q83XK4
B	4	GLY	-	expression tag	UNP Q83XK4
B	5	SER	-	expression tag	UNP Q83XK4
B	158	ALA	GLU	conflict	UNP Q83XK4
B	159	ALA	GLU	conflict	UNP Q83XK4
C	1	GLY	-	expression tag	UNP Q83XK4
C	2	ALA	-	expression tag	UNP Q83XK4
C	3	MET	-	expression tag	UNP Q83XK4
C	4	GLY	-	expression tag	UNP Q83XK4
C	5	SER	-	expression tag	UNP Q83XK4
C	158	ALA	GLU	conflict	UNP Q83XK4
C	159	ALA	GLU	conflict	UNP Q83XK4

*Continued on next page...*

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	GLY	-	expression tag	UNP Q83XK4
D	2	ALA	-	expression tag	UNP Q83XK4
D	3	MET	-	expression tag	UNP Q83XK4
D	4	GLY	-	expression tag	UNP Q83XK4
D	5	SER	-	expression tag	UNP Q83XK4
D	158	ALA	GLU	conflict	UNP Q83XK4
D	159	ALA	GLU	conflict	UNP Q83XK4

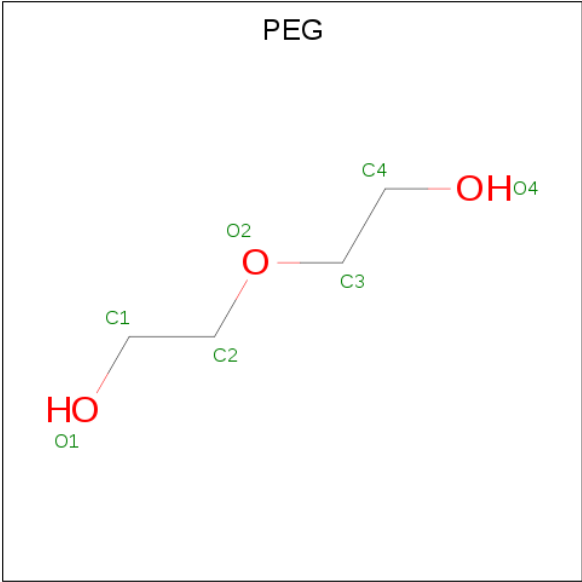
- 
- The chemical structure of FAD (Flavin Adenine Dinucleotide) is shown. It consists of a riboflavin moiety (top) linked to a ribitol moiety (middle), which is further linked to an adenosine moiety (bottom). The riboflavin moiety includes a ribityl side chain. The adenosine moiety includes an adenine base and a ribose sugar. The structure is labeled with various atoms and bonds, including C, N, O, and P, and is shown in a 3D representation.

- Molecule 3 is 3-ACETILPYRIDINE ADENINE DINUCLEOTIDE PHOSPHATE (three-letter code: NA0) (formula:  $C_{22}H_{29}N_6O_{17}P_3$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			48	22	6	17	3		
3	B	1	Total	C	N	O	P	0	0
			48	22	6	17	3		
3	C	1	Total	C	N	O	P	0	0
			48	22	6	17	3		
3	D	1	Total	C	N	O	P	0	0
			48	22	6	17	3		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 7 4 3	0	0
4	A	1	Total C O 7 4 3	0	0
4	A	1	Total C O 7 4 3	0	0
4	A	1	Total C O 7 4 3	0	0
4	B	1	Total C O 7 4 3	0	0
4	B	1	Total C O 7 4 3	0	0
4	B	1	Total C O 7 4 3	0	0
4	B	1	Total C O 7 4 3	0	0
4	C	1	Total C O 7 4 3	0	0
4	C	1	Total C O 7 4 3	0	0
4	C	1	Total C O 7 4 3	0	0
4	D	1	Total C O 7 4 3	0	0
4	D	1	Total C O 7 4 3	0	0
4	D	1	Total C O 7 4 3	0	0
4	D	1	Total C O 7 4 3	0	0

- Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C<sub>8</sub>H<sub>18</sub>N<sub>2</sub>O<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
5	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
5	D	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

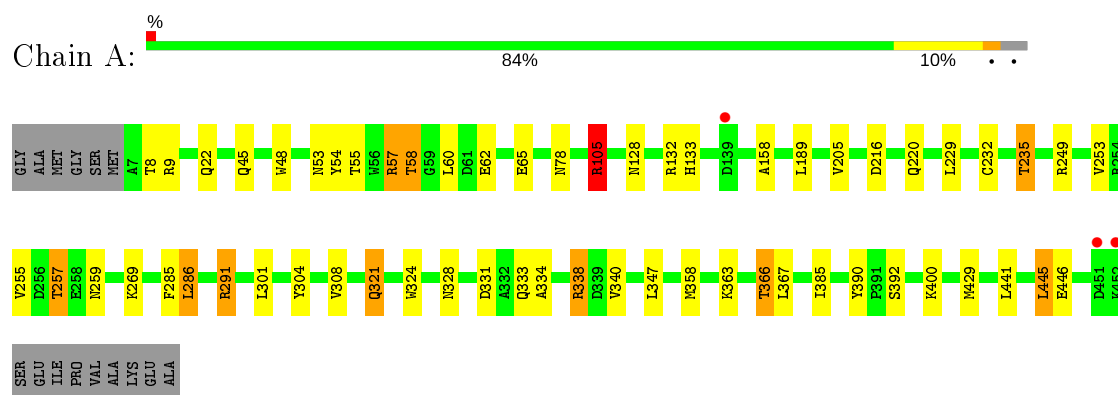
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	285	Total	O	0	0
			285	285		
6	B	293	Total	O	0	0
			293	293		
6	C	261	Total	O	0	0
			261	261		
6	D	255	Total	O	0	0
			255	255		

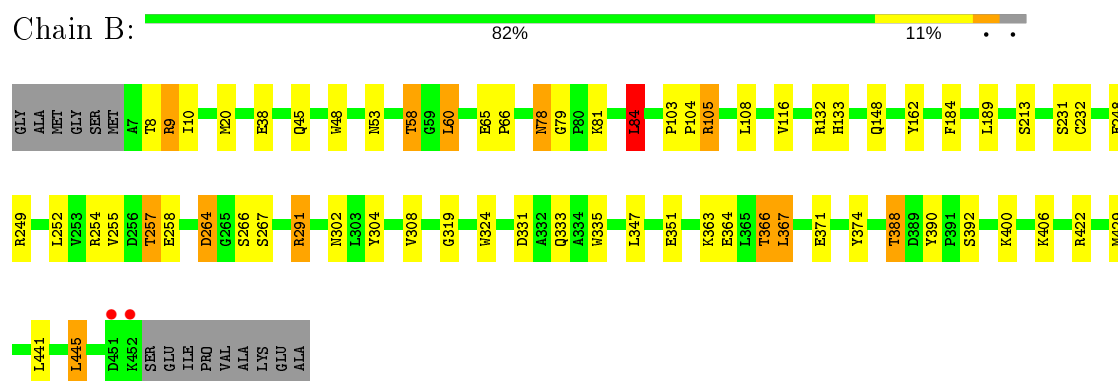
### 3 Residue-property plots [i](#)

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.

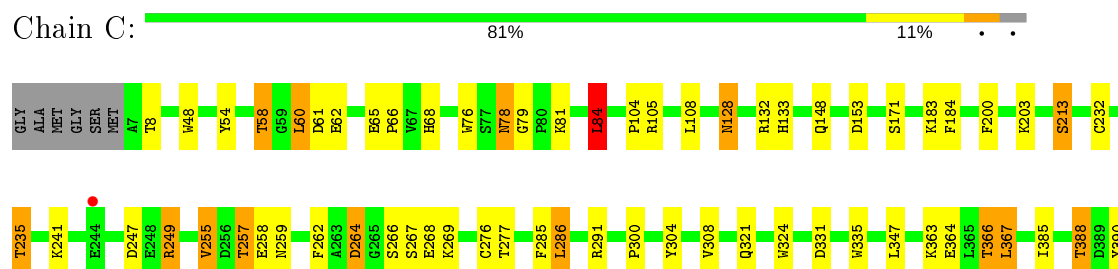
#### • Molecule 1: FLAVIN-CONTAINING MONOOXYGENASE



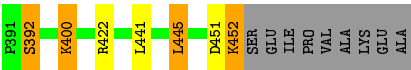
#### • Molecule 1: FLAVIN-CONTAINING MONOOXYGENASE




#### • Molecule 1: FLAVIN-CONTAINING MONOOXYGENASE







● Molecule 1: FLAVIN-CONTAINING MONOOXYGENASE

Chain D:  85% 10% ● ●



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	219.75Å 219.75Å 130.62Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	61.78 – 2.20 57.06 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (61.78-2.20) 99.8 (57.06-2.20)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.33 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.174 , 0.202 0.175 , 0.203	Depositor DCC
$R_{free}$ test set	9065 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.1	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 48.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.033 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	16288	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.42% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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: EPE, NA0, PEG, 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	0.69	0/3774	0.83	9/5124 (0.2%)
1	B	0.70	0/3774	0.78	7/5124 (0.1%)
1	C	0.70	0/3774	0.72	4/5124 (0.1%)
1	D	0.69	0/3774	0.72	5/5124 (0.1%)
All	All	0.70	0/15096	0.77	25/20496 (0.1%)

There are no bond length outliers.

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	105	ARG	NE-CZ-NH2	-14.64	112.98	120.30
1	B	105	ARG	NE-CZ-NH2	-13.96	113.32	120.30
1	A	57	ARG	NE-CZ-NH2	-11.94	114.33	120.30
1	A	291	ARG	NE-CZ-NH2	-11.71	114.44	120.30
1	D	291	ARG	NE-CZ-NH2	-11.20	114.70	120.30
1	B	291	ARG	NE-CZ-NH2	-11.18	114.71	120.30
1	A	105	ARG	NE-CZ-NH1	10.92	125.76	120.30
1	A	57	ARG	NE-CZ-NH1	10.40	125.50	120.30
1	B	105	ARG	NE-CZ-NH1	9.19	124.90	120.30
1	C	291	ARG	NE-CZ-NH2	-8.54	116.03	120.30
1	A	291	ARG	NE-CZ-NH1	8.52	124.56	120.30
1	C	445	LEU	CA-CB-CG	7.96	133.61	115.30
1	B	445	LEU	CA-CB-CG	7.92	133.51	115.30
1	A	445	LEU	CA-CB-CG	7.77	133.18	115.30
1	D	445	LEU	CA-CB-CG	7.68	132.96	115.30
1	D	291	ARG	NE-CZ-NH1	6.57	123.58	120.30
1	D	84	LEU	CA-CB-CG	6.48	130.20	115.30
1	B	105	ARG	CG-CD-NE	-6.42	98.32	111.80
1	B	291	ARG	NE-CZ-NH1	6.40	123.50	120.30
1	B	84	LEU	CA-CB-CG	6.13	129.40	115.30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	105	ARG	CG-CD-NE	-6.09	99.00	111.80
1	C	84	LEU	CA-CB-CG	6.04	129.18	115.30
1	A	338	ARG	CG-CD-NE	-5.83	99.57	111.80
1	D	84	LEU	CB-CG-CD2	5.05	119.59	111.00
1	C	291	ARG	NE-CZ-NH1	5.00	122.80	120.30

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	3660	0	3450	31	0
1	B	3660	0	3450	36	0
1	C	3660	0	3450	53	0
1	D	3660	0	3450	27	0
2	A	53	0	31	0	0
2	B	53	0	31	0	0
2	C	53	0	31	0	0
2	D	53	0	31	0	0
3	A	48	0	26	3	0
3	B	48	0	26	2	0
3	C	48	0	26	4	0
3	D	48	0	26	2	0
4	A	28	0	40	2	0
4	B	28	0	40	0	0
4	C	21	0	30	4	0
4	D	28	0	40	1	0
5	A	15	0	17	0	0
5	B	15	0	17	0	0
5	D	15	0	18	1	0
6	A	285	0	0	7	0
6	B	293	0	0	4	0
6	C	261	0	0	4	0
6	D	255	0	0	1	0
All	All	16288	0	14230	145	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.

All (145) 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:249:ARG:CG	1:C:249:ARG:HH11	1.54	1.16
1:C:249:ARG:HG2	1:C:249:ARG:HH11	1.12	1.09
1:C:247:ASP:OD2	1:C:249:ARG:NH1	2.03	0.91
1:C:451:ASP:O	1:C:452:LYS:HB2	1.72	0.88
1:A:235:THR:HG23	3:A:501:NA0:O1X	1.79	0.83
1:D:259:ASN:HD21	4:D:1456:PEG:H22	1.42	0.82
1:C:235:THR:HG23	3:C:501:NA0:O1X	1.80	0.81
1:B:257:THR:HG22	1:B:258:GLU:HG3	1.63	0.80
1:C:249:ARG:HG3	1:C:249:ARG:HH11	1.46	0.79
1:D:132:ARG:HH21	1:D:148:GLN:HE21	1.31	0.79
1:C:62:GLU:OE1	6:C:2036:HOH:O	2.02	0.78
1:C:249:ARG:HG2	1:C:249:ARG:NH1	1.92	0.77
1:C:388:THR:HG22	1:C:390:TYR:H	1.48	0.77
1:C:132:ARG:HH21	1:C:148:GLN:HE21	1.33	0.77
1:D:324:TRP:H	1:D:377:GLN:HE22	1.33	0.76
1:C:249:ARG:CG	1:C:249:ARG:NH1	2.28	0.75
1:C:249:ARG:NH2	1:C:268:GLU:OE2	2.20	0.75
1:D:324:TRP:HA	3:D:501:NA0:HAA2	1.69	0.75
1:C:259:ASN:HD21	4:C:1455:PEG:H31	1.54	0.73
1:A:257:THR:CG2	6:A:2170:HOH:O	2.36	0.72
1:B:324:TRP:HA	3:B:501:NA0:HAA2	1.70	0.72
1:D:132:ARG:HH21	1:D:148:GLN:NE2	1.89	0.70
1:C:264:ASP:HB3	1:C:266:SER:H	1.56	0.69
1:C:132:ARG:HH21	1:C:148:GLN:NE2	1.91	0.68
1:D:264:ASP:HB3	1:D:266:SER:H	1.59	0.68
1:C:249:ARG:NH1	1:C:249:ARG:HG3	2.07	0.68
1:B:264:ASP:HB3	1:B:266:SER:H	1.59	0.67
1:B:132:ARG:HH21	1:B:148:GLN:HE21	1.42	0.67
1:C:388:THR:CG2	1:C:390:TYR:H	2.07	0.67
1:A:390:TYR:O	6:A:2246:HOH:O	2.13	0.66
1:C:78:ASN:HD22	1:C:79:GLY:N	1.94	0.65
1:C:258:GLU:HG2	4:C:1454:PEG:H22	1.79	0.65
1:A:257:THR:HG21	6:A:2170:HOH:O	1.98	0.63
1:A:324:TRP:HA	3:A:501:NA0:HAA2	1.82	0.62
1:D:324:TRP:CE3	3:D:501:NA0:HAA3	2.36	0.61
1:B:319:GLY:H	1:B:333:GLN:HE22	1.47	0.60
1:B:388:THR:HG22	1:B:390:TYR:H	1.66	0.60

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:335:TRP:HB3	1:C:388:THR:HG21	1.83	0.60
1:C:200:PHE:HA	1:C:203:LYS:HD2	1.81	0.60
1:C:285:PHE:CD1	1:C:286:LEU:HD13	2.37	0.60
1:A:385:ILE:HD12	1:A:392:SER:HA	1.83	0.60
1:B:132:ARG:HH21	1:B:148:GLN:NE2	1.99	0.59
1:A:57:ARG:NH2	1:D:175:VAL:O	2.27	0.59
1:B:388:THR:CG2	1:B:390:TYR:H	2.16	0.59
1:C:259:ASN:HD21	4:C:1455:PEG:C3	2.15	0.59
1:C:61:ASP:HB2	6:C:2036:HOH:O	2.04	0.58
1:C:324:TRP:HA	3:C:501:NA0:HAA2	1.87	0.56
1:A:324:TRP:CE3	3:A:501:NA0:HAA3	2.40	0.56
1:B:363:LYS:O	1:B:366:THR:HB	2.05	0.56
1:A:321:GLN:NE2	1:A:333:GLN:HE22	2.05	0.55
6:B:2139:HOH:O	1:C:58:THR:HG23	2.07	0.55
1:A:62:GLU:HG2	6:A:2045:HOH:O	2.07	0.55
1:B:9:ARG:HG3	1:B:38:GLU:HB2	1.89	0.54
1:A:363:LYS:O	1:A:366:THR:HB	2.08	0.54
1:B:324:TRP:CE3	3:B:501:NA0:HAA3	2.43	0.54
1:A:321:GLN:HE22	1:A:333:GLN:HE22	1.56	0.53
1:B:335:TRP:HB3	1:B:388:THR:HG21	1.90	0.53
1:A:446:GLU:HG2	6:A:2277:HOH:O	2.09	0.53
1:A:55:THR:OG1	1:A:57:ARG:HG3	2.08	0.53
1:C:249:ARG:HD2	1:C:262:PHE:CD2	2.45	0.52
1:A:358:MET:CE	6:A:2222:HOH:O	2.58	0.52
1:C:235:THR:CG2	3:C:501:NA0:O1X	2.57	0.52
1:C:285:PHE:HD1	1:C:286:LEU:HD13	1.74	0.51
1:B:364:GLU:HA	1:B:367:LEU:HD22	1.91	0.51
1:D:10:ILE:HD12	1:D:162:TYR:HB2	1.91	0.51
1:D:325:TYR:H	1:D:377:GLN:HE21	1.58	0.51
1:B:319:GLY:H	1:B:333:GLN:NE2	2.09	0.50
1:B:78:ASN:HD22	1:B:79:GLY:N	2.09	0.50
1:A:9:ARG:HH12	1:A:158:ALA:HB1	1.77	0.50
1:B:65:GLU:OE2	1:B:132:ARG:NH2	2.37	0.49
1:D:78:ASN:HD22	1:D:79:GLY:N	2.09	0.49
1:B:81:LYS:O	1:B:84:LEU:HD22	2.11	0.49
1:C:363:LYS:O	1:C:366:THR:HB	2.13	0.49
1:B:232:CYS:HA	1:B:249:ARG:O	2.12	0.49
1:C:78:ASN:HD22	1:C:79:GLY:H	1.60	0.49
1:B:304:TYR:HB3	1:B:308:VAL:HB	1.94	0.49
1:A:363:LYS:HG2	4:A:1456:PEG:H32	1.95	0.48
1:B:58:THR:HG23	6:C:2124:HOH:O	2.13	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259:ASN:HD21	4:A:1454:PEG:H32	1.78	0.48
1:A:321:GLN:H	1:A:321:GLN:NE2	2.12	0.48
1:D:65:GLU:OE2	1:D:132:ARG:NH2	2.38	0.47
1:B:406:LYS:HD3	6:B:2161:HOH:O	2.14	0.47
1:C:81:LYS:O	1:C:84:LEU:HD22	2.14	0.47
1:D:54:TYR:HB2	1:D:105:ARG:CZ	2.43	0.47
1:A:291:ARG:NH2	1:D:153:ASP:OD1	2.41	0.47
1:A:232:CYS:HA	1:A:249:ARG:O	2.15	0.46
1:C:385:ILE:HD12	1:C:392:SER:HA	1.96	0.46
1:D:324:TRP:N	1:D:377:GLN:HE22	2.07	0.46
1:C:184:PHE:HB2	1:C:255:VAL:CG1	2.45	0.46
6:A:2141:HOH:O	1:D:58:THR:HG23	2.16	0.46
1:B:231:SER:HB2	1:B:248:GLU:HG2	1.97	0.46
1:D:385:ILE:HD12	1:D:392:SER:HA	1.99	0.45
1:B:10:ILE:HD12	1:B:162:TYR:HB2	1.98	0.45
1:C:257:THR:HG22	1:C:258:GLU:HG3	1.99	0.45
1:C:304:TYR:HB3	1:C:308:VAL:HB	1.98	0.45
1:C:65:GLU:OE2	1:C:132:ARG:NH2	2.35	0.45
1:C:259:ASN:ND2	4:C:1455:PEG:H31	2.28	0.44
1:D:231:SER:OG	1:D:248:GLU:HG2	2.17	0.44
1:D:371:GLU:HA	1:D:374:TYR:CZ	2.52	0.44
1:C:60:LEU:HD12	1:C:66:PRO:HA	2.00	0.44
1:C:385:ILE:O	6:C:2218:HOH:O	2.21	0.44
1:C:400:LYS:HD3	1:C:400:LYS:HA	1.69	0.44
1:B:103:PRO:HA	1:B:104:PRO:HD3	1.87	0.44
1:C:232:CYS:HA	1:C:249:ARG:O	2.17	0.44
1:B:331:ASP:HB3	1:B:390:TYR:CE1	2.53	0.43
1:A:58:THR:HG23	6:D:2125:HOH:O	2.17	0.43
1:C:331:ASP:HB3	1:C:390:TYR:CE1	2.53	0.43
1:D:132:ARG:NH2	1:D:148:GLN:HE21	2.09	0.43
1:C:277:THR:HA	3:C:501:NAO:O4B	2.18	0.43
1:D:304:TYR:HB3	1:D:308:VAL:HB	2.00	0.43
1:C:364:GLU:HA	1:C:367:LEU:HD22	1.99	0.43
1:C:108:LEU:HA	1:C:108:LEU:HD23	1.87	0.43
1:B:351:GLU:HG3	6:B:2219:HOH:O	2.18	0.43
1:B:371:GLU:HA	1:B:374:TYR:CE2	2.54	0.43
1:D:200:PHE:HA	1:D:203:LYS:HD2	2.01	0.43
1:A:331:ASP:HB3	1:A:390:TYR:CE1	2.53	0.43
1:C:213:SER:HB3	1:C:276:CYS:HB3	2.01	0.43
1:C:300:PRO:HD2	1:C:321:GLN:HG3	2.01	0.43
1:A:216:ASP:O	1:A:220:GLN:HG2	2.19	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:22:GLN:HA	1:D:334:ALA:HB1	2.01	0.42
1:C:76:TRP:HA	1:C:104:PRO:HA	2.02	0.42
1:A:65:GLU:OE2	1:A:132:ARG:NH2	2.40	0.42
1:C:54:TYR:HB2	1:C:105:ARG:CZ	2.49	0.42
1:C:128:ASN:HD22	1:C:128:ASN:HA	1.71	0.42
1:A:285:PHE:CD1	1:A:286:LEU:HD13	2.54	0.42
1:B:108:LEU:HD23	1:B:108:LEU:HA	1.86	0.42
1:B:184:PHE:HB2	1:B:255:VAL:CG1	2.49	0.42
1:A:45:GLN:NE2	1:A:53:ASN:HD22	2.18	0.42
1:B:60:LEU:HD12	1:B:66:PRO:HA	2.02	0.42
1:B:20:MET:HB3	1:B:116:VAL:HG11	2.02	0.42
5:D:1453:EPE:H51	5:D:1453:EPE:H82	1.64	0.41
1:A:304:TYR:HB3	1:A:308:VAL:HB	2.02	0.41
1:B:319:GLY:N	1:B:333:GLN:HE22	2.16	0.41
1:D:348:PRO:HB2	1:D:352:GLU:HB2	2.02	0.41
1:D:145:VAL:O	1:D:157:SER:HA	2.20	0.41
1:B:291:ARG:NH2	1:C:153:ASP:OD1	2.45	0.41
1:A:22:GLN:HA	1:A:334:ALA:HB1	2.02	0.41
1:D:364:GLU:HA	1:D:367:LEU:HD22	2.03	0.41
1:B:252:LEU:HD11	1:B:255:VAL:HG23	2.02	0.41
1:B:257:THR:CG2	6:B:2169:HOH:O	2.69	0.41
1:A:205:VAL:HB	1:A:229:LEU:HD23	2.03	0.40
1:D:324:TRP:H	1:D:377:GLN:NE2	2.08	0.40
1:B:45:GLN:NE2	1:B:53:ASN:HD22	2.18	0.40
1:C:68:HIS:CE1	1:C:171:SER:OG	2.74	0.40
1:A:54:TYR:HB2	1:A:105:ARG:CZ	2.52	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	444/461 (96%)	427 (96%)	17 (4%)	0	100	100
1	B	444/461 (96%)	428 (96%)	16 (4%)	0	100	100
1	C	444/461 (96%)	428 (96%)	16 (4%)	0	100	100
1	D	444/461 (96%)	430 (97%)	14 (3%)	0	100	100
All	All	1776/1844 (96%)	1713 (96%)	63 (4%)	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	387/397 (98%)	360 (93%)	27 (7%)	15	16
1	B	387/397 (98%)	361 (93%)	26 (7%)	16	18
1	C	387/397 (98%)	358 (92%)	29 (8%)	13	14
1	D	387/397 (98%)	364 (94%)	23 (6%)	19	23
All	All	1548/1588 (98%)	1443 (93%)	105 (7%)	16	17

All (105) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	THR
1	A	48	TRP
1	A	58	THR
1	A	60	LEU
1	A	78	ASN
1	A	105	ARG
1	A	128	ASN
1	A	133	HIS
1	A	189	LEU
1	A	235	THR
1	A	253	VAL
1	A	255	VAL
1	A	257	THR

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	269	LYS
1	A	286	LEU
1	A	301	LEU
1	A	321	GLN
1	A	328	ASN
1	A	338	ARG
1	A	340	VAL
1	A	347	LEU
1	A	366	THR
1	A	367	LEU
1	A	400	LYS
1	A	429	MET
1	A	441	LEU
1	A	445	LEU
1	B	8	THR
1	B	9	ARG
1	B	48	TRP
1	B	58	THR
1	B	60	LEU
1	B	78	ASN
1	B	84	LEU
1	B	105	ARG
1	B	133	HIS
1	B	189	LEU
1	B	213	SER
1	B	254	ARG
1	B	257	THR
1	B	264	ASP
1	B	267	SER
1	B	302	ASN
1	B	347	LEU
1	B	366	THR
1	B	367	LEU
1	B	388	THR
1	B	392	SER
1	B	400	LYS
1	B	422	ARG
1	B	429	MET
1	B	441	LEU
1	B	445	LEU
1	C	8	THR
1	C	48	TRP

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	58	THR
1	C	60	LEU
1	C	78	ASN
1	C	84	LEU
1	C	128	ASN
1	C	133	HIS
1	C	183	LYS
1	C	213	SER
1	C	235	THR
1	C	241	LYS
1	C	249	ARG
1	C	255	VAL
1	C	257	THR
1	C	264	ASP
1	C	267	SER
1	C	269	LYS
1	C	286	LEU
1	C	347	LEU
1	C	366	THR
1	C	367	LEU
1	C	388	THR
1	C	392	SER
1	C	400	LYS
1	C	422	ARG
1	C	441	LEU
1	C	445	LEU
1	C	452	LYS
1	D	8	THR
1	D	9	ARG
1	D	48	TRP
1	D	58	THR
1	D	60	LEU
1	D	78	ASN
1	D	84	LEU
1	D	128	ASN
1	D	189	LEU
1	D	207	LEU
1	D	244	GLU
1	D	249	ARG
1	D	264	ASP
1	D	269	LYS
1	D	347	LEU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	D	367	LEU
1	D	392	SER
1	D	400	LYS
1	D	422	ARG
1	D	441	LEU
1	D	445	LEU
1	D	450	SER
1	D	452	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	GLN
1	A	63	ASN
1	A	78	ASN
1	A	128	ASN
1	A	133	HIS
1	A	259	ASN
1	A	321	GLN
1	A	328	ASN
1	B	22	GLN
1	B	45	GLN
1	B	78	ASN
1	B	133	HIS
1	B	148	GLN
1	B	259	ASN
1	B	302	ASN
1	B	333	GLN
1	C	45	GLN
1	C	78	ASN
1	C	128	ASN
1	C	133	HIS
1	C	141	GLN
1	C	148	GLN
1	C	259	ASN
1	D	78	ASN
1	D	128	ASN
1	D	133	HIS
1	D	148	GLN
1	D	259	ASN
1	D	377	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 ⓘ

26 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	EPE	B	1457	-	15,15,15	0.86	1 (6%)	18,20,20	1.86	5 (27%)
4	PEG	A	1456	-	6,6,6	0.43	0	5,5,5	0.71	0
2	FAD	A	500	-	51,58,58	1.28	6 (11%)	60,89,89	1.78	9 (15%)
4	PEG	C	1454	-	6,6,6	0.49	0	5,5,5	0.59	0
4	PEG	D	1456	-	6,6,6	0.42	0	5,5,5	0.39	0
3	NA0	B	501	-	45,52,52	0.77	0	56,80,80	1.39	5 (8%)
4	PEG	C	1453	-	6,6,6	0.56	0	5,5,5	0.41	0
4	PEG	B	1455	-	6,6,6	0.35	0	5,5,5	0.61	0
4	PEG	B	1456	-	6,6,6	0.57	0	5,5,5	0.43	0
5	EPE	D	1453	-	15,15,15	0.87	1 (6%)	18,20,20	1.99	5 (27%)
4	PEG	B	1454	-	6,6,6	0.45	0	5,5,5	0.27	0
2	FAD	D	500	-	51,58,58	1.46	7 (13%)	60,89,89	1.76	10 (16%)
4	PEG	A	1455	-	6,6,6	0.43	0	5,5,5	0.47	0
4	PEG	B	1453	-	6,6,6	0.39	0	5,5,5	0.40	0
4	PEG	A	1454	-	6,6,6	0.51	0	5,5,5	0.37	0
5	EPE	A	1457	-	15,15,15	0.94	1 (6%)	18,20,20	1.97	4 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	PEG	D	1457	-	6,6,6	0.52	0	5,5,5	0.52	0
4	PEG	A	1453	-	6,6,6	0.42	0	5,5,5	0.42	0
2	FAD	B	500	-	51,58,58	1.32	7 (13%)	60,89,89	1.74	10 (16%)
4	PEG	D	1455	-	6,6,6	0.47	0	5,5,5	0.38	0
4	PEG	D	1454	-	6,6,6	0.38	0	5,5,5	0.52	0
3	NA0	C	501	-	45,52,52	0.74	0	56,80,80	1.25	6 (10%)
3	NA0	A	501	-	45,52,52	0.71	0	56,80,80	1.44	5 (8%)
4	PEG	C	1455	-	6,6,6	0.42	0	5,5,5	0.47	0
2	FAD	C	500	-	51,58,58	1.29	5 (9%)	60,89,89	1.76	9 (15%)
3	NA0	D	501	-	45,52,52	0.70	0	56,80,80	1.25	4 (7%)

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	EPE	B	1457	-	-	3/9/19/19	0/1/1/1
4	PEG	A	1456	-	-	3/4/4/4	-
2	FAD	A	500	-	-	3/30/50/50	0/6/6/6
4	PEG	C	1454	-	-	1/4/4/4	-
4	PEG	D	1456	-	-	2/4/4/4	-
3	NA0	B	501	-	-	9/31/67/67	0/5/5/5
4	PEG	C	1453	-	-	3/4/4/4	-
4	PEG	B	1455	-	-	1/4/4/4	-
4	PEG	B	1456	-	-	1/4/4/4	-
5	EPE	D	1453	-	-	3/9/19/19	0/1/1/1
4	PEG	B	1454	-	-	2/4/4/4	-
2	FAD	D	500	-	-	3/30/50/50	0/6/6/6
4	PEG	A	1455	-	-	3/4/4/4	-
4	PEG	B	1453	-	-	2/4/4/4	-
4	PEG	A	1454	-	-	2/4/4/4	-
5	EPE	A	1457	-	-	2/9/19/19	0/1/1/1
4	PEG	D	1457	-	-	1/4/4/4	-
4	PEG	A	1453	-	-	2/4/4/4	-
2	FAD	B	500	-	-	3/30/50/50	0/6/6/6
4	PEG	D	1455	-	-	1/4/4/4	-
4	PEG	D	1454	-	-	2/4/4/4	-

Continued on next page...

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NA0	C	501	-	-	14/31/67/67	0/5/5/5
3	NA0	A	501	-	-	11/31/67/67	0/5/5/5
4	PEG	C	1455	-	-	1/4/4/4	-
2	FAD	C	500	-	-	3/30/50/50	0/6/6/6
3	NA0	D	501	-	-	9/31/67/67	0/5/5/5

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	500	FAD	C10-N1	4.83	1.39	1.33
2	D	500	FAD	C4X-N5	4.40	1.39	1.33
2	C	500	FAD	C2A-N3A	4.12	1.38	1.32
2	A	500	FAD	C4X-N5	4.04	1.39	1.33
2	B	500	FAD	C4X-N5	3.94	1.39	1.33
2	C	500	FAD	C10-N1	3.87	1.38	1.33
2	D	500	FAD	C1'-N10	3.78	1.52	1.48
2	A	500	FAD	C2A-N3A	3.75	1.38	1.32
2	A	500	FAD	C10-N1	3.64	1.37	1.33
2	B	500	FAD	C2A-N3A	3.58	1.37	1.32
2	C	500	FAD	C4X-N5	3.43	1.38	1.33
5	A	1457	EPE	C10-S	3.36	1.82	1.77
2	B	500	FAD	C10-N1	3.33	1.37	1.33
2	D	500	FAD	C2A-N3A	3.29	1.37	1.32
2	B	500	FAD	C1'-N10	3.12	1.51	1.48
2	D	500	FAD	C4-N3	3.06	1.38	1.33
2	B	500	FAD	C4-N3	2.83	1.38	1.33
5	B	1457	EPE	C10-S	2.83	1.81	1.77
2	D	500	FAD	C2A-N1A	2.81	1.39	1.33
5	D	1453	EPE	C10-S	2.71	1.81	1.77
2	A	500	FAD	C4-N3	2.58	1.37	1.33
2	A	500	FAD	C1'-N10	2.52	1.50	1.48
2	C	500	FAD	C4-N3	2.39	1.37	1.33
2	B	500	FAD	C5X-N5	2.36	1.39	1.35
2	C	500	FAD	C1'-N10	2.30	1.50	1.48
2	B	500	FAD	C2A-N1A	2.24	1.38	1.33
2	A	500	FAD	C2A-N1A	2.09	1.37	1.33
2	D	500	FAD	C5X-N5	2.01	1.38	1.35

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	500	FAD	C4-N3-C2	6.38	120.53	115.14
2	A	500	FAD	N3A-C2A-N1A	-6.21	118.97	128.68
2	A	500	FAD	C4-N3-C2	6.17	120.35	115.14
2	C	500	FAD	N3A-C2A-N1A	-6.12	119.11	128.68
3	A	501	NA0	N3A-C2A-N1A	-6.07	119.19	128.68
2	D	500	FAD	N3A-C2A-N1A	-5.95	119.38	128.68
2	B	500	FAD	C1'-N10-C9A	5.86	122.91	118.29
2	B	500	FAD	N3A-C2A-N1A	-5.69	119.78	128.68
2	D	500	FAD	C4-N3-C2	5.65	119.91	115.14
2	B	500	FAD	C4-N3-C2	5.44	119.74	115.14
3	B	501	NA0	N3A-C2A-N1A	-5.12	120.68	128.68
3	C	501	NA0	N3A-C2A-N1A	-5.11	120.69	128.68
2	A	500	FAD	C1'-N10-C9A	5.05	122.27	118.29
3	D	501	NA0	N3A-C2A-N1A	-4.95	120.94	128.68
2	D	500	FAD	C1'-N10-C9A	4.82	122.09	118.29
5	A	1457	EPE	C5-N4-C3	4.68	119.36	108.83
5	D	1453	EPE	C5-N4-C3	4.45	118.85	108.83
5	A	1457	EPE	C7-N4-C5	4.41	122.50	111.23
2	A	500	FAD	C4X-N5-C5X	4.27	121.04	116.77
2	C	500	FAD	C1'-N10-C9A	4.25	121.64	118.29
3	B	501	NA0	C2B-C3B-C4B	-4.18	92.91	101.99
2	C	500	FAD	C4X-N5-C5X	4.17	120.94	116.77
2	D	500	FAD	C5X-C9A-N10	4.08	120.67	117.72
5	B	1457	EPE	C5-N4-C3	4.01	117.86	108.83
5	D	1453	EPE	C7-N4-C3	3.81	120.99	111.23
2	D	500	FAD	C4X-N5-C5X	3.79	120.56	116.77
2	C	500	FAD	O2'-C2'-C1'	-3.73	100.61	109.59
5	B	1457	EPE	O2S-S-C10	3.73	111.40	106.92
2	B	500	FAD	C4X-N5-C5X	3.42	120.19	116.77
5	D	1453	EPE	C7-N4-C5	3.40	119.94	111.23
5	D	1453	EPE	O2S-S-C10	3.39	111.00	106.92
3	A	501	NA0	C2B-C3B-C4B	-3.33	94.76	101.99
2	C	500	FAD	C4X-C4-N3	-3.33	118.88	123.43
3	A	501	NA0	C1B-N9A-C4A	-3.13	121.15	126.64
3	B	501	NA0	C1B-N9A-C4A	-3.07	121.24	126.64
2	B	500	FAD	C5X-C9A-N10	2.96	119.86	117.72
5	B	1457	EPE	C6-N1-C2	2.87	115.30	108.83
3	D	501	NA0	C2B-C3B-C4B	-2.87	95.77	101.99
2	B	500	FAD	C4X-C4-N3	-2.86	119.53	123.43
2	A	500	FAD	C5X-C9A-N10	2.85	119.78	117.72
2	C	500	FAD	C5X-C9A-N10	2.85	119.78	117.72
2	D	500	FAD	O5'-C5'-C4'	-2.84	101.77	109.36
2	A	500	FAD	O2'-C2'-C1'	-2.84	102.75	109.59

Continued on next page...



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	NA0	O2B-P2B-O1X	-2.82	98.51	109.39
3	D	501	NA0	C1B-N9A-C4A	-2.78	121.75	126.64
3	C	501	NA0	C2B-C3B-C4B	-2.78	95.95	101.99
5	B	1457	EPE	C7-N4-C3	2.65	118.01	111.23
2	B	500	FAD	O2'-C2'-C1'	-2.57	103.40	109.59
5	A	1457	EPE	O3S-S-C10	2.56	109.91	105.77
2	A	500	FAD	C10-C4X-N5	-2.54	119.50	121.26
2	A	500	FAD	C4X-C4-N3	-2.53	119.97	123.43
5	A	1457	EPE	C7-N4-C3	2.48	117.58	111.23
3	A	501	NA0	O4B-C4B-C5B	2.44	117.41	109.37
5	D	1453	EPE	C6-N1-C2	2.44	114.31	108.83
3	C	501	NA0	C1B-N9A-C4A	-2.43	122.38	126.64
2	B	500	FAD	C10-C4X-N5	-2.42	119.58	121.26
3	B	501	NA0	O2B-P2B-O1X	-2.42	100.07	109.39
3	C	501	NA0	O3X-P2B-O2X	2.40	116.82	107.64
2	D	500	FAD	O2'-C2'-C1'	-2.27	104.12	109.59
2	D	500	FAD	C4X-C4-N3	-2.26	120.34	123.43
2	C	500	FAD	O4B-C1B-C2B	-2.25	103.64	106.93
2	D	500	FAD	C4A-C5A-N7A	-2.22	107.09	109.40
2	A	500	FAD	O5'-C5'-C4'	-2.17	103.58	109.36
3	B	501	NA0	O4B-C4B-C5B	2.13	116.39	109.37
5	B	1457	EPE	C7-N4-C5	2.12	116.65	111.23
3	C	501	NA0	PA-O3-PN	-2.09	125.64	132.83
2	D	500	FAD	C9A-C5X-N5	-2.08	119.10	122.36
2	B	500	FAD	O4B-C1B-C2B	-2.05	103.94	106.93
3	C	501	NA0	O4B-C4B-C5B	2.04	116.10	109.37
3	D	501	NA0	O3X-P2B-O2X	2.04	115.45	107.64
2	C	500	FAD	C10-C4X-N5	-2.02	119.86	121.26
2	B	500	FAD	O5'-C5'-C4'	-2.02	103.97	109.36

There are no chirality outliers.

All (90) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500	FAD	N10-C1'-C2'-O2'
3	B	501	NA0	C5D-O5D-PN-O1N
3	B	501	NA0	C5D-O5D-PN-O2N
3	B	501	NA0	C2B-O2B-P2B-O1X
3	B	501	NA0	C5B-O5B-PA-O3
3	B	501	NA0	C5B-O5B-PA-O2A
5	D	1453	EPE	C10-C9-N1-C2
5	D	1453	EPE	C8-C7-N4-C5

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
2	D	500	FAD	N10-C1'-C2'-O2'
5	A	1457	EPE	C8-C7-N4-C5
5	A	1457	EPE	S-C10-C9-N1
2	B	500	FAD	N10-C1'-C2'-O2'
2	B	500	FAD	N10-C1'-C2'-C3'
3	C	501	NA0	C5D-O5D-PN-O1N
3	C	501	NA0	C5D-O5D-PN-O2N
3	C	501	NA0	C2B-O2B-P2B-O1X
3	C	501	NA0	C5B-O5B-PA-O3
3	C	501	NA0	C5B-O5B-PA-O2A
3	A	501	NA0	C5D-O5D-PN-O1N
3	A	501	NA0	C5D-O5D-PN-O2N
3	A	501	NA0	C2B-O2B-P2B-O1X
3	A	501	NA0	C5B-O5B-PA-O3
3	A	501	NA0	C5B-O5B-PA-O2A
3	A	501	NA0	C5B-O5B-PA-O1A
2	C	500	FAD	N10-C1'-C2'-O2'
3	D	501	NA0	C5D-O5D-PN-O1N
3	D	501	NA0	C5D-O5D-PN-O2N
3	D	501	NA0	C2B-O2B-P2B-O1X
3	D	501	NA0	C5B-O5B-PA-O3
3	D	501	NA0	C5B-O5B-PA-O2A
4	B	1456	PEG	C1-C2-O2-C3
4	C	1455	PEG	O1-C1-C2-O2
4	C	1453	PEG	O2-C3-C4-O4
4	A	1453	PEG	O1-C1-C2-O2
4	A	1456	PEG	C4-C3-O2-C2
4	A	1456	PEG	O1-C1-C2-O2
4	C	1453	PEG	O1-C1-C2-O2
4	A	1455	PEG	O2-C3-C4-O4
4	A	1454	PEG	O2-C3-C4-O4
4	D	1457	PEG	O2-C3-C4-O4
4	A	1456	PEG	O2-C3-C4-O4
4	D	1454	PEG	O1-C1-C2-O2
4	D	1456	PEG	O2-C3-C4-O4
4	B	1453	PEG	O2-C3-C4-O4
3	C	501	NA0	C4N-C3N-C7N-CAA
3	C	501	NA0	C4N-C3N-C7N-O7N
4	A	1453	PEG	O2-C3-C4-O4
3	C	501	NA0	PA-O3-PN-O5D
4	A	1455	PEG	C1-C2-O2-C3
4	D	1454	PEG	C1-C2-O2-C3

*Continued on next page...*

*Continued from previous page...*

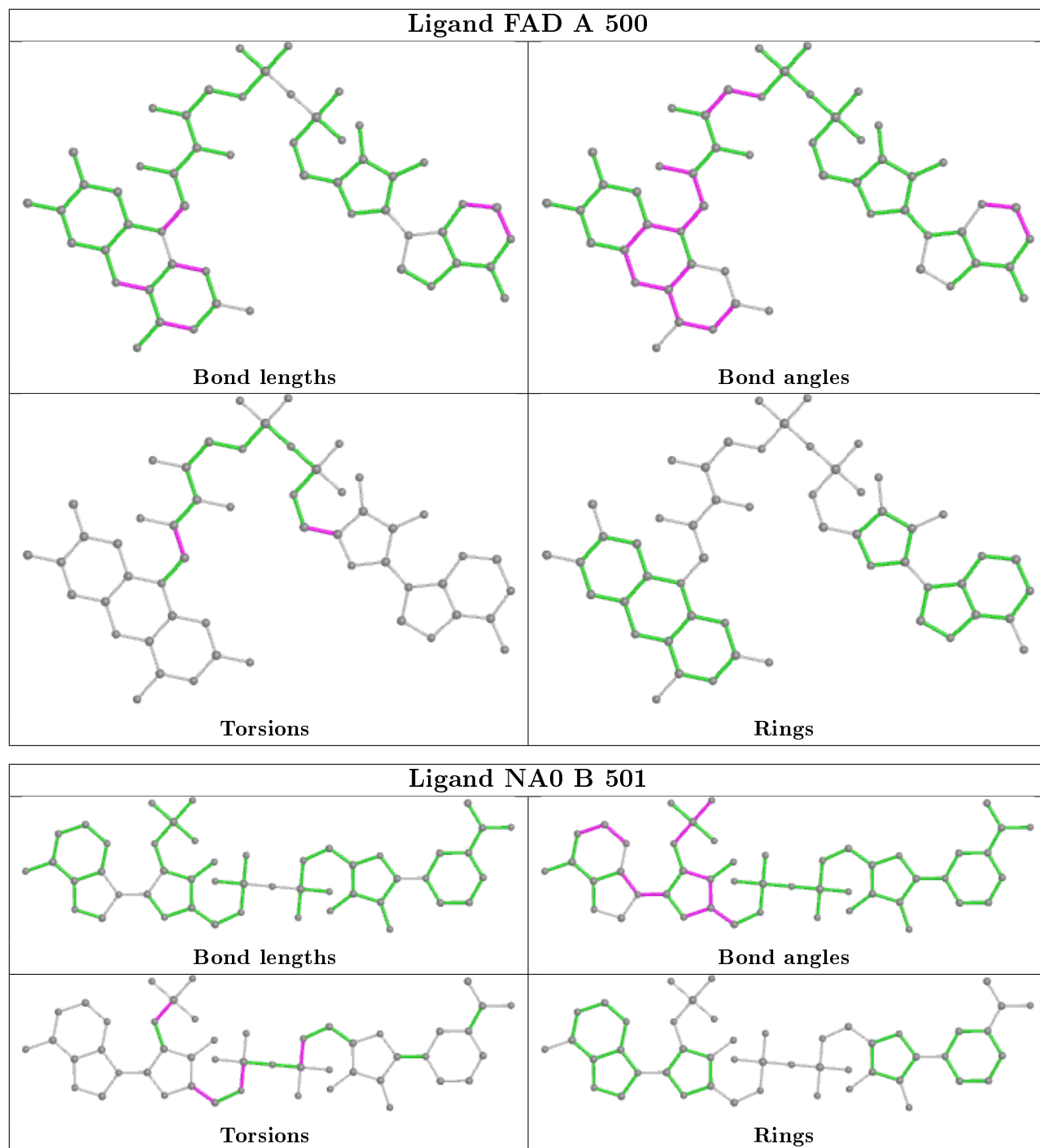
Mol	Chain	Res	Type	Atoms
3	C	501	NA0	C2N-C3N-C7N-CAA
4	D	1455	PEG	C1-C2-O2-C3
4	B	1454	PEG	C1-C2-O2-C3
5	B	1457	EPE	N4-C7-C8-O8
3	B	501	NA0	C5B-O5B-PA-O1A
3	C	501	NA0	C5B-O5B-PA-O1A
3	D	501	NA0	C5B-O5B-PA-O1A
4	A	1454	PEG	C1-C2-O2-C3
5	B	1457	EPE	C9-C10-S-O1S
2	A	500	FAD	N10-C1'-C2'-C3'
2	D	500	FAD	N10-C1'-C2'-C3'
2	C	500	FAD	N10-C1'-C2'-C3'
4	B	1453	PEG	C4-C3-O2-C2
4	C	1453	PEG	C1-C2-O2-C3
4	C	1454	PEG	C4-C3-O2-C2
4	D	1456	PEG	C1-C2-O2-C3
3	D	501	NA0	O4B-C4B-C5B-O5B
2	D	500	FAD	O4B-C4B-C5B-O5B
3	C	501	NA0	PN-O3-PA-O1A
3	A	501	NA0	PN-O3-PA-O2A
3	A	501	NA0	C3B-C2B-O2B-P2B
4	B	1455	PEG	O1-C1-C2-O2
5	D	1453	EPE	N4-C7-C8-O8
3	A	501	NA0	C1B-C2B-O2B-P2B
5	B	1457	EPE	C8-C7-N4-C3
2	A	500	FAD	O4B-C4B-C5B-O5B
2	C	500	FAD	O4B-C4B-C5B-O5B
3	B	501	NA0	C5D-O5D-PN-O3
3	B	501	NA0	C2B-O2B-P2B-O2X
3	C	501	NA0	C5D-O5D-PN-O3
3	A	501	NA0	C5D-O5D-PN-O3
3	D	501	NA0	C5D-O5D-PN-O3
3	D	501	NA0	C2B-O2B-P2B-O2X
4	A	1455	PEG	O1-C1-C2-O2
3	B	501	NA0	O4B-C4B-C5B-O5B
3	C	501	NA0	O4B-C4B-C5B-O5B
3	A	501	NA0	O4B-C4B-C5B-O5B
3	C	501	NA0	PN-O3-PA-O2A
2	B	500	FAD	O4B-C4B-C5B-O5B
4	B	1454	PEG	O1-C1-C2-O2

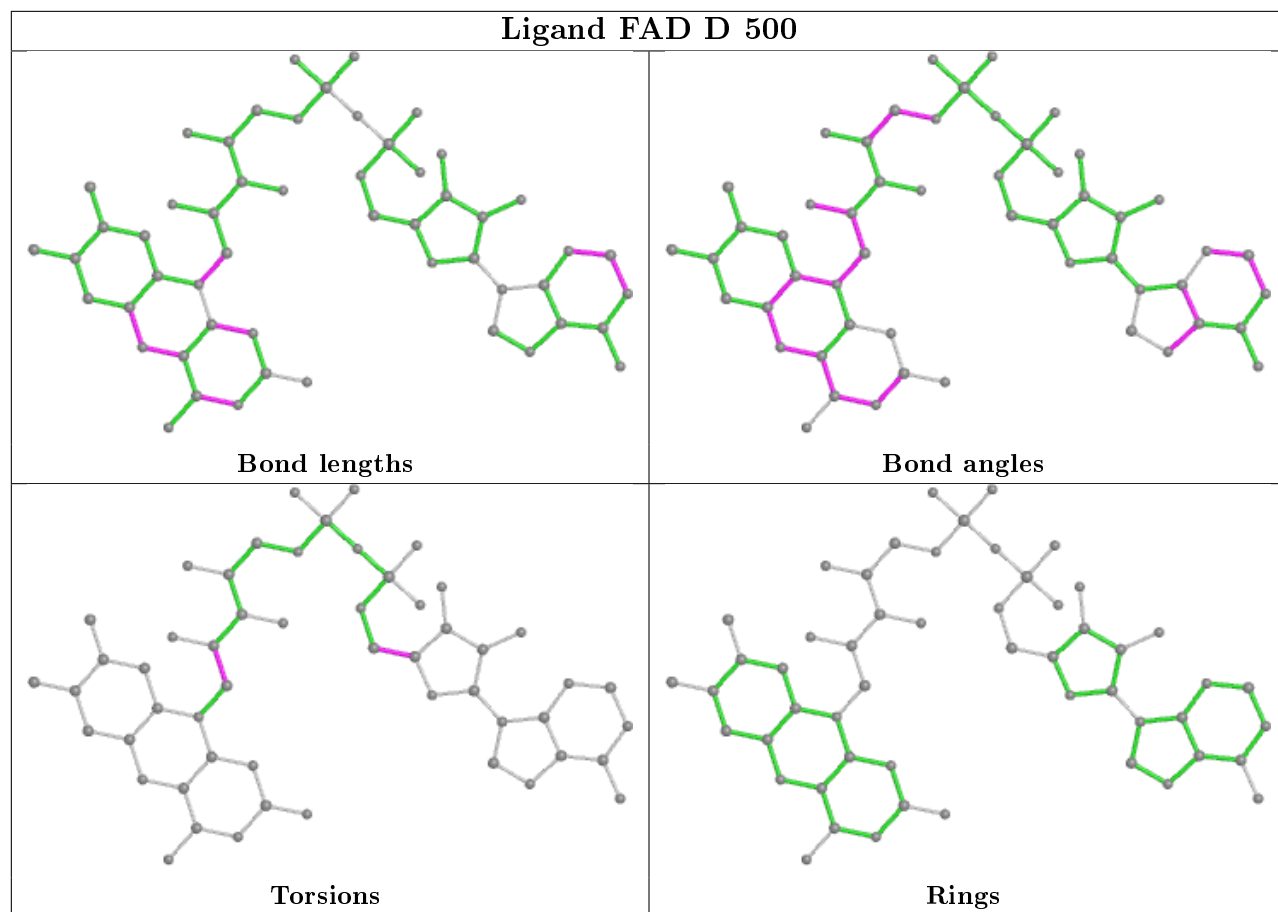
There are no ring outliers.

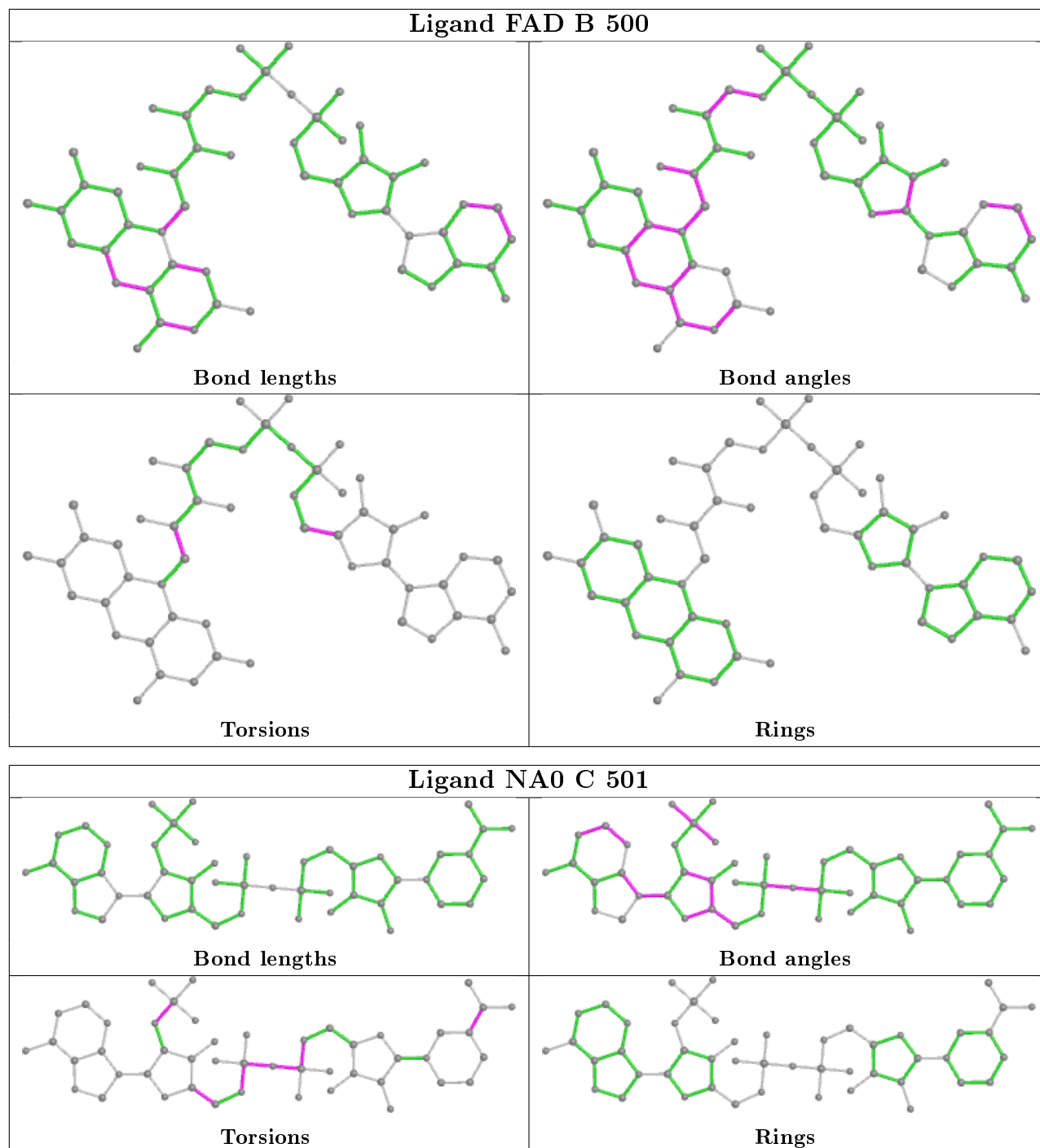
10 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1456	PEG	1	0
4	C	1454	PEG	1	0
4	D	1456	PEG	1	0
3	B	501	NA0	2	0
5	D	1453	EPE	1	0
4	A	1454	PEG	1	0
3	C	501	NA0	4	0
3	A	501	NA0	3	0
4	C	1455	PEG	3	0
3	D	501	NA0	2	0

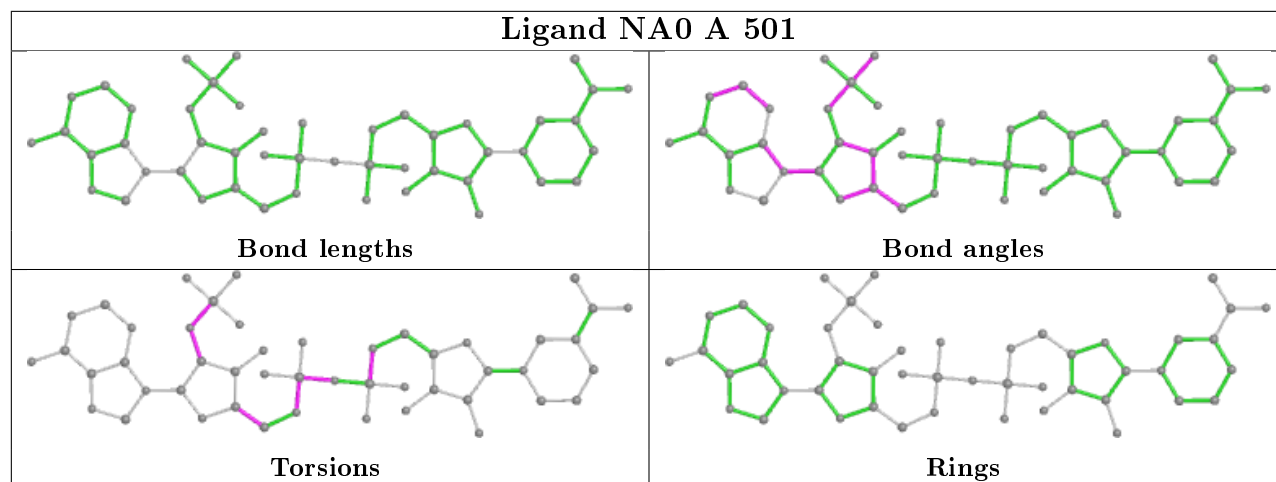
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



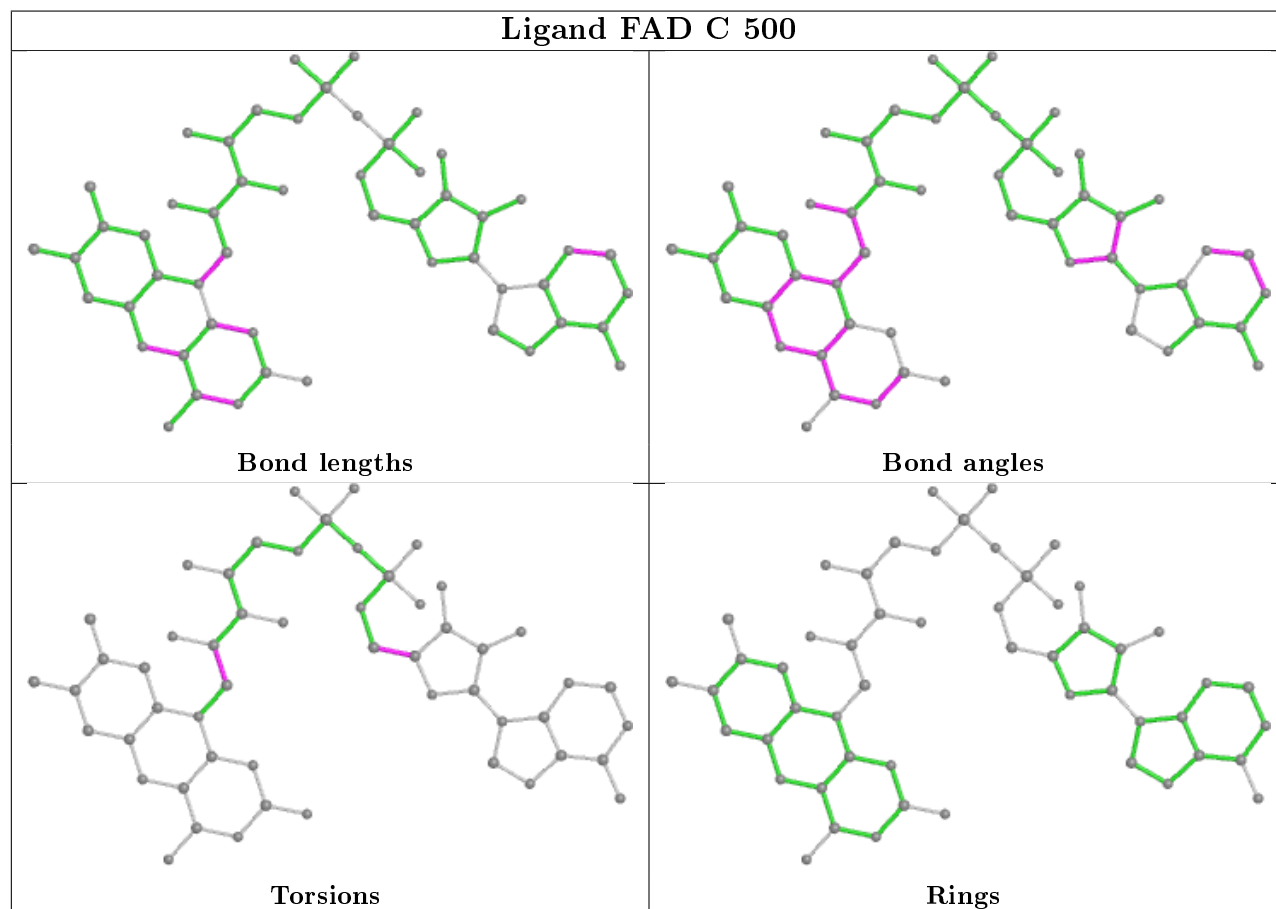




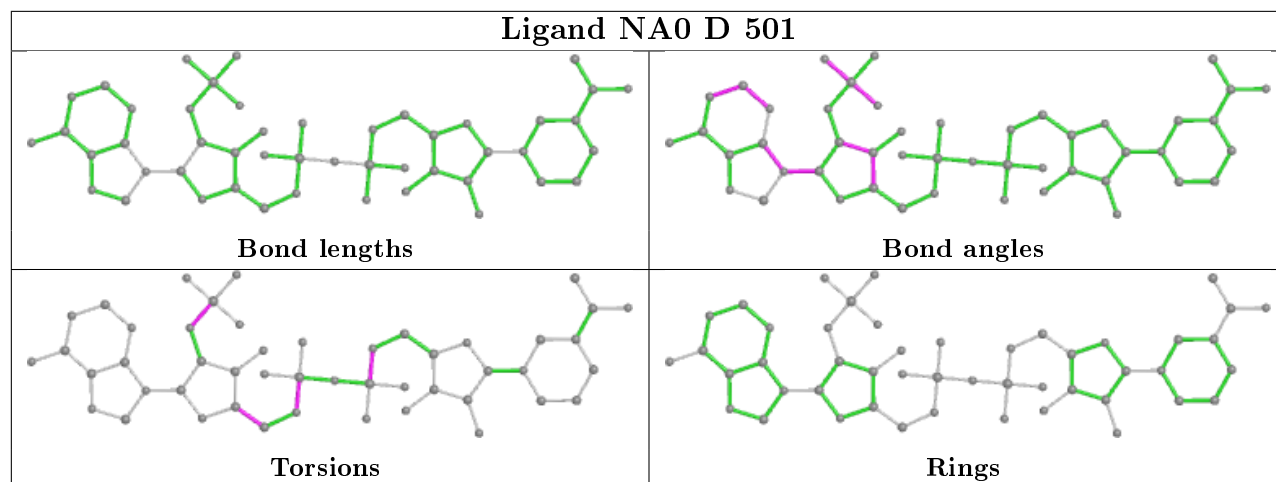
## Ligand NAO A 501



## Ligand FAD C 500







## 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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	446/461 (96%)	-0.77	3 (0%) 87 86	15, 23, 35, 54	0
1	B	446/461 (96%)	-0.68	2 (0%) 92 91	14, 22, 34, 54	0
1	C	446/461 (96%)	-0.62	1 (0%) 95 94	14, 23, 35, 52	0
1	D	446/461 (96%)	-0.73	2 (0%) 92 91	14, 23, 35, 54	0
All	All	1784/1844 (96%)	-0.70	8 (0%) 92 91	14, 23, 35, 54	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	451	ASP	3.3
1	D	452	LYS	2.6
1	A	451	ASP	2.5
1	A	452	LYS	2.5
1	B	452	LYS	2.4
1	C	244	GLU	2.2
1	A	139	ASP	2.2
1	B	451	ASP	2.0

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

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

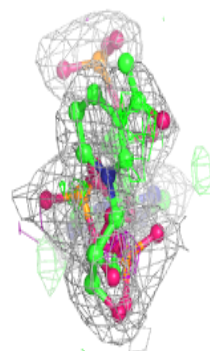
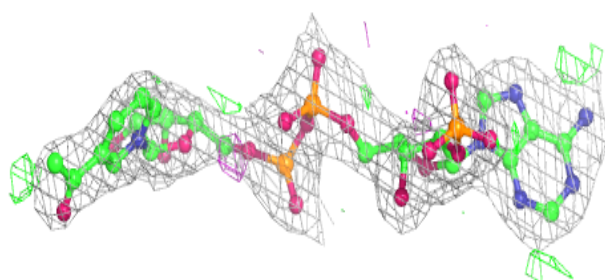
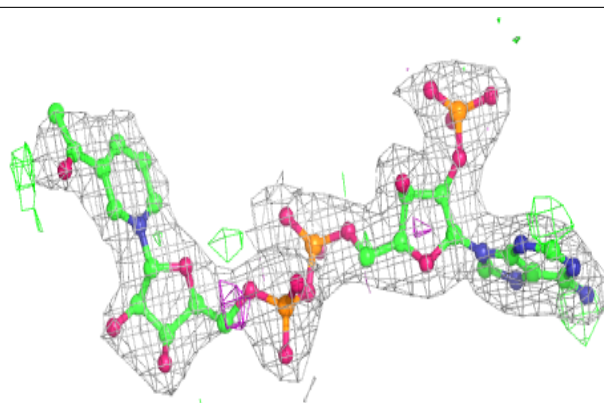
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	PEG	D	1457	7/7	0.74	0.20	49,50,52,52	0
4	PEG	A	1455	7/7	0.79	0.19	50,53,54,55	0
4	PEG	B	1456	7/7	0.81	0.14	45,47,48,48	0
4	PEG	C	1453	7/7	0.81	0.25	28,40,43,45	0
4	PEG	B	1455	7/7	0.81	0.21	53,53,55,56	0
4	PEG	A	1454	7/7	0.85	0.16	46,47,49,50	0
4	PEG	B	1453	7/7	0.87	0.15	50,50,52,55	0
4	PEG	D	1454	7/7	0.88	0.13	42,43,49,50	0
4	PEG	A	1456	7/7	0.89	0.14	42,43,44,45	0
4	PEG	C	1454	7/7	0.89	0.17	40,43,45,45	0
4	PEG	C	1455	7/7	0.90	0.24	49,49,51,52	0
4	PEG	A	1453	7/7	0.92	0.12	32,37,39,40	0
4	PEG	B	1454	7/7	0.93	0.13	42,47,49,49	0
4	PEG	D	1455	7/7	0.93	0.18	37,40,46,47	0
5	EPE	B	1457	15/15	0.94	0.14	39,47,52,52	0
5	EPE	A	1457	15/15	0.95	0.12	45,49,51,51	0
4	PEG	D	1456	7/7	0.95	0.21	47,49,51,52	0
3	NA0	A	501	48/48	0.96	0.10	26,32,39,45	0
3	NA0	C	501	48/48	0.97	0.10	25,33,40,44	0
5	EPE	D	1453	15/15	0.97	0.10	34,38,43,44	0
3	NA0	B	501	48/48	0.97	0.10	26,33,39,45	0
3	NA0	D	501	48/48	0.97	0.09	25,33,39,45	0
2	FAD	A	500	53/53	0.98	0.09	12,16,20,23	0
2	FAD	D	500	53/53	0.98	0.09	14,16,20,23	0
2	FAD	C	500	53/53	0.98	0.10	12,16,20,22	0
2	FAD	B	500	53/53	0.98	0.09	12,16,19,21	0

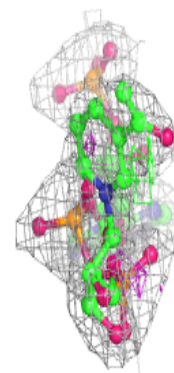
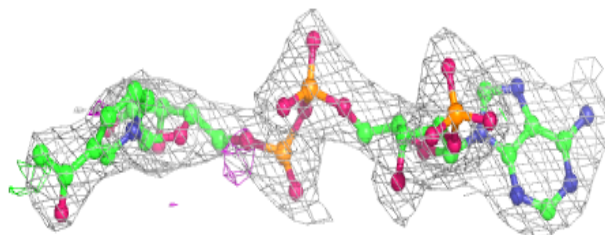
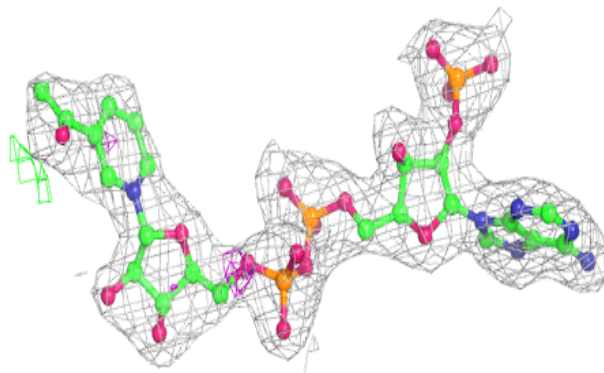
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around NA0 A 501:**

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

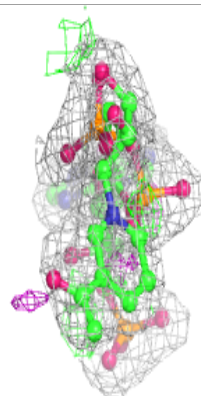
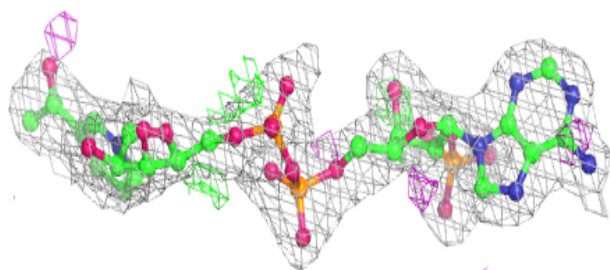
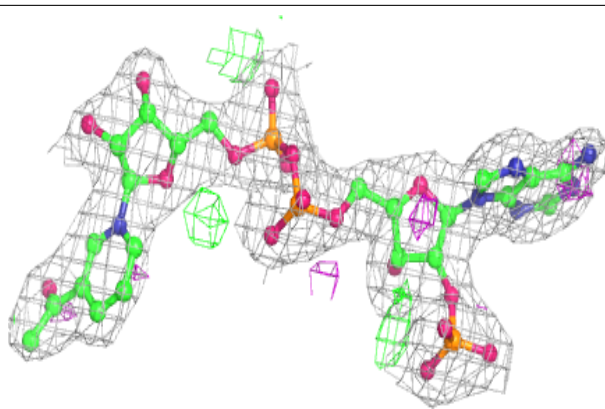
**Electron density around NA0 C 501:**

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

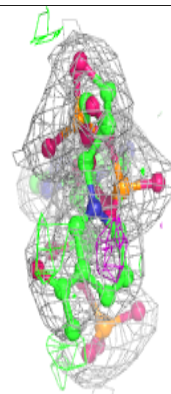
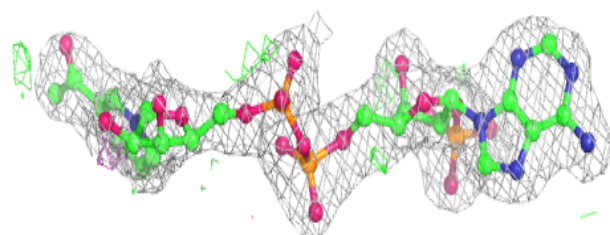
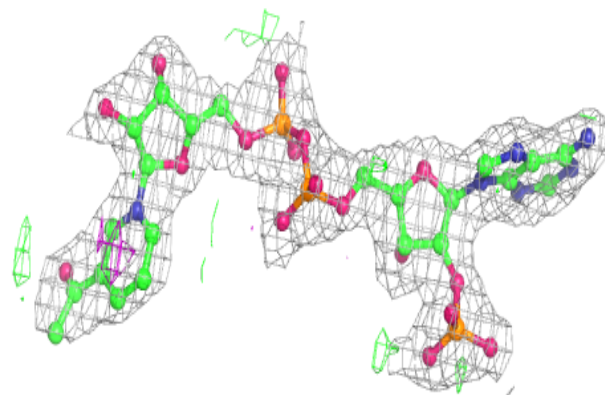


**Electron density around NA0 B 501:**

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

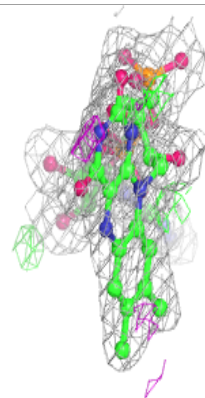
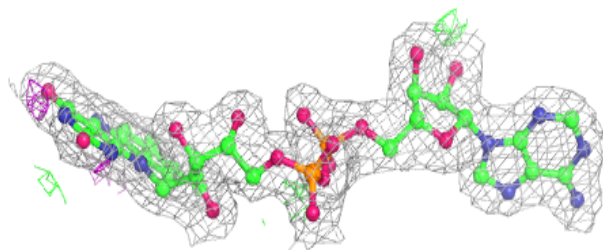
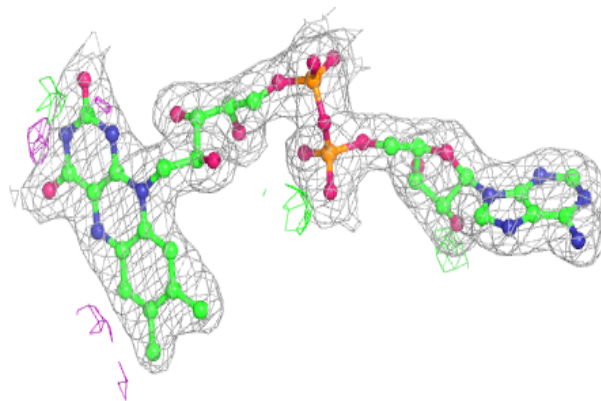
**Electron density around NA0 D 501:**

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

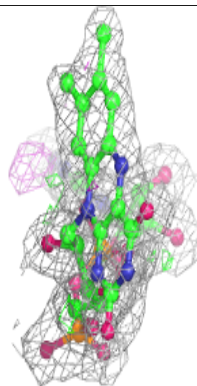
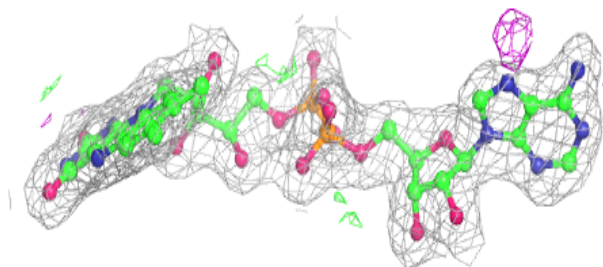
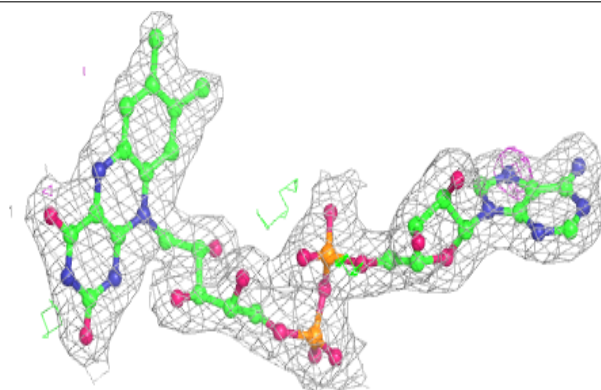


**Electron density around FAD A 500:**

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

**Electron density around FAD D 500:**

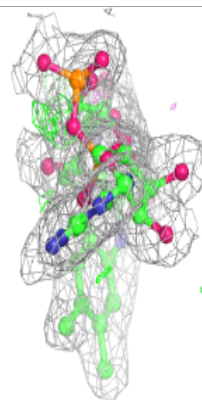
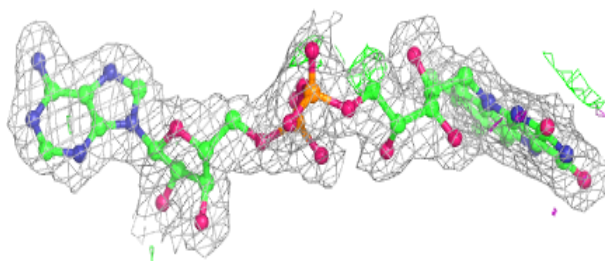
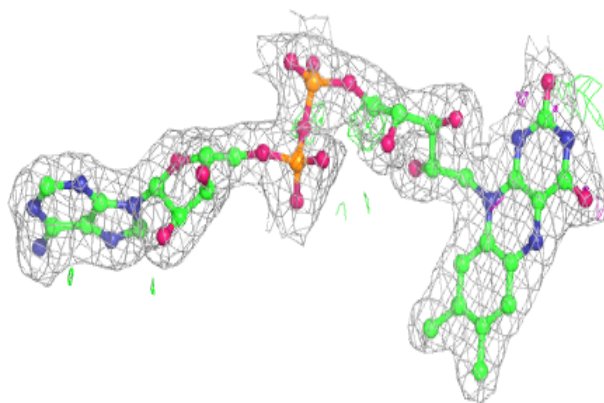
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



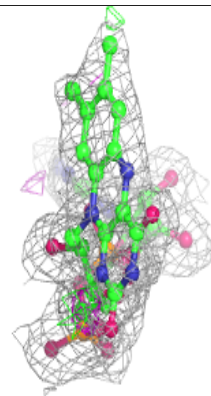
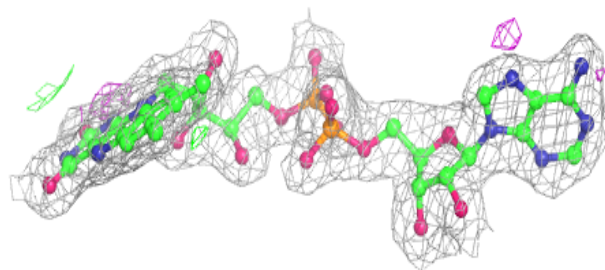
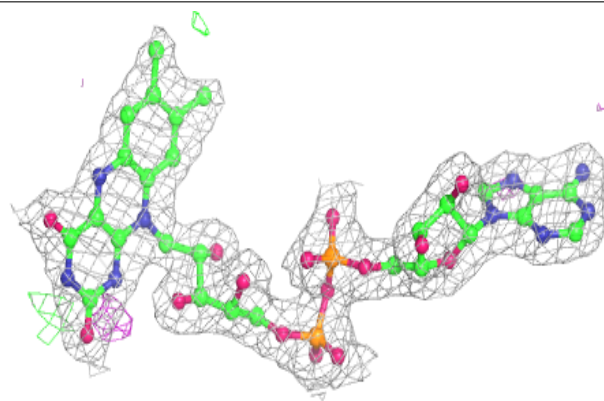


**Electron density around FAD C 500:**

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

**Electron density around FAD B 500:**

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



## 6.5 Other polymers

There are no such residues in this entry.