wwPDB X-ray Structure Validation Summary Report (i)

May 15, 2020 – 11:29 pm BST

PDB ID	:	1F0X
Title	:	CRYSTAL STRUCTURE OF D-LACTATE DEHYDROGENASE, A PERIPHERAL MEMBRANE RESPIRATORY ENZYME.
Authors	:	Dym, O.; Pratt, E.A.; Ho, C.; Eisenberg, D.
Deposited on	:	2000-05-17
Resolution	:	1.90 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 (i) symbol.

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

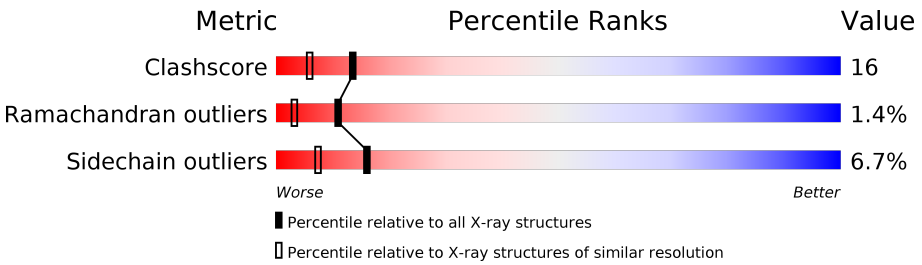
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	571	63% 21% • • 12%
1	B	571	63% 21% • • 12%

2 Entry composition (i)

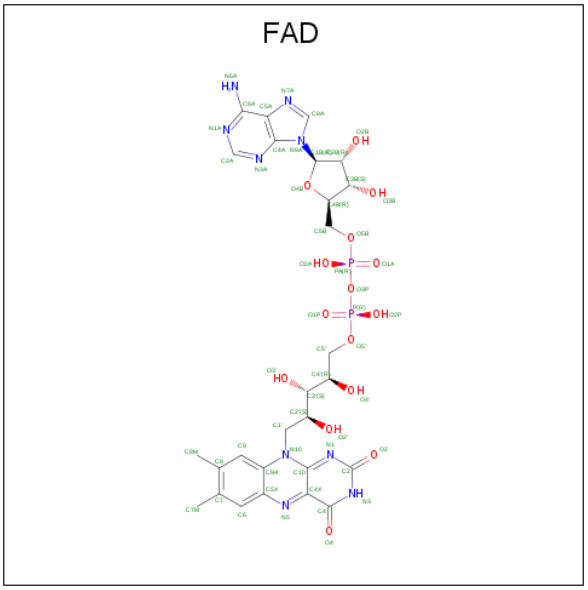
There are 3 unique types of molecules in this entry. The entry contains 8393 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 D-LACTATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	502	3983	2515	706	748	14	0	0	0
1	B	502	3983	2515	706	748	14	0	0	0

- 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
			Total	C	N	O	P		
2	A	1	53	27	9	15	2	0	0
2	B	1	53	27	9	15	2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	179	179	179	0	0
			Total	O		
3	B	142	142	142	0	0

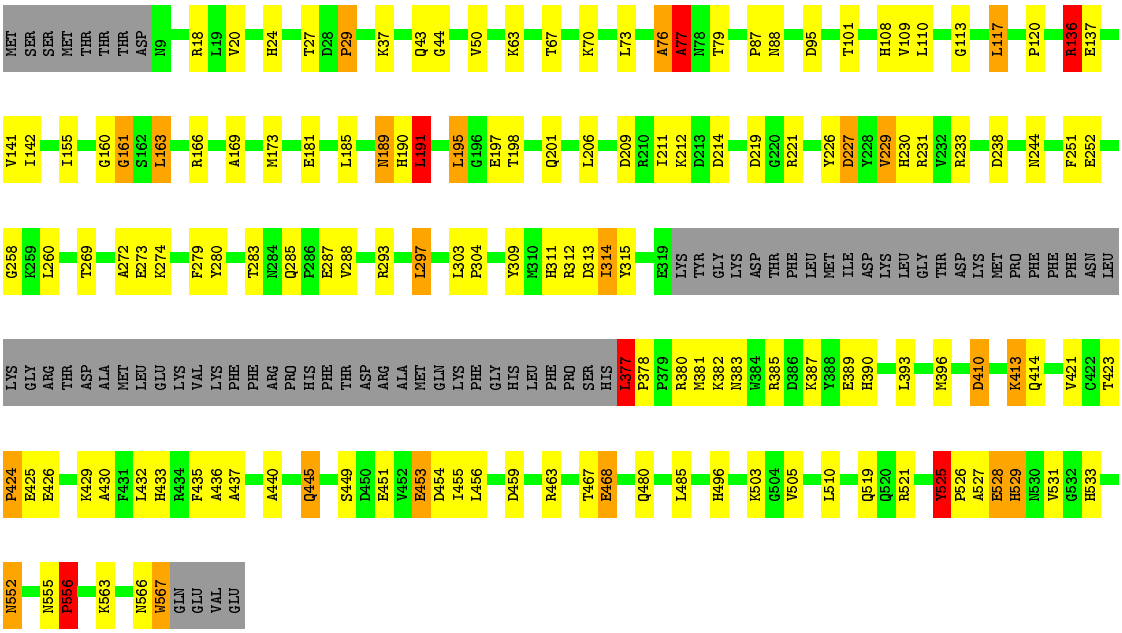
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

Note EDS was not executed.

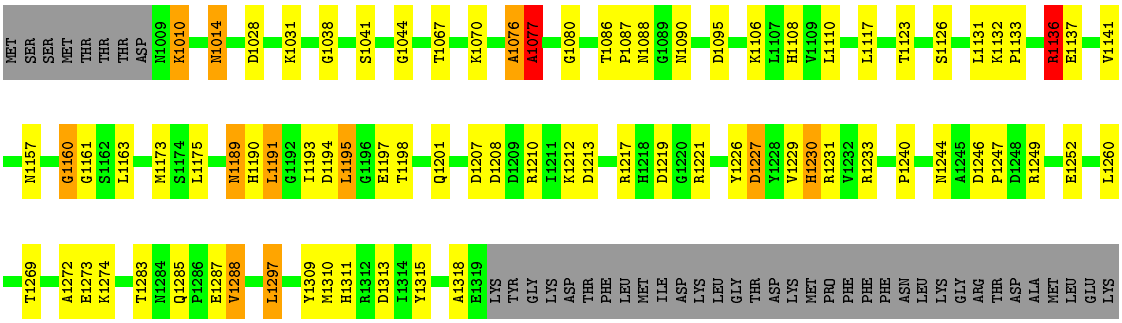
- Molecule 1: D-LACTATE DEHYDROGENASE

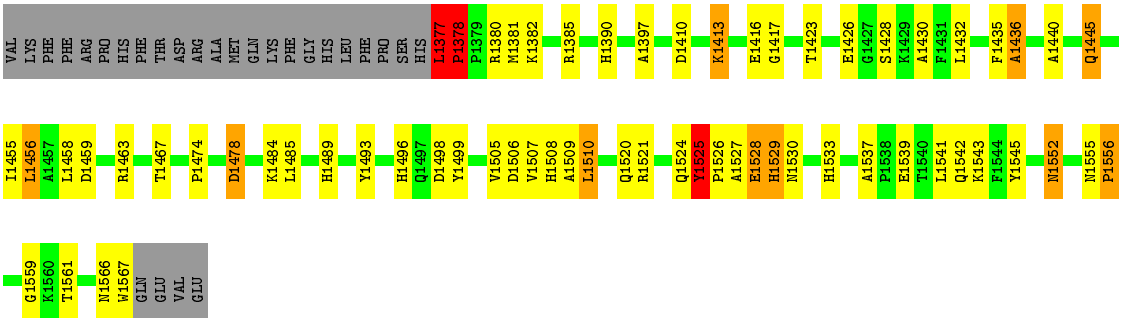
Chain A:



- Molecule 1: D-LACTATE DEHYDROGENASE

Chain B:




VAL
LYS
PHE
PHE
ARG
PRO
HIS
PHE
THR
ASP
ARG
ALA
MET
GLN
LYS
PHE
GLY
HIS
LEU
PHE
PRO
SER
HIS
I1377
P1378
P1379
R1380
M1381
K1382
R1385
H1390
A1397
D1410
K1413
E1416
G1417
T1423
E1426
G1427
S1428
K1429
A1430
F1431
L1432
F1435
A1436
A1440
Q1445
I1455
L1456
A1457
L1458
D1459
R1463
T1467
P1474
D1478
K1484
L1485
H1489
Y1493
H1496
Q1497
D1498
Y1499
V1505
D1506
V1507
H1508
A1509
L1510
Q1520
R1521
Q1524
Y1525
P1526
A1527
E1528
H1529
N1530
H1533
A1537
P1538
E1539
T1540
L1541
Q1542
K1543
F1544
Y1545
N1552
N1555
P1556
G1559
K1560
T1561
N1566
W1567
GLN
GLU
VAL
GLU

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	69.01Å 74.19Å 102.00Å 90.00° 95.73° 90.00°	Depositor
Resolution (Å)	18.00 – 1.90	Depositor
% Data completeness (in resolution range)	96.5 (18.00-1.90)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.209 , 0.248	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8393	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

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: 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	0.91	5/4072 (0.1%)	1.05	20/5511 (0.4%)
1	B	0.95	8/4072 (0.2%)	1.03	20/5511 (0.4%)
All	All	0.93	13/8144 (0.2%)	1.04	40/11022 (0.4%)

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1528	GLU	CD-OE1	23.52	1.51	1.25
1	A	528	GLU	CD-OE1	17.23	1.44	1.25
1	B	1528	GLU	CB-CG	11.16	1.73	1.52
1	A	528	GLU	CB-CG	10.24	1.71	1.52
1	A	77	ALA	N-CA	7.53	1.61	1.46

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	377	LEU	C-N-CD	-18.31	80.32	120.60
1	B	1377	LEU	C-N-CD	-11.09	96.19	120.60
1	A	377	LEU	C-N-CA	10.30	165.25	122.00
1	A	525	TYR	C-N-CD	10.14	149.70	128.40
1	B	1528	GLU	CG-CD-OE2	-9.75	98.80	118.30

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	3983	0	3900	130	2
1	B	3983	0	3900	120	2
2	A	53	0	31	6	0
2	B	53	0	31	6	0
3	A	179	0	0	4	0
3	B	142	0	0	8	0
All	All	8393	0	7862	255	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 16.

The worst 5 of 255 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:B:1285:GLN:O	1:B:1288:VAL:HG12	1.52	1.09
1:B:1076:ALA:O	1:B:1077:ALA:HB3	1.47	1.09
1:A:212:LYS:HD2	1:B:1520:GLN:HE22	1.17	1.08
1:A:76:ALA:O	1:A:77:ALA:HB3	1.41	1.08
1:A:285:GLN:O	1:A:288:VAL:HG12	1.55	1.07

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:ASP:OD1	1:B:1010:LYS:NZ[1_445]	2.01	0.19
1:A:238:ASP:N	1:B:1010:LYS:NZ[1_445]	2.19	0.01

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	498/571 (87%)	474 (95%)	16 (3%)	8 (2%)	9 2
1	B	498/571 (87%)	474 (95%)	18 (4%)	6 (1%)	13 4
All	All	996/1142 (87%)	948 (95%)	34 (3%)	14 (1%)	11 3

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	274	LYS
1	A	378	PRO
1	B	1274	LYS
1	B	1378	PRO
1	A	77	ALA

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	421/484 (87%)	393 (93%)	28 (7%)	16 7
1	B	421/484 (87%)	393 (93%)	28 (7%)	16 7
All	All	842/968 (87%)	786 (93%)	56 (7%)	16 7

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	525	TYR
1	B	1136	ARG
1	B	1478	ASP
1	A	552	ASN
1	B	1010	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	433	HIS

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Mol	Chain	Res	Type
1	A	552	ASN
1	B	1433	HIS
1	A	480	GLN
1	B	1014	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	FAD	A	600	-	51,58,58	3.29	22 (43%)	60,89,89	2.35	16 (26%)
2	FAD	B	1600	-	51,58,58	3.40	26 (50%)	60,89,89	2.26	17 (28%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FAD	A	600	-	-	3/30/50/50	0/6/6/6
2	FAD	B	1600	-	-	2/30/50/50	0/6/6/6

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1600	FAD	C5'-C4'	-12.34	1.34	1.51
2	A	600	FAD	C5'-C4'	-10.97	1.36	1.51
2	A	600	FAD	C4X-C10	9.43	1.48	1.38
2	B	1600	FAD	C4X-C10	8.42	1.47	1.38
2	B	1600	FAD	C9A-N10	6.60	1.47	1.38

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	600	FAD	C4-N3-C2	9.77	123.39	115.14
2	B	1600	FAD	C4-N3-C2	8.67	122.47	115.14
2	B	1600	FAD	C4'-C3'-C2'	-5.99	100.91	113.36
2	A	600	FAD	O5B-PA-O1A	-5.44	87.82	109.07
2	A	600	FAD	C4X-C4-N3	-5.12	116.42	123.43

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	600	FAD	PA-O3P-P-O2P
2	B	1600	FAD	PA-O3P-P-O2P
2	B	1600	FAD	O4B-C4B-C5B-O5B
2	A	600	FAD	O4B-C4B-C5B-O5B
2	A	600	FAD	C3B-C4B-C5B-O5B

There are no ring outliers.

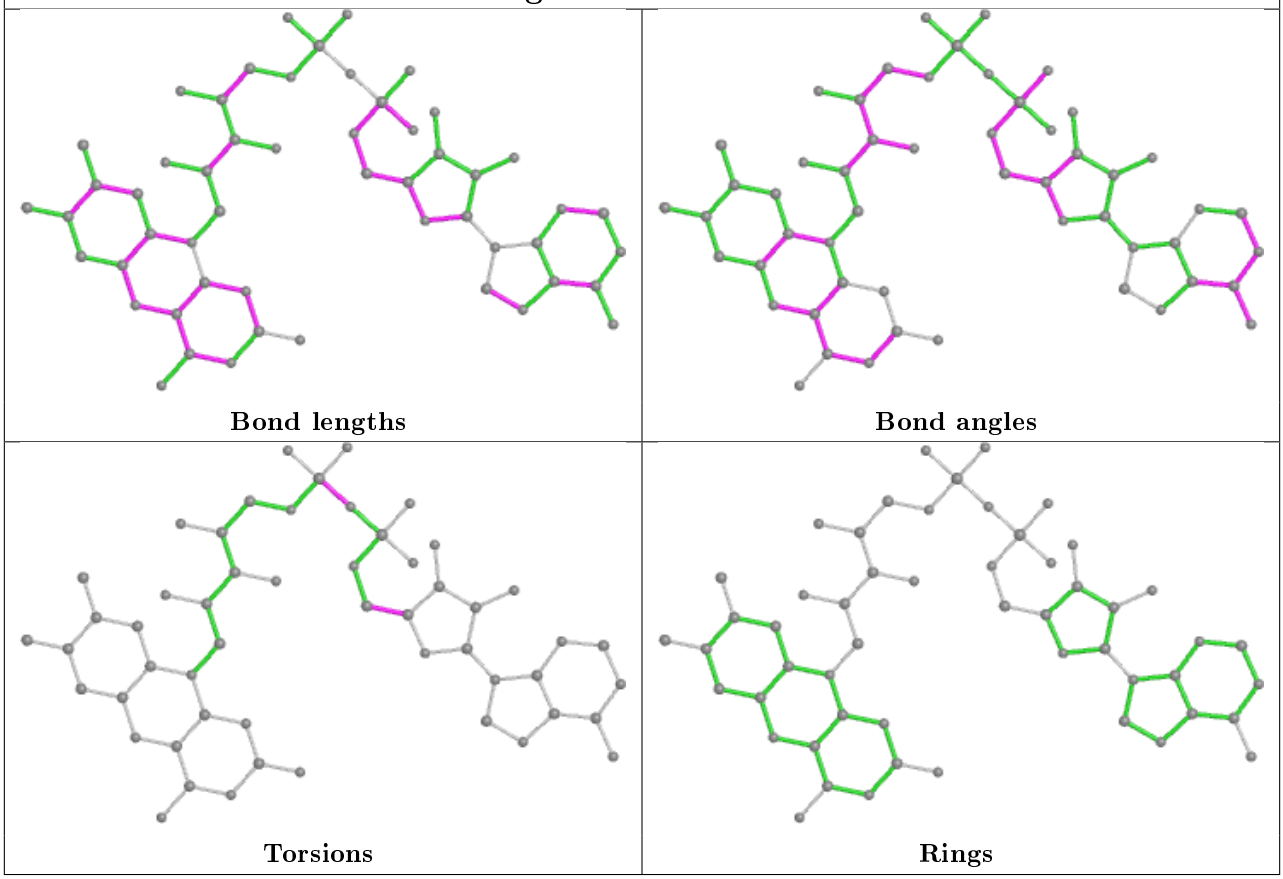
2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	600	FAD	6	0
2	B	1600	FAD	6	0

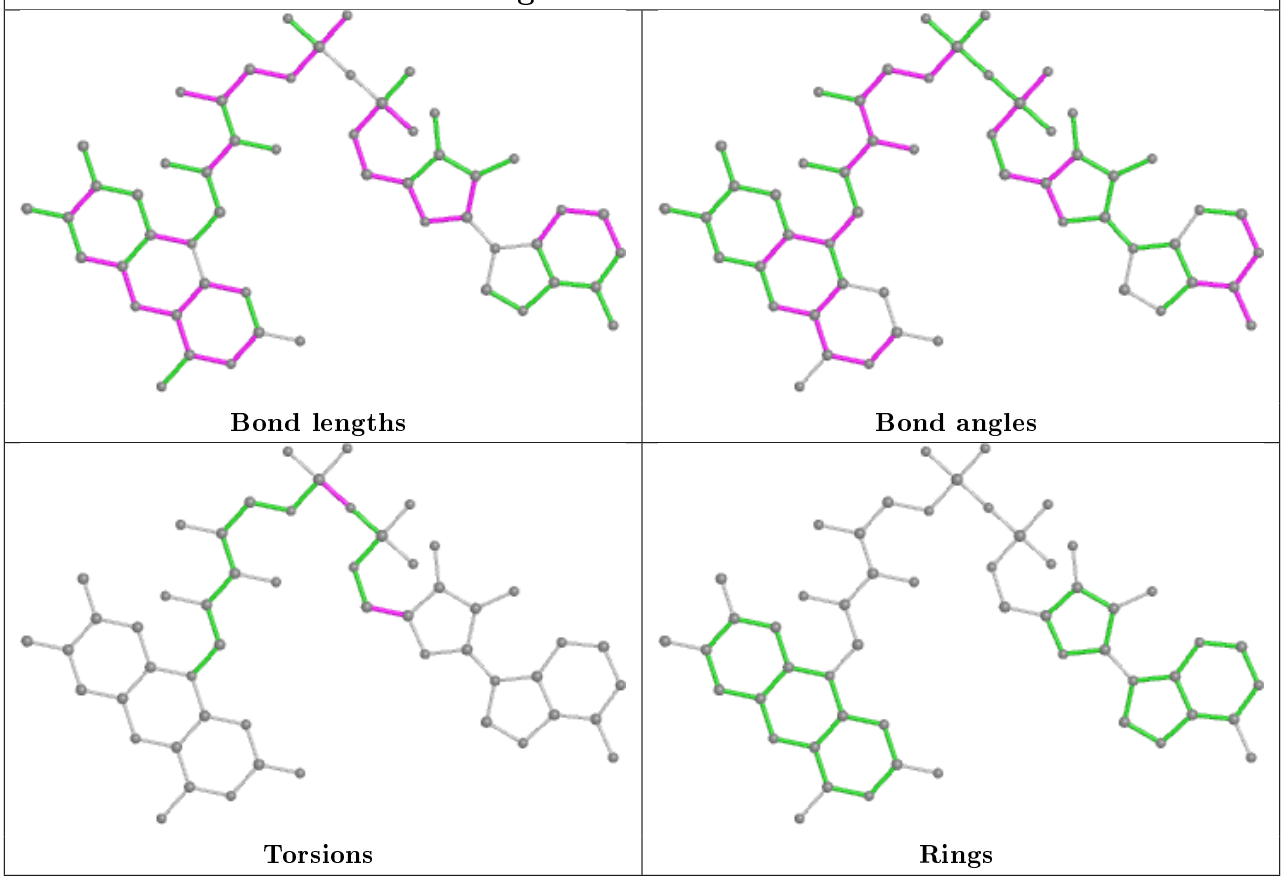
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less then 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 FAD A 600



Ligand FAD B 1600



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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.