wwPDB X-ray Structure Validation Summary Report (i)

Jan 30, 2024 – 09:41 PM EST

PDB ID	:	1JNR
Title	:	Structure of adenylylsulfate reductase from the hyperthermophilic Archaeoglobus fulgidus at 1.6 resolution
Authors	:	Fritz, G.; Roth, A.; Schiffer, A.; Buechert, T.; Bourenkov, G.; Bartunik, H.D.; Huber, H.; Stetter, K.O.; Kroneck, P.M.H.; Ermler, U.
Deposited on	:	2001-07-25
Resolution	:	1.60 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

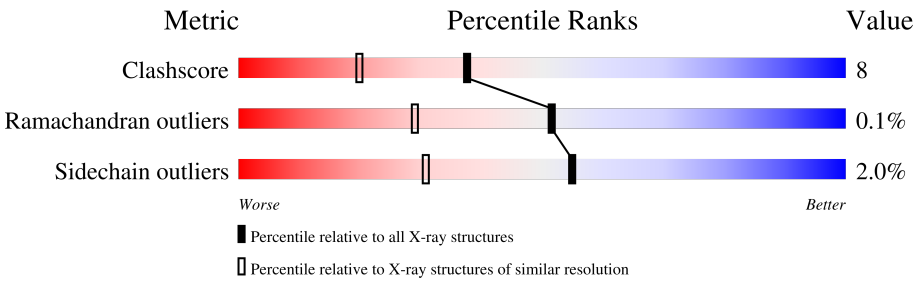
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.60 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	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	643	84% 14% •
1	C	643	86% 13% •
2	B	150	83% 13% • •
2	D	150	88% 11% •

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 14542 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 adenylylsulfate reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	642	5199	3364	855	950	30	0	8	0
1	C	642	5205	3369	853	953	30	0	11	0

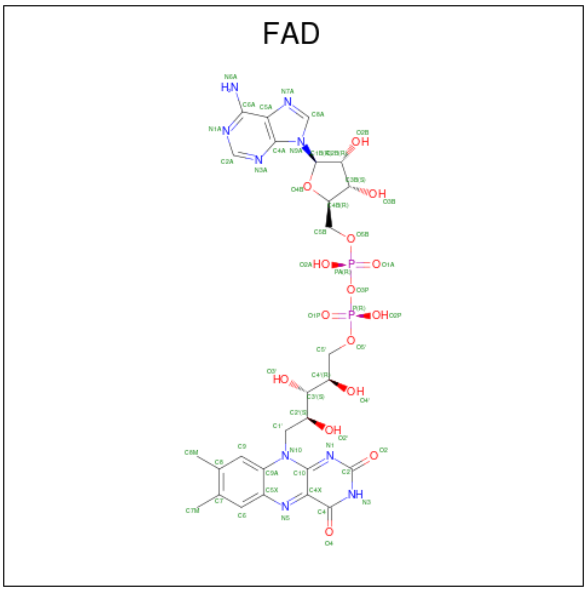
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	183	ASN	LYS	conflict	UNP O28603
C	183	ASN	LYS	conflict	UNP O28603

- Molecule 2 is a protein called adenylylsulfate reductase.

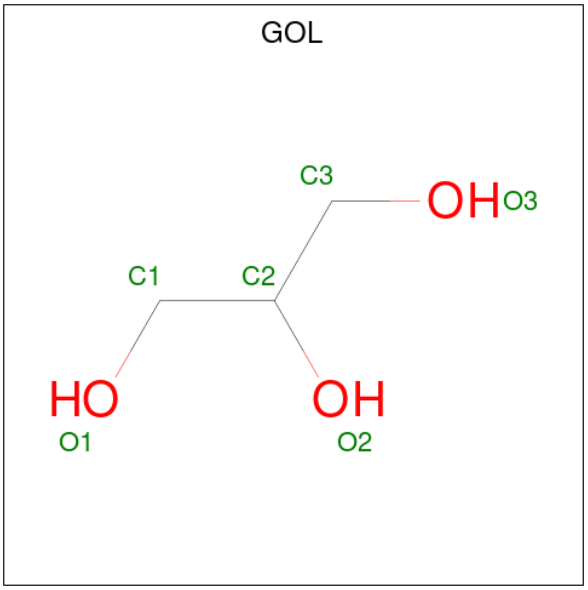
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	149	1176	747	193	220	16	0	1	0
2	D	149	1176	747	193	220	16	0	1	0

- Molecule 3 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		
3	A	1	53	27	9	15	2	0	0
			Total	C	N	O	P		
3	C	1	53	27	9	15	2	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	6	3	3	0	0
			Total	C	O		
4	C	1	6	3	3	0	0

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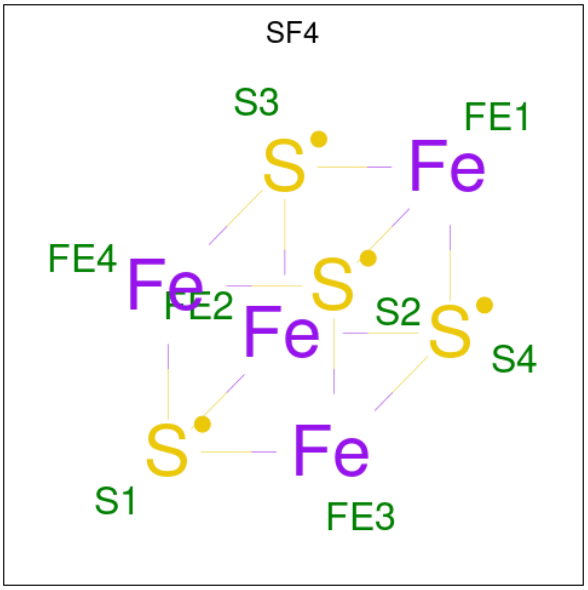
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total C O 6 3 3	0	0
4	C	1	Total C O 6 3 3	0	0

- Molecule 5 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Fe S 8 4 4	0	0
5	B	1	Total Fe S 8 4 4	0	0
5	D	1	Total Fe S 8 4 4	0	0
5	D	1	Total Fe S 8 4 4	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	584	Total O 587 587	0	3
6	B	170	Total O 171 171	0	1
6	C	649	Total O 659 659	0	10

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	D	205	207	207	0	2

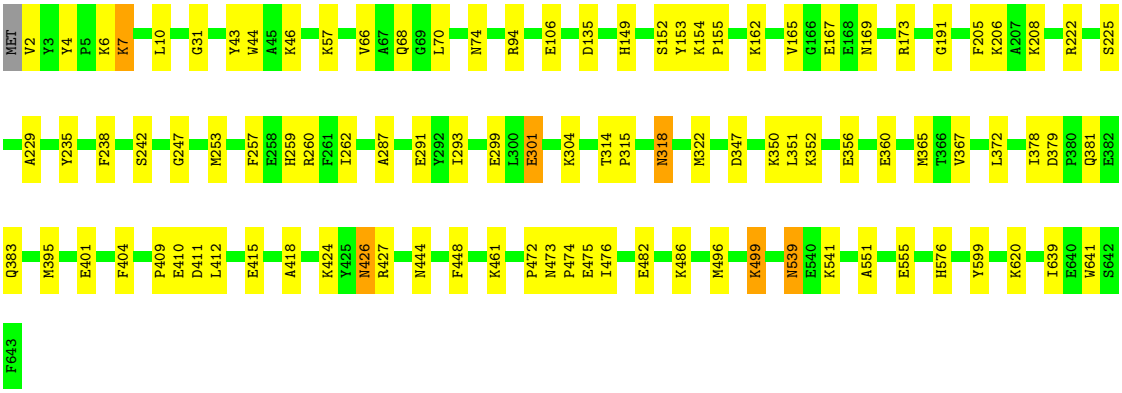
3 Residue-property plots (i)

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

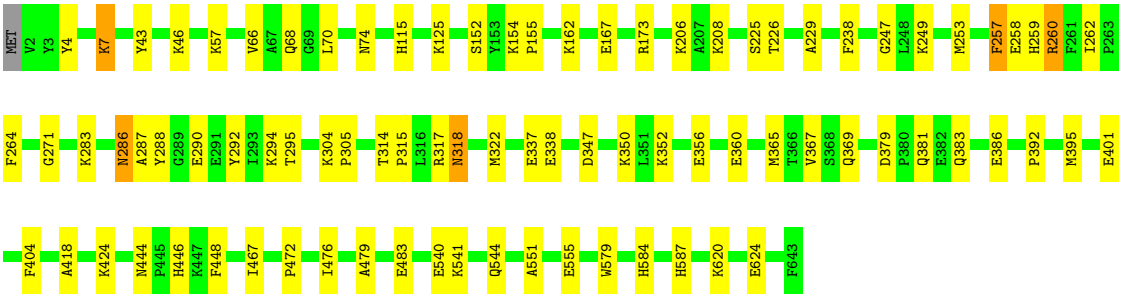
• Molecule 1: adenylylsulfate reductase

Chain A:



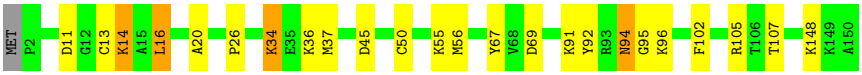
• Molecule 1: adenylylsulfate reductase

Chain C:



• Molecule 2: adenylylsulfate reductase

Chain B:



• Molecule 2: adenylylsulfate reductase

Chain D:

88%
11%

MET
P2
K14
A15
L16
E17
R18
T19
A20
C25
P26
K34
E35
K36
M37
D45
Y67
V68
D69
K96
Y97
L98
F102
E134
P135
A150

4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	72.60Å 113.50Å 193.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.59 – 1.60	Depositor
% Data completeness (in resolution range)	90.5 (27.59-1.60)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.180 , 0.202	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	14542	wwPDB-VP
Average B, all atoms (Å^2)	15.0	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: GOL, FAD, SF4

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	0.30	0/5372	0.58	0/7269
1	C	0.31	0/5393	0.60	0/7300
2	B	0.30	0/1210	0.65	0/1632
2	D	0.32	0/1210	0.66	0/1632
All	All	0.30	0/13185	0.60	0/17833

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	5199	0	5094	92	0
1	C	5205	0	5100	84	0
2	B	1176	0	1151	26	0
2	D	1176	0	1151	16	0
3	A	53	0	29	2	0
3	C	53	0	29	0	0
4	A	6	0	8	0	0
4	C	18	0	24	4	0
5	B	16	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	16	0	0	1	0
6	A	587	0	0	6	0
6	B	171	0	0	3	0
6	C	659	0	0	6	0
6	D	207	0	0	3	0
All	All	14542	0	12586	194	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 8.

The worst 5 of 194 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)
2:B:13:CYS:HB3	2:B:16:LEU:HD21	1.23	1.17
1:A:4:TYR:CE2	1:C:4:TYR:CD1	2.47	1.02
1:A:4:TYR:CE1	1:C:4:TYR:CE1	2.64	0.85
1:A:4:TYR:CE2	1:C:4:TYR:HD1	1.93	0.85
1:A:106:GLU:HB3	1:A:639[B]:ILE:HD13	1.58	0.85

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	648/643 (101%)	627 (97%)	21 (3%)	0	100 100
1	C	650/643 (101%)	631 (97%)	19 (3%)	0	100 100
2	B	148/150 (99%)	142 (96%)	4 (3%)	2 (1%)	11 2
2	D	148/150 (99%)	146 (99%)	2 (1%)	0	100 100
All	All	1594/1586 (100%)	1546 (97%)	46 (3%)	2 (0%)	51 29

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	14	LYS
2	B	34	LYS

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	533/526 (101%)	518 (97%)	15 (3%)	43	18
1	C	536/526 (102%)	527 (98%)	9 (2%)	60	38
2	B	130/130 (100%)	127 (98%)	3 (2%)	50	25
2	D	130/130 (100%)	129 (99%)	1 (1%)	81	70
All	All	1329/1312 (101%)	1301 (98%)	28 (2%)	55	29

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	539	ASN
2	D	69	ASP
2	B	94	ASN
1	C	395[B]	MET
2	B	69	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	115	HIS
1	C	310	GLN
2	D	145	GLN
1	C	286	ASN
1	C	318	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

10 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	SF4	B	1110	2	0,12,12	-	-	-		
4	GOL	C	6501	-	5,5,5	1.08	0	5,5,5	0.67	0
4	GOL	A	6503	-	5,5,5	0.85	0	5,5,5	0.96	1 (20%)
4	GOL	C	6504	-	5,5,5	0.76	0	5,5,5	0.70	0
3	FAD	A	1000	-	53,58,58	4.36	35 (66%)	68,89,89	2.26	25 (36%)
5	SF4	D	3110	2	0,12,12	-	-	-		
5	SF4	D	3100	2	0,12,12	-	-	-		
3	FAD	C	3000	-	53,58,58	4.24	32 (60%)	68,89,89	2.23	20 (29%)
5	SF4	B	1100	2	0,12,12	-	-	-		
4	GOL	C	6505	-	5,5,5	0.79	0	5,5,5	1.14	1 (20%)

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	SF4	B	1110	2	-	-	0/6/5/5
4	GOL	C	6501	-	-	2/4/4/4	-
4	GOL	A	6503	-	-	4/4/4/4	-
4	GOL	C	6504	-	-	4/4/4/4	-
3	FAD	A	1000	-	-	1/30/50/50	0/6/6/6
5	SF4	D	3110	2	-	-	0/6/5/5
5	SF4	D	3100	2	-	-	0/6/5/5
3	FAD	C	3000	-	-	2/30/50/50	0/6/6/6
5	SF4	B	1100	2	-	-	0/6/5/5
4	GOL	C	6505	-	-	4/4/4/4	-

The worst 5 of 67 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1000	FAD	C2B-C1B	10.07	1.69	1.53
3	C	3000	FAD	C9A-C5X	9.86	1.57	1.41
3	A	1000	FAD	C1'-N10	-9.48	1.24	1.48
3	A	1000	FAD	C9A-C5X	9.24	1.56	1.41
3	A	1000	FAD	C5'-C4'	9.21	1.64	1.51

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	3000	FAD	O4B-C1B-C2B	-7.25	96.33	106.93
3	A	1000	FAD	O4B-C1B-C2B	-6.99	96.71	106.93
3	A	1000	FAD	O4B-C4B-C3B	6.35	117.67	105.11
3	C	3000	FAD	O4B-C4B-C3B	6.26	117.50	105.11
3	A	1000	FAD	C2B-C3B-C4B	-5.46	92.04	102.64

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	6503	GOL	C1-C2-C3-O3
4	A	6503	GOL	O2-C2-C3-O3
4	C	6501	GOL	C1-C2-C3-O3
4	C	6504	GOL	O1-C1-C2-C3
4	C	6504	GOL	C1-C2-C3-O3

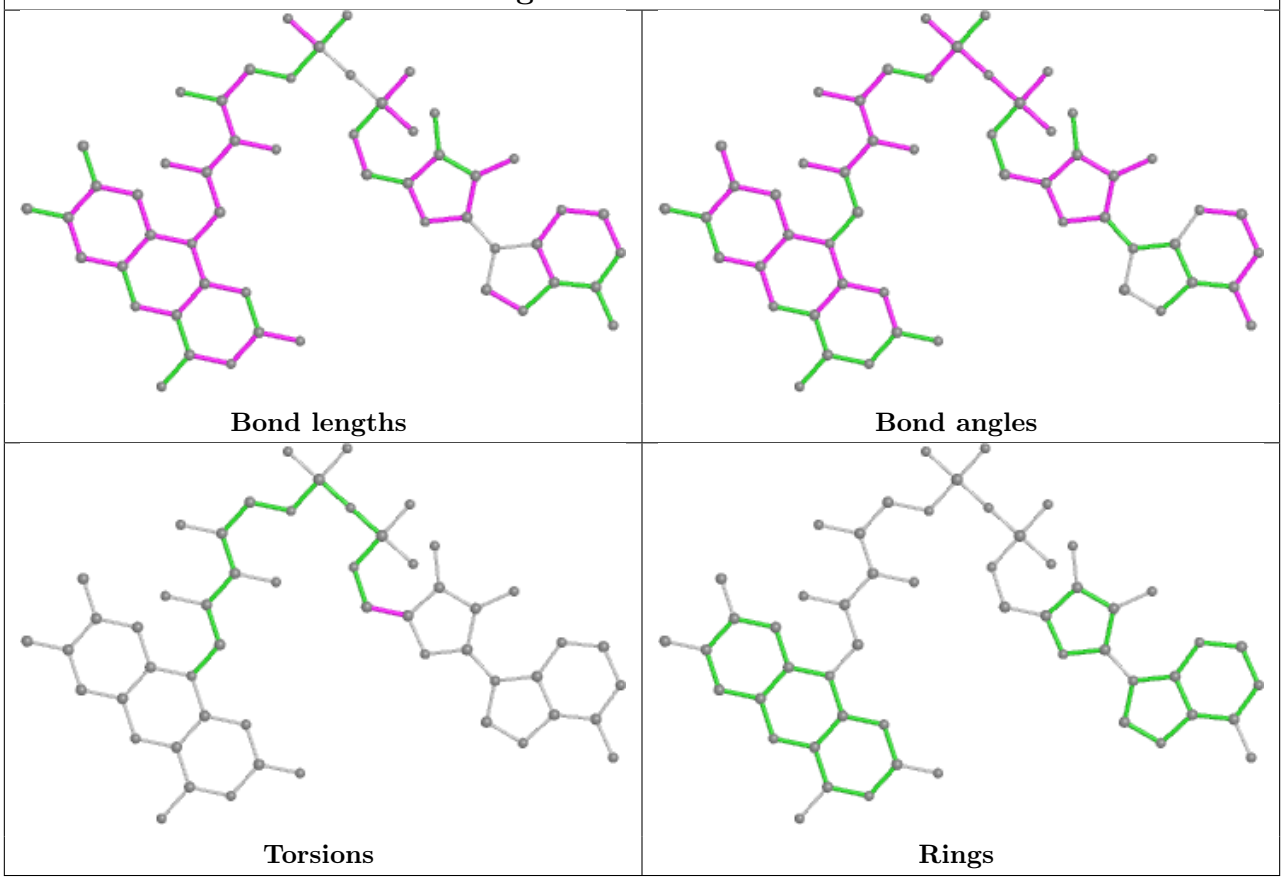
There are no ring outliers.

5 monomers are involved in 8 short contacts:

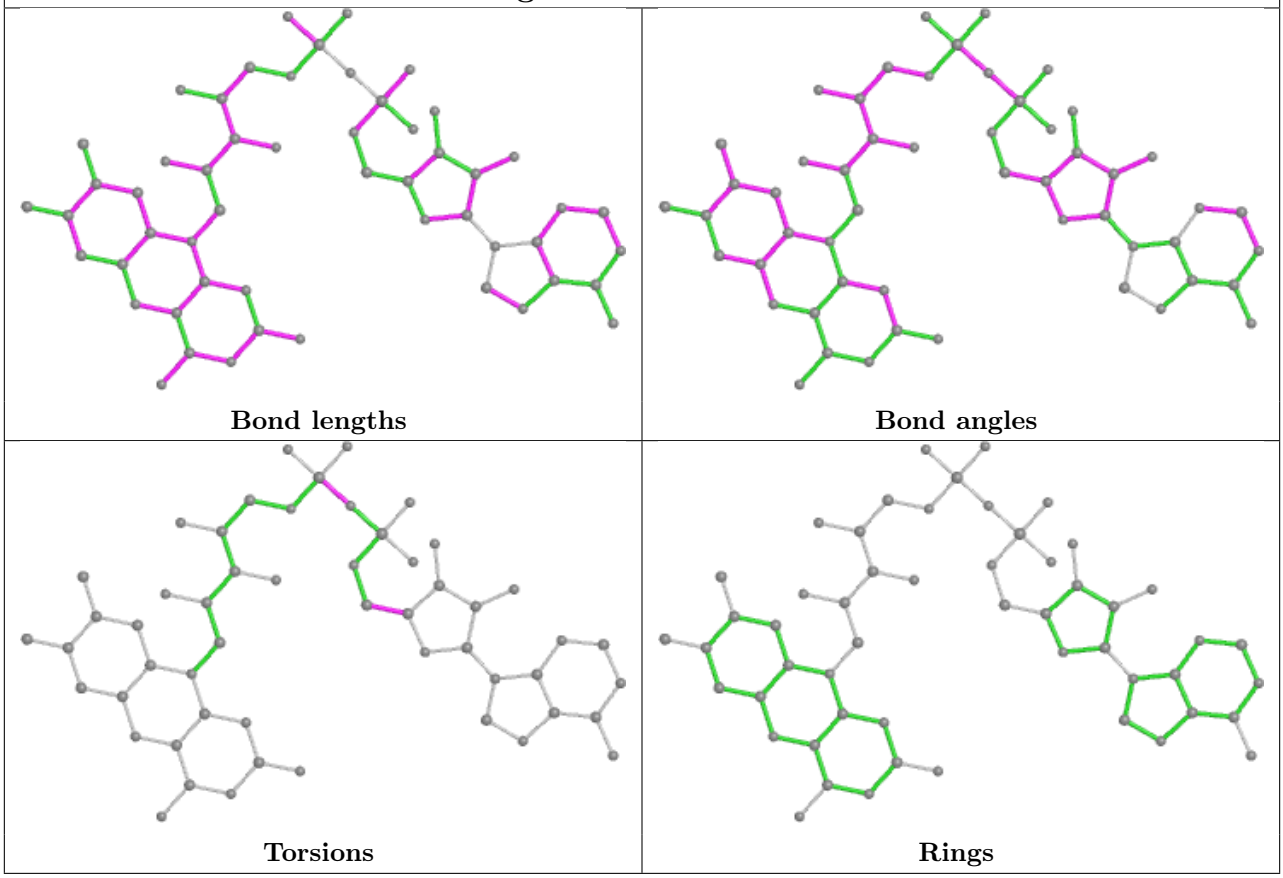
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1110	SF4	1	0
4	C	6504	GOL	3	0
3	A	1000	FAD	2	0
5	D	3110	SF4	1	0
4	C	6505	GOL	1	0

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 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 1000



Ligand FAD C 3000



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.