Full wwPDB X-ray Structure Validation Report (i)

Oct 3, 2023 – 03:16 AM EDT

PDB ID	:	6OXD
Title	:	Structure of Mycobacterium tuberculosis methylmalonyl-CoA mutase with adenosyl cobalamin
Authors	:	Purchal, M.; Ruetz, M.; Banerjee, R.; Koutmos, M.
Deposited on	:	2019-05-13
Resolution	:	2.00 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*
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	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
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)	:	2.35.1

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 2.00 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 21256 atoms, of which 9990 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 Methylmalonyl-CoA mutase large subunit.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	736	11127	3527	5528	996	1061	15	0	2	0

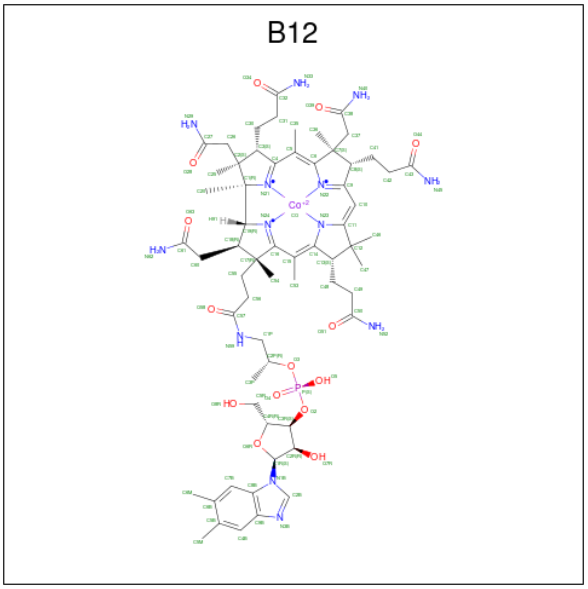
- Molecule 2 is a protein called Methylmalonyl-CoA mutase small subunit.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	B	590	8746	2746	4365	806	819	10	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

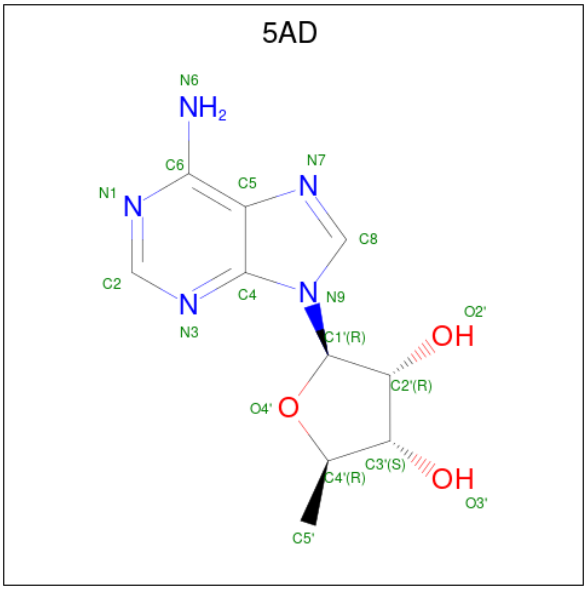
Chain	Residue	Modelled	Actual	Comment	Reference
B	1	SER	-	expression tag	UNP A0A045IZR3
B	2	VAL	MET	variant	UNP A0A045IZR3

- Molecule 3 is COBALAMIN (three-letter code: B12) (formula: $C_{62}H_{89}CoN_{13}O_{14}P$) (labeled as "Ligand of Interest" by depositor).



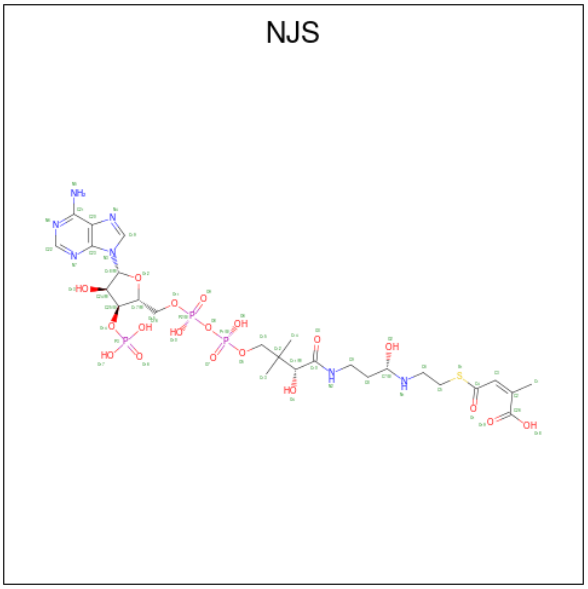
Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
			Total	C	Co	H	N	O	P		
3	A	1	177	62	1	86	13	14	1	0	0

- Molecule 4 is 5'-DEOXYADENOSINE (three-letter code: 5AD) (formula: $C_{10}H_{13}N_5O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
4	A	1	29	10	11	5	3	0	0

- Molecule 5 is Itaconyl coenzyme A (three-letter code: NJS) (formula: $C_{26}H_{42}N_7O_{19}P_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
5	A	1	56	26	7	19	3	1	0	0

- Molecule 6 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	K		
6	A	1	1	1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	555	555	555	0	0
			Total	O		
7	B	565	565	565	0	0

MolProbity and EDS failed to run properly - this section is therefore empty.

3 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	76.58Å 104.96Å 194.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.80 – 2.00	Depositor
% Data completeness (in resolution range)	97.9 (29.80-2.00)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.51 (at 2.00Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.159 , 0.197	Depositor
Wilson B-factor (Å^2)	28.4	Xtriage
Anisotropy	0.320	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	21256	wwPDB-VP
Average B, all atoms (Å^2)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

4 Model quality (i)

4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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	$\#\|Z\| > 2$
4	5AD	A	1001	5	17,20,20	4.45	7 (41%)	15,30,30	3.46	7 (46%)
5	NJS	A	1002	4	48,58,58	2.38	12 (25%)	61,86,86	2.32	14 (22%)
3	B12	A	1000	1	90,101,101	1.39	15 (16%)	137,166,166	2.74	33 (24%)

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
4	5AD	A	1001	5	-	0/0/20/20	0/3/3/3
5	NJS	A	1002	4	-	11/53/75/75	0/3/3/3
3	B12	A	1000	1	-	7/52/223/223	0/3/11/11

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1001	5AD	O4'-C1'	12.29	1.58	1.41
4	A	1001	5AD	C3'-C4'	9.11	1.65	1.52
5	A	1002	NJS	O12-C17	8.52	1.64	1.45
5	A	1002	NJS	C25-C17	-6.65	1.35	1.52
4	A	1001	5AD	C3'-C2'	-6.44	1.35	1.53
5	A	1002	NJS	O12-C18	-5.98	1.32	1.41
4	A	1001	5AD	O4'-C4'	-5.01	1.29	1.44
5	A	1002	NJS	C10-N2	4.92	1.44	1.33
3	A	1000	B12	C19-N24	-4.78	1.39	1.48
5	A	1002	NJS	O13-C24	-4.36	1.32	1.43
3	A	1000	B12	C9-N22	4.17	1.41	1.30
3	A	1000	B12	C14-N23	3.80	1.39	1.35
5	A	1002	NJS	P3-O14	3.70	1.66	1.59
3	A	1000	B12	C12-C11	-3.17	1.46	1.52
3	A	1000	B12	C6B-C5B	3.15	1.48	1.40
4	A	1001	5AD	C2-N3	2.93	1.36	1.32
3	A	1000	B12	C8B-C9B	2.85	1.46	1.40
5	A	1002	NJS	C21-N5	2.80	1.44	1.34
5	A	1002	NJS	C3-C4	2.74	1.51	1.47
3	A	1000	B12	C16-C15	-2.63	1.37	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1000	B12	C1-C19	-2.63	1.49	1.55
4	A	1001	5AD	C6-N6	2.47	1.43	1.34
4	A	1001	5AD	O2'-C2'	2.44	1.48	1.43
3	A	1000	B12	C1-C2	-2.40	1.53	1.58
3	A	1000	B12	C14-C15	2.33	1.48	1.38
3	A	1000	B12	C25-C2	-2.26	1.49	1.54
3	A	1000	B12	C10-C9	2.26	1.45	1.39
5	A	1002	NJS	C24-C18	2.21	1.57	1.53
3	A	1000	B12	C56-C57	2.14	1.55	1.51
3	A	1000	B12	C46-C12	-2.12	1.49	1.54
5	A	1002	NJS	C26-C2	2.12	1.54	1.49
3	A	1000	B12	P-O3	2.07	1.65	1.60
5	A	1002	NJS	O19-C26	2.01	1.28	1.22
5	A	1002	NJS	O18-C26	-2.00	1.24	1.30

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1000	B12	C20-C1-C19	-14.32	95.56	109.36
5	A	1002	NJS	C3-C4-S1	11.24	125.27	111.24
3	A	1000	B12	C20-C1-N21	-10.91	92.37	110.27
3	A	1000	B12	C19-C1-N21	8.14	110.50	102.16
5	A	1002	NJS	O1-C4-C3	-7.95	115.74	125.50
3	A	1000	B12	C47-C12-C46	7.67	122.32	109.35
4	A	1001	5AD	C5-C6-N6	7.22	131.32	120.35
3	A	1000	B12	C18-C19-N24	7.04	113.02	102.31
3	A	1000	B12	C13-C12-C11	-6.96	93.09	100.97
4	A	1001	5AD	C5'-C4'-C3'	-6.59	108.78	115.70
3	A	1000	B12	C12-C11-C10	-6.08	115.45	123.37
3	A	1000	B12	C18-C17-C16	6.05	108.03	100.67
3	A	1000	B12	C1-C19-C18	5.84	131.46	121.88
3	A	1000	B12	C2-C1-N21	5.49	109.42	101.77
4	A	1001	5AD	N6-C6-N1	-5.26	107.66	118.57
3	A	1000	B12	C2P-C1P-N59	-5.21	105.26	112.93
4	A	1001	5AD	N3-C2-N1	-5.20	120.55	128.68
3	A	1000	B12	C2-C1-C19	5.08	126.61	118.60
3	A	1000	B12	C54-C17-C18	-4.73	106.00	112.98
5	A	1002	NJS	N7-C22-N6	-4.67	121.39	128.68
3	A	1000	B12	C46-C12-C13	-4.34	95.05	112.72
3	A	1000	B12	O6R-C1R-C2R	-3.67	101.56	106.93
3	A	1000	B12	C15-C14-N23	-3.63	121.83	126.26
5	A	1002	NJS	O5-C15-C12	-3.54	104.86	110.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1000	B12	C17-C16-C15	3.43	131.66	126.26
3	A	1000	B12	C12-C13-C14	3.20	107.61	102.26
4	A	1001	5AD	O4'-C1'-C2'	-3.16	102.31	106.93
5	A	1002	NJS	C5-C6-N1	-3.01	103.67	112.05
3	A	1000	B12	C47-C12-C11	2.97	120.78	110.08
3	A	1000	B12	C17-C16-N24	-2.96	106.58	111.15
3	A	1000	B12	C48-C13-C14	-2.92	101.21	108.49
3	A	1000	B12	C47-C12-C13	-2.84	101.14	112.72
3	A	1000	B12	C13-C14-C15	2.82	128.64	124.32
3	A	1000	B12	C12-C11-N23	2.72	115.62	111.83
5	A	1002	NJS	C5-S1-C4	-2.66	96.45	99.80
3	A	1000	B12	C55-C17-C18	2.64	116.25	111.15
4	A	1001	5AD	O3'-C3'-C2'	2.58	120.18	111.82
3	A	1000	B12	C60-C18-C19	2.52	121.19	114.62
5	A	1002	NJS	C18-N3-C23	-2.50	122.25	126.64
3	A	1000	B12	C26-C2-C3	2.49	111.82	107.41
5	A	1002	NJS	C14-C12-C15	2.47	112.27	108.23
5	A	1002	NJS	C9-N2-C10	-2.43	118.26	122.59
4	A	1001	5AD	C1'-N9-C4	-2.43	122.38	126.64
3	A	1000	B12	C54-C17-C55	-2.41	105.27	109.25
5	A	1002	NJS	C1-C2-C3	-2.32	117.39	123.87
3	A	1000	B12	C36-C7-C37	2.24	114.50	110.80
5	A	1002	NJS	C24-C25-C17	2.19	107.11	103.22
5	A	1002	NJS	C9-C8-C7	-2.18	109.19	114.17
3	A	1000	B12	C8-C7-C6	2.13	104.58	100.92
5	A	1002	NJS	P2-O8-P1	-2.13	125.53	132.83
3	A	1000	B12	C26-C2-C1	2.10	113.28	110.01
3	A	1000	B12	C17-C18-C19	-2.08	99.18	102.36
5	A	1002	NJS	O6-P1-O5	2.04	117.24	107.75
3	A	1000	B12	C20-C1-C2	2.01	116.64	113.28

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1002	NJS	C1-C2-C26-O18
5	A	1002	NJS	C1-C2-C26-O19
5	A	1002	NJS	C3-C4-S1-C5
5	A	1002	NJS	O1-C4-S1-C5
5	A	1002	NJS	O2-C7-C8-C9
3	A	1000	B12	C42-C41-C8-C9
5	A	1002	NJS	C3-C2-C26-O18

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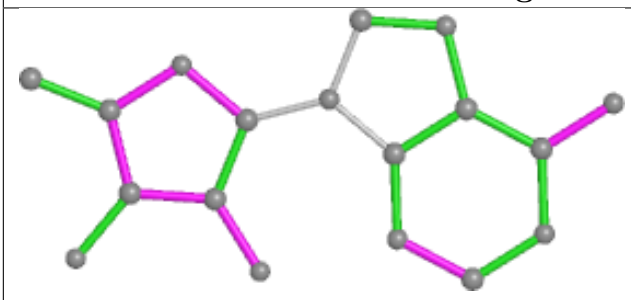
Mol	Chain	Res	Type	Atoms
5	A	1002	NJS	C3-C2-C26-O19
5	A	1002	NJS	N1-C7-C8-C9
5	A	1002	NJS	C25-O14-P3-O15
3	A	1000	B12	C2P-O3-P-O2
5	A	1002	NJS	P1-O8-P2-O10
3	A	1000	B12	C55-C56-C57-O58
3	A	1000	B12	C30-C31-C32-O34
3	A	1000	B12	C55-C56-C57-N59
5	A	1002	NJS	C6-C5-S1-C4
3	A	1000	B12	C30-C31-C32-N33
3	A	1000	B12	C3-C30-C31-C32

There are no ring outliers.

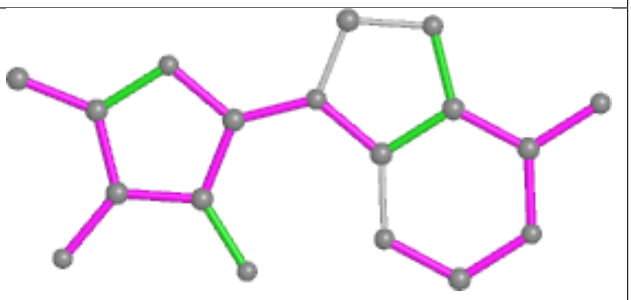
No monomer is involved in short contacts.

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.

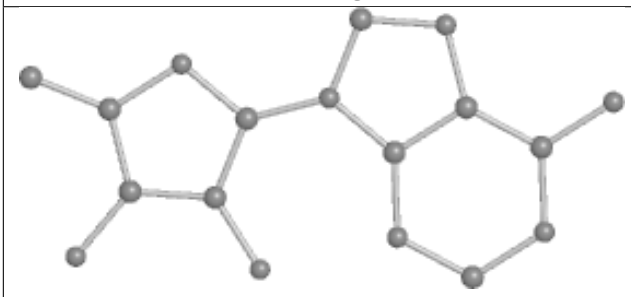
Ligand 5AD A 1001



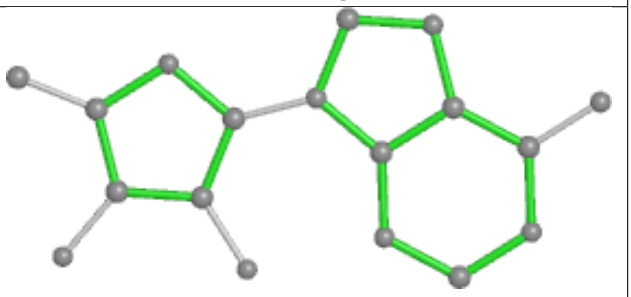
Bond lengths



Bond angles

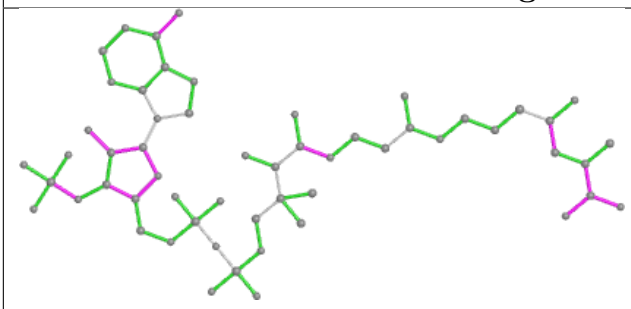


Torsions

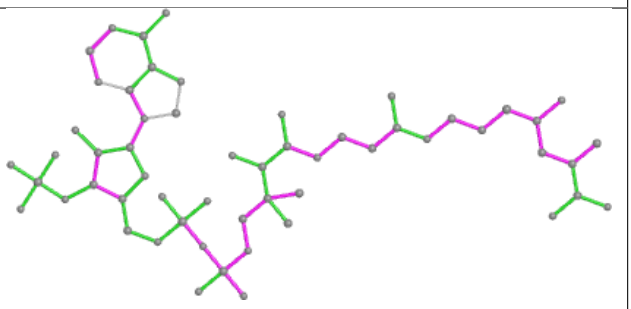


Rings

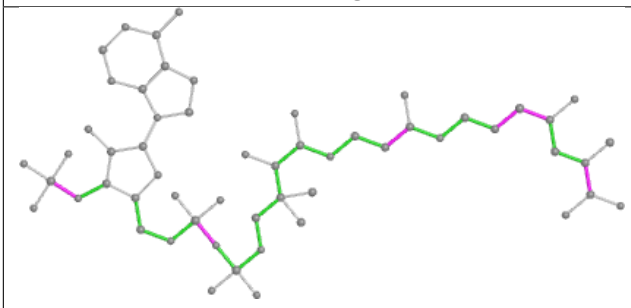
Ligand NJS A 1002



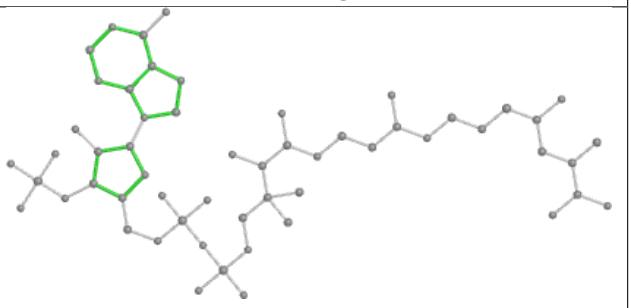
Bond lengths



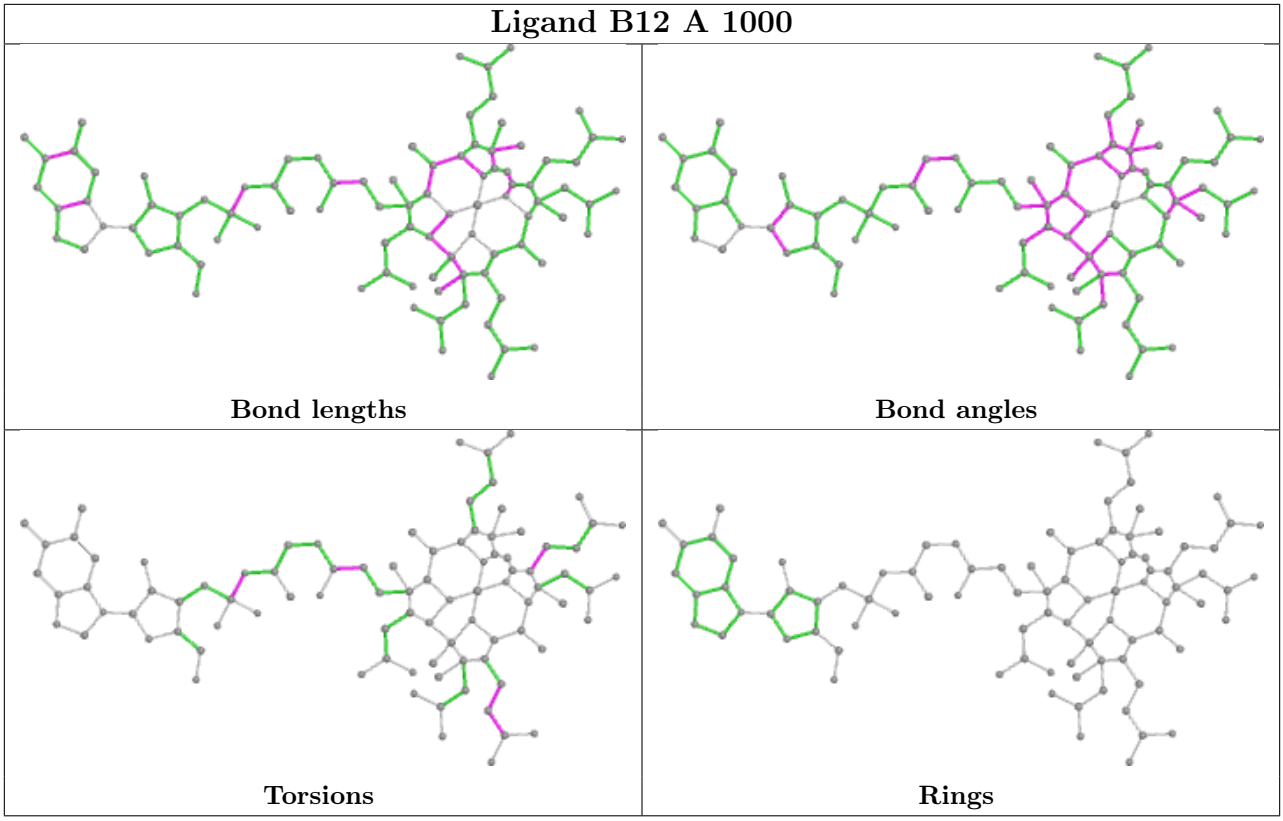
Bond angles



Torsions



Rings



4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

5 Fit of model and data (i)

5.1 Protein, DNA and RNA chains (i)

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

5.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.