

wwPDB X-ray Structure Validation Summary Report (i)

May 23, 2020 – 08:47 pm BST

PDB ID : 1KHR

Title: Crystal Structure of Vat(D) in Complex with Virginiamycin and Coenzyme A

Authors: Sugantino, M.; Roderick, S.L.

Deposited on : 2001-11-30

Resolution : 2.80 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)

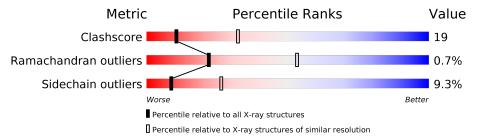
Validation Pipeline (wwPDB-VP) : 2.11

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 2.80 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\AA)}) \end{array}$
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)

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	209	59%	36%					
1	В	209	72%	22% • •					
1	С	209	64%	32%					
1	D	209	57%	34% 8% •					
1	Е	209	56%	37% • •					
1	F	209	63%	32%					



2 Entry composition (i)

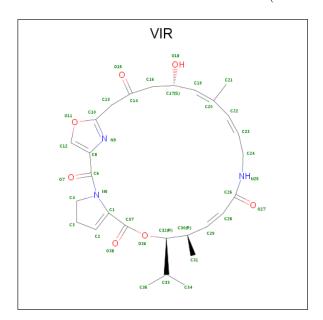
There are 4 unique types of molecules in this entry. The entry contains 10192 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 STREPTOGRAMIN A ACETYLTRANSFERASE.

Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf	Trace
1	A	206	Total	С	N	О	S	0	0	0
1	Λ	200	1611	1037	265	300	9	0	0	
1	В	205	Total	С	N	О	S	0	0	0
1	Ъ	200	1609	1036	265	299	9	0	U	
1	С	206	Total	С	N	О	S	0	0	0
1		200	1618	1041	266	302	9		U	U
1	D	206	Total	С	N	O	S	0	0	0
1	D	200	1622	1046	267	300	9	U	U	
1	E	204	Total	С	N	Ο	S	0	0	0
1	12	204	1606	1034	264	300	8		U	U
1	F	206	Total	С	N	О	S	0	0	0
1	1'	200	1612	1038	267	298	9	U	U	U

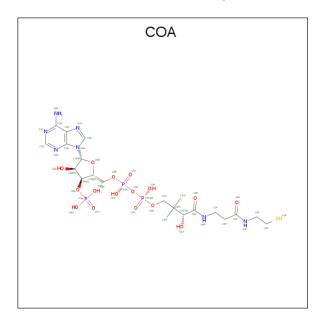
• Molecule 2 is VIRGINIAMYCIN M1 (three-letter code: VIR) (formula: C₂₈H₃₅N₃O₇).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O 38 28 3 7	0	0
2	A	1	Total C N O 38 28 3 7	0	0
2	E	1	Total C N O 38 28 3 7	0	0

 \bullet Molecule 3 is COENZYME A (three-letter code: COA) (formula: $\mathrm{C_{21}H_{36}N_{7}O_{16}P_{3}S}).$



Mol	Chain	Residues		A	ton	ıs			ZeroOcc	AltConf		
3	A	1	Total	С	N	О	Р	S	0	0		
)	Λ	1	48	21	7	16	3	1	0	0		
3	В	1	Total	С	N	О	Р	S	0	0		
)	Ъ	1	48	21	7	16	3	1	0	U		
3	С	1	Total C N O P S	0	0							
3		1	48	21	7	16	3	1	U	U		
3	D	1	Total	С	N	Ο	Р	S	0	0		
)	ט	1	48	21	7	16	3	1	0	0		
3	E	E	L.	1	Total	С	N	Ο	Р	S	0	0
	ינו	1	48	21	7	16	3	1	0	U		
3	F	1	Total	С	N	О	Р	S	0	0		
	1"	I.	48	21	7	16	3	1	U	U		

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	15	Total O 15 15	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	22	Total O 22 22	0	0
4	С	16	Total O 16 16	0	0
4	D	23	Total O 23 23	0	0
4	E	23	Total O 23 23	0	0
4	F	13	Total O 13 13	0	0



Chain D:

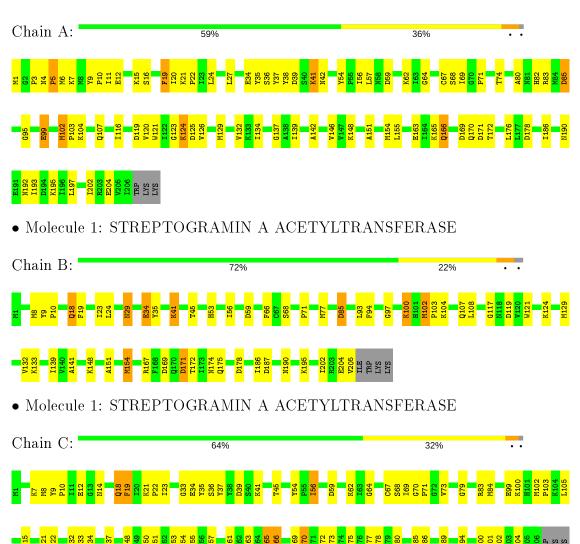
3 Residue-property plots (i)

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.

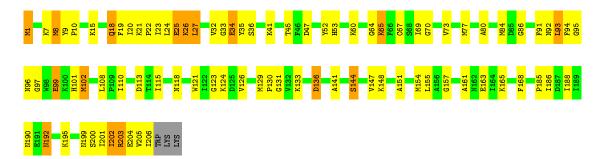
Note EDS was not executed.

• Molecule 1: STREPTOGRAMIN A ACETYLTRANSFERASE

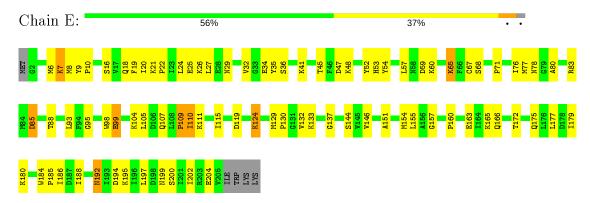
• Molecule 1: STREPTOGRAMIN A ACETYLTRANSFERASE



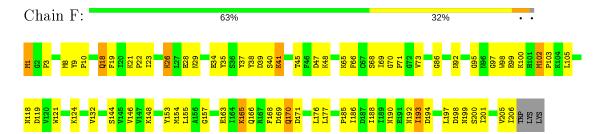




• Molecule 1: STREPTOGRAMIN A ACETYLTRANSFERASE



• Molecule 1: STREPTOGRAMIN A ACETYLTRANSFERASE





4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	F 2 2 2	Depositor	
Cell constants	186.10Å 185.90Å 186.90Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	99.00 - 2.80	Depositor	
% Data completeness	91.4 (99.00-2.80)	Depositor	
(in resolution range)	31.4 (33.00 2.00)	Depositor	
R_{merge}	0.09	Depositor	
R_{sym}	(Not available)	Depositor	
Refinement program	X-PLOR 3.851	Depositor	
R, R_{free}	0.186 , 0.251	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	10192	wwPDB-VP	
Average B, all atoms (Å ²)	21.0	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: COA, VIR

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		
MIOI		RMSZ	# Z >5	RMSZ	# Z > 5	
1	A	0.39	0/1650	0.65	0/2242	
1	В	0.41	0/1648	0.69	0/2238	
1	С	0.41	0/1657	0.68	0/2250	
1	D	0.40	0/1661	0.64	0/2254	
1	E	0.39	0/1645	0.68	0/2234	
1	F	0.39	0/1651	0.68	$1/2241 \; (0.0\%)$	
All	All	0.40	0/9912	0.67	$1/13459 \ (0.0\%)$	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
1	F	166	GLN	N-CA-C	-5.86	95.17	111.00

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	1611	0	1581	75	0
1	В	1609	0	1585	43	0
1	С	1618	0	1591	47	0
1	D	1622	0	1612	75	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Ε	1606	0	1582	64	0
1	F	1612	0	1590	49	0
2	A	76	0	67	20	0
2	Ε	38	0	33	7	0
3	A	48	0	32	4	0
3	В	48	0	32	1	0
3	С	48	0	32	8	0
3	D	48	0	32	11	0
3	Ε	48	0	32	2	0
3	F	48	0	32	2	0
4	A	15	0	0	5	0
4	В	22	0	0	4	0
4	$^{\mathrm{C}}$	16	0	0	2	0
4	D	23	0	0	1	0
4	Ε	23	0	0	3	0
4	F	13	0	0	0	0
All	All	10192	0	9833	369	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 19.

The worst 5 of 369 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{array}{l} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{array}$	$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
1:E:57:LEU:HB3	1:E:110:ILE:HD11	1.25	1.18
1:D:199:ASN:O	1:D:202:ILE:CD1	2.10	0.97
1:A:82:HIS:HE2	3:C:303:COA:HS1	1.03	0.87
1:D:199:ASN:O	1:D:202:ILE:HD11	1.74	0.86
2:A:402:VIR:H311	2:A:402:VIR:H352	1.57	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	Perce	\mathbf{ntiles}
1	A	204/209~(98%)	188 (92%)	13 (6%)	3 (2%)	10	33
1	В	$203/209 \; (97\%)$	192 (95%)	10 (5%)	1 (0%)	29	61
1	С	204/209~(98%)	190 (93%)	12 (6%)	2 (1%)	15	44
1	D	204/209~(98%)	186 (91%)	18 (9%)	0	100	100
1	E	$202/209 \ (97\%)$	181 (90%)	20 (10%)	1 (0%)	29	61
1	F	204/209~(98%)	189 (93%)	14 (7%)	1 (0%)	29	61
All	All	1221/1254 (97%)	1126 (92%)	87 (7%)	8 (1%)	22	53

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	${f Res}$	Type
1	С	34	GLU
1	A	64	GLY
1	E	109	PRO
1	A	5	PRO
1	A	42	ASN

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	Perce	entiles
1	A	173/183 (94%)	158 (91%)	15 (9%)	10	30
1	В	173/183 (94%)	160 (92%)	13 (8%)	13	37
1	С	174/183 (95%)	160 (92%)	14 (8%)	12	34
1	D	176/183 (96%)	153 (87%)	23 (13%)	4	12
1	E	174/183 (95%)	156 (90%)	18 (10%)	7	21
1	F	173/183 (94%)	159 (92%)	14 (8%)	11	33
All	All	1043/1098 (95%)	946 (91%)	97 (9%)	9	26

5 of 97 residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	D	8	MET
1	D	93	LEU
1	F	102	MET
1	D	18	GLN
1	D	34	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	Ε	42	ASN
1	E	58	ASN
1	Е	192	ASN
1	D	166	GLN
1	D	192	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)

9 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	Tune	Chain	Res	Link	Вс	ond leng	gths	В	ond ang	gles
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	$\mid \# Z > 2$	Counts	RMSZ	# Z >2
3	COA	A	301	_	41,50,50	1.11	1 (2%)	52,75,75	1.39	5 (9%)
2	VIR	Е	403	-	34,40,40	2.31	9 (26%)	36,55,55	2.21	8 (22%)
2	VIR	A	402	-	34,40,40	2.40	9 (26%)	36,55,55	2.99	13 (36%)
3	COA	В	302	-	41,50,50	1.32	5 (12%)	52,75,75	1.17	1 (1%)
3	COA	F	306	-	41,50,50	1.31	5 (12%)	52,75,75	1.17	1 (1%)
2	VIR	A	401	-	34,40,40	2.03	7 (20%)	36,55,55	2.75	11 (30%)
3	COA	С	303	-	41,50,50	1.31	5 (12%)	52,75,75	1.17	2 (3%)
3	COA	D	304	_	41,50,50	1.01	1 (2%)	52,75,75	1.59	9 (17%)
3	COA	Е	305	-	41,50,50	1.14	2 (4%)	52,75,75	1.33	7 (13%)

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
3	COA	A	301	-	-	10/44/64/64	0/3/3/3
2	VIR	Е	403	-	-	11/42/58/58	0/2/3/3
2	VIR	A	402	-	-	19/42/58/58	0/2/3/3
3	COA	В	302	-	-	11/44/64/64	0/3/3/3
3	COA	F	306	-	-	11/44/64/64	0/3/3/3
2	VIR	A	401	-	-	10/42/58/58	0/2/3/3
3	COA	С	303	-	-	3/44/64/64	0/3/3/3
3	COA	D	304	-	-	13/44/64/64	0/3/3/3
3	COA	Е	305	-	-	11/44/64/64	0/3/3/3

The worst 5 of 44 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
2	A	402	VIR	C28-C29	-8.77	1.11	1.32
2	A	401	VIR	C28-C29	-8.19	1.13	1.32
2	Е	403	VIR	C28-C29	-8.05	1.13	1.32
2	Е	403	VIR	C1-N5	5.41	1.46	1.39
2	Е	403	VIR	C28-C26	5.22	1.59	1.48

The worst 5 of 57 bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
2	Α	402	VIR	C28-C26-N25	-9.41	97.23	114.97
2	A	401	VIR	C28-C26-N25	-8.89	98.21	114.97
2	E	403	VIR	C28-C26-N25	-7.98	99.93	114.97
2	A	402	VIR	O27-C26-C28	6.66	138.21	123.03
2	A	401	VIR	O27-C26-C28	6.28	137.34	123.03

There are no chirality outliers.

5 of 99 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	301	COA	O4B-C4B-C5B-O5B
3	A	301	COA	C5B-O5B-P1A-O1A
3	A	301	COA	CCP-O6A-P2A-O4A
3	A	301	COA	CCP-O6A-P2A-O5A
3	A	301	COA	S1P-C2P-C3P-N4P

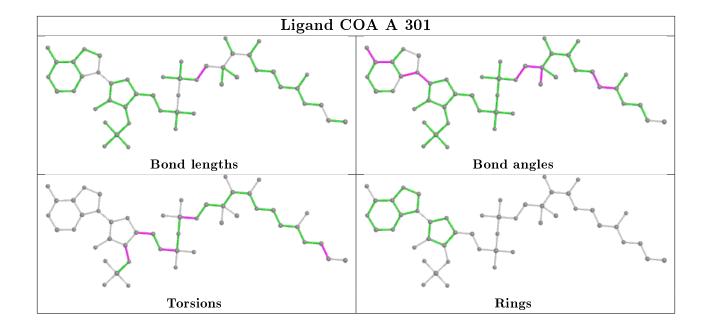
There are no ring outliers.

9 monomers are involved in 53 short contacts:

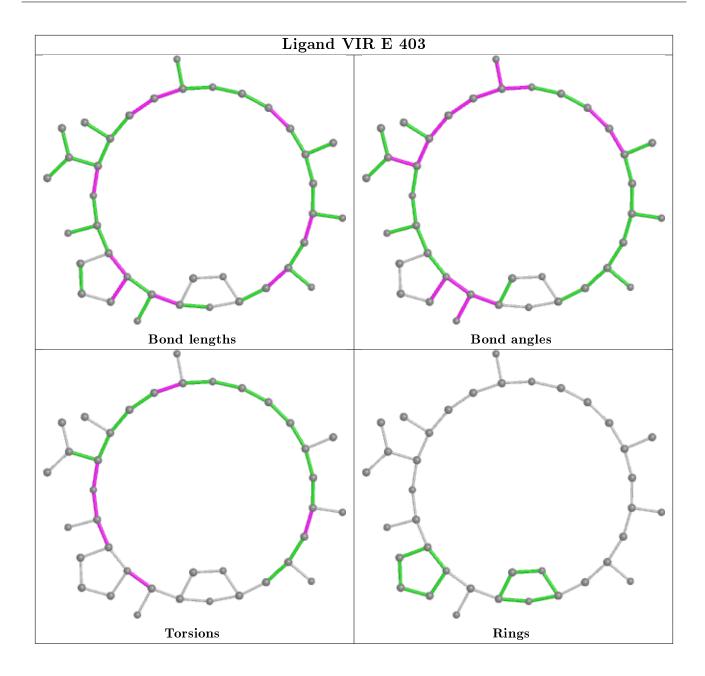
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	301	COA	4	0
2	E	403	VIR	7	0
2	A	402	VIR	11	0
3	В	302	COA	1	0
3	F	306	COA	2	0
2	A	401	VIR	9	0
3	С	303	COA	8	0
3	D	304	COA	11	0
3	Ε	305	COA	2	0

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 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.

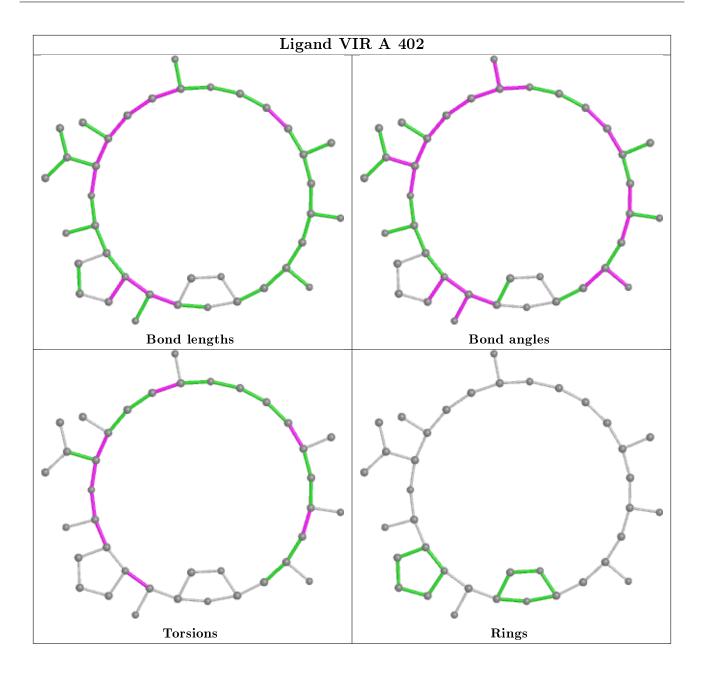




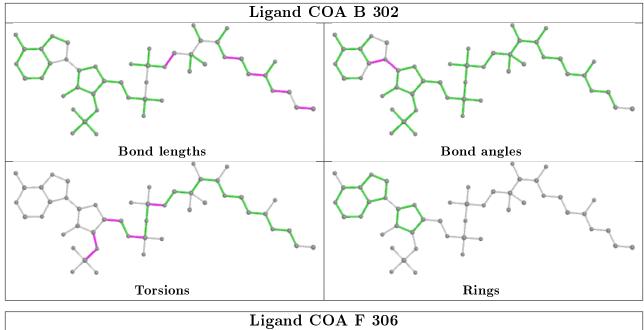


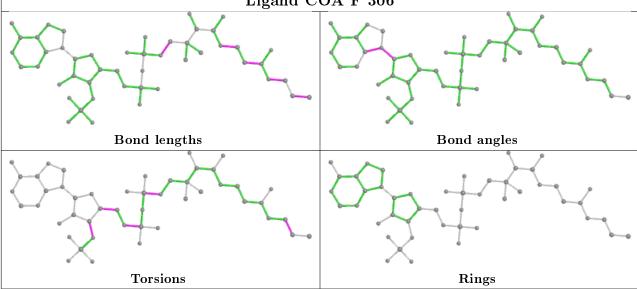




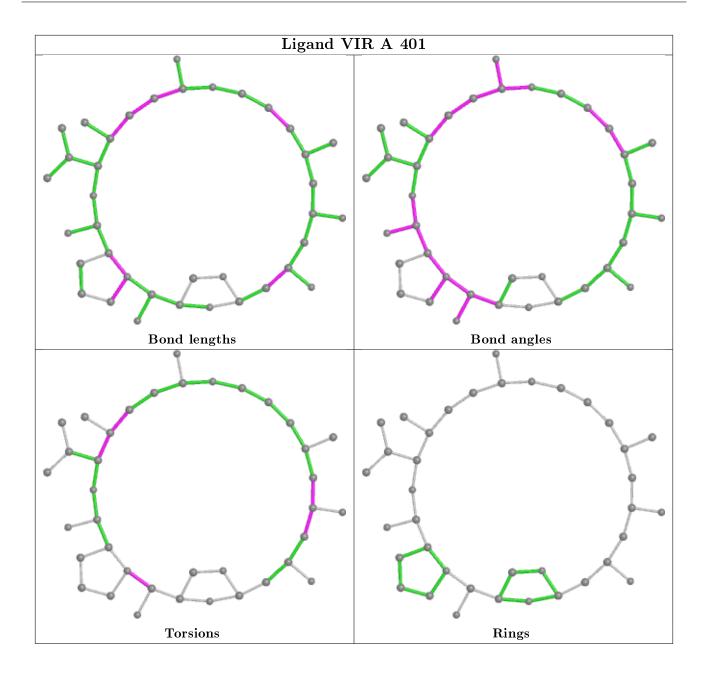




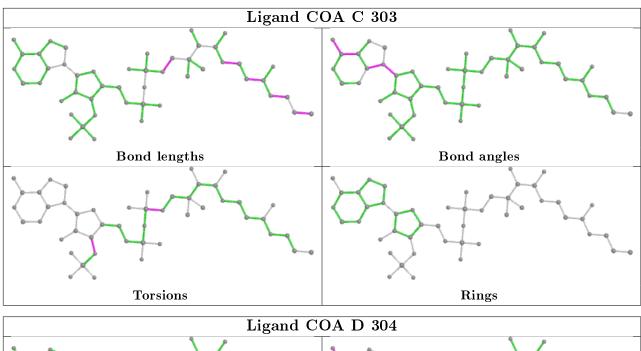


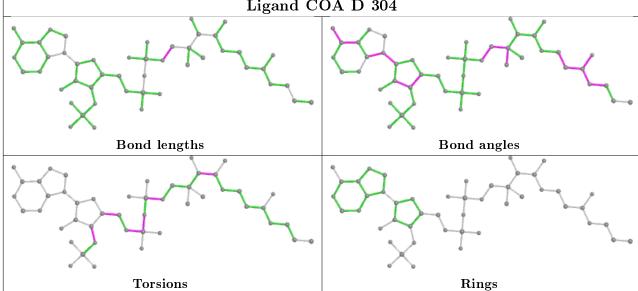




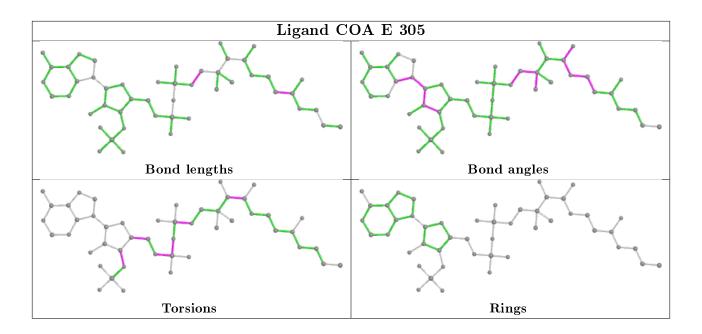












5.7 Other polymers (i)

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.

