



# wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 15, 2024 – 03:30 PM EST

PDB ID : 2NMT  
Title : MYRISTOYL-COA:PROTEIN N-MYRISTOYLTRANSFERASE BOUND  
TO MYRISTOYL-COA AND PEPTIDE ANALOGS  
Authors : Fuetterer, K.; Bhatnagar, R.S.; Waksman, G.  
Deposited on : 1998-07-14  
Resolution : 2.90 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](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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

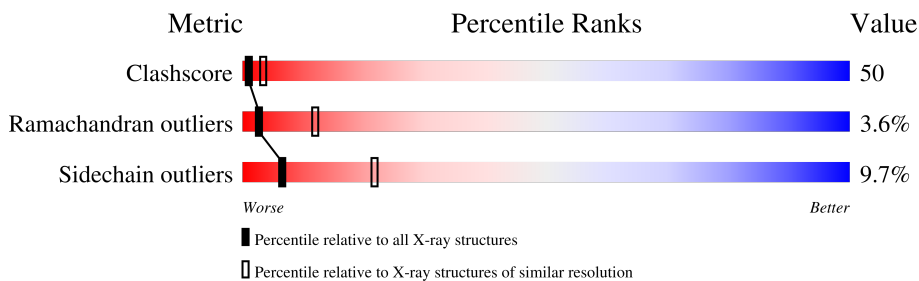
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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	180529	2564 (2.90-2.90)
Ramachandran outliers	177936	2514 (2.90-2.90)
Sidechain outliers	177891	2516 (2.90-2.90)

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 of 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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	422	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GOL	A	804	-	-	X	-
4	GOL	A	807	-	-	X	-

## 2 Entry composition [i](#)

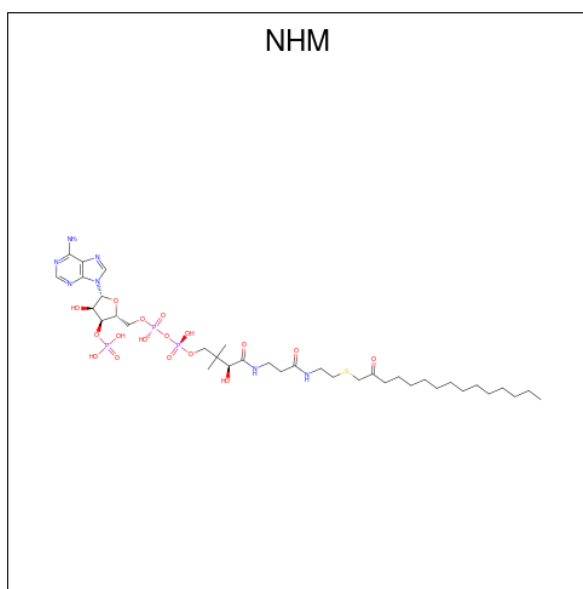
There are 5 unique types of molecules in this entry. The entry contains 3601 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 MYRISTOYL-COA\;PROTEIN N-MYRISTOYLTRANSFERASE.

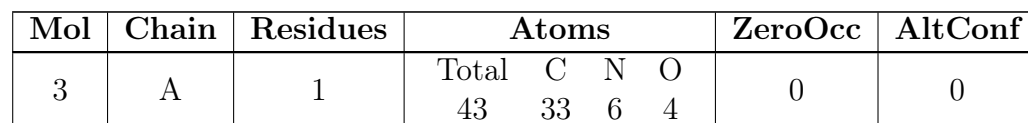
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	422	3388	2190	558	630	10	0	0	0

- Molecule 2 is S-(2-OXO)PENTADECYLCOA (three-letter code: NHM) (formula:  $C_{36}H_{64}N_7O_{17}P_3S$ ).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
2	A	1	64	36	7	17	3	1	0	0

- Molecule 3 is [CYCLOHEXYLETHYL]-[[[4-[2-METHYL-1-IMIDAZOLYL-BUTYL]PHENYL]ACETYL]-SERYL]-LYSINYL]-AMINE (three-letter code: MIM) (formula:  $C_{33}H_{52}N_6O_4$ ).



- GOL
- 
- The diagram shows the skeletal structure of 1,2,3-propanetriol (glycerol). The carbon backbone is represented by three vertices labeled C1, C2, and C3 in green. C1 is on the left, C2 is in the middle, and C3 is on the right. Each carbon is bonded to a hydroxyl group (OH) shown in red. The hydroxyl group on C1 is labeled O1 in green below it. The hydroxyl group on C2 is labeled O2 in green below it. The hydroxyl group on C3 is labeled O3 in green to its right. The bonds between the carbons and the hydroxyl groups are shown as black lines.

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



*Continued from previous page...*

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

- Molecule 5 is water.

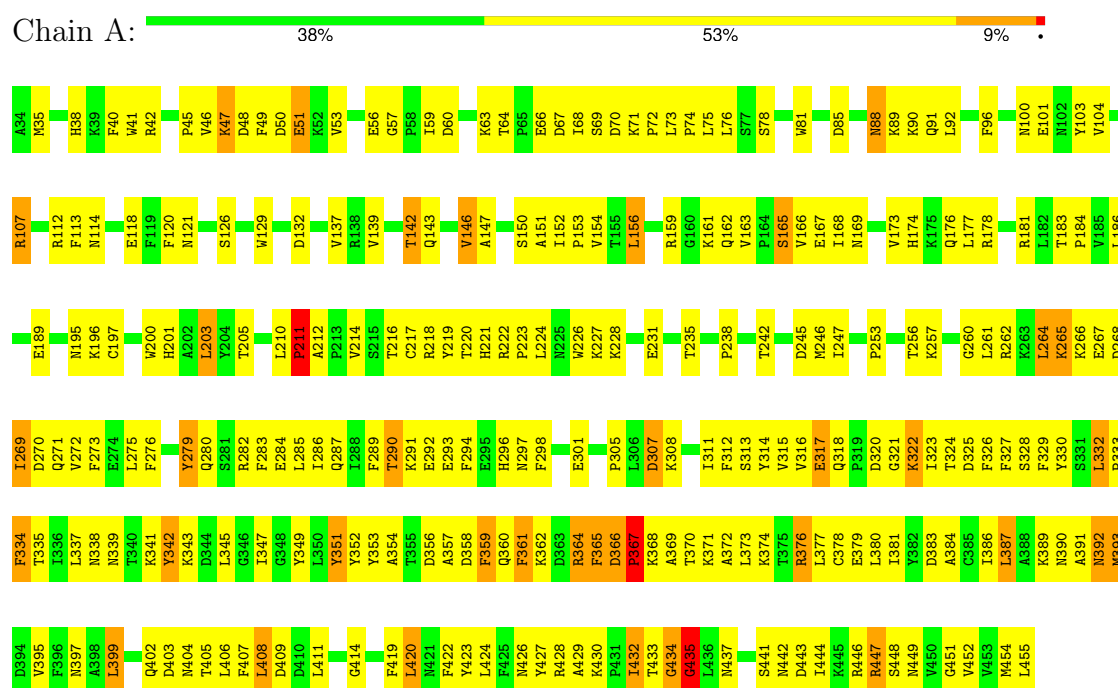
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	34	Total	O	0	0
			34	34		

### 3 Residue-property plots

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: MYRISTOYL-COA\;PROTEIN N-MYRISTOYLTRANSFERASE



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.40 Å   105.40 Å   106.70 Å 90.00°   90.00°   120.00°	Depositor
Resolution (Å)	30.00 – 2.90	Depositor
% Data completeness (in resolution range)	91.7 (30.00-2.90)	Depositor
$R_{merge}$	0.04	Depositor
$R_{sym}$	0.04	Depositor
Refinement program	CNS 0.3	Depositor
R, $R_{free}$	0.228 , 0.297	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3601	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MIM, NHM

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	0.74	0/3477	0.99	5/4726 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	399	LEU	N-CA-C	6.85	129.49	111.00
1	A	435	GLY	N-CA-C	6.65	129.74	113.10
1	A	434	GLY	N-CA-C	-5.77	98.69	113.10
1	A	290	THR	N-CA-C	-5.68	95.67	111.00
1	A	335	THR	N-CA-C	-5.56	95.98	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	279	TYR	Sidechain
1	A	342	TYR	Sidechain



## 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	3388	0	3257	346	2
2	A	64	0	60	8	0
3	A	43	0	52	6	0
4	A	72	0	95	15	4
5	A	34	0	0	6	0
All	All	3601	0	3464	349	4

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 50.

The worst 5 of 349 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:A:383:ASP:O	1:A:387:LEU:HD23	1.64	0.96
1:A:316:VAL:HB	1:A:325:ASP:HB2	1.45	0.95
1:A:47:LYS:HB3	1:A:212:ALA:CB	2.02	0.90
1:A:269:ILE:CG2	1:A:291:LYS:HE3	2.02	0.90
1:A:364:ARG:HA	1:A:364:ARG:HH11	1.35	0.89

All (4) 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)
4:A:811:GOL:O1	4:A:811:GOL:O1[5_556]	1.32	0.88
4:A:811:GOL:O3	4:A:811:GOL:O3[5_556]	1.99	0.21
1:A:245:ASP:OD2	4:A:809:GOL:O2[6_666]	2.04	0.16
1:A:70:ASP:OD2	4:A:811:GOL:O1[5_556]	2.12	0.08

## 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	420/422 (100%)	348 (83%)	57 (14%)	15 (4%)	<b>3</b> <b>12</b>

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	47	LYS
1	A	211	PRO
1	A	264	LEU
1	A	269	ILE
1	A	322	LYS

### 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	362/381 (95%)	327 (90%)	35 (10%)	<b>6</b> <b>22</b>

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	367	PRO
1	A	373	LEU
1	A	393	MET
1	A	211	PRO
1	A	203	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	195	ASN
1	A	421	ASN
1	A	225	ASN
1	A	426	ASN
1	A	397	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

14 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	$\# Z  > 2$
4	GOL	A	801	-	5,5,5	0.85	0	5,5,5	0.54	0
2	NHM	A	500	-	60,66,66	1.58	8 (13%)	74,92,92	1.28	5 (6%)
4	GOL	A	804	-	5,5,5	1.97	1 (20%)	5,5,5	0.66	0
4	GOL	A	810	-	5,5,5	1.15	0	5,5,5	0.64	0
4	GOL	A	802	-	5,5,5	1.32	1 (20%)	5,5,5	0.69	0
4	GOL	A	812	-	5,5,5	0.95	1 (20%)	5,5,5	0.54	0
4	GOL	A	805	-	5,5,5	0.87	0	5,5,5	0.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	GOL	A	806	-	5,5,5	0.89	0	5,5,5	0.62	0
4	GOL	A	807	-	5,5,5	0.86	0	5,5,5	0.60	0
4	GOL	A	808	-	5,5,5	1.14	1 (20%)	5,5,5	0.55	0
4	GOL	A	809	-	5,5,5	0.98	0	5,5,5	0.93	0
3	MIM	A	700	-	44,45,45	1.60	12 (27%)	51,57,57	1.57	10 (19%)
4	GOL	A	811	-	5,5,5	0.99	1 (20%)	5,5,5	0.38	0
4	GOL	A	803	-	5,5,5	1.10	0	5,5,5	0.59	0

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	GOL	A	801	-	-	0/4/4/4	-
2	NHM	A	500	-	-	17/61/81/81	0/3/3/3
4	GOL	A	804	-	-	0/4/4/4	-
4	GOL	A	810	-	-	2/4/4/4	-
4	GOL	A	802	-	-	2/4/4/4	-
4	GOL	A	812	-	-	2/4/4/4	-
4	GOL	A	805	-	-	2/4/4/4	-
4	GOL	A	806	-	-	0/4/4/4	-
4	GOL	A	807	-	-	2/4/4/4	-
4	GOL	A	808	-	-	0/4/4/4	-
4	GOL	A	809	-	-	1/4/4/4	-
3	MIM	A	700	-	-	17/40/48/48	0/3/3/3
4	GOL	A	811	-	-	2/4/4/4	-
4	GOL	A	803	-	-	2/4/4/4	-

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	NHM	C4A-N3A	7.31	1.45	1.35
4	A	804	GOL	O2-C2	-4.28	1.30	1.43
2	A	500	NHM	O4X-C1X	3.66	1.45	1.40
2	A	500	NHM	P1A-O2A	3.30	1.62	1.50
3	A	700	MIM	C5B-C0B	3.08	1.45	1.38

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	NHM	O4X-C1X-N9A	7.25	118.35	108.75
3	A	700	MIM	CBY-CAY-NY	-4.76	98.83	111.88
3	A	700	MIM	CAB-CB-NS	3.25	120.94	115.88
2	A	500	NHM	C2-C3-N4	-3.04	106.08	112.41
2	A	500	NHM	CP-C1M-C2M	2.83	121.55	115.55

There are no chirality outliers.

5 of 49 torsion outliers are listed below:

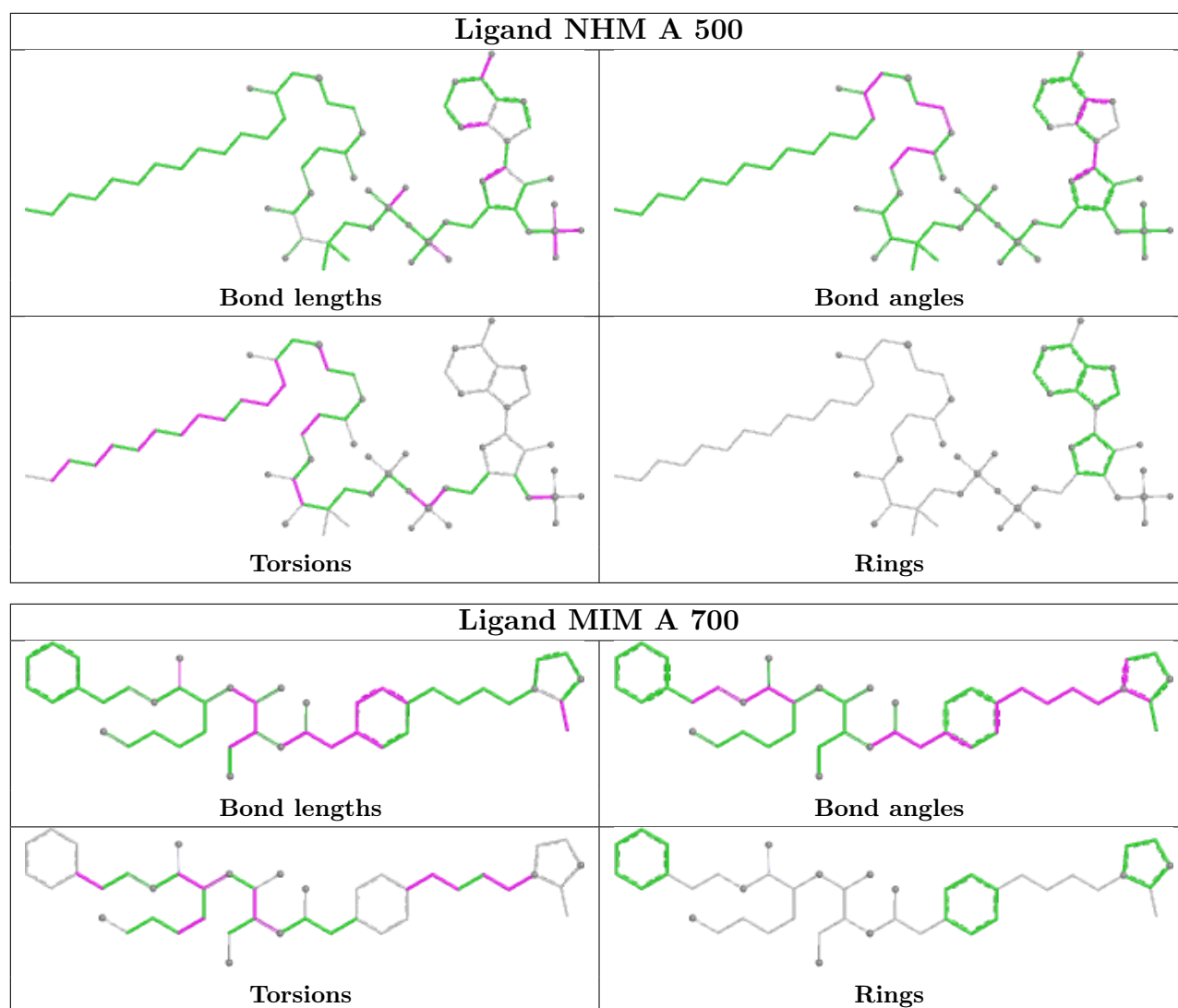
Mol	Chain	Res	Type	Atoms
3	A	700	MIM	C8B-C9B-NAB-CBB
3	A	700	MIM	C8B-C9B-NAB-CEB
3	A	700	MIM	CAY-CBY-CGY-CKY
4	A	803	GOL	C1-C2-C3-O3
4	A	805	GOL	C1-C2-C3-O3

There are no ring outliers.

10 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	NHM	8	0
4	A	804	GOL	5	0
4	A	810	GOL	1	0
4	A	812	GOL	1	0
4	A	805	GOL	2	0
4	A	807	GOL	4	0
4	A	809	GOL	1	1
3	A	700	MIM	6	0
4	A	811	GOL	0	3
4	A	803	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 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.



## 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

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.