wwPDB X-ray Structure Validation Summary Report (i)

Aug 21, 2020 – 12:17 AM BST

PDB ID	:	6QRM
Title	:	HsNMT1 in complex with both MyrCoA and GNCFSKRRAA substrates
Authors	:	Dian, C.; Riviere, F.B.; Asensio, T.; Giglione, C.; Meinnel, T.
Deposited on	:	2019-02-19
Resolution	:	2.30 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 (i)) were used in the production of this report:

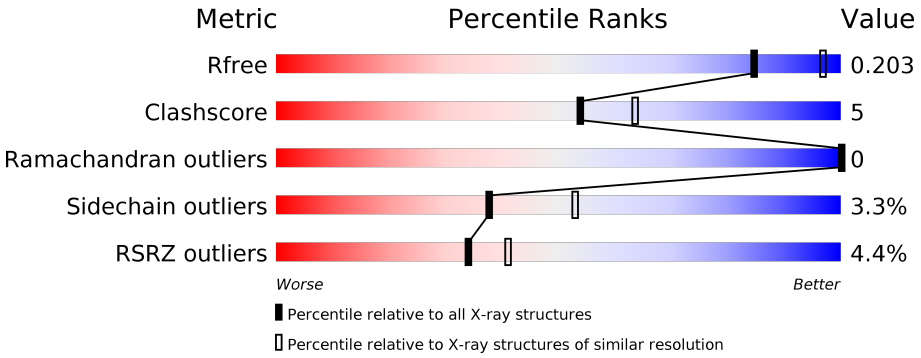
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 2.30 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))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	402	3% 83% 14%
1	B	402	4% 86% 10%
2	C	10	50% 30% 20%
2	D	10	60% 40% 40% 10% 10%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7003 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 Glycylpeptide N-tetradecanoyltransferase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	392	Total	C	N	O	S	0	1	0
			3168	2053	531	567	17			
1	B	391	Total	C	N	O	S	0	1	0
			3166	2050	533	566	17			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	95	GLY	-	expression tag	UNP P30419
A	96	GLY	-	expression tag	UNP P30419
A	97	SER	-	expression tag	UNP P30419
A	98	GLU	-	expression tag	UNP P30419
B	95	GLY	-	expression tag	UNP P30419
B	96	GLY	-	expression tag	UNP P30419
B	97	SER	-	expression tag	UNP P30419
B	98	GLU	-	expression tag	UNP P30419

- Molecule 2 is a protein called Apoptosis-inducing factor 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	8	Total	C	N	O	S	0	0	0
			54	33	10	10	1			
2	D	9	Total	C	N	O	S	0	0	0
			67	39	16	11	1			

There are 10 discrepancies between the modelled and reference sequences:

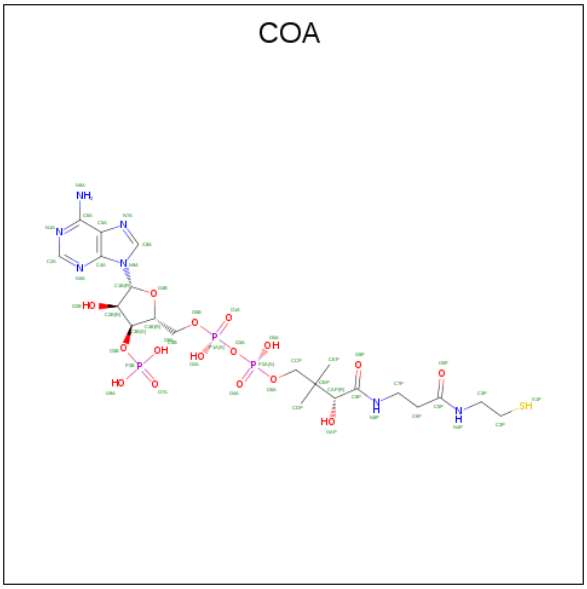
Chain	Residue	Modelled	Actual	Comment	Reference
C	2	ASN	GLY	engineered mutation	UNP Q96NN9
C	7	ARG	PRO	engineered mutation	UNP Q96NN9
C	8	ARG	LYS	conflict	UNP Q96NN9
C	9	ALA	PRO	conflict	UNP Q96NN9

Continued on next page...

Continued from previous page...

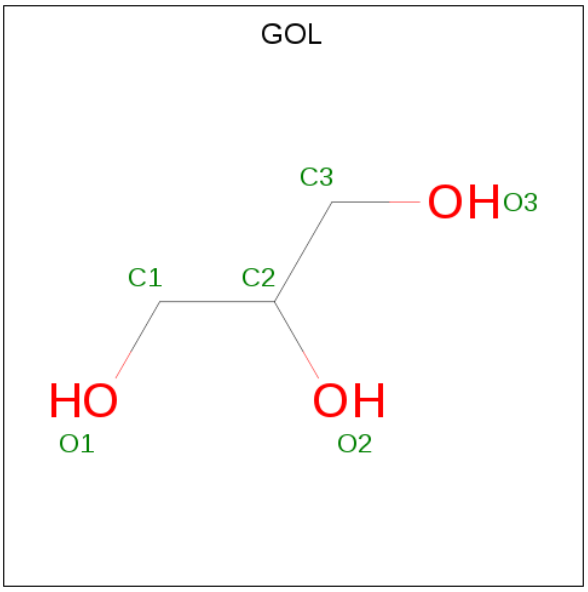
Chain	Residue	Modelled	Actual	Comment	Reference
C	10	ALA	VAL	conflict	UNP Q96NN9
D	2	ASN	GLY	engineered mutation	UNP Q96NN9
D	7	ARG	PRO	engineered mutation	UNP Q96NN9
D	8	ARG	LYS	conflict	UNP Q96NN9
D	9	ALA	PRO	conflict	UNP Q96NN9
D	10	ALA	VAL	conflict	UNP Q96NN9

- Molecule 3 is COENZYME A (three-letter code: COA) (formula: $C_{21}H_{36}N_7O_{16}P_3S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
3	A	1	48	21	7	16	3	1	0	0

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

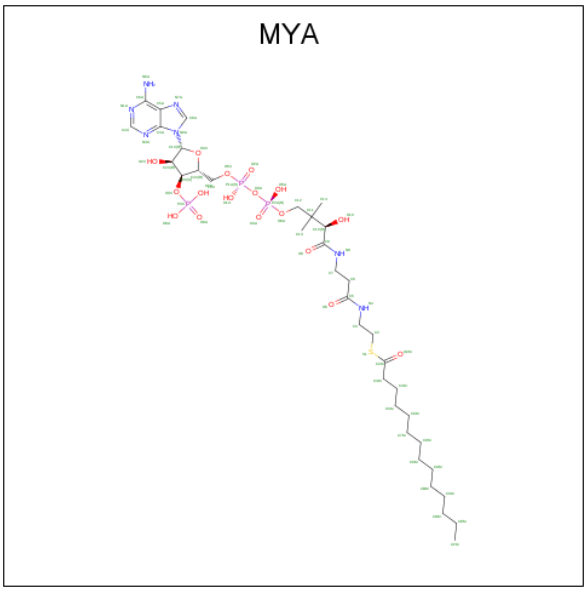


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

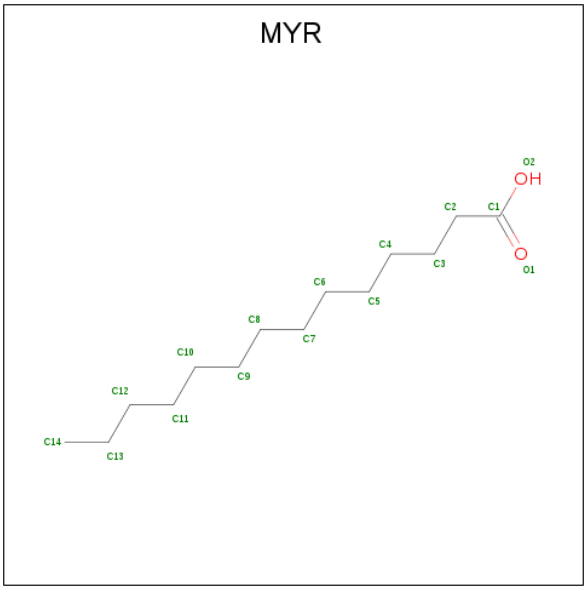
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Cl 1 1	0	0
5	A	1	Total Cl 1 1	0	0

- Molecule 6 is TETRADECANOYL-COA (three-letter code: MYA) (formula: $C_{35}H_{62}N_7O_{17}P_3S$) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	B	1	Total	C	N	O	P	S	0	0
			63	35	7	17	3	1		

- Molecule 7 is MYRISTIC ACID (three-letter code: MYR) (formula: $C_{14}H_{28}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			15	14	1		

- Molecule 8 is water.

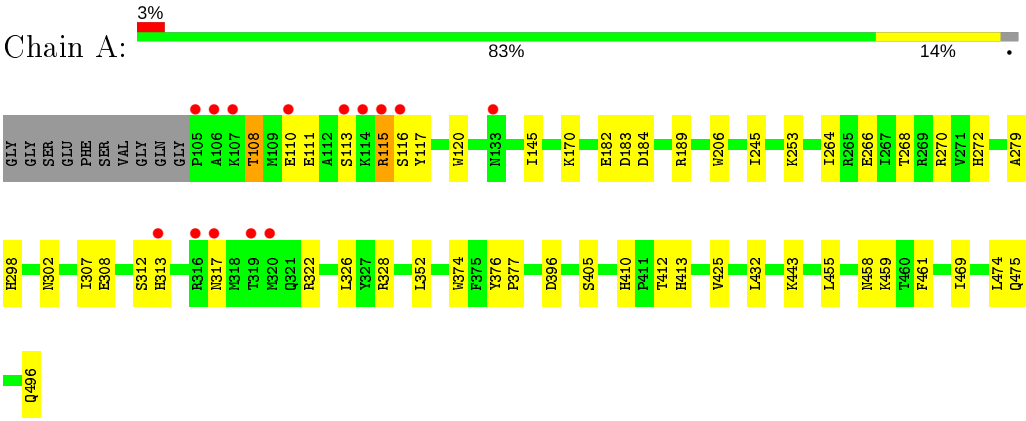
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	193	Total O 193 193	0	0
8	B	198	Total O 198 198	0	0
8	C	1	Total O 1 1	0	0
8	D	4	Total O 4 4	0	0

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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.

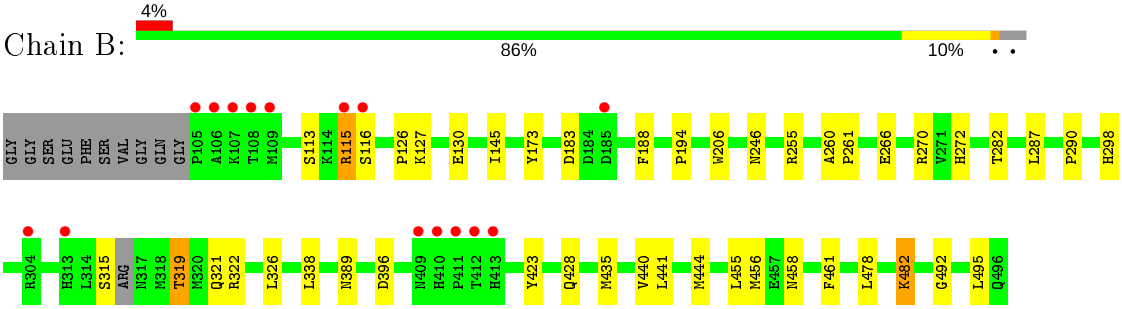
- Molecule 1: Glycylpeptide N-tetradecanoyltransferase 1

Chain A:



- Molecule 1: Glycylpeptide N-tetradecanoyltransferase 1

Chain B:

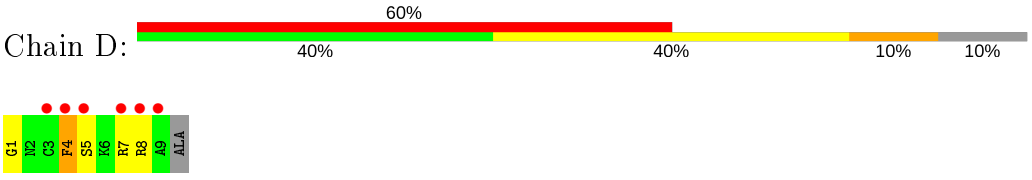


- Molecule 2: Apoptosis-inducing factor 3

Chain C:

- Molecule 2: Apoptosis-inducing factor 3

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	79.44Å 178.93Å 58.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.91 – 2.30 48.91 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.91-2.30) 99.5 (48.91-2.30)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.06 (at 2.29Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.172 , 0.203 0.173 , 0.203	Depositor DCC
R_{free} test set	1916 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	29.6	Xtriage
Anisotropy	0.507	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 46.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7003	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.26 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.2789e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: COA, GOL, MYR, MYA, CL

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	0.42	0/3258	0.57	0/4433
1	B	0.45	0/3255	0.60	0/4427
2	C	0.48	0/54	0.80	0/70
2	D	0.41	0/67	0.72	0/87
All	All	0.44	0/6634	0.59	0/9017

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

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	3168	0	3126	35	0
1	B	3166	0	3122	29	0
2	C	54	0	44	3	0
2	D	67	0	63	7	0
3	A	48	0	32	2	0
4	A	12	0	16	2	0
4	B	12	0	16	2	0
5	A	1	0	0	1	0
5	B	1	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	63	0	58	2	0
7	C	15	0	27	6	0
8	A	193	0	0	1	0
8	B	198	0	0	0	0
8	C	1	0	0	0	0
8	D	4	0	0	0	0
All	All	7003	0	6504	69	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 5.

The worst 5 of 69 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)
3:A:501:COA:C1B	3:A:501:COA:O4B	1.67	1.17
1:A:115:ARG:NH1	1:A:116:SER:O	2.23	0.71
1:A:295:ARG:HD3	1:A:469:ILE:HD11	1.80	0.63
1:A:410:HIS:HD2	1:A:412:THR:H	1.46	0.63
6:B:501:MYA:C2M	2:D:1:GLY:HA3	2.33	0.58

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	391/402 (97%)	379 (97%)	12 (3%)	0	100	100
1	B	388/402 (96%)	376 (97%)	12 (3%)	0	100	100
2	C	6/10 (60%)	5 (83%)	1 (17%)	0	100	100
2	D	7/10 (70%)	7 (100%)	0	0	100	100
All	All	792/824 (96%)	767 (97%)	25 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	346/362 (96%)	335 (97%)	11 (3%)	39	54
1	B	346/362 (96%)	337 (97%)	9 (3%)	46	63
2	C	5/7 (71%)	4 (80%)	1 (20%)	1	1
2	D	6/7 (86%)	4 (67%)	2 (33%)	0	0
All	All	703/738 (95%)	680 (97%)	23 (3%)	38	53

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	455	LEU
1	B	115	ARG
2	D	4	PHE
1	B	113	SER
1	B	255	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	410	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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)

Of 9 ligands modelled in this entry, 2 are monoatomic - leaving 7 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	$\#\|Z\| > 2$
7	MYR	C	101	2	14,14,15	0.51	0	13,13,15	1.06	1 (7%)
4	GOL	B	502	-	5,5,5	0.54	0	5,5,5	0.39	0
4	GOL	A	503	-	5,5,5	0.58	0	5,5,5	0.49	0
6	MYA	B	501	-	54,65,65	1.36	8 (14%)	67,91,91	1.53	7 (10%)
4	GOL	B	503	-	5,5,5	0.44	0	5,5,5	0.62	0
3	COA	A	501	-	41,50,50	4.32	12 (29%)	52,75,75	1.80	5 (9%)
4	GOL	A	502	-	5,5,5	0.45	0	5,5,5	0.67	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
7	MYR	C	101	2	-	4/11/12/13	-
4	GOL	B	502	-	-	2/4/4/4	-
4	GOL	A	503	-	-	2/4/4/4	-
6	MYA	B	501	-	-	2/59/80/80	0/3/3/3
4	GOL	B	503	-	-	4/4/4/4	-
3	COA	A	501	-	-	8/44/64/64	0/3/3/3
4	GOL	A	502	-	-	2/4/4/4	-

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	COA	O4B-C1B	18.59	1.67	1.41
3	A	501	COA	C2B-C1B	-13.68	1.33	1.53
3	A	501	COA	C5P-N4P	6.63	1.48	1.33
3	A	501	COA	C9P-N8P	6.62	1.48	1.33
3	A	501	COA	O4B-C4B	-5.86	1.31	1.45

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	501	COA	C5A-C6A-N6A	8.11	132.68	120.35
6	B	501	MYA	N3A-C2A-N1A	-6.96	117.79	128.68
3	A	501	COA	N3A-C2A-N1A	-5.94	119.40	128.68
3	A	501	COA	N6A-C6A-N1A	-5.08	108.03	118.57
6	B	501	MYA	O2M-C2M-C3M	5.00	117.93	109.02

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	503	GOL	C1-C2-C3-O3
3	A	501	COA	C3B-O3B-P3B-O8A
3	A	501	COA	C5B-O5B-P1A-O3A
7	C	101	MYR	C4-C5-C6-C7
4	B	502	GOL	C1-C2-C3-O3

There are no ring outliers.

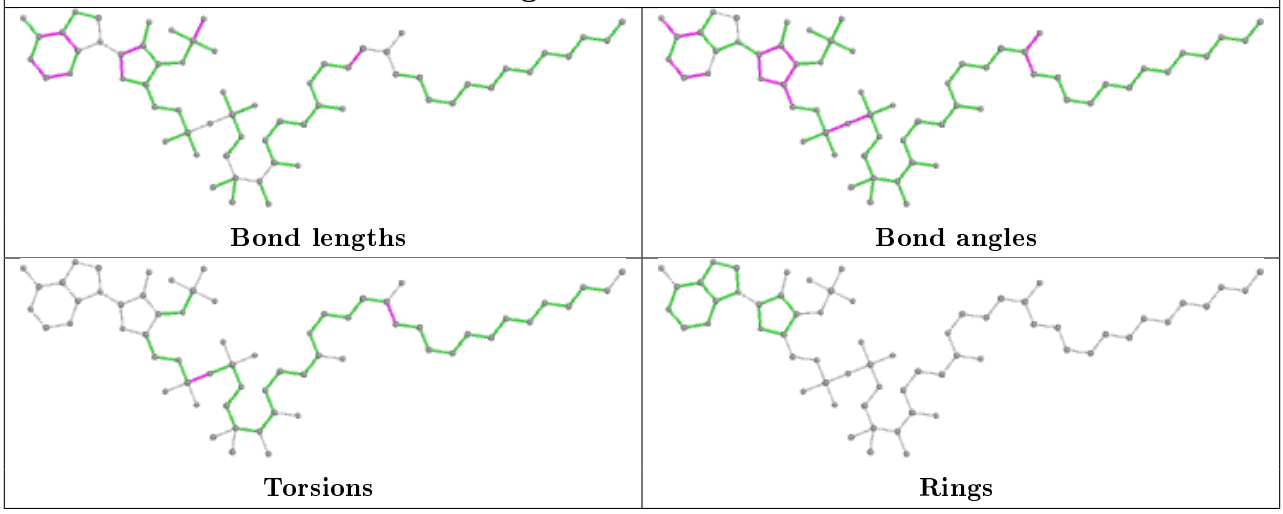
6 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	101	MYR	6	0
4	B	502	GOL	1	0
6	B	501	MYA	2	0
4	B	503	GOL	1	0
3	A	501	COA	2	0
4	A	502	GOL	2	0

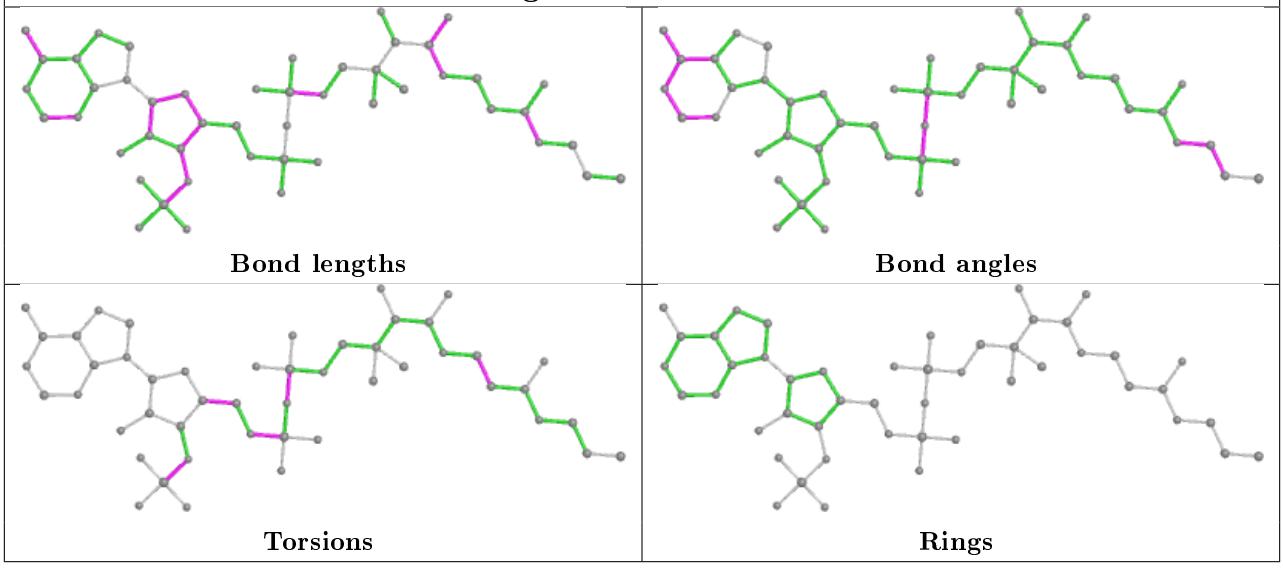
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

Ligand MYA B 501



Ligand COA A 501



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	392/402 (97%)	-0.09	14 (3%) 42 49	15, 29, 59, 76	0
1	B	391/402 (97%)	-0.10	15 (3%) 40 47	13, 25, 62, 79	0
2	C	8/10 (80%)	0.57	0 100 100	33, 40, 51, 53	0
2	D	9/10 (90%)	2.93	6 (66%) 0 0	37, 53, 68, 80	0
All	All	800/824 (97%)	-0.06	35 (4%) 34 41	13, 27, 61, 80	0

The worst 5 of 35 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	106	ALA	5.7
2	D	4	PHE	4.8
2	D	3	CYS	4.6
1	B	108	THR	4.1
1	A	106	ALA	4.1

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

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

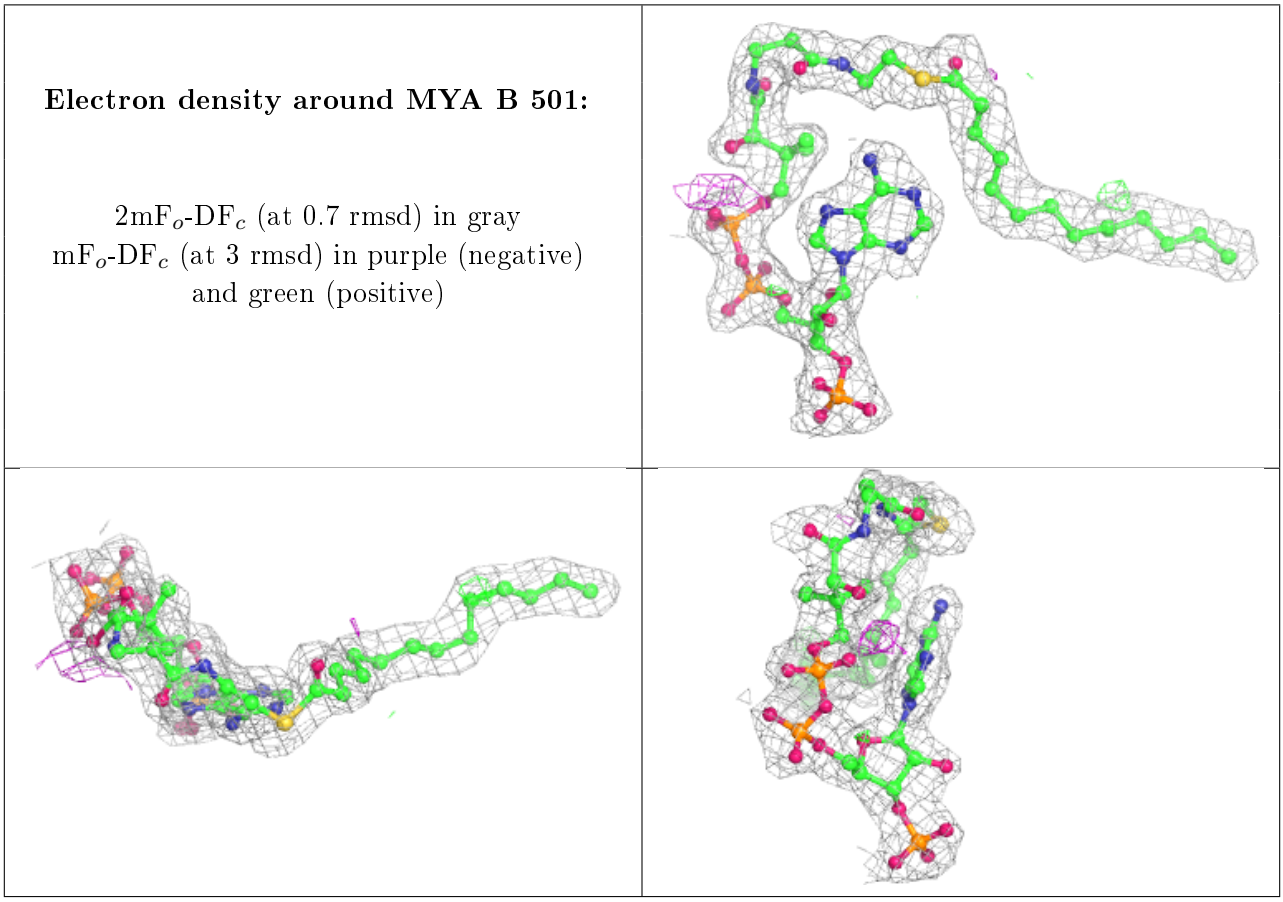
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	GOL	B	503	6/6	0.91	0.22	26,31,34,36	0
4	GOL	A	502	6/6	0.91	0.13	30,34,35,40	0
6	MYA	B	501	63/63	0.92	0.14	13,30,37,42	0
3	COA	A	501	48/48	0.93	0.18	30,42,50,51	0
7	MYR	C	101	15/16	0.93	0.15	18,21,29,31	0
4	GOL	B	502	6/6	0.96	0.13	19,21,24,27	0
4	GOL	A	503	6/6	0.97	0.12	25,30,31,31	0
5	CL	B	504	1/1	0.98	0.11	35,35,35,35	0
5	CL	A	504	1/1	0.99	0.05	37,37,37,37	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

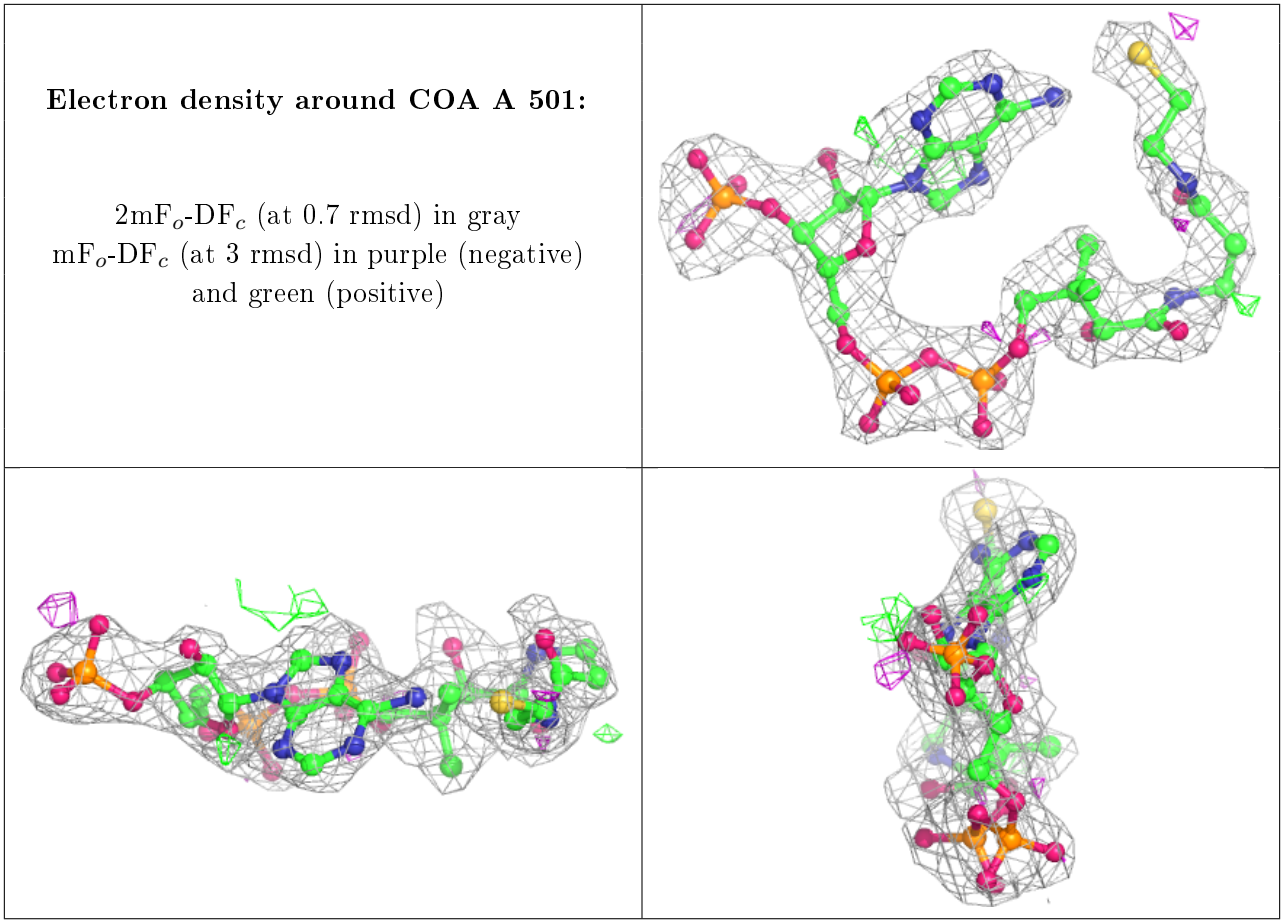
Electron density around MYA B 501:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around COA A 501:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.