



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:09 PM UTC

PDB ID : 7OWO / pdb_00007owo
Title : HsNMT1 in complex with both MyrCoA and N-acetylated KSFSKPR peptide
Authors : Dian, C.; Giglione, C.; Meinnel, T.
Deposited on : 2021-06-18
Resolution : 1.70 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

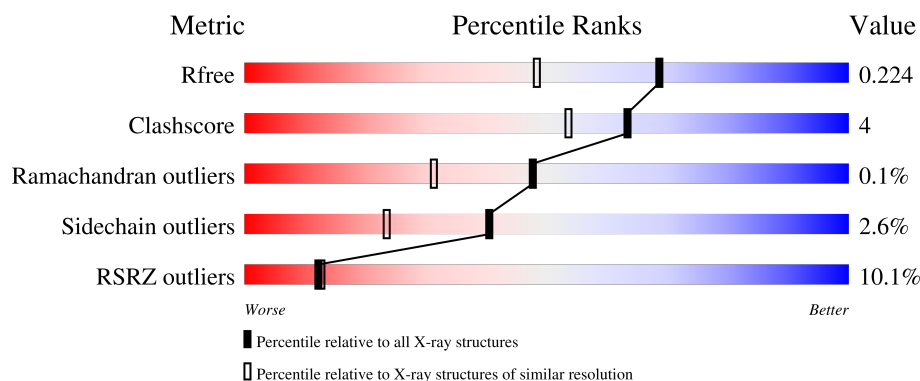
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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 $\leq 5\%$. 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	9% 89% 8% .
1	B	402	9% 86% 10% .
2	D	8	12% 50% 50%
2	F	8	75% 62% 38%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7372 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
			3155	2048	527	563	17			
1	B	389	Total	C	N	O	S	0	9	0
			3212	2078	534	583	17			

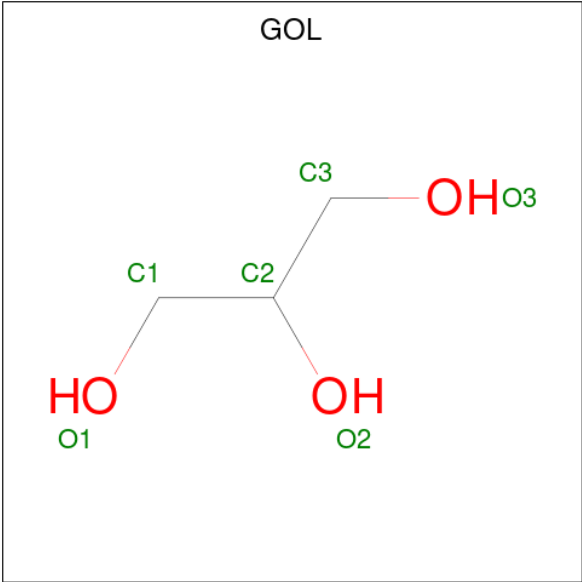
There are 8 discrepancies between the modelled and reference sequences:

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 N-Acetyl-LYS-SER-PHE-SER-LYS-PRO-ARG.

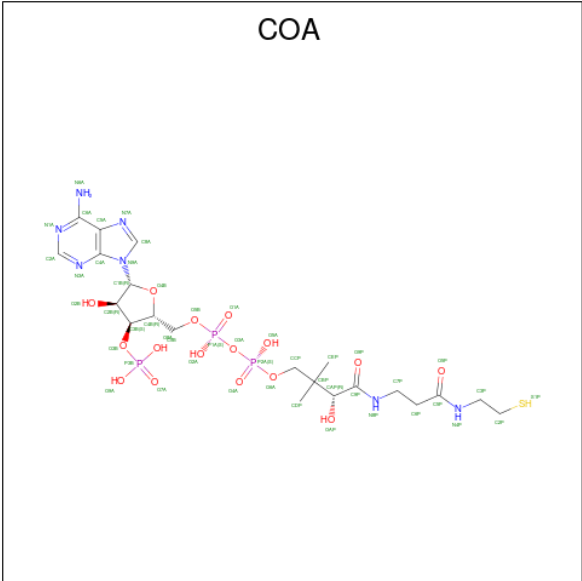
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	8	Total	C	N	O	0	1	0
			66	43	11	12			
2	F	8	Total	C	N	O	0	1	0
			62	40	10	12			

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



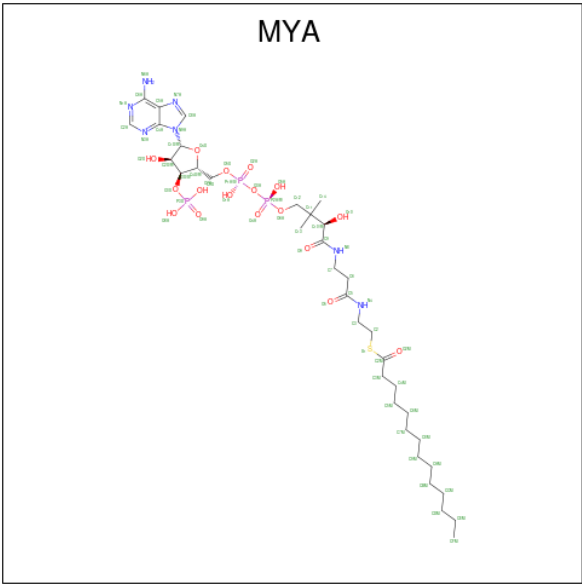
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is COENZYME A (CCD ID: COA) (formula: $C_{21}H_{36}N_7O_{16}P_3S$) (labeled as "Ligand of Interest" by depositor).



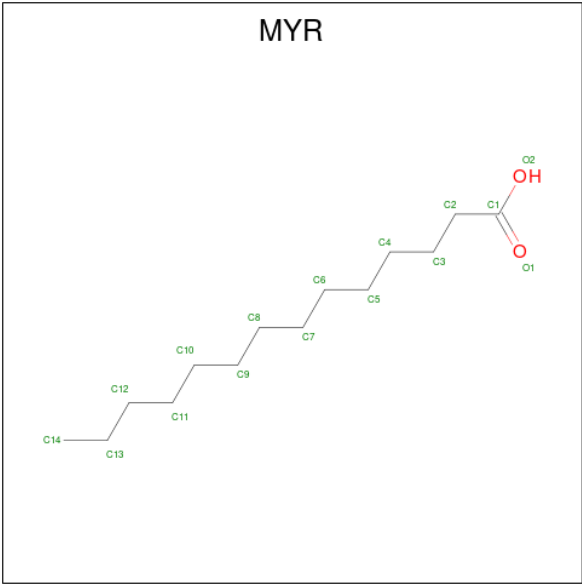
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	S	0	1
			48	21	7	16	3	1		

- Molecule 5 is TETRADECANOYL-COA (CCD ID: MYA) (formula: C₃₅H₆₂N₇O₁₇P₃S) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 6 is MYRISTIC ACID (CCD ID: MYR) (formula: C₁₄H₂₈O₂) (labeled as "Ligand of Interest" by depositor).



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

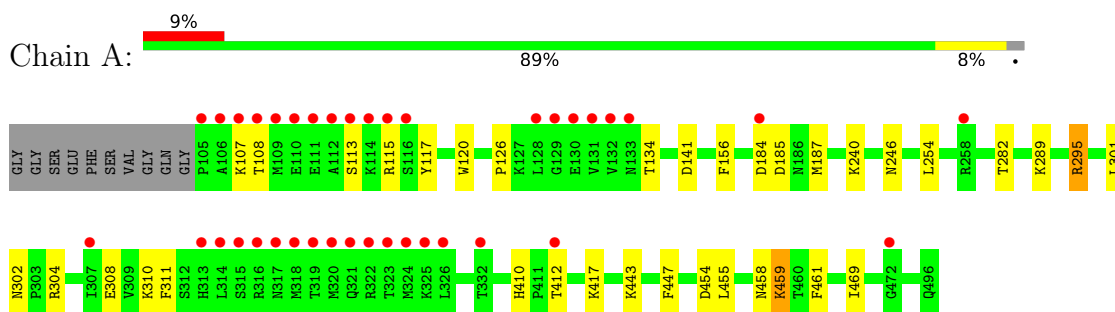
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	320	Total	O	0	0
			320	320		
7	B	352	Total	O	0	3
			352	352		
7	D	3	Total	O	0	0
			3	3		
7	F	1	Total	O	0	0
			1	1		

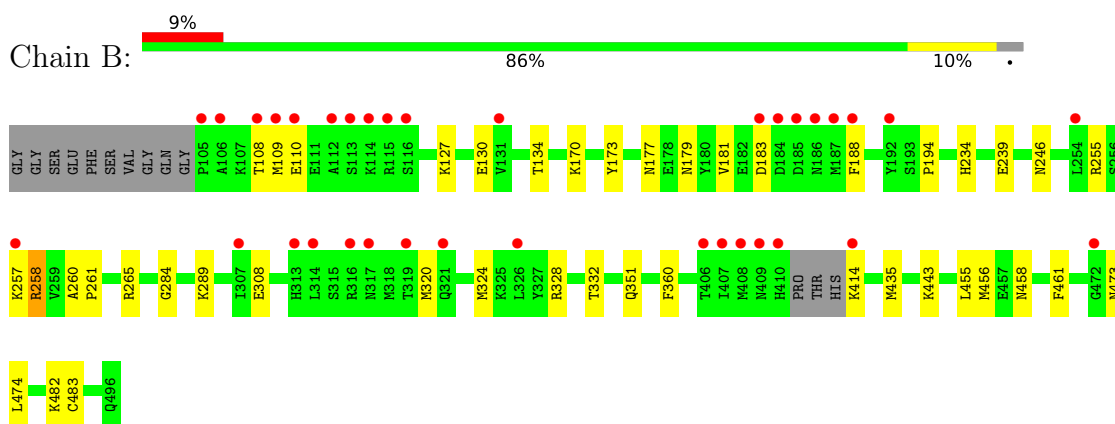
3 Residue-property plots

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 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.

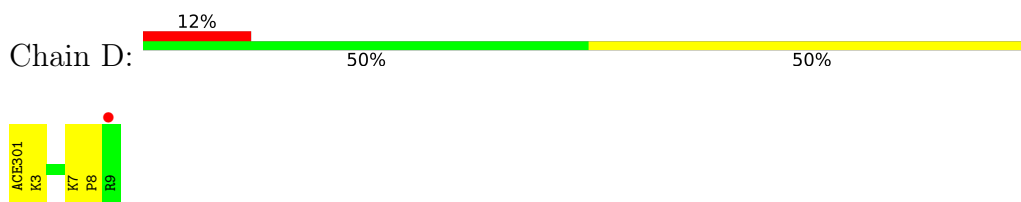
- Molecule 1: Glycylpeptide N-tetradecanoyltransferase 1



- Molecule 1: Glycylpeptide N-tetradecanoyltransferase 1



- Molecule 2: N-Acetyl-LYS-SER-PHE-SER-LYS-PRO-ARG



- Molecule 2: N-Acetyl-LYS-SER-PHE-SER-LYS-PRO-ARG

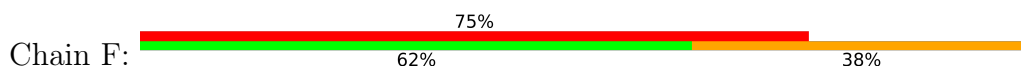


Diagram illustrating the restriction sites for ACE601, K3, S4, F5, S6, K7, P8, and R9 on a 1000 bp DNA fragment. The fragment is divided into two regions: an orange region (ACE601, K3, S4) and a green region (F5, S6, K7, P8, R9). Red dots indicate the positions of the restriction sites.

4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	79.31 Å 178.29 Å 58.17 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.72 – 1.70 48.72 – 1.70	Depositor EDS
% Data completeness (in resolution range)	86.8 (48.72-1.70) 86.8 (48.72-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.55 (at 1.70 Å)	Xtriage
Refinement program	PHENIX 1.17_3644	Depositor
R, R_{free}	0.183 , 0.223 0.184 , 0.224	Depositor DCC
R_{free} test set	3943 reflections (4.30%)	wwPDB-VP
Wilson B-factor (Å ²)	18.2	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 38.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7372	wwPDB-VP
Average B, all atoms (Å ²)	26.0	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 25.46 % 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 3.1599e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: MYA, MYR, COA, GOL, ACE

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	0.27	0/3245	0.46	0/4416
1	B	0.30	0/3298	0.51	0/4481
2	D	0.20	0/65	0.98	1/83 (1.2%)
2	F	0.51	0/61	1.15	1/79 (1.3%)
All	All	0.29	0/6669	0.50	2/9059 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	601	ACE	C-N-CA	8.67	147.72	121.70
2	D	301	ACE	C-N-CA	6.41	140.93	121.70

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	3155	0	3098	19	0
1	B	3212	0	3157	29	0
2	D	66	0	66	6	0
2	F	62	0	58	7	0
3	A	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	6	0	8	0	0
4	A	48	0	32	1	0
5	A	63	0	56	0	0
5	B	63	0	58	1	0
6	D	15	0	26	0	0
7	A	320	0	0	4	0
7	B	352	0	0	7	0
7	D	3	0	0	0	0
7	F	1	0	0	0	0
All	All	7372	0	6567	53	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 4.

All (53) 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)
4:A:502[A]:COA:C1B	4:A:502[A]:COA:O4B	1.63	1.20
1:B:234:HIS:HD2	1:B:239[B]:GLU:HG3	1.51	0.76
1:A:410:HIS:HD2	1:A:412:THR:H	1.31	0.75
1:A:302:ASN:OD1	1:A:443:LYS:NZ	2.23	0.70
1:B:173:TYR:CE2	1:B:194:PRO:HG3	2.29	0.68
1:A:240:LYS:NZ	7:A:602:HOH:O	2.23	0.65
1:A:141:ASP:OD2	7:A:601:HOH:O	2.14	0.64
1:B:320:MET:HG3	1:B:324:MET:HE2	1.81	0.63
1:A:459:LYS:NZ	7:A:604:HOH:O	2.33	0.60
1:B:130:GLU:O	1:B:289:LYS:HE3	2.04	0.57
1:A:246:ASN:OD1	2:D:3[B]:LYS:HE2	2.05	0.57
1:B:170:LYS:HA	1:B:173:TYR:CE2	2.41	0.56
1:B:443:LYS:NZ	7:B:608:HOH:O	2.39	0.54
1:B:246:ASN:OD1	2:F:3[B]:LYS:HE3	2.09	0.52
1:B:458:ASN:HA	1:B:461:PHE:CE2	2.44	0.51
1:A:282:THR:OG1	2:D:3[B]:LYS:HD2	2.11	0.51
1:A:458:ASN:HA	1:A:461:PHE:CE2	2.46	0.51
1:B:234:HIS:CD2	1:B:239[B]:GLU:HG3	2.40	0.49
1:A:301:LEU:O	1:A:443:LYS:NZ	2.37	0.48
1:A:304:ARG:HG2	1:A:308:GLU:OE1	2.14	0.48
1:B:177[B]:ASN:ND2	7:B:616:HOH:O	2.47	0.48
1:B:183:ASP:OD2	1:B:188:PHE:N	2.37	0.47
1:B:179:ASN:O	1:B:255:ARG:NH2	2.47	0.47
1:B:170:LYS:HA	1:B:173:TYR:CD2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:473:ASN:O	2:F:4:SER:OG	2.18	0.47
5:B:501:MYA:S1	2:F:3[B]:LYS:HD3	2.54	0.47
1:B:414:LYS:O	7:B:601:HOH:O	2.20	0.47
1:A:187:MET:HE1	1:A:310:LYS:HB2	1.97	0.46
1:B:181:VAL:HG22	2:F:601:ACE:H2	1.97	0.46
1:A:117:TYR:HB3	1:A:120:TRP:HB2	1.98	0.45
1:A:454:ASP:HB2	1:A:459:LYS:HD2	1.98	0.45
1:B:127:LYS:HB2	1:B:130:GLU:HG3	1.98	0.45
1:B:351:GLN:NE2	7:B:611:HOH:O	2.44	0.45
7:B:685:HOH:O	2:F:3[A]:LYS:HD2	2.16	0.45
1:B:284:GLY:H	2:F:601:ACE:C	2.25	0.44
1:A:311:PHE:O	2:D:8:PRO:HD2	2.17	0.44
1:B:265:ARG:HD2	7:B:607:HOH:O	2.18	0.43
1:B:482:LYS:HB3	7:B:665:HOH:O	2.19	0.42
1:B:435:MET:HG3	1:B:461:PHE:CE2	2.55	0.42
7:A:641:HOH:O	2:D:3[B]:LYS:HE3	2.20	0.41
1:A:185:ASP:OD1	2:D:7:LYS:HE3	2.19	0.41
1:A:417:LYS:HG2	1:A:447:PHE:CD1	2.55	0.41
1:A:295:ARG:HE	1:A:469:ILE:HD11	1.86	0.41
2:D:3[B]:LYS:NZ	2:D:3[B]:LYS:HB2	2.33	0.41
1:B:181:VAL:CG2	2:F:601:ACE:H2	2.51	0.41
1:B:260:ALA:HB3	1:B:261:PRO:HD3	2.03	0.40
1:B:134:THR:O	1:B:483:CYS:HA	2.21	0.40
1:B:360:PHE:CE1	1:B:456:MET:HA	2.57	0.40
1:A:126:PRO:HB2	1:A:289:LYS:HD3	2.04	0.40
1:A:156:PHE:CZ	1:A:254:LEU:HD21	2.56	0.40
1:B:257[B]:LYS:O	1:B:258:ARG:HG2	2.22	0.40

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%)	380 (97%)	11 (3%)	0	100	100
1	B	394/402 (98%)	383 (97%)	11 (3%)	0	100	100
2	D	7/8 (88%)	5 (71%)	2 (29%)	0	100	100
2	F	7/8 (88%)	5 (71%)	0	2 (29%)	0	0
All	All	799/820 (97%)	773 (97%)	24 (3%)	2 (0%)	48	22

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	3[A]	LYS
2	F	3[B]	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	340/362 (94%)	331 (97%)	9 (3%)	40	23
1	B	351/362 (97%)	343 (98%)	8 (2%)	44	27
2	D	7/7 (100%)	7 (100%)	0	100	100
2	F	6/7 (86%)	5 (83%)	1 (17%)	2	0
All	All	704/738 (95%)	686 (97%)	18 (3%)	40	23

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	107	LYS
1	A	108	THR
1	A	113	SER
1	A	115	ARG
1	A	134	THR
1	A	184	ASP
1	A	295	ARG
1	A	455	LEU
1	A	459	LYS

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Mol	Chain	Res	Type
1	B	108	THR
1	B	109	MET
1	B	110	GLU
1	B	258	ARG
1	B	308	GLU
1	B	328	ARG
1	B	332	THR
1	B	455	LEU
2	F	4	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	186	ASN
1	A	232	ASN
1	A	410	HIS
1	A	458	ASN
1	B	144	ASN
1	B	351	GLN
1	B	458	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](#)

6 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
6	MYR	D	401[A]	2	13,14,15	0.44	0	12,13,15	0.43	0
4	COA	A	502[A]	-	47,50,50	2.97	20 (42%)	69,75,75	2.00	15 (21%)
5	MYA	B	501	-	63,65,65	1.41	12 (19%)	85,91,91	1.64	16 (18%)
5	MYA	A	503[B]	-	63,65,65	1.29	10 (15%)	85,91,91	1.63	15 (17%)
3	GOL	B	502	-	5,5,5	1.12	0	5,5,5	0.83	0
3	GOL	A	501	-	5,5,5	1.35	1 (20%)	5,5,5	0.87	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
6	MYR	D	401[A]	2	-	1/12/12/13	-
4	COA	A	502[A]	-	-	7/48/64/64	0/3/3/3
5	MYA	B	501	-	-	2/64/80/80	0/3/3/3
5	MYA	A	503[B]	-	-	4/64/80/80	0/3/3/3
3	GOL	B	502	-	-	0/4/4/4	-
3	GOL	A	501	-	-	0/4/4/4	-

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	502[A]	COA	O4B-C1B	9.39	1.63	1.42
4	A	502[A]	COA	C2B-C1B	-6.15	1.34	1.53
4	A	502[A]	COA	C5P-N4P	6.02	1.47	1.33
4	A	502[A]	COA	P2A-O3A	6.01	1.66	1.59
4	A	502[A]	COA	O4B-C4B	-5.80	1.32	1.45
4	A	502[A]	COA	C6A-N6A	5.74	1.48	1.34
4	A	502[A]	COA	C9P-N8P	5.39	1.46	1.33
5	B	501	MYA	P2A-O3A	4.00	1.63	1.59
4	A	502[A]	COA	P3B-O3B	3.61	1.65	1.59
5	A	503[B]	MYA	C2A-N3A	3.52	1.40	1.33
4	A	502[A]	COA	P1A-O3A	3.41	1.63	1.59
5	A	503[B]	MYA	C2A-N1A	3.40	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	501	MYA	C2A-N3A	3.37	1.39	1.33
4	A	502[A]	COA	C2A-N3A	3.29	1.39	1.33
5	B	501	MYA	C2A-N1A	3.29	1.39	1.33
5	A	503[B]	MYA	C3M-C2M	3.16	1.54	1.50
5	A	503[B]	MYA	C5A-N7A	-2.95	1.33	1.39
4	A	502[A]	COA	C6P-C5P	2.91	1.57	1.51
5	B	501	MYA	C3M-C2M	2.73	1.53	1.50
5	A	503[B]	MYA	C5A-C4A	-2.71	1.34	1.39
4	A	502[A]	COA	O5P-C5P	-2.68	1.17	1.23
5	B	501	MYA	C5A-N7A	-2.63	1.34	1.39
4	A	502[A]	COA	P1A-O5B	2.59	1.69	1.59
5	A	503[B]	MYA	C5A-C6A	-2.57	1.33	1.41
5	B	501	MYA	C5A-C4A	-2.53	1.34	1.39
4	A	502[A]	COA	C5A-N7A	-2.52	1.34	1.39
4	A	502[A]	COA	O3B-C3B	-2.50	1.35	1.44
4	A	502[A]	COA	C5A-C4A	-2.49	1.34	1.39
4	A	502[A]	COA	P2A-O6A	2.39	1.68	1.59
5	B	501	MYA	C2M-S1	2.32	1.81	1.76
5	B	501	MYA	P1A-O3A	2.32	1.62	1.59
5	A	503[B]	MYA	C8A-N9A	-2.30	1.33	1.37
5	B	501	MYA	C5A-C6A	-2.27	1.34	1.41
4	A	502[A]	COA	O9P-C9P	-2.26	1.19	1.23
4	A	502[A]	COA	C3B-C4B	2.21	1.58	1.52
5	B	501	MYA	P3X-O3X	2.20	1.63	1.59
5	B	501	MYA	P3X-O8A	-2.14	1.46	1.54
5	B	501	MYA	C8A-N9A	-2.06	1.34	1.37
5	A	503[B]	MYA	C4A-N9A	-2.06	1.33	1.37
4	A	502[A]	COA	C4A-N9A	-2.05	1.33	1.37
3	A	501	GOL	C1-C2	2.02	1.59	1.51
5	A	503[B]	MYA	P3X-O8A	-2.02	1.47	1.54
5	A	503[B]	MYA	P2A-O3A	2.00	1.61	1.59

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	503[B]	MYA	N3A-C2A-N1A	-6.58	118.62	128.58
5	B	501	MYA	N3A-C2A-N1A	-6.43	118.85	128.58
4	A	502[A]	COA	N6A-C6A-N1A	-6.26	104.43	118.38
4	A	502[A]	COA	N3A-C2A-N1A	-5.39	120.42	128.58
4	A	502[A]	COA	C5A-C6A-N6A	4.93	135.49	123.29
4	A	502[A]	COA	C4A-N9A-C1B	-4.80	115.41	126.63
4	A	502[A]	COA	C5A-C4A-N3A	-4.60	120.38	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	502[A]	COA	N9A-C8A-N7A	-4.49	107.56	113.94
5	B	501	MYA	C5A-C4A-N3A	-4.35	120.72	126.72
5	A	503[B]	MYA	C5A-C4A-N3A	-4.34	120.74	126.72
5	A	503[B]	MYA	N9A-C8A-N7A	-4.16	108.03	113.94
4	A	502[A]	COA	C1B-N9A-C8A	4.06	136.11	127.09
5	B	501	MYA	N9A-C8A-N7A	-3.95	108.34	113.94
5	B	501	MYA	O2M-C2M-C3M	-3.67	119.75	123.98
5	B	501	MYA	C2X-C3X-C4X	-3.49	97.12	103.24
5	A	503[B]	MYA	C2X-C3X-C4X	-3.25	97.54	103.24
4	A	502[A]	COA	C2A-N3A-C4A	3.23	119.72	111.83
5	B	501	MYA	C2A-N3A-C4A	3.15	119.52	111.83
4	A	502[A]	COA	C3P-N4P-C5P	-3.12	117.02	122.82
5	A	503[B]	MYA	C2A-N3A-C4A	3.11	119.43	111.83
4	A	502[A]	COA	C6P-C5P-N4P	3.10	121.98	116.34
4	A	502[A]	COA	C5A-N7A-C8A	3.05	108.25	103.45
5	B	501	MYA	C5A-N7A-C8A	3.05	108.24	103.45
5	B	501	MYA	C4A-C5A-N7A	-3.01	107.14	110.58
5	A	503[B]	MYA	C5A-N7A-C8A	2.97	108.12	103.45
5	B	501	MYA	O4X-C1X-N9A	2.89	113.64	108.09
5	A	503[B]	MYA	O2M-C2M-C3M	-2.80	120.75	123.98
5	B	501	MYA	C5A-C4A-N9A	2.78	108.84	105.81
5	A	503[B]	MYA	C5A-C6A-N6A	-2.74	116.50	123.29
5	A	503[B]	MYA	C6A-C5A-C4A	2.68	120.83	117.18
4	A	502[A]	COA	N3A-C4A-N9A	2.64	131.65	127.17
5	B	501	MYA	P3X-O3X-C3X	-2.62	116.42	123.43
4	A	502[A]	COA	C4A-N9A-C8A	2.61	108.48	105.74
5	A	503[B]	MYA	O4X-C1X-N9A	2.60	113.08	108.09
5	B	501	MYA	C3M-C2M-S1	2.55	116.44	113.40
5	B	501	MYA	C6A-C5A-C4A	2.49	120.58	117.18
4	A	502[A]	COA	C4A-C5A-N7A	-2.49	107.74	110.58
5	A	503[B]	MYA	C4A-C5A-N7A	-2.45	107.78	110.58
5	A	503[B]	MYA	P3X-O3X-C3X	-2.45	116.90	123.43
5	A	503[B]	MYA	N3A-C4A-N9A	2.44	131.31	127.17
4	A	502[A]	COA	O5P-C5P-N4P	-2.41	118.31	123.03
5	A	503[B]	MYA	C2-C3-N4	-2.28	107.66	112.41
5	A	503[B]	MYA	C4A-N9A-C8A	2.28	108.13	105.74
5	B	501	MYA	C4M-C3M-C2M	-2.25	107.31	112.27
5	B	501	MYA	C5A-C6A-N6A	-2.21	117.81	123.29
5	B	501	MYA	O3X-P3X-O9A	-2.09	101.87	109.33

There are no chirality outliers.

All (14) torsion outliers are listed below:

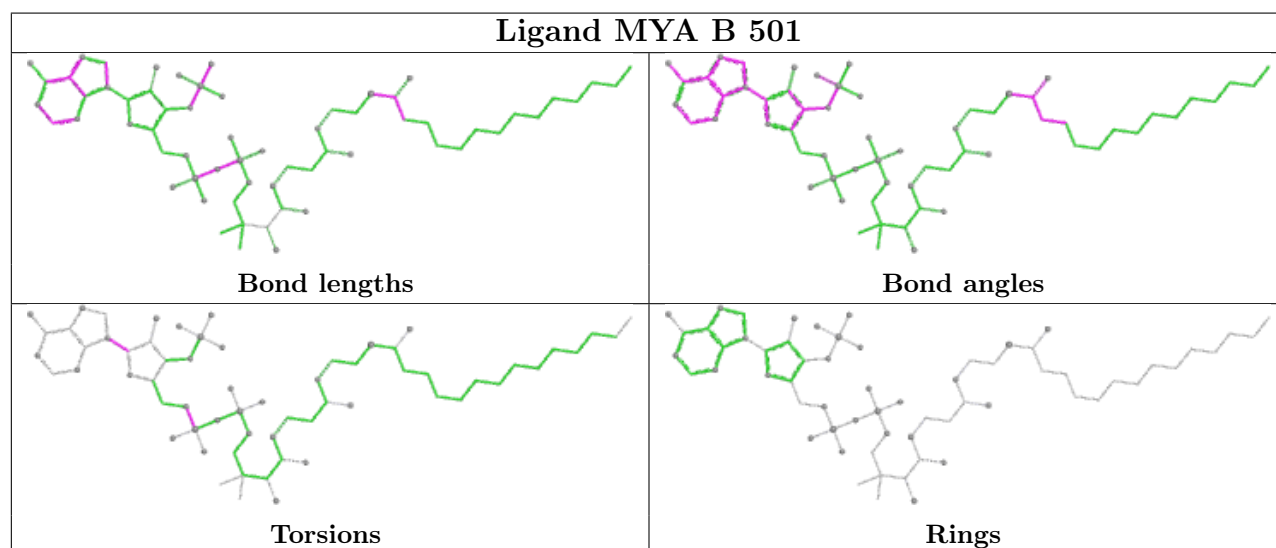
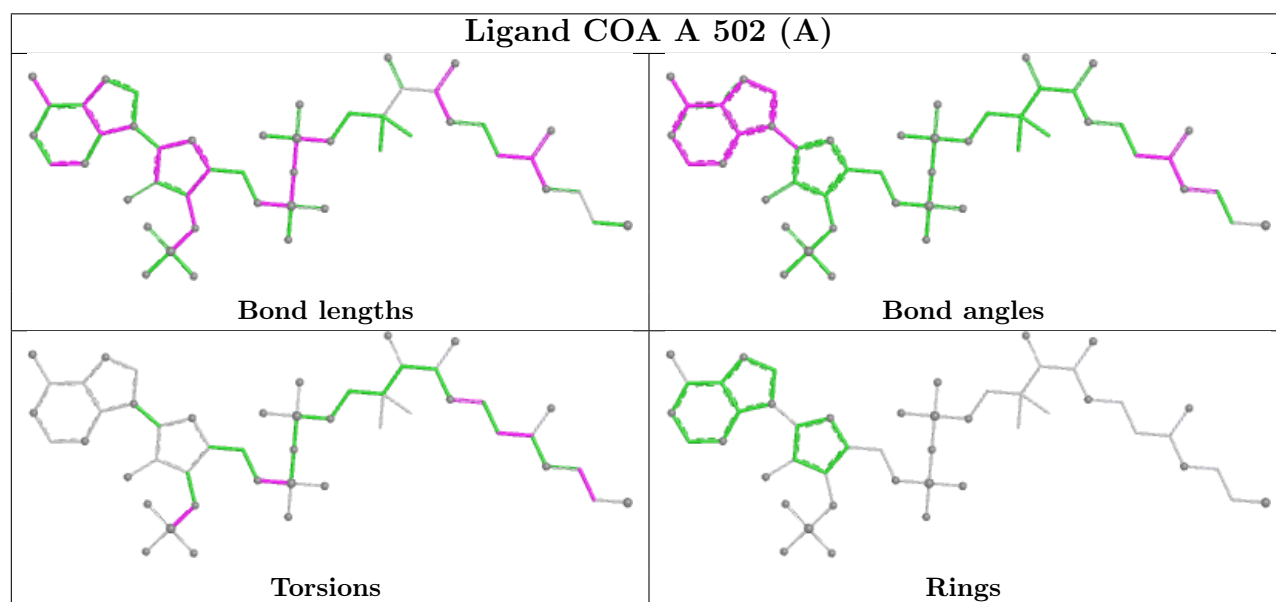
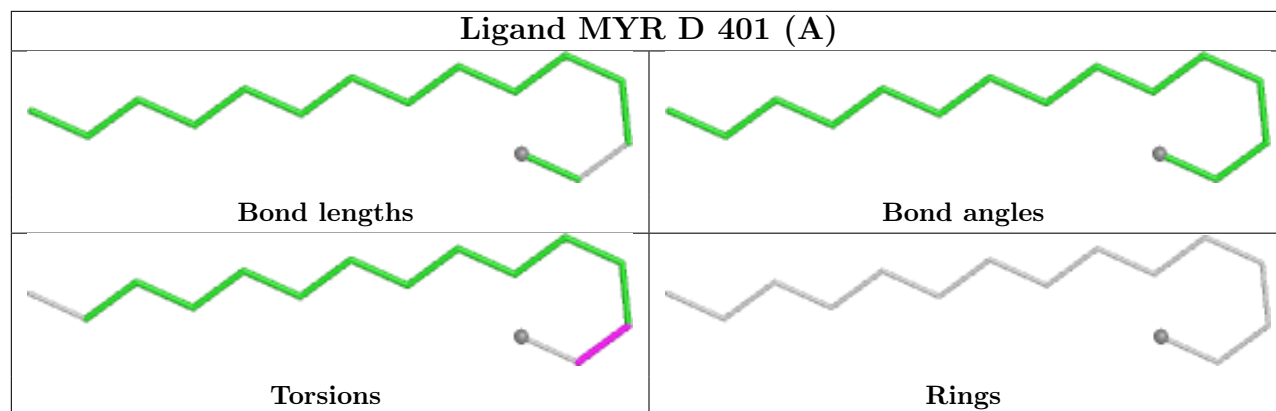
Mol	Chain	Res	Type	Atoms
4	A	502[A]	COA	C5B-O5B-P1A-O2A
4	A	502[A]	COA	C5B-O5B-P1A-O3A
4	A	502[A]	COA	S1P-C2P-C3P-N4P
6	D	401[A]	MYR	O1-C1-C2-C3
5	A	503[B]	MYA	C2X-C1X-N9A-C8A
5	B	501	MYA	C2X-C1X-N9A-C8A
5	B	501	MYA	C5X-O5X-P1A-O2A
4	A	502[A]	COA	C6P-C7P-N8P-C9P
5	A	503[B]	MYA	O2M-C2M-S1-C2
5	A	503[B]	MYA	P1A-O3A-P2A-O4A
4	A	502[A]	COA	C3B-O3B-P3B-O8A
4	A	502[A]	COA	O5P-C5P-C6P-C7P
4	A	502[A]	COA	N4P-C5P-C6P-C7P
5	A	503[B]	MYA	P1A-O3A-P2A-O5A

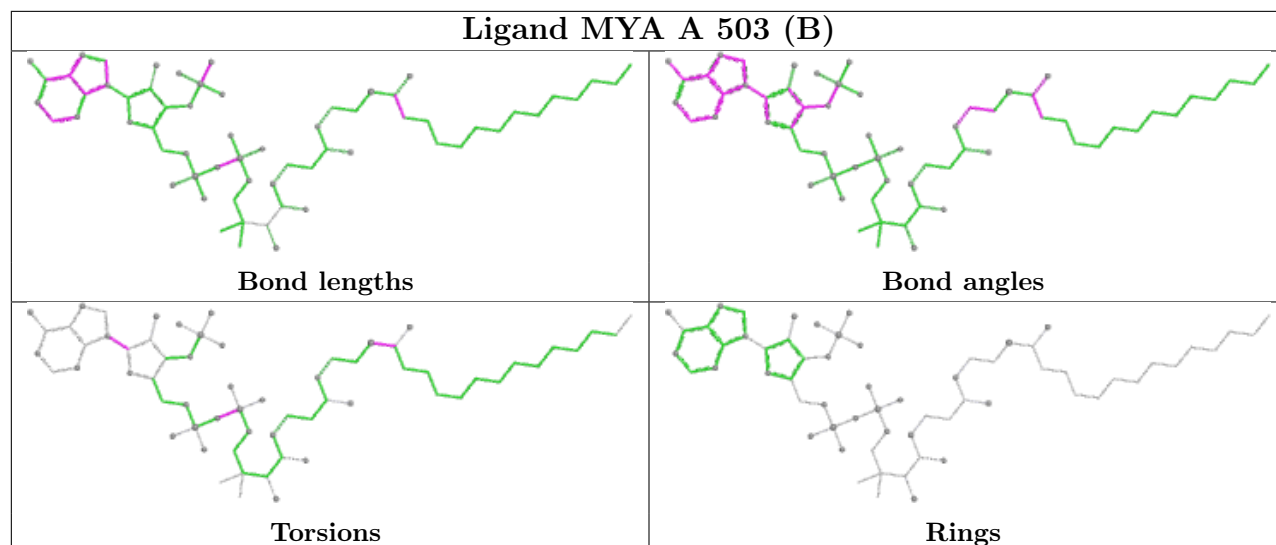
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	502[A]	COA	1	0
5	B	501	MYA	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

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, 95th 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%)	0.34	38 (9%) 13 14	11, 23, 54, 80	1 (0%)
1	B	389/402 (96%)	0.25	35 (8%) 15 16	9, 20, 56, 78	9 (2%)
2	D	7/8 (87%)	1.50	1 (14%) 6 5	15, 36, 43, 53	1 (14%)
2	F	7/8 (87%)	2.78	6 (85%) 0 0	21, 51, 53, 65	1 (14%)
All	All	795/820 (96%)	0.32	80 (10%) 12 13	9, 21, 56, 80	12 (1%)

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	105	PRO	5.3
1	B	106	ALA	4.8
1	A	106	ALA	4.4
1	A	131	VAL	4.1
1	A	315	SER	4.0
2	F	3[A]	LYS	4.0
1	A	116	SER	3.8
1	A	318	MET	3.6
1	B	472	GLY	3.6
1	B	257[A]	LYS	3.5
1	A	319	THR	3.5
1	B	410	HIS	3.5
1	B	313	HIS	3.4
2	F	8	PRO	3.4
1	B	316	ARG	3.4
1	A	109	MET	3.3
1	B	408	MET	3.2
1	A	108	THR	3.2
1	B	314	LEU	3.2
1	A	313	HIS	3.2
1	B	254	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	105	PRO	3.1
1	B	184	ASP	3.0
1	A	114	LYS	3.0
2	F	4	SER	2.9
1	B	115	ARG	2.9
1	B	109	MET	2.9
1	A	110	GLU	2.9
1	A	112	ALA	2.9
1	A	129	GLY	2.9
1	A	321	GLN	2.9
1	A	320	MET	2.9
1	A	316	ARG	2.8
1	A	111	GLU	2.8
1	B	108	THR	2.8
1	A	128	LEU	2.7
1	A	314	LEU	2.7
1	A	472	GLY	2.6
1	B	317	ASN	2.6
1	B	192	TYR	2.6
1	A	317	ASN	2.6
1	A	133	ASN	2.6
2	F	9	ARG	2.6
1	B	185	ASP	2.5
1	B	186	ASN	2.5
2	F	7	LYS	2.5
1	B	414	LYS	2.5
1	B	187	MET	2.5
1	B	409	ASN	2.4
1	A	307	ILE	2.4
1	B	116	SER	2.4
1	B	319	THR	2.4
1	B	114	LYS	2.4
1	B	131	VAL	2.4
1	A	332	THR	2.3
1	A	322	ARG	2.3
1	A	325	LYS	2.3
1	B	188	PHE	2.3
1	A	132	VAL	2.3
1	A	323	THR	2.2
1	A	107	LYS	2.2
1	A	324	MET	2.2
2	F	5	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	112	ALA	2.2
1	B	307	ILE	2.2
1	A	113	SER	2.2
1	A	258[A]	ARG	2.1
1	B	110	GLU	2.1
1	B	407	ILE	2.1
1	A	115	ARG	2.1
1	A	130	GLU	2.1
1	A	184	ASP	2.1
1	B	113	SER	2.1
1	B	183	ASP	2.1
1	B	321	GLN	2.1
1	A	326	LEU	2.1
1	B	326	LEU	2.1
1	A	412	THR	2.0
1	B	406	THR	2.0
2	D	9	ARG	2.0

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 ⓘ

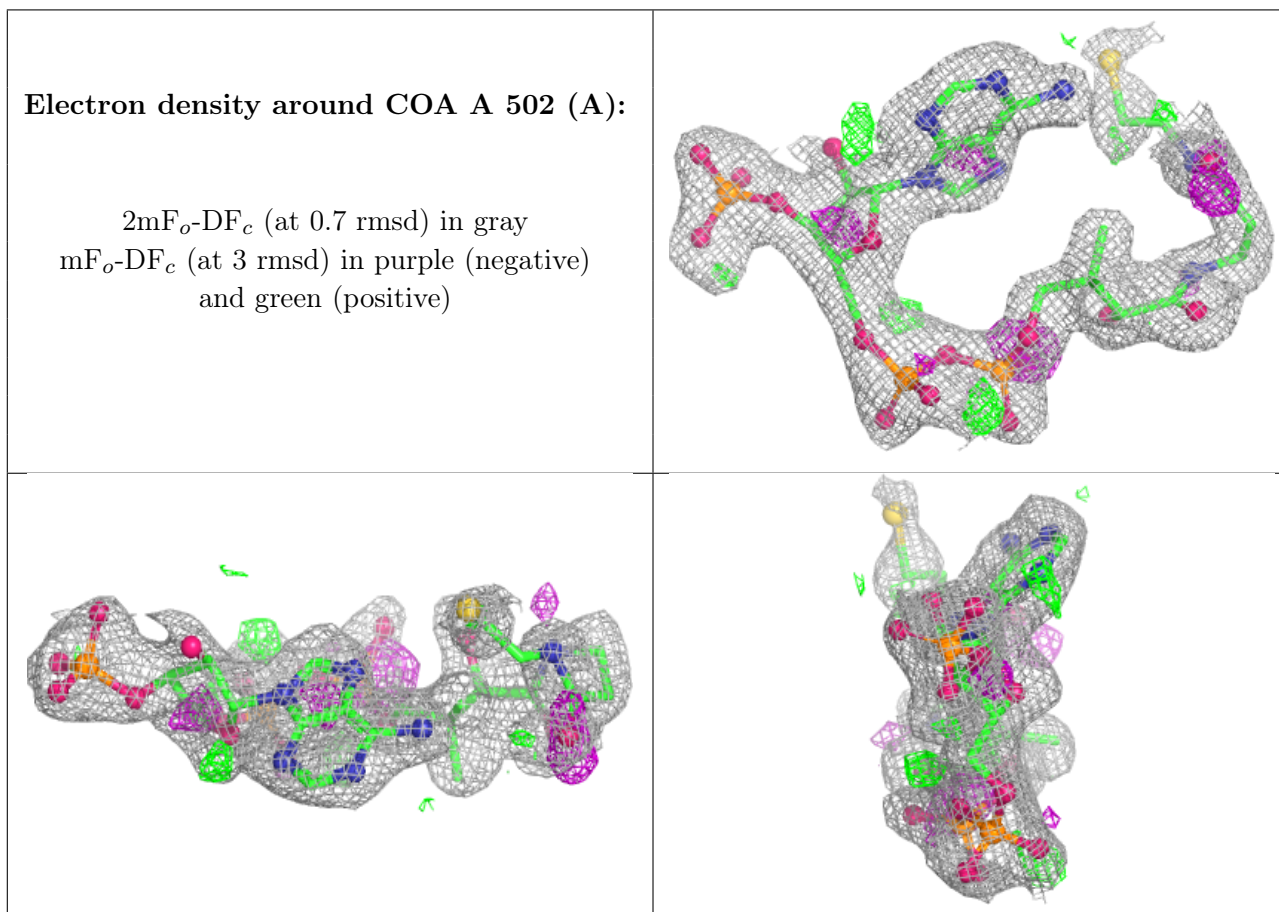
There are no oligosaccharides in this entry.

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, 95th 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.

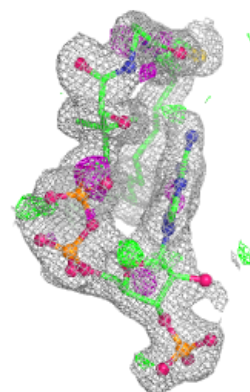
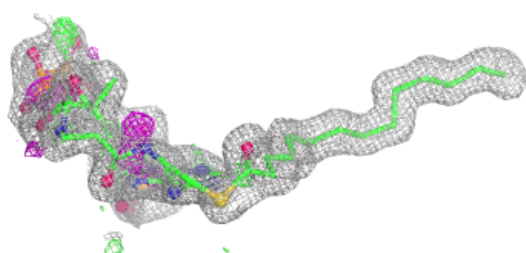
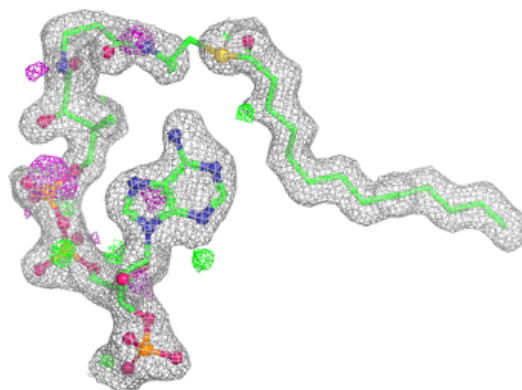
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	COA	A	502[A]	48/48	0.83	0.13	23,36,42,51	48
5	MYA	A	503[B]	63/63	0.87	0.11	13,29,40,44	63
5	MYA	B	501	63/63	0.91	0.10	9,32,42,44	0
3	GOL	A	501	6/6	0.96	0.07	20,25,26,27	0
6	MYR	D	401[A]	15/16	0.96	0.05	13,15,21,22	15
3	GOL	B	502	6/6	0.97	0.06	13,17,20,25	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.

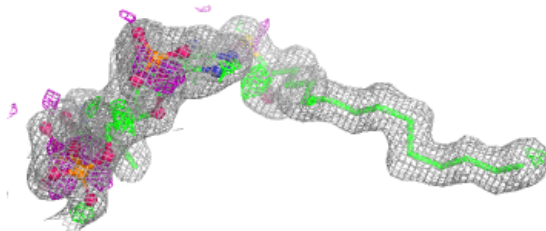
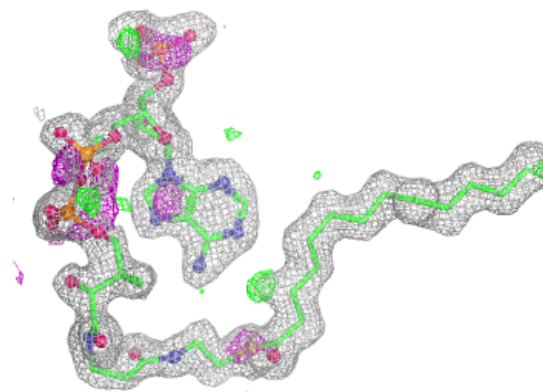


Electron density around MYA A 503 (B):

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

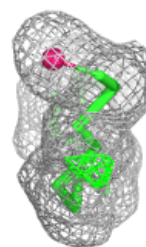
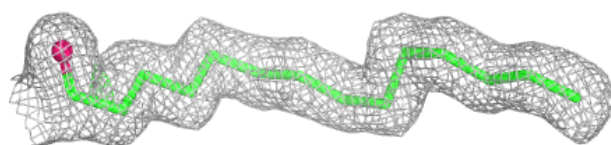
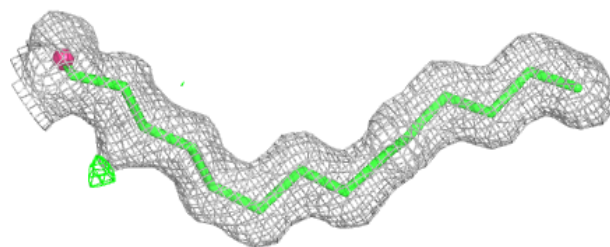
**Electron density around MYA B 501:**

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



Electron density around MYR D 401 (A):

$2mF_o-DF_c$ (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.