



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 06:36 pm BST

PDB ID : 6GNT
Title : Crystal Structure of Leishmania major N-Myristoyltransferase (NMT) With Bound Myristoyl-CoA and a Quionlinyl aryl sulphonamide ligand
Authors : Robinson, D.A.; Harrison, J.R.; Brand, S.; Smith, V.C.; Thompson, S.; Smith, A.; Davies, K.; Mok, N.Y.; Torrie, L.S.; Collie, I.; Hallyburton, I.; Norval, S.; Simeons, F.R.C.; Stojanovski, L.; Frearson, J.A.; Brenk, R.; Wyatt, P.G.; Gilbert, I.H.; Read, K.D.
Deposited on : 2018-05-31
Resolution : 1.60 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 following versions of software and data (see [references ⓘ](#)) 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 : 2.11
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) : 2.11

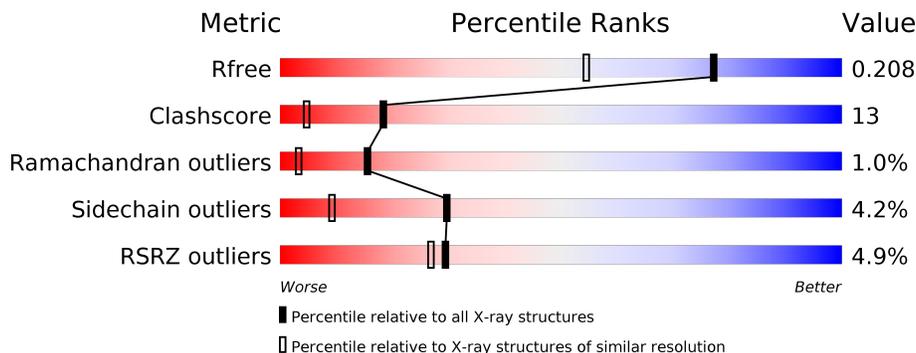
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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 $\leq 5\%$. 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	411	

2 Entry composition [i](#)

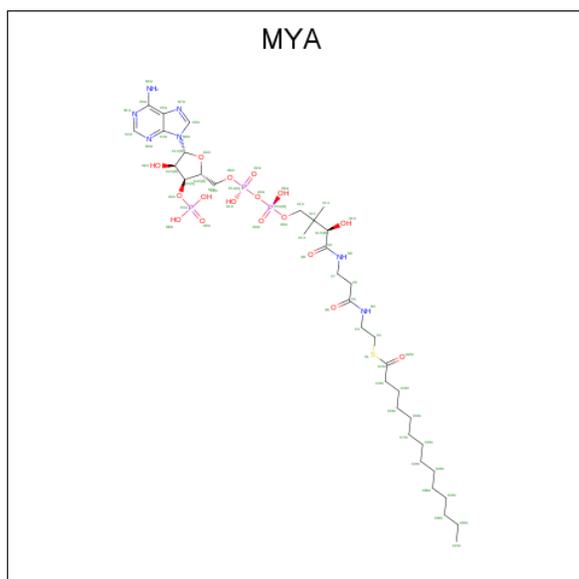
There are 5 unique types of molecules in this entry. The entry contains 3737 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

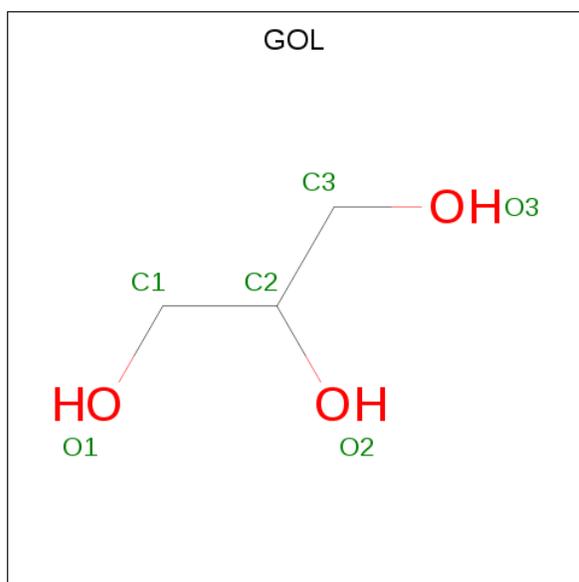
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	411	3343	2162	560	606	15	0	2	0

- Molecule 2 is TETRADECANOYL-COA (three-letter code: MYA) (formula: $C_{35}H_{62}N_7O_{17}P_3S$).



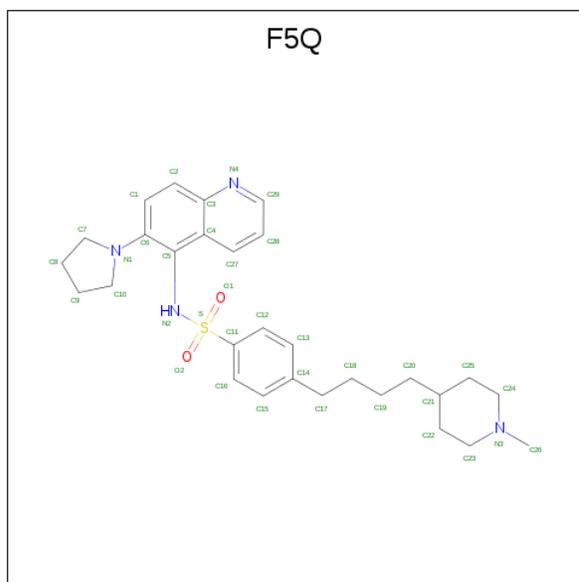
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
2	A	1	63	35	7	17	3	1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is 4-[4-(1-methylpiperidin-4-yl)butyl]-{N}-(6-pyrrolidin-1-ylquinolin-5-yl)benzenesulfonamide (three-letter code: F5Q) (formula: $C_{29}H_{38}N_4O_2S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			36	29	4	2	1		

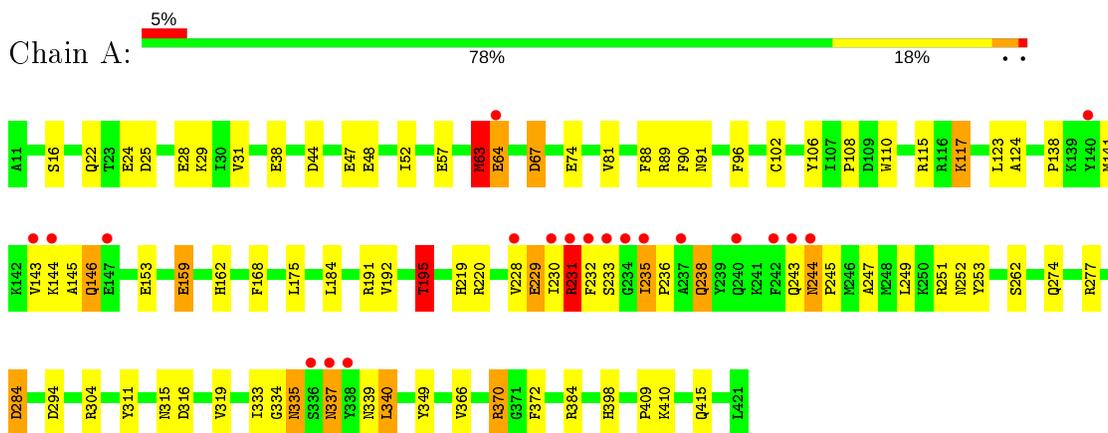
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	289	Total 289	O 289	0	0

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 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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	48.76 Å 90.84 Å 53.68 Å 90.00° 114.85° 90.00°	Depositor
Resolution (Å)	19.97 – 1.60 45.42 – 1.60	Depositor EDS
% Data completeness (in resolution range)	98.0 (19.97-1.60) 98.1 (45.42-1.60)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 1.60 Å)	Xtrriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.168 , 0.200 0.175 , 0.208	Depositor DCC
R_{free} test set	2782 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	18.3	Xtrriage
Anisotropy	0.323	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.026 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3737	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.30% of the height of the origin peak. No significant pseudotranslation is detected.*

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, GOL, F5Q

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	1.27	10/3448 (0.3%)	1.19	23/4696 (0.5%)

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	1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	67	ASP	CB-CG	8.70	1.70	1.51
1	A	67	ASP	CG-OD1	6.39	1.40	1.25
1	A	159	GLU	CB-CG	6.19	1.64	1.52
1	A	229	GLU	CG-CD	6.12	1.61	1.51
1	A	24	GLU	CD-OE2	5.79	1.32	1.25
1	A	88	PHE	CD1-CE1	5.22	1.49	1.39
1	A	168	PHE	CG-CD1	5.19	1.46	1.38
1	A	415	GLN	CG-CD	5.16	1.62	1.51
1	A	372	PHE	CE2-CZ	5.09	1.47	1.37
1	A	191	ARG	CZ-NH1	5.02	1.39	1.33

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	67	ASP	CB-CG-OD1	8.96	126.37	118.30
1	A	384	ARG	NE-CZ-NH1	8.20	124.40	120.30
1	A	115	ARG	CB-CG-CD	-7.62	91.78	111.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	115	ARG	NE-CZ-NH2	-7.10	116.75	120.30
1	A	340	LEU	CA-CB-CG	7.02	131.44	115.30
1	A	294	ASP	CB-CG-OD1	6.91	124.52	118.30
1	A	195	THR	N-CA-CB	-6.51	97.92	110.30
1	A	384	ARG	NE-CZ-NH2	-6.43	117.08	120.30
1	A	195	THR	OG1-CB-CG2	6.43	124.78	110.00
1	A	63	MET	CG-SD-CE	6.25	110.21	100.20
1	A	304	ARG	NE-CZ-NH2	-6.09	117.25	120.30
1	A	304	ARG	CG-CD-NE	-6.01	99.17	111.80
1	A	96	PHE	CB-CG-CD1	-5.92	116.66	120.80
1	A	89	ARG	NE-CZ-NH2	-5.61	117.50	120.30
1	A	220	ARG	NE-CZ-NH2	-5.54	117.53	120.30
1	A	67	ASP	CB-CA-C	5.45	121.30	110.40
1	A	44	ASP	CB-CG-OD2	-5.39	113.44	118.30
1	A	349	TYR	CB-CG-CD2	-5.35	117.79	121.00
1	A	64	GLU	OE1-CD-OE2	-5.33	116.90	123.30
1	A	294	ASP	CB-CG-OD2	-5.27	113.56	118.30
1	A	340	LEU	CB-CG-CD2	5.27	119.96	111.00
1	A	370	ARG	NE-CZ-NH2	-5.23	117.68	120.30
1	A	349	TYR	CB-CG-CD1	5.00	124.00	121.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	231	ARG	Peptide

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	3343	0	3246	89	0
2	A	63	0	58	0	0
3	A	6	0	8	0	0
4	A	36	0	0	1	0
5	A	289	0	0	49	0
All	All	3737	0	3312	90	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 13.

All (90) 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:175:LEU:HG	5:A:1359:HOH:O	1.17	1.30
1:A:102:CYS:HB3	5:A:1358:HOH:O	1.29	1.26
1:A:25:ASP:HB3	5:A:1322:HOH:O	1.30	1.26
1:A:63:MET:SD	5:A:1146:HOH:O	1.93	1.25
1:A:67:ASP:HB3	5:A:1351:HOH:O	1.31	1.21
1:A:146:GLN:HE21	1:A:146:GLN:HA	1.28	0.99
1:A:143:VAL:HA	5:A:1110:HOH:O	1.64	0.97
1:A:48:GLU:OE1	5:A:1102:HOH:O	1.85	0.94
1:A:110:TRP:HZ2	1:A:195:THR:HG21	1.35	0.91
1:A:106:TYR:CE2	5:A:1358:HOH:O	2.23	0.91
1:A:146:GLN:NE2	5:A:1105:HOH:O	2.02	0.91
1:A:141:MET:HG2	5:A:1329:HOH:O	0.73	0.91
1:A:238:GLN:HE21	1:A:238:GLN:N	1.70	0.88
1:A:238:GLN:HE21	1:A:238:GLN:H	0.89	0.88
1:A:238:GLN:H	1:A:238:GLN:NE2	1.72	0.88
1:A:146:GLN:HB2	5:A:1110:HOH:O	1.75	0.85
1:A:146:GLN:NE2	1:A:146:GLN:HA	1.90	0.85
1:A:334:GLY:N	5:A:1101:HOH:O	1.71	0.84
1:A:315:ASN:HA	5:A:1116:HOH:O	1.76	0.83
1:A:315:ASN:CA	5:A:1116:HOH:O	2.28	0.81
1:A:228:VAL:HG11	1:A:249:LEU:HD21	1.64	0.79
1:A:335:ASN:O	5:A:1104:HOH:O	2.01	0.79
1:A:229:GLU:HB3	5:A:1337:HOH:O	1.84	0.77
1:A:47:GLU:OE1	5:A:1106:HOH:O	2.04	0.75
1:A:110:TRP:CZ2	1:A:195:THR:HG21	2.19	0.74
1:A:153:GLU:HG3	5:A:1331:HOH:O	1.87	0.73
1:A:235:ILE:HA	1:A:236:PRO:C	2.11	0.71
1:A:124:ALA:HB1	1:A:184:LEU:HD11	1.72	0.71
1:A:274:GLN:HE22	1:A:319:VAL:H	1.38	0.71
1:A:228:VAL:CG1	1:A:249:LEU:HD21	2.21	0.71
1:A:146:GLN:CA	1:A:146:GLN:HE21	2.04	0.70
1:A:243:GLN:O	1:A:245:PRO:HD3	1.91	0.70
1:A:74:GLU:OE1	5:A:1108:HOH:O	2.10	0.70
1:A:64:GLU:OE1	5:A:1109:HOH:O	2.11	0.68
1:A:398:HIS:HD2	5:A:1371:HOH:O	1.76	0.67
1:A:274:GLN:NE2	1:A:319:VAL:H	1.92	0.67
1:A:277:ARG:NH2	5:A:1113:HOH:O	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:VAL:HG12	1:A:141:MET:HE1	1.78	0.66
1:A:252:ASN:HB2	5:A:1313:HOH:O	1.95	0.66
1:A:91:ASN:HD22	1:A:340:LEU:HD21	1.63	0.63
1:A:284:ASP:CG	5:A:1111:HOH:O	2.36	0.62
1:A:143:VAL:O	5:A:1110:HOH:O	2.17	0.60
1:A:63:MET:HB3	1:A:102:CYS:SG	2.42	0.59
1:A:143:VAL:HG22	5:A:1353:HOH:O	2.02	0.59
1:A:229:GLU:O	1:A:232:PHE:CD2	2.56	0.59
1:A:31:VAL:HB	1:A:141:MET:CE	2.33	0.58
1:A:143:VAL:CA	5:A:1110:HOH:O	2.34	0.58
1:A:228:VAL:HG11	1:A:249:LEU:CD2	2.33	0.57
1:A:145:ALA:C	5:A:1105:HOH:O	2.43	0.56
1:A:230:ILE:O	1:A:231:ARG:HB2	2.05	0.56
1:A:123:LEU:HD13	1:A:175:LEU:HD11	1.88	0.55
1:A:57:GLU:HB3	1:A:117:LYS:HZ3	1.74	0.53
1:A:410:LYS:HE3	5:A:1270:HOH:O	2.09	0.53
1:A:192:VAL:O	1:A:195:THR:HG22	2.09	0.52
1:A:16:SER:HA	1:A:22:GLN:HE22	1.75	0.52
1:A:138:PRO:HG2	1:A:409:PRO:HG2	1.92	0.52
1:A:251:ARG:HG2	5:A:1325:HOH:O	2.10	0.52
1:A:141:MET:CG	5:A:1329:HOH:O	1.63	0.51
1:A:316:ASP:N	5:A:1116:HOH:O	2.42	0.51
1:A:339:ASN:HB2	5:A:1311:HOH:O	2.10	0.51
1:A:247:ALA:HB1	1:A:251:ARG:HH12	1.76	0.51
1:A:253:TYR:HB3	5:A:1145:HOH:O	2.11	0.51
1:A:25:ASP:CB	5:A:1322:HOH:O	2.15	0.51
1:A:311:TYR:CE2	1:A:366:VAL:HG11	2.46	0.51
1:A:143:VAL:C	5:A:1110:HOH:O	2.49	0.51
1:A:31:VAL:HG22	5:A:1284:HOH:O	2.12	0.50
4:A:1003:F5Q:N2	4:A:1003:F5Q:C7	2.75	0.49
1:A:232:PHE:CZ	5:A:1352:HOH:O	2.54	0.49
1:A:52:ILE:HD12	5:A:1314:HOH:O	2.12	0.49
1:A:146:GLN:CB	5:A:1110:HOH:O	2.49	0.48
1:A:16:SER:HA	1:A:22:GLN:NE2	2.29	0.47
1:A:52:ILE:O	1:A:52:ILE:HD12	2.14	0.47
1:A:219:HIS:HD2	5:A:1354:HOH:O	1.96	0.47
1:A:31:VAL:CG1	1:A:141:MET:HE1	2.43	0.46
1:A:162:HIS:HE1	5:A:1368:HOH:O	1.99	0.46
1:A:31:VAL:CB	1:A:141:MET:CE	2.94	0.46
1:A:232:PHE:CD1	1:A:232:PHE:O	2.69	0.45
1:A:31:VAL:HA	1:A:141:MET:CE	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:335:ASN:C	5:A:1107:HOH:O	2.54	0.45
1:A:141:MET:SD	1:A:144:LYS:HD2	2.58	0.44
1:A:31:VAL:CB	1:A:141:MET:HE1	2.47	0.44
1:A:370:ARG:NH2	5:A:1126:HOH:O	2.51	0.44
1:A:52:ILE:CD1	5:A:1314:HOH:O	2.66	0.44
1:A:81:VAL:HB	1:A:90:PHE:HD2	1.83	0.44
1:A:277:ARG:CZ	5:A:1113:HOH:O	2.62	0.43
1:A:337:ASN:N	1:A:337:ASN:OD1	2.50	0.43
1:A:235:ILE:CA	1:A:236:PRO:C	2.86	0.43
1:A:262:SER:HA	5:A:1103:HOH:O	2.19	0.42
1:A:333:ILE:O	5:A:1112:HOH:O	2.22	0.42
1:A:284:ASP:OD2	5:A:1111:HOH:O	2.21	0.41

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	411/411 (100%)	385 (94%)	22 (5%)	4 (1%)	15 3

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	231	ARG
1	A	233	SER
1	A	235	ILE
1	A	244	ASN

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	356/362 (98%)	341 (96%)	15 (4%)	30 9

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	GLU
1	A	29	LYS
1	A	38	GLU
1	A	63	MET
1	A	108	PRO
1	A	117	LYS
1	A	146	GLN
1	A	159	GLU
1	A	195	THR
1	A	231	ARG
1	A	238	GLN
1	A	244	ASN
1	A	284	ASP
1	A	335	ASN
1	A	337	ASN

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

Mol	Chain	Res	Type
1	A	22	GLN
1	A	91	ASN
1	A	146	GLN
1	A	162	HIS
1	A	238	GLN
1	A	252	ASN
1	A	274	GLN

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](#)

3 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	F5Q	A	1003	-	40,40,40	2.04	10 (25%)	52,56,56	2.42	19 (36%)
3	GOL	A	1002	-	5,5,5	0.85	0	5,5,5	1.40	1 (20%)
2	MYA	A	1001	-	54,65,65	1.01	3 (5%)	67,91,91	1.66	11 (16%)

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	F5Q	A	1003	-	-	7/22/39/39	0/5/5/5
3	GOL	A	1002	-	-	0/4/4/4	-
2	MYA	A	1001	-	-	3/59/80/80	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1003	F5Q	C11-S	-8.00	1.64	1.76
4	A	1003	F5Q	O1-S	5.22	1.49	1.43
4	A	1003	F5Q	S-N2	3.42	1.69	1.63
4	A	1003	F5Q	O2-S	3.41	1.47	1.43
4	A	1003	F5Q	C29-N4	2.61	1.37	1.32
4	A	1003	F5Q	C3-N4	-2.58	1.32	1.37
2	A	1001	MYA	P2A-O5A	-2.30	1.44	1.55
4	A	1003	F5Q	C17-C14	2.28	1.58	1.51
4	A	1003	F5Q	C26-N3	2.20	1.51	1.46
2	A	1001	MYA	C3X-C4X	-2.10	1.47	1.52
4	A	1003	F5Q	C7-N1	2.09	1.50	1.47
4	A	1003	F5Q	C16-C11	2.07	1.42	1.38
2	A	1001	MYA	P1A-O1A	-2.06	1.45	1.55

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1003	F5Q	O1-S-O2	-6.80	111.19	119.55
2	A	1001	MYA	N3A-C2A-N1A	-5.60	119.92	128.68
4	A	1003	F5Q	C23-N3-C24	5.17	116.75	109.52
4	A	1003	F5Q	C20-C21-C25	-5.08	99.97	112.11
2	A	1001	MYA	C5A-C6A-N6A	4.53	127.24	120.35
4	A	1003	F5Q	C26-N3-C24	-4.53	103.89	110.66
2	A	1001	MYA	O2M-C2M-C3M	4.11	116.35	109.02
4	A	1003	F5Q	C29-N4-C3	4.10	123.28	116.93
4	A	1003	F5Q	C25-C24-N3	-3.73	106.22	111.22
4	A	1003	F5Q	C22-C21-C25	-3.65	100.41	109.33
4	A	1003	F5Q	O1-S-C11	3.55	112.33	107.97
2	A	1001	MYA	C2A-N1A-C6A	3.48	124.70	118.75
4	A	1003	F5Q	C12-C11-S	3.44	123.51	119.77
4	A	1003	F5Q	C1-C6-N1	-3.41	116.87	122.30
2	A	1001	MYA	O5-C5-N4	3.26	129.17	123.01
4	A	1003	F5Q	C28-C29-N4	-3.19	119.05	123.94
4	A	1003	F5Q	C11-S-N2	3.08	110.71	106.83
4	A	1003	F5Q	C26-N3-C23	3.06	115.24	110.66
4	A	1003	F5Q	O2-S-C11	-2.57	104.80	107.97
4	A	1003	F5Q	C4-C3-N4	-2.56	120.11	122.83
4	A	1003	F5Q	C18-C19-C20	-2.43	105.02	113.62
4	A	1003	F5Q	C17-C14-C13	2.42	127.34	121.23
2	A	1001	MYA	O5-C5-C6	-2.36	117.70	122.02
2	A	1001	MYA	C2X-C3X-C4X	2.24	107.20	103.22
2	A	1001	MYA	C3-C2-S1	-2.20	105.35	114.36
2	A	1001	MYA	O4X-C4X-C5X	-2.19	102.17	109.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	MYA	P2A-O3A-P1A	-2.17	125.37	132.83
4	A	1003	F5Q	C17-C14-C15	-2.17	115.74	121.23
2	A	1001	MYA	O5A-P2A-O4A	2.13	122.76	112.24
3	A	1002	GOL	O1-C1-C2	-2.09	100.19	110.20
4	A	1003	F5Q	C24-C25-C21	-2.03	106.86	111.99

There are no chirality outliers.

All (10) torsion outliers are listed below:

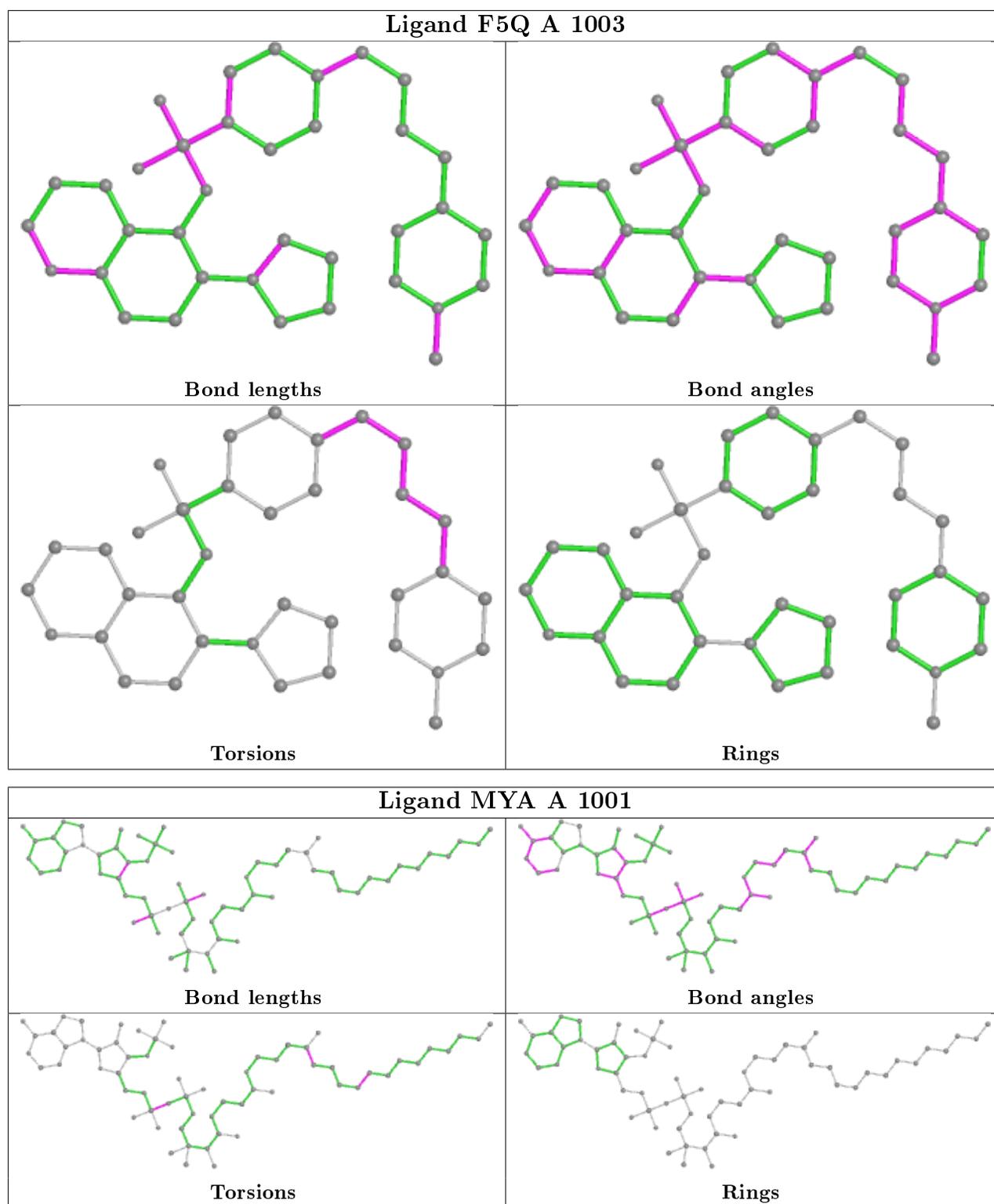
Mol	Chain	Res	Type	Atoms
4	A	1003	F5Q	C19-C20-C21-C22
4	A	1003	F5Q	C14-C17-C18-C19
4	A	1003	F5Q	C17-C18-C19-C20
4	A	1003	F5Q	C19-C20-C21-C25
4	A	1003	F5Q	C18-C19-C20-C21
2	A	1001	MYA	S1-C2M-C3M-C4M
4	A	1003	F5Q	C13-C14-C17-C18
4	A	1003	F5Q	C15-C14-C17-C18
2	A	1001	MYA	C5M-C6M-C7M-C8M
2	A	1001	MYA	P2A-O3A-P1A-O2A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1003	F5Q	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

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	411/411 (100%)	-0.08	20 (4%) 29 27	12, 19, 51, 83	3 (0%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	235	ILE	11.4
1	A	232	PHE	10.5
1	A	234	GLY	7.1
1	A	242	PHE	6.2
1	A	336	SER	5.9
1	A	237	ALA	5.9
1	A	233	SER	5.9
1	A	243	GLN	5.4
1	A	231	ARG	4.1
1	A	337	ASN	4.1
1	A	144	LYS	4.1
1	A	147	GLU	4.0
1	A	244	ASN	3.9
1	A	338	TYR	3.5
1	A	64	GLU	3.3
1	A	228	VAL	3.3
1	A	140	TYR	2.8
1	A	230	ILE	2.4
1	A	240	GLN	2.4
1	A	143	VAL	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

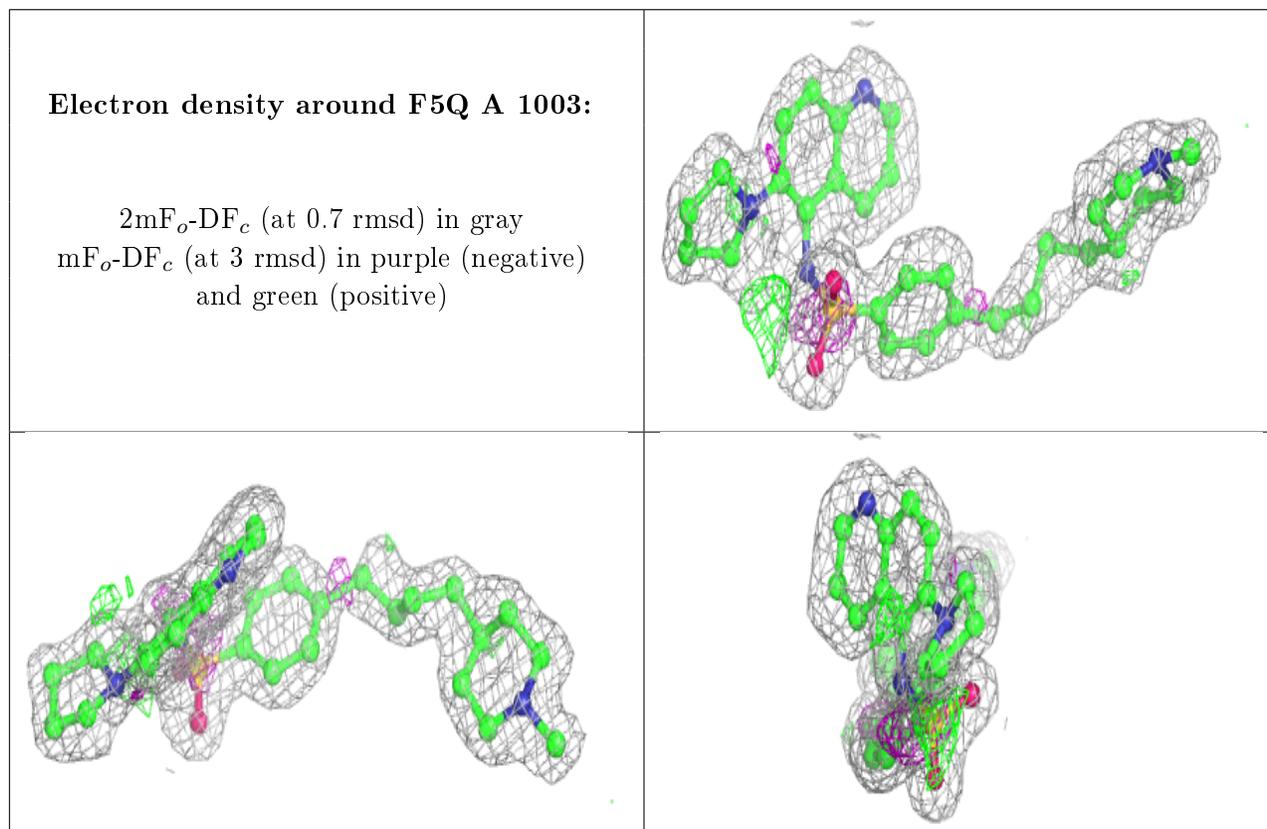
There are no carbohydrates in this entry.

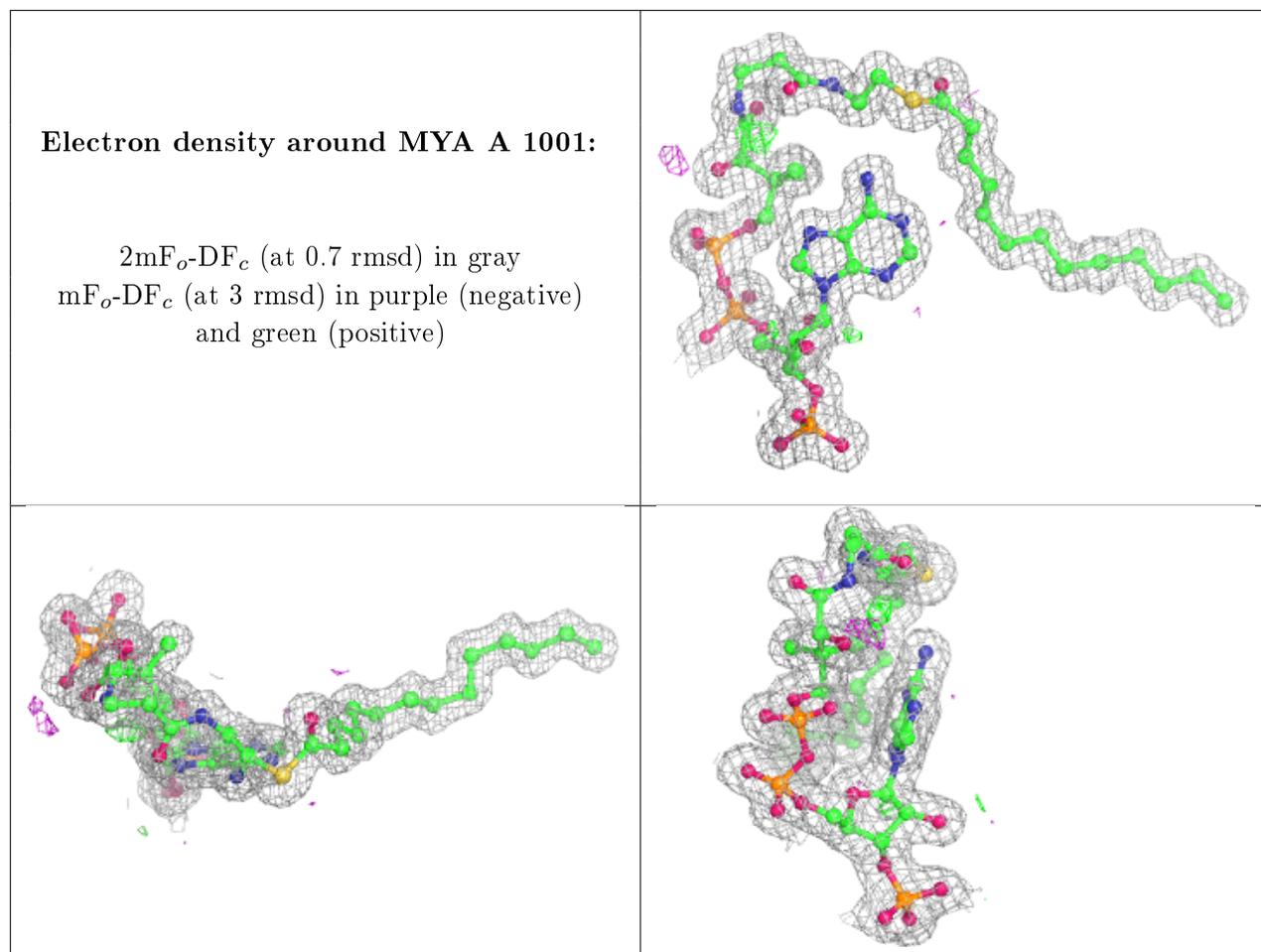
6.4 Ligands [i](#)

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
3	GOL	A	1002	6/6	0.92	0.14	22,29,30,31	0
4	F5Q	A	1003	36/36	0.94	0.09	16,22,30,35	0
2	MYA	A	1001	63/63	0.98	0.07	10,14,19,23	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.