



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 19, 2026 – 12:01 AM UTC

PDB ID : 5KMD / pdb_00005kmd
Title : Structure of CavAb in complex with amlodipine
Authors : Tang, L.; Gamal EL-Din, T.M.; Swanson, T.M.; Pryde, D.C.; Scheuer, T.;
Zheng, N.; Catterall, W.A.
Deposited on : 2016-06-26
Resolution : 3.20 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 ⓘ 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

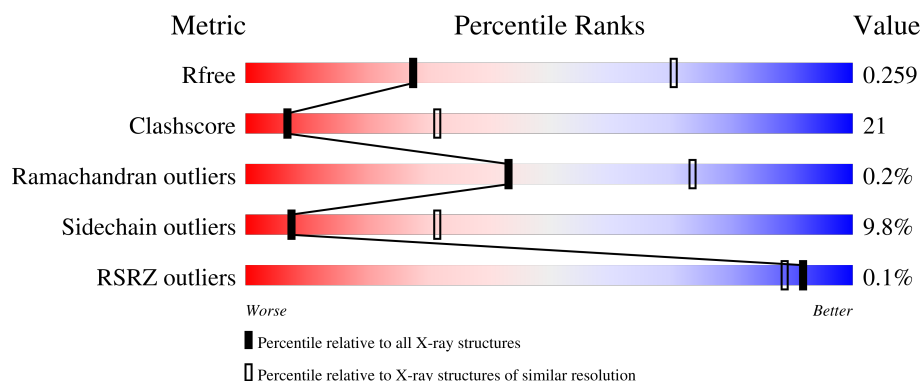
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	285	40% 31% 6% 23%
1	B	285	38% 33% 6% 23%
1	C	285	41% 31% 5% 23%
1	D	285	47% 25% 5% 23%

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	6UB	C	1304	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7380 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 Ion transport protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	0	0
			1798	1225	268	295	10			
1	B	219	Total	C	N	O	S	0	0	0
			1798	1225	268	295	10			
1	C	219	Total	C	N	O	S	0	0	0
			1798	1225	268	295	10			
1	D	219	Total	C	N	O	S	0	0	0
			1798	1225	268	295	10			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	983	MET	-	initiating methionine	UNP A8EVM5
A	984	ASP	-	expression tag	UNP A8EVM5
A	985	TYR	-	expression tag	UNP A8EVM5
A	986	LYS	-	expression tag	UNP A8EVM5
A	987	ASP	-	expression tag	UNP A8EVM5
A	988	ASP	-	expression tag	UNP A8EVM5
A	989	ASP	-	expression tag	UNP A8EVM5
A	990	ASP	-	expression tag	UNP A8EVM5
A	991	LYS	-	expression tag	UNP A8EVM5
A	992	GLY	-	expression tag	UNP A8EVM5
A	993	SER	-	expression tag	UNP A8EVM5
A	994	LEU	-	expression tag	UNP A8EVM5
A	995	VAL	-	expression tag	UNP A8EVM5
A	996	PRO	-	expression tag	UNP A8EVM5
A	997	ARG	-	expression tag	UNP A8EVM5
A	998	GLY	-	expression tag	UNP A8EVM5
A	999	SER	-	expression tag	UNP A8EVM5
A	1000	HIS	-	expression tag	UNP A8EVM5
A	1177	ASP	GLU	conflict	UNP A8EVM5
A	1178	ASP	SER	conflict	UNP A8EVM5
A	1181	ASN	MET	conflict	UNP A8EVM5

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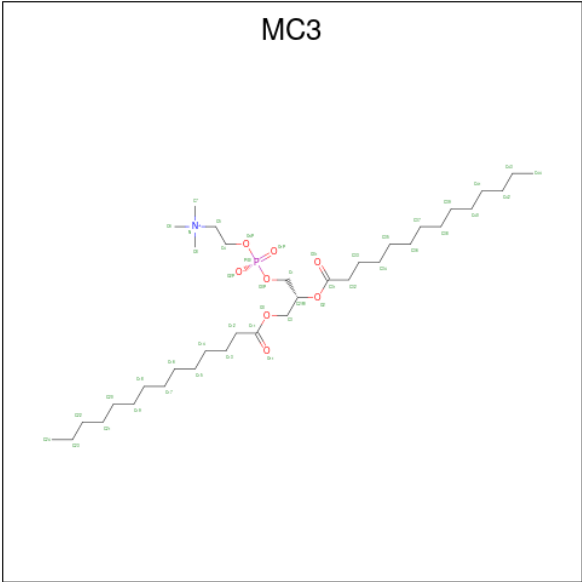
Chain	Residue	Modelled	Actual	Comment	Reference
A	1195	TYR	TRP	conflict	UNP A8EVM5
B	983	MET	-	initiating methionine	UNP A8EVM5
B	984	ASP	-	expression tag	UNP A8EVM5
B	985	TYR	-	expression tag	UNP A8EVM5
B	986	LYS	-	expression tag	UNP A8EVM5
B	987	ASP	-	expression tag	UNP A8EVM5
B	988	ASP	-	expression tag	UNP A8EVM5
B	989	ASP	-	expression tag	UNP A8EVM5
B	990	ASP	-	expression tag	UNP A8EVM5
B	991	LYS	-	expression tag	UNP A8EVM5
B	992	GLY	-	expression tag	UNP A8EVM5
B	993	SER	-	expression tag	UNP A8EVM5
B	994	LEU	-	expression tag	UNP A8EVM5
B	995	VAL	-	expression tag	UNP A8EVM5
B	996	PRO	-	expression tag	UNP A8EVM5
B	997	ARG	-	expression tag	UNP A8EVM5
B	998	GLY	-	expression tag	UNP A8EVM5
B	999	SER	-	expression tag	UNP A8EVM5
B	1000	HIS	-	expression tag	UNP A8EVM5
B	1177	ASP	GLU	conflict	UNP A8EVM5
B	1178	ASP	SER	conflict	UNP A8EVM5
B	1181	ASN	MET	conflict	UNP A8EVM5
B	1195	TYR	TRP	conflict	UNP A8EVM5
C	983	MET	-	initiating methionine	UNP A8EVM5
C	984	ASP	-	expression tag	UNP A8EVM5
C	985	TYR	-	expression tag	UNP A8EVM5
C	986	LYS	-	expression tag	UNP A8EVM5
C	987	ASP	-	expression tag	UNP A8EVM5
C	988	ASP	-	expression tag	UNP A8EVM5
C	989	ASP	-	expression tag	UNP A8EVM5
C	990	ASP	-	expression tag	UNP A8EVM5
C	991	LYS	-	expression tag	UNP A8EVM5
C	992	GLY	-	expression tag	UNP A8EVM5
C	993	SER	-	expression tag	UNP A8EVM5
C	994	LEU	-	expression tag	UNP A8EVM5
C	995	VAL	-	expression tag	UNP A8EVM5
C	996	PRO	-	expression tag	UNP A8EVM5
C	997	ARG	-	expression tag	UNP A8EVM5
C	998	GLY	-	expression tag	UNP A8EVM5
C	999	SER	-	expression tag	UNP A8EVM5
C	1000	HIS	-	expression tag	UNP A8EVM5
C	1177	ASP	GLU	conflict	UNP A8EVM5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1178	ASP	SER	conflict	UNP A8EVM5
C	1181	ASN	MET	conflict	UNP A8EVM5
C	1195	TYR	TRP	conflict	UNP A8EVM5
D	983	MET	-	initiating methionine	UNP A8EVM5
D	984	ASP	-	expression tag	UNP A8EVM5
D	985	TYR	-	expression tag	UNP A8EVM5
D	986	LYS	-	expression tag	UNP A8EVM5
D	987	ASP	-	expression tag	UNP A8EVM5
D	988	ASP	-	expression tag	UNP A8EVM5
D	989	ASP	-	expression tag	UNP A8EVM5
D	990	ASP	-	expression tag	UNP A8EVM5
D	991	LYS	-	expression tag	UNP A8EVM5
D	992	GLY	-	expression tag	UNP A8EVM5
D	993	SER	-	expression tag	UNP A8EVM5
D	994	LEU	-	expression tag	UNP A8EVM5
D	995	VAL	-	expression tag	UNP A8EVM5
D	996	PRO	-	expression tag	UNP A8EVM5
D	997	ARG	-	expression tag	UNP A8EVM5
D	998	GLY	-	expression tag	UNP A8EVM5
D	999	SER	-	expression tag	UNP A8EVM5
D	1000	HIS	-	expression tag	UNP A8EVM5
D	1177	ASP	GLU	conflict	UNP A8EVM5
D	1178	ASP	SER	conflict	UNP A8EVM5
D	1181	ASN	MET	conflict	UNP A8EVM5
D	1195	TYR	TRP	conflict	UNP A8EVM5

- Molecule 2 is 1,2-DIMYRISTOYL-RAC-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: MC3) (formula: C₃₆H₇₂NO₈P).



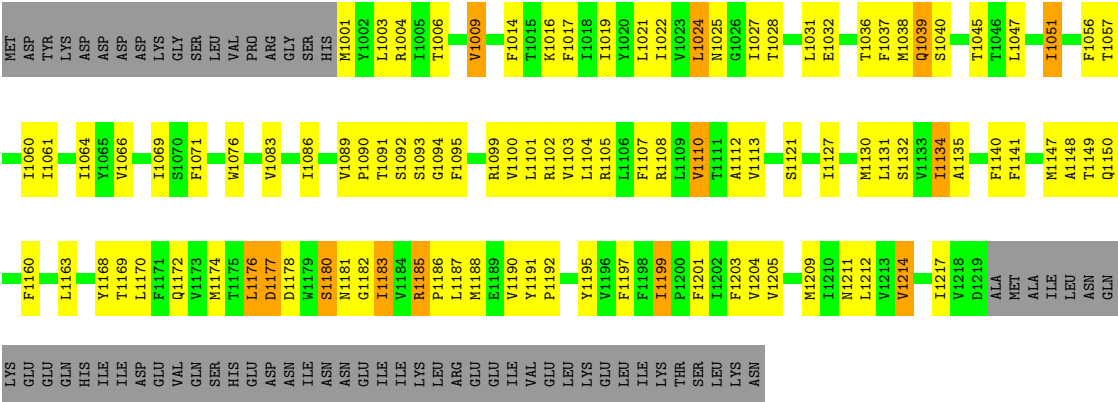
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C			0	0
			6	6				
2	A	1	Total	C			0	0
			6	6				
2	A	1	Total	C	O	P	0	0
			21	13	7	1		
2	A	1	Total	C	O	P	0	0
			21	13	7	1		
2	A	1	Total	C	O	P	0	0
			10	3	6	1		
2	A	1	Total	C	O	P	0	0
			10	3	6	1		
2	A	1	Total	C	O	P	0	0
			10	3	6	1		
2	B	1	Total	C			0	0
			6	6				
2	B	1	Total	C	O	P	0	0
			21	13	7	1		
2	B	1	Total	C	O	P	0	0
			10	3	6	1		
2	C	1	Total	C	O	P	0	0
			10	3	6	1		
2	C	1	Total	C	O	P	0	0
			10	3	6	1		
2	D	1	Total	C			0	0
			6	6				
2	D	1	Total	C	O	P	0	0
			10	3	6	1		

- | Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|-----------------|---------|---------|
| 3 | C | 1 | Total Ca
1 1 | 0 | 0 |
| 3 | D | 1 | Total Ca
1 1 | 0 | 0 |

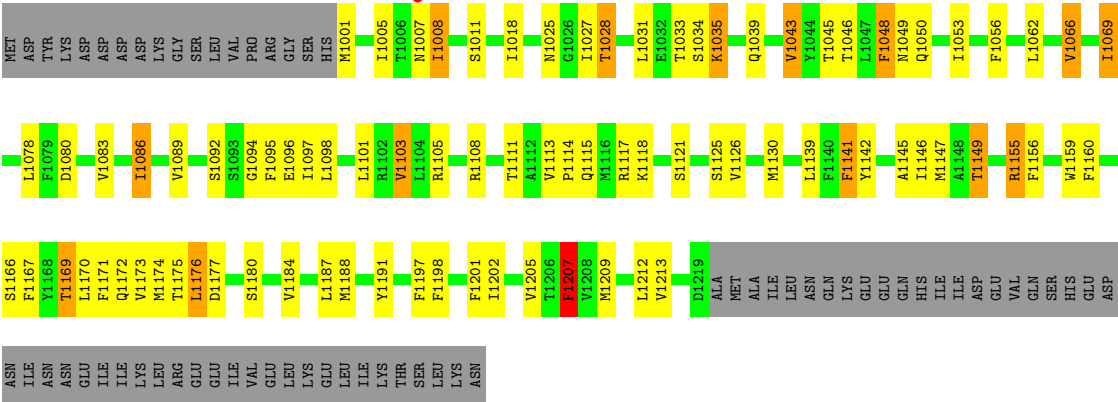
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- The chemical structure of 6UB (6-aminouracil) is shown in its tautomeric form. The structure features a pyrimidine ring with an amino group (NH₂) at the 6-position. The ring is connected to a side chain that includes a carbonyl group (C=O) and a methylene group (CH₂). The side chain is further connected to a methylene group (CH₂) and an amino group (NH₂). The structure is labeled with various residues and atoms, including N28, C24, C26, C27, O25, OAF, OAS, CAL, CAA, CAI, CAJ, CAZ, CBA, CAX, CAY, CAV, CBB(S), CAC, CAT, CAU, OAE, OAG, OAP, and CAB. The structure is shown in a 3D representation with a black wedge bond indicating stereochemistry.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	C	1	Total	C	Cl	N	O	0	0
			28	20	1	2	5		

- | Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|----------------|---------|---------|
| 5 | C | 1 | Total O
1 1 | 0 | 0 |



● Molecule 1: Ion transport protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants a, b, c, α , β , γ	125.64Å 125.53Å 191.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.85 – 3.20 29.85 – 3.20	Depositor EDS
% Data completeness (in resolution range)	86.4 (29.85-3.20) 86.4 (29.85-3.20)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 3.11Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.233 , 0.277 0.212 , 0.259	Depositor DCC
R_{free} test set	2353 reflections (4.22%)	wwPDB-VP
Wilson B-factor (Å ²)	77.4	Xtriage
Anisotropy	0.465	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 59.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.440 for k,h,-l	Xtriage
Reported twinning fraction	0.500 for H, K, L 0.500 for K, H, -L	Depositor
Outliers	0 of 48489 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7380	wwPDB-VP
Average B, all atoms (Å ²)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.30% 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: 6UB, MC3, CA

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	0.90	1/1848 (0.1%)	1.27	15/2515 (0.6%)
1	B	0.81	1/1848 (0.1%)	1.25	7/2515 (0.3%)
1	C	0.89	1/1848 (0.1%)	1.31	15/2515 (0.6%)
1	D	0.80	1/1848 (0.1%)	1.25	9/2515 (0.4%)
All	All	0.85	4/7392 (0.1%)	1.27	46/10060 (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	B	0	1
1	D	0	1
All	All	0	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1169	THR	CA-C	5.93	1.60	1.52
1	C	1180	SER	C-O	5.83	1.28	1.23
1	B	1181	ASN	C-O	-5.72	1.17	1.24
1	D	1169	THR	CA-CB	5.09	1.61	1.53

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1181	ASN	N-CA-C	-9.72	100.54	111.82
1	B	1068	ARG	CB-CA-C	-8.35	106.94	116.54
1	C	1181	ASN	N-CA-C	-7.67	102.89	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	1180	SER	N-CA-C	7.54	122.72	111.04
1	C	1178	ASP	N-CA-C	-7.36	101.22	111.52

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	1181	ASN	Mainchain
1	D	1207	PHE	Mainchain

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	1798	0	1868	97	0
1	B	1798	0	1868	113	0
1	C	1798	0	1868	66	0
1	D	1798	0	1868	66	0
2	A	84	0	69	7	0
2	B	37	0	32	6	0
2	C	20	0	10	0	0
2	D	16	0	13	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	C	28	0	0	1	0
5	C	1	0	0	0	0
All	All	7380	0	7596	317	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 21.

The worst 5 of 317 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:B:1002:TYR:HA	1:B:1004:ARG:HH11	1.17	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1005:ILE:O	1:A:1008:ILE:HG22	1.57	1.03
1:B:1174:MET:HG3	1:B:1205:VAL:HG11	1.36	1.02
1:A:1108:ARG:O	1:A:1111:THR:HG22	1.69	0.91
1:B:1002:TYR:HA	1:B:1004:ARG:NH1	1.87	0.90

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	217/285 (76%)	205 (94%)	12 (6%)	0	100	100
1	B	217/285 (76%)	212 (98%)	5 (2%)	0	100	100
1	C	217/285 (76%)	204 (94%)	12 (6%)	1 (0%)	24	59
1	D	217/285 (76%)	205 (94%)	11 (5%)	1 (0%)	24	59
All	All	868/1140 (76%)	826 (95%)	40 (5%)	2 (0%)	43	73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	1094	GLY
1	C	1131	LEU

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	202/264 (76%)	183 (91%)	19 (9%)	8	33
1	B	202/264 (76%)	178 (88%)	24 (12%)	5	23
1	C	202/264 (76%)	187 (93%)	15 (7%)	13	43
1	D	202/264 (76%)	181 (90%)	21 (10%)	7	28
All	All	808/1056 (76%)	729 (90%)	79 (10%)	7	31

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1199	ILE
1	D	1126	VAL
1	D	1028	THR
1	D	1069	ILE
1	D	1166	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1050	GLN
1	C	1067	HIS

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](#)

Of 17 ligands modelled in this entry, 2 are monoatomic - leaving 15 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
4	6UB	C	1304	-	28,29,29	4.48	14 (50%)	38,39,39	5.64	22 (57%)
2	MC3	A	1306	-	9,9,45	1.02	1 (11%)	10,12,53	0.95	0
2	MC3	B	1302	-	20,20,45	1.95	3 (15%)	22,24,53	1.49	2 (9%)
2	MC3	B	1303	-	9,9,45	1.14	1 (11%)	10,12,53	0.94	1 (10%)
2	MC3	A	1301	-	5,5,45	0.38	0	4,4,53	0.40	0
2	MC3	C	1303	-	9,9,45	1.00	0	10,12,53	0.94	0
2	MC3	B	1301	-	5,5,45	0.51	0	4,4,53	0.64	0
2	MC3	A	1305	-	9,9,45	0.96	0	10,12,53	1.28	1 (10%)
2	MC3	D	1303	-	9,9,45	0.97	1 (11%)	10,12,53	0.77	0
2	MC3	C	1302	-	9,9,45	1.17	1 (11%)	10,12,53	1.28	1 (10%)
2	MC3	A	1303	-	20,20,45	1.85	5 (25%)	22,24,53	1.60	3 (13%)
2	MC3	A	1307	-	9,9,45	0.91	0	10,12,53	1.14	0
2	MC3	A	1304	-	20,20,45	1.80	3 (15%)	22,24,53	1.57	2 (9%)
2	MC3	D	1302	-	5,5,45	0.58	0	4,4,53	0.31	0
2	MC3	A	1302	-	5,5,45	0.67	0	4,4,53	0.37	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	6UB	C	1304	-	-	17/22/42/42	0/2/2/2
2	MC3	A	1306	-	-	4/8/8/49	-
2	MC3	B	1302	-	-	12/22/22/49	-
2	MC3	B	1303	-	-	8/8/8/49	-
2	MC3	A	1301	-	-	0/3/3/49	-
2	MC3	C	1303	-	-	3/8/8/49	-
2	MC3	B	1301	-	-	1/3/3/49	-
2	MC3	A	1305	-	-	3/8/8/49	-
2	MC3	D	1303	-	-	4/8/8/49	-
2	MC3	C	1302	-	-	4/8/8/49	-
2	MC3	A	1303	-	-	14/22/22/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	A	1307	-	-	5/8/8/49	-
2	MC3	A	1304	-	-	10/22/22/49	-
2	MC3	D	1302	-	-	2/3/3/49	-
2	MC3	A	1302	-	-	2/3/3/49	-

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1304	6UB	CAU-CAX	10.34	1.66	1.47
4	C	1304	6UB	CAT-NAP	9.80	1.51	1.38
4	C	1304	6UB	CAW-NAP	9.57	1.52	1.37
4	C	1304	6UB	CBA-CBB	9.14	1.66	1.53
2	B	1302	MC3	O11-C11	6.44	1.41	1.22

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1304	6UB	CAT-NAP-CAW	-25.90	100.58	122.35
4	C	1304	6UB	CBB-CAX-CAT	-9.55	110.01	120.86
4	C	1304	6UB	OAQ-CAU-CAX	7.21	125.57	112.31
4	C	1304	6UB	CBA-CBB-CAX	7.15	125.16	110.95
4	C	1304	6UB	CBA-CAZ-CLAG	6.64	127.21	120.41

There are no chirality outliers.

5 of 89 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1303	MC3	C1-O3P-P-O1P
2	A	1303	MC3	C1-O3P-P-O2P
2	A	1303	MC3	C1-O3P-P-O4P
2	A	1303	MC3	C4-O4P-P-O1P
2	A	1303	MC3	C4-O4P-P-O2P

There are no ring outliers.

7 monomers are involved in 14 short contacts:

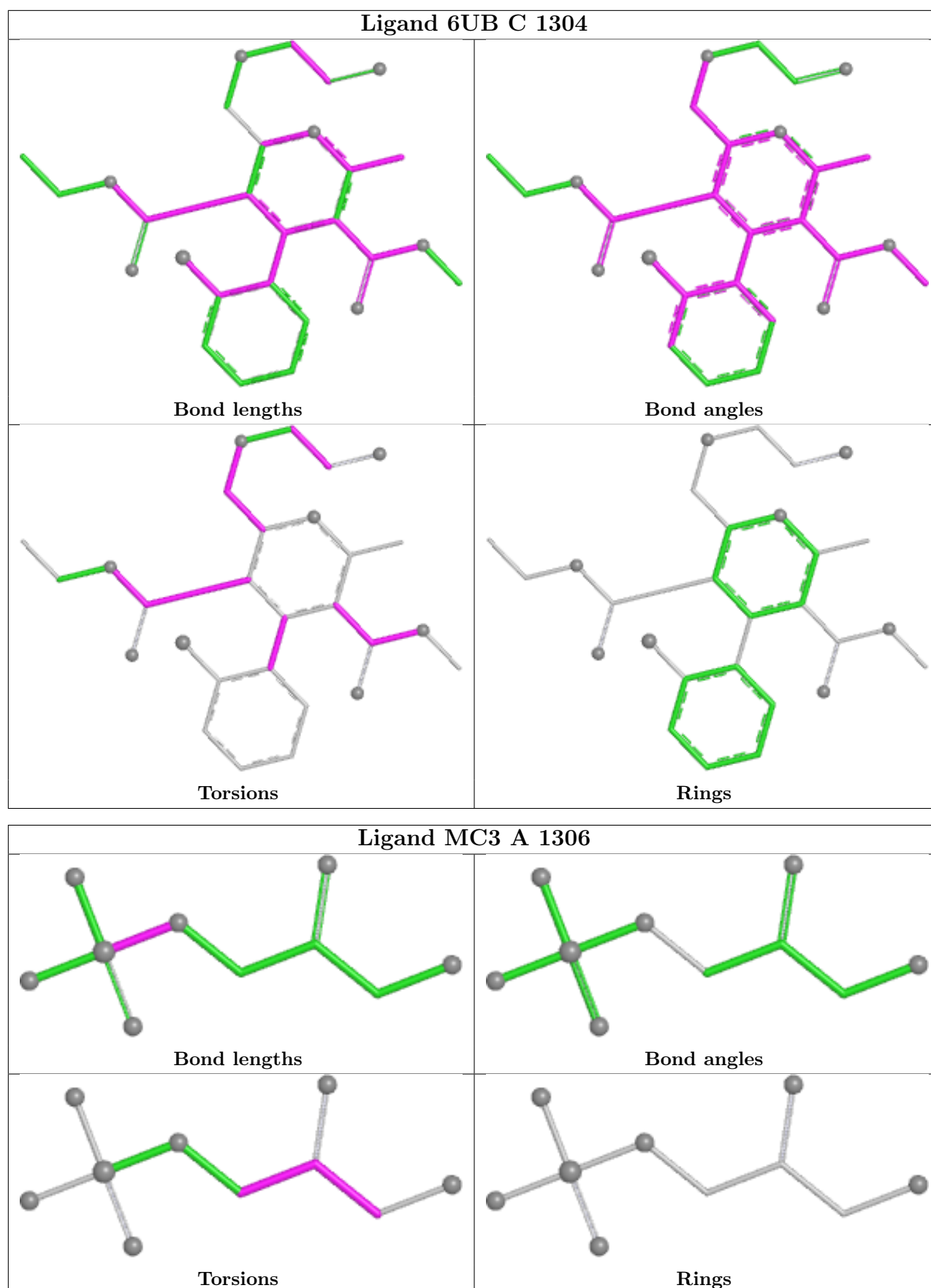
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	1304	6UB	1	0
2	B	1302	MC3	1	0
2	B	1303	MC3	4	0

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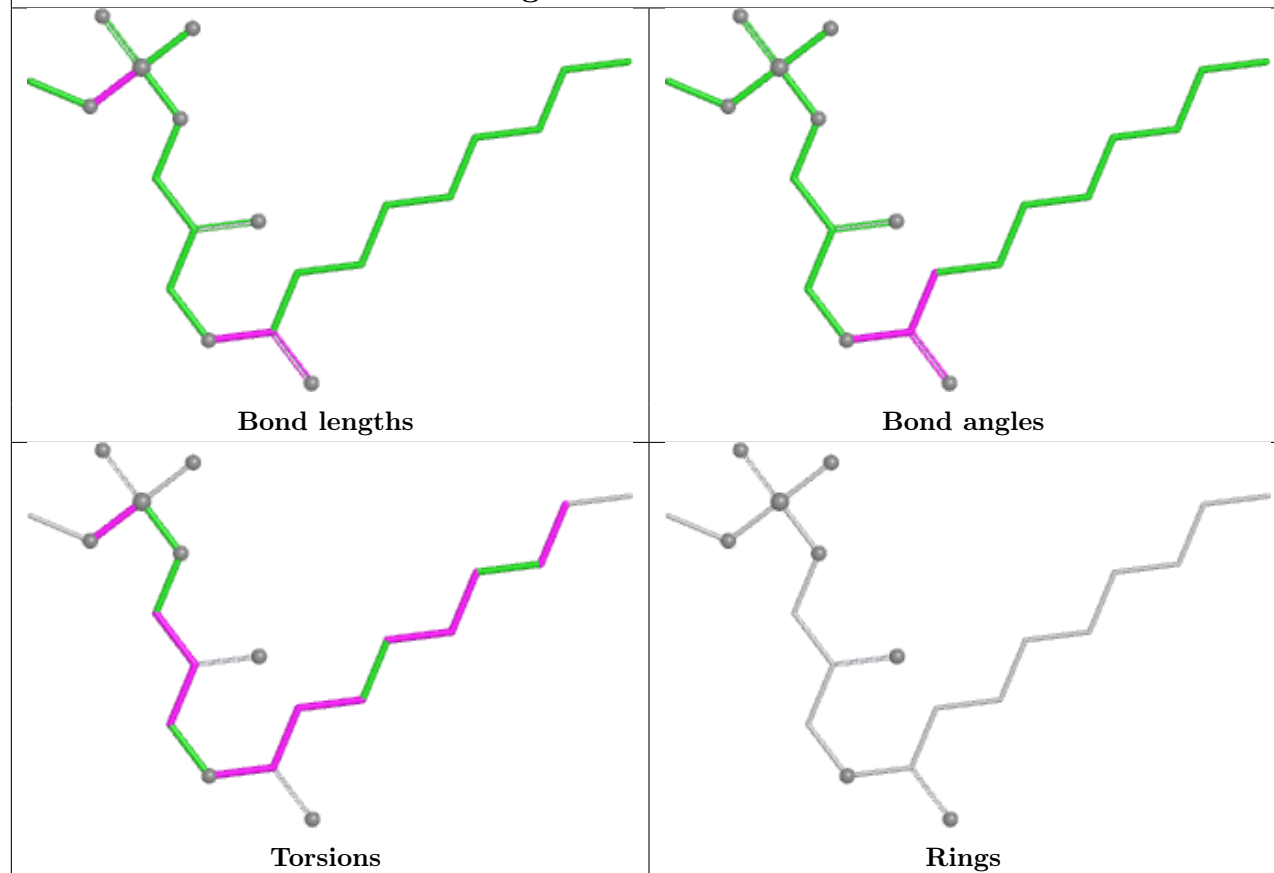
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1301	MC3	1	0
2	A	1303	MC3	3	0
2	A	1304	MC3	2	0
2	A	1302	MC3	2	0

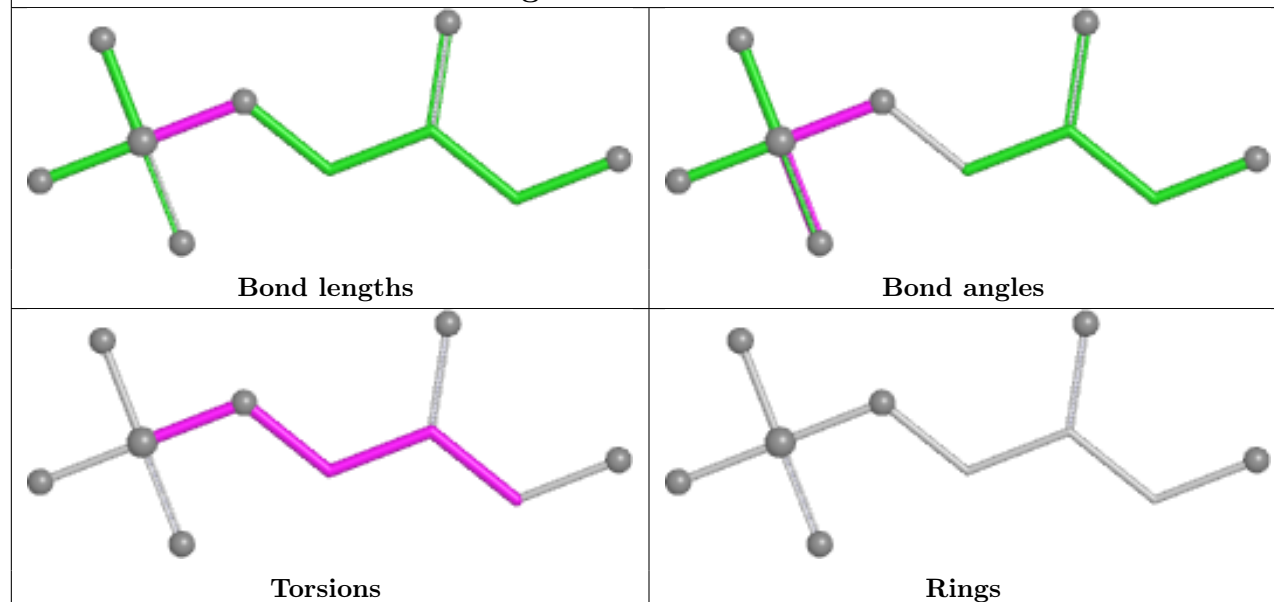
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

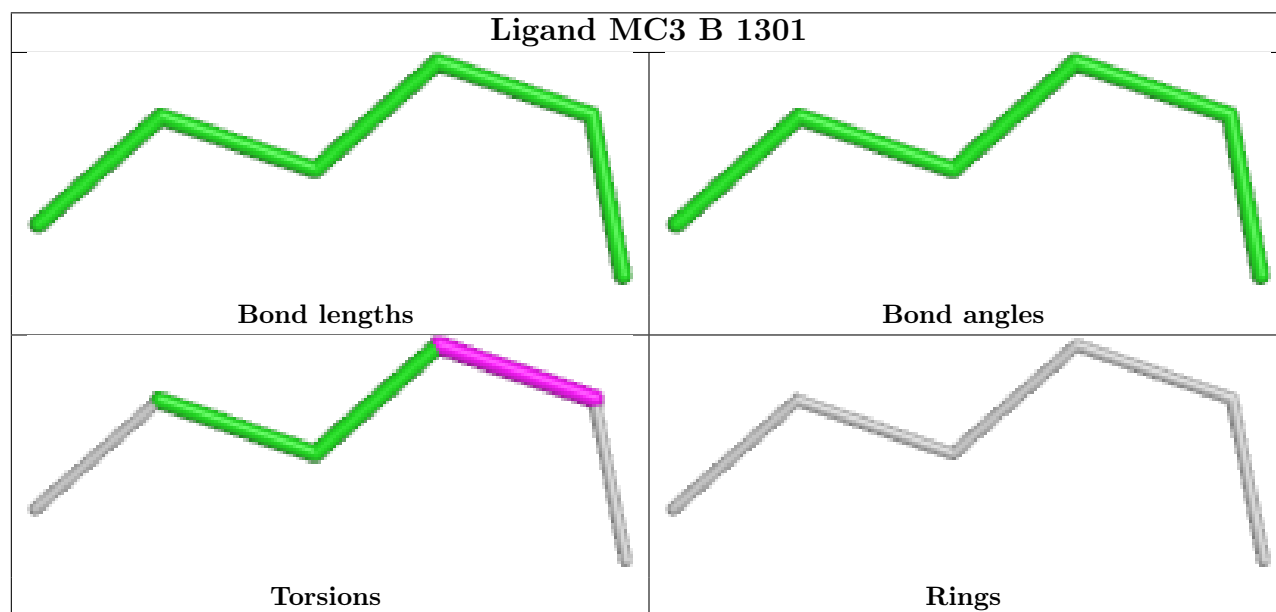
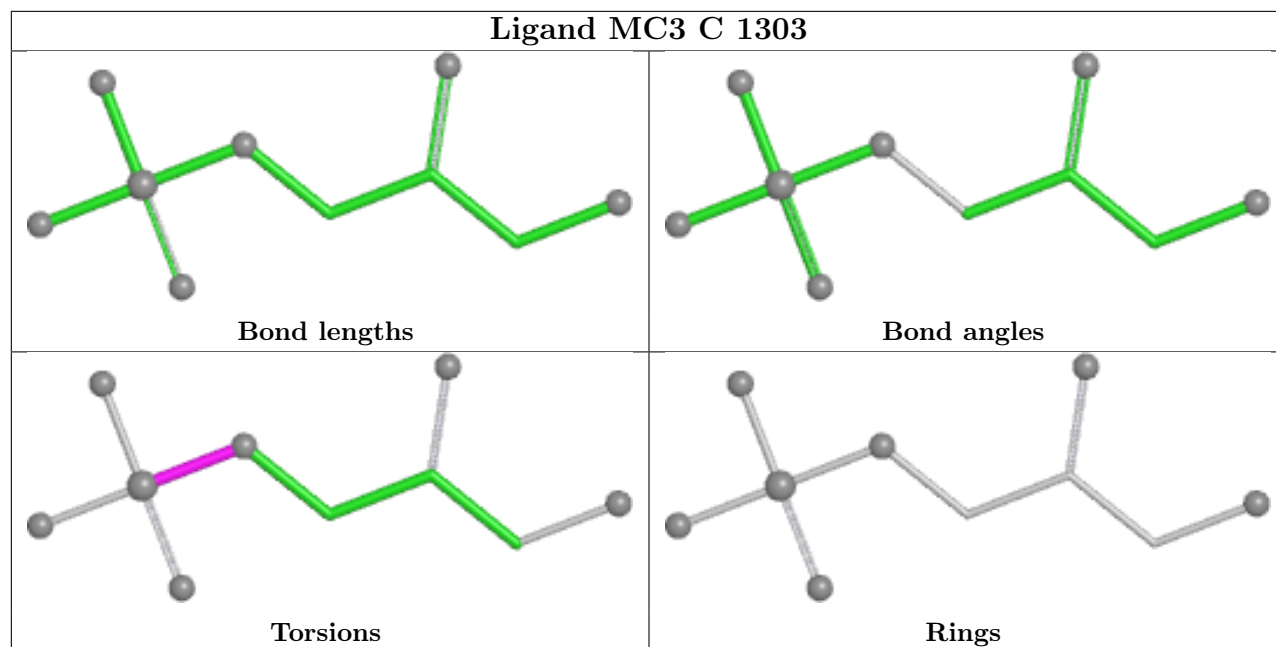


Ligand MC3 B 1302

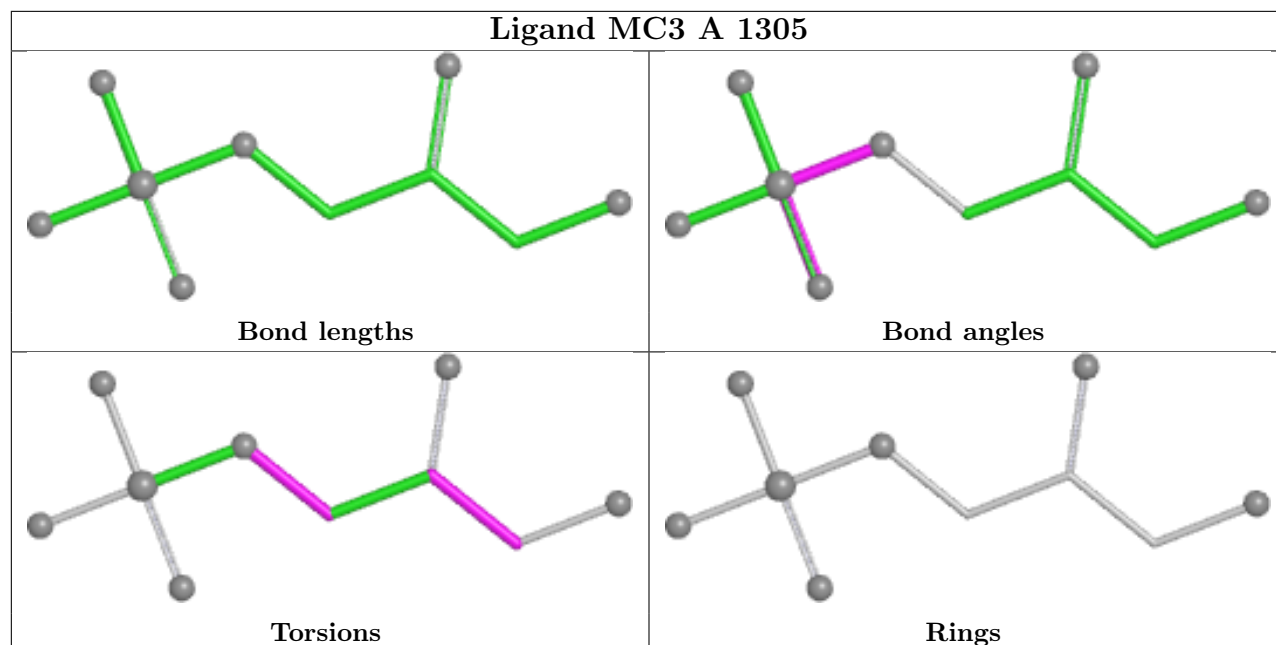


Ligand MC3 B 1303

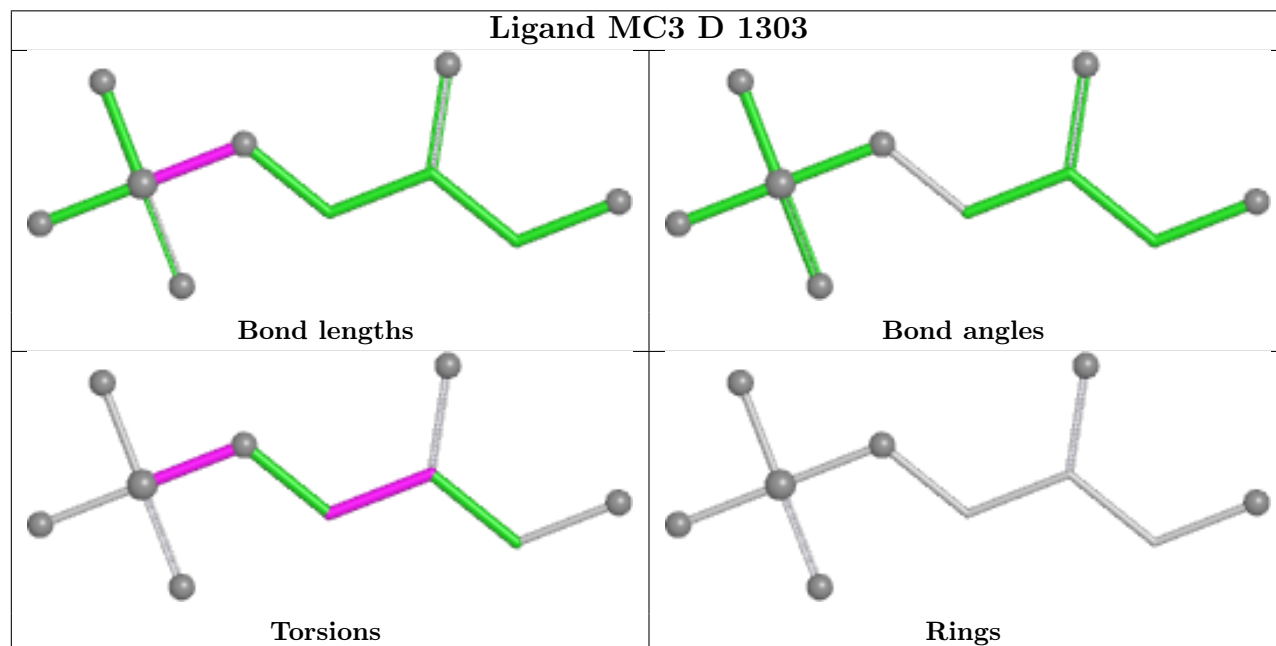


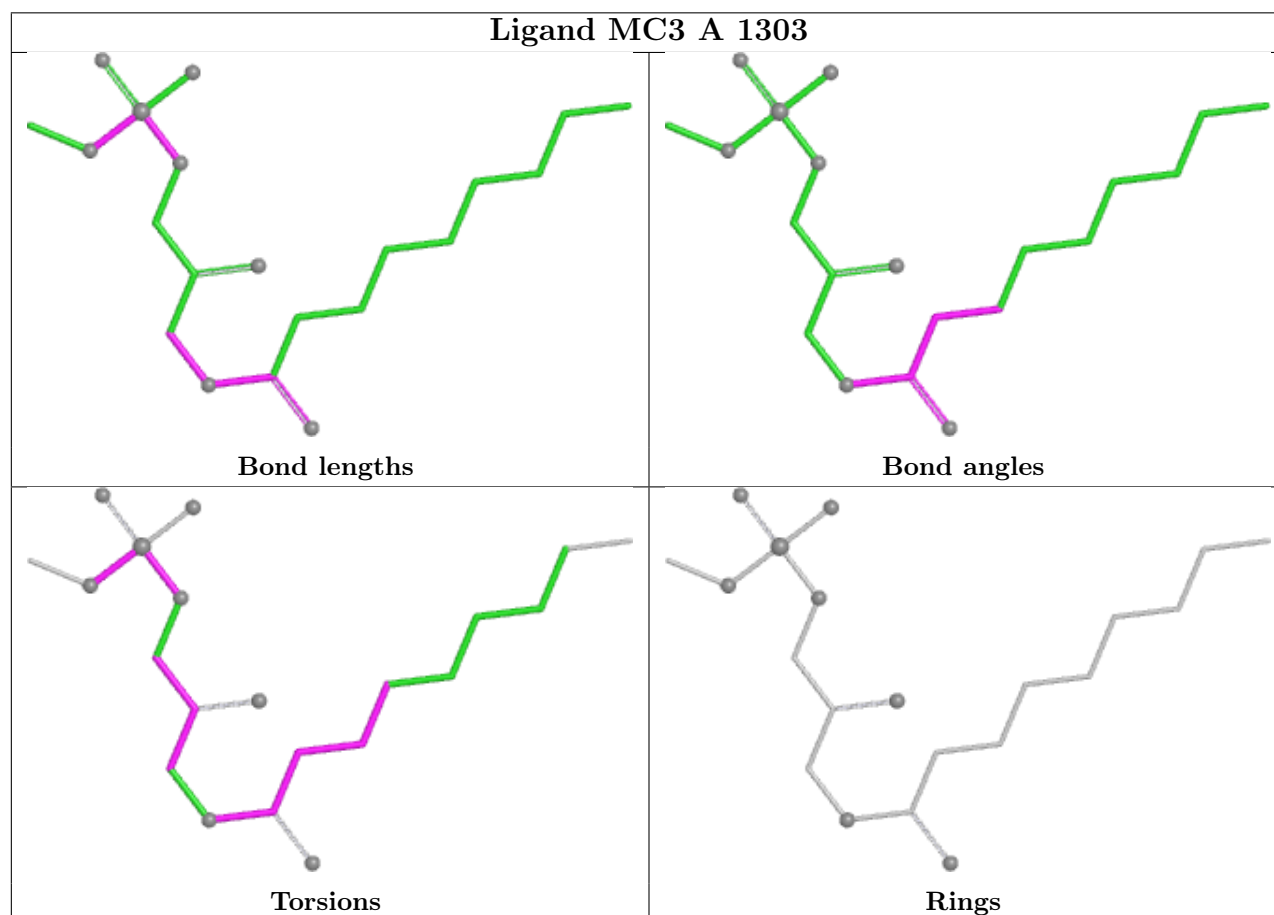
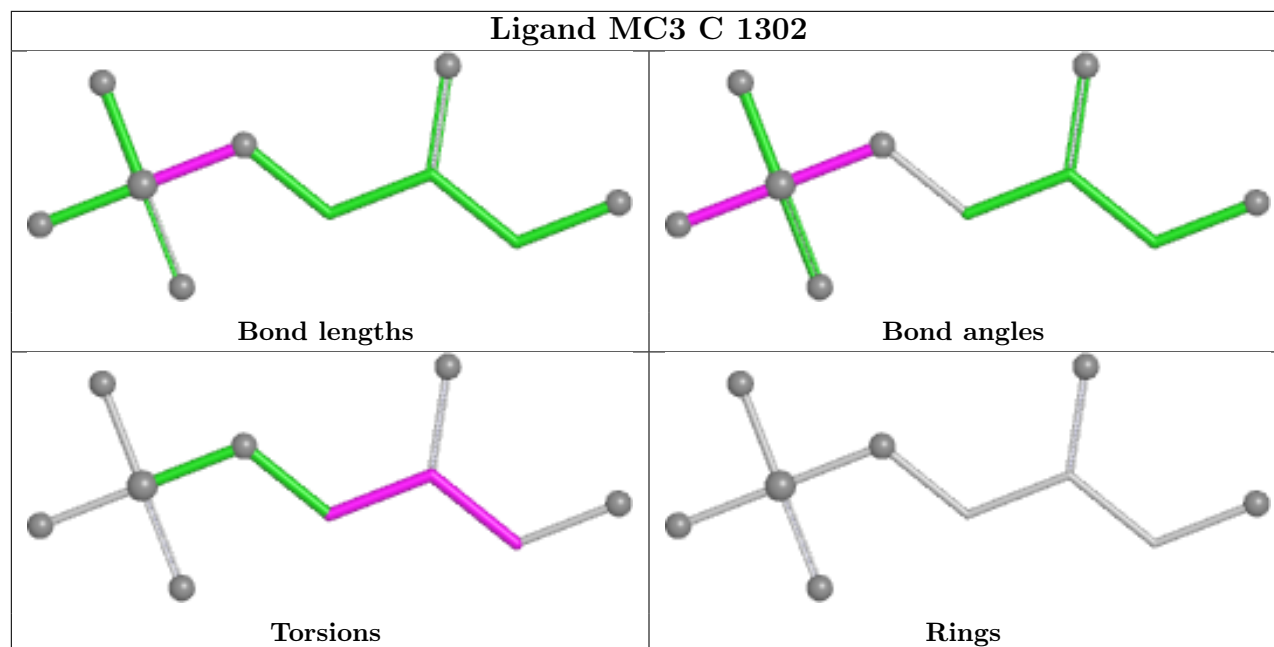


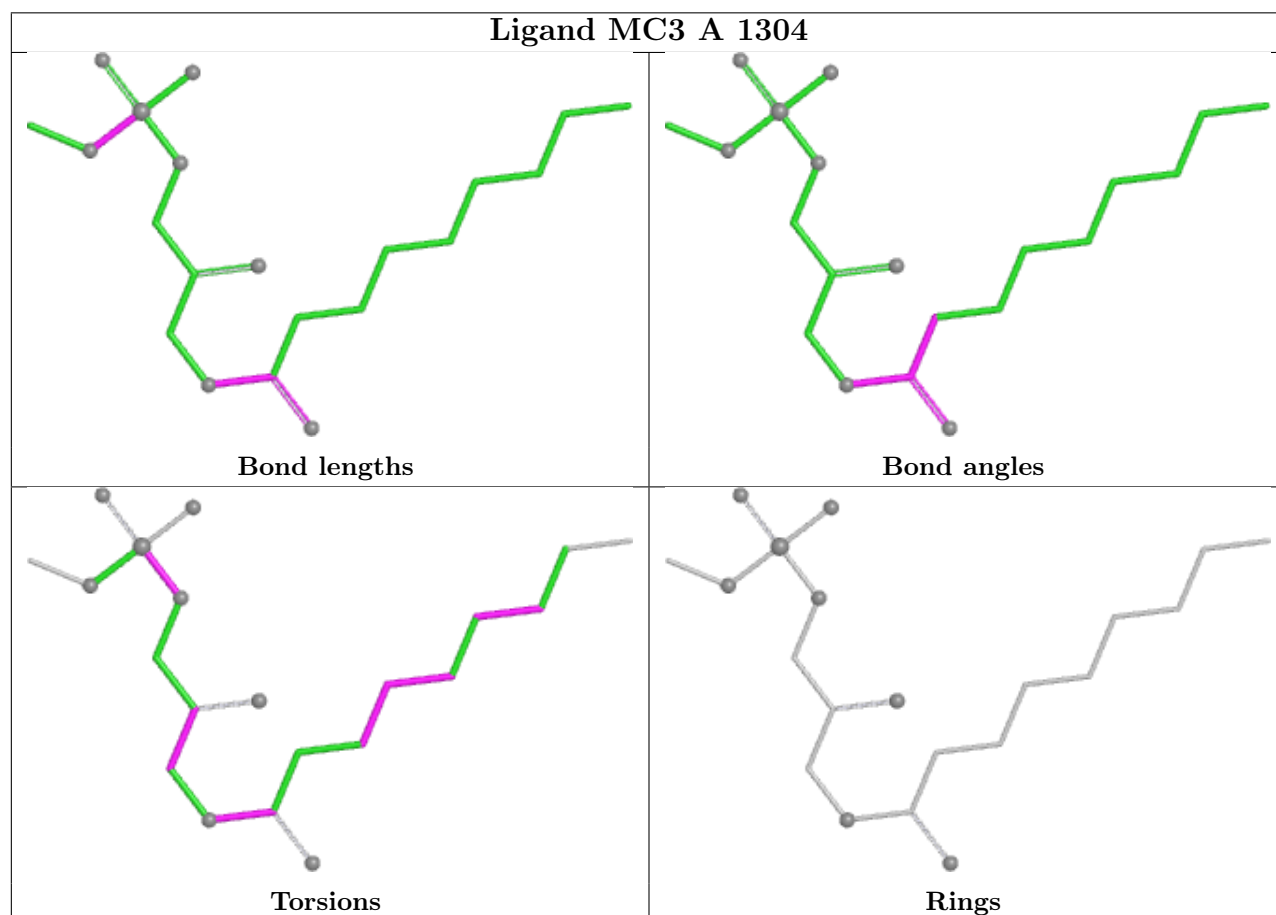
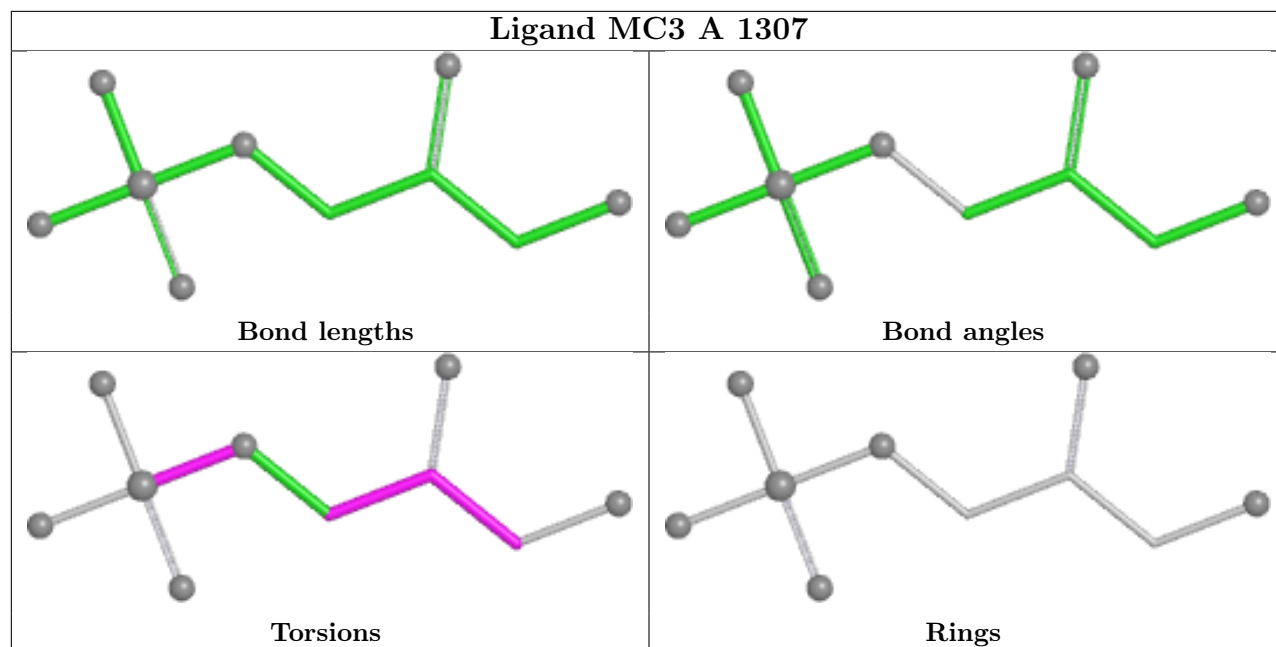
Ligand MC3 A 1305

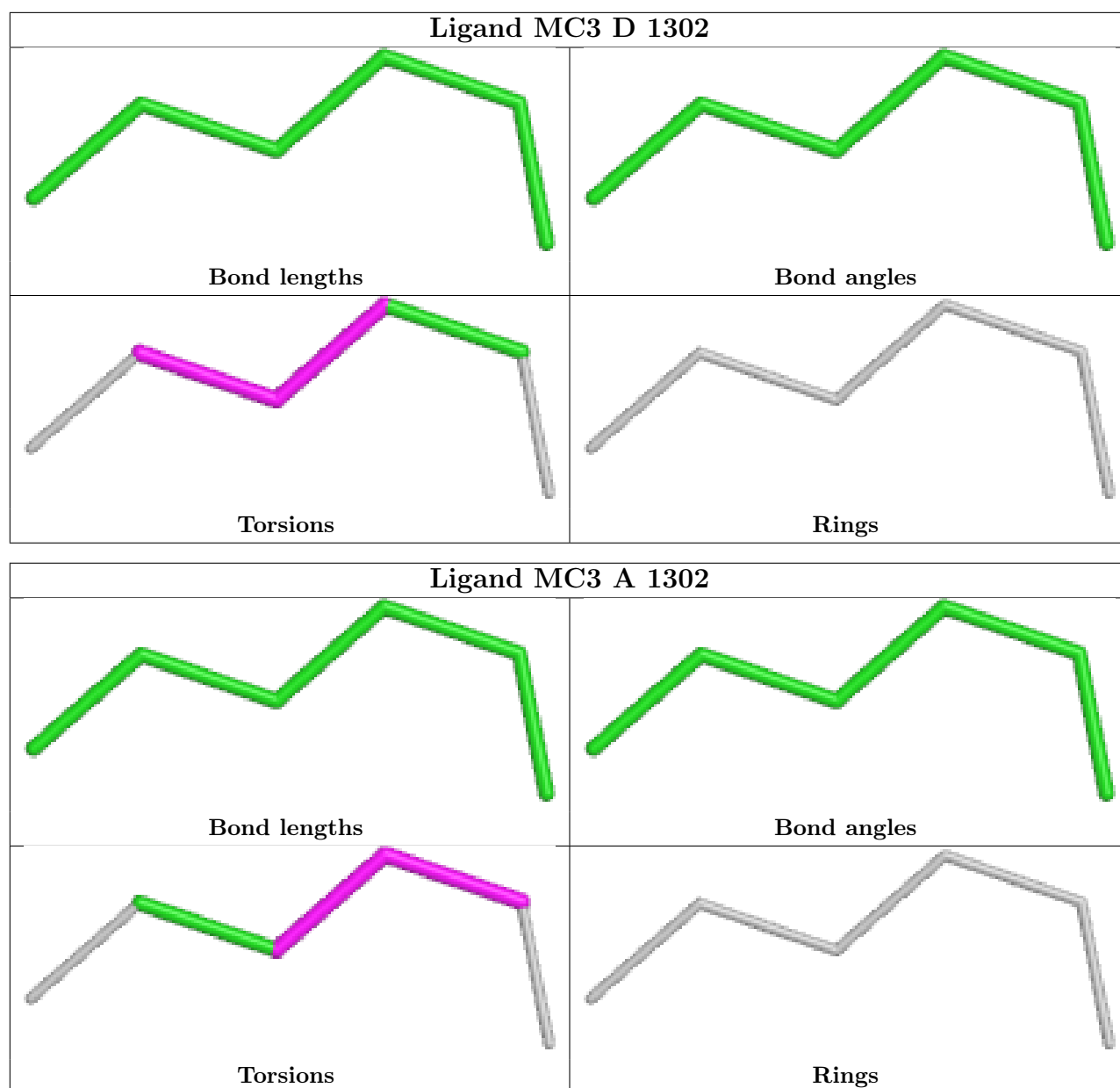


Ligand MC3 D 1303









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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	219/285 (76%)	-1.17	0 100 100	16, 101, 174, 220	0
1	B	219/285 (76%)	-1.21	0 100 100	24, 103, 161, 191	0
1	C	219/285 (76%)	-1.18	0 100 100	21, 101, 164, 199	0
1	D	219/285 (76%)	-1.16	1 (0%) 87 76	24, 103, 158, 201	0
All	All	876/1140 (76%)	-1.18	1 (0%) 92 89	16, 102, 165, 220	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	1007	ASN	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 oligosaccharides 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
2	MC3	A	1301	6/46	0.97	0.08	28,36,41,44	0

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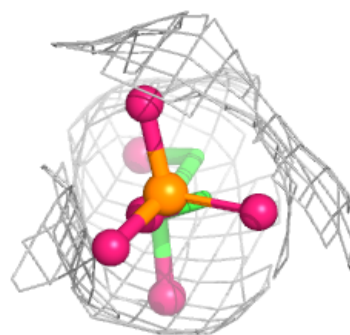
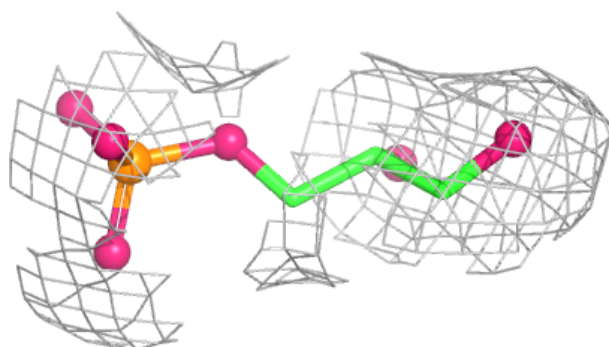
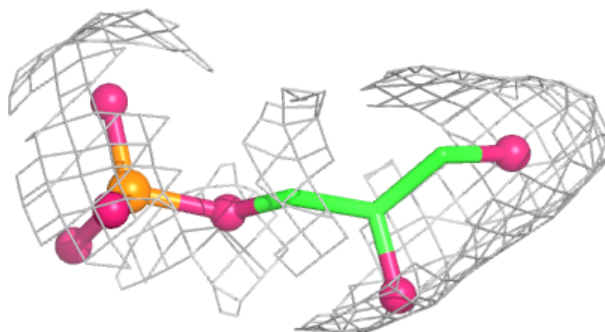
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MC3	D	1303	10/46	0.97	0.04	81,112,129,133	0
2	MC3	B	1303	10/46	0.98	0.05	58,68,104,113	0
2	MC3	C	1303	10/46	0.98	0.06	90,107,113,115	0
2	MC3	D	1302	6/46	0.98	0.09	34,36,43,46	0
2	MC3	A	1306	10/46	0.98	0.06	93,115,124,127	0
2	MC3	A	1307	10/46	0.99	0.05	103,116,125,130	0
2	MC3	B	1301	6/46	0.99	0.05	18,22,26,27	0
2	MC3	B	1302	21/46	0.99	0.06	57,67,88,95	0
2	MC3	A	1303	21/46	0.99	0.05	60,86,107,116	0
2	MC3	C	1302	10/46	0.99	0.06	57,81,109,109	0
2	MC3	A	1304	21/46	0.99	0.05	44,66,83,85	0
2	MC3	A	1305	10/46	0.99	0.03	60,89,114,118	0
2	MC3	A	1302	6/46	0.99	0.05	25,28,35,37	0
3	CA	C	1301	1/1	0.99	0.03	56,56,56,56	0
3	CA	D	1301	1/1	0.99	0.03	39,39,39,39	0
4	6UB	C	1304	28/28	0.99	0.07	45,87,115,121	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.

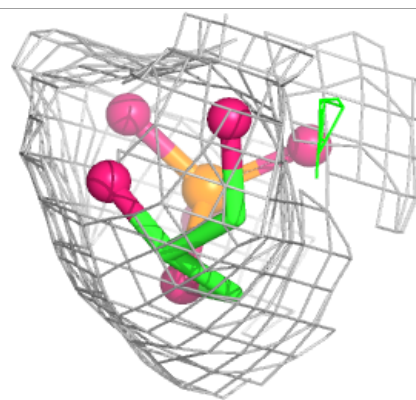
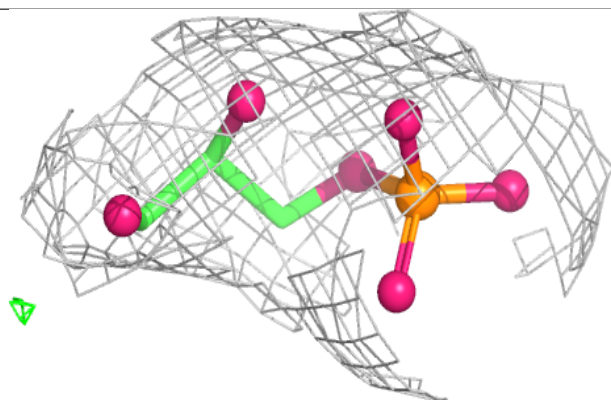
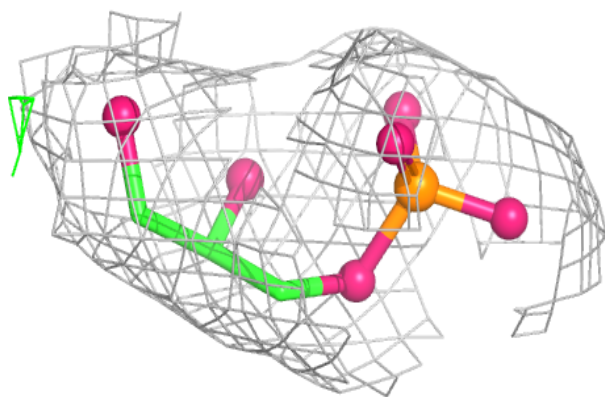
Electron density around MC3 D 1303:

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

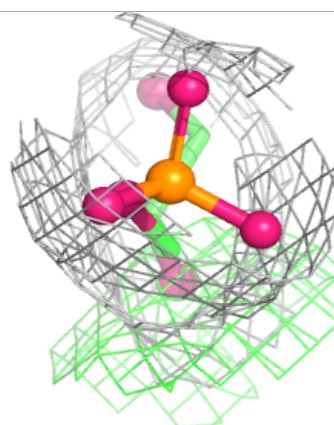
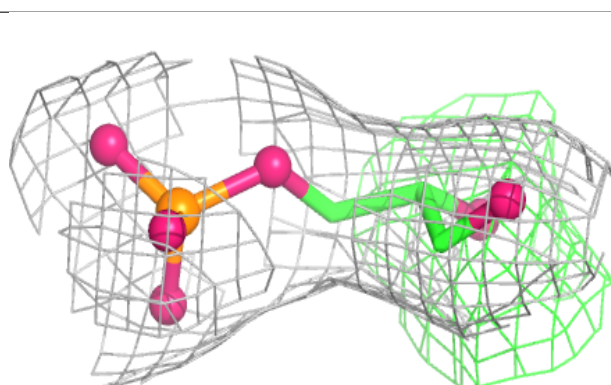
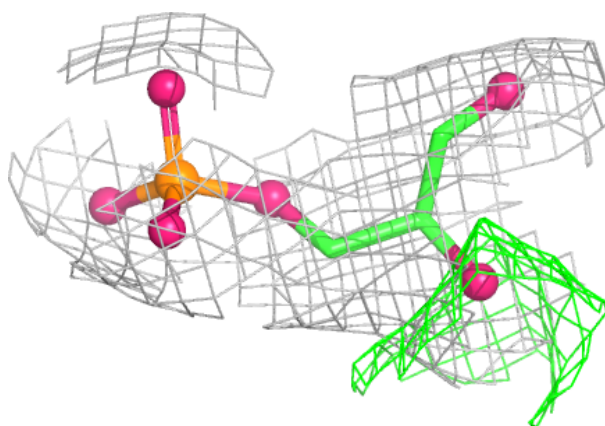


Electron density around MC3 B 1303:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

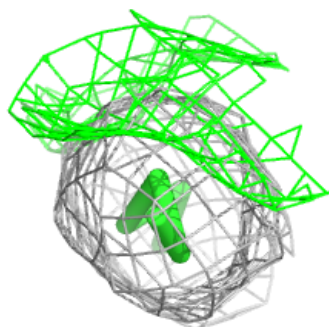
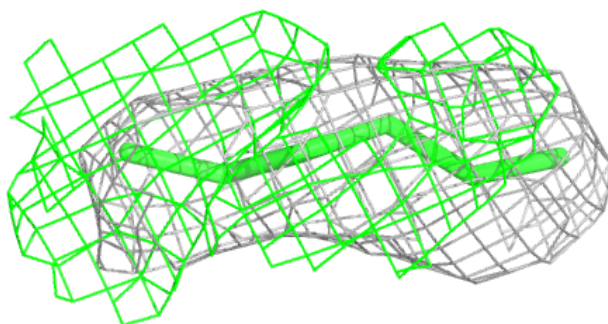
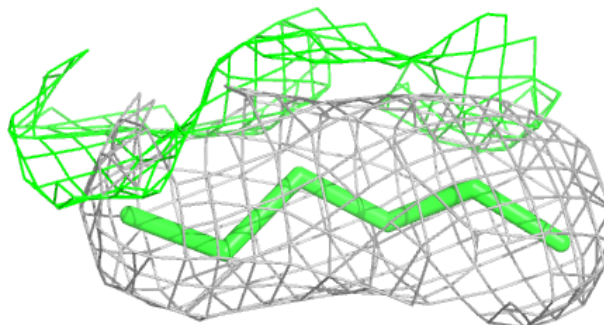
**Electron density around MC3 C 1303:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

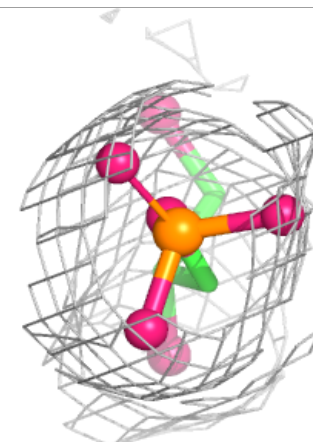
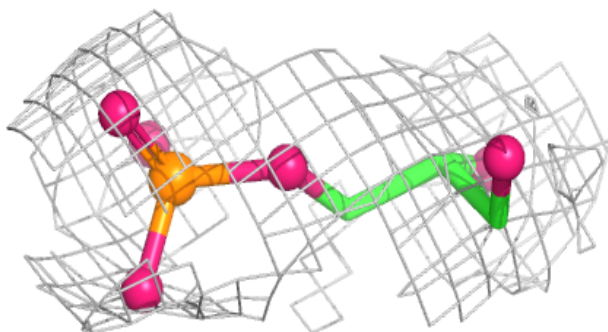
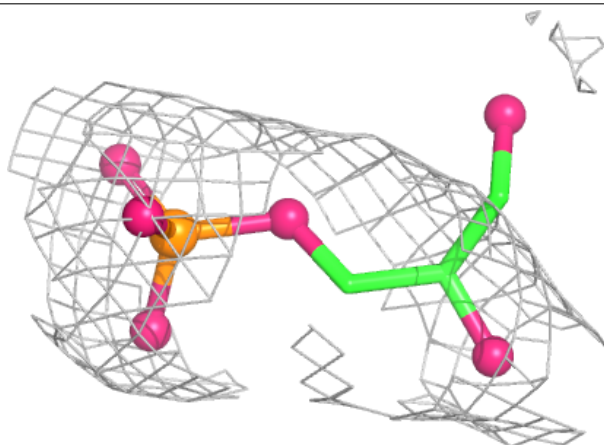


Electron density around MC3 D 1302:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

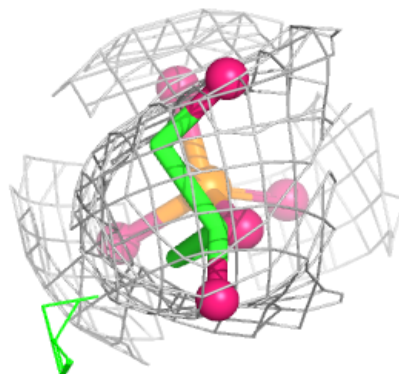
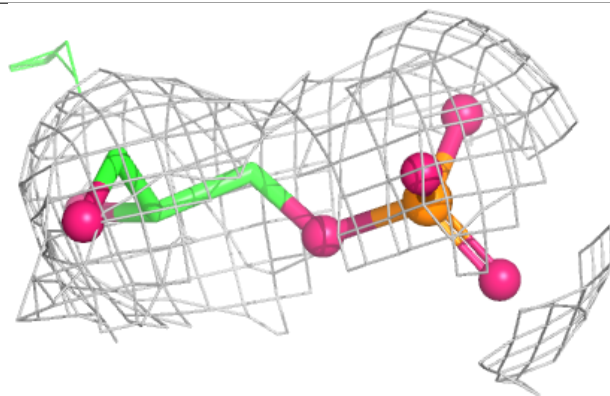
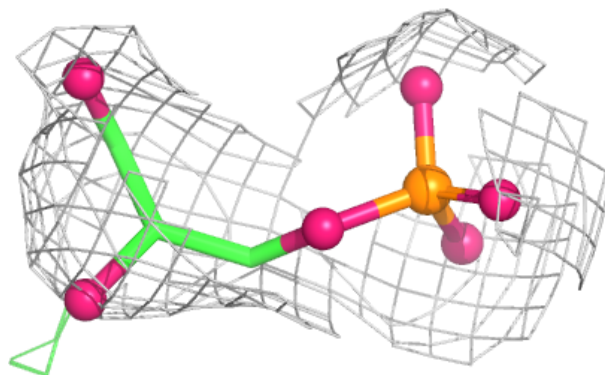
**Electron density around MC3 A 1306:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

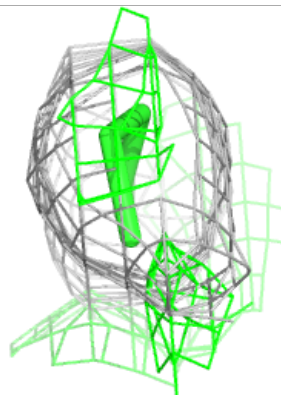
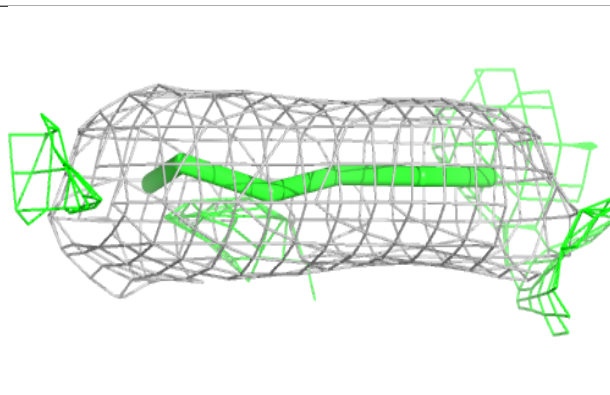
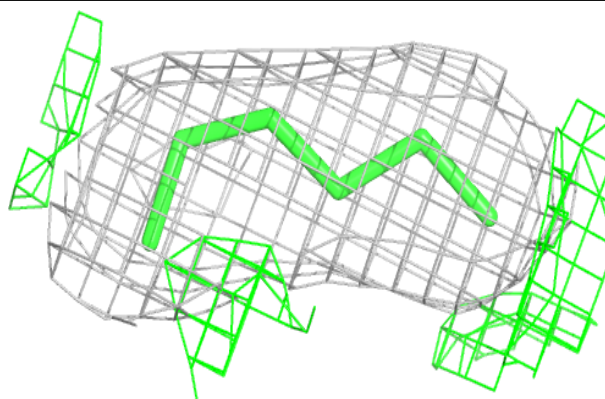


Electron density around MC3 A 1307:

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and green (positive)

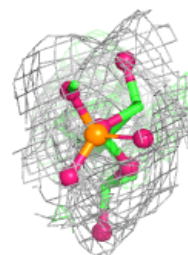
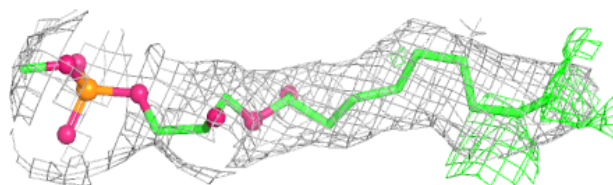
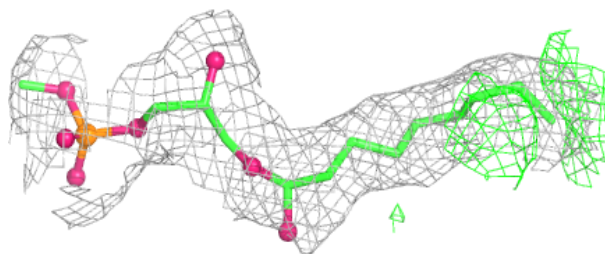
**Electron density around MC3 B 1301:**

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and green (positive)

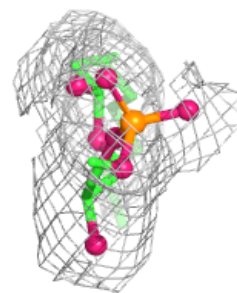
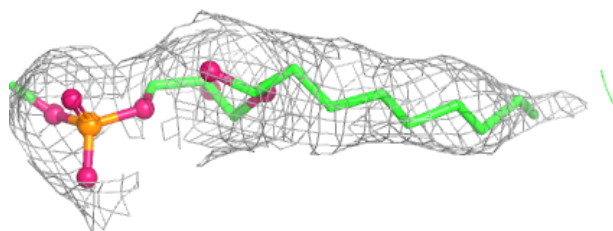


Electron density around MC3 B 1302:

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and green (positive)

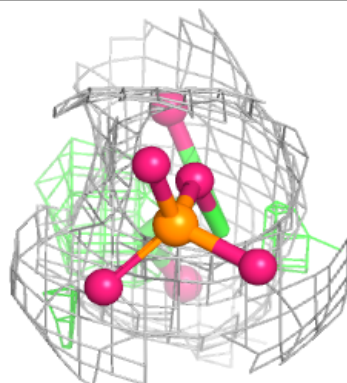
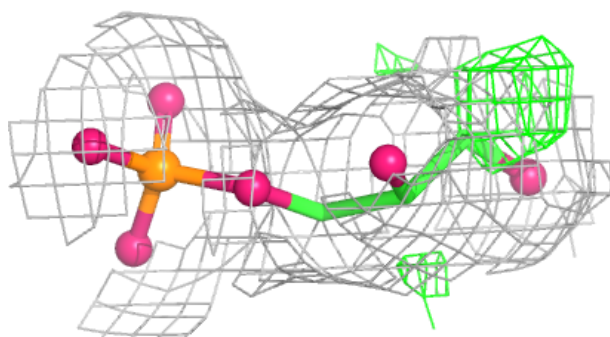
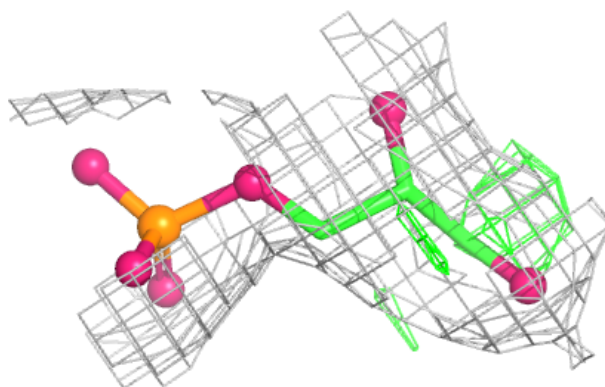
**Electron density around MC3 A 1303:**

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and green (positive)

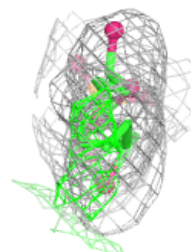
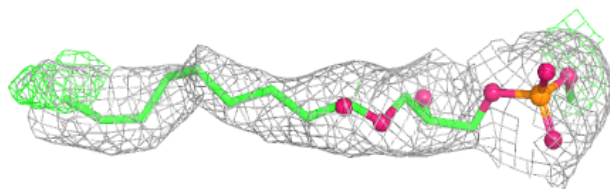
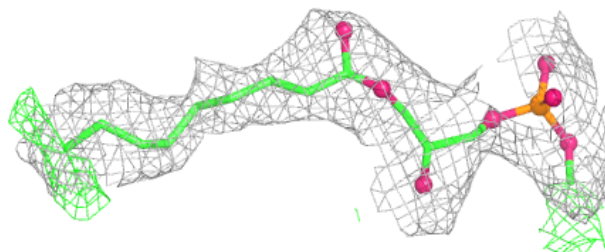


Electron density around MC3 C 1302:

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and green (positive)

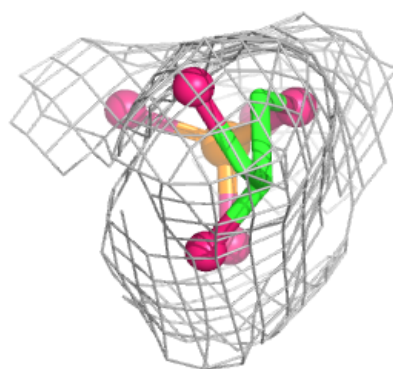
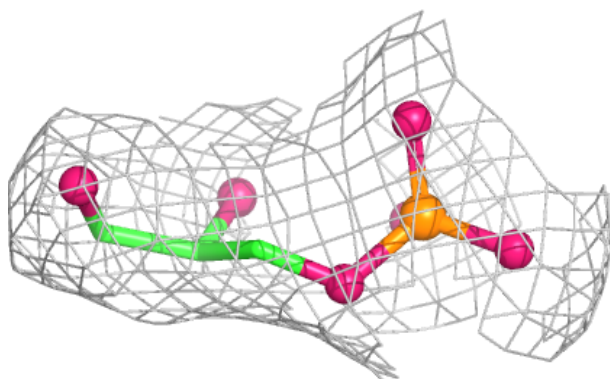
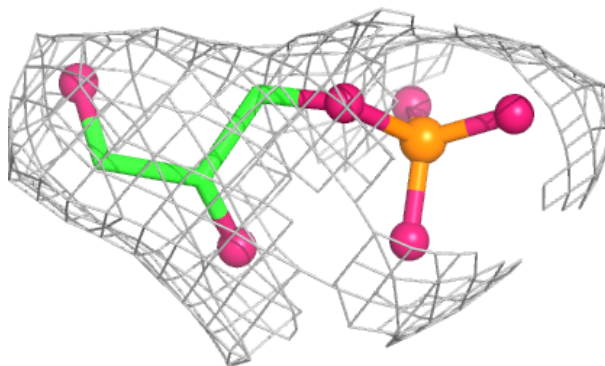
**Electron density around MC3 A 1304:**

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and green (positive)

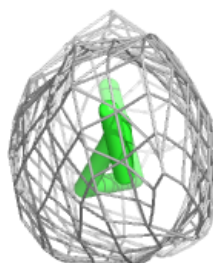
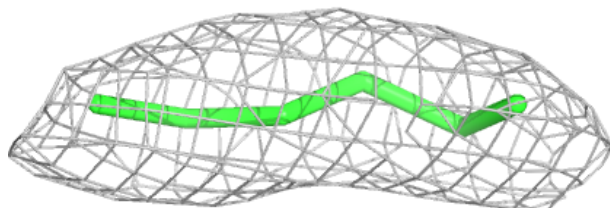
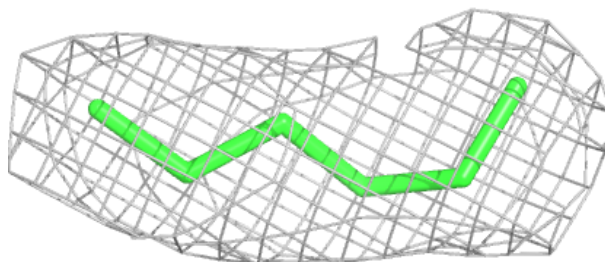


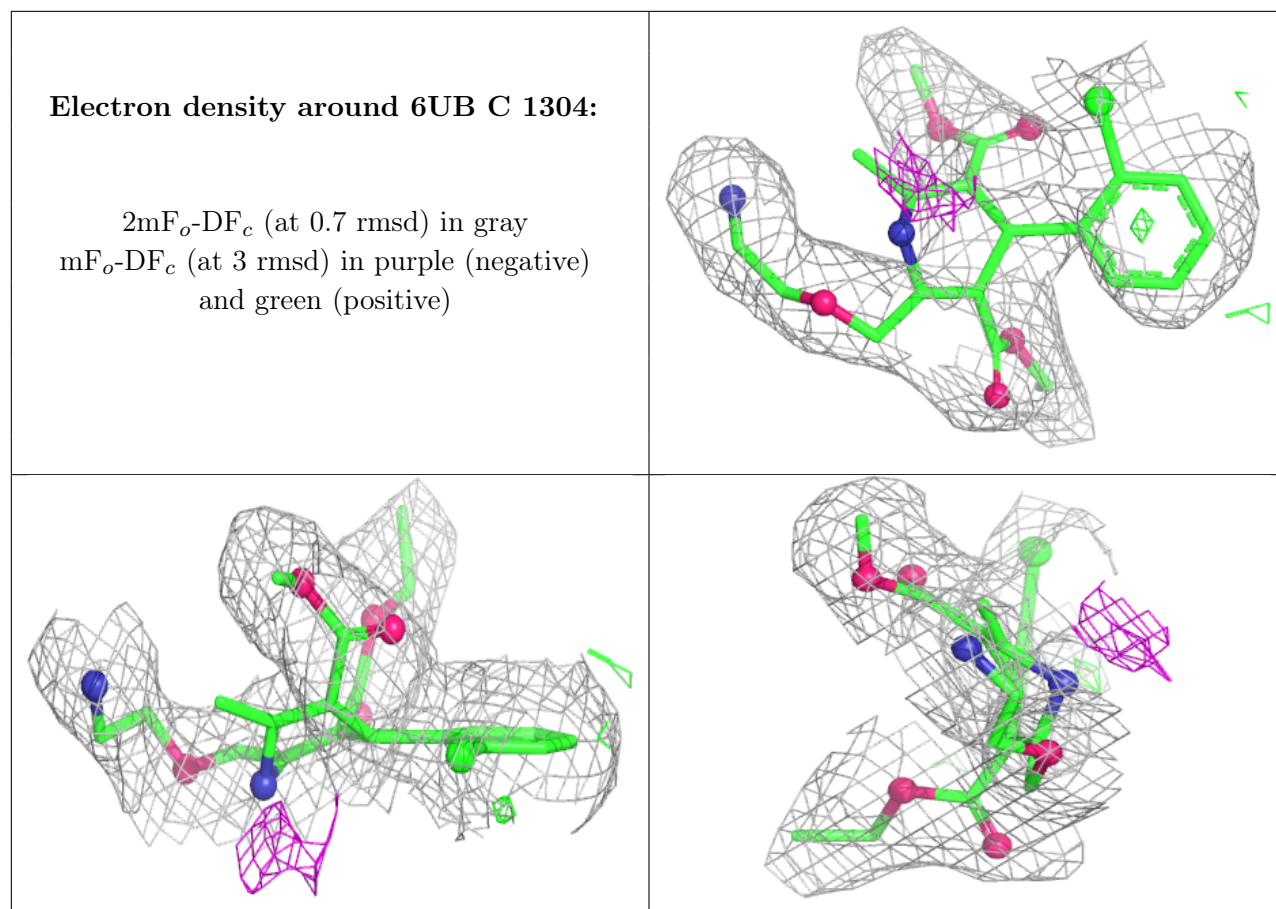
Electron density around MC3 A 1305:

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

**Electron density around MC3 A 1302:**

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





6.5 Other polymers ⓘ

There are no such residues in this entry.