



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 4, 2026 – 11:49 PM UTC

PDB ID : 2BYR / pdb_00002byr
Title : CRYSTAL STRUCTURE OF ACHBP FROM APLYSIA CALIFORNICA in complex with methyllycaconitine
Authors : Hansen, S.B.; Sulzenbacher, G.; Huxford, T.; Marchot, P.; Taylor, P.; Bourne, Y.
Deposited on : 2005-08-03
Resolution : 2.45 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

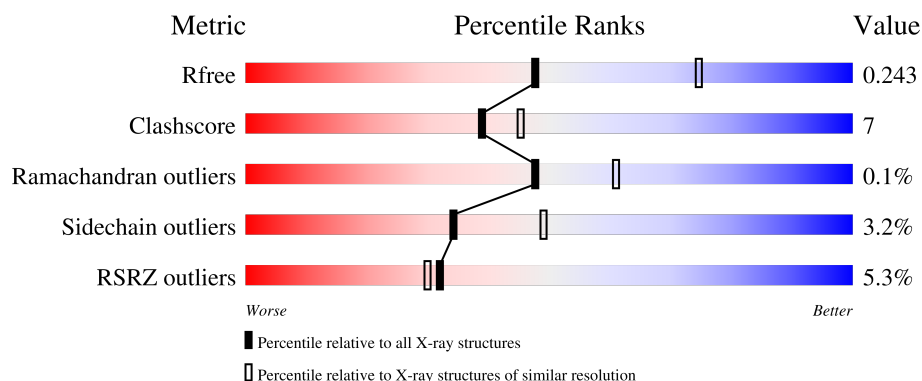
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	227	
1	B	227	
1	C	227	
1	D	227	

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Mol	Chain	Length	Quality of chain
1	E	227	2%83%11%6%
1	F	227	6%78%13%8%
1	G	227	6%82%7%10%
1	H	227	16%78%10%10%
1	I	227	5%83%11%6%
1	J	227	2%85%8%7%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 18062 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 ACETYLCHOLINE-BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	213	Total	C	N	O	S	0	7	0
			1737	1096	289	342	10			
1	B	210	Total	C	N	O	S	0	8	0
			1714	1082	288	334	10			
1	C	210	Total	C	N	O	S	0	5	0
			1699	1073	284	333	9			
1	D	211	Total	C	N	O	S	0	6	0
			1720	1084	290	337	9			
1	E	214	Total	C	N	O	S	0	4	0
			1733	1090	290	343	10			
1	F	209	Total	C	N	O	S	0	6	0
			1700	1074	284	333	9			
1	G	205	Total	C	N	O	S	0	1	0
			1637	1035	267	326	9			
1	H	204	Total	C	N	O	S	0	1	0
			1634	1032	270	324	8			
1	I	213	Total	C	N	O	S	0	4	0
			1724	1085	287	343	9			
1	J	212	Total	C	N	O	S	0	5	0
			1718	1084	285	339	10			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	TYR	-	expression tag	UNP Q8WSF8
A	-6	LYS	-	expression tag	UNP Q8WSF8
A	-5	ASP	-	expression tag	UNP Q8WSF8
A	-4	ASP	-	expression tag	UNP Q8WSF8
A	-3	ASP	-	expression tag	UNP Q8WSF8
A	-2	ASP	-	expression tag	UNP Q8WSF8
A	-1	LYS	-	expression tag	UNP Q8WSF8
A	0	LEU	-	expression tag	UNP Q8WSF8
B	-7	TYR	-	expression tag	UNP Q8WSF8

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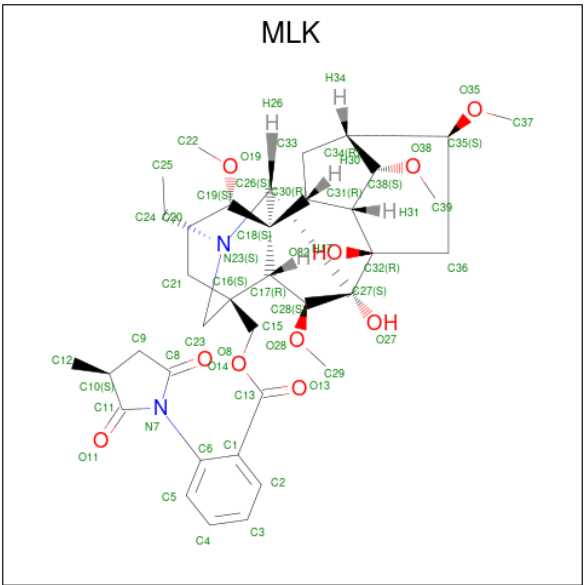
Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	LYS	-	expression tag	UNP Q8WSF8
B	-5	ASP	-	expression tag	UNP Q8WSF8
B	-4	ASP	-	expression tag	UNP Q8WSF8
B	-3	ASP	-	expression tag	UNP Q8WSF8
B	-2	ASP	-	expression tag	UNP Q8WSF8
B	-1	LYS	-	expression tag	UNP Q8WSF8
B	0	LEU	-	expression tag	UNP Q8WSF8
C	-7	TYR	-	expression tag	UNP Q8WSF8
C	-6	LYS	-	expression tag	UNP Q8WSF8
C	-5	ASP	-	expression tag	UNP Q8WSF8
C	-4	ASP	-	expression tag	UNP Q8WSF8
C	-3	ASP	-	expression tag	UNP Q8WSF8
C	-2	ASP	-	expression tag	UNP Q8WSF8
C	-1	LYS	-	expression tag	UNP Q8WSF8
C	0	LEU	-	expression tag	UNP Q8WSF8
D	-7	TYR	-	expression tag	UNP Q8WSF8
D	-6	LYS	-	expression tag	UNP Q8WSF8
D	-5	ASP	-	expression tag	UNP Q8WSF8
D	-4	ASP	-	expression tag	UNP Q8WSF8
D	-3	ASP	-	expression tag	UNP Q8WSF8
D	-2	ASP	-	expression tag	UNP Q8WSF8
D	-1	LYS	-	expression tag	UNP Q8WSF8
D	0	LEU	-	expression tag	UNP Q8WSF8
E	-7	TYR	-	expression tag	UNP Q8WSF8
E	-6	LYS	-	expression tag	UNP Q8WSF8
E	-5	ASP	-	expression tag	UNP Q8WSF8
E	-4	ASP	-	expression tag	UNP Q8WSF8
E	-3	ASP	-	expression tag	UNP Q8WSF8
E	-2	ASP	-	expression tag	UNP Q8WSF8
E	-1	LYS	-	expression tag	UNP Q8WSF8
E	0	LEU	-	expression tag	UNP Q8WSF8
F	-7	TYR	-	expression tag	UNP Q8WSF8
F	-6	LYS	-	expression tag	UNP Q8WSF8
F	-5	ASP	-	expression tag	UNP Q8WSF8
F	-4	ASP	-	expression tag	UNP Q8WSF8
F	-3	ASP	-	expression tag	UNP Q8WSF8
F	-2	ASP	-	expression tag	UNP Q8WSF8
F	-1	LYS	-	expression tag	UNP Q8WSF8
F	0	LEU	-	expression tag	UNP Q8WSF8
G	-7	TYR	-	expression tag	UNP Q8WSF8
G	-6	LYS	-	expression tag	UNP Q8WSF8
G	-5	ASP	-	expression tag	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-4	ASP	-	expression tag	UNP Q8WSF8
G	-3	ASP	-	expression tag	UNP Q8WSF8
G	-2	ASP	-	expression tag	UNP Q8WSF8
G	-1	LYS	-	expression tag	UNP Q8WSF8
G	0	LEU	-	expression tag	UNP Q8WSF8
H	-7	TYR	-	expression tag	UNP Q8WSF8
H	-6	LYS	-	expression tag	UNP Q8WSF8
H	-5	ASP	-	expression tag	UNP Q8WSF8
H	-4	ASP	-	expression tag	UNP Q8WSF8
H	-3	ASP	-	expression tag	UNP Q8WSF8
H	-2	ASP	-	expression tag	UNP Q8WSF8
H	-1	LYS	-	expression tag	UNP Q8WSF8
H	0	LEU	-	expression tag	UNP Q8WSF8
I	-7	TYR	-	expression tag	UNP Q8WSF8
I	-6	LYS	-	expression tag	UNP Q8WSF8
I	-5	ASP	-	expression tag	UNP Q8WSF8
I	-4	ASP	-	expression tag	UNP Q8WSF8
I	-3	ASP	-	expression tag	UNP Q8WSF8
I	-2	ASP	-	expression tag	UNP Q8WSF8
I	-1	LYS	-	expression tag	UNP Q8WSF8
I	0	LEU	-	expression tag	UNP Q8WSF8
J	-7	TYR	-	expression tag	UNP Q8WSF8
J	-6	LYS	-	expression tag	UNP Q8WSF8
J	-5	ASP	-	expression tag	UNP Q8WSF8
J	-4	ASP	-	expression tag	UNP Q8WSF8
J	-3	ASP	-	expression tag	UNP Q8WSF8
J	-2	ASP	-	expression tag	UNP Q8WSF8
J	-1	LYS	-	expression tag	UNP Q8WSF8
J	0	LEU	-	expression tag	UNP Q8WSF8

- Molecule 2 is METHYLLYCACONITINE (CCD ID: MLK) (formula: C₃₇H₅₀N₂O₁₀).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			49	37	2	10		
2	B	1	Total	C	N	O	0	0
			49	37	2	10		
2	C	1	Total	C	N	O	0	0
			49	37	2	10		
2	D	1	Total	C	N	O	0	0
			49	37	2	10		
2	E	1	Total	C	N	O	0	0
			49	37	2	10		
2	F	1	Total	C	N	O	0	0
			49	37	2	10		
2	G	1	Total	C	N	O	0	0
			49	37	2	10		
2	H	1	Total	C	N	O	0	0
			49	37	2	10		
2	I	1	Total	C	N	O	0	0
			49	37	2	10		
2	J	1	Total	C	N	O	0	0
			49	37	2	10		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	113	Total	O	0	0
			113	113		
3	B	91	Total	O	0	0
			91	91		

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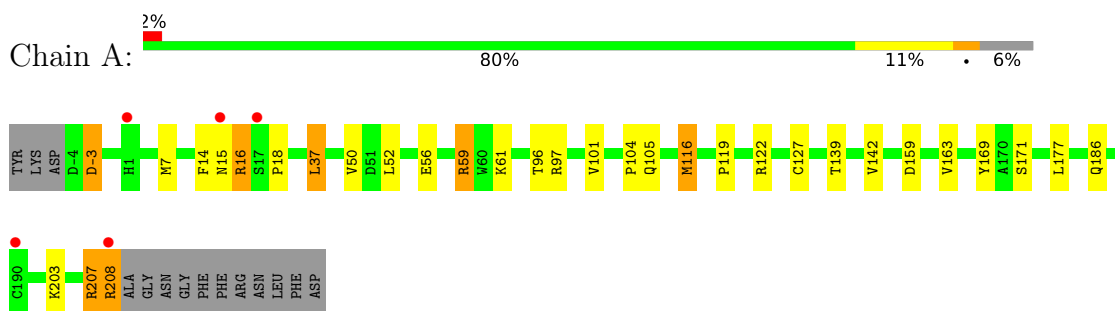
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	54	Total 54	O 54	0	0
3	D	58	Total 58	O 58	0	0
3	E	88	Total 88	O 88	0	0
3	F	32	Total 32	O 32	0	0
3	G	23	Total 23	O 23	0	0
3	H	14	Total 14	O 14	0	0
3	I	29	Total 29	O 29	0	0
3	J	54	Total 54	O 54	0	0

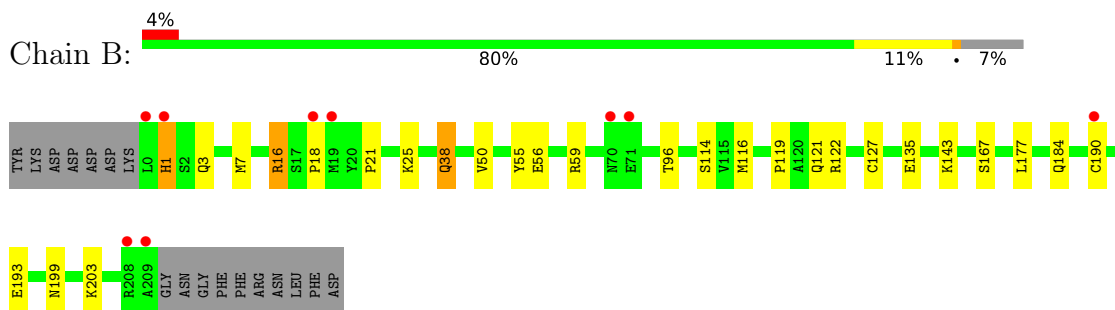
3 Residue-property plots [i](#)

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.

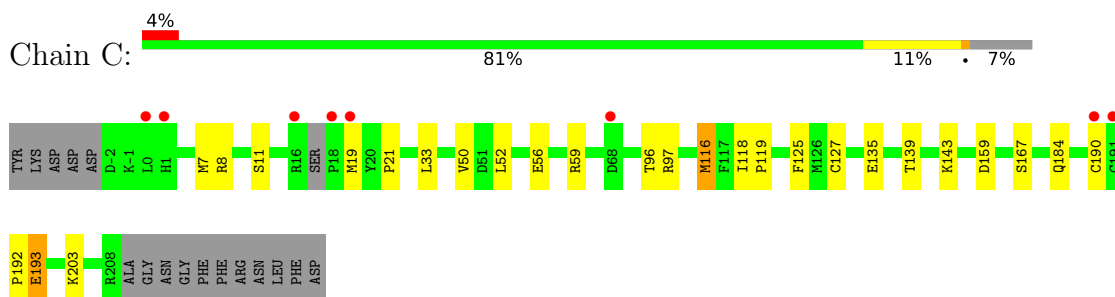
• Molecule 1: ACETYLCHOLINE-BINDING PROTEIN



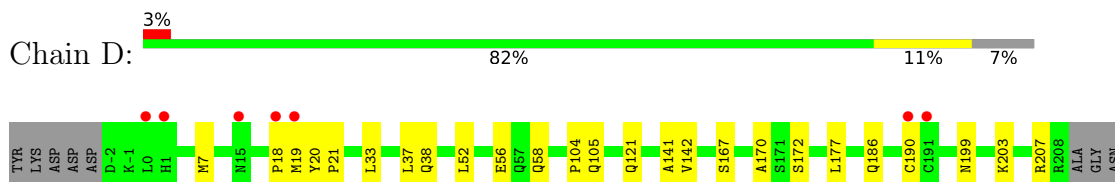
• Molecule 1: ACETYLCHOLINE-BINDING PROTEIN



• Molecule 1: ACETYLCHOLINE-BINDING PROTEIN



• Molecule 1: ACETYLCHOLINE-BINDING PROTEIN



GLY
PHE
PHE
ARG
ARG
ASN
LEU
PHE
ASP

● Molecule 1: ACETYLCHOLINE-BINDING PROTEIN

Chain E: 

Tyr Lys D-5 D-4 D-3 M7 R16 R17 R18 K25 T30 Q38 V50 V51 V52 E56 Q57 Q58 R59 V101 Q105 M116 P119 R122 F125 M126 C127 V142 K143 K157 S167 E175 Q184 C190 R207 R208 Ala Gly Asn Gly

PHE
PHE
ASN
ASN
LEU
PHE
ASP

● Molecule 1: ACETYLCHOLINE-BINDING PROTEIN

Chain F: 

Tyr Lys Asp Asp Asp Lys L0 H1 N5 L6 M7 F14 M15 M16 S17 P18 M19 Y20 L33 G34 F35 Q38 V50 D51 L52 E56 R59 M70 E71 Y72 G73 M74 I75 V99 Q105 M116 P119 A120 Q121 R122 C127 S134 A141 V142

K143 V148 D159 S167 Y168 Y169 A170 S172 E175 C190 E193 N199 R207 R208 Ala Gly Asn Gly Phe Phe Arg Arg Asn Leu Phe Asp

● Molecule 1: ACETYLCHOLINE-BINDING PROTEIN

Chain G: 

Tyr Lys Asp Asp Asp Asp Lys Leu His Ser Q3 A4 N5 L6 M7 P18 M19 Y20 P21 L33 T36 L37 Q38 E56 D57 Q58 E71 Y72 T96 P119 S134 A138 V142 K157 T160 L177 Q186 C190 C191 P192 L200 K203 F204

R205 E206 R207 Arg Ala Asn Gly Phe Phe Arg Arg Asn Leu Phe Asp

● Molecule 1: ACETYLCHOLINE-BINDING PROTEIN

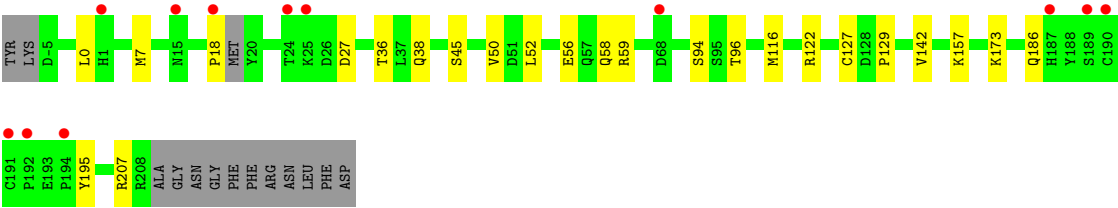
Chain H: 

Tyr Lys Asp Asp Asp Asp Lys Leu H1 S2 Q3 A4 N5 F14 M15 R16 SER PRO MET Y20 P28 L33 Q38 D39 T40 L52 Y55 W67 M70 E71 Y72 G73 V101 Q105 S114 R122 F125 C140 A141 V142 K143 Y149 F152 E153

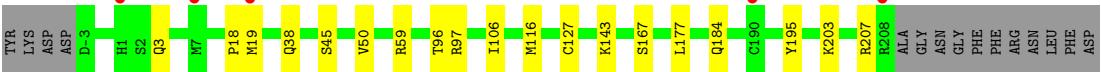
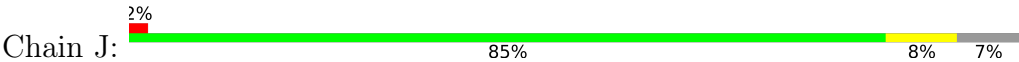
I154 D155 L156 K157 T160 D161 S167 Y168 Y169 S171 S172 K173 Y174 E175 A179 R183 Q184 V185 Q186 H187 Y188 C190 C191 P192 E193 P194 Y195 I196 L200 R205 E206 R207 Arg Ala Gly Asn Gly Phe Phe Arg Arg Asn Leu Phe Asp

● Molecule 1: ACETYLCHOLINE-BINDING PROTEIN

Chain I: 



● Molecule 1: ACETYLCHOLINE-BINDING PROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	67.27Å 135.78Å 147.29Å 90.00° 99.46° 90.00°	Depositor
Resolution (Å)	20.00 – 2.45 20.00 – 2.45	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-2.45) 98.3 (20.00-2.45)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.193 , 0.232 0.212 , 0.243	Depositor DCC
R_{free} test set	1891 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å ²)	36.8	Xtriage
Anisotropy	0.237	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18062	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.38% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MLK

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	0.61	0/1806	0.74	0/2458
1	B	0.59	0/1787	0.74	0/2432
1	C	0.57	0/1761	0.70	0/2397
1	D	0.53	0/1785	0.70	0/2430
1	E	0.59	0/1790	0.70	0/2437
1	F	0.50	0/1765	0.72	0/2405
1	G	0.50	0/1681	0.69	0/2293
1	H	0.47	0/1677	0.68	0/2286
1	I	0.50	0/1779	0.69	0/2422
1	J	0.55	0/1779	0.66	0/2422
All	All	0.54	0/17610	0.70	0/23982

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	C	0	1
1	D	0	1
1	F	0	1
1	G	0	1
1	H	0	1
All	All	0	6

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	1	HIS	Peptide
1	C	190	CYS	Peptide
1	D	190	CYS	Peptide
1	F	0	LEU	Peptide
1	G	190	CYS	Peptide

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	1737	0	1672	35	0
1	B	1714	0	1655	29	0
1	C	1699	0	1634	15	0
1	D	1720	0	1656	24	0
1	E	1733	0	1661	21	0
1	F	1700	0	1637	33	0
1	G	1637	0	1565	13	0
1	H	1634	0	1563	15	0
1	I	1724	0	1650	34	0
1	J	1718	0	1652	19	0
2	A	49	0	50	3	0
2	B	49	0	50	2	0
2	C	49	0	50	2	0
2	D	49	0	50	2	0
2	E	49	0	50	7	0
2	F	49	0	50	6	0
2	G	49	0	50	3	0
2	H	49	0	50	4	0
2	I	49	0	50	6	0
2	J	49	0	50	3	0
3	A	113	0	0	1	0
3	B	91	0	0	3	0
3	C	54	0	0	0	0
3	D	58	0	0	1	0
3	E	88	0	0	2	0
3	F	32	0	0	1	0
3	G	23	0	0	0	0
3	H	14	0	0	0	0
3	I	29	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	J	54	0	0	0	0
All	All	18062	0	16845	235	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 7.

The worst 5 of 235 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:59[B]:ARG:HD3	1:A:116[B]:MET:CE	1.17	1.60
1:A:59[B]:ARG:CD	1:A:116[B]:MET:HE2	1.43	1.46
1:I:59[B]:ARG:CG	1:I:116[B]:MET:CE	1.94	1.46
1:I:59[B]:ARG:CG	1:I:116[B]:MET:HE3	1.42	1.46
1:I:59[B]:ARG:HG3	1:I:116[B]:MET:CE	1.60	1.19

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	218/227 (96%)	213 (98%)	5 (2%)	0	100	100
1	B	216/227 (95%)	211 (98%)	4 (2%)	1 (0%)	24	32
1	C	211/227 (93%)	206 (98%)	5 (2%)	0	100	100
1	D	215/227 (95%)	209 (97%)	4 (2%)	2 (1%)	14	17
1	E	216/227 (95%)	211 (98%)	5 (2%)	0	100	100
1	F	213/227 (94%)	206 (97%)	7 (3%)	0	100	100
1	G	204/227 (90%)	201 (98%)	3 (2%)	0	100	100
1	H	201/227 (88%)	194 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	213/227 (94%)	206 (97%)	7 (3%)	0	100	100
1	J	215/227 (95%)	211 (98%)	4 (2%)	0	100	100
All	All	2122/2270 (94%)	2068 (98%)	51 (2%)	3 (0%)	48	61

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	18	PRO
1	D	19	MET
1	D	18	PRO

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	201/205 (98%)	188 (94%)	13 (6%)	15	21
1	B	198/205 (97%)	191 (96%)	7 (4%)	32	46
1	C	195/205 (95%)	187 (96%)	8 (4%)	27	40
1	D	198/205 (97%)	195 (98%)	3 (2%)	57	70
1	E	199/205 (97%)	194 (98%)	5 (2%)	42	56
1	F	196/205 (96%)	188 (96%)	8 (4%)	27	40
1	G	187/205 (91%)	179 (96%)	8 (4%)	26	38
1	H	186/205 (91%)	176 (95%)	10 (5%)	20	29
1	I	198/205 (97%)	193 (98%)	5 (2%)	42	56
1	J	198/205 (97%)	196 (99%)	2 (1%)	68	77
All	All	1956/2050 (95%)	1887 (96%)	69 (4%)	34	46

5 of 69 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	175	GLU

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Mol	Chain	Res	Type
1	H	186	GLN
1	I	142	VAL
1	C	33[B]	LEU
1	C	33[A]	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	5	ASN
1	H	38	GLN
1	F	184	GLN
1	G	15	ASN
1	H	162	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

10 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
2	MLK	F	301	-	56,56,56	1.58	9 (16%)	82,92,92	1.16	12 (14%)
2	MLK	A	301	-	56,56,56	1.49	7 (12%)	82,92,92	1.43	10 (12%)
2	MLK	D	301	-	56,56,56	1.58	7 (12%)	82,92,92	1.41	11 (13%)
2	MLK	C	301	-	56,56,56	1.56	8 (14%)	82,92,92	1.26	10 (12%)
2	MLK	H	301	-	56,56,56	1.45	7 (12%)	82,92,92	1.49	13 (15%)
2	MLK	E	301	-	56,56,56	1.52	9 (16%)	82,92,92	1.33	11 (13%)
2	MLK	I	301	-	56,56,56	1.51	7 (12%)	82,92,92	1.35	10 (12%)
2	MLK	B	301	-	56,56,56	1.63	7 (12%)	82,92,92	1.41	8 (9%)
2	MLK	G	301	-	56,56,56	1.54	7 (12%)	82,92,92	1.28	12 (14%)
2	MLK	J	301	-	56,56,56	1.45	7 (12%)	82,92,92	1.37	12 (14%)

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
2	MLK	F	301	-	-	2/24/141/141	0/2/8/8
2	MLK	A	301	-	-	0/24/141/141	0/2/8/8
2	MLK	D	301	-	-	0/24/141/141	0/2/8/8
2	MLK	C	301	-	-	0/24/141/141	0/2/8/8
2	MLK	H	301	-	-	0/24/141/141	0/2/8/8
2	MLK	E	301	-	-	0/24/141/141	0/2/8/8
2	MLK	I	301	-	-	0/24/141/141	0/2/8/8
2	MLK	B	301	-	-	0/24/141/141	0/2/8/8
2	MLK	G	301	-	-	0/24/141/141	0/2/8/8
2	MLK	J	301	-	-	0/24/141/141	0/2/8/8

The worst 5 of 75 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	301	MLK	C1-C6	5.80	1.49	1.41
2	E	301	MLK	C1-C6	5.60	1.49	1.41
2	D	301	MLK	C1-C6	5.54	1.49	1.41
2	C	301	MLK	C1-C6	5.44	1.49	1.41
2	B	301	MLK	C11-N7	-5.38	1.32	1.40

The worst 5 of 109 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	MLK	O27-C27-C26	6.95	116.85	110.45
2	D	301	MLK	O27-C27-C26	5.01	115.06	110.45
2	A	301	MLK	O27-C27-C26	4.70	114.78	110.45
2	I	301	MLK	O27-C27-C26	4.55	114.63	110.45
2	I	301	MLK	C10-C11-N7	4.46	110.94	108.24

There are no chirality outliers.

All (2) torsion outliers are listed below:

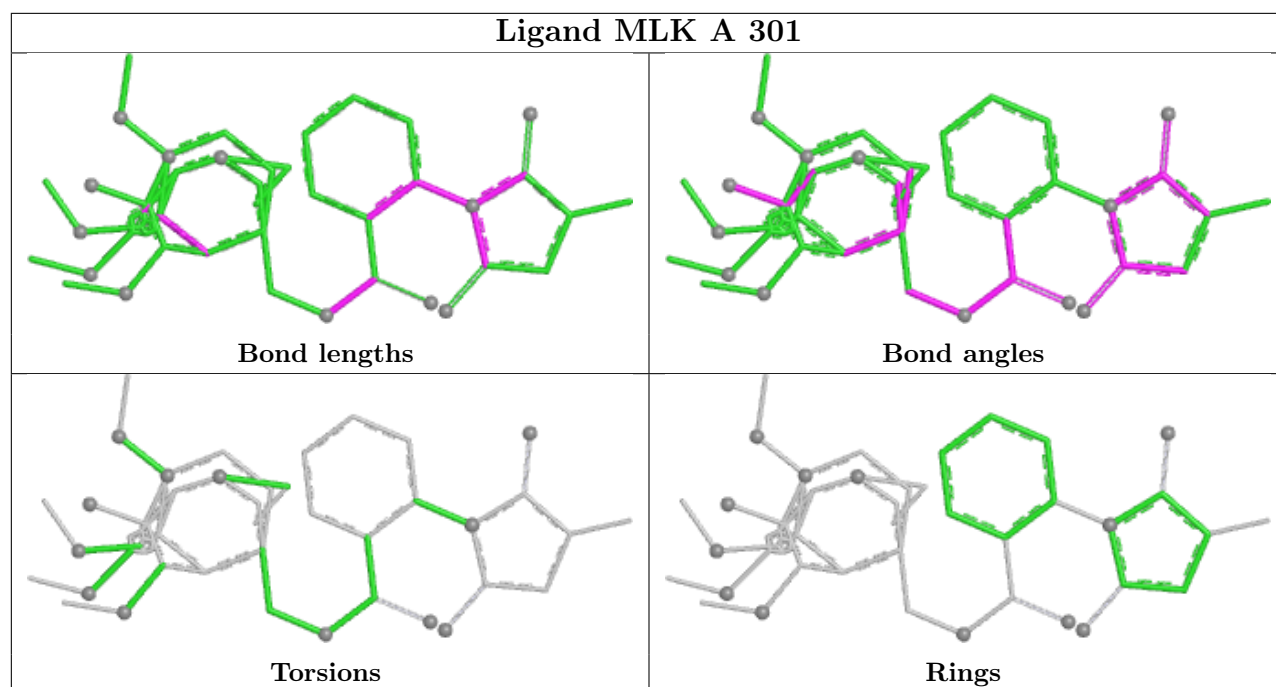
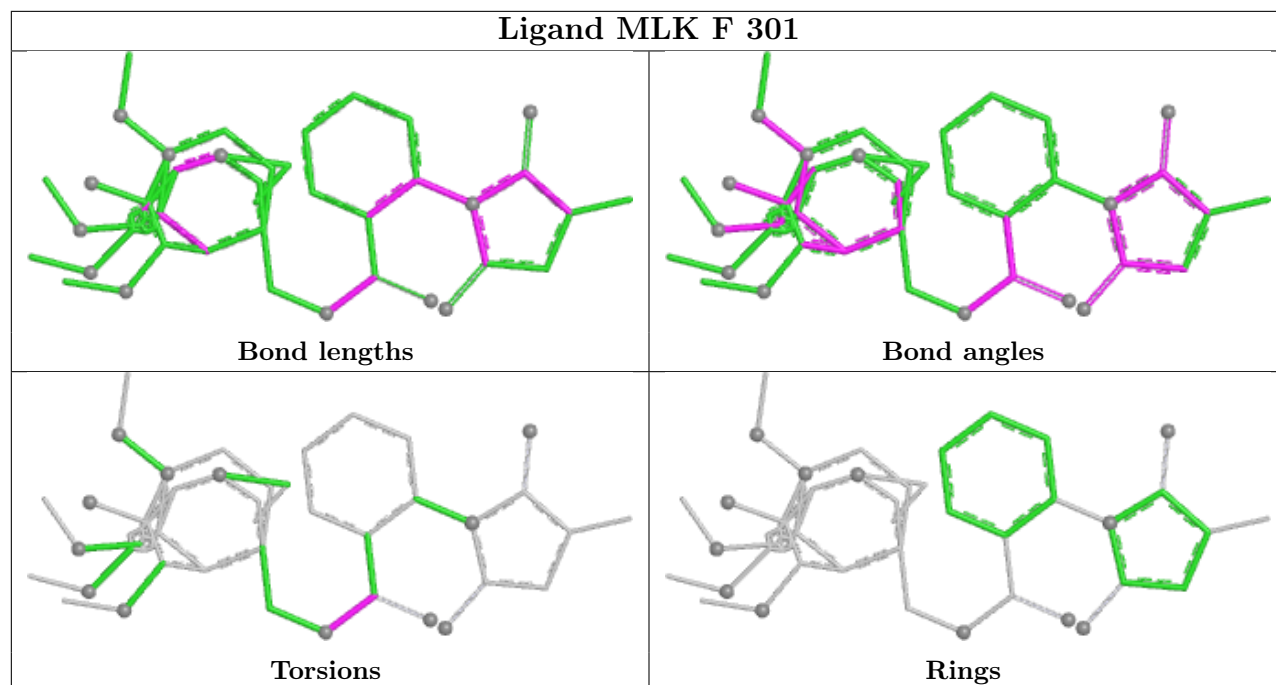
Mol	Chain	Res	Type	Atoms
2	F	301	MLK	O13-C13-O14-C15
2	F	301	MLK	C1-C13-O14-C15

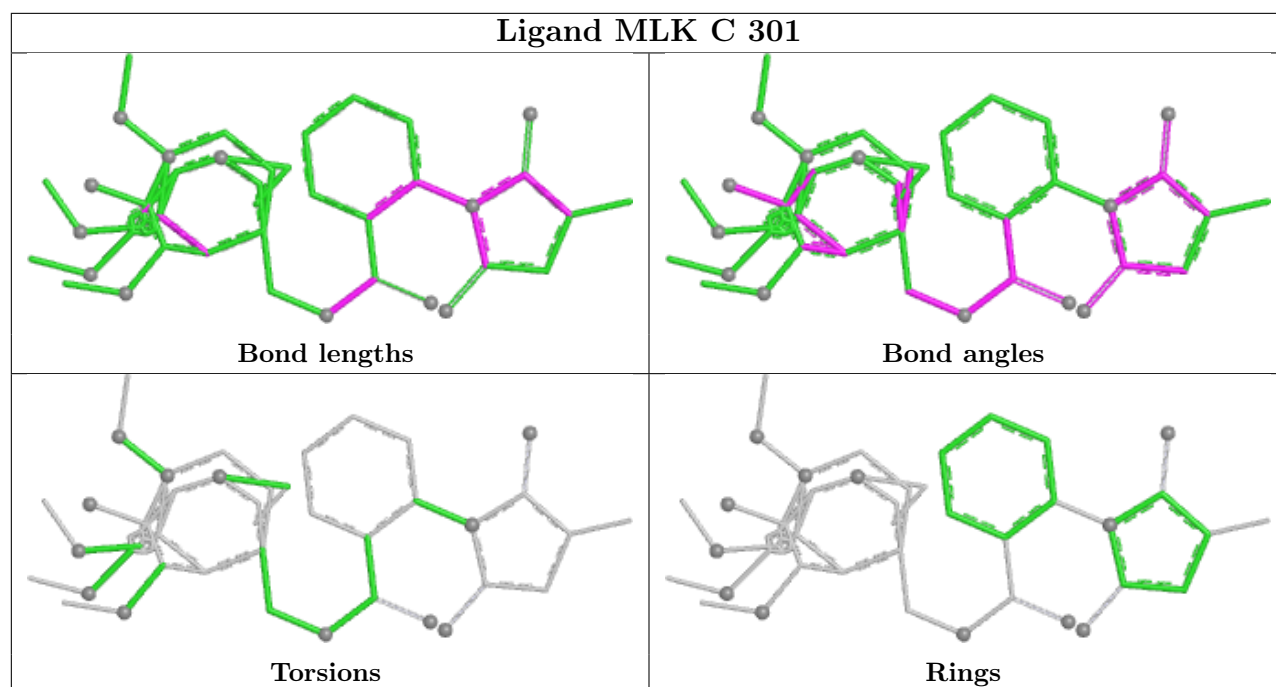
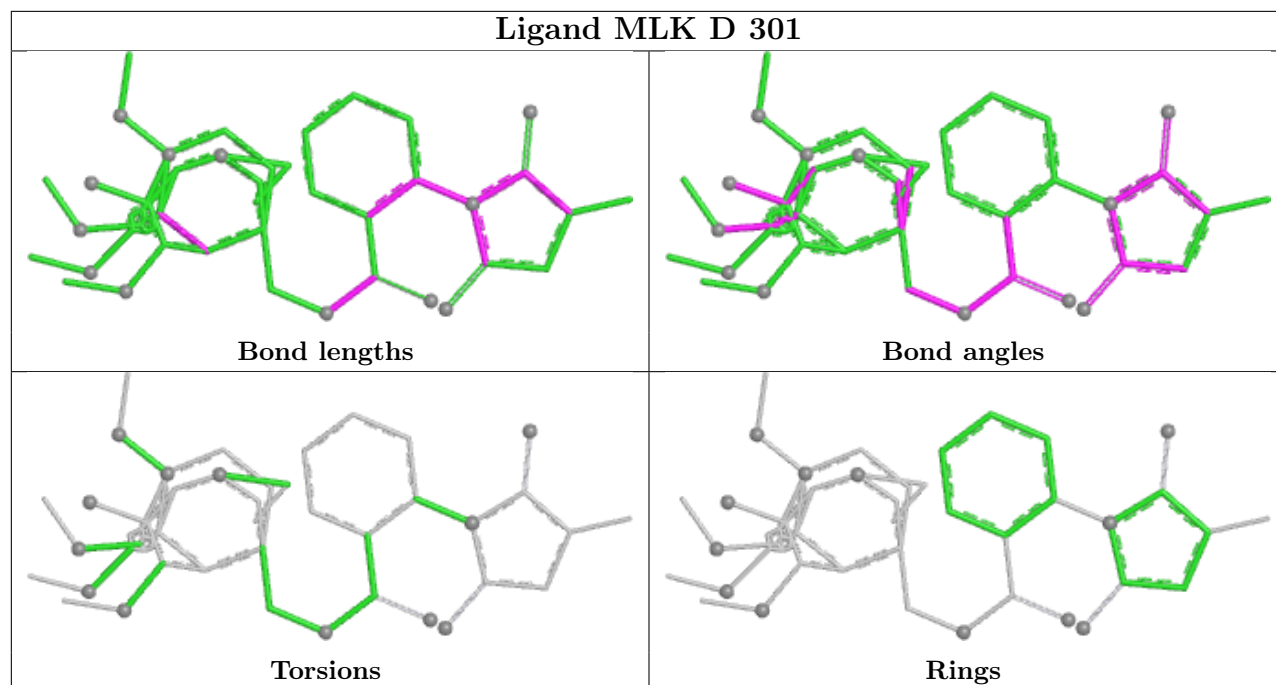
There are no ring outliers.

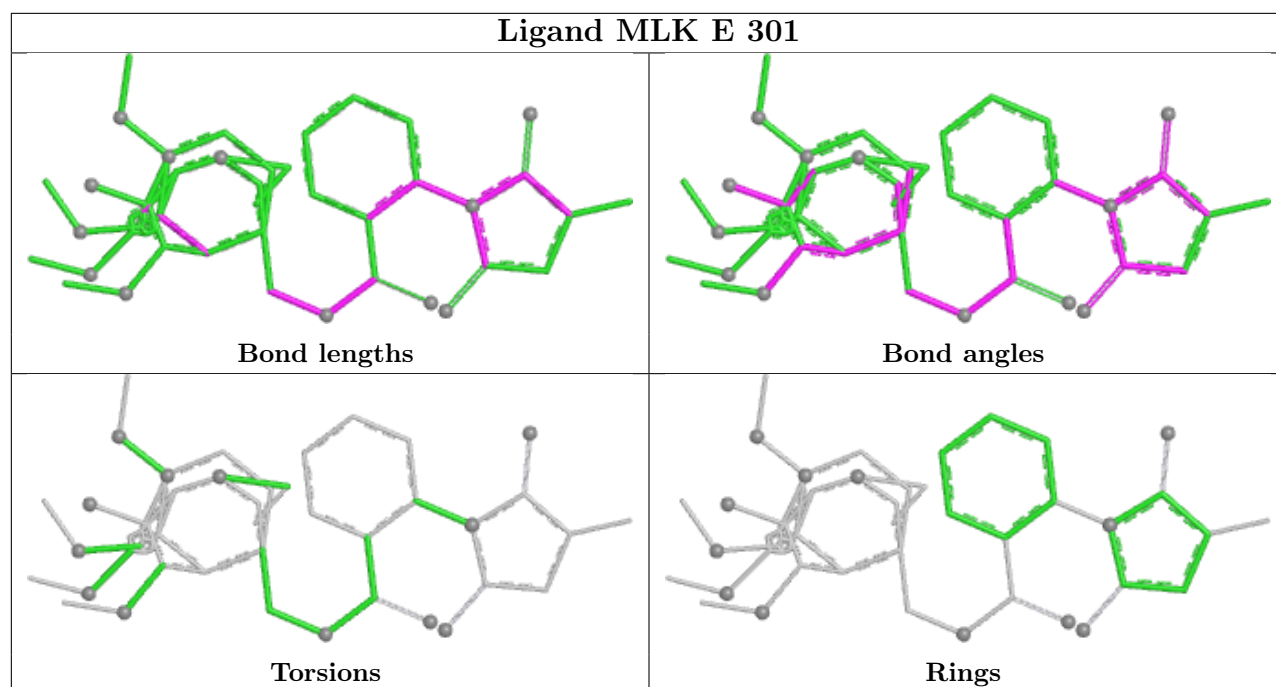
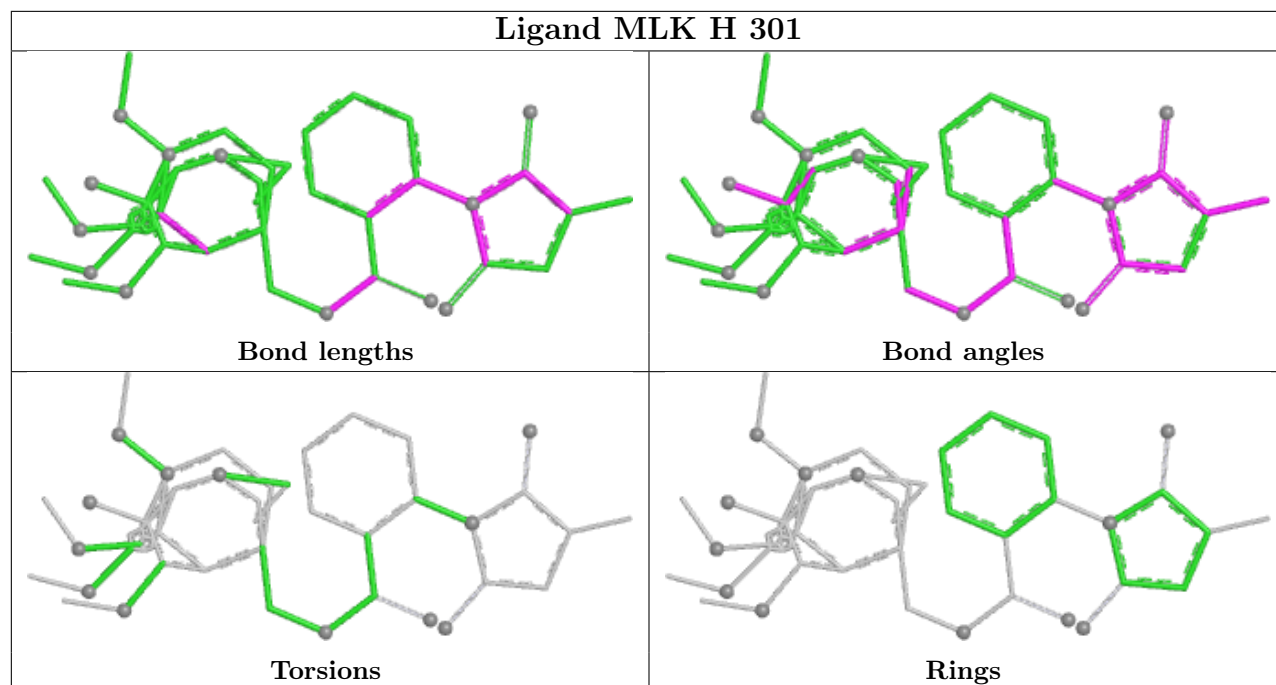
10 monomers are involved in 38 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	301	MLK	6	0
2	A	301	MLK	3	0
2	D	301	MLK	2	0
2	C	301	MLK	2	0
2	H	301	MLK	4	0
2	E	301	MLK	7	0
2	I	301	MLK	6	0
2	B	301	MLK	2	0
2	G	301	MLK	3	0
2	J	301	MLK	3	0

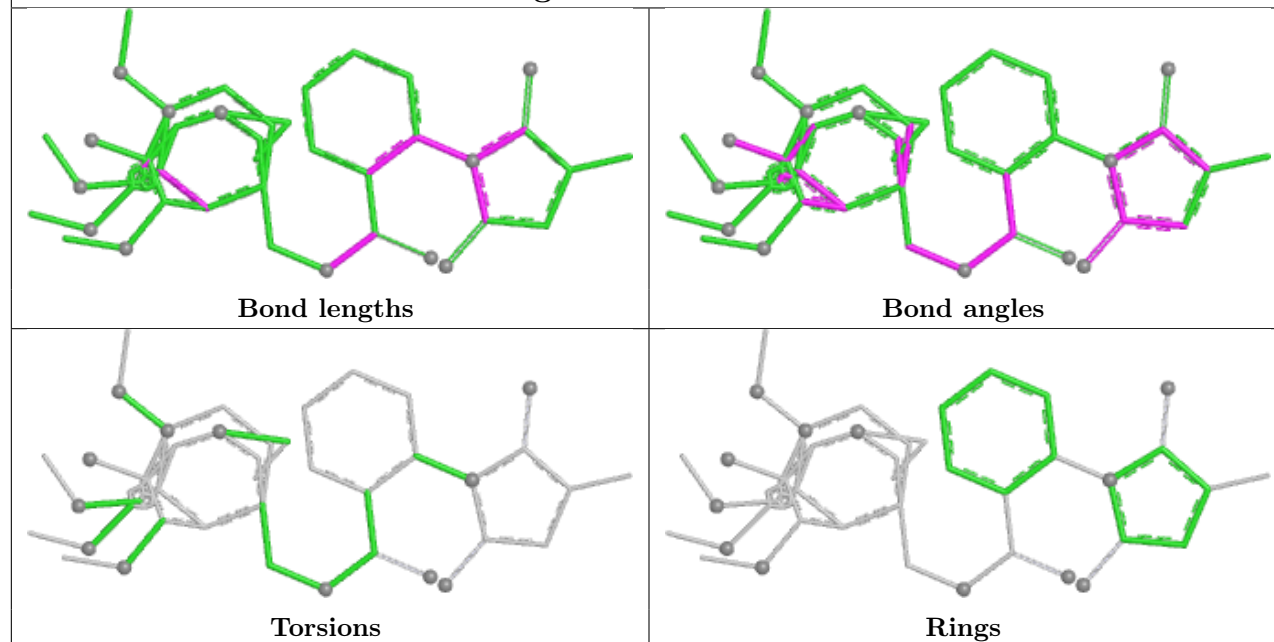
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



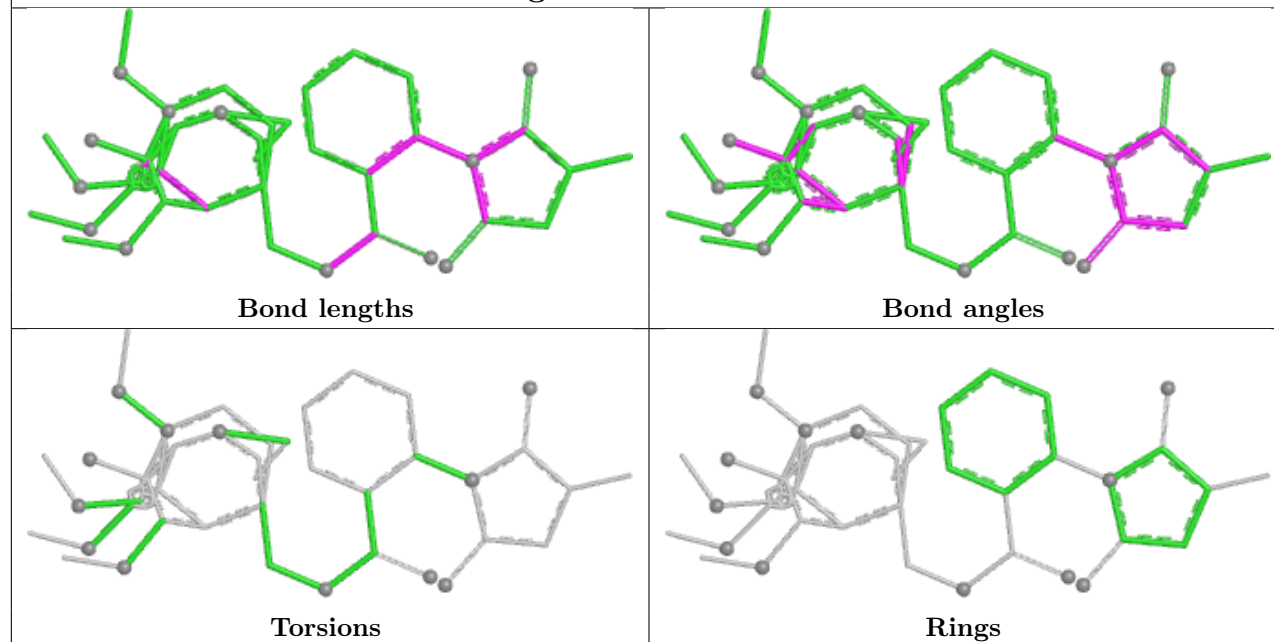


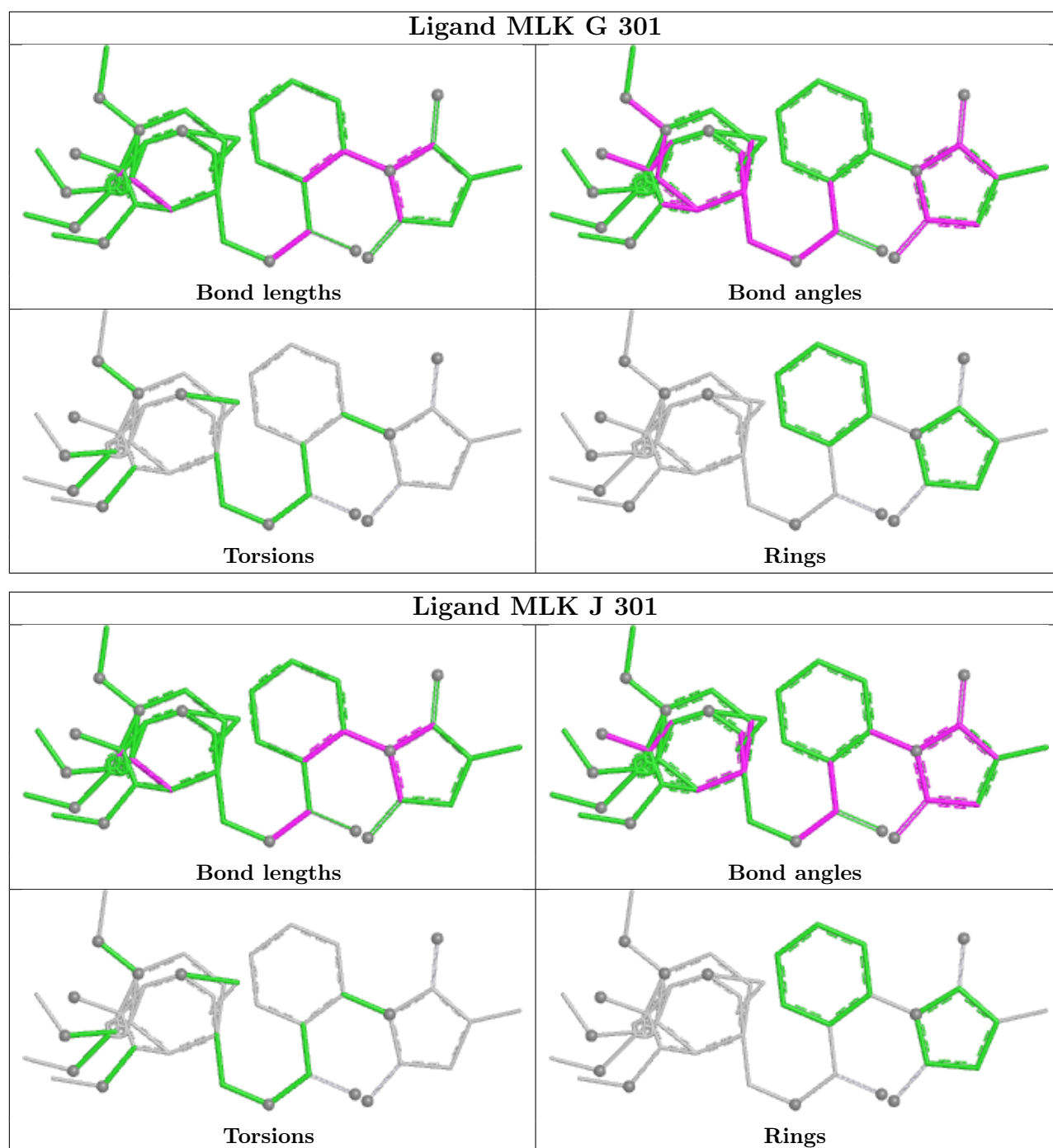


Ligand MLK I 301



Ligand MLK B 301





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	213/227 (93%)	-0.13	5 (2%) 61 63	12, 28, 56, 77	7 (3%)
1	B	210/227 (92%)	-0.06	9 (4%) 40 39	14, 31, 62, 78	8 (3%)
1	C	210/227 (92%)	0.03	8 (3%) 44 44	17, 38, 67, 96	5 (2%)
1	D	211/227 (92%)	0.19	7 (3%) 49 50	15, 39, 74, 85	6 (2%)
1	E	214/227 (94%)	-0.04	4 (1%) 66 67	16, 30, 65, 92	4 (1%)
1	F	209/227 (92%)	0.55	13 (6%) 26 24	22, 48, 75, 92	6 (2%)
1	G	205/227 (90%)	0.71	13 (6%) 26 23	33, 55, 85, 95	1 (0%)
1	H	204/227 (89%)	1.24	36 (17%) 4 3	28, 65, 95, 106	1 (0%)
1	I	213/227 (93%)	0.60	12 (5%) 30 27	24, 51, 92, 100	4 (1%)
1	J	212/227 (93%)	0.15	5 (2%) 59 62	20, 39, 69, 99	5 (2%)
All	All	2101/2270 (92%)	0.32	112 (5%) 32 30	12, 43, 81, 106	47 (2%)

The worst 5 of 112 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	190	CYS	6.9
1	B	209	ALA	6.1
1	H	4	ALA	3.9
1	F	0	LEU	3.8
1	G	18	PRO	3.7

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 [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

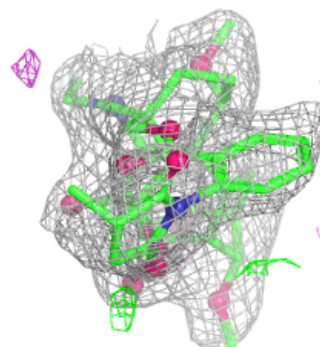
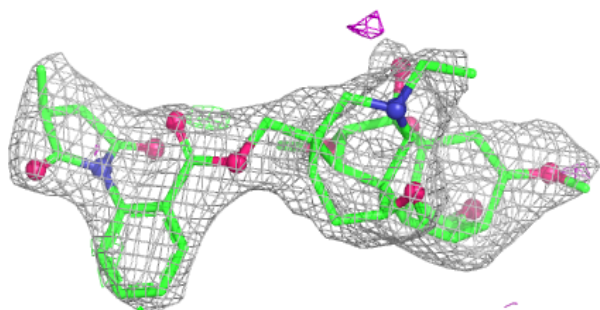
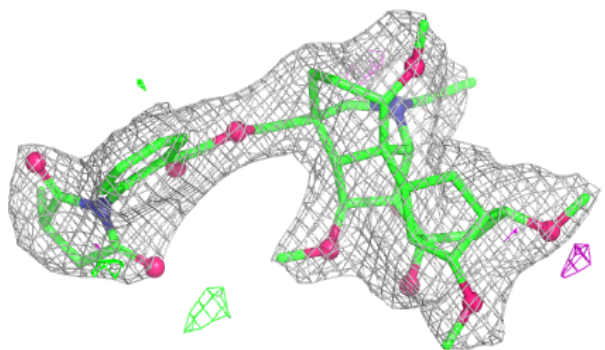
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MLK	H	301	49/49	0.85	0.13	51,52,59,59	0
2	MLK	I	301	49/49	0.85	0.12	49,52,56,57	0
2	MLK	G	301	49/49	0.88	0.12	45,46,56,56	0
2	MLK	F	301	49/49	0.92	0.10	43,44,48,48	0
2	MLK	A	301	49/49	0.93	0.09	28,30,40,40	0
2	MLK	D	301	49/49	0.93	0.09	39,40,45,45	0
2	MLK	B	301	49/49	0.94	0.08	23,25,31,32	0
2	MLK	E	301	49/49	0.94	0.08	27,28,37,38	0
2	MLK	C	301	49/49	0.94	0.08	30,32,40,40	0
2	MLK	J	301	49/49	0.95	0.08	30,33,39,39	0

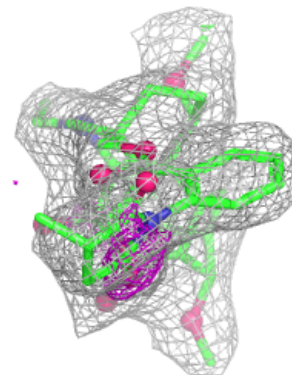
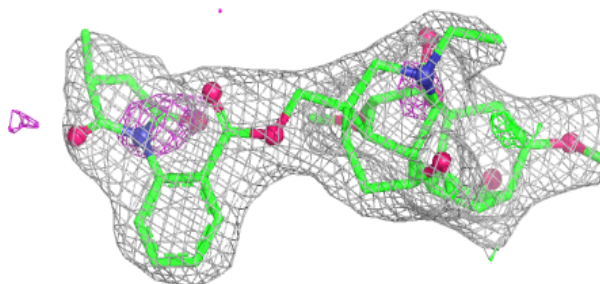
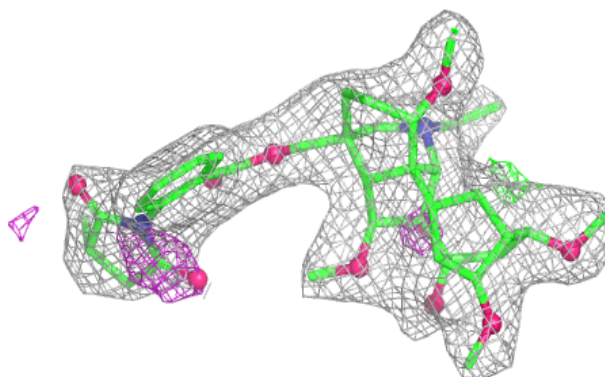
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around MLK H 301:

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

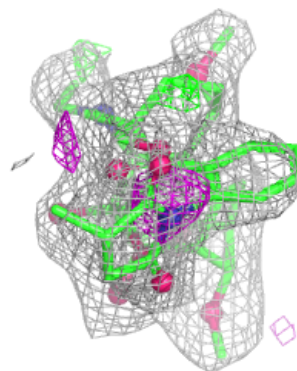
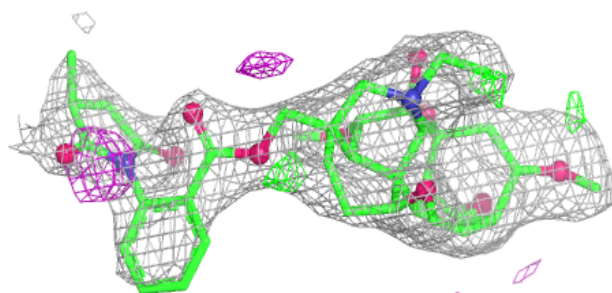
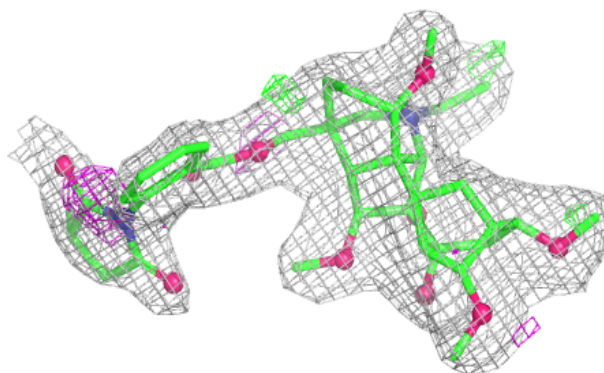
**Electron density around MLK I 301:**

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

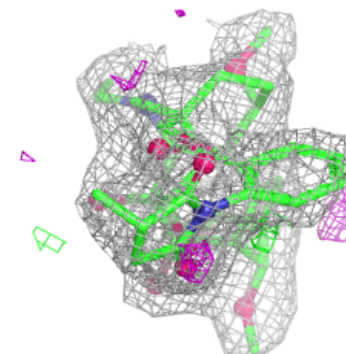
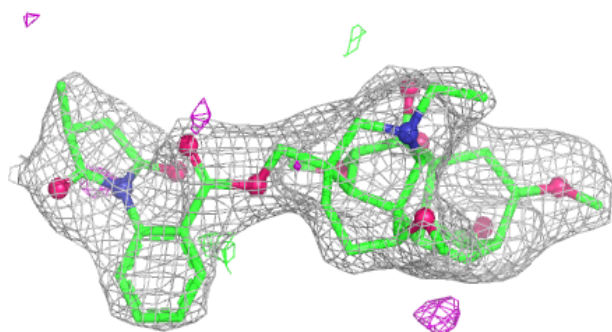
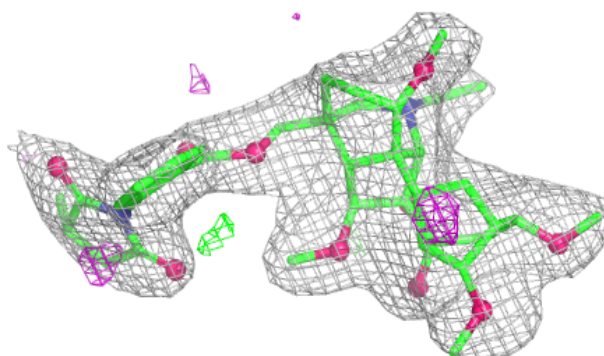


Electron density around MLK G 301:

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

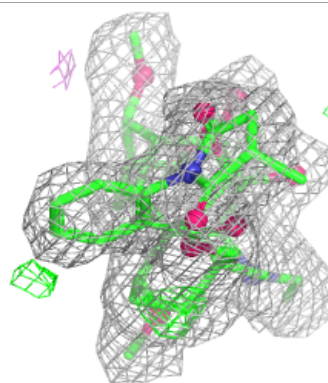
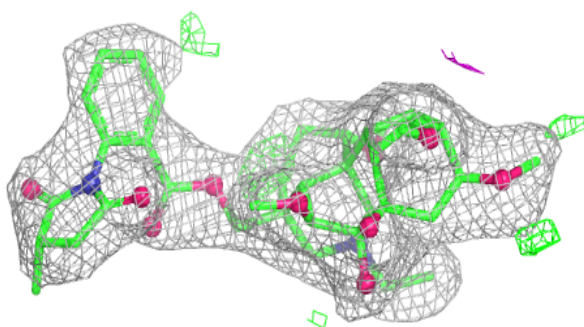
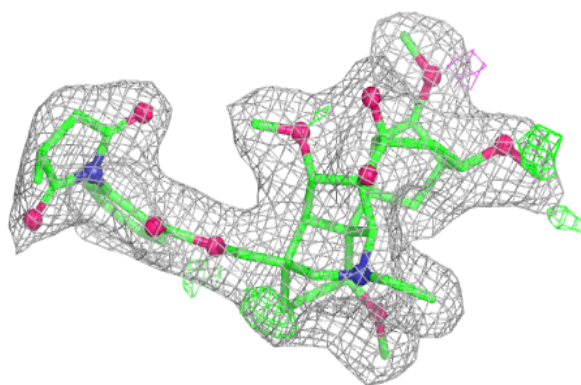
**Electron density around MLK F 301:**

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

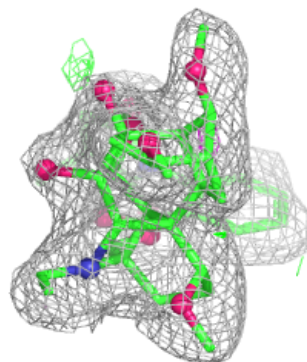
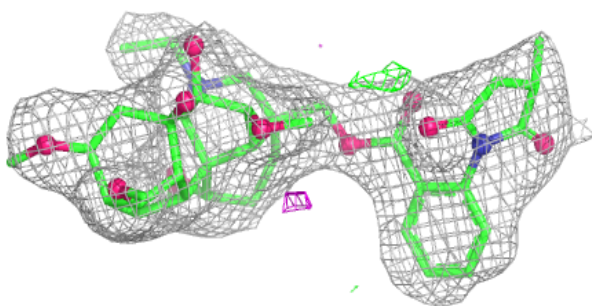
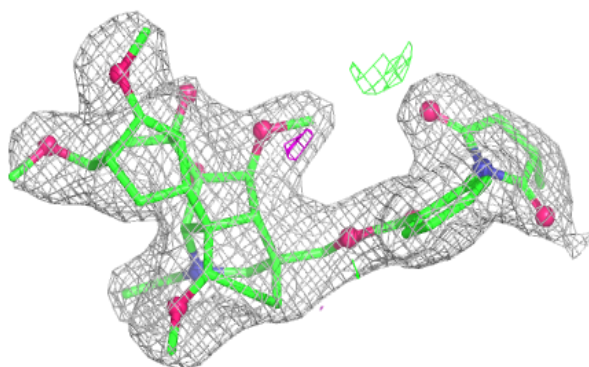


Electron density around MLK A 301:

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

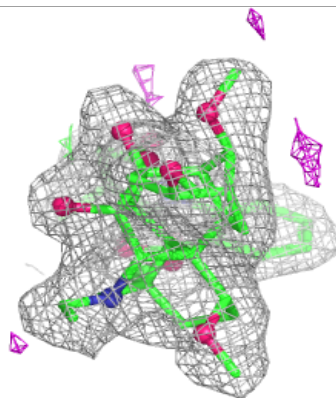
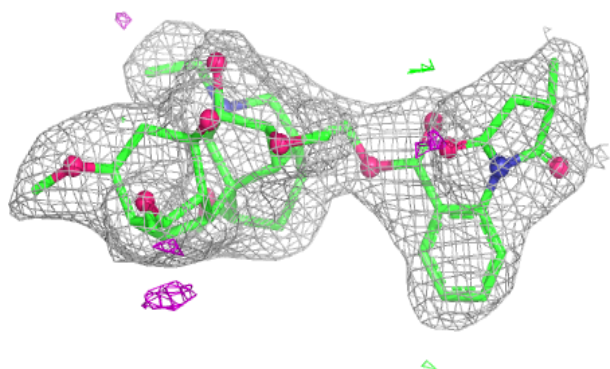
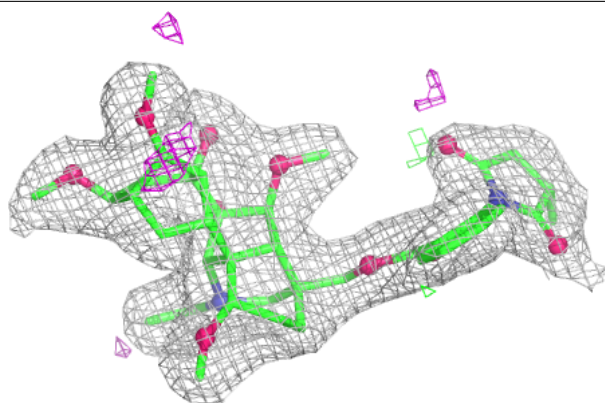
**Electron density around MLK D 301:**

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

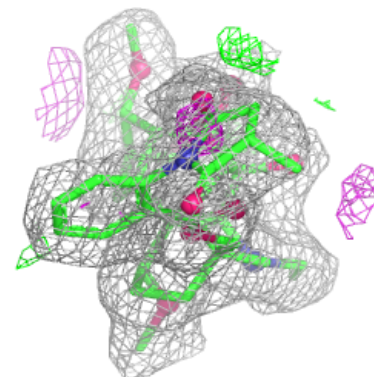
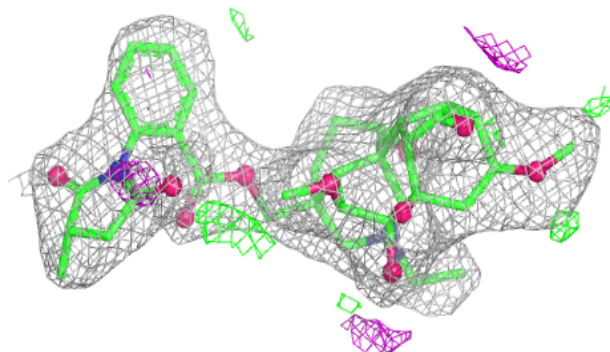
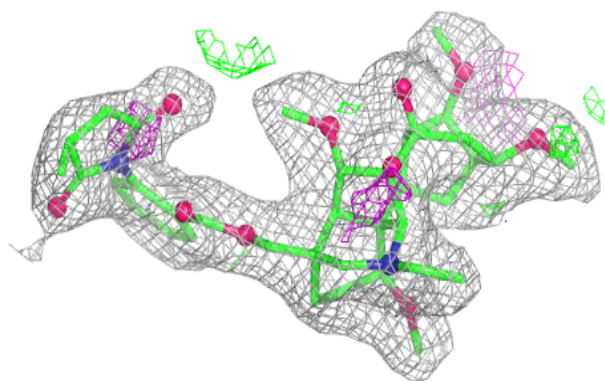


Electron density around MLK B 301:

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

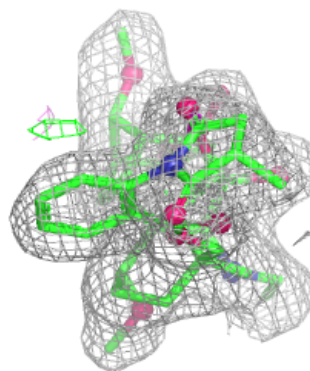
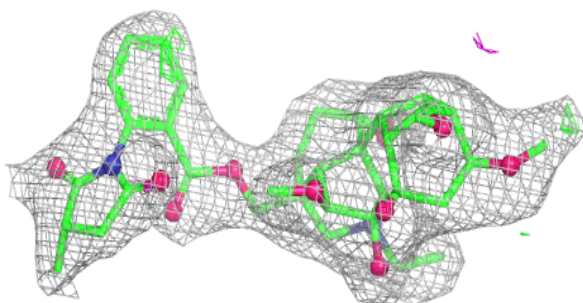
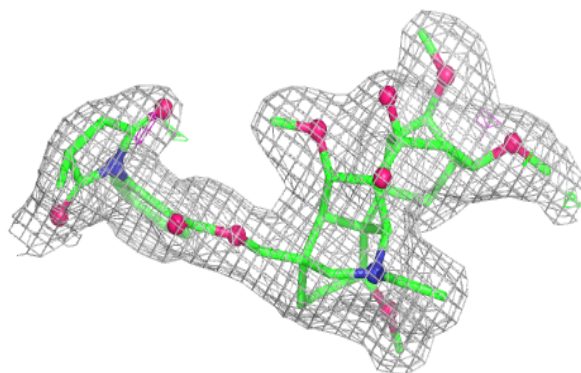
**Electron density around MLK E 301:**

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

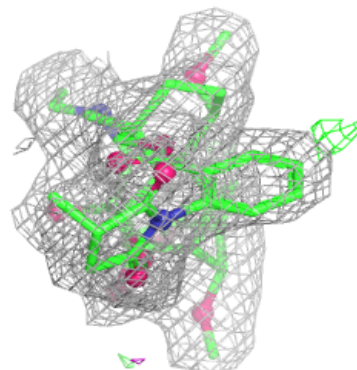
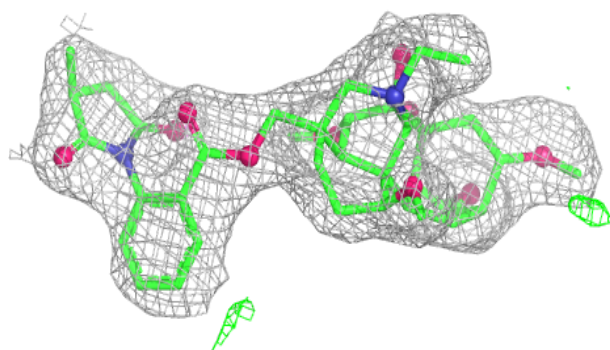
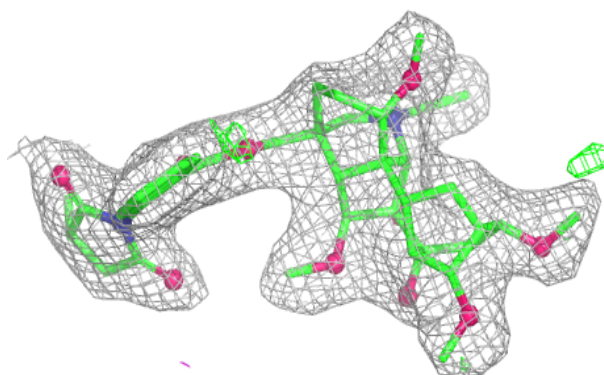


Electron density around MLK C 301:

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

**Electron density around MLK J 301:**

$2mF_o-DF_c$ (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.