



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 05:13 PM UTC

PDB ID : 3W9J / pdb_00003w9j
Title : Structural basis for the inhibition of bacterial multidrug exporters
Authors : Sakurai, K.; Nakashima, R.; Hayashi, K.; Yamaguchi, A.
Deposited on : 2013-04-04
Resolution : 3.15 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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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

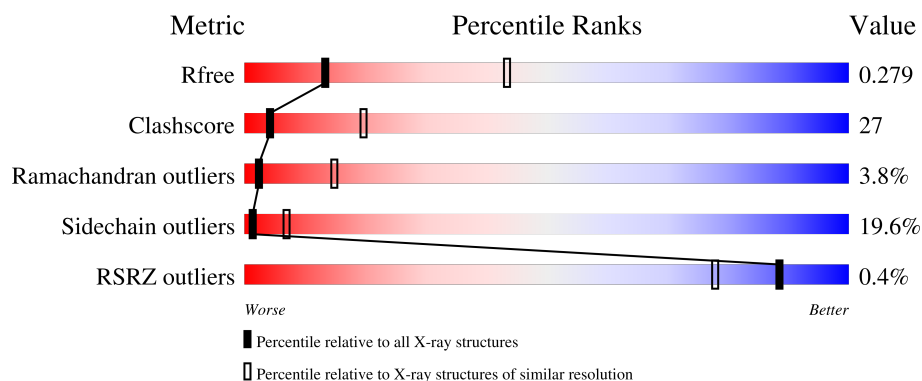
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.15 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	2361 (3.20-3.12)
Clashscore	190562	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)

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	1052	
1	B	1052	
1	C	1052	
1	D	1052	
1	E	1052	

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Mol	Chain	Length	Quality of chain
1	F	1052	% 45% 40% 11% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 47358 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 Multidrug resistance protein MexB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1018	Total	C	N	O	S	0	0	0
			7724	4975	1280	1429	40			
1	B	1030	Total	C	N	O	S	0	0	0
			7812	5027	1298	1447	40			
1	C	1030	Total	C	N	O	S	0	0	0
			7812	5027	1298	1447	40			
1	D	1019	Total	C	N	O	S	0	0	0
			7735	4984	1281	1430	40			
1	E	1030	Total	C	N	O	S	0	0	0
			7812	5027	1298	1447	40			
1	F	1033	Total	C	N	O	S	0	0	0
			7840	5046	1302	1452	40			

There are 36 discrepancies between the modelled and reference sequences:

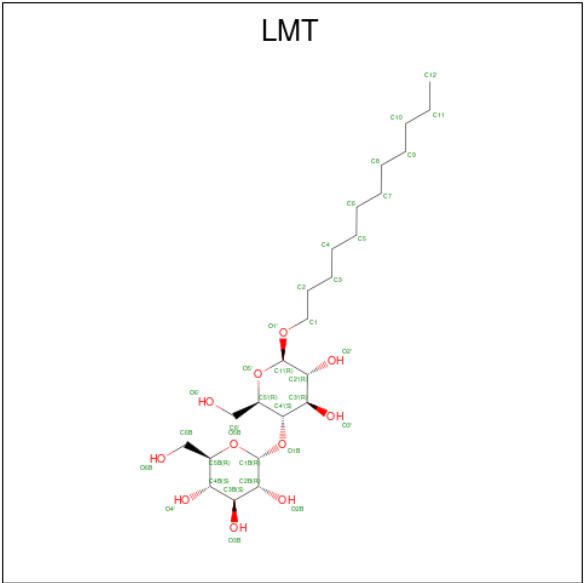
Chain	Residue	Modelled	Actual	Comment	Reference
A	1047	HIS	-	expression tag	UNP P52002
A	1048	HIS	-	expression tag	UNP P52002
A	1049	HIS	-	expression tag	UNP P52002
A	1050	HIS	-	expression tag	UNP P52002
A	1051	HIS	-	expression tag	UNP P52002
A	1052	HIS	-	expression tag	UNP P52002
B	1047	HIS	-	expression tag	UNP P52002
B	1048	HIS	-	expression tag	UNP P52002
B	1049	HIS	-	expression tag	UNP P52002
B	1050	HIS	-	expression tag	UNP P52002
B	1051	HIS	-	expression tag	UNP P52002
B	1052	HIS	-	expression tag	UNP P52002
C	1047	HIS	-	expression tag	UNP P52002
C	1048	HIS	-	expression tag	UNP P52002
C	1049	HIS	-	expression tag	UNP P52002
C	1050	HIS	-	expression tag	UNP P52002
C	1051	HIS	-	expression tag	UNP P52002

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1052	HIS	-	expression tag	UNP P52002
D	1047	HIS	-	expression tag	UNP P52002
D	1048	HIS	-	expression tag	UNP P52002
D	1049	HIS	-	expression tag	UNP P52002
D	1050	HIS	-	expression tag	UNP P52002
D	1051	HIS	-	expression tag	UNP P52002
D	1052	HIS	-	expression tag	UNP P52002
E	1047	HIS	-	expression tag	UNP P52002
E	1048	HIS	-	expression tag	UNP P52002
E	1049	HIS	-	expression tag	UNP P52002
E	1050	HIS	-	expression tag	UNP P52002
E	1051	HIS	-	expression tag	UNP P52002
E	1052	HIS	-	expression tag	UNP P52002
F	1047	HIS	-	expression tag	UNP P52002
F	1048	HIS	-	expression tag	UNP P52002
F	1049	HIS	-	expression tag	UNP P52002
F	1050	HIS	-	expression tag	UNP P52002
F	1051	HIS	-	expression tag	UNP P52002
F	1052	HIS	-	expression tag	UNP P52002

- Molecule 2 is DODECYL-BETA-D-MALTOSIDE (CCD ID: LMT) (formula: C₂₄H₄₆O₁₁).



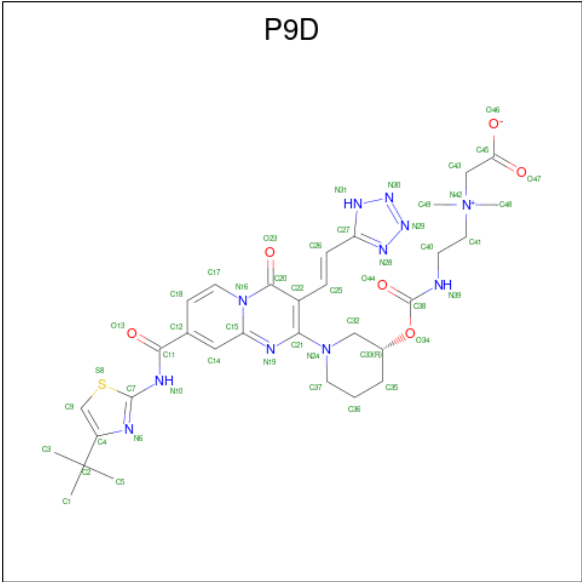
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			35	24	11		
2	A	1	Total	C	O	0	0
			35	24	11		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			35	24	11		
2	B	1	Total	C	O	0	0
			35	24	11		
2	B	1	Total	C	O	0	0
			35	24	11		
2	B	1	Total	C	O	0	0
			35	24	11		
2	C	1	Total	C	O	0	0
			35	24	11		
2	D	1	Total	C	O	0	0
			35	24	11		
2	D	1	Total	C	O	0	0
			35	24	11		
2	D	1	Total	C	O	0	0
			35	24	11		
2	E	1	Total	C	O	0	0
			35	24	11		
2	E	1	Total	C	O	0	0
			35	24	11		
2	E	1	Total	C	O	0	0
			35	24	11		
2	F	1	Total	C	O	0	0
			35	24	11		
2	F	1	Total	C	O	0	0
			35	24	11		

- Molecule 3 is [{2-[(3R)-1-{8-[(4-tert-butyl-1,3-thiazol-2-yl)carbamoyl]-4-oxo-3-[(E)-2-(1H-tetrazol-5-yl)ethenyl]-4H-pyrido[1,2-a]pyrimidin-2-yl}piperidin-3-yl]oxy}carbonyl)amino]ethyl}(dimethyl)ammonio]acetate (CCD ID: P9D) (formula: C₃₁H₃₉N₁₁O₆S).

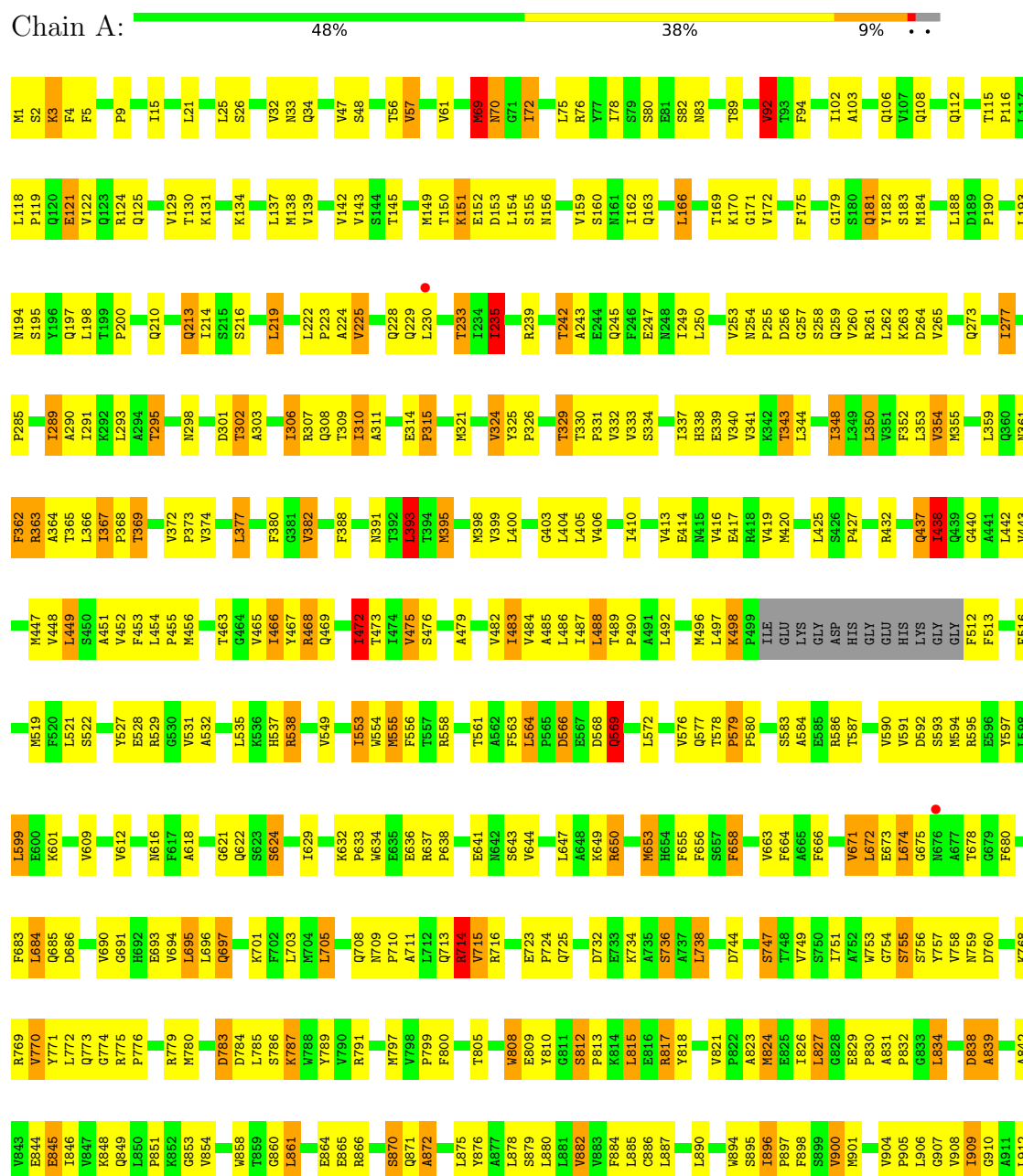


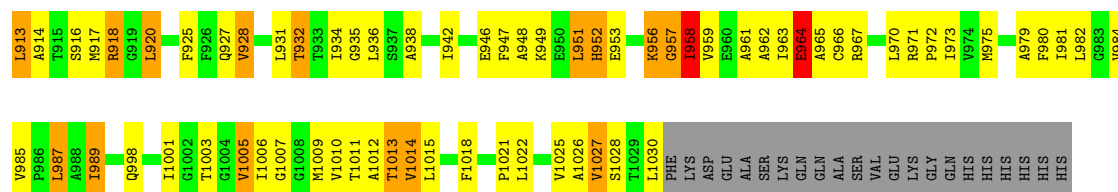
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	S	0	0
			49	31	11	6	1		
3	E	1	Total	C	N	O	S	0	0
			49	31	11	6	1		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

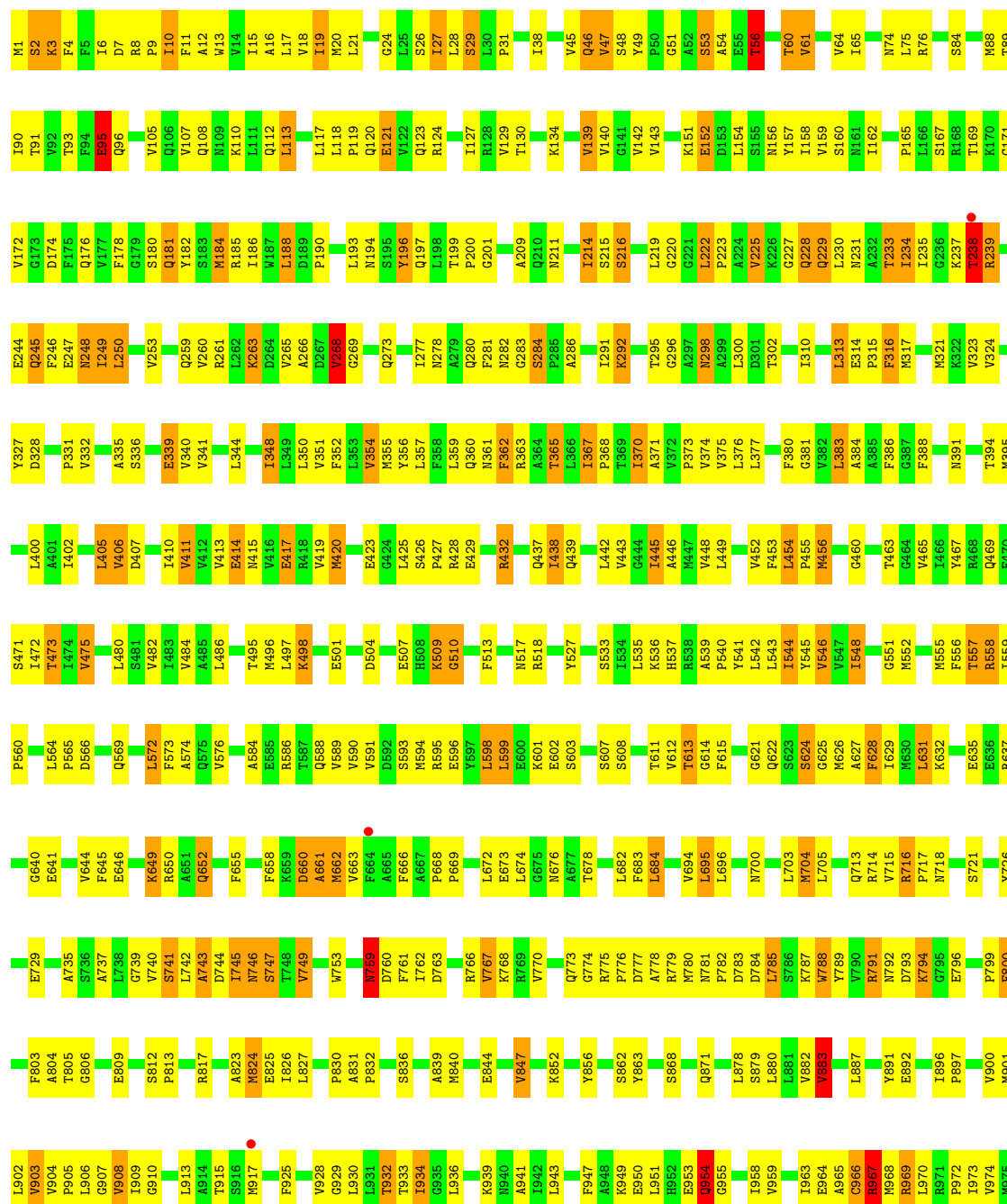
• Molecule 1: Multidrug resistance protein MexB

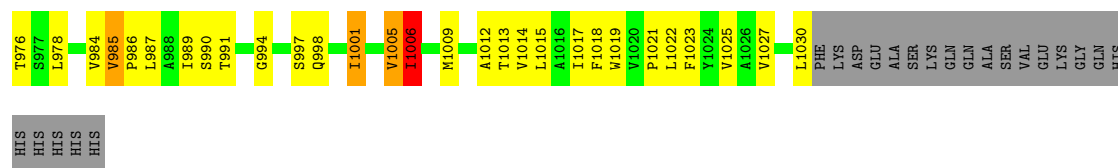




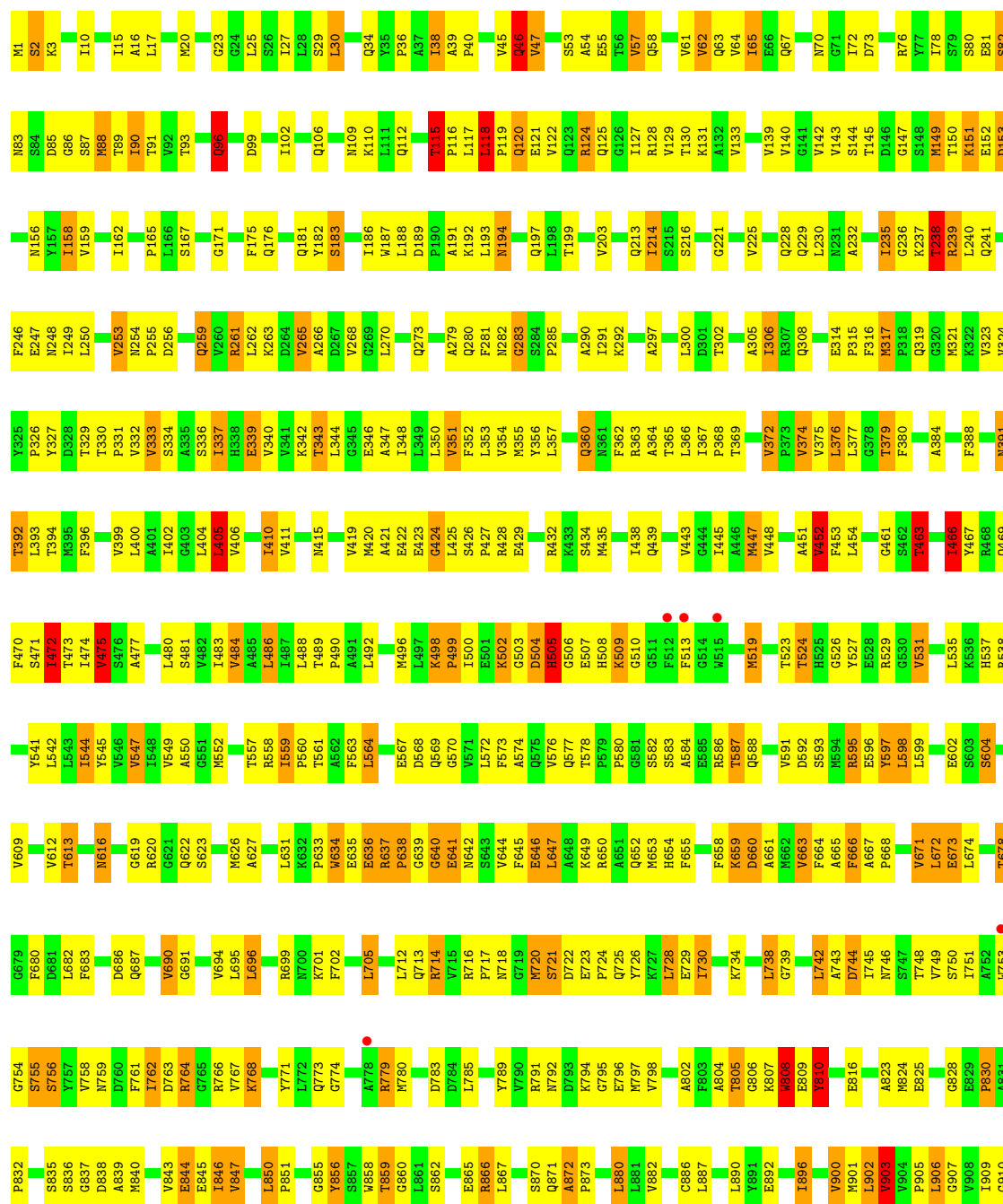
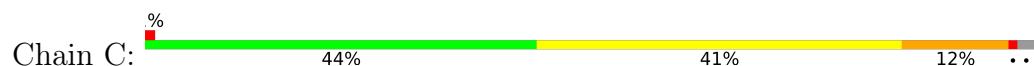
Molecule 1: Multidrug resistance protein MexB

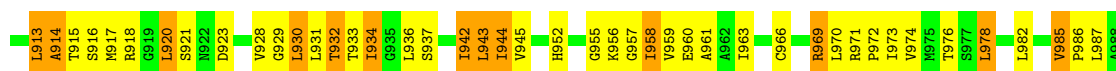
Chain B: 48% 39% 10% ..





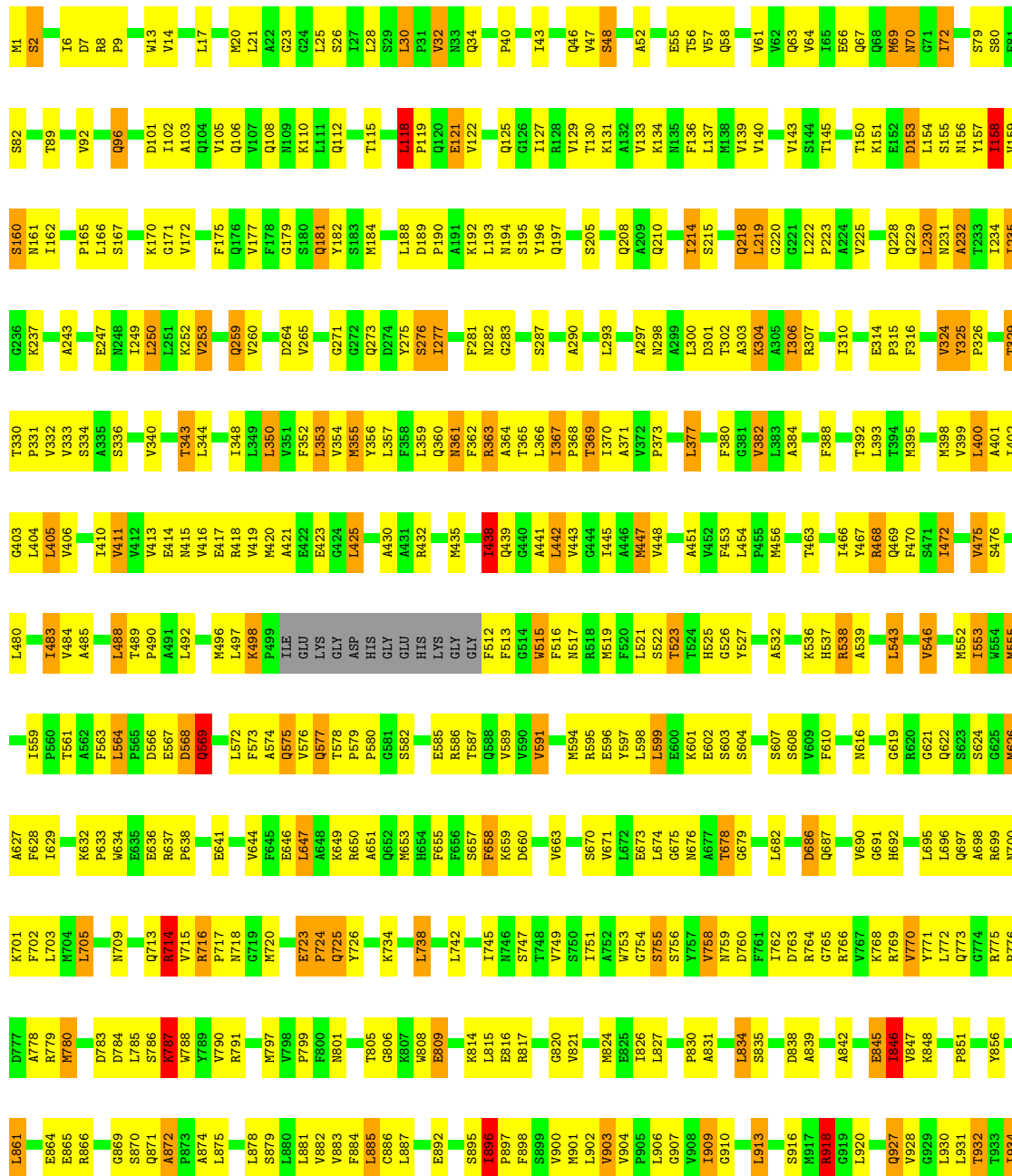
• Molecule 1: Multidrug resistance protein MexB

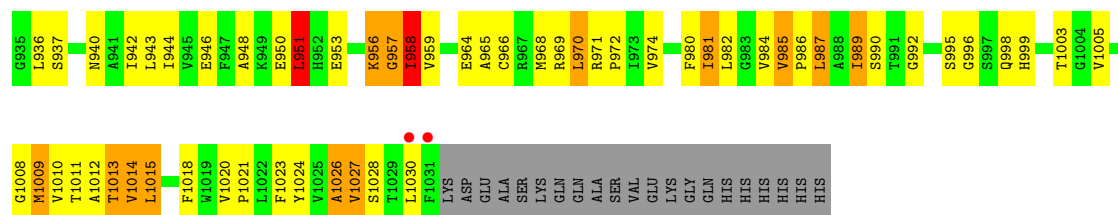




• Molecule 1: Multidrug resistance protein MexB

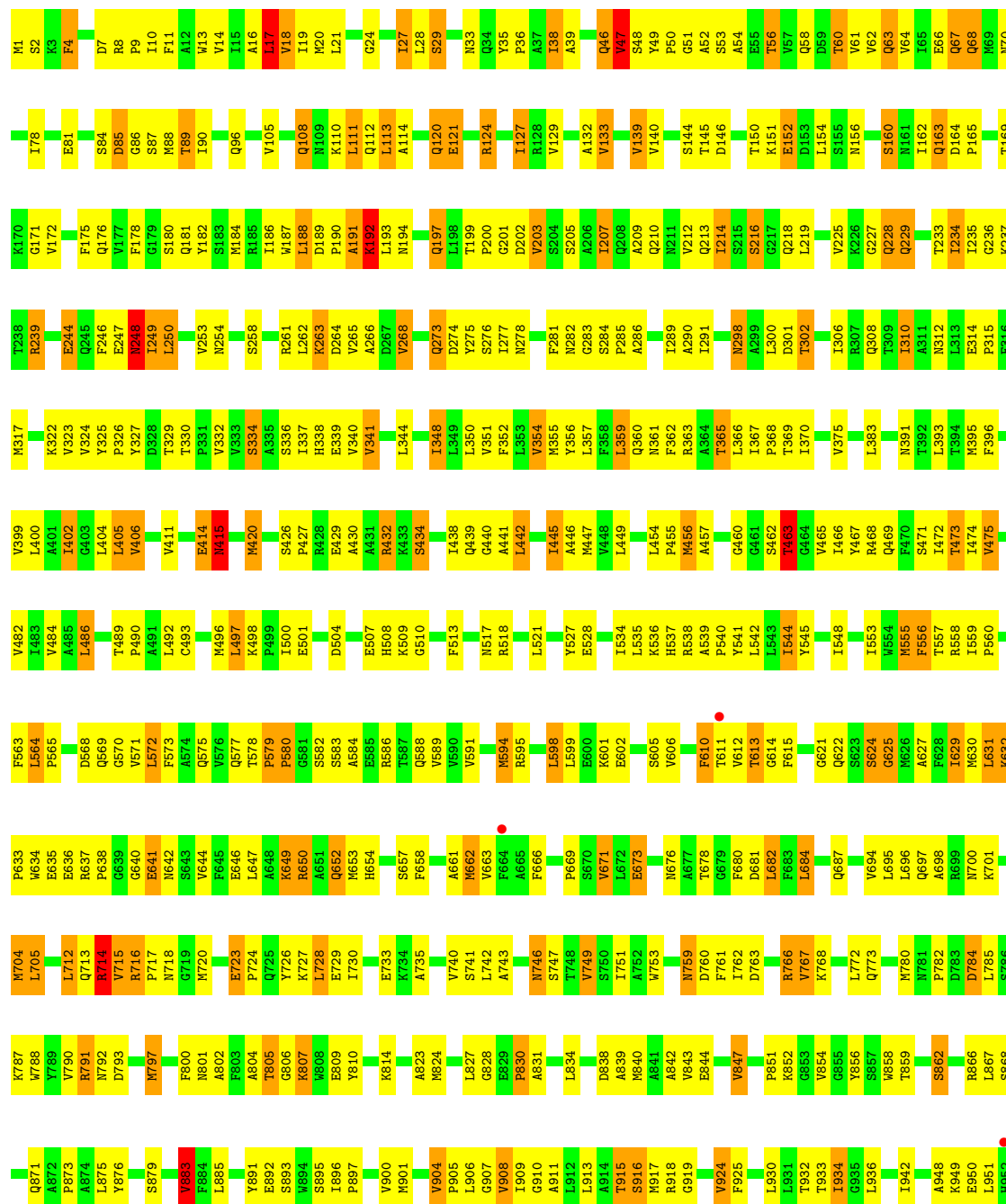
Chain D: 45% 41% 10% . .

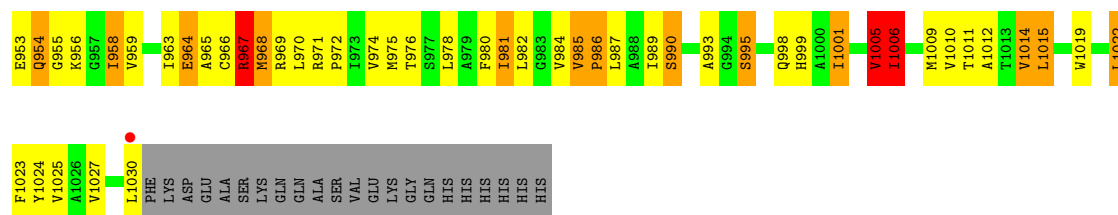




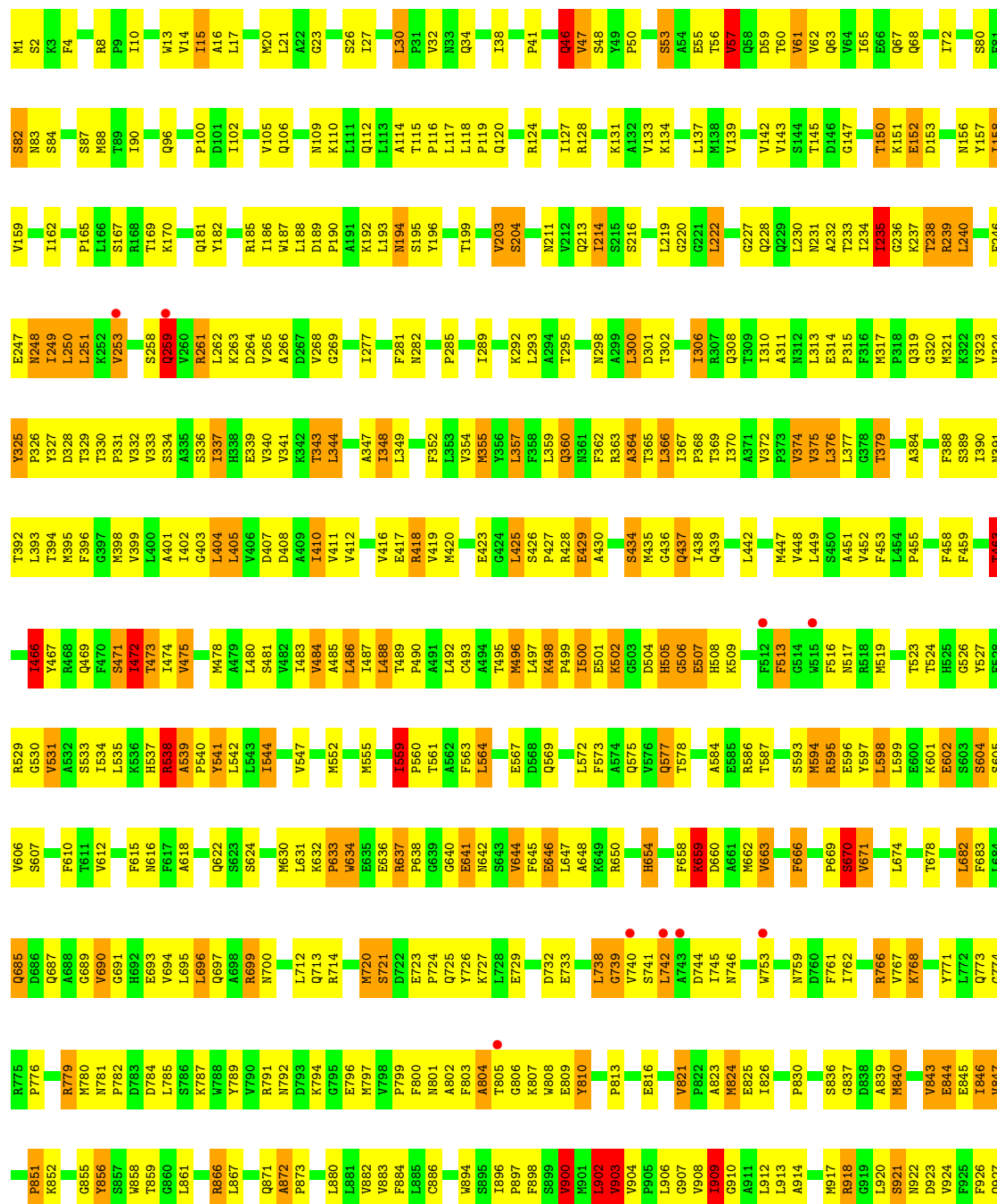
• Molecule 1: Multidrug resistance protein MexB

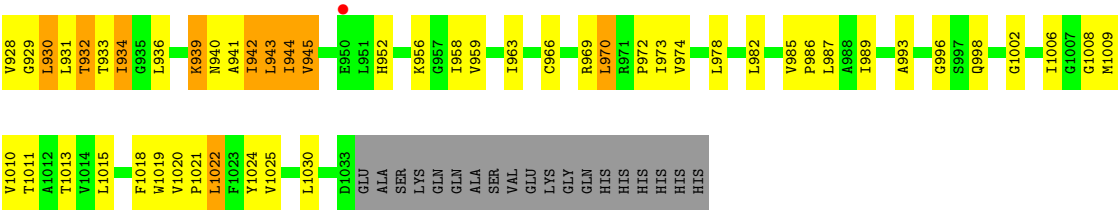
Chain E: 45% 39% 12% ..





• Molecule 1: Multidrug resistance protein MexB





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	126.20Å 137.03Å 152.28Å 85.75° 68.93° 87.39°	Depositor
Resolution (Å)	42.19 – 3.15 42.19 – 3.15	Depositor EDS
% Data completeness (in resolution range)	97.3 (42.19-3.15) 97.3 (42.19-3.15)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 3.12Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.202 , 0.279 0.202 , 0.279	Depositor DCC
R_{free} test set	7980 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	80.1	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 57.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	47358	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.64% 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: LMT, P9D

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	0.76	2/7880 (0.0%)	1.16	31/10712 (0.3%)
1	B	0.76	0/7971	1.15	26/10833 (0.2%)
1	C	0.71	0/7971	1.16	31/10833 (0.3%)
1	D	0.73	1/7892 (0.0%)	1.14	30/10728 (0.3%)
1	E	0.74	0/7971	1.14	28/10833 (0.3%)
1	F	0.73	0/8000	1.16	31/10871 (0.3%)
All	All	0.74	3/47685 (0.0%)	1.15	177/64810 (0.3%)

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
1	D	0	2
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	697	GLN	C-N	8.33	1.44	1.33
1	A	498	LYS	CA-C	6.07	1.60	1.52
1	D	498	LYS	CA-C	5.41	1.59	1.52

The worst 5 of 177 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	812	SER	CA-C-N	10.18	130.45	119.87
1	A	812	SER	C-N-CA	10.18	130.45	119.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	723	GLU	N-CA-C	9.19	118.70	108.14
1	A	675	GLY	N-CA-C	-9.01	102.30	111.85
1	F	325	TYR	CA-C-N	8.46	128.59	119.28

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	951	LEU	Peptide
1	D	691	GLY	Peptide
1	D	951	LEU	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	7724	0	7864	403	0
1	B	7812	0	7944	427	0
1	C	7812	0	7944	500	0
1	D	7735	0	7873	443	0
1	E	7812	0	7944	448	0
1	F	7840	0	7970	459	0
2	A	105	0	138	5	0
2	B	105	0	138	5	0
2	C	35	0	46	6	0
2	D	105	0	138	5	0
2	E	105	0	138	9	0
2	F	70	0	92	7	0
3	B	49	0	39	8	0
3	E	49	0	39	8	0
All	All	47358	0	48307	2597	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 27.

The worst 5 of 2597 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:D:780:MET:CE	1:F:220:GLY:HA2	1.75	1.17
1:C:142:VAL:HG21	1:C:321:MET:HE3	1.16	1.13
1:E:958:ILE:HD12	1:E:958:ILE:H	1.11	1.10
1:F:239:ARG:HG2	1:F:239:ARG:HH11	1.11	1.10
1:B:469:GLN:O	1:B:473:THR:HG22	1.52	1.10

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	1014/1052 (96%)	861 (85%)	122 (12%)	31 (3%)	3	18
1	B	1028/1052 (98%)	874 (85%)	127 (12%)	27 (3%)	4	21
1	C	1028/1052 (98%)	844 (82%)	129 (12%)	55 (5%)	1	9
1	D	1015/1052 (96%)	846 (83%)	130 (13%)	39 (4%)	2	15
1	E	1028/1052 (98%)	865 (84%)	127 (12%)	36 (4%)	3	16
1	F	1031/1052 (98%)	862 (84%)	125 (12%)	44 (4%)	2	13
All	All	6144/6312 (97%)	5152 (84%)	760 (12%)	232 (4%)	2	15

5 of 232 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	69	MET
1	A	70	ASN
1	A	498	LYS
1	A	673	GLU
1	A	714	ARG

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	833/860 (97%)	678 (81%)	155 (19%)	1	8
1	B	841/860 (98%)	676 (80%)	165 (20%)	1	7
1	C	841/860 (98%)	677 (80%)	164 (20%)	1	7
1	D	834/860 (97%)	681 (82%)	153 (18%)	2	8
1	E	841/860 (98%)	660 (78%)	181 (22%)	1	5
1	F	844/860 (98%)	676 (80%)	168 (20%)	1	7
All	All	5034/5160 (98%)	4048 (80%)	986 (20%)	1	7

5 of 986 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	900	VAL
1	F	434	SER
1	D	608	SER
1	F	379	THR
1	F	767	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 182 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	927	GLN
1	E	746	ASN
1	E	67	GLN
1	E	273	GLN
1	F	104	GLN

5.3.3 RNA ⓘ

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](#)

17 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	LMT	B	2002	-	36,36,36	0.77	1 (2%)	47,47,47	1.77	11 (23%)
2	LMT	D	2002	-	36,36,36	0.66	1 (2%)	47,47,47	1.35	4 (8%)
3	P9D	B	2001	-	53,53,53	2.38	16 (30%)	62,77,77	2.61	22 (35%)
2	LMT	F	2002	-	36,36,36	0.85	1 (2%)	47,47,47	1.36	5 (10%)
2	LMT	A	2001	-	36,36,36	0.76	1 (2%)	47,47,47	1.25	5 (10%)
2	LMT	D	2001	-	36,36,36	0.94	2 (5%)	47,47,47	1.47	7 (14%)
2	LMT	A	2003	-	36,36,36	0.69	1 (2%)	47,47,47	1.64	11 (23%)
2	LMT	E	2002	-	36,36,36	0.97	1 (2%)	47,47,47	1.47	9 (19%)
2	LMT	C	2001	-	36,36,36	0.71	1 (2%)	47,47,47	1.32	5 (10%)
2	LMT	E	2004	-	36,36,36	0.69	1 (2%)	47,47,47	1.11	3 (6%)
2	LMT	D	2003	-	36,36,36	0.81	1 (2%)	47,47,47	1.38	6 (12%)
2	LMT	B	2004	-	36,36,36	0.48	0	47,47,47	1.02	3 (6%)
2	LMT	F	2001	-	36,36,36	0.82	1 (2%)	47,47,47	2.00	13 (27%)
3	P9D	E	2001	-	53,53,53	2.40	15 (28%)	62,77,77	2.36	11 (17%)
2	LMT	B	2003	-	36,36,36	0.83	1 (2%)	47,47,47	1.61	10 (21%)
2	LMT	E	2003	-	36,36,36	0.76	1 (2%)	47,47,47	1.51	5 (10%)
2	LMT	A	2002	-	36,36,36	0.85	1 (2%)	47,47,47	1.74	15 (31%)

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	LMT	B	2002	-	-	12/21/61/61	0/2/2/2
2	LMT	D	2002	-	-	9/21/61/61	0/2/2/2
3	P9D	B	2001	-	-	24/39/49/49	0/5/5/5
2	LMT	F	2002	-	-	12/21/61/61	0/2/2/2
2	LMT	A	2001	-	-	14/21/61/61	0/2/2/2
2	LMT	D	2001	-	-	16/21/61/61	0/2/2/2
2	LMT	A	2003	-	-	11/21/61/61	0/2/2/2
2	LMT	E	2002	-	-	10/21/61/61	0/2/2/2
2	LMT	C	2001	-	-	14/21/61/61	0/2/2/2
2	LMT	E	2004	-	-	10/21/61/61	0/2/2/2
2	LMT	D	2003	-	-	7/21/61/61	0/2/2/2
2	LMT	B	2004	-	-	9/21/61/61	0/2/2/2
2	LMT	F	2001	-	-	12/21/61/61	0/2/2/2
3	P9D	E	2001	-	-	21/39/49/49	1/5/5/5
2	LMT	B	2003	-	-	8/21/61/61	0/2/2/2
2	LMT	E	2003	-	-	14/21/61/61	0/2/2/2
2	LMT	A	2002	-	-	13/21/61/61	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2001	P9D	C7-S8	-8.30	1.62	1.74
3	E	2001	P9D	C7-S8	-7.12	1.64	1.74
3	E	2001	P9D	O34-C38	6.54	1.46	1.35
3	B	2001	P9D	N30-N29	6.05	1.41	1.30
3	E	2001	P9D	C9-C4	5.59	1.41	1.35

The worst 5 of 145 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	2001	P9D	C9-S8-C7	10.64	96.67	88.40
3	E	2001	P9D	C9-S8-C7	9.26	95.60	88.40
3	B	2001	P9D	N31-C27-N28	6.77	117.45	108.92
3	E	2001	P9D	C4-C9-S8	-6.72	104.42	111.32
3	B	2001	P9D	C4-C9-S8	-6.26	104.90	111.32

There are no chirality outliers.

5 of 216 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	2001	LMT	O5'-C1'-O1'-C1
2	A	2002	LMT	C3'-C4'-O1B-C1B
2	B	2004	LMT	C2-C1-O1'-C1'
2	D	2001	LMT	C2'-C1'-O1'-C1
2	D	2001	LMT	O5'-C1'-O1'-C1

All (1) ring outliers are listed below:

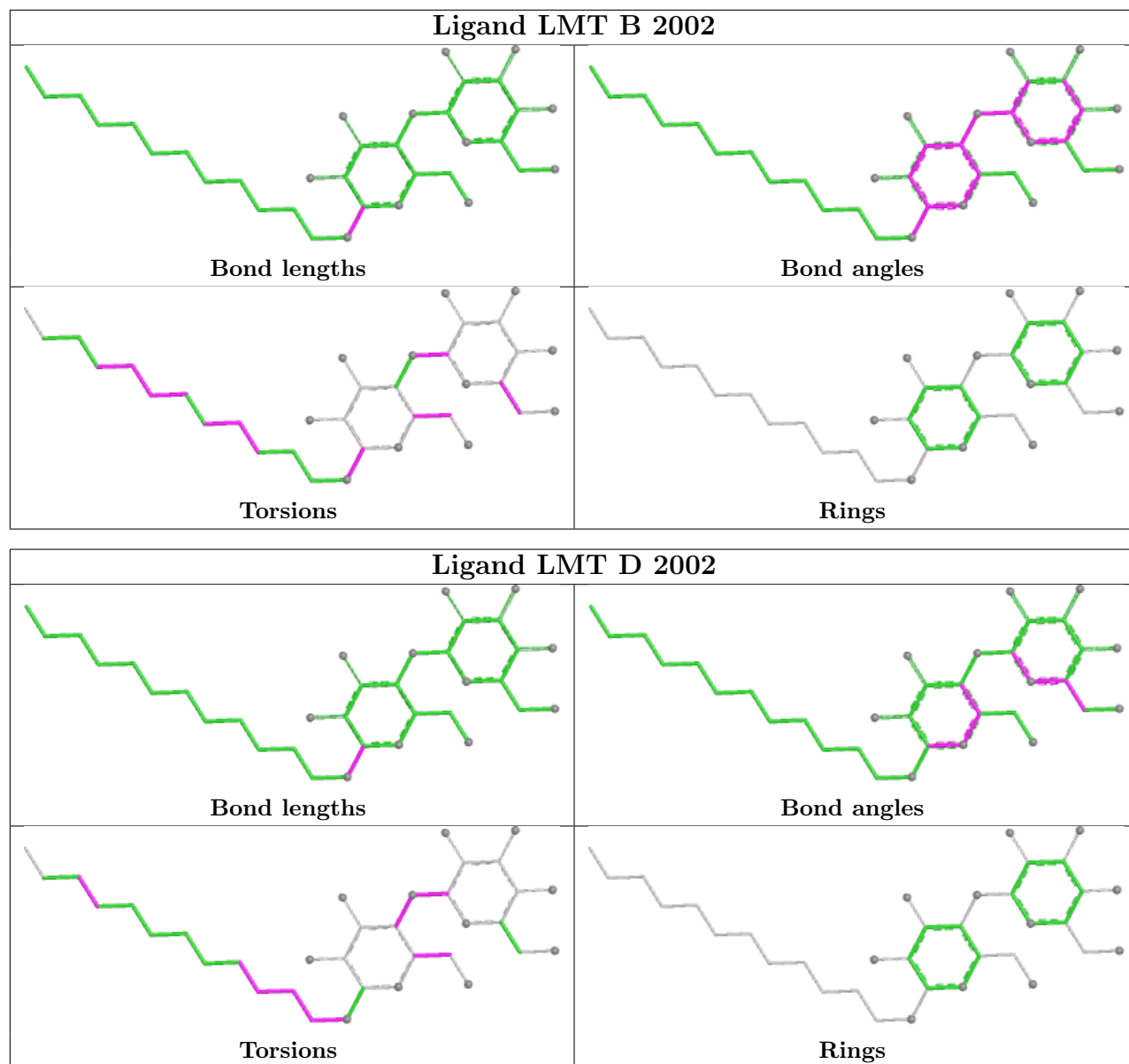
Mol	Chain	Res	Type	Atoms
3	E	2001	P9D	C32-C33-C35-C36-C37-N24

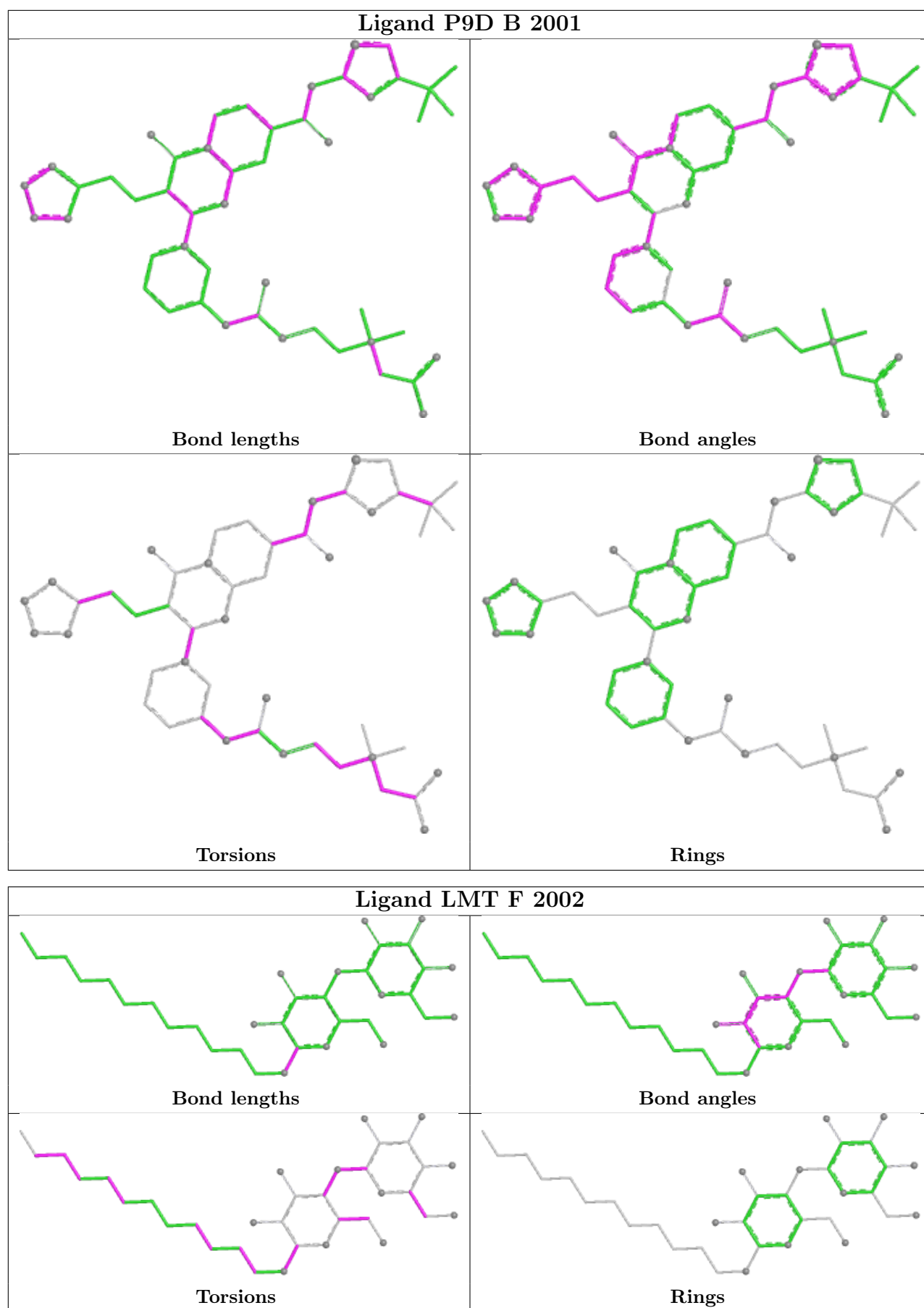
16 monomers are involved in 53 short contacts:

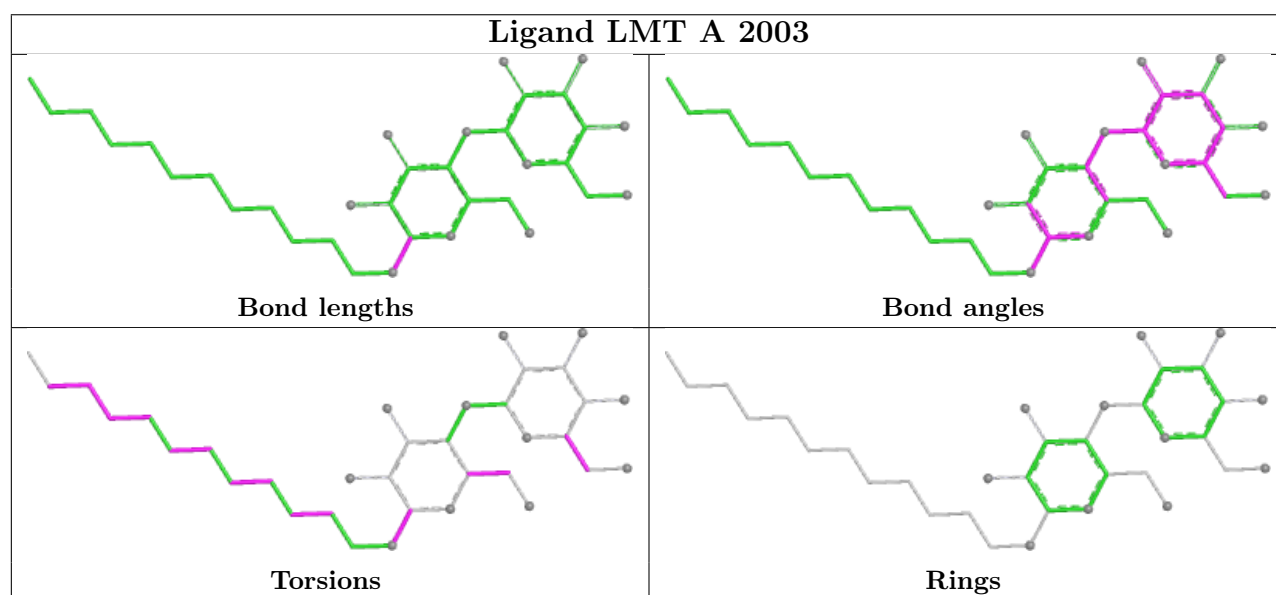
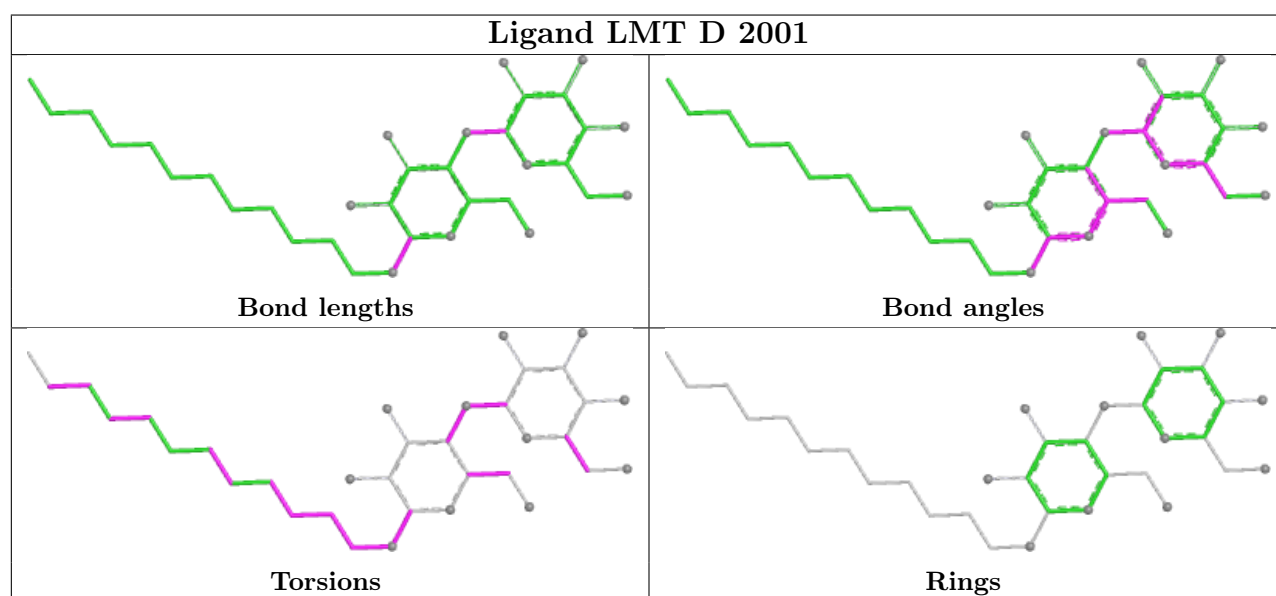
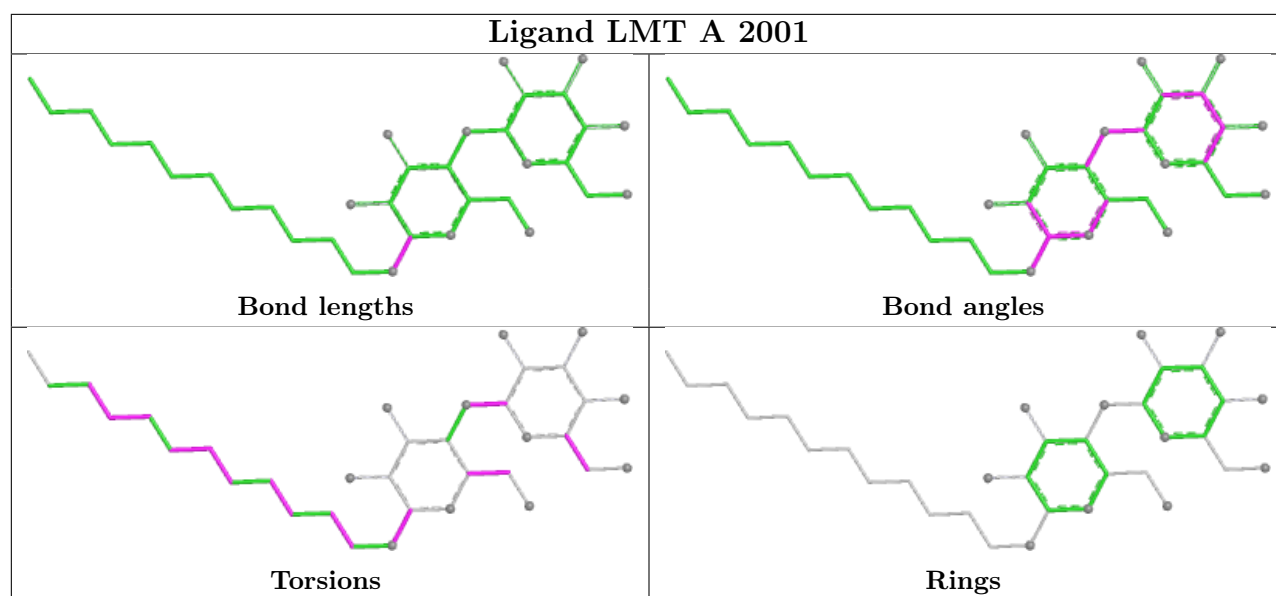
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2002	LMT	2	0
2	D	2002	LMT	1	0
3	B	2001	P9D	8	0
2	F	2002	LMT	3	0
2	A	2001	LMT	2	0
2	D	2001	LMT	2	0
2	A	2003	LMT	1	0
2	E	2002	LMT	8	0
2	C	2001	LMT	6	0
2	D	2003	LMT	2	0
2	B	2004	LMT	1	0
2	F	2001	LMT	4	0
3	E	2001	P9D	8	0
2	B	2003	LMT	2	0
2	E	2003	LMT	1	0
2	A	2002	LMT	2	0

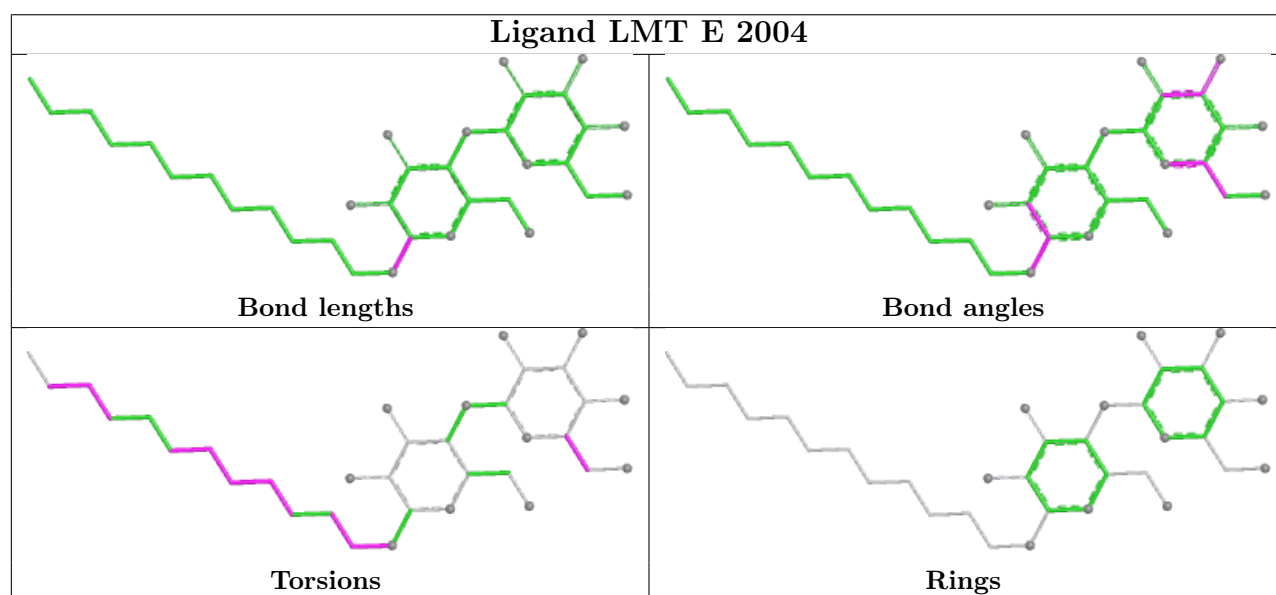
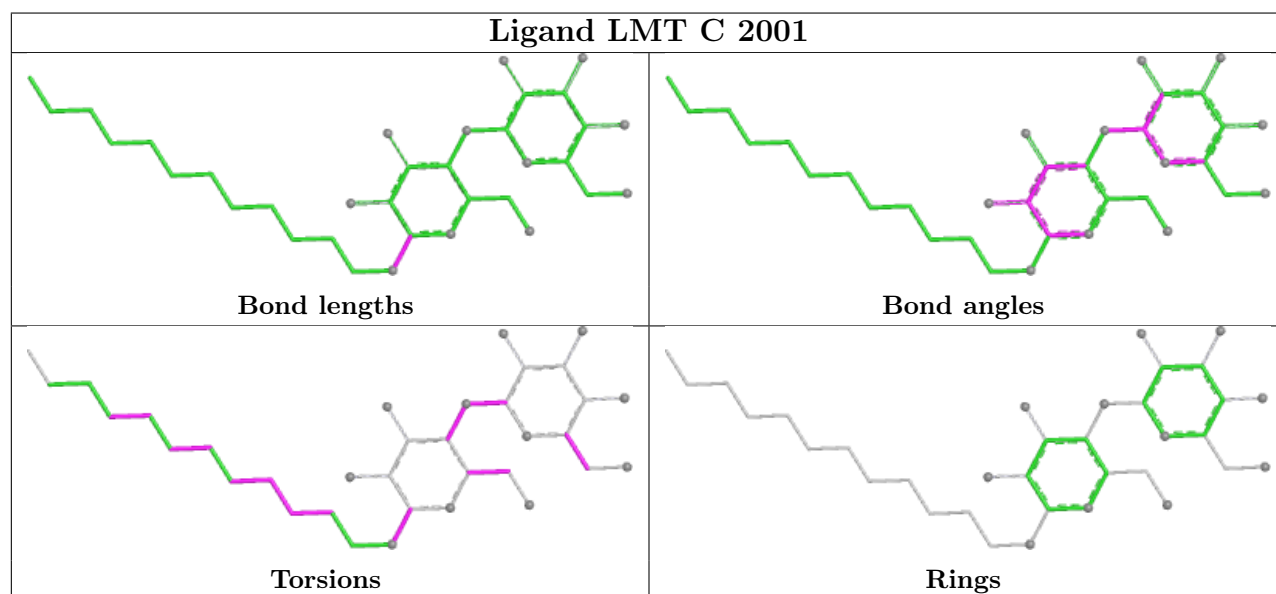
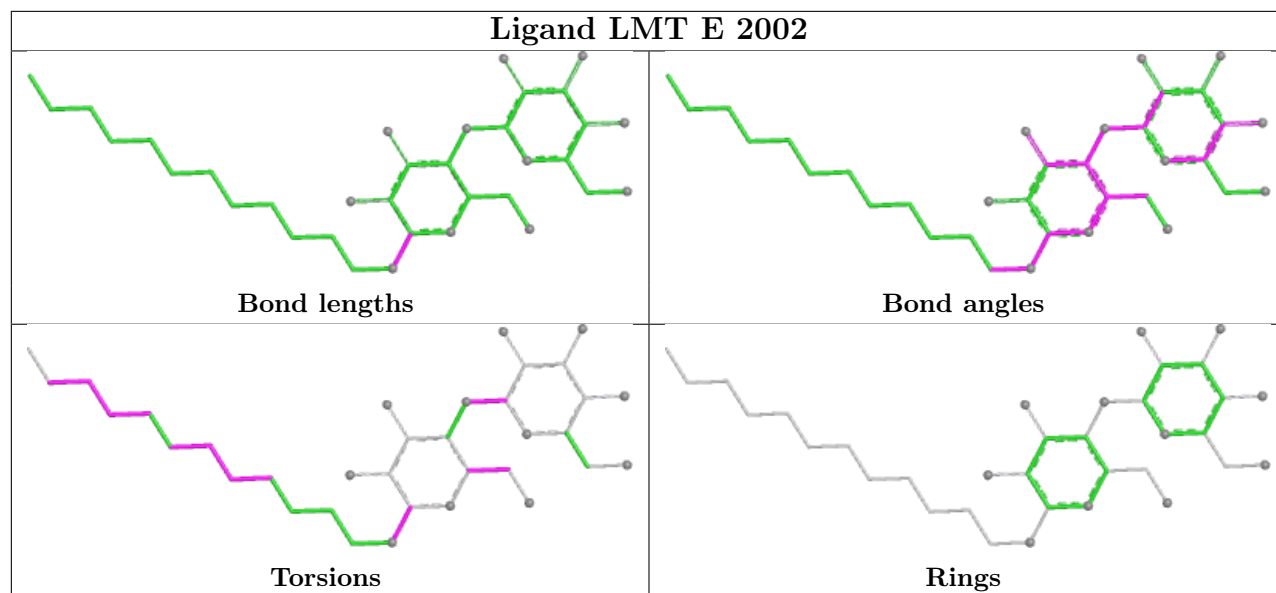
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

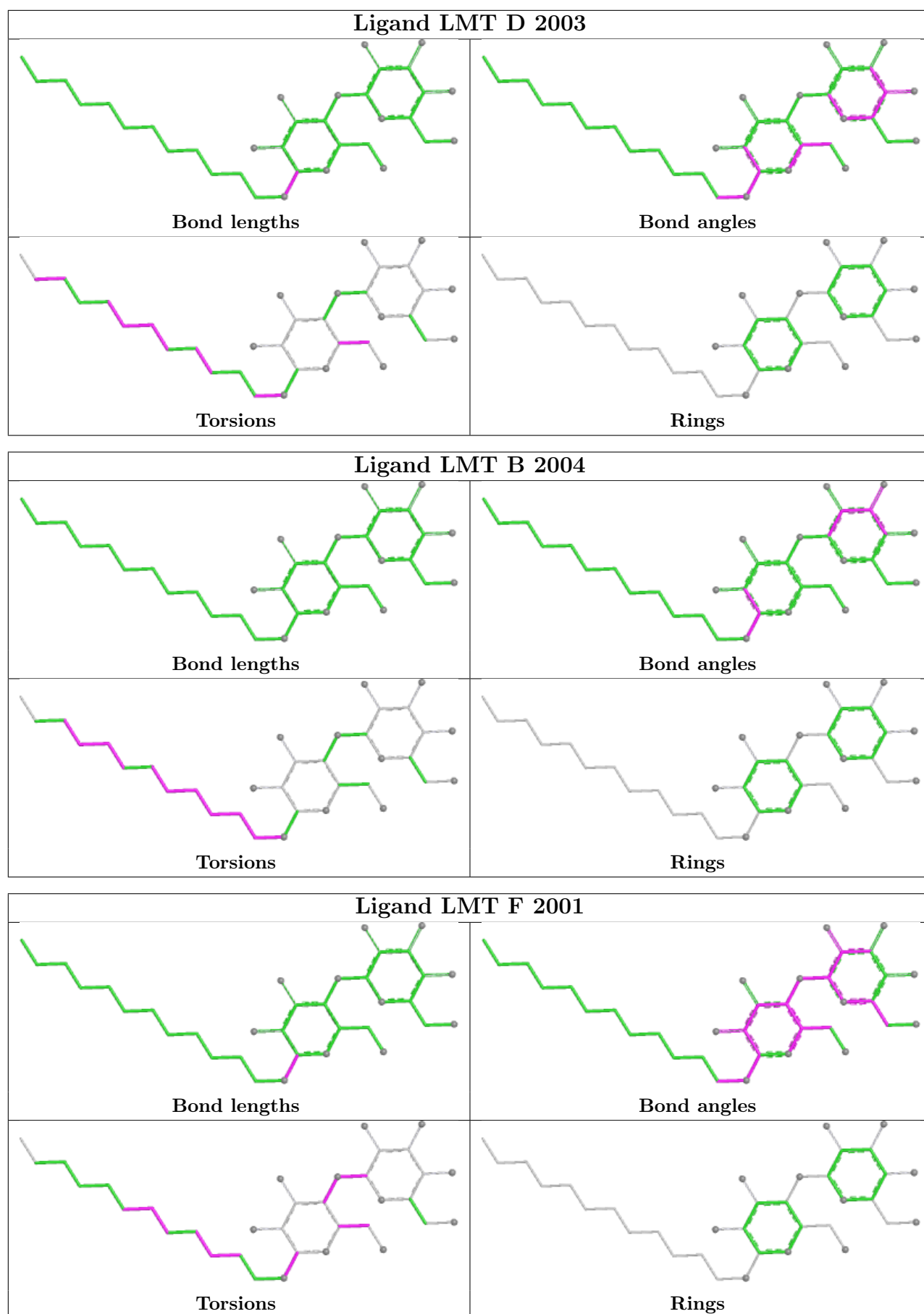
any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

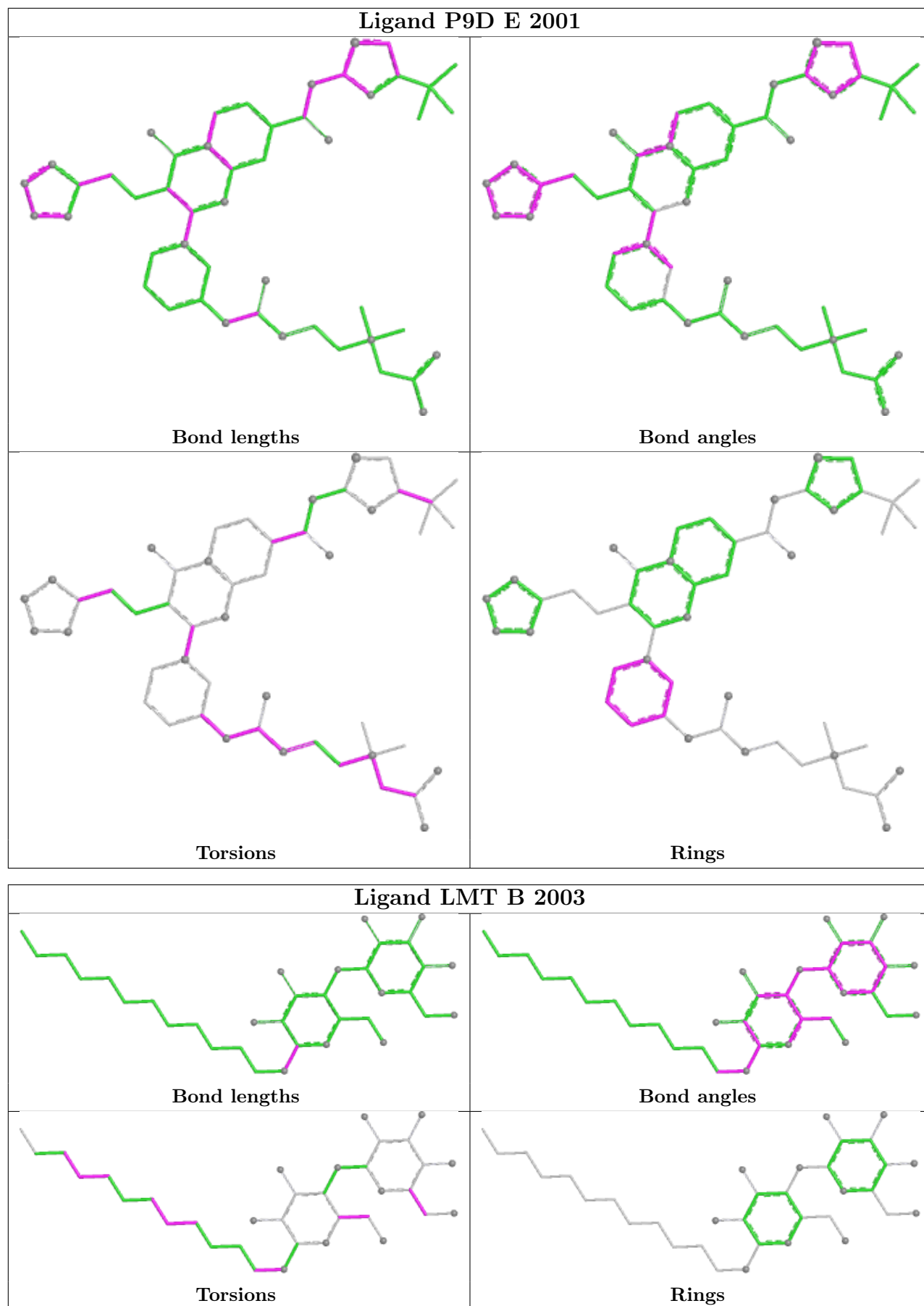


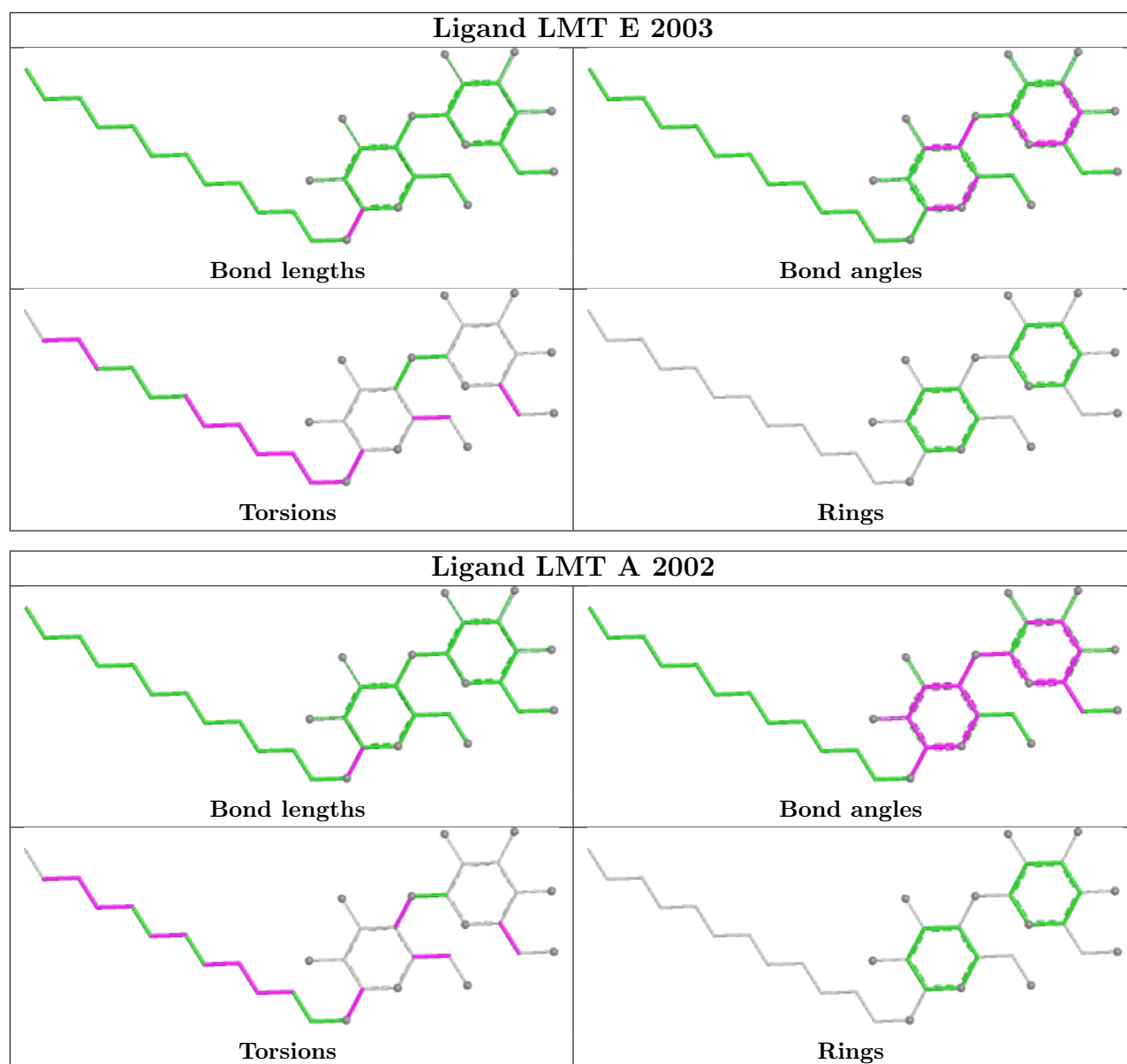












5.7 Other polymers [i](#)

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	1018/1052 (96%)	-0.40	2 (0%) 91 84	39, 75, 112, 164	0
1	B	1030/1052 (97%)	-0.47	3 (0%) 90 81	40, 73, 113, 152	0
1	C	1030/1052 (97%)	-0.23	6 (0%) 85 72	43, 87, 143, 201	0
1	D	1019/1052 (96%)	-0.39	2 (0%) 91 84	47, 78, 117, 160	0
1	E	1030/1052 (97%)	-0.38	4 (0%) 88 78	46, 78, 124, 162	0
1	F	1033/1052 (98%)	-0.29	10 (0%) 79 62	45, 79, 129, 264	0
All	All	6160/6312 (97%)	-0.36	27 (0%) 88 78	39, 78, 124, 264	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	1031	PHE	5.8
1	F	740	VAL	4.1
1	F	742	LEU	3.5
1	A	676	ASN	3.3
1	D	1030	LEU	3.1

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

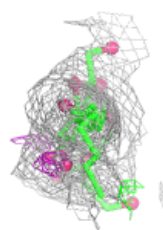
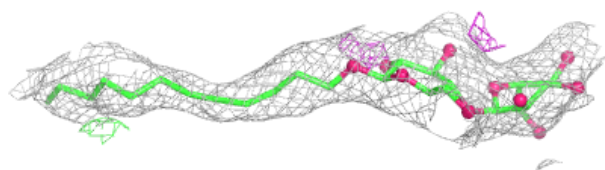
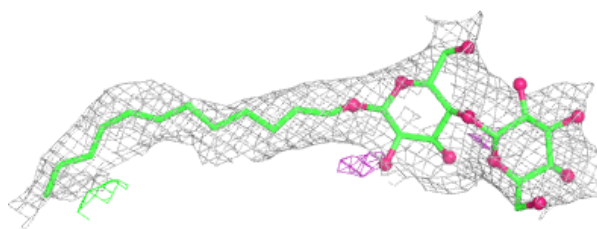
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	LMT	C	2001	35/35	0.79	0.12	80,105,146,151	0
2	LMT	F	2001	35/35	0.80	0.13	82,104,126,139	0
2	LMT	D	2003	35/35	0.84	0.14	70,98,134,144	0
2	LMT	F	2002	35/35	0.85	0.12	76,118,147,148	0
2	LMT	A	2001	35/35	0.87	0.21	43,66,94,103	35
2	LMT	D	2001	35/35	0.89	0.21	47,65,79,89	35
2	LMT	A	2003	35/35	0.89	0.11	64,90,115,120	0
2	LMT	E	2002	35/35	0.90	0.15	67,106,124,132	0
2	LMT	E	2003	35/35	0.90	0.11	67,94,108,124	0
2	LMT	B	2002	35/35	0.92	0.14	63,106,135,137	0
2	LMT	E	2004	35/35	0.92	0.10	67,74,100,103	0
2	LMT	B	2003	35/35	0.92	0.10	71,82,104,111	0
2	LMT	A	2002	35/35	0.92	0.10	60,86,132,142	0
2	LMT	D	2002	35/35	0.93	0.10	69,111,137,144	0
2	LMT	B	2004	35/35	0.94	0.09	62,69,78,84	0
3	P9D	E	2001	49/49	0.94	0.10	60,78,108,123	0
3	P9D	B	2001	49/49	0.95	0.09	53,71,85,108	0

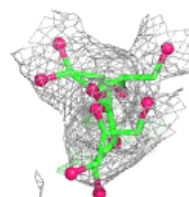
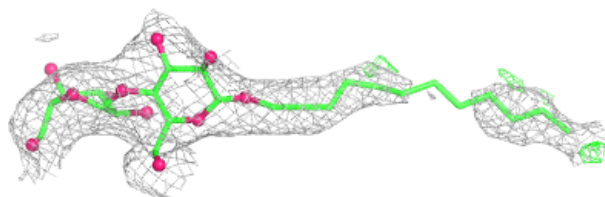
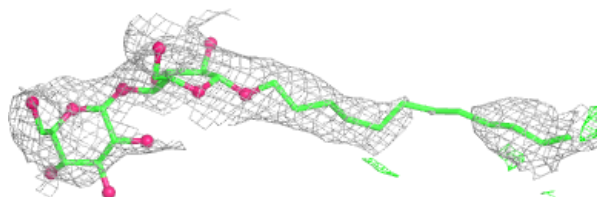
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around LMT C 2001:

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

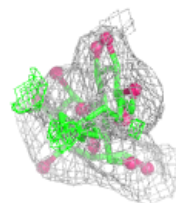
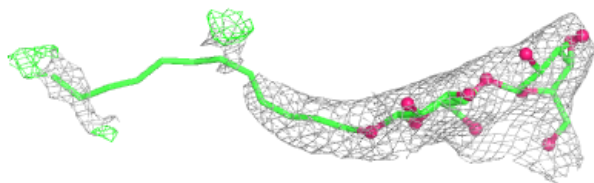
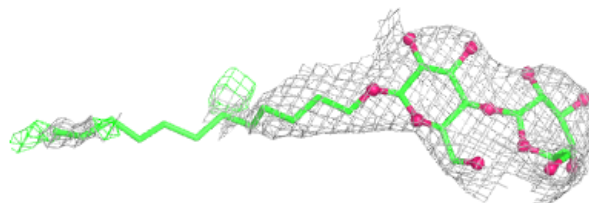
**Electron density around LMT F 2001:**

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

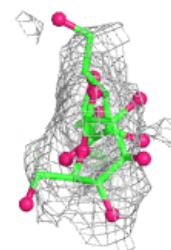
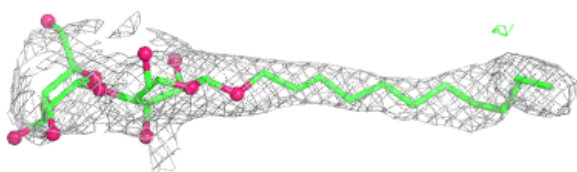
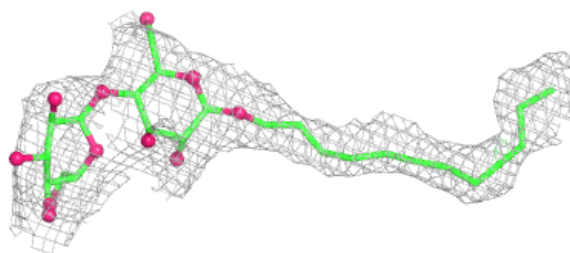


Electron density around LMT D 2003:

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

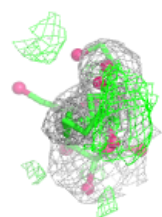
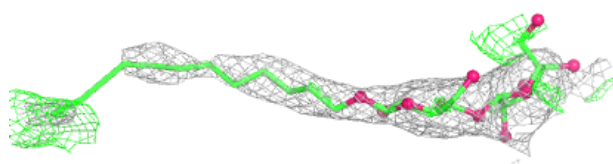
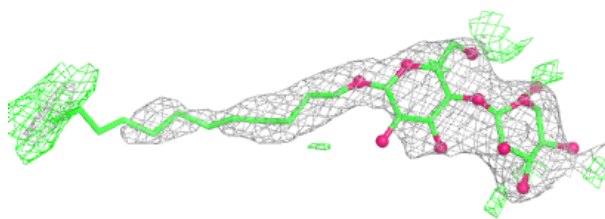
**Electron density around LMT F 2002:**

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

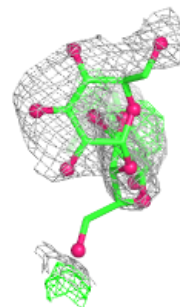
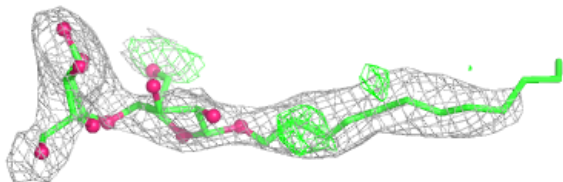
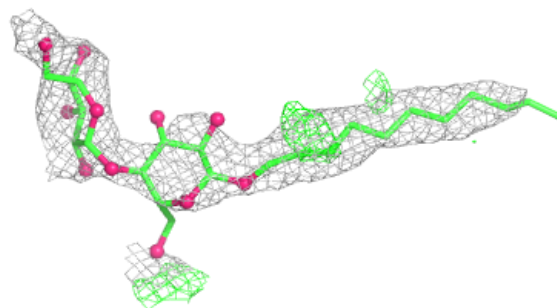


Electron density around LMT A 2001:

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

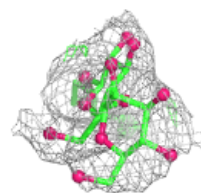
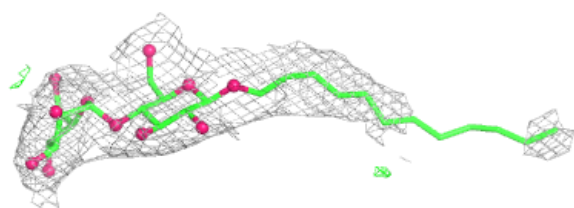
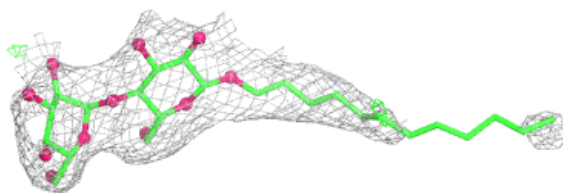
**Electron density around LMT D 2001:**

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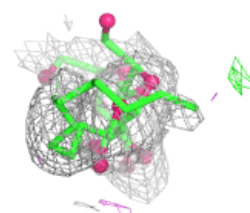
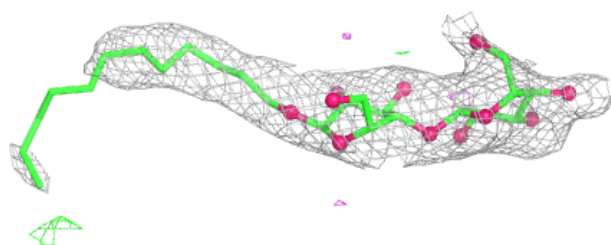
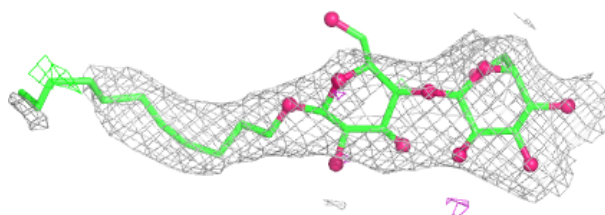


Electron density around LMT A 2003:

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

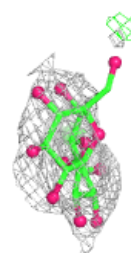
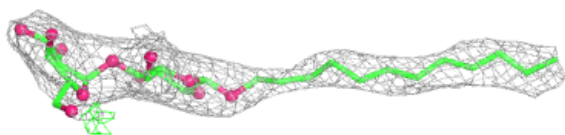
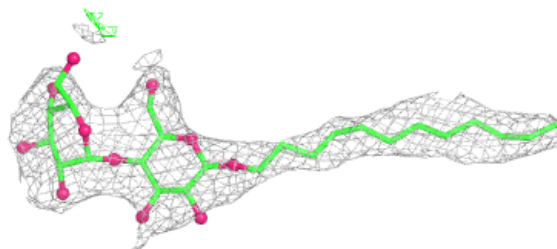
**Electron density around LMT E 2002:**

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

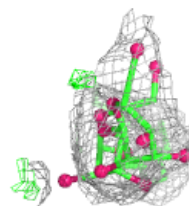
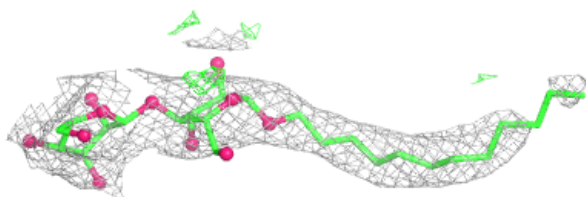
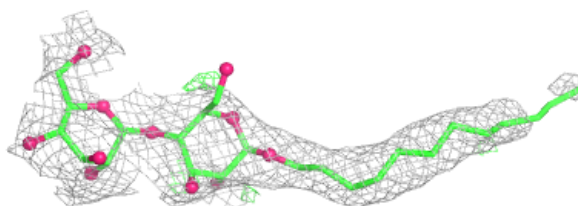


Electron density around LMT E 2003:

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

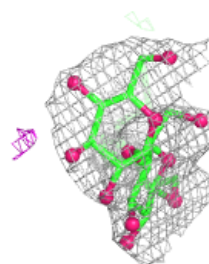
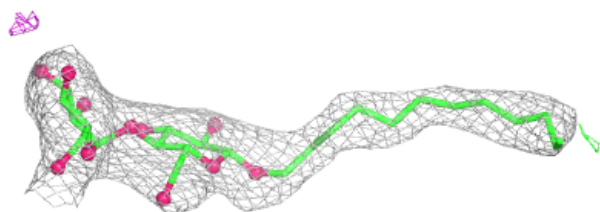
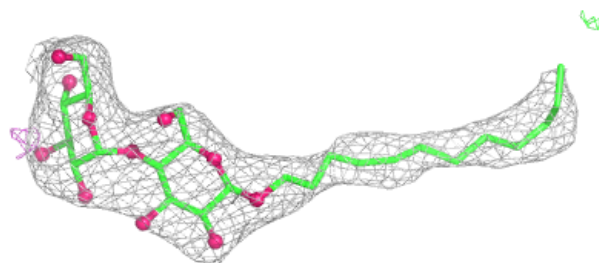
**Electron density around LMT B 2002:**

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and green (positive)

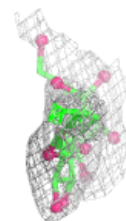
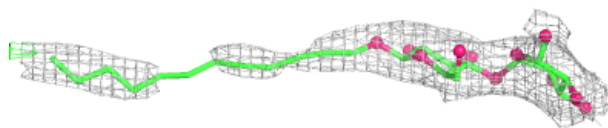
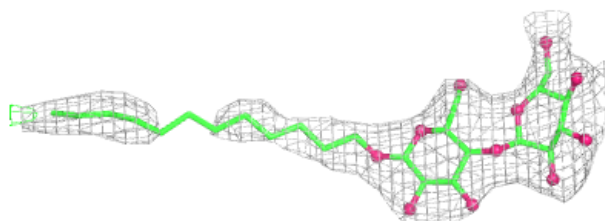


Electron density around LMT E 2004:

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

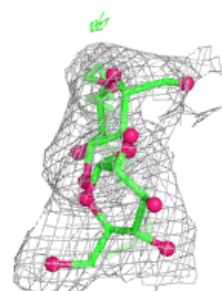
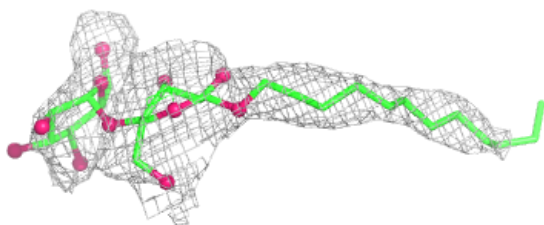
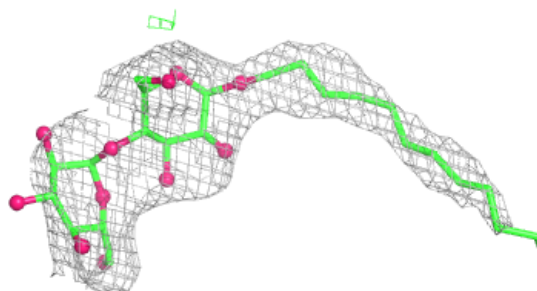
**Electron density around LMT B 2003:**

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

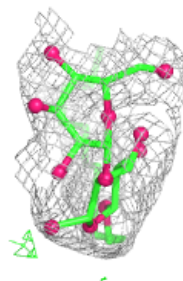
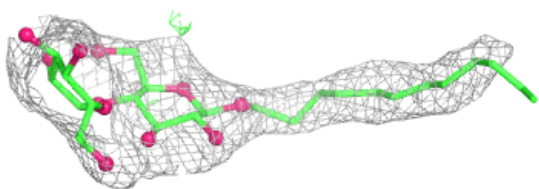
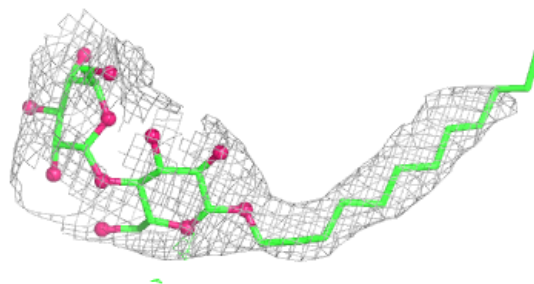


Electron density around LMT A 2002:

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

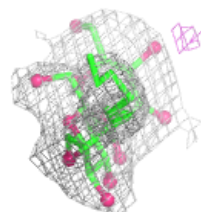
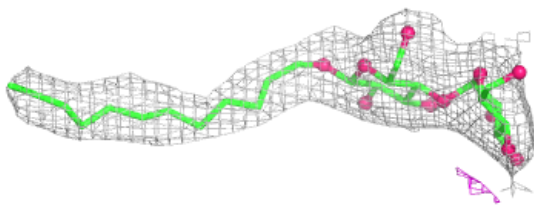
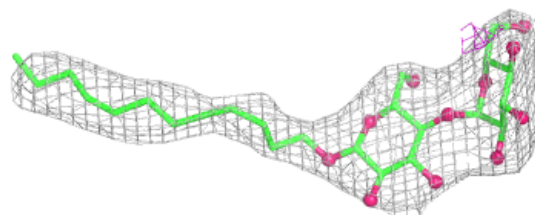
**Electron density around LMT D 2002:**

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

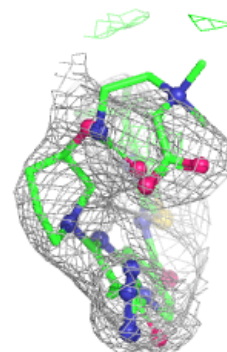
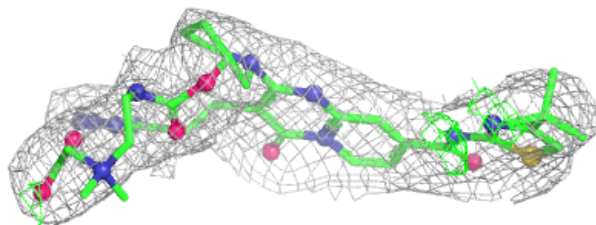
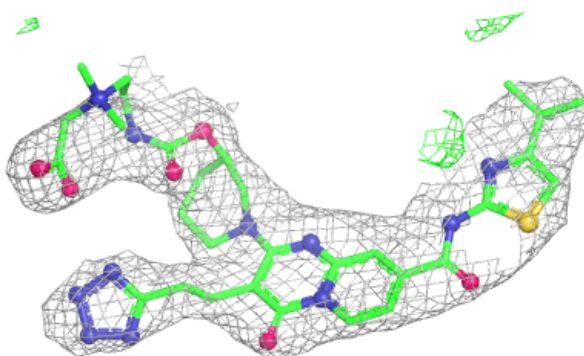


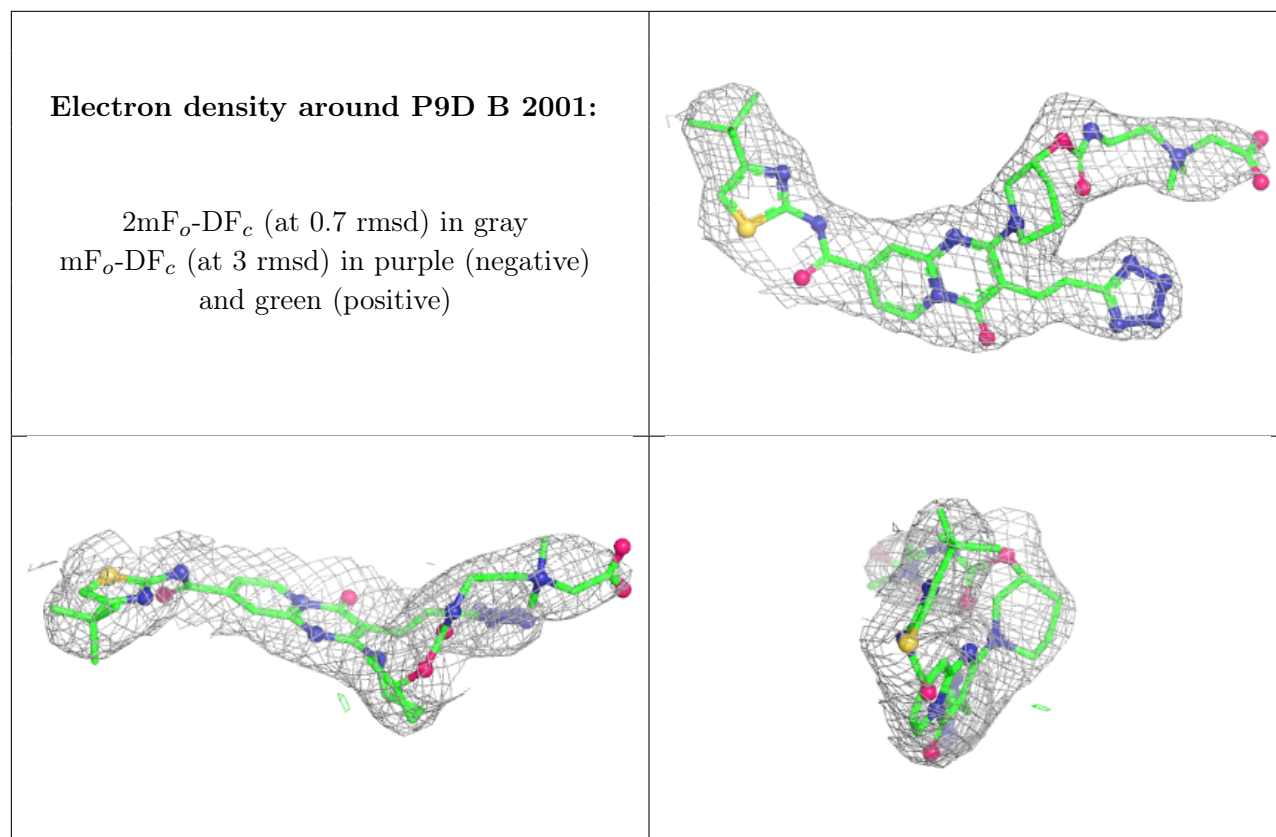
Electron density around LMT B 2004:

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

**Electron density around P9D E 2001:**

$2mF_o-DF_c$ (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.