



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:05 AM UTC

PDB ID : 4HFC / pdb_00004hfc
Title : The GLIC pentameric Ligand-Gated Ion Channel F14'A ethanol-sensitive mutant complexed to 2-bromo-ethanol
Authors : Sauguet, L.; Howard, R.J.; Malherbe, L.; Lee, U.S.; Corringer, P.J.; Harris, R.A.; Delarue, M.
Deposited on : 2012-10-05
Resolution : 3.05 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

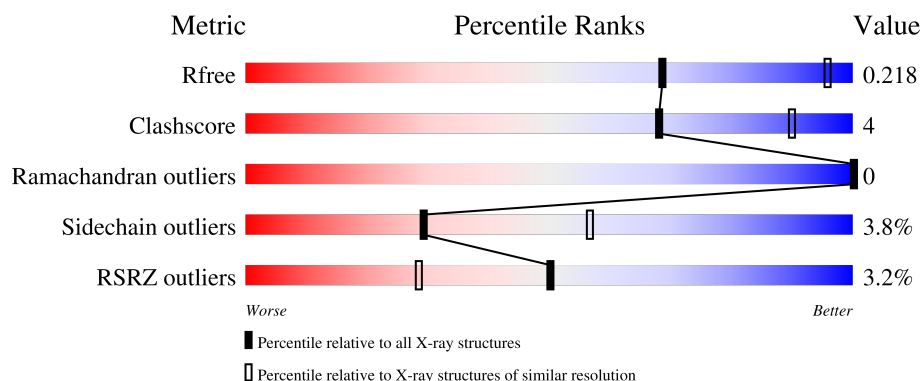
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

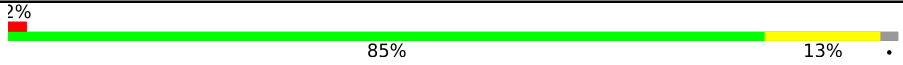
The reported resolution of this entry is 3.05 Å.

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	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

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	317	
1	B	317	
1	C	317	
1	D	317	

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Mol	Chain	Length	Quality of chain
1	E	317	

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
3	BRJ	A	402	-	-	-	X
3	BRJ	C	404	-	-	-	X
3	BRJ	D	404	-	-	-	X
3	BRJ	E	405	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 12984 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.

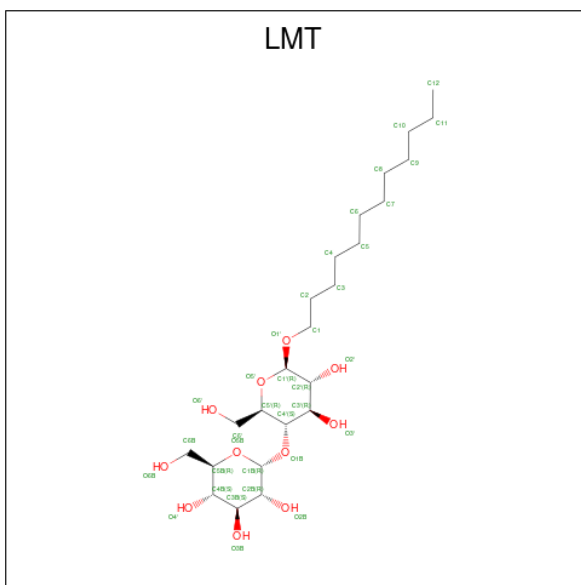
- Molecule 1 is a protein called Proton-gated ion channel.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	311	Total	C	N	O	S	0	0	0
			2519	1658	404	453	4			
1	B	311	Total	C	N	O	S	0	0	0
			2519	1658	404	453	4			
1	C	311	Total	C	N	O	S	0	0	0
			2519	1658	404	453	4			
1	D	311	Total	C	N	O	S	0	0	0
			2519	1658	404	453	4			
1	E	311	Total	C	N	O	S	0	0	0
			2519	1658	404	453	4			

There are 10 discrepancies between the modelled and reference sequences:

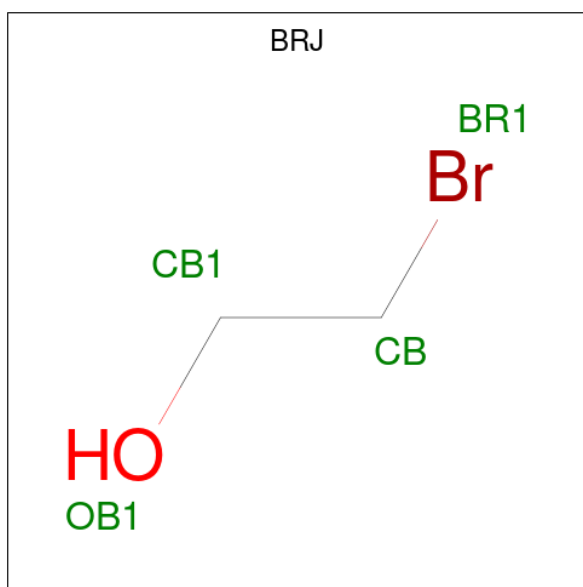
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	-	expression tag	UNP Q7NDN8
A	238	ALA	PHE	engineered mutation	UNP Q7NDN8
B	1	ALA	-	expression tag	UNP Q7NDN8
B	238	ALA	PHE	engineered mutation	UNP Q7NDN8
C	1	ALA	-	expression tag	UNP Q7NDN8
C	238	ALA	PHE	engineered mutation	UNP Q7NDN8
D	1	ALA	-	expression tag	UNP Q7NDN8
D	238	ALA	PHE	engineered mutation	UNP Q7NDN8
E	1	ALA	-	expression tag	UNP Q7NDN8
E	238	ALA	PHE	engineered mutation	UNP Q7NDN8

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



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C 12 12	0	0
2	B	1	Total C 12 12	0	0
2	C	1	Total C 12 12	0	0
2	C	1	Total C 12 12	0	0
2	D	1	Total C 12 12	0	0
2	E	1	Total C 12 12	0	0

- Molecule 3 is 2-BROMOETHANOL (CCD ID: BRJ) (formula: $\text{C}_2\text{H}_5\text{BrO}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	Br	C	O	0	0
			4	1	2	1		
3	B	1	Total	Br	C	O	0	0
			4	1	2	1		
3	C	1	Total	Br	C	O	0	0
			4	1	2	1		
3	D	1	Total	Br	C	O	0	0
			4	1	2	1		
3	E	1	Total	Br	C	O	0	0
			4	1	2	1		

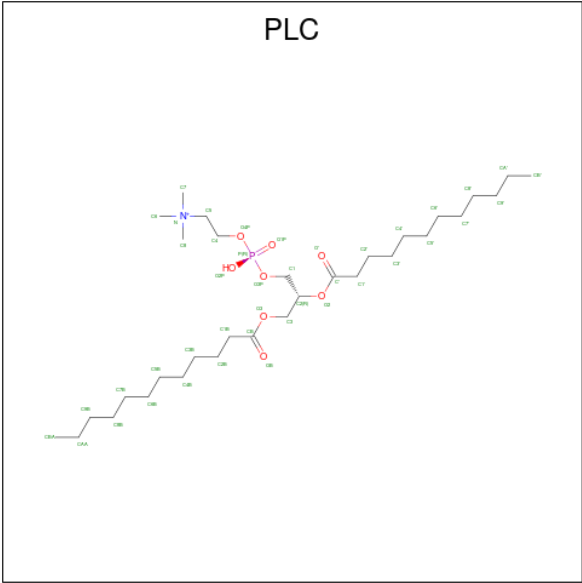
- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	Cl	0	0
			3	3		
4	B	1	Total	Cl	0	0
			1	1		
4	C	1	Total	Cl	0	0
			1	1		
4	D	1	Total	Cl	0	0
			1	1		
4	E	1	Total	Cl	0	0
			1	1		

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total Na 2 2	0	0
5	B	1	Total Na 1 1	0	0
5	C	1	Total Na 1 1	0	0
5	D	1	Total Na 1 1	0	0
5	E	1	Total Na 1 1	0	0

- Molecule 6 is DIUNDECYL PHOSPHATIDYL CHOLINE (CCD ID: PLC) (formula: C₃₂H₆₅NO₈P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C N O P 34 24 1 8 1	0	0
6	B	1	Total C N O P 34 24 1 8 1	0	0
6	C	1	Total C N O P 34 24 1 8 1	0	0
6	D	1	Total C N O P 34 24 1 8 1	0	0
6	E	1	Total C N O P 34 24 1 8 1	0	0

- Molecule 7 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		
7	D	1	Total	C	O	0	0
			4	2	2		
7	E	1	Total	C	O	0	0
			4	2	2		
7	E	1	Total	C	O	0	0
			4	2	2		

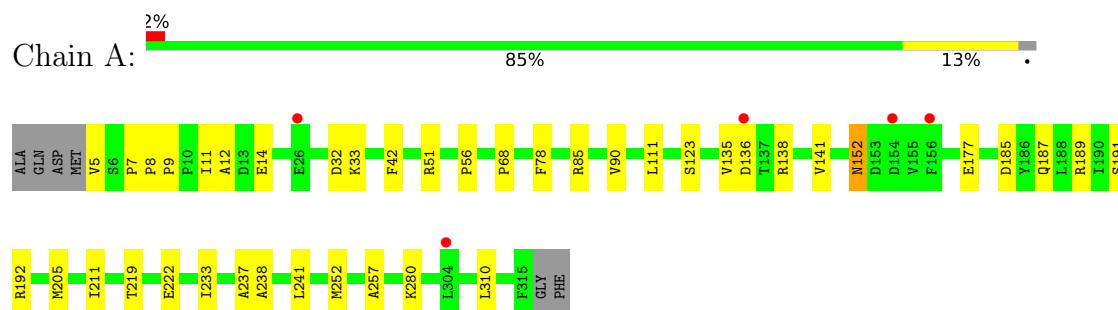
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	16	Total	O	0	0
			16	16		
8	B	21	Total	O	0	0
			21	21		
8	C	19	Total	O	0	0
			19	19		
8	D	22	Total	O	0	0
			22	22		
8	E	16	Total	O	0	0
			16	16		

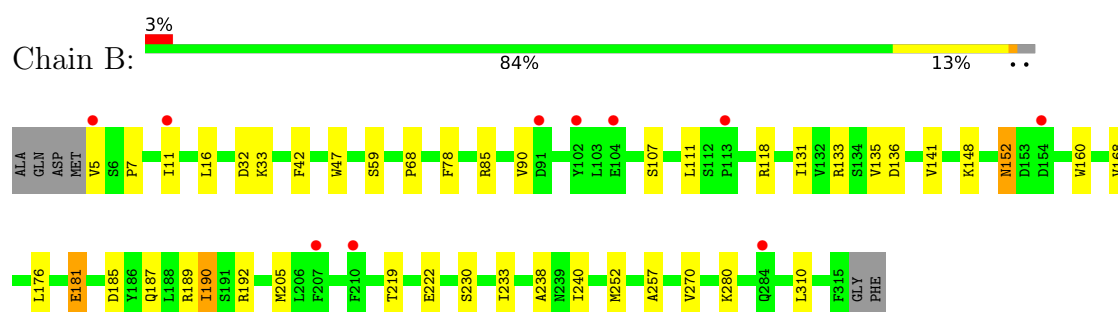
3 Residue-property plots [i](#)

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.

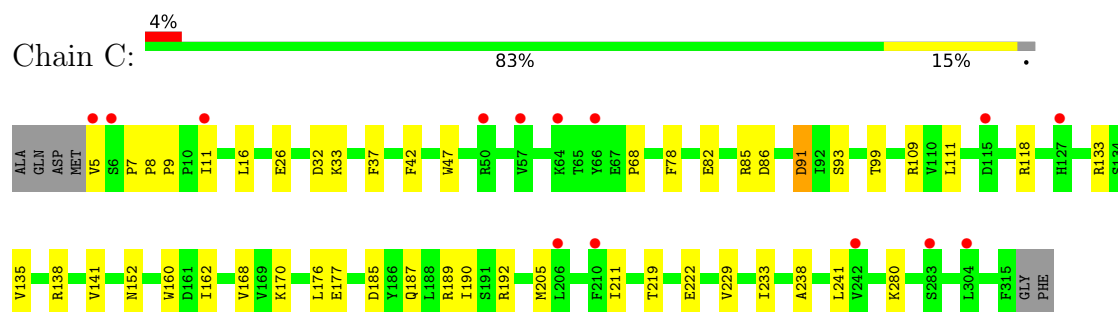
- Molecule 1: Proton-gated ion channel



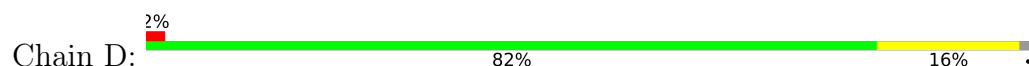
- Molecule 1: Proton-gated ion channel

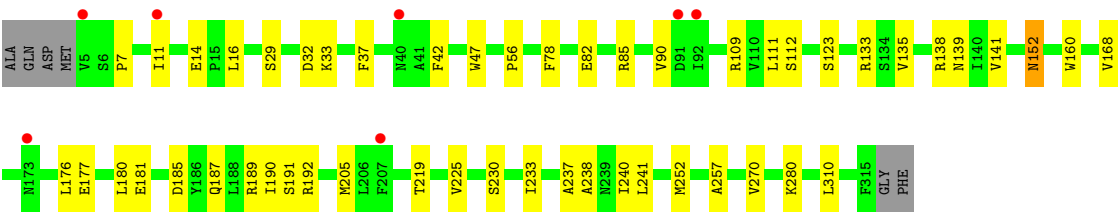


- Molecule 1: Proton-gated ion channel

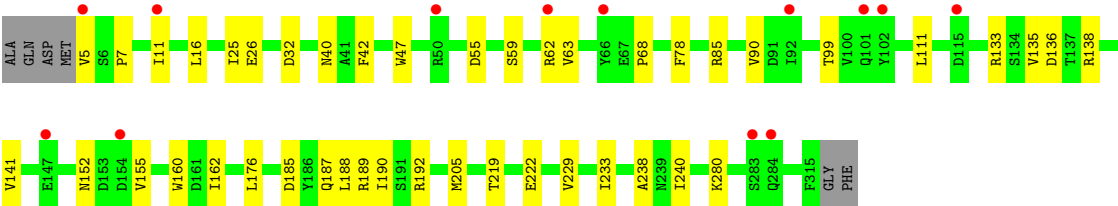
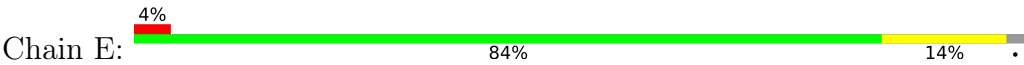


- Molecule 1: Proton-gated ion channel





● Molecule 1: Proton-gated ion channel



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	180.88Å 133.14Å 159.35Å 90.00° 102.22° 90.00°	Depositor
Resolution (Å)	30.00 – 3.05 30.00 – 3.05	Depositor EDS
% Data completeness (in resolution range)	99.8 (30.00-3.05) 99.6 (30.00-3.05)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.63 (at 3.07Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.192 , 0.220 (Not available) , 0.218	Depositor DCC
R_{free} test set	3540 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	74.5	Xtriage
Anisotropy	0.370	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 60.8	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	12984	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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: ACT, LMT, NA, PLC, BRJ, CL

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	0.87	1/2586 (0.0%)	1.26	11/3536 (0.3%)
1	B	0.88	1/2586 (0.0%)	1.25	8/3536 (0.2%)
1	C	0.88	0/2586	1.25	13/3536 (0.4%)
1	D	0.86	0/2586	1.22	8/3536 (0.2%)
1	E	0.87	0/2586	1.23	6/3536 (0.2%)
All	All	0.87	2/12930 (0.0%)	1.24	46/17680 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	12	ALA	CA-C	5.07	1.55	1.52
1	B	190	ILE	CG1-CD1	-5.03	1.32	1.51

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	5	VAL	CA-C-N	6.79	133.13	122.26
1	B	5	VAL	C-N-CA	6.79	133.13	122.26
1	C	5	VAL	CA-C-N	6.67	132.94	122.26
1	C	5	VAL	C-N-CA	6.67	132.94	122.26
1	E	5	VAL	CA-C-N	6.36	132.44	122.26
1	E	5	VAL	C-N-CA	6.36	132.44	122.26
1	A	56	PRO	CA-C-N	5.95	128.14	120.70
1	A	56	PRO	C-N-CA	5.95	128.14	120.70
1	B	152	ASN	CA-CB-CG	5.93	118.53	112.60
1	D	152	ASN	CA-CB-CG	5.77	118.37	112.60
1	E	152	ASN	CA-CB-CG	5.72	118.32	112.60
1	C	42	PHE	CA-CB-CG	5.68	119.48	113.80
1	C	26	GLU	CB-CG-CD	5.61	122.14	112.60
1	D	56	PRO	CA-C-N	5.52	127.60	120.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	56	PRO	C-N-CA	5.52	127.60	120.70
1	E	68	PRO	CA-C-N	5.50	127.65	120.28
1	E	68	PRO	C-N-CA	5.50	127.65	120.28
1	D	185	ASP	CA-CB-CG	5.47	118.08	112.60
1	C	91	ASP	CA-CB-CG	5.47	118.07	112.60
1	A	152	ASN	CA-CB-CG	5.43	118.03	112.60
1	A	177	GLU	CA-C-N	5.35	129.72	122.07
1	A	177	GLU	C-N-CA	5.35	129.72	122.07
1	A	185	ASP	CA-CB-CG	5.35	117.95	112.60
1	C	152	ASN	CA-CB-CG	5.34	117.94	112.60
1	D	181	GLU	CB-CG-CD	5.32	121.64	112.60
1	D	14	GLU	CB-CG-CD	5.31	121.63	112.60
1	B	185	ASP	CA-CB-CG	5.30	117.90	112.60
1	C	168	VAL	CA-C-N	5.27	128.80	120.47
1	C	168	VAL	C-N-CA	5.27	128.80	120.47
1	E	185	ASP	CA-CB-CG	5.24	117.84	112.60
1	A	68	PRO	CA-C-N	5.23	127.29	120.28
1	A	68	PRO	C-N-CA	5.23	127.29	120.28
1	A	5	VAL	CA-C-N	5.23	131.42	122.38
1	A	5	VAL	C-N-CA	5.23	131.42	122.38
1	D	168	VAL	CA-C-N	5.22	128.72	120.47
1	D	168	VAL	C-N-CA	5.22	128.72	120.47
1	C	68	PRO	CA-C-N	5.22	127.27	120.28
1	C	68	PRO	C-N-CA	5.22	127.27	120.28
1	B	68	PRO	CA-C-N	5.19	127.24	120.28
1	B	68	PRO	C-N-CA	5.19	127.24	120.28
1	A	14	GLU	CB-CG-CD	5.19	121.42	112.60
1	C	185	ASP	CA-CB-CG	5.18	117.78	112.60
1	B	168	VAL	CA-C-N	5.17	128.64	120.47
1	B	168	VAL	C-N-CA	5.17	128.64	120.47
1	C	37	PHE	CA-CB-CG	5.05	118.85	113.80
1	C	86	ASP	CA-CB-CG	5.03	117.63	112.60

There are no chirality outliers.

There are no planarity outliers.

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	2519	0	2541	17	0
1	B	2519	0	2541	19	0
1	C	2519	0	2541	19	0
1	D	2519	0	2541	26	0
1	E	2519	0	2541	19	0
2	A	12	0	23	0	0
2	B	12	0	23	2	0
2	C	24	0	46	1	0
2	D	12	0	23	1	0
2	E	12	0	23	0	0
3	A	4	0	3	1	0
3	B	4	0	3	1	0
3	C	4	0	3	1	0
3	D	4	0	3	1	0
3	E	4	0	3	0	0
4	A	3	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
5	A	2	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
6	A	34	0	42	0	0
6	B	34	0	42	1	0
6	C	34	0	42	1	0
6	D	34	0	42	0	0
6	E	34	0	42	0	0
7	B	8	0	6	0	0
7	D	4	0	3	0	0
7	E	8	0	6	0	0
8	A	16	0	0	0	0
8	B	21	0	0	0	0
8	C	19	0	0	0	0
8	D	22	0	0	1	0
8	E	16	0	0	0	0
All	All	12984	0	13083	93	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (93) 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:78:PHE:HE2	1:A:85:ARG:HD3	1.40	0.84
1:B:78:PHE:HE2	1:B:85:ARG:HD3	1.44	0.83
1:D:78:PHE:HE2	1:D:85:ARG:HD3	1.43	0.81
1:C:78:PHE:HE2	1:C:85:ARG:HD3	1.45	0.81
1:B:205:MET:HE2	1:B:238:ALA:HB1	1.62	0.80
1:E:78:PHE:HE2	1:E:85:ARG:HD3	1.45	0.80
1:D:205:MET:HE2	1:D:238:ALA:HB1	1.64	0.80
1:E:205:MET:HE2	1:E:238:ALA:HB1	1.65	0.78
1:C:205:MET:HE2	1:C:238:ALA:HB1	1.65	0.76
1:B:7:PRO:HG3	1:B:135:VAL:HG21	1.68	0.75
1:A:205:MET:HE2	1:A:238:ALA:HB1	1.67	0.75
1:A:78:PHE:CE2	1:A:85:ARG:HD3	2.23	0.71
1:C:78:PHE:CE2	1:C:85:ARG:HD3	2.27	0.70
1:D:78:PHE:CE2	1:D:85:ARG:HD3	2.26	0.69
1:B:78:PHE:CE2	1:B:85:ARG:HD3	2.26	0.69
1:D:139:ASN:ND2	1:D:180:LEU:HD13	2.07	0.69
1:C:7:PRO:HG3	1:C:135:VAL:HG21	1.75	0.68
1:E:78:PHE:CE2	1:E:85:ARG:HD3	2.27	0.67
1:A:7:PRO:HG3	1:A:135:VAL:HG21	1.75	0.67
1:D:7:PRO:HG3	1:D:135:VAL:HG21	1.78	0.64
1:E:7:PRO:HG3	1:E:135:VAL:HG21	1.78	0.64
1:D:139:ASN:HB3	8:D:503:HOH:O	1.99	0.62
1:D:139:ASN:HD22	1:D:180:LEU:HD13	1.66	0.59
1:C:118:ARG:HH22	6:C:406:PLC:H72	1.67	0.59
1:A:32:ASP:OD1	1:A:192:ARG:NH2	2.35	0.58
1:B:32:ASP:OD1	1:B:192:ARG:NH2	2.36	0.58
1:C:32:ASP:OD1	1:C:192:ARG:NH2	2.35	0.55
1:A:252:MET:HE3	1:A:257:ALA:HA	1.87	0.55
1:E:26:GLU:HB2	1:E:40:ASN:HB3	1.89	0.55
1:D:32:ASP:OD1	1:D:192:ARG:NH2	2.36	0.54
1:E:160:TRP:CE3	1:E:190:ILE:HD12	2.42	0.54
1:E:32:ASP:OD1	1:E:192:ARG:NH2	2.39	0.54
1:B:160:TRP:CE3	1:B:190:ILE:HD12	2.43	0.53
1:B:118:ARG:HH12	6:B:407:PLC:H72	1.74	0.52
1:C:133:ARG:NH1	1:C:176:LEU:O	2.42	0.51
1:D:252:MET:HE3	1:D:257:ALA:HA	1.93	0.51
1:B:131:ILE:HD11	1:B:181:GLU:HG2	1.92	0.51
1:B:133:ARG:NH1	1:B:176:LEU:O	2.44	0.50
1:B:252:MET:HE3	1:B:257:ALA:HA	1.92	0.50
1:C:160:TRP:CE3	1:C:190:ILE:HD12	2.47	0.50
1:E:62:ARG:HD2	1:E:63:VAL:HG23	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:241:LEU:HD22	1:E:240:ILE:HG12	1.93	0.49
1:A:241:LEU:HD22	1:B:240:ILE:HG12	1.94	0.49
1:E:16:LEU:HD11	1:E:47:TRP:HB2	1.93	0.49
1:D:82:GLU:HG2	1:D:111:LEU:CD1	2.43	0.49
3:A:402:BRJ:BR1	1:E:238:ALA:HB2	2.68	0.48
1:E:133:ARG:NH1	1:E:176:LEU:O	2.46	0.48
1:D:82:GLU:HG3	1:D:109:ARG:HB3	1.95	0.47
1:D:123:SER:HA	1:D:191:SER:HA	1.97	0.47
1:A:9:PRO:HD3	1:A:51:ARG:HD3	1.97	0.46
1:D:133:ARG:NH1	1:D:176:LEU:O	2.47	0.46
1:A:187:GLN:OE1	1:A:189:ARG:NH2	2.43	0.46
1:D:29:SER:O	1:D:37:PHE:HA	2.15	0.46
1:E:55:ASP:O	1:E:59:SER:HB2	2.15	0.46
1:C:187:GLN:OE1	1:C:189:ARG:NH2	2.43	0.45
1:C:162:ILE:HA	1:C:190:ILE:HG22	1.97	0.45
1:E:42:PHE:HE1	1:E:90:VAL:HG21	1.81	0.45
1:B:238:ALA:HB2	3:C:404:BRJ:BR1	2.72	0.45
1:D:16:LEU:HD11	1:D:47:TRP:HB2	1.99	0.45
1:A:310:LEU:HD23	1:A:310:LEU:HA	1.88	0.44
1:D:135:VAL:HG23	1:D:138:ARG:H	1.83	0.44
1:C:238:ALA:HB2	3:D:404:BRJ:BR1	2.72	0.44
1:E:25:ILE:O	1:E:155:VAL:HG22	2.19	0.43
1:C:211:ILE:HG12	1:D:270:VAL:HG11	2.01	0.43
1:C:241:LEU:HD22	1:D:240:ILE:HG12	2.00	0.43
1:A:42:PHE:HE1	1:A:90:VAL:HG21	1.84	0.43
1:A:8:PRO:HA	1:A:9:PRO:HD3	1.96	0.42
1:A:123:SER:HA	1:A:191:SER:HA	2.01	0.42
1:A:211:ILE:HG12	1:B:270:VAL:HG11	2.00	0.42
1:B:42:PHE:HE1	1:B:90:VAL:HG21	1.85	0.42
1:B:187:GLN:OE1	1:B:189:ARG:NH2	2.46	0.42
2:B:401:LMT:H81	2:C:402:LMT:H71	2.02	0.42
1:C:16:LEU:HD11	1:C:47:TRP:HB2	2.02	0.42
1:D:230:SER:CB	1:E:229:VAL:HG11	2.49	0.42
1:B:16:LEU:HD11	1:B:47:TRP:HB2	2.02	0.42
1:D:237:ALA:HA	2:D:401:LMT:H82	2.01	0.42
1:E:135:VAL:HG23	1:E:138:ARG:H	1.84	0.42
1:A:135:VAL:HG23	1:A:138:ARG:H	1.85	0.41
1:D:42:PHE:HE1	1:D:90:VAL:HG21	1.84	0.41
1:D:160:TRP:CE3	1:D:190:ILE:HD12	2.55	0.41
1:C:82:GLU:HG3	1:C:109:ARG:HB3	2.01	0.41
1:E:187:GLN:OE1	1:E:189:ARG:NH2	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:237:ALA:HB2	2:B:401:LMT:H122	2.03	0.41
1:B:230:SER:CB	1:C:229:VAL:HG11	2.50	0.41
1:C:8:PRO:HA	1:C:9:PRO:HD3	1.91	0.41
1:C:135:VAL:HG23	1:C:138:ARG:H	1.85	0.41
1:D:133:ARG:NH1	1:D:177:GLU:HB2	2.36	0.41
1:A:238:ALA:HB2	3:B:403:BRJ:BR1	2.75	0.41
1:B:310:LEU:HD23	1:B:310:LEU:HA	1.89	0.40
1:D:310:LEU:HD23	1:D:310:LEU:HA	1.90	0.40
1:D:187:GLN:OE1	1:D:189:ARG:NH2	2.45	0.40
1:B:148:LYS:HE3	1:C:177:GLU:HB3	2.04	0.40
1:E:162:ILE:HG23	1:E:188:LEU:HD11	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	309/317 (98%)	300 (97%)	9 (3%)	0	100	100
1	B	309/317 (98%)	298 (96%)	11 (4%)	0	100	100
1	C	309/317 (98%)	301 (97%)	8 (3%)	0	100	100
1	D	309/317 (98%)	301 (97%)	8 (3%)	0	100	100
1	E	309/317 (98%)	300 (97%)	9 (3%)	0	100	100
All	All	1545/1585 (98%)	1500 (97%)	45 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	279/283 (99%)	269 (96%)	10 (4%)	31	58
1	B	279/283 (99%)	266 (95%)	13 (5%)	23	51
1	C	279/283 (99%)	267 (96%)	12 (4%)	26	53
1	D	279/283 (99%)	270 (97%)	9 (3%)	34	60
1	E	279/283 (99%)	270 (97%)	9 (3%)	34	60
All	All	1395/1415 (99%)	1342 (96%)	53 (4%)	29	57

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	ILE
1	A	33	LYS
1	A	111	LEU
1	A	136	ASP
1	A	141	VAL
1	A	152	ASN
1	A	219	THR
1	A	222	GLU
1	A	233	ILE
1	A	280	LYS
1	B	11	ILE
1	B	33	LYS
1	B	59	SER
1	B	107	SER
1	B	111	LEU
1	B	136	ASP
1	B	141	VAL
1	B	152	ASN
1	B	181	GLU
1	B	219	THR
1	B	222	GLU
1	B	233	ILE
1	B	280	LYS
1	C	11	ILE
1	C	33	LYS
1	C	91	ASP
1	C	93	SER

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Mol	Chain	Res	Type
1	C	99	THR
1	C	111	LEU
1	C	141	VAL
1	C	170	LYS
1	C	219	THR
1	C	222	GLU
1	C	233	ILE
1	C	280	LYS
1	D	11	ILE
1	D	33	LYS
1	D	112	SER
1	D	141	VAL
1	D	152	ASN
1	D	219	THR
1	D	225	VAL
1	D	233	ILE
1	D	280	LYS
1	E	11	ILE
1	E	99	THR
1	E	111	LEU
1	E	136	ASP
1	E	141	VAL
1	E	219	THR
1	E	222	GLU
1	E	233	ILE
1	E	280	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	152	ASN
1	A	239	ASN
1	B	152	ASN
1	B	239	ASN
1	C	152	ASN
1	C	239	ASN
1	D	152	ASN
1	D	239	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 34 ligands modelled in this entry, 13 are monoatomic - leaving 21 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	$\# Z > 2$
3	BRJ	E	405	-	3,3,3	0.82	0	2,2,2	0.52	0
2	LMT	C	401	-	11,11,36	0.75	0	10,10,47	0.53	0
3	BRJ	C	404	-	3,3,3	0.89	0	2,2,2	0.56	0
6	PLC	D	406	-	33,33,41	1.21	3 (9%)	39,41,49	1.53	5 (12%)
7	ACT	E	404	-	3,3,3	1.30	0	3,3,3	0.85	0
2	LMT	C	402	-	11,11,36	0.52	0	10,10,47	0.50	0
2	LMT	E	401	-	11,11,36	0.43	0	10,10,47	0.69	0
2	LMT	A	401	-	11,11,36	0.58	0	10,10,47	0.57	0
6	PLC	E	407	-	33,33,41	1.26	3 (9%)	39,41,49	1.52	5 (12%)
2	LMT	D	401	-	11,11,36	0.57	0	10,10,47	0.58	0
6	PLC	C	406	-	33,33,41	1.28	5 (15%)	39,41,49	1.45	5 (12%)
7	ACT	E	403	-	3,3,3	1.29	0	3,3,3	0.66	0
3	BRJ	B	403	-	3,3,3	0.91	0	2,2,2	0.82	0
7	ACT	B	404	-	3,3,3	1.15	0	3,3,3	1.21	0
3	BRJ	A	402	-	3,3,3	0.93	0	2,2,2	0.32	0
6	PLC	B	407	-	33,33,41	1.22	2 (6%)	39,41,49	1.57	5 (12%)
7	ACT	B	405	-	3,3,3	1.08	0	3,3,3	1.20	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	BRJ	D	404	-	3,3,3	0.95	0	2,2,2	0.62	0
6	PLC	A	408	-	33,33,41	1.23	3 (9%)	39,41,49	1.55	5 (12%)
2	LMT	B	401	-	11,11,36	0.42	0	10,10,47	0.71	0
7	ACT	D	403	-	3,3,3	1.16	0	3,3,3	0.81	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
2	LMT	C	402	-	-	0/9/9/61	-
6	PLC	A	408	-	-	23/37/37/45	-
3	BRJ	A	402	-	-	1/1/1/1	-
2	LMT	B	401	-	-	2/9/9/61	-
2	LMT	E	401	-	-	3/9/9/61	-
3	BRJ	E	405	-	-	0/1/1/1	-
6	PLC	B	407	-	-	21/37/37/45	-
2	LMT	C	401	-	-	3/9/9/61	-
2	LMT	A	401	-	-	0/9/9/61	-
3	BRJ	C	404	-	-	0/1/1/1	-
6	PLC	D	406	-	-	21/37/37/45	-
6	PLC	E	407	-	-	19/37/37/45	-
2	LMT	D	401	-	-	0/9/9/61	-
6	PLC	C	406	-	-	20/37/37/45	-
3	BRJ	B	403	-	-	0/1/1/1	-
3	BRJ	D	404	-	-	0/1/1/1	-

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	407	PLC	O2-C'	3.24	1.43	1.34
6	A	408	PLC	O2-C'	3.11	1.43	1.34
6	E	407	PLC	O2-C'	3.00	1.42	1.34
6	D	406	PLC	O2-C'	2.98	1.42	1.34
6	C	406	PLC	O2-C'	2.89	1.42	1.34
6	E	407	PLC	C3-C2	2.70	1.59	1.50
6	A	408	PLC	C3-C2	2.43	1.58	1.50
6	C	406	PLC	C3-C2	2.41	1.58	1.50
6	C	406	PLC	O3-CB	2.30	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	407	PLC	P-O1P	2.28	1.58	1.50
6	C	406	PLC	C5-C4	2.24	1.58	1.51
6	C	406	PLC	P-O1P	2.20	1.58	1.50
6	A	408	PLC	P-O1P	2.20	1.58	1.50
6	D	406	PLC	P-O1P	2.18	1.58	1.50
6	B	407	PLC	P-O1P	2.10	1.58	1.50
6	D	406	PLC	C3-C2	2.01	1.57	1.50

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	407	PLC	O2-C'-O'	-4.79	112.50	123.70
6	B	407	PLC	O2-C'-O'	-4.55	113.06	123.70
6	C	406	PLC	O2-C'-O'	-4.54	113.09	123.70
6	B	407	PLC	C2-O2-C'	4.53	128.64	117.80
6	D	406	PLC	O2-C'-C1'	4.51	121.24	111.48
6	B	407	PLC	O2-C'-C1'	4.47	121.15	111.48
6	D	406	PLC	C2-O2-C'	4.37	128.25	117.80
6	A	408	PLC	C2-O2-C'	4.35	128.20	117.80
6	A	408	PLC	O2-C'-O'	-4.33	113.57	123.70
6	D	406	PLC	O2-C'-O'	-4.33	113.59	123.70
6	C	406	PLC	C2-O2-C'	4.30	128.08	117.80
6	E	407	PLC	O2-C'-C1'	4.24	120.65	111.48
6	A	408	PLC	O2-C'-C1'	4.23	120.64	111.48
6	E	407	PLC	C2-O2-C'	4.19	127.83	117.80
6	C	406	PLC	O2-C'-C1'	3.95	120.02	111.48
6	A	408	PLC	O4P-P-O1P	-2.87	97.54	108.94
6	A	408	PLC	O2P-P-O3P	2.76	120.08	107.57
6	D	406	PLC	O2P-P-O3P	2.70	119.80	107.57
6	B	407	PLC	O2P-P-O3P	2.67	119.66	107.57
6	B	407	PLC	O4P-P-O1P	-2.66	98.39	108.94
6	D	406	PLC	O4P-P-O1P	-2.62	98.57	108.94
6	E	407	PLC	O4P-P-O1P	-2.58	98.72	108.94
6	E	407	PLC	O2P-P-O3P	2.56	119.17	107.57
6	C	406	PLC	O4P-P-O1P	-2.47	99.15	108.94
6	C	406	PLC	O2P-P-O3P	2.46	118.70	107.57

There are no chirality outliers.

All (113) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	408	PLC	C1'-C'-O2-C2

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Mol	Chain	Res	Type	Atoms
6	A	408	PLC	C1-O3P-P-O1P
6	A	408	PLC	C1-O3P-P-O2P
6	A	408	PLC	C1-O3P-P-O4P
6	B	407	PLC	C1'-C'-O2-C2
6	B	407	PLC	C1-O3P-P-O1P
6	B	407	PLC	C1-O3P-P-O2P
6	B	407	PLC	C1-O3P-P-O4P
6	B	407	PLC	C4-O4P-P-O1P
6	C	406	PLC	C1'-C'-O2-C2
6	C	406	PLC	C1-O3P-P-O2P
6	C	406	PLC	C1-O3P-P-O4P
6	C	406	PLC	C4-O4P-P-O1P
6	D	406	PLC	C1'-C'-O2-C2
6	D	406	PLC	C1-O3P-P-O1P
6	D	406	PLC	C1-O3P-P-O2P
6	D	406	PLC	C1-O3P-P-O4P
6	D	406	PLC	C4-O4P-P-O1P
6	E	407	PLC	C1'-C'-O2-C2
6	E	407	PLC	C1-O3P-P-O1P
6	E	407	PLC	C1-O3P-P-O2P
6	E	407	PLC	C1-O3P-P-O4P
6	E	407	PLC	C4-O4P-P-O1P
6	C	406	PLC	O'-C'-O2-C2
6	E	407	PLC	O'-C'-O2-C2
6	A	408	PLC	O'-C'-O2-C2
6	B	407	PLC	O'-C'-O2-C2
6	D	406	PLC	O'-C'-O2-C2
6	E	407	PLC	C4-C5-N-C8
6	A	408	PLC	CB-C1B-C2B-C3B
6	C	406	PLC	C'-C1'-C2'-C3'
6	B	407	PLC	C4-C5-N-C7
6	C	406	PLC	CB-C1B-C2B-C3B
6	D	406	PLC	CB-C1B-C2B-C3B
6	A	408	PLC	C'-C1'-C2'-C3'
6	B	407	PLC	C'-C1'-C2'-C3'
6	B	407	PLC	CB-C1B-C2B-C3B
6	E	407	PLC	C'-C1'-C2'-C3'
6	E	407	PLC	CB-C1B-C2B-C3B
6	D	406	PLC	C'-C1'-C2'-C3'
6	A	408	PLC	C4-C5-N-C8
6	B	407	PLC	C4-C5-N-C8
6	D	406	PLC	C4-C5-N-C6

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Mol	Chain	Res	Type	Atoms
6	D	406	PLC	C4-C5-N-C7
6	D	406	PLC	C4-C5-N-C8
6	E	407	PLC	C4-C5-N-C6
6	E	407	PLC	C4-C5-N-C7
6	A	408	PLC	C4-C5-N-C6
6	D	406	PLC	C3B-C4B-C5B-C6B
6	D	406	PLC	C1'-C2'-C3'-C4'
6	C	406	PLC	C3B-C4B-C5B-C6B
6	A	408	PLC	C1'-C2'-C3'-C4'
6	A	408	PLC	C3B-C4B-C5B-C6B
6	B	407	PLC	C1'-C2'-C3'-C4'
6	A	408	PLC	C4-C5-N-C7
6	B	407	PLC	C4-C5-N-C6
6	B	407	PLC	C3B-C4B-C5B-C6B
2	C	401	LMT	C4-C5-C6-C7
2	C	401	LMT	C2-C3-C4-C5
6	C	406	PLC	C4-C5-N-C8
6	A	408	PLC	O3P-C1-C2-C3
6	B	407	PLC	O3P-C1-C2-C3
6	E	407	PLC	O3P-C1-C2-C3
6	E	407	PLC	C3B-C4B-C5B-C6B
6	A	408	PLC	C4B-C5B-C6B-C7B
6	D	406	PLC	O3P-C1-C2-C3
6	E	407	PLC	C1'-C2'-C3'-C4'
6	A	408	PLC	O3P-C1-C2-O2
6	C	406	PLC	O3P-C1-C2-O2
6	D	406	PLC	O3P-C1-C2-O2
2	E	401	LMT	C7-C8-C9-C10
6	B	407	PLC	C4B-C5B-C6B-C7B
6	C	406	PLC	O3P-C1-C2-C3
6	E	407	PLC	O3P-C1-C2-O2
6	E	407	PLC	C4B-C5B-C6B-C7B
6	A	408	PLC	O4P-C4-C5-N
6	B	407	PLC	O4P-C4-C5-N
6	C	406	PLC	O4P-C4-C5-N
6	D	406	PLC	O4P-C4-C5-N
6	E	407	PLC	O4P-C4-C5-N
6	C	406	PLC	C4-C5-N-C6
6	B	407	PLC	O3P-C1-C2-O2
6	C	406	PLC	C4-C5-N-C7
6	A	408	PLC	C4-O4P-P-O1P
6	A	408	PLC	C4-O4P-P-O3P

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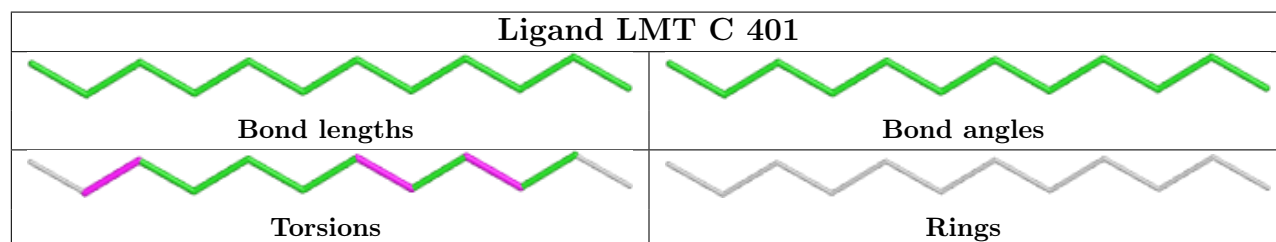
Mol	Chain	Res	Type	Atoms
6	C	406	PLC	C1-O3P-P-O1P
6	D	406	PLC	C1-C2-O2-C'
2	E	401	LMT	C4-C5-C6-C7
6	B	407	PLC	C1-C2-O2-C'
6	C	406	PLC	C1-C2-O2-C'
6	E	407	PLC	C3-C2-O2-C'
6	D	406	PLC	C1B-C2B-C3B-C4B
2	C	401	LMT	C9-C10-C11-C12
6	B	407	PLC	C1B-C2B-C3B-C4B
3	A	402	BRJ	BR1-CB-CB1-OB1
6	D	406	PLC	C4B-C5B-C6B-C7B
6	B	407	PLC	C2B-C1B-CB-O3
6	A	408	PLC	C2B-C1B-CB-O3
6	C	406	PLC	C1B-C2B-C3B-C4B
6	C	406	PLC	C2B-C1B-CB-O3
6	A	408	PLC	C2B-C3B-C4B-C5B
6	A	408	PLC	C1-C2-O2-C'
2	E	401	LMT	C11-C10-C9-C8
6	D	406	PLC	C2B-C1B-CB-O3
2	B	401	LMT	C11-C10-C9-C8
2	B	401	LMT	C7-C8-C9-C10
6	C	406	PLC	C1'-C2'-C3'-C4'
6	B	407	PLC	C2B-C1B-CB-OB
6	A	408	PLC	C2B-C1B-CB-OB
6	C	406	PLC	C2B-C1B-CB-OB
6	A	408	PLC	O2-C'-C1'-C2'
6	D	406	PLC	C2B-C1B-CB-OB
6	E	407	PLC	C2B-C1B-CB-O3

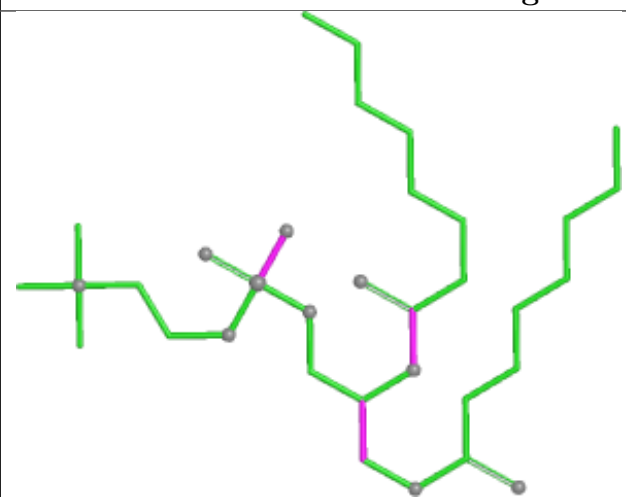
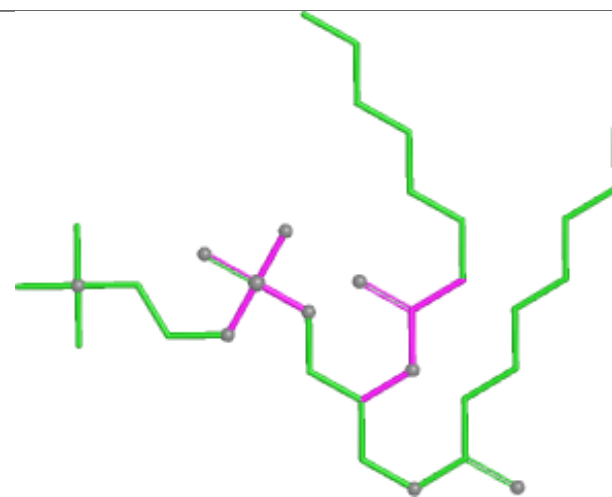
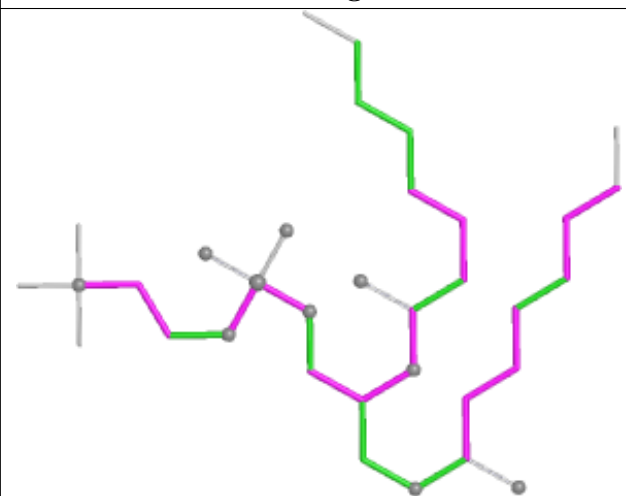
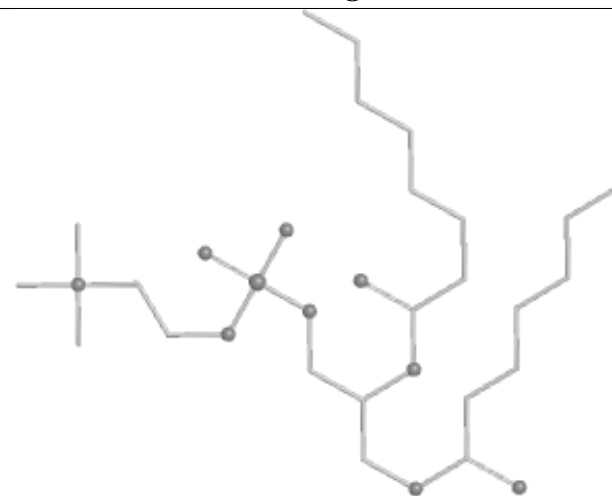
There are no ring outliers.

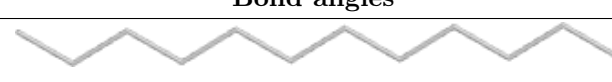
9 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	404	BRJ	1	0
2	C	402	LMT	1	0
2	D	401	LMT	1	0
6	C	406	PLC	1	0
3	B	403	BRJ	1	0
3	A	402	BRJ	1	0
6	B	407	PLC	1	0
3	D	404	BRJ	1	0
2	B	401	LMT	2	0

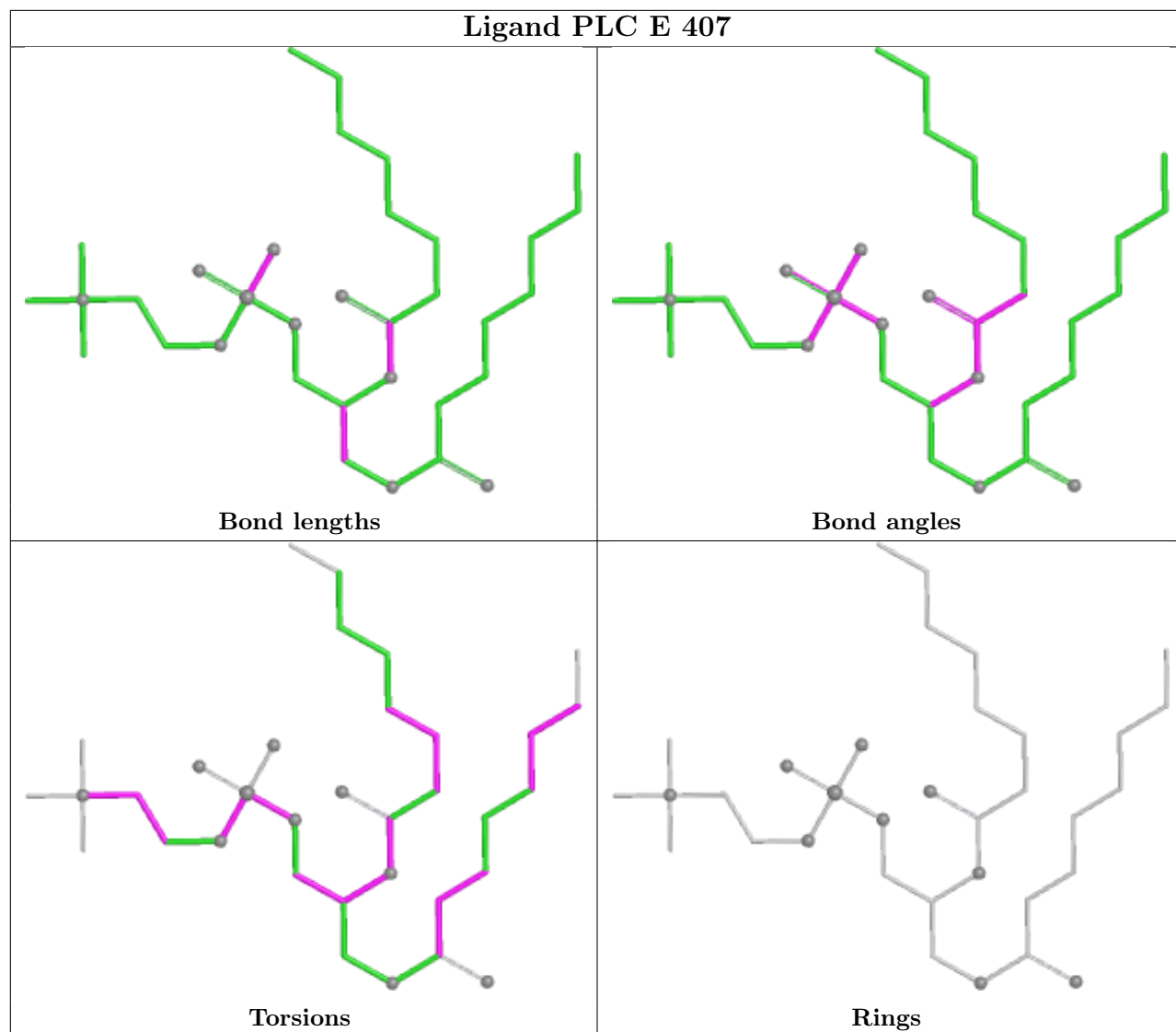
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

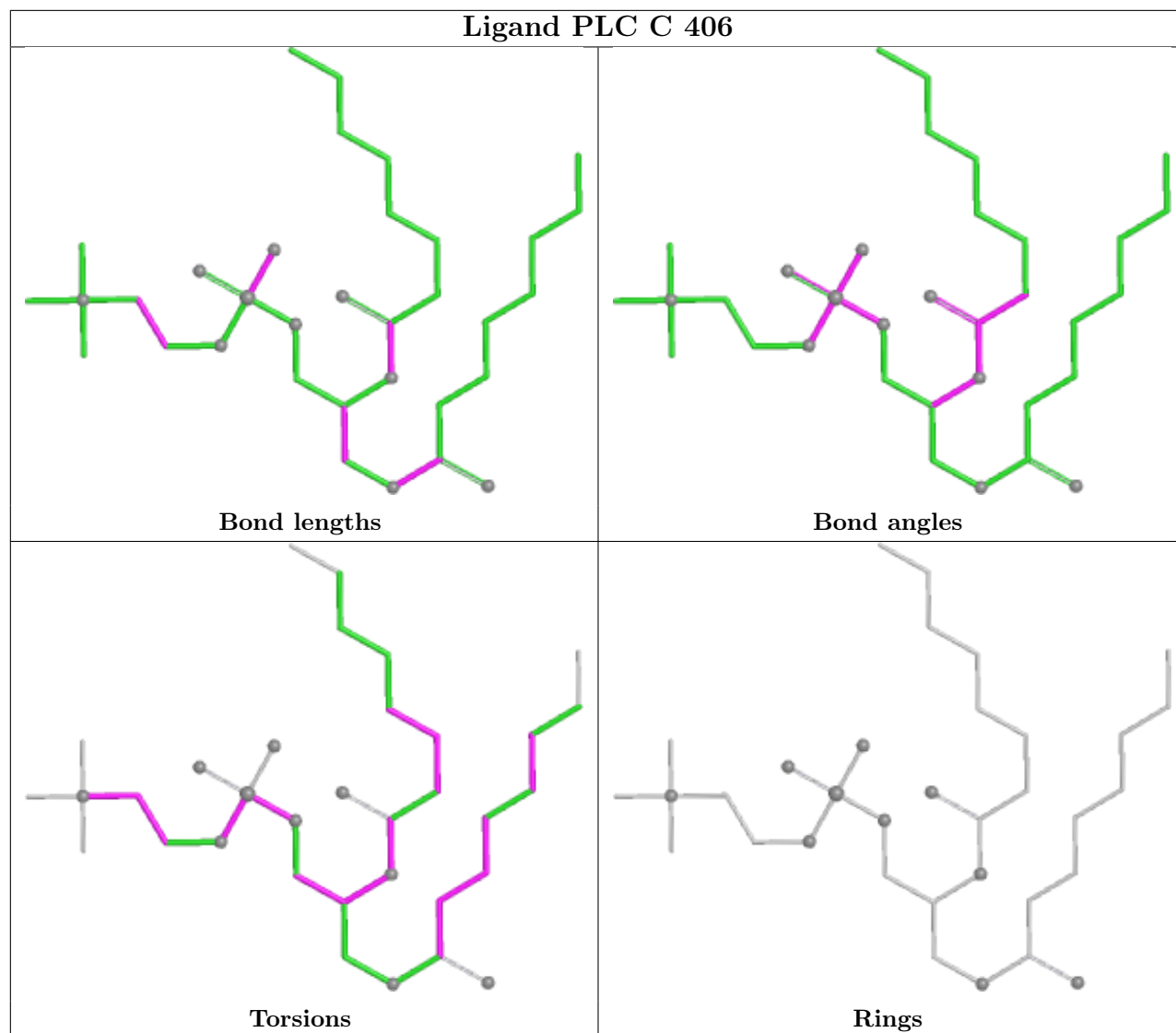


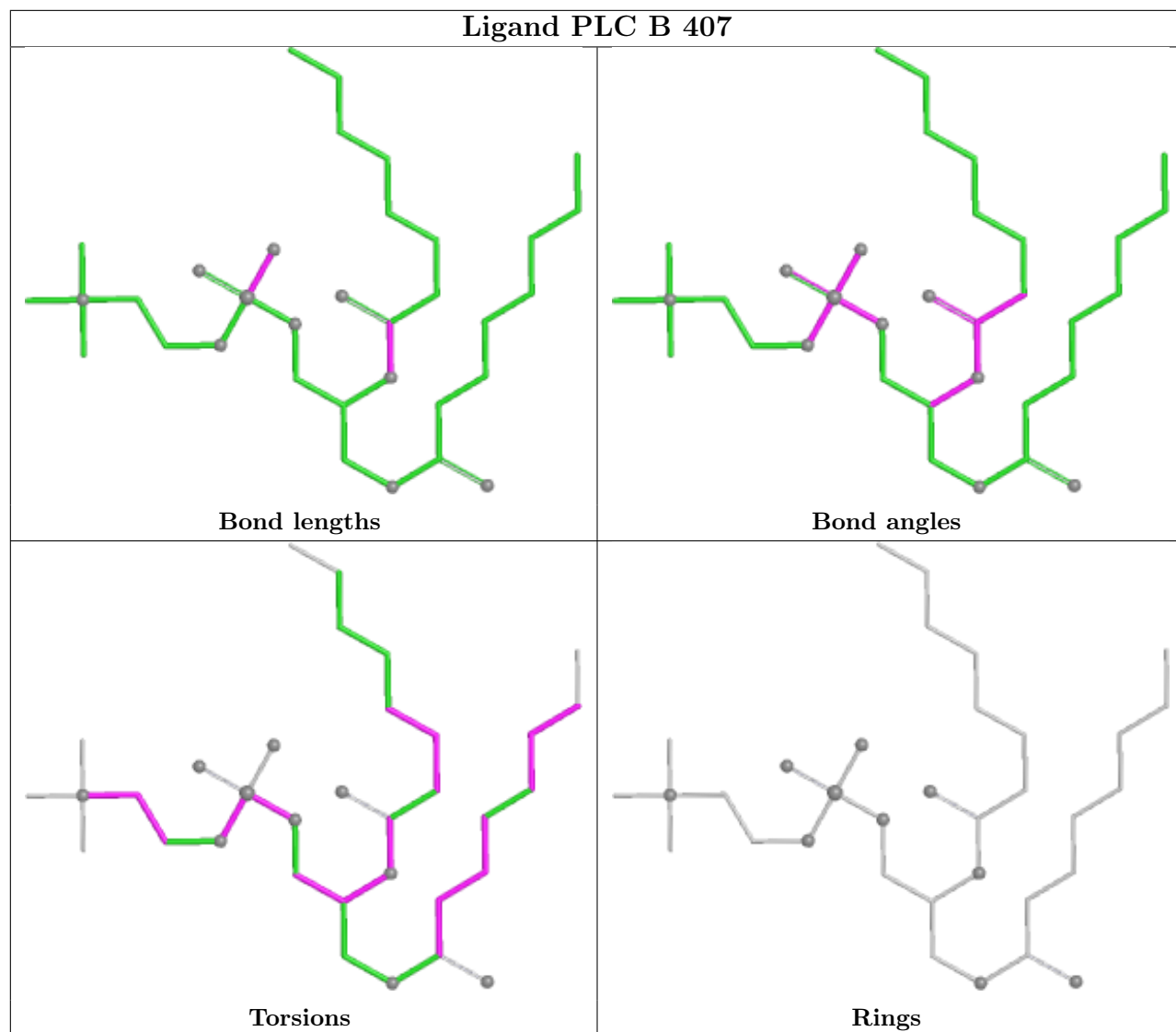
Ligand PLC D 406	
	
Bond lengths	Bond angles
	
Torsions	Rings

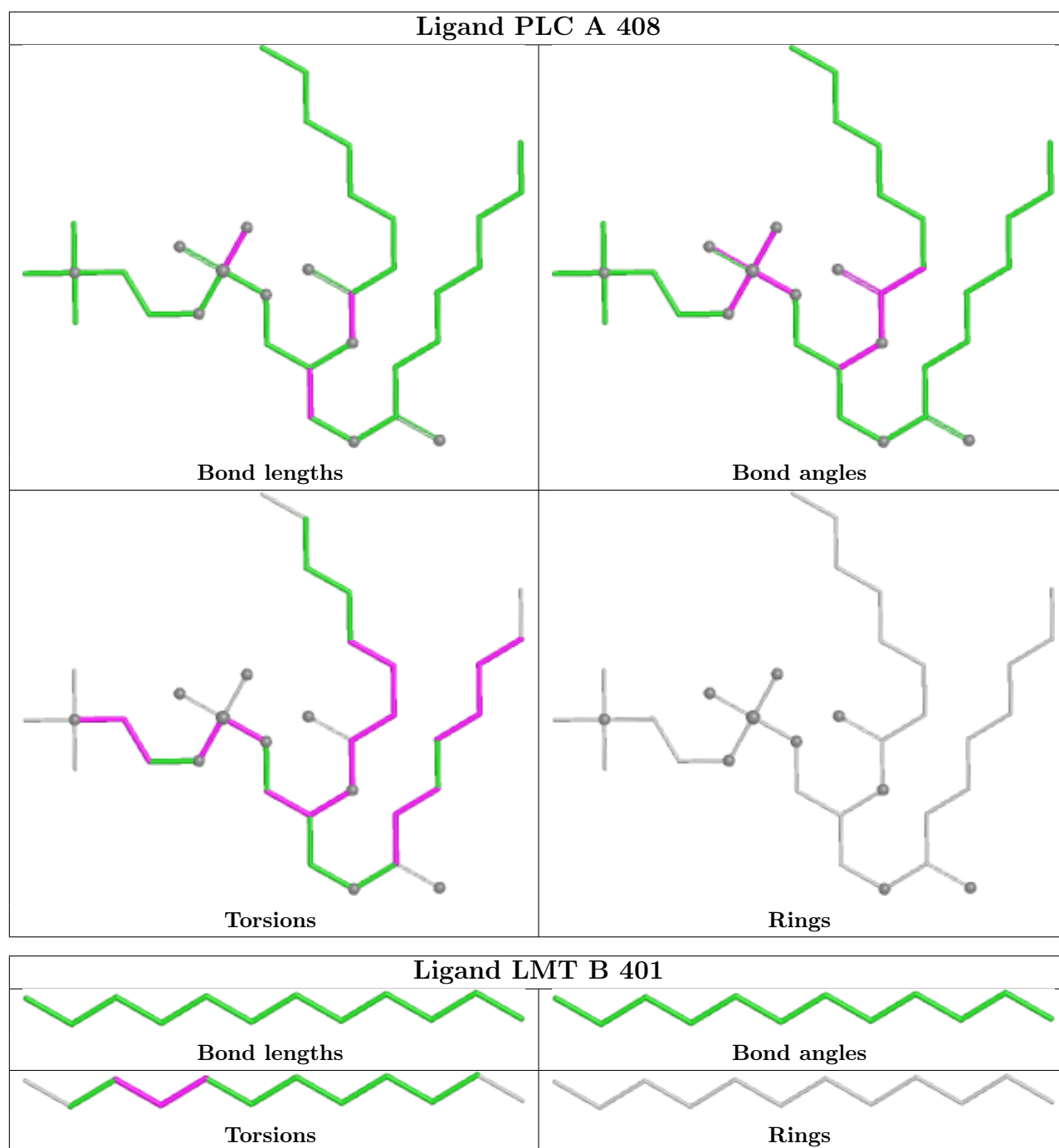
Ligand LMT E 401	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand PLC E 407









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	311/317 (98%)	0.06	5 (1%) 70 47	60, 83, 117, 162	0
1	B	311/317 (98%)	0.13	10 (3%) 50 28	57, 80, 112, 139	0
1	C	311/317 (98%)	0.18	14 (4%) 38 20	61, 83, 118, 174	0
1	D	311/317 (98%)	0.20	7 (2%) 61 38	61, 83, 118, 170	0
1	E	311/317 (98%)	0.15	13 (4%) 40 21	62, 83, 120, 164	0
All	All	1555/1585 (98%)	0.14	49 (3%) 50 28	57, 83, 118, 174	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	5	VAL	5.4
1	B	104	GLU	3.6
1	B	5	VAL	3.6
1	B	154	ASP	3.5
1	E	147	GLU	3.4
1	E	115	ASP	3.4
1	E	283	SER	3.3
1	D	91	ASP	3.2
1	B	11	ILE	3.2
1	C	6	SER	3.2
1	E	92	ILE	3.1
1	C	5	VAL	2.8
1	E	62	ARG	2.8
1	C	127	HIS	2.8
1	C	206	LEU	2.8
1	E	11	ILE	2.8
1	B	102	TYR	2.8
1	C	66	TYR	2.8
1	A	156	PHE	2.7
1	E	5	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	57	VAL	2.7
1	A	136	ASP	2.7
1	B	207	PHE	2.6
1	C	115	ASP	2.6
1	C	50	ARG	2.6
1	A	304	LEU	2.6
1	E	50	ARG	2.6
1	E	101	GLN	2.5
1	B	113	PRO	2.5
1	B	91	ASP	2.5
1	E	284	GLN	2.4
1	D	92	ILE	2.4
1	C	64	LYS	2.3
1	D	11	ILE	2.3
1	D	207	PHE	2.2
1	C	242	VAL	2.2
1	B	284	GLN	2.2
1	C	283	SER	2.2
1	C	304	LEU	2.1
1	D	40	ASN	2.1
1	D	173	ASN	2.1
1	C	210	PHE	2.1
1	E	154	ASP	2.1
1	B	210	PHE	2.1
1	C	11	ILE	2.1
1	A	26	GLU	2.1
1	E	102	TYR	2.0
1	E	66	TYR	2.0
1	A	154	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

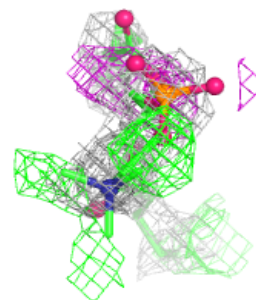
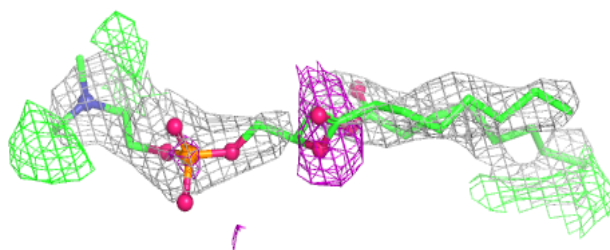
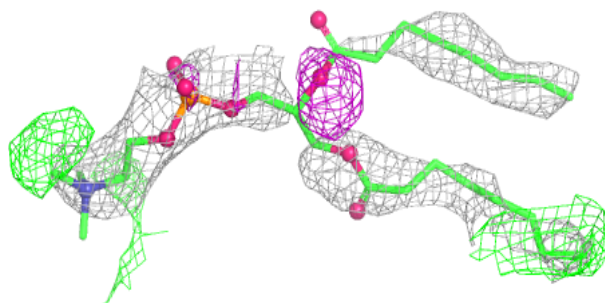
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	PLC	E	407	34/42	0.67	0.37	95,138,169,171	0
6	PLC	B	407	34/42	0.70	0.38	115,143,165,167	0
6	PLC	D	406	34/42	0.70	0.34	102,136,174,174	0
3	BRJ	A	402	4/4	0.70	0.55	194,196,201,207	0
6	PLC	A	408	34/42	0.74	0.34	108,141,170,170	0
3	BRJ	D	404	4/4	0.75	0.46	181,184,190,197	0
6	PLC	C	406	34/42	0.76	0.31	111,139,169,169	0
3	BRJ	C	404	4/4	0.76	0.54	219,221,225,229	0
2	LMT	A	401	12/35	0.76	0.24	93,95,101,102	0
3	BRJ	E	405	4/4	0.77	0.53	204,206,210,214	0
5	NA	E	406	1/1	0.79	0.30	96,96,96,96	0
2	LMT	C	402	12/35	0.79	0.27	106,110,119,119	0
3	BRJ	B	403	4/4	0.80	0.36	176,179,185,193	0
2	LMT	C	401	12/35	0.81	0.22	69,81,94,95	0
5	NA	B	406	1/1	0.82	0.29	84,84,84,84	0
2	LMT	E	401	12/35	0.85	0.22	81,98,118,120	0
2	LMT	D	401	12/35	0.87	0.21	85,97,107,107	0
5	NA	D	405	1/1	0.88	0.28	95,95,95,95	0
5	NA	A	407	1/1	0.89	0.17	86,86,86,86	0
7	ACT	E	404	4/4	0.89	0.19	75,80,80,81	0
2	LMT	B	401	12/35	0.90	0.19	94,97,98,98	0
5	NA	A	406	1/1	0.91	0.62	89,89,89,89	0
7	ACT	B	404	4/4	0.91	0.19	85,86,86,87	0
5	NA	C	405	1/1	0.91	0.14	76,76,76,76	0
7	ACT	B	405	4/4	0.93	0.14	86,89,90,95	0
7	ACT	E	403	4/4	0.95	0.13	93,95,95,98	0
4	CL	E	402	1/1	0.95	0.09	58,58,58,58	0
4	CL	A	405	1/1	0.96	0.12	74,74,74,74	0
7	ACT	D	403	4/4	0.96	0.13	87,90,90,99	0
4	CL	C	403	1/1	0.98	0.05	53,53,53,53	0
4	CL	B	402	1/1	0.98	0.05	57,57,57,57	0
4	CL	D	402	1/1	0.99	0.04	57,57,57,57	0
4	CL	A	404	1/1	0.99	0.08	83,83,83,83	0
4	CL	A	403	1/1	0.99	0.05	56,56,56,56	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.

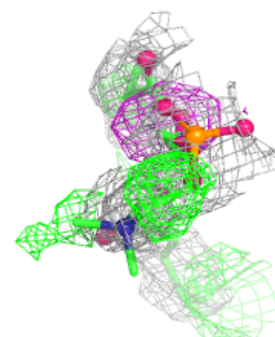
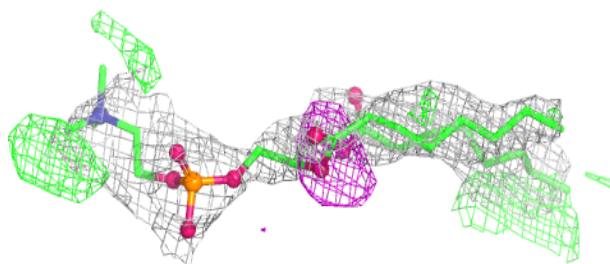
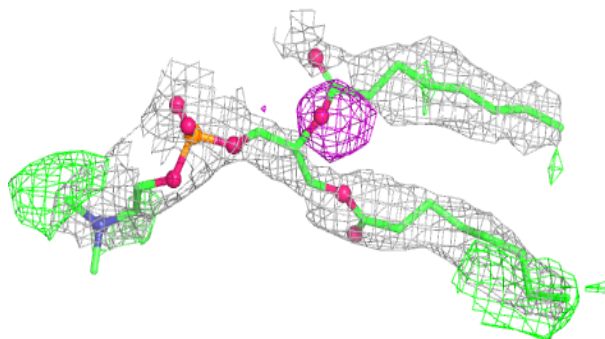
Electron density around PLC E 407:

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



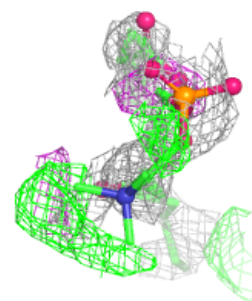
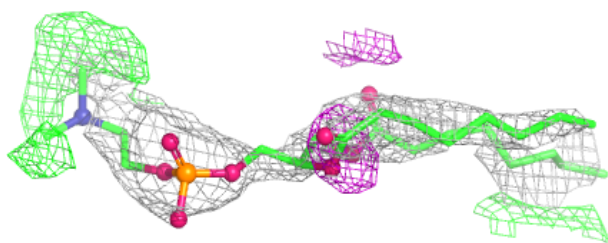
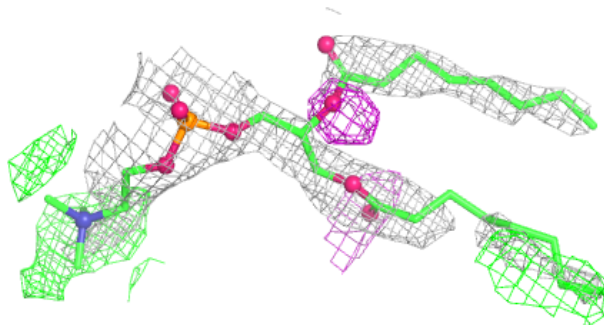
Electron density around PLC B 407:

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

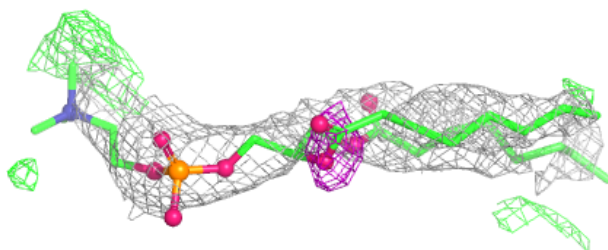
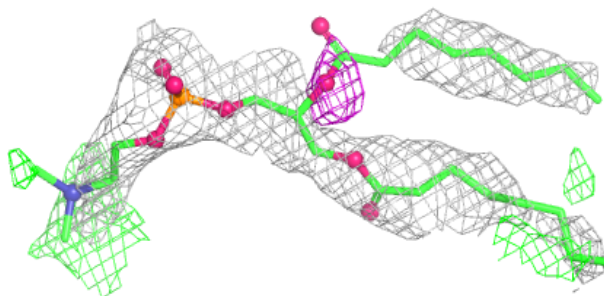


Electron density around PLC D 406:

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

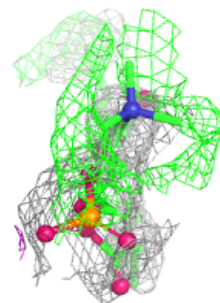
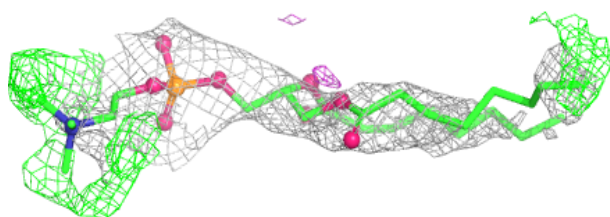
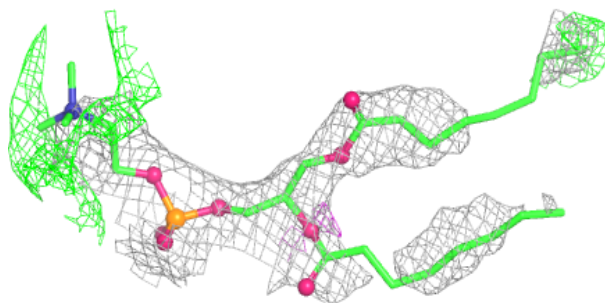
**Electron density around PLC A 408:**

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

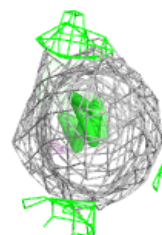
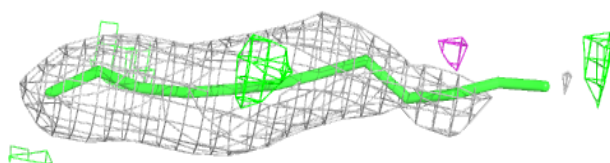
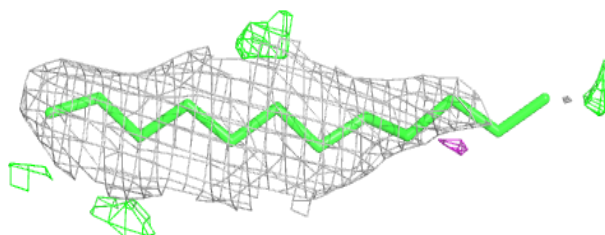


Electron density around PLC C 406:

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

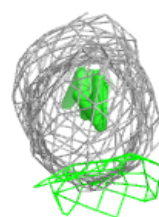
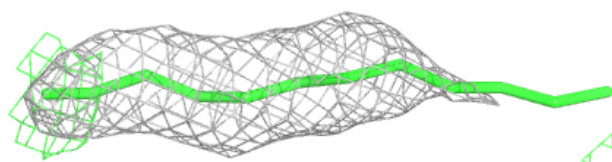
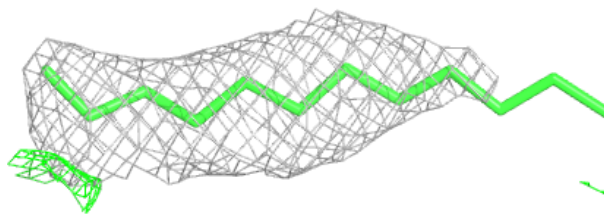
**Electron density around LMT C 401:**

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

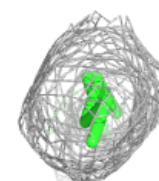
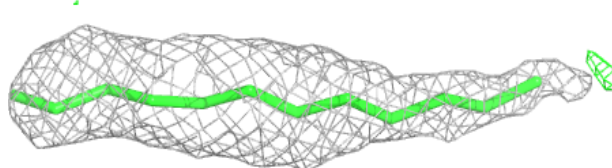
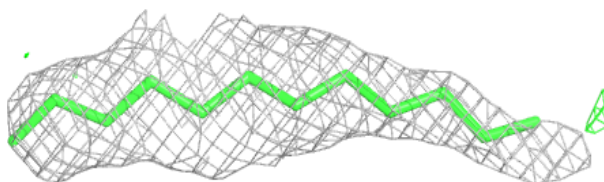


Electron density around LMT E 401:

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

**Electron density around LMT B 401:**

$2mF_o-DF_c$ (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.