



# Full wwPDB EM Validation Report ⓘ

Oct 21, 2024 – 04:46 PM JST

PDB ID : 8I5X  
EMDB ID : EMD-35197  
Title : Structure of human Nav1.7 in complex with Vinpocetine  
Authors : Wu, Q.R.; Yan, N.  
Deposited on : 2023-01-26  
Resolution : 2.90 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

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:

EMDB validation analysis : 0.0.1.dev113  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

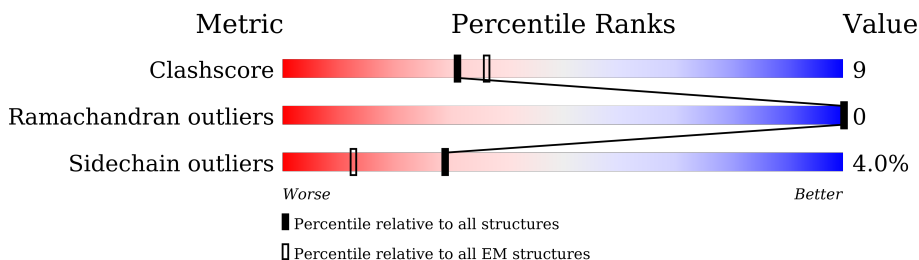
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.90 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)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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 EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2028	 9% 48% 14% 37%
2	B	218	 5% 57% 21% 21%
3	C	215	 43% 43% 12% 45%
4	D	2	 50% 100%
4	E	2	 50% 50%
4	F	2	 100%

## 2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 13590 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Sodium channel protein type 9 subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1273	Total	C	N	O	S	1	0
			10273	6810	1615	1771	77		

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-39	TRP	-	expression tag	UNP Q15858
A	-38	SER	-	expression tag	UNP Q15858
A	-37	HIS	-	expression tag	UNP Q15858
A	-36	PRO	-	expression tag	UNP Q15858
A	-35	GLN	-	expression tag	UNP Q15858
A	-34	PHE	-	expression tag	UNP Q15858
A	-33	GLU	-	expression tag	UNP Q15858
A	-32	LYS	-	expression tag	UNP Q15858
A	-31	GLY	-	expression tag	UNP Q15858
A	-30	GLY	-	expression tag	UNP Q15858
A	-29	GLY	-	expression tag	UNP Q15858
A	-28	ALA	-	expression tag	UNP Q15858
A	-27	ARG	-	expression tag	UNP Q15858
A	-26	GLY	-	expression tag	UNP Q15858
A	-25	GLY	-	expression tag	UNP Q15858
A	-24	SER	-	expression tag	UNP Q15858
A	-23	GLY	-	expression tag	UNP Q15858
A	-22	GLY	-	expression tag	UNP Q15858
A	-21	GLY	-	expression tag	UNP Q15858
A	-20	SER	-	expression tag	UNP Q15858
A	-19	TRP	-	expression tag	UNP Q15858
A	-18	SER	-	expression tag	UNP Q15858
A	-17	HIS	-	expression tag	UNP Q15858
A	-16	PRO	-	expression tag	UNP Q15858
A	-15	GLN	-	expression tag	UNP Q15858
A	-14	PHE	-	expression tag	UNP Q15858
A	-13	GLU	-	expression tag	UNP Q15858
A	-12	LYS	-	expression tag	UNP Q15858

*Continued on next page...*

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	GLY	-	expression tag	UNP Q15858
A	-10	PHE	-	expression tag	UNP Q15858
A	-9	ASP	-	expression tag	UNP Q15858
A	-8	TYR	-	expression tag	UNP Q15858
A	-7	LYS	-	expression tag	UNP Q15858
A	-6	ASP	-	expression tag	UNP Q15858
A	-5	ASP	-	expression tag	UNP Q15858
A	-4	ASP	-	expression tag	UNP Q15858
A	-3	ASP	-	expression tag	UNP Q15858
A	-2	LYS	-	expression tag	UNP Q15858
A	-1	GLY	-	expression tag	UNP Q15858
A	0	THR	-	expression tag	UNP Q15858

- Molecule 2 is a protein called Sodium channel subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	173	Total	C	N	O	S	0	0
			1416	902	232	272	10		

- Molecule 3 is a protein called Sodium channel subunit beta-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	119	Total	C	N	O	S	4	0
			980	615	172	183	10		

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



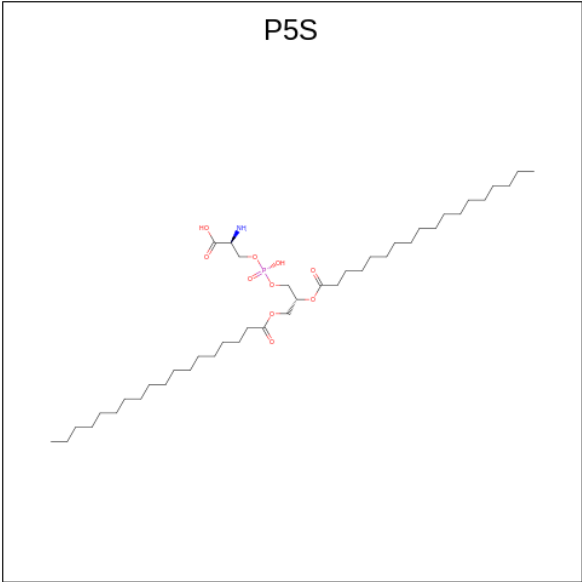
Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	2	Total	C	N	O	0	0
			28	16	2	10		
4	E	2	Total	C	N	O	0	0
			28	16	2	10		
4	F	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



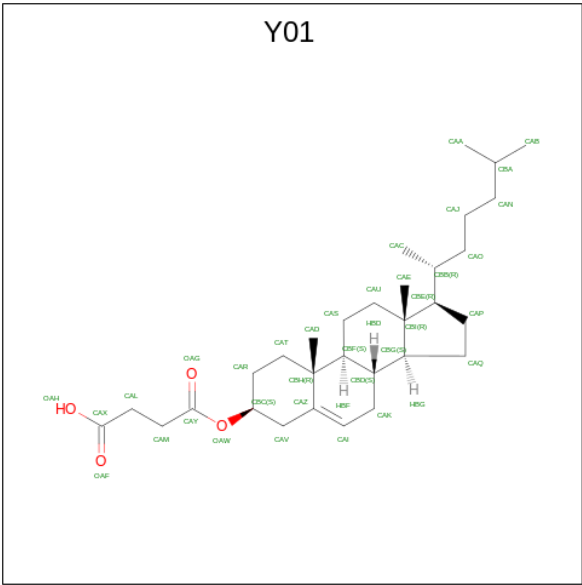
Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 6 is O-[(R)-{[(2R)-2,3-bis(octadecanoyloxy)propyl]oxy}(hydroxy)phosphoryl]-L-serine (three-letter code: P5S) (formula: C<sub>42</sub>H<sub>82</sub>NO<sub>10</sub>P).



Mol	Chain	Residues	Atoms					AltConf
6	A	1	Total	C	N	O	P	0
			35	24	1	9	1	

- Molecule 7 is CHOLESTEROL HEMISUCCINATE (three-letter code: Y01) (formula: C<sub>31</sub>H<sub>50</sub>O<sub>4</sub>).



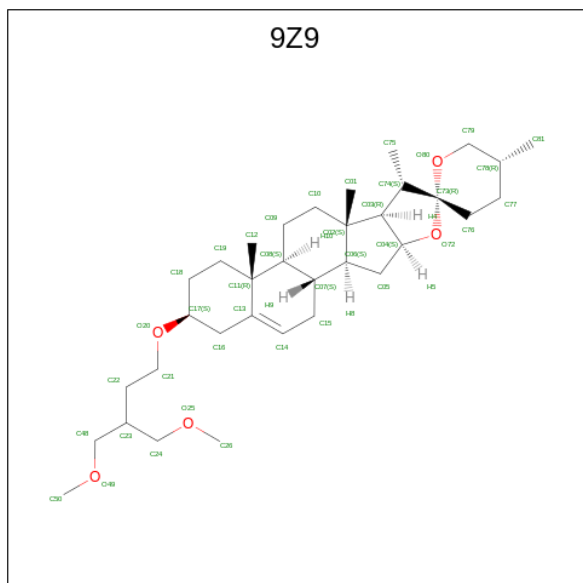
Mol	Chain	Residues	Atoms			AltConf
7	A	1	Total	C	O	0
			35	31	4	
7	A	1	Total	C	O	0
			35	31	4	
7	A	1	Total	C	O	0
			35	31	4	

Continued on next page...

Continued from previous page...

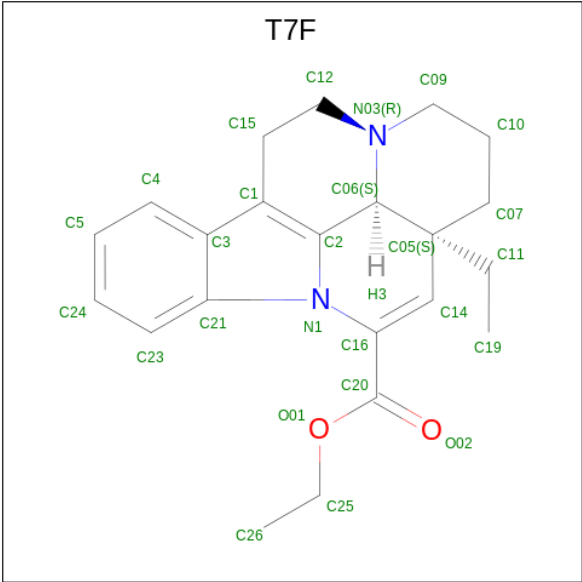
Mol	Chain	Residues	Atoms			AltConf
7	A	1	Total	C	O	0
			35	31	4	
7	A	1	Total	C	O	0
			35	31	4	

- Molecule 8 is (3beta,14beta,17beta,25R)-3-[4-methoxy-3-(methoxymethyl)butoxy]spirost-5-en (three-letter code: 9Z9) (formula: C<sub>34</sub>H<sub>56</sub>O<sub>5</sub>).



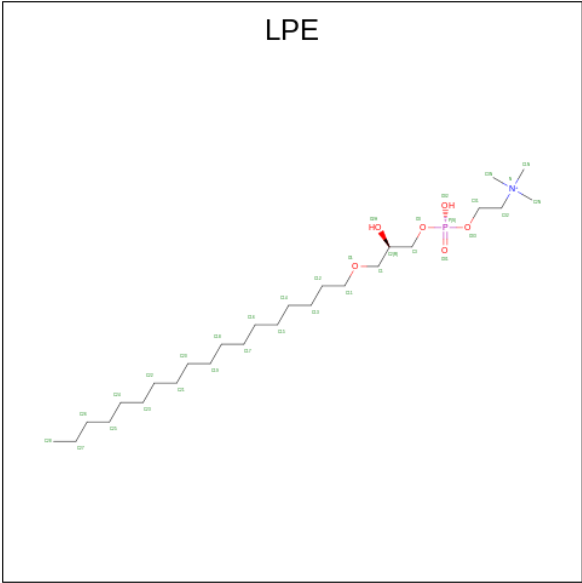
Mol	Chain	Residues	Atoms			AltConf
8	A	1	Total	C	O	0
			39	34	5	

- Molecule 9 is Vinpocetine (three-letter code: T7F) (formula: C<sub>22</sub>H<sub>26</sub>N<sub>2</sub>O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
9	A	1	Total	C	N	O	0
			26	22	2	2	

- Molecule 10 is 1-O-OCTADECYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: LPE) (formula: C<sub>26</sub>H<sub>57</sub>NO<sub>6</sub>P).



Mol	Chain	Residues	Atoms					AltConf
10	A	1	Total	C	N	O	P	0
			25	17	1	6	1	
10	A	1	Total	C	N	O	P	0
			18	10	1	6	1	

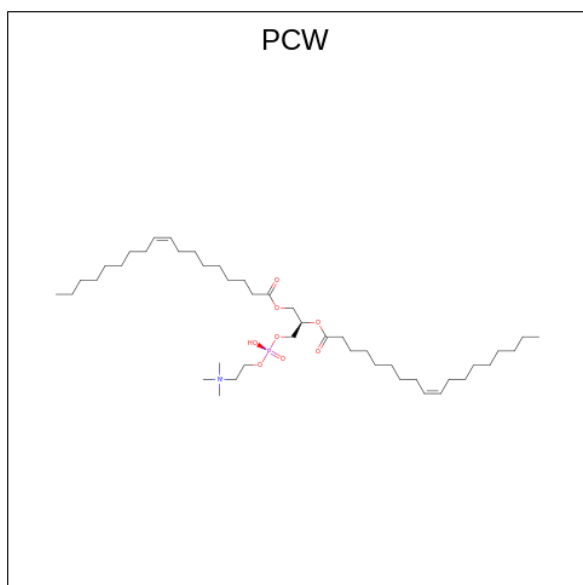
Continued on next page...



*Continued from previous page...*

Mol	Chain	Residues	Atoms					AltConf
10	A	1	Total	C	N	O	P	0
			28	20	1	6	1	
10	A	1	Total	C	N	O	P	0
			25	17	1	6	1	
10	A	1	Total	C	N	O	P	0
			25	17	1	6	1	
10	A	1	Total	C	N	O	P	0
			25	17	1	6	1	
10	A	1	Total	C	N	O	P	0
			25	17	1	6	1	
10	A	1	Total	C	N	O	P	0
			25	17	1	6	1	
10	B	1	Total	C	N	O	P	0
			17	9	1	6	1	

- Molecule 11 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PCW) (formula:  $C_{44}H_{85}NO_8P$ ).



Mol	Chain	Residues	Atoms					AltConf
11	A	1	Total	C	N	O	P	0
			50	40	1	8	1	
11	A	1	Total	C	N	O	P	0
			47	37	1	8	1	

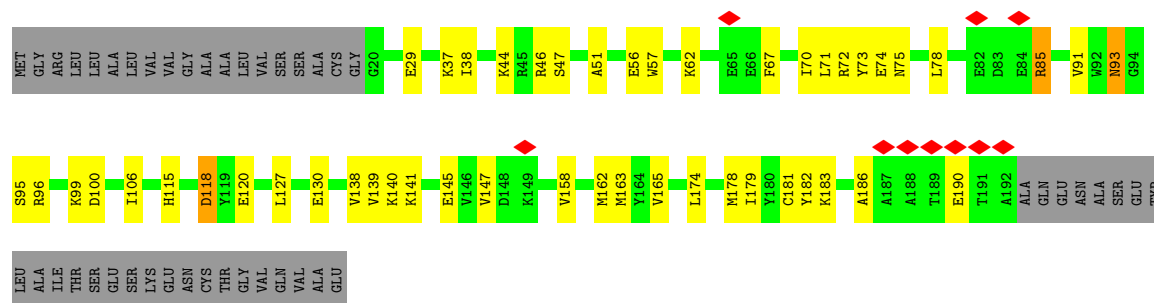
*Continued on next page...*

*Continued from previous page...*

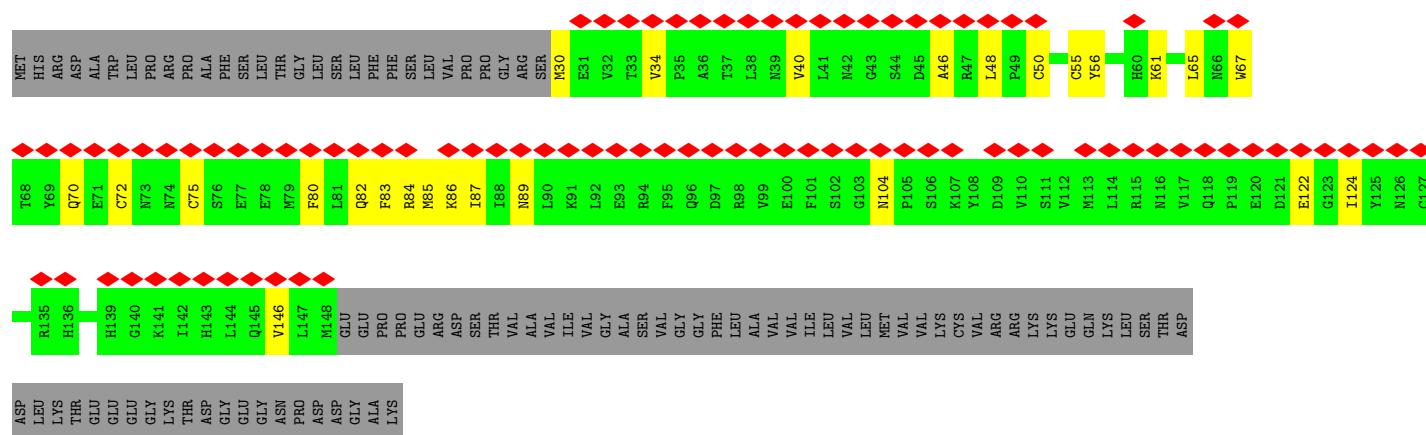
Mol	Chain	Residues	Atoms					AltConf
11	A	1	Total	C	N	O	P	0
			44	34	1	8	1	
11	A	1	Total	C	N	O	P	0
			44	34	1	8	1	
11	A	1	Total	C	N	O	P	0
			44	34	1	8	1	







• Molecule 3: Sodium channel subunit beta-2



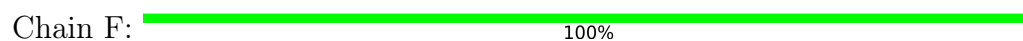
• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	304324	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.288	Depositor
Minimum map value	-2.226	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.075	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	277.12, 277.12, 277.12	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0825, 1.0825, 1.0825	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PCW, 9Z9, Y01, P5S, NAG, T7F, LPE

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	0.28	0/10524	0.47	1/14258 (0.0%)
2	B	0.26	0/1442	0.50	0/1949
3	C	0.26	0/1011	0.50	0/1367
All	All	0.28	0/12977	0.48	1/17574 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	398	LEU	CA-CB-CG	5.28	127.44	115.30

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	10273	0	10498	193	0
2	B	1416	0	1380	28	0
3	C	980	0	935	16	0
4	D	28	0	25	0	0
4	E	28	0	25	0	0
4	F	28	0	25	0	0
5	A	28	0	26	1	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	42	0	39	2	0
6	A	35	0	45	1	0
7	A	175	0	245	3	0
8	A	39	0	0	2	0
9	A	26	0	0	0	0
10	A	246	0	339	8	0
10	B	17	0	19	5	0
11	A	229	0	317	4	0
All	All	13590	0	13918	237	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 9.

All (237) 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:1324:VAL:HG11	1:A:1455:VAL:HG21	1.59	0.84
1:A:211:SER:O	1:A:215:THR:HG23	1.89	0.71
3:C:61:LYS:HA	3:C:85:MET:CE	2.21	0.70
3:C:61:LYS:HA	3:C:85:MET:HE3	1.74	0.67
1:A:932:MET:HE1	1:A:945:LEU:HD23	1.78	0.66
1:A:1755:TYR:O	1:A:1759:ILE:HD12	1.97	0.65
1:A:730:TRP:HA	1:A:733:PHE:CE2	2.32	0.64
1:A:1452:PHE:O	1:A:1455:VAL:HG22	1.98	0.64
2:B:51:ALA:HB2	2:B:127:LEU:HD13	1.80	0.63
1:A:1608:LEU:O	1:A:1612:ILE:HD12	1.99	0.62
2:B:162:MET:HA	2:B:165:VAL:HG22	1.81	0.62
1:A:182:THR:HG22	1:A:185:ARG:HD3	1.81	0.62
1:A:1194:PHE:HD1	10:B:304:LPE:H32	1.64	0.61
1:A:86:LYS:HB2	1:A:102:ALA:HB3	1.83	0.61
2:B:158:VAL:O	2:B:162:MET:HG3	2.01	0.61
1:A:1756:ILE:O	1:A:1760:LEU:HG	2.01	0.61
1:A:1451:LEU:O	1:A:1455:VAL:HG13	2.01	0.61
7:A:2025:Y01:HAC1	7:A:2025:Y01:HAE2	1.81	0.60
2:B:44:LYS:NZ	2:B:100:ASP:OD2	2.30	0.60
1:A:862:SER:HG	1:A:1447:PHE:HE1	1.50	0.60
3:C:65:LEU:HB3	3:C:83:PHE:HB3	1.83	0.60
1:A:910:MET:HG2	1:A:919:ILE:HD12	1.84	0.59
1:A:1481:TYR:CE1	10:A:2017:LPE:H1N3	2.37	0.59
1:A:1349:GLU:HG3	1:A:1351:ILE:HG23	1.84	0.59
1:A:180:GLU:N	1:A:180:GLU:OE1	2.36	0.59

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:75:ASN:OD1	2:B:99:LYS:NZ	2.36	0.59
1:A:1177:ILE:HD12	1:A:1177:ILE:H	1.68	0.58
1:A:1759:ILE:HG21	8:A:2006:9Z9:C10	2.33	0.58
1:A:814:LEU:O	1:A:818:LEU:HG	2.03	0.58
1:A:1003:LYS:HE2	1:A:1007:ARG:HH21	1.68	0.58
1:A:1452:PHE:CE2	1:A:1456:ILE:CD1	2.87	0.57
1:A:1502:ASN:HB3	1:A:1505:GLN:HB2	1.86	0.57
1:A:1641:LEU:HD22	10:A:2016:LPE:H132	1.85	0.57
2:B:85:ARG:O	2:B:115:HIS:NE2	2.30	0.57
1:A:1197:PHE:O	1:A:1201:MET:HG2	2.05	0.57
1:A:1324:VAL:CG1	1:A:1455:VAL:HG11	2.35	0.57
1:A:1325:LEU:O	1:A:1329:LEU:HG	2.05	0.57
1:A:1519:ILE:O	1:A:1523:VAL:HG13	2.05	0.57
1:A:1235:TYR:CE2	1:A:1239:LEU:HD11	2.41	0.56
2:B:96:ARG:NH2	5:B:301:NAG:O7	2.38	0.56
1:A:1315:ILE:HA	1:A:1318:ILE:HG12	1.86	0.56
1:A:13:VAL:HG23	1:A:76:GLU:HG3	1.88	0.56
1:A:993:THR:HG22	1:A:997:LYS:HE3	1.87	0.56
1:A:1324:VAL:HG11	1:A:1455:VAL:HG11	1.87	0.56
1:A:1504:ILE:O	1:A:1508:ILE:HG13	2.05	0.56
1:A:1676:ASN:O	1:A:1680:ASN:ND2	2.39	0.55
2:B:118:ASP:OD1	2:B:118:ASP:N	2.38	0.55
1:A:1400:LEU:HD21	1:A:1744:ILE:HD11	1.87	0.55
1:A:1607:THR:O	1:A:1611:VAL:HG23	2.07	0.55
3:C:122:GLU:OE2	3:C:146:VAL:O	2.25	0.55
1:A:97:ILE:O	1:A:97:ILE:HD12	2.06	0.55
1:A:90:VAL:HG11	1:A:120:ILE:HG21	1.88	0.55
1:A:1752:VAL:O	1:A:1756:ILE:HG13	2.06	0.55
1:A:392:TYR:OH	1:A:1633:LEU:O	2.25	0.54
1:A:1535:GLU:HG2	1:A:1547:LEU:HD13	1.89	0.54
1:A:1491:LYS:HB2	11:A:2023:PCW:H61	1.88	0.53
3:C:40:VAL:HG11	3:C:46:ALA:HB2	1.90	0.53
1:A:139:ASN:O	1:A:143:MET:HG3	2.08	0.53
1:A:1402:VAL:HA	1:A:1408:TRP:HB3	1.89	0.53
1:A:388:LEU:O	1:A:392:TYR:HB3	2.07	0.53
1:A:1463:GLN:HA	1:A:1466:LYS:HE3	1.91	0.53
10:A:2018:LPE:H12	10:A:2019:LPE:H142	1.90	0.53
3:C:61:LYS:HA	3:C:85:MET:SD	2.49	0.53
1:A:98:PHE:HB3	1:A:100:PHE:CE1	2.43	0.52
1:A:186:ASP:HB3	1:A:189:ASN:HB2	1.90	0.52
1:A:101:ASN:HD22	1:A:179:GLY:HA3	1.74	0.52

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:819:SER:O	1:A:822:GLU:HG3	2.09	0.52
2:B:181:CYS:SG	10:B:304:LPE:H3N1	2.50	0.52
1:A:396:LEU:HD22	1:A:1633:LEU:HD12	1.91	0.52
1:A:1585:VAL:HA	1:A:1588:ILE:HD12	1.90	0.52
1:A:1191:HIS:CG	10:B:304:LPE:H322	2.45	0.52
1:A:392:TYR:CZ	1:A:1637:LEU:HB2	2.45	0.51
1:A:1625:LYS:O	1:A:1631:ARG:NH1	2.44	0.51
1:A:215:THR:HG21	1:A:887:LEU:HD21	1.92	0.51
1:A:1738:PHE:HD1	10:A:2012:LPE:H2N3	1.76	0.51
1:A:1647:ILE:HG21	1:A:1754:MET:HG3	1.93	0.51
1:A:177:CYS:HB2	1:A:184:LEU:HD12	1.93	0.51
1:A:285:THR:O	1:A:289:ILE:HG12	2.10	0.51
1:A:1408:TRP:O	1:A:1412:MET:HG3	2.11	0.51
1:A:287:GLU:H	1:A:287:GLU:CD	2.13	0.50
2:B:72:ARG:NH2	2:B:74:GLU:OE1	2.34	0.50
3:C:86:LYS:HG2	3:C:87:ILE:N	2.27	0.50
1:A:266:LEU:O	1:A:1610:ARG:NH1	2.45	0.50
1:A:810:ILE:O	1:A:814:LEU:HD12	2.12	0.50
1:A:1430:SER:HB3	1:A:1433:MET:HG2	1.94	0.50
1:A:88:PHE:CE1	1:A:100:PHE:HB2	2.46	0.49
1:A:101:ASN:OD1	1:A:103:THR:N	2.32	0.49
1:A:266:LEU:HD21	1:A:1614:LEU:HD11	1.94	0.49
1:A:1337:ILE:O	1:A:1341:ASN:ND2	2.45	0.49
1:A:1643:ALA:O	1:A:1647:ILE:HG13	2.12	0.49
1:A:128:PHE:O	1:A:132:ILE:HG12	2.12	0.49
1:A:774:ASN:O	1:A:778:ILE:HG23	2.12	0.49
1:A:782:VAL:O	1:A:786:ILE:HG23	2.12	0.49
1:A:949:MET:SD	11:A:2014:PCW:C43	3.00	0.49
1:A:1500:PRO:HG2	1:A:1505:GLN:HB3	1.93	0.49
1:A:1584:VAL:HG12	1:A:1588:ILE:HD11	1.95	0.49
1:A:235:VAL:O	1:A:239:ILE:HG12	2.13	0.49
1:A:1293:ARG:O	1:A:1296:ARG:HG3	2.12	0.49
1:A:1443:PHE:HA	1:A:1447:PHE:HD2	1.77	0.49
2:B:38:ILE:HG22	2:B:57:TRP:HH2	1.78	0.49
2:B:67:PHE:CE1	2:B:120:GLU:HG3	2.48	0.49
1:A:751:THR:HG23	1:A:845:LEU:HD22	1.95	0.49
1:A:355:PHE:HE2	1:A:952:MET:HE1	1.78	0.48
1:A:360:GLN:HE22	1:A:1696:THR:HG21	1.79	0.48
1:A:1376:VAL:HG12	1:A:1377:SER:N	2.28	0.48
2:B:62:LYS:NZ	2:B:145:GLU:OE2	2.47	0.48
1:A:133:MET:HG3	1:A:227:VAL:HG23	1.95	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:VAL:HG11	1:A:883:VAL:HG22	1.96	0.48
1:A:878:PHE:O	1:A:882:VAL:HG12	2.13	0.48
2:B:186:ALA:O	2:B:190:GLU:HG3	2.13	0.48
1:A:1348:TYR:CD1	1:A:1384:ASN:HB2	2.49	0.48
1:A:737:ILE:HD13	1:A:740:ILE:HD12	1.95	0.48
1:A:1370:CYS:O	1:A:1374:MET:HG3	2.13	0.48
3:C:34:VAL:HG12	3:C:50:CYS:HA	1.96	0.48
1:A:268:MET:HG2	1:A:1537:GLU:HG2	1.95	0.48
1:A:251:LEU:HD13	1:A:1630:ILE:HB	1.96	0.48
1:A:1212:GLU:O	1:A:1212:GLU:HG3	2.14	0.47
1:A:1288:SER:O	1:A:1291:THR:HG22	2.14	0.47
10:A:2019:LPE:H11	10:A:2020:LPE:H1N3	1.96	0.47
3:C:86:LYS:HG2	3:C:87:ILE:H	1.79	0.47
3:C:72:CYS:H	3:C:75:CYS:HB2	1.79	0.47
1:A:77:ASP:HA	1:A:89:ILE:HD13	1.95	0.47
1:A:158:THR:O	1:A:162:ILE:HG12	2.14	0.47
2:B:57:TRP:HB2	2:B:71:LEU:HG	1.95	0.47
1:A:1290:ARG:O	1:A:1293:ARG:HG3	2.14	0.47
1:A:1573:TYR:CE1	1:A:1579:ASN:HB3	2.50	0.47
1:A:1627:ALA:HA	10:A:2021:LPE:H1N2	1.96	0.47
3:C:70:GLN:HG3	3:C:124:ILE:HB	1.96	0.47
1:A:391:PHE:CZ	1:A:1754:MET:HB3	2.49	0.47
1:A:394:ILE:O	1:A:398:LEU:HB2	2.15	0.47
1:A:1385:LEU:O	1:A:1388:ASN:ND2	2.47	0.47
1:A:1519:ILE:HD12	1:A:1520:SER:N	2.30	0.47
1:A:1583:PHE:O	1:A:1586:VAL:HG22	2.15	0.46
1:A:410:GLN:OE1	1:A:410:GLN:HA	2.15	0.46
1:A:300:ARG:HB3	2:B:130:GLU:OE1	2.16	0.46
1:A:1201:MET:HE3	1:A:1233:PHE:HE1	1.80	0.46
1:A:1228:TYR:O	1:A:1232:ILE:HG13	2.16	0.46
2:B:174:LEU:HD13	10:B:304:LPE:H11	1.97	0.46
1:A:875:ILE:O	1:A:879:ILE:HG13	2.15	0.46
1:A:1585:VAL:HG11	1:A:1622:ARG:HD2	1.97	0.46
3:C:67:TRP:HB3	3:C:80:PHE:CZ	2.51	0.46
1:A:139:ASN:OD1	1:A:220:ARG:HD3	2.16	0.46
1:A:1530:VAL:O	1:A:1534:VAL:HG23	2.16	0.45
1:A:1178:TRP:HZ2	6:A:2002:P5S:H46	1.82	0.45
1:A:116:ARG:O	1:A:120:ILE:HG12	2.17	0.45
1:A:1588:ILE:HG23	11:A:2024:PCW:H252	1.99	0.45
1:A:1318:ILE:HB	1:A:1319:PRO:HD3	1.99	0.45
3:C:48:LEU:HD23	3:C:48:LEU:HA	1.81	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:861:ASN:ND2	1:A:974:ASP:OD2	2.50	0.45
3:C:122:GLU:HG2	3:C:146:VAL:HG23	1.99	0.45
1:A:746:VAL:O	1:A:750:ILE:HG12	2.16	0.45
1:A:360:GLN:HG3	1:A:390:SER:OG	2.17	0.44
1:A:1484:ALA:O	1:A:1487:LYS:HG3	2.17	0.44
1:A:215:THR:HG21	1:A:887:LEU:CD2	2.48	0.44
1:A:1458:ASP:O	1:A:1462:GLN:NE2	2.50	0.44
1:A:391:PHE:HE1	1:A:1758:VAL:HG21	1.81	0.44
1:A:92:ASN:HB3	1:A:124:VAL:HG12	1.99	0.44
1:A:1476:GLU:OE1	1:A:1476:GLU:N	2.50	0.44
1:A:1656:PHE:O	1:A:1660:ILE:HG12	2.17	0.44
1:A:101:ASN:OD1	1:A:102:ALA:N	2.50	0.44
1:A:1759:ILE:HG21	8:A:2006:9Z9:C09	2.47	0.44
1:A:336:ASN:HB2	1:A:340:GLY:HA2	2.00	0.44
1:A:325:PRO:HG3	2:B:46:ARG:HD3	2.00	0.44
1:A:890:LYS:HB2	1:A:890:LYS:HE2	1.82	0.43
1:A:182:THR:HG23	1:A:184:LEU:H	1.82	0.43
1:A:357:LEU:HD23	1:A:363:TRP:HB2	1.99	0.43
1:A:1328:CYS:SG	1:A:1448:THR:HG23	2.58	0.43
1:A:89:ILE:HD11	1:A:99:ARG:HE	1.83	0.43
2:B:29:GLU:OE2	2:B:147:VAL:HG22	2.18	0.43
2:B:37:LYS:HE3	2:B:93:ASN:HB3	2.00	0.43
1:A:730:TRP:HA	1:A:733:PHE:CD2	2.53	0.43
1:A:1492:LYS:H	1:A:1492:LYS:HD2	1.84	0.43
2:B:91:VAL:HG21	5:B:301:NAG:H62	2.01	0.43
1:A:729:TYR:HA	1:A:732:LYS:HD3	2.00	0.43
1:A:1347:PHE:HB3	1:A:1385:LEU:HD13	2.01	0.43
2:B:73:TYR:HB2	2:B:78:LEU:HD12	2.01	0.43
1:A:1324:VAL:HG11	1:A:1455:VAL:CG2	2.40	0.42
1:A:1406:LYS:HE3	1:A:1698:ALA:HA	2.01	0.42
1:A:1408:TRP:HD1	1:A:1408:TRP:H	1.66	0.42
1:A:1478:GLN:HG2	10:A:2016:LPE:H311	2.01	0.42
1:A:1481:TYR:HE1	10:A:2017:LPE:H1N3	1.80	0.42
7:A:2003:Y01:HAU2	7:A:2003:Y01:HAC1	2.01	0.42
1:A:248:VAL:HG21	1:A:400:VAL:HG21	2.01	0.42
1:A:1232:ILE:HD11	2:B:163:MET:HA	2.00	0.42
1:A:731:ILE:HA	1:A:734:LYS:HD3	2.01	0.42
1:A:98:PHE:CE2	1:A:124:VAL:HG13	2.55	0.42
1:A:1222:ILE:HA	1:A:1225:ILE:HD12	2.02	0.42
1:A:1582:ASP:O	1:A:1586:VAL:HG13	2.18	0.42
1:A:247:ASP:OD1	1:A:247:ASP:N	2.53	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1352:ASN:O	1:A:1356:GLY:N	2.53	0.42
1:A:1378:GLN:OE1	1:A:1378:GLN:HA	2.19	0.42
1:A:249:MET:O	1:A:253:VAL:HG23	2.19	0.42
1:A:945:LEU:O	1:A:949:MET:HG2	2.19	0.42
1:A:1452:PHE:CZ	1:A:1456:ILE:HD11	2.55	0.42
1:A:1608:LEU:HG	1:A:1612:ILE:HD11	2.01	0.42
1:A:817:THR:O	1:A:821:VAL:HG23	2.20	0.42
1:A:1250:TYR:HB3	7:A:2004:Y01:HAU1	2.01	0.42
1:A:1355:ASP:C	1:A:1355:ASP:OD1	2.58	0.42
1:A:1375:ASN:HB2	5:A:2007:NAG:O5	2.17	0.42
1:A:1191:HIS:ND1	10:B:304:LPE:H322	2.35	0.42
1:A:890:LYS:O	1:A:894:GLU:HG2	2.20	0.41
1:A:1635:PHE:HB2	11:A:2023:PCW:H11	2.02	0.41
1:A:16:THR:O	1:A:19:SER:OG	2.34	0.41
1:A:892:TYR:CE1	1:A:910:MET:HG3	2.55	0.41
1:A:733:PHE:O	1:A:737:ILE:HG12	2.20	0.41
1:A:1624:VAL:HA	1:A:1630:ILE:HD11	2.02	0.41
2:B:71:LEU:HD21	2:B:106:ILE:HG21	2.00	0.41
2:B:138:VAL:HG12	2:B:139:VAL:N	2.35	0.41
1:A:30:ARG:NH2	1:A:84:ASP:OD2	2.54	0.41
1:A:99:ARG:HG2	1:A:99:ARG:HH11	1.85	0.41
1:A:120:ILE:HD13	1:A:173:ALA:HB1	2.00	0.41
1:A:212:ALA:HB1	1:A:216:PHE:CZ	2.55	0.41
1:A:798:MET:H	1:A:798:MET:HG2	1.72	0.41
1:A:1365:PRO:HD2	1:A:1369:GLU:HG3	2.02	0.41
1:A:1566:LEU:HD12	1:A:1566:LEU:HA	1.92	0.41
1:A:995:ILE:HG23	1:A:999:ILE:HD12	2.03	0.41
1:A:184:LEU:HD22	1:A:190[B]:TRP:CZ2	2.56	0.41
1:A:1707:ILE:HD13	1:A:1740:PHE:HE2	1.86	0.41
1:A:814:LEU:HA	1:A:817:THR:HG22	2.02	0.41
1:A:153:LYS:HD3	1:A:157:TYR:OH	2.21	0.41
1:A:228:ILE:HB	1:A:231:LEU:HD22	2.02	0.41
1:A:950:MET:O	1:A:954:ILE:HG12	2.19	0.41
1:A:1467:LEU:HD21	1:A:1472:ILE:HG22	2.03	0.41
2:B:56:GLU:HG2	2:B:72:ARG:HB2	2.03	0.41
3:C:82:GLN:NE2	3:C:84:ARG:CG	2.84	0.41
1:A:318:SER:OG	1:A:321:SER:OG	2.36	0.41
1:A:1703:LEU:O	1:A:1706:PRO:HD2	2.21	0.41
2:B:70:ILE:HD12	2:B:71:LEU:HD23	2.02	0.41
1:A:897:CYS:HB2	3:C:56:TYR:CE1	2.56	0.40
1:A:360:GLN:NE2	1:A:386:ILE:HD12	2.36	0.40

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:803:TYR:CZ	1:A:809:ASN:HB3	2.56	0.40
1:A:1759:ILE:HG23	1:A:1763:PHE:CE2	2.56	0.40
1:A:54:GLU:O	1:A:97:ILE:HD11	2.21	0.40
1:A:273:HIS:CE1	1:A:317:PHE:HE1	2.39	0.40
1:A:410:GLN:O	1:A:413:ILE:HG13	2.21	0.40
1:A:1507:CYS:HA	1:A:1510:ASP:OD2	2.21	0.40
2:B:179:ILE:O	2:B:183:LYS:HG2	2.20	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 PDB entries followed by that with respect to all EM entries.

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	1262/2028 (62%)	1241 (98%)	21 (2%)	0	100	100
2	B	171/218 (78%)	167 (98%)	4 (2%)	0	100	100
3	C	120/215 (56%)	117 (98%)	3 (2%)	0	100	100
All	All	1553/2461 (63%)	1525 (98%)	28 (2%)	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 PDB entries followed by that with respect to all EM entries.

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	1136/1807 (63%)	1093 (96%)	43 (4%)	28	63
2	B	157/190 (83%)	148 (94%)	9 (6%)	17	47
3	C	114/193 (59%)	110 (96%)	4 (4%)	31	66
All	All	1407/2190 (64%)	1351 (96%)	56 (4%)	29	61

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	VAL
1	A	57	LYS
1	A	75	LEU
1	A	88	PHE
1	A	92	ASN
1	A	130	MET
1	A	150	ASP
1	A	198	PHE
1	A	307	GLU
1	A	348	SER
1	A	362	TYR
1	A	403	MET
1	A	405	TYR
1	A	734	LYS
1	A	736	CYS
1	A	742	MET
1	A	747	ASP
1	A	781	LEU
1	A	822	GLU
1	A	837	PHE
1	A	910	MET
1	A	912	ASP
1	A	964	LEU
1	A	1195	GLU
1	A	1222	ILE
1	A	1288	SER
1	A	1290	ARG
1	A	1331	PHE
1	A	1355	ASP
1	A	1375	ASN
1	A	1406	LYS
1	A	1408	TRP
1	A	1424	GLN
1	A	1456	ILE

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	1487	LYS
1	A	1492	LYS
1	A	1528	ASN
1	A	1536	LYS
1	A	1582	ASP
1	A	1620	ILE
1	A	1630	ILE
1	A	1640	SER
1	A	1661	PHE
2	B	47	SER
2	B	85	ARG
2	B	93	ASN
2	B	95	SER
2	B	118	ASP
2	B	140	LYS
2	B	141	LYS
2	B	178	MET
2	B	182	TYR
3	C	30	MET
3	C	55	CYS
3	C	89	ASN
3	C	104	ASN

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

Mol	Chain	Res	Type
1	A	92	ASN
3	C	82	GLN

### 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 ⓘ

6 monosaccharides are modelled in this entry.



In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	NAG	D	1	4,1	14,14,15	0.45	0	17,19,21	0.46	0
4	NAG	D	2	4	14,14,15	0.27	0	17,19,21	0.35	0
4	NAG	E	1	4,1	14,14,15	0.37	0	17,19,21	0.85	1 (5%)
4	NAG	E	2	4	14,14,15	0.25	0	17,19,21	0.52	0
4	NAG	F	1	4,2	14,14,15	0.25	0	17,19,21	0.53	0
4	NAG	F	2	4	14,14,15	0.23	0	17,19,21	0.42	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	D	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1
4	NAG	E	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	E	2	4	-	2/6/23/26	0/1/1/1
4	NAG	F	1	4,2	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	1	NAG	O4-C4-C3	2.22	115.48	110.35

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	1	NAG	O5-C5-C6-O6
4	F	2	NAG	O5-C5-C6-O6

*Continued on next page...*

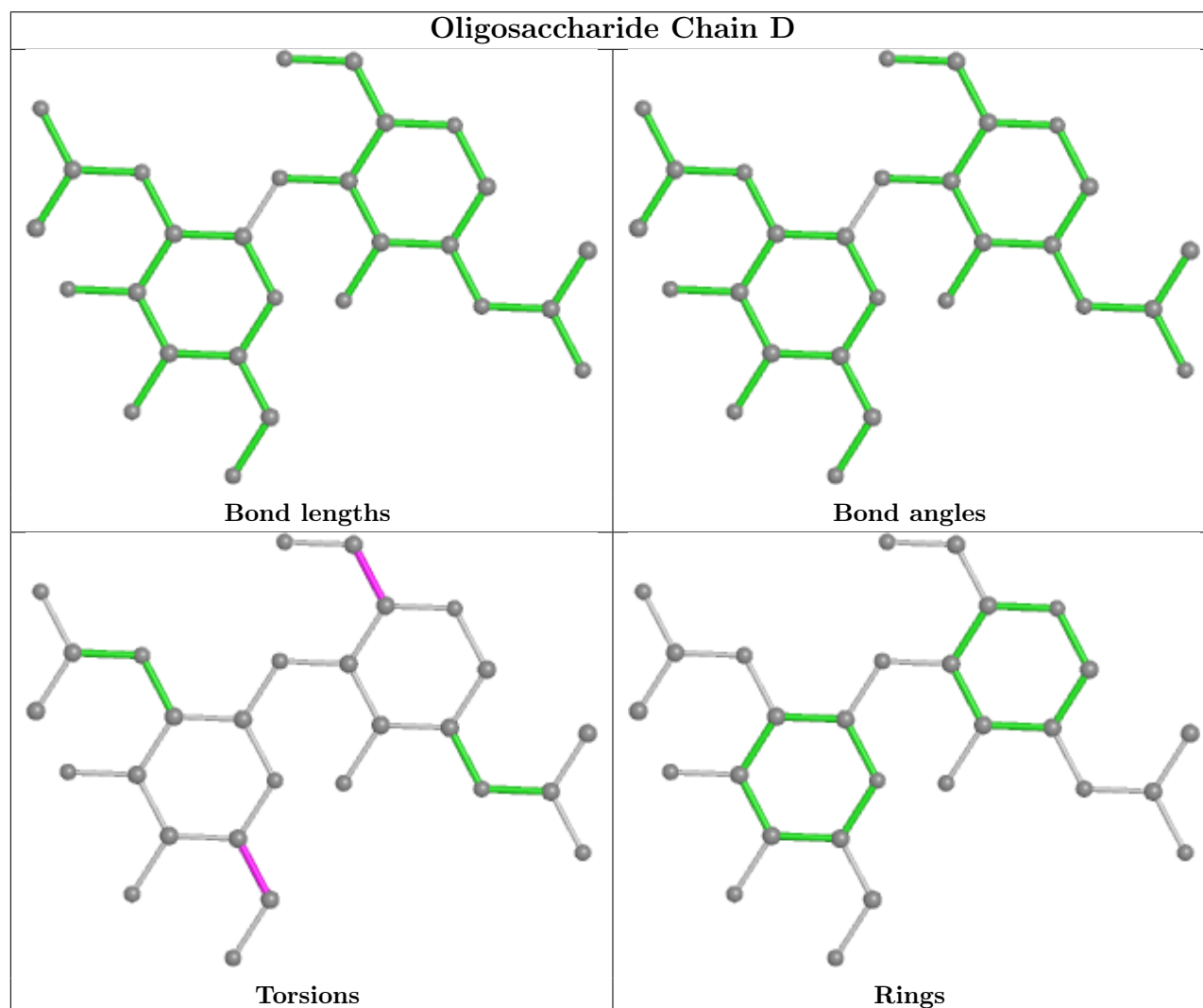
*Continued from previous page...*

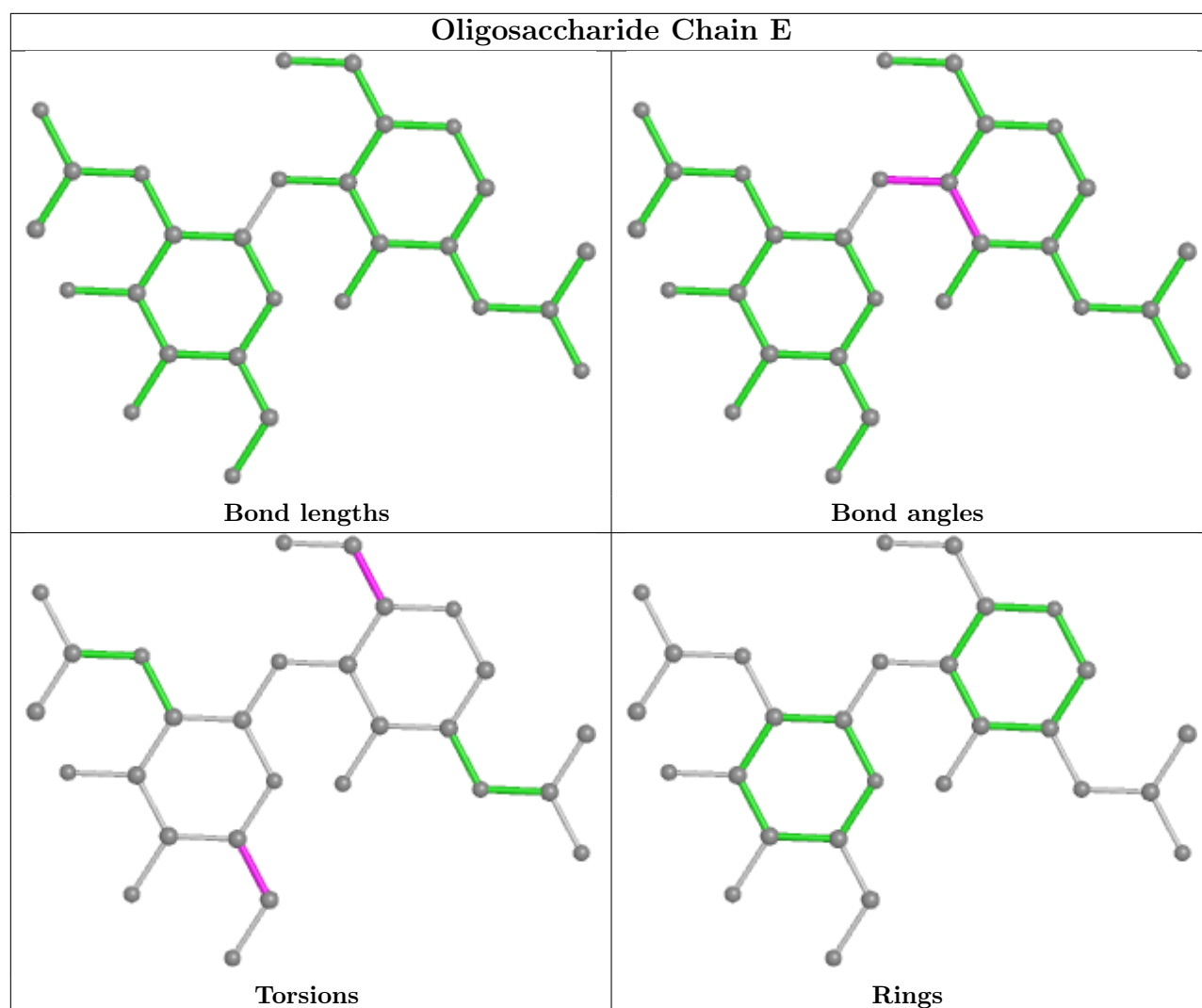
Mol	Chain	Res	Type	Atoms
4	E	2	NAG	O5-C5-C6-O6
4	D	1	NAG	C4-C5-C6-O6
4	F	2	NAG	C4-C5-C6-O6
4	D	2	NAG	C4-C5-C6-O6
4	E	2	NAG	C4-C5-C6-O6
4	D	2	NAG	O5-C5-C6-O6
4	F	1	NAG	O5-C5-C6-O6
4	F	1	NAG	C4-C5-C6-O6
4	E	1	NAG	O5-C5-C6-O6

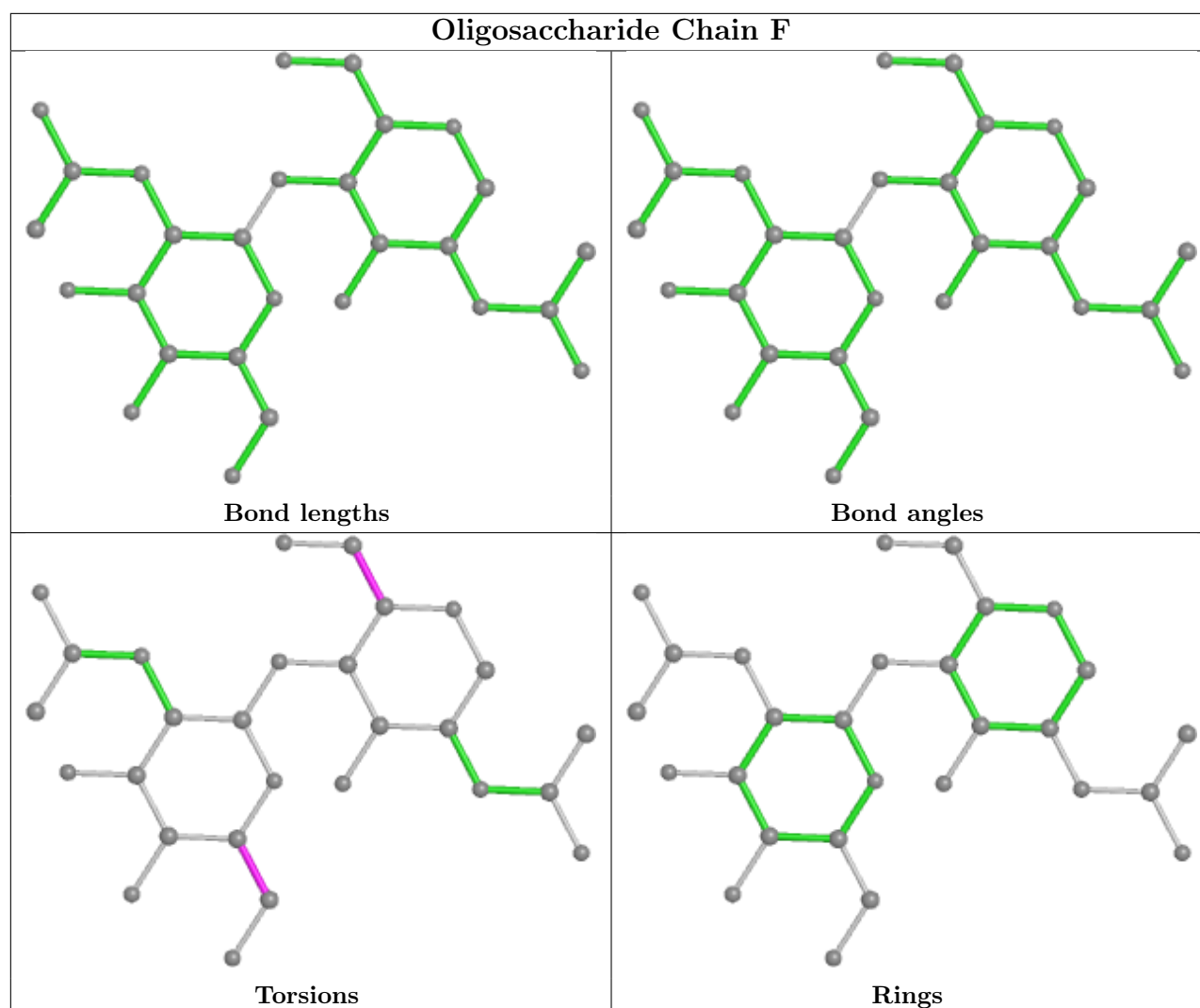
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.







## 5.6 Ligand geometry [i](#)

29 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	$\# Z  > 2$
10	LPE	A	2016	-	24,24,33	0.28	0	28,30,39	0.38	0
7	Y01	A	2003	-	38,38,38	0.45	0	57,57,57	0.50	0
7	Y01	A	2005	-	38,38,38	0.43	0	57,57,57	0.49	0
11	PCW	A	2015	-	43,43,53	0.36	0	49,51,61	0.40	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
11	PCW	A	2024	-	43,43,53	0.31	0	49,51,61	0.32	0
8	9Z9	A	2006	-	44,44,44	0.29	0	66,68,68	0.63	0
7	Y01	A	2025	-	38,38,38	0.49	0	57,57,57	0.53	0
7	Y01	A	2008	-	38,38,38	0.44	0	57,57,57	0.48	0
11	PCW	A	2014	-	46,46,53	0.48	0	52,54,61	0.35	0
9	T7F	A	2009	-	24,30,30	2.61	8 (33%)	22,46,46	3.10	7 (31%)
10	LPE	A	2010	-	24,24,33	0.37	0	25,27,39	0.43	0
10	LPE	A	2021	-	24,24,33	0.28	0	28,30,39	0.35	0
10	LPE	A	2019	-	24,24,33	0.27	0	28,30,39	0.35	0
10	LPE	B	304	-	16,16,33	0.35	0	20,22,39	0.41	0
11	PCW	A	2023	-	43,43,53	0.41	0	49,51,61	0.34	0
10	LPE	A	2018	-	24,24,33	0.28	0	28,30,39	0.33	0
10	LPE	A	2022	-	24,24,33	0.27	0	28,30,39	0.41	0
7	Y01	A	2004	-	38,38,38	0.44	0	57,57,57	0.48	0
11	PCW	A	2011	-	49,49,53	0.46	0	55,57,61	0.30	0
5	NAG	B	303	2	14,14,15	0.24	0	17,19,21	0.38	0
10	LPE	A	2017	-	24,24,33	0.29	0	28,30,39	0.35	0
5	NAG	A	2001	1	14,14,15	0.33	0	17,19,21	0.37	0
10	LPE	A	2020	-	24,24,33	0.28	0	28,30,39	0.40	0
10	LPE	A	2012	-	17,17,33	0.40	0	21,23,39	0.41	0
5	NAG	B	301	2	14,14,15	0.23	0	17,19,21	0.38	0
10	LPE	A	2013	-	27,27,33	0.26	0	31,33,39	0.33	0
5	NAG	A	2007	1	14,14,15	0.93	1 (7%)	17,19,21	0.90	1 (5%)
5	NAG	B	302	2	14,14,15	0.22	0	17,19,21	0.45	0
6	P5S	A	2002	-	33,34,53	0.45	0	36,40,60	0.51	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
10	LPE	A	2016	-	-	9/25/25/34	-
7	Y01	A	2003	-	-	10/19/77/77	0/4/4/4
7	Y01	A	2005	-	-	7/19/77/77	0/4/4/4
11	PCW	A	2015	-	-	21/47/47/57	-
11	PCW	A	2024	-	-	4/47/47/57	-
8	9Z9	A	2006	-	-	6/12/100/100	0/6/6/6
7	Y01	A	2025	-	-	11/19/77/77	0/4/4/4
7	Y01	A	2008	-	-	7/19/77/77	0/4/4/4

Continued on next page...

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	PCW	A	2014	-	-	23/50/50/57	-
9	T7F	A	2009	-	-	6/10/45/45	0/4/5/5
10	LPE	A	2010	-	-	14/25/25/34	-
10	LPE	A	2021	-	-	5/25/25/34	-
10	LPE	A	2019	-	-	4/25/25/34	-
10	LPE	B	304	-	-	6/17/17/34	-
11	PCW	A	2023	-	-	20/47/47/57	-
10	LPE	A	2018	-	-	4/25/25/34	-
10	LPE	A	2022	-	-	7/25/25/34	-
7	Y01	A	2004	-	-	0/19/77/77	0/4/4/4
11	PCW	A	2011	-	-	29/53/53/57	-
5	NAG	B	303	2	-	2/6/23/26	0/1/1/1
10	LPE	A	2017	-	-	14/25/25/34	-
5	NAG	A	2001	1	-	2/6/23/26	0/1/1/1
10	LPE	A	2020	-	-	8/25/25/34	-
10	LPE	A	2012	-	-	7/18/18/34	-
5	NAG	B	301	2	-	2/6/23/26	0/1/1/1
10	LPE	A	2013	-	-	6/28/28/34	-
5	NAG	A	2007	1	-	1/6/23/26	0/1/1/1
5	NAG	B	302	2	-	2/6/23/26	0/1/1/1
6	P5S	A	2002	-	-	12/39/39/59	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	2009	T7F	C15-C1	-6.49	1.39	1.51
9	A	2009	T7F	C21-N1	-5.04	1.32	1.39
9	A	2009	T7F	C12-N03	4.94	1.56	1.47
9	A	2009	T7F	C2-C06	-4.25	1.47	1.52
9	A	2009	T7F	O01-C20	3.40	1.40	1.33
5	A	2007	NAG	O5-C1	3.09	1.48	1.43
9	A	2009	T7F	C05-C14	2.91	1.56	1.51
9	A	2009	T7F	C2-N1	-2.78	1.31	1.36
9	A	2009	T7F	C16-C20	2.33	1.53	1.48

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	2009	T7F	C12-N03-C09	9.97	129.26	110.00
9	A	2009	T7F	O01-C20-C16	6.09	120.03	110.90
9	A	2009	T7F	C19-C11-C05	-5.17	110.46	115.66
9	A	2009	T7F	C12-C15-C1	3.97	118.19	111.64
5	A	2007	NAG	C1-O5-C5	3.44	116.86	112.19
9	A	2009	T7F	C12-N03-C06	-3.15	104.24	110.82
9	A	2009	T7F	C07-C10-C09	-2.27	106.85	110.69
9	A	2009	T7F	C25-O01-C20	-2.17	112.65	116.50

There are no chirality outliers.

All (249) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	2002	P5S	O-C-CA-N
6	A	2002	P5S	C2-C3-O16-P12
6	A	2002	P5S	N-CA-CB-OG
7	A	2003	Y01	CAM-CAY-OAW-CBC
8	A	2006	9Z9	C48-C23-C24-O25
8	A	2006	9Z9	C24-C23-C48-O49
9	A	2009	T7F	C06-C05-C11-C19
9	A	2009	T7F	C14-C05-C11-C19
9	A	2009	T7F	N1-C16-C20-O01
9	A	2009	T7F	C14-C16-C20-O01
9	A	2009	T7F	C14-C16-C20-O02
10	A	2010	LPE	O1-C1-C2-O2H
10	A	2010	LPE	C3-O3-P-O31
10	A	2010	LPE	O33-C31-C32-N
10	A	2012	LPE	O1-C1-C2-O2H
10	A	2012	LPE	O33-C31-C32-N
10	A	2013	LPE	C3-O3-P-O31
10	A	2016	LPE	C31-O33-P-O31
10	A	2017	LPE	C31-O33-P-O3
10	A	2017	LPE	C31-O33-P-O31
10	A	2018	LPE	C31-O33-P-O31
10	A	2019	LPE	C3-O3-P-O31
10	A	2020	LPE	C32-C31-O33-P
10	A	2022	LPE	C31-O33-P-O3
10	A	2022	LPE	C31-O33-P-O31
10	A	2022	LPE	C32-C31-O33-P
10	B	304	LPE	C3-O3-P-O31
10	B	304	LPE	C32-C31-O33-P
10	B	304	LPE	O33-C31-C32-N
11	A	2014	PCW	C1-O3P-P-O1P

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
11	A	2014	PCW	C1-O3P-P-O2P
11	A	2014	PCW	C1-O3P-P-O4P
11	A	2015	PCW	C1-O3P-P-O4P
11	A	2015	PCW	C4-O4P-P-O1P
11	A	2015	PCW	C4-O4P-P-O3P
11	A	2023	PCW	C1-O3P-P-O2P
11	A	2024	PCW	C1-O3P-P-O2P
11	A	2011	PCW	C38-C39-C40-C41
7	A	2003	Y01	OAG-CAY-OAW-CBC
7	A	2008	Y01	CAJ-CAO-CBB-CBE
10	A	2010	LPE	O2H-C2-C3-O3
5	B	303	NAG	O5-C5-C6-O6
11	A	2015	PCW	C32-C31-O2-C2
5	B	302	NAG	C4-C5-C6-O6
7	A	2003	Y01	CAJ-CAO-CBB-CBE
7	A	2005	Y01	CAJ-CAO-CBB-CBE
5	A	2001	NAG	O5-C5-C6-O6
7	A	2003	Y01	CAJ-CAO-CBB-CAC
7	A	2005	Y01	CAJ-CAO-CBB-CAC
7	A	2008	Y01	CAJ-CAO-CBB-CAC
11	A	2015	PCW	O31-C31-O2-C2
7	A	2025	Y01	CAJ-CAO-CBB-CBE
10	A	2017	LPE	O2H-C2-C3-O3
11	A	2011	PCW	C31-C32-C33-C34
5	A	2001	NAG	C4-C5-C6-O6
11	A	2015	PCW	C12-C11-O3-C3
11	A	2015	PCW	C18-C19-C20-C21
6	A	2002	P5S	OXT-C-CA-N
7	A	2025	Y01	CAJ-CAO-CBB-CAC
5	B	301	NAG	C4-C5-C6-O6
5	B	302	NAG	O5-C5-C6-O6
5	B	303	NAG	C4-C5-C6-O6
11	A	2015	PCW	O11-C11-O3-C3
10	A	2017	LPE	O1-C1-C2-O2H
10	A	2010	LPE	C3-O3-P-O33
10	A	2012	LPE	C31-O33-P-O3
10	A	2016	LPE	C31-O33-P-O3
10	A	2020	LPE	C31-O33-P-O3
10	B	304	LPE	C31-O33-P-O3
11	A	2011	PCW	C1-O3P-P-O4P
11	A	2023	PCW	C1-O3P-P-O4P
10	A	2010	LPE	C1-C2-C3-O3

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
11	A	2015	PCW	C12-C13-C14-C15
10	A	2010	LPE	O1-C1-C2-C3
10	A	2017	LPE	O1-C1-C2-C3
11	A	2014	PCW	C35-C36-C37-C38
11	A	2011	PCW	C33-C34-C35-C36
11	A	2011	PCW	C13-C14-C15-C16
11	A	2015	PCW	C14-C15-C16-C17
11	A	2023	PCW	C20-C21-C22-C23
10	A	2010	LPE	C16-C17-C18-C19
11	A	2015	PCW	C22-C23-C24-C25
11	A	2014	PCW	C15-C16-C17-C18
11	A	2023	PCW	C18-C19-C20-C21
11	A	2011	PCW	C12-C11-O3-C3
11	A	2023	PCW	C14-C15-C16-C17
11	A	2011	PCW	C24-C25-C26-C27
11	A	2023	PCW	C22-C23-C24-C25
11	A	2011	PCW	O31-C31-O2-C2
11	A	2011	PCW	O11-C11-O3-C3
10	A	2010	LPE	C13-C14-C15-C16
11	A	2011	PCW	C32-C31-O2-C2
8	A	2006	9Z9	C22-C23-C24-O25
8	A	2006	9Z9	C22-C23-C48-O49
10	A	2017	LPE	C11-C12-C13-C14
11	A	2011	PCW	C35-C36-C37-C38
10	A	2017	LPE	O1-C11-C12-C13
11	A	2011	PCW	C21-C22-C23-C24
11	A	2014	PCW	C34-C35-C36-C37
5	B	301	NAG	O5-C5-C6-O6
6	A	2002	P5S	C39-C38-O37-C2
11	A	2014	PCW	C14-C15-C16-C17
7	A	2003	Y01	CAN-CAJ-CAO-CBB
11	A	2014	PCW	C12-C13-C14-C15
6	A	2002	P5S	C3-O16-P12-OG
11	A	2011	PCW	O3P-C1-C2-C3
11	A	2014	PCW	C12-C11-O3-C3
7	A	2003	Y01	CAR-CBC-OAW-CAY
10	A	2012	LPE	O1-C1-C2-C3
10	A	2022	LPE	O1-C1-C2-C3
11	A	2014	PCW	C38-C39-C40-C41
11	A	2023	PCW	O3-C11-C12-C13
10	A	2017	LPE	C13-C14-C15-C16
10	A	2010	LPE	C11-C12-C13-C14

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
11	A	2015	PCW	O3P-C1-C2-C3
10	A	2018	LPE	C2-C3-O3-P
8	A	2006	9Z9	C23-C48-O49-C50
10	A	2010	LPE	O1-C11-C12-C13
10	A	2017	LPE	C16-C17-C18-C19
11	A	2011	PCW	C18-C19-C20-C21
10	A	2022	LPE	C2-C1-O1-C11
11	A	2011	PCW	C12-C13-C14-C15
11	A	2014	PCW	O11-C11-O3-C3
11	A	2011	PCW	C25-C26-C27-C28
11	A	2023	PCW	O2-C2-C3-O3
11	A	2015	PCW	C23-C24-C25-C26
7	A	2005	Y01	CAO-CBB-CBE-CBI
6	A	2002	P5S	O47-C38-O37-C2
11	A	2023	PCW	C2-C1-O3P-P
7	A	2005	Y01	CAO-CBB-CBE-CAP
10	A	2020	LPE	C2-C1-O1-C11
7	A	2005	Y01	CAC-CBB-CBE-CBI
7	A	2025	Y01	CAJ-CAN-CBA-CAB
10	A	2020	LPE	O1-C1-C2-O2H
11	A	2023	PCW	C1-C2-C3-O3
10	A	2010	LPE	C2-C1-O1-C11
11	A	2023	PCW	O3P-C1-C2-O2
7	A	2003	Y01	CAV-CBC-OAW-CAY
10	A	2010	LPE	C12-C13-C14-C15
7	A	2008	Y01	CAO-CBB-CBE-CBI
11	A	2014	PCW	C18-C19-C20-C21
11	A	2011	PCW	C23-C24-C25-C26
10	A	2018	LPE	C31-O33-P-O3
10	A	2019	LPE	C3-O3-P-O33
11	A	2014	PCW	C4-O4P-P-O3P
10	A	2013	LPE	C2-C3-O3-P
10	A	2010	LPE	C3-O3-P-O32
10	A	2012	LPE	C31-O33-P-O31
10	A	2016	LPE	C31-O33-P-O32
10	A	2020	LPE	C31-O33-P-O31
10	B	304	LPE	C31-O33-P-O31
11	A	2011	PCW	C1-O3P-P-O1P
11	A	2015	PCW	C1-O3P-P-O1P
11	A	2015	PCW	C4-O4P-P-O2P
11	A	2023	PCW	C1-O3P-P-O1P
6	A	2002	P5S	C1-C2-C3-O16

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
11	A	2023	PCW	O3P-C1-C2-C3
7	A	2005	Y01	CAC-CBB-CBE-CAP
10	A	2017	LPE	C32-C31-O33-P
8	A	2006	9Z9	C23-C24-O25-C26
11	A	2011	PCW	O3P-C1-C2-O2
11	A	2015	PCW	O3P-C1-C2-O2
7	A	2008	Y01	CAO-CBB-CBE-CAP
7	A	2008	Y01	CAC-CBB-CBE-CBI
7	A	2025	Y01	CAC-CBB-CBE-CBI
10	A	2017	LPE	O33-C31-C32-N
10	A	2018	LPE	O33-C31-C32-N
10	A	2019	LPE	O33-C31-C32-N
10	A	2020	LPE	O33-C31-C32-N
10	A	2021	LPE	O33-C31-C32-N
10	A	2022	LPE	O33-C31-C32-N
11	A	2011	PCW	O4P-C4-C5-N
11	A	2014	PCW	O4P-C4-C5-N
11	A	2015	PCW	O4P-C4-C5-N
11	A	2023	PCW	O4P-C4-C5-N
11	A	2024	PCW	O4P-C4-C5-N
11	A	2023	PCW	C17-C18-C19-C20
10	A	2016	LPE	C12-C11-O1-C1
11	A	2023	PCW	C19-C20-C21-C22
10	A	2012	LPE	C12-C11-O1-C1
6	A	2002	P5S	C45-C46-C48-C49
7	A	2025	Y01	CAO-CAJ-CAN-CBA
10	A	2012	LPE	C3-O3-P-O33
10	A	2013	LPE	C3-O3-P-O33
10	A	2013	LPE	C31-O33-P-O3
10	A	2020	LPE	C3-O3-P-O33
10	A	2021	LPE	C3-O3-P-O33
10	A	2021	LPE	C31-O33-P-O3
10	B	304	LPE	C3-O3-P-O33
11	A	2011	PCW	C4-O4P-P-O3P
11	A	2024	PCW	C1-O3P-P-O4P
11	A	2014	PCW	C39-C40-C41-C42
11	A	2014	PCW	C36-C37-C38-C39
7	A	2025	Y01	CAO-CBB-CBE-CAP
11	A	2015	PCW	C21-C22-C23-C24
11	A	2011	PCW	O2-C2-C3-O3
11	A	2024	PCW	O2-C2-C3-O3
11	A	2023	PCW	O11-C11-C12-C13

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
7	A	2003	Y01	CAM-CAL-CAX-OAF
7	A	2008	Y01	CAC-CBB-CBE-CAP
7	A	2003	Y01	CAM-CAL-CAX-OAH
10	A	2016	LPE	C31-C32-N-C2N
10	A	2017	LPE	C2-C1-O1-C11
7	A	2025	Y01	CAN-CAJ-CAO-CBB
10	A	2013	LPE	C2-C1-O1-C11
5	A	2007	NAG	C4-C5-C6-O6
10	A	2017	LPE	C1-C2-C3-O3
10	A	2019	LPE	C1-C2-C3-O3
11	A	2011	PCW	C32-C33-C34-C35
10	A	2016	LPE	O1-C11-C12-C13
11	A	2015	PCW	O3-C11-C12-C13
7	A	2003	Y01	CAL-CAM-CAY-OAW
6	A	2002	P5S	O37-C2-C3-O16
9	A	2009	T7F	C26-C25-O01-C20
10	A	2022	LPE	O1-C1-C2-O2H
7	A	2025	Y01	CAM-CAL-CAX-OAF
7	A	2025	Y01	CAC-CBB-CBE-CAP
11	A	2014	PCW	C19-C20-C21-C22
11	A	2023	PCW	C16-C17-C18-C19
11	A	2023	PCW	C35-C36-C37-C38
11	A	2014	PCW	C4-C5-N-C8
11	A	2014	PCW	O3-C11-C12-C13
7	A	2008	Y01	CAR-CBC-OAW-CAY
11	A	2014	PCW	O2-C31-C32-C33
11	A	2011	PCW	C20-C21-C22-C23
11	A	2014	PCW	O31-C31-O2-C2
7	A	2025	Y01	CAM-CAL-CAX-OAH
7	A	2025	Y01	CAJ-CAN-CBA-CAA
10	A	2016	LPE	C12-C13-C14-C15
11	A	2011	PCW	O2-C31-C32-C33
11	A	2023	PCW	C33-C34-C35-C36
11	A	2015	PCW	C2-C1-O3P-P
7	A	2005	Y01	CAR-CBC-OAW-CAY
6	A	2002	P5S	C3-O16-P12-O13
10	A	2013	LPE	C31-O33-P-O31
10	A	2017	LPE	C3-O3-P-O31
10	A	2020	LPE	C3-O3-P-O31
10	A	2021	LPE	C3-O3-P-O31
10	A	2021	LPE	C31-O33-P-O31
11	A	2011	PCW	C4-C5-N-C6

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
11	A	2014	PCW	O31-C31-C32-C33
6	A	2002	P5S	C1-C2-O37-C38
11	A	2015	PCW	C32-C33-C34-C35
10	A	2016	LPE	C31-C32-N-C1N
10	A	2016	LPE	C31-C32-N-C3N
11	A	2014	PCW	C17-C18-C19-C20
11	A	2011	PCW	O31-C31-C32-C33
11	A	2011	PCW	O3-C11-C12-C13
11	A	2011	PCW	O11-C11-C12-C13

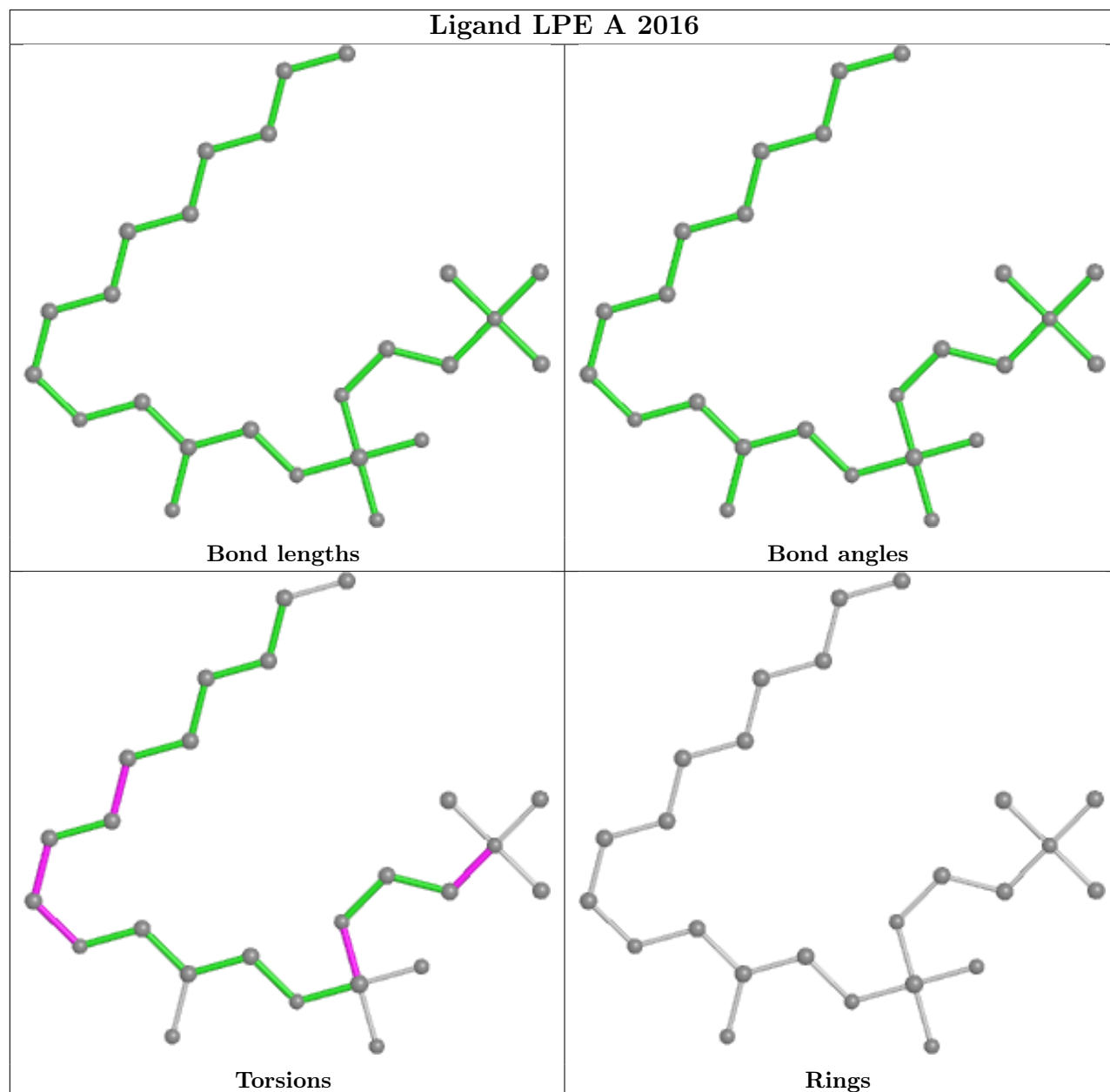
There are no ring outliers.

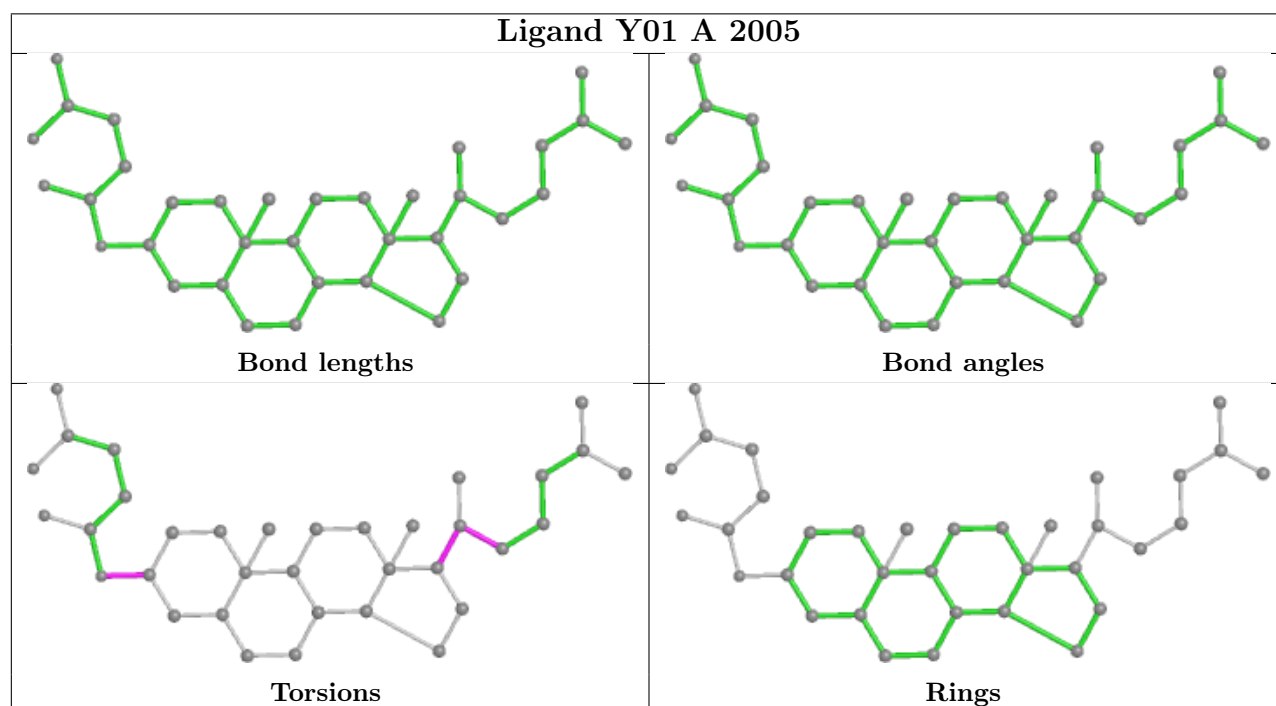
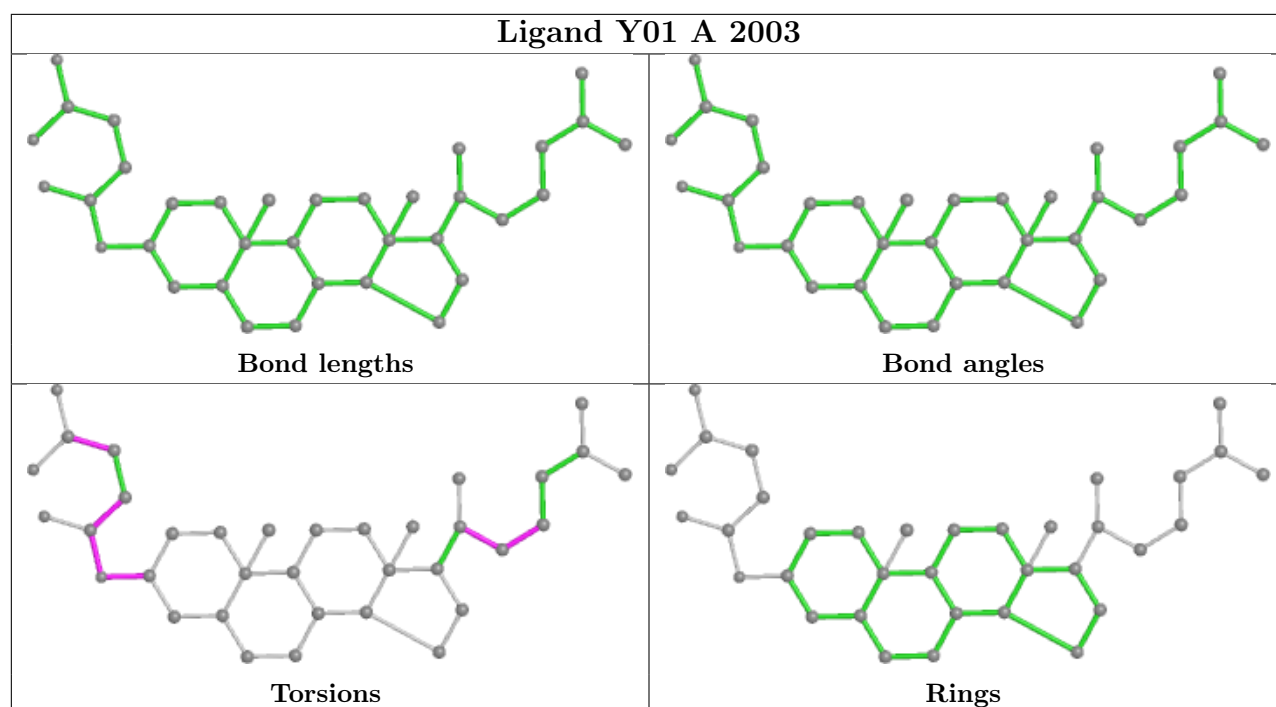
18 monomers are involved in 26 short contacts:

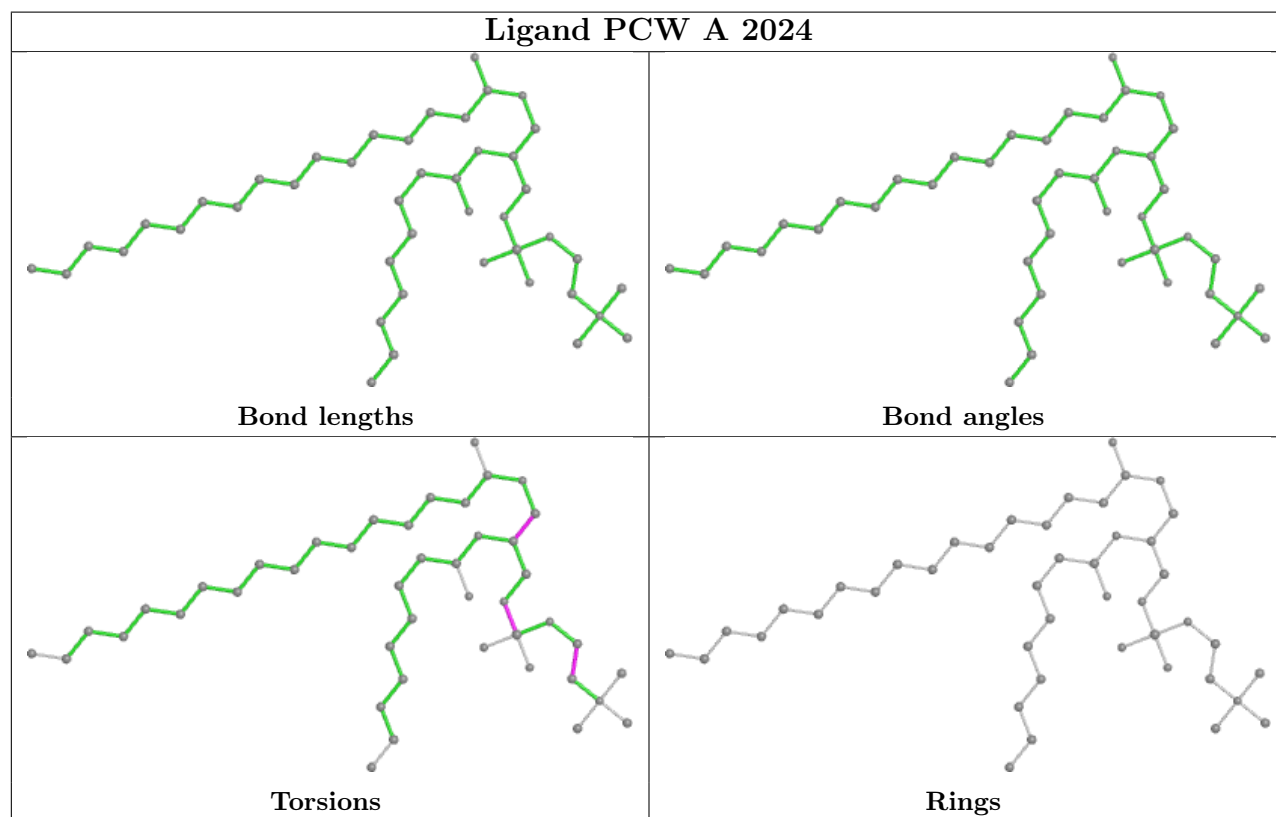
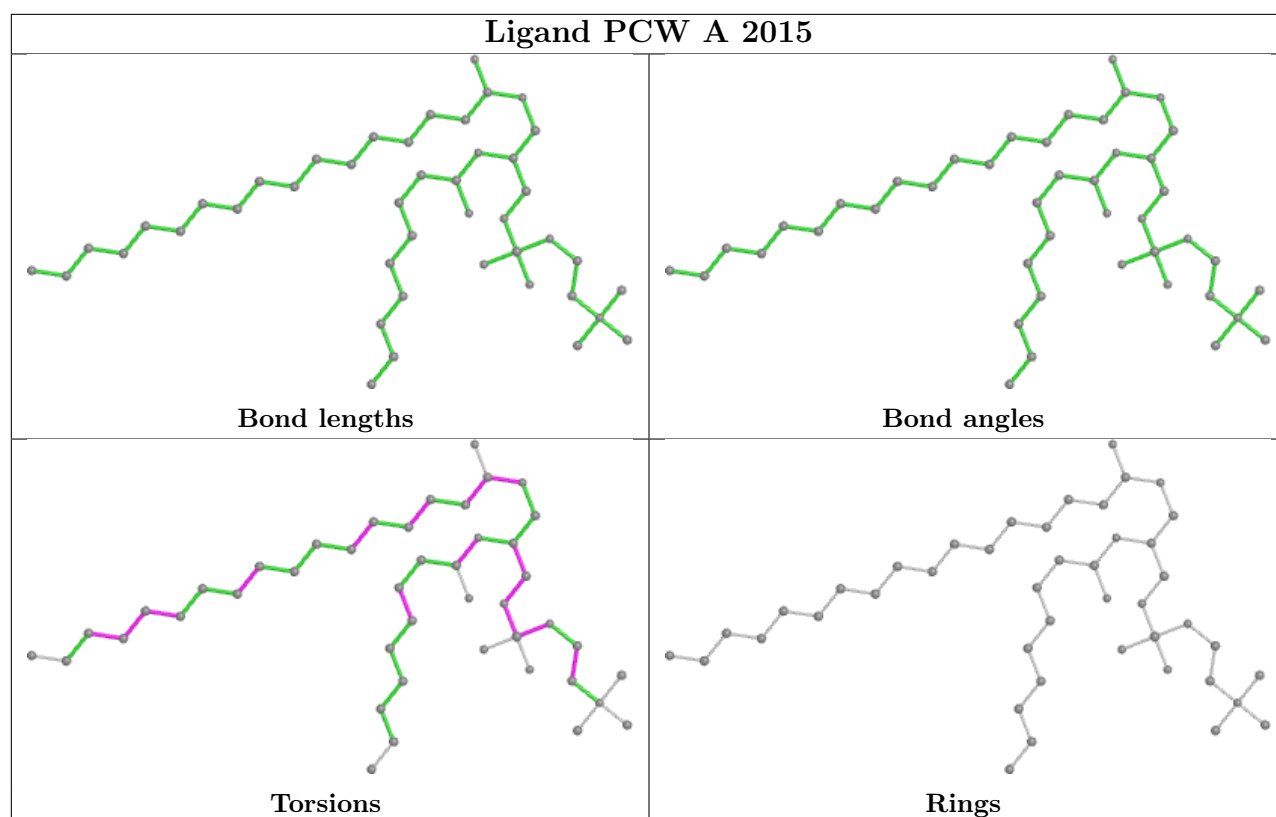
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	A	2016	LPE	2	0
7	A	2003	Y01	1	0
11	A	2024	PCW	1	0
8	A	2006	9Z9	2	0
7	A	2025	Y01	1	0
11	A	2014	PCW	1	0
10	A	2021	LPE	1	0
10	A	2019	LPE	2	0
10	B	304	LPE	5	0
11	A	2023	PCW	2	0
10	A	2018	LPE	1	0
7	A	2004	Y01	1	0
10	A	2017	LPE	2	0
10	A	2020	LPE	1	0
10	A	2012	LPE	1	0
5	B	301	NAG	2	0
5	A	2007	NAG	1	0
6	A	2002	P5S	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

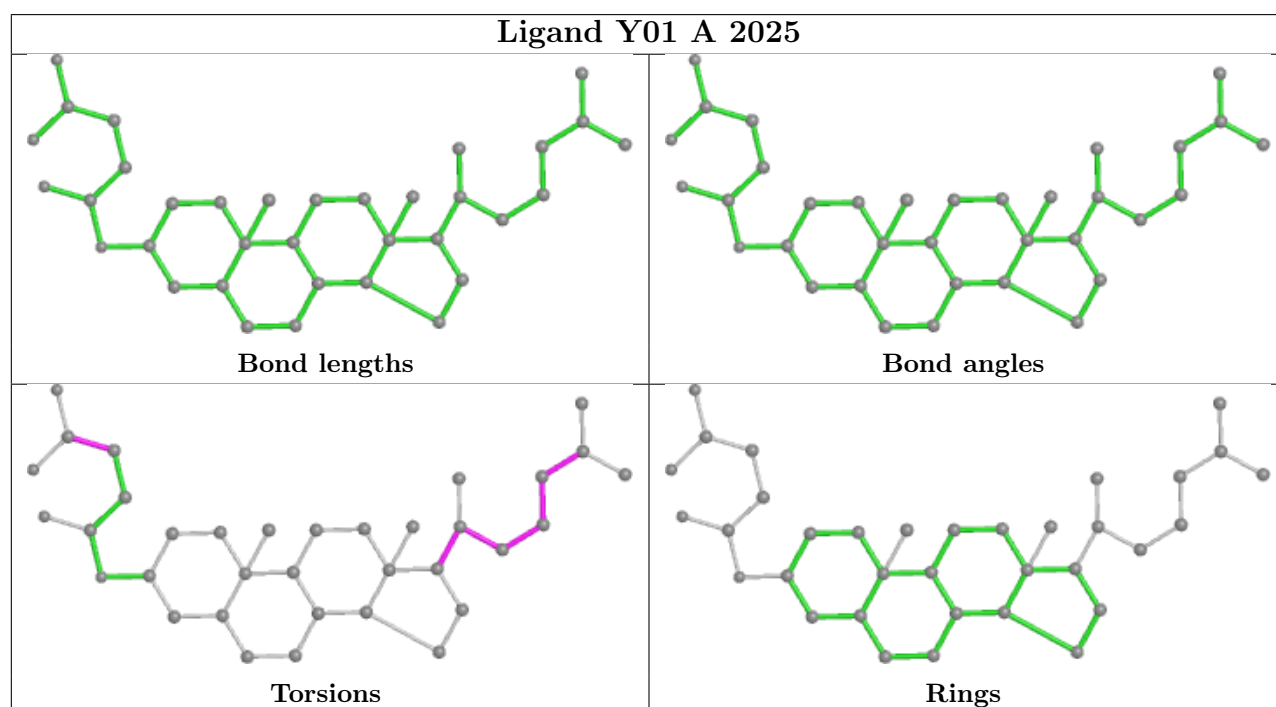
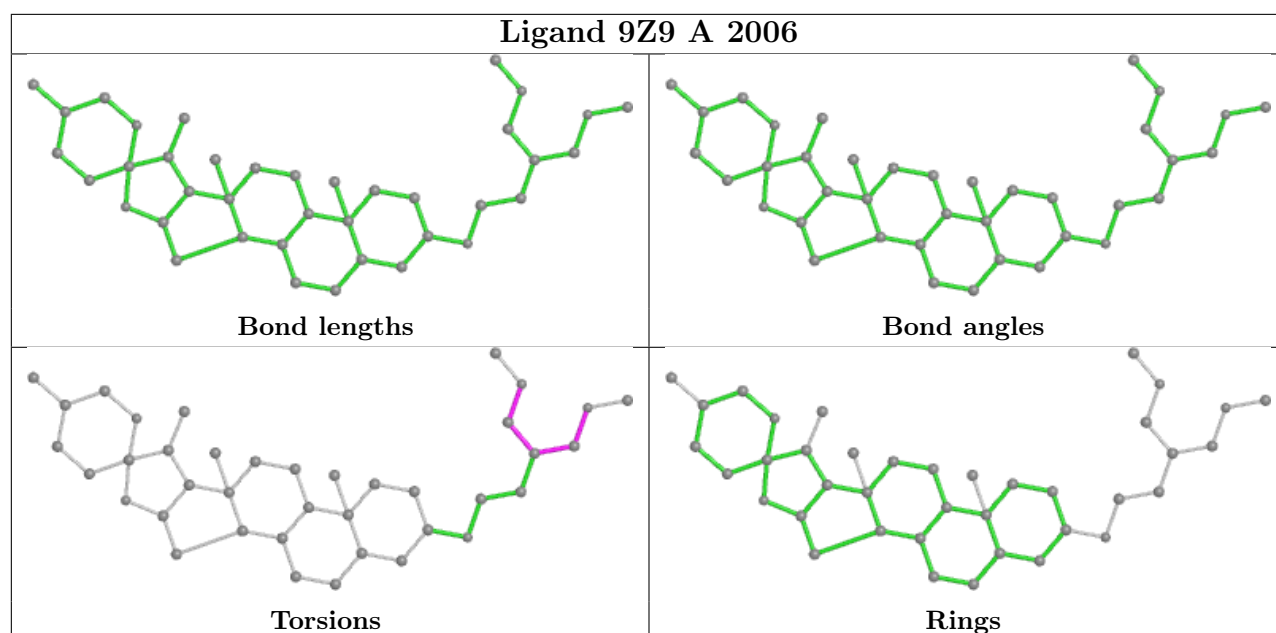
any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

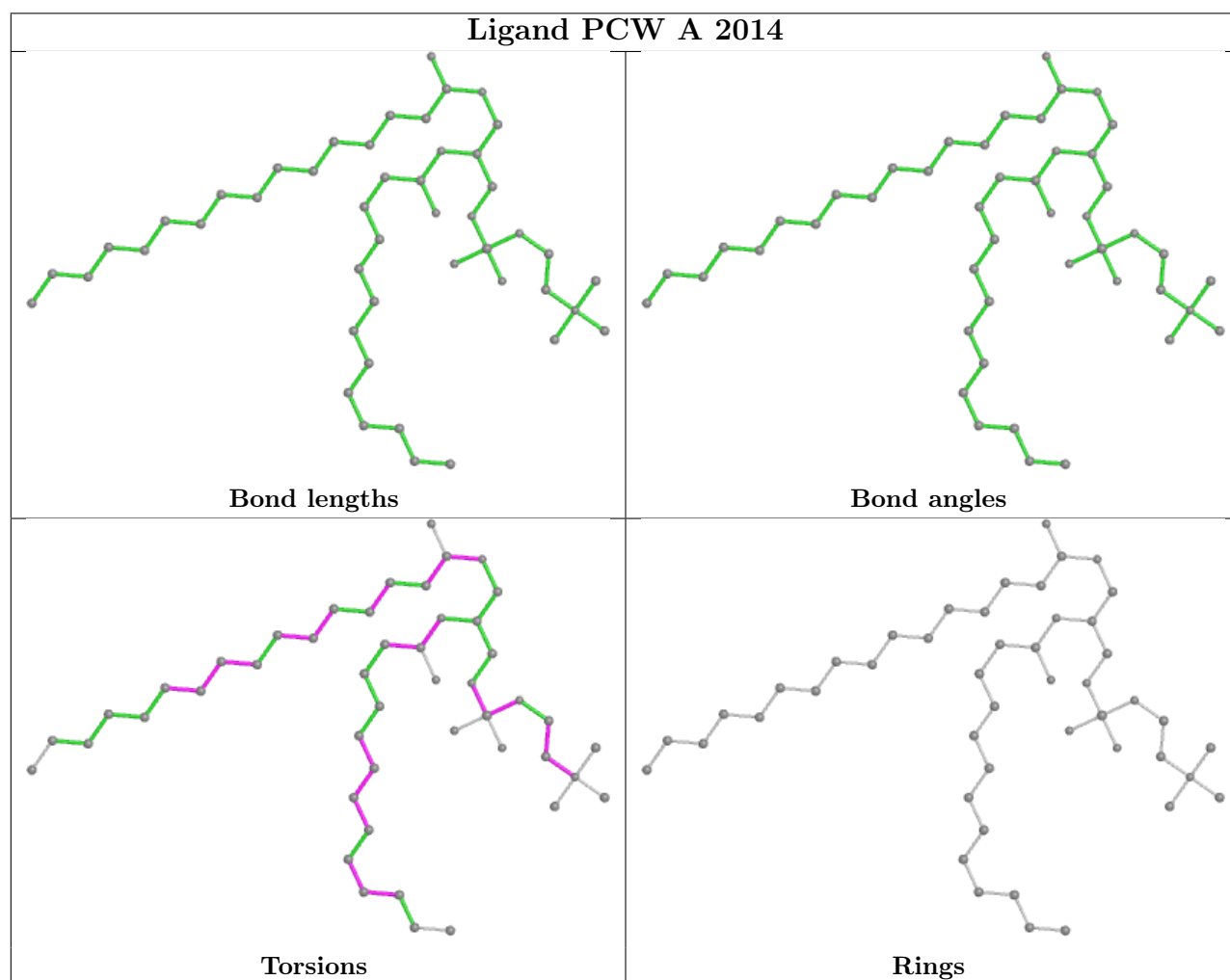
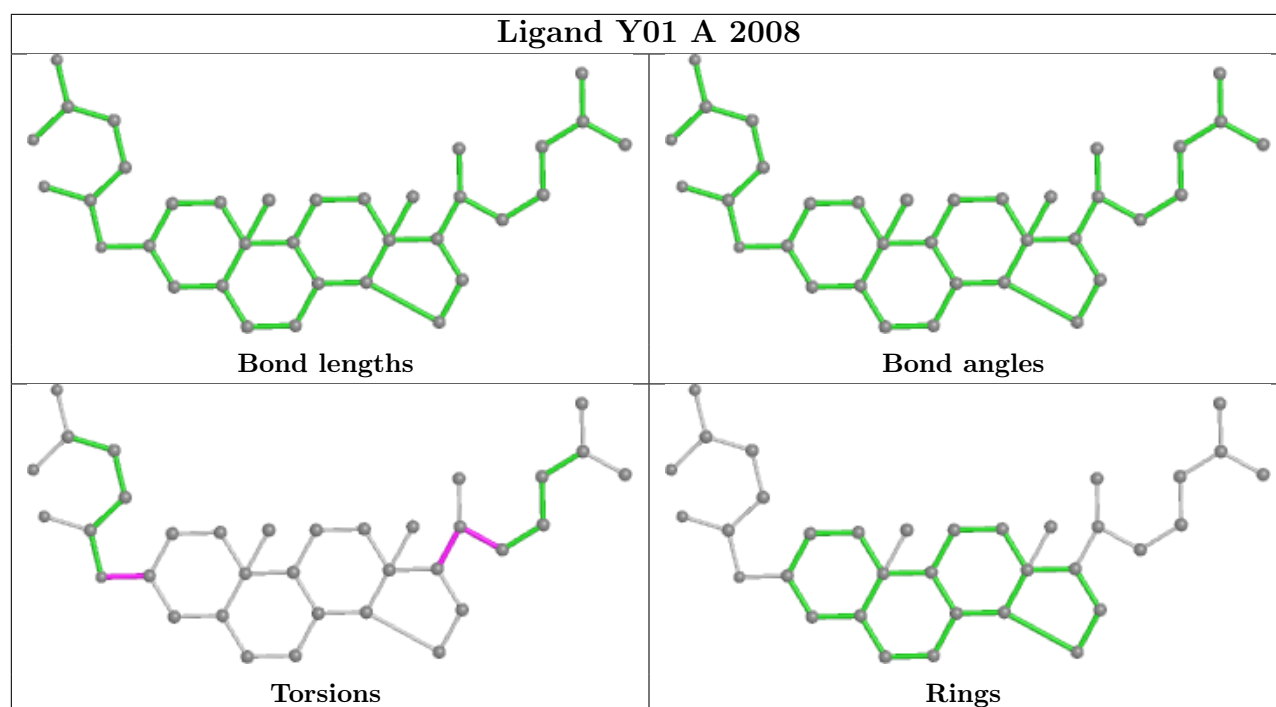


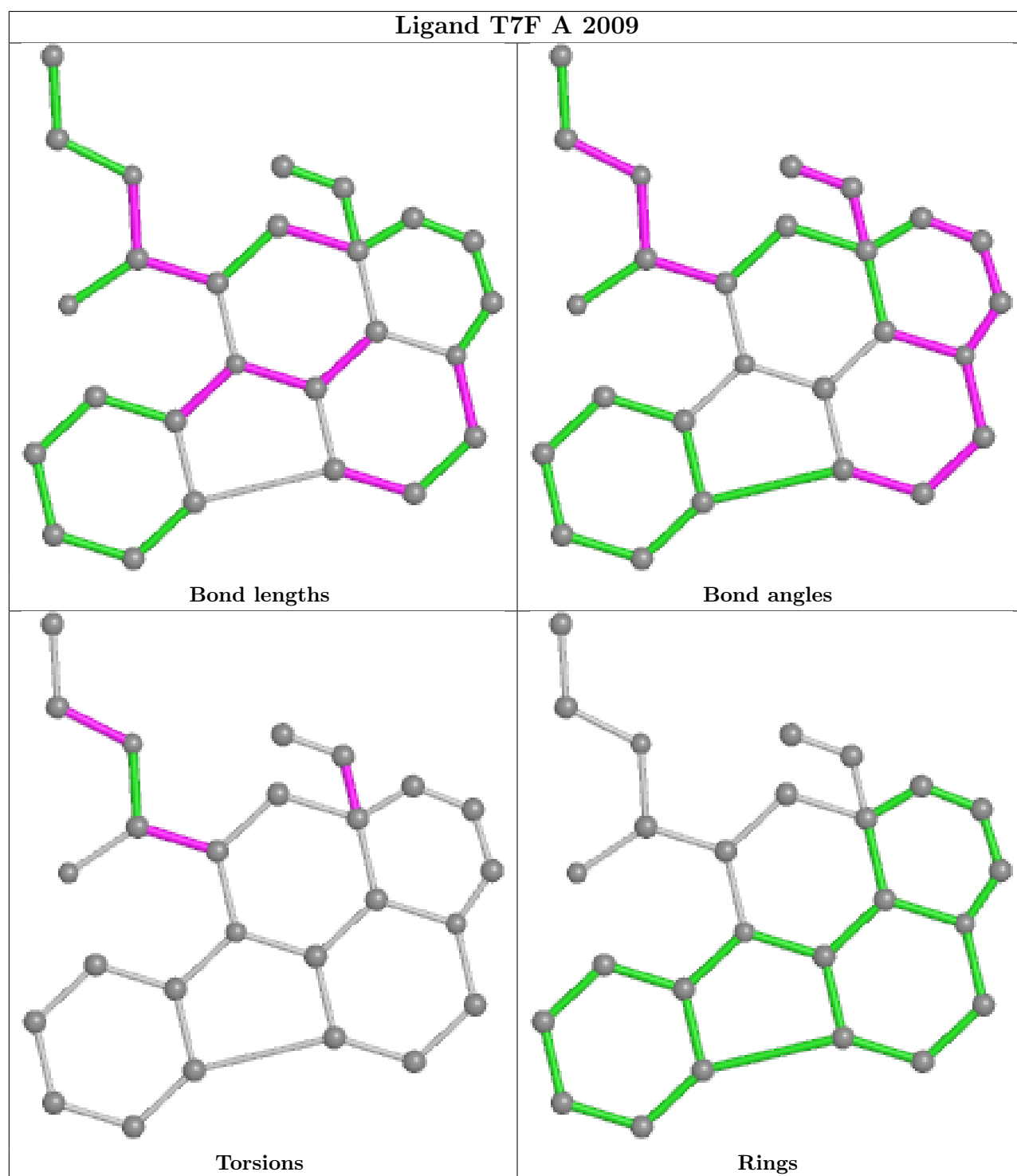


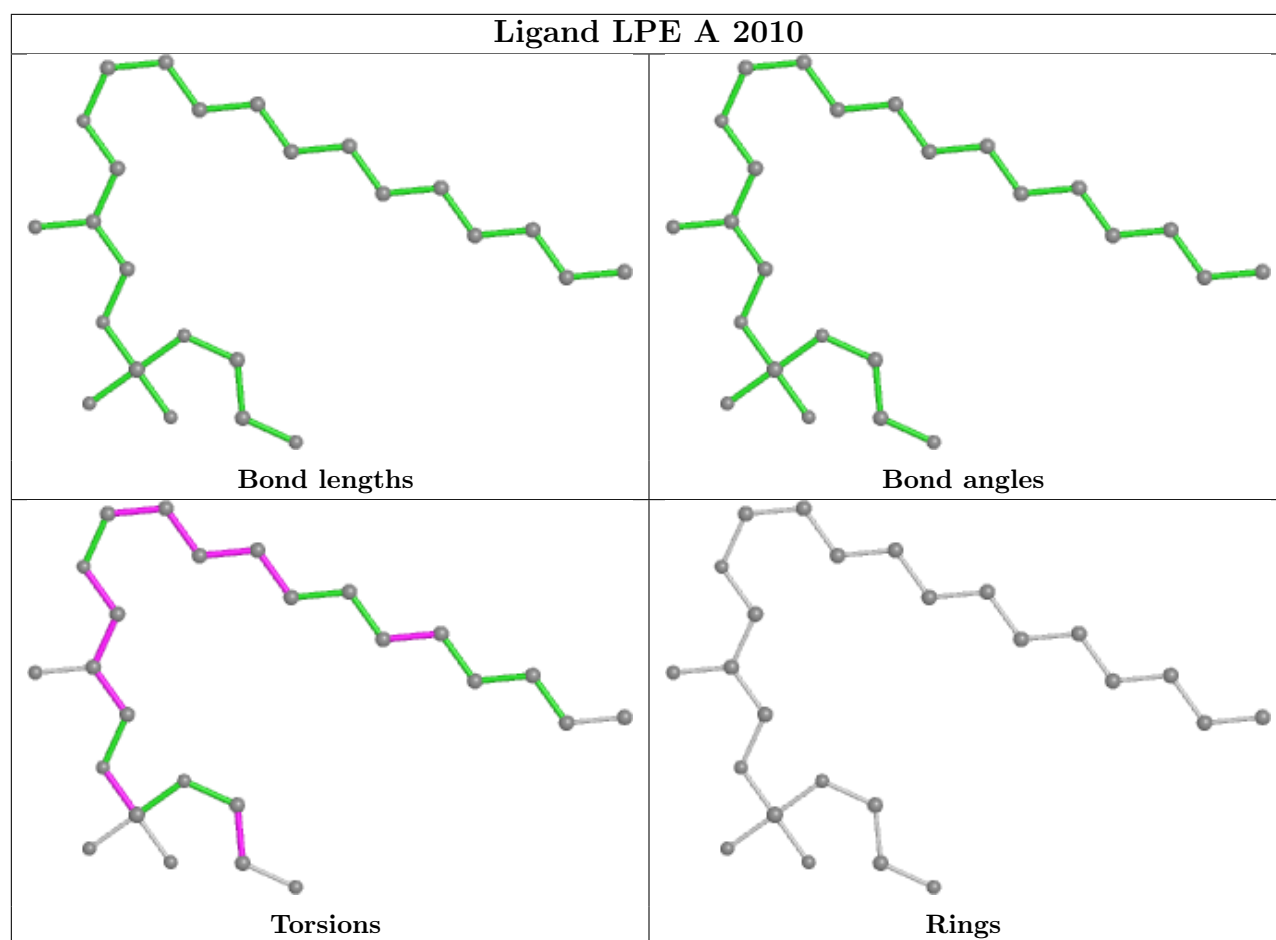


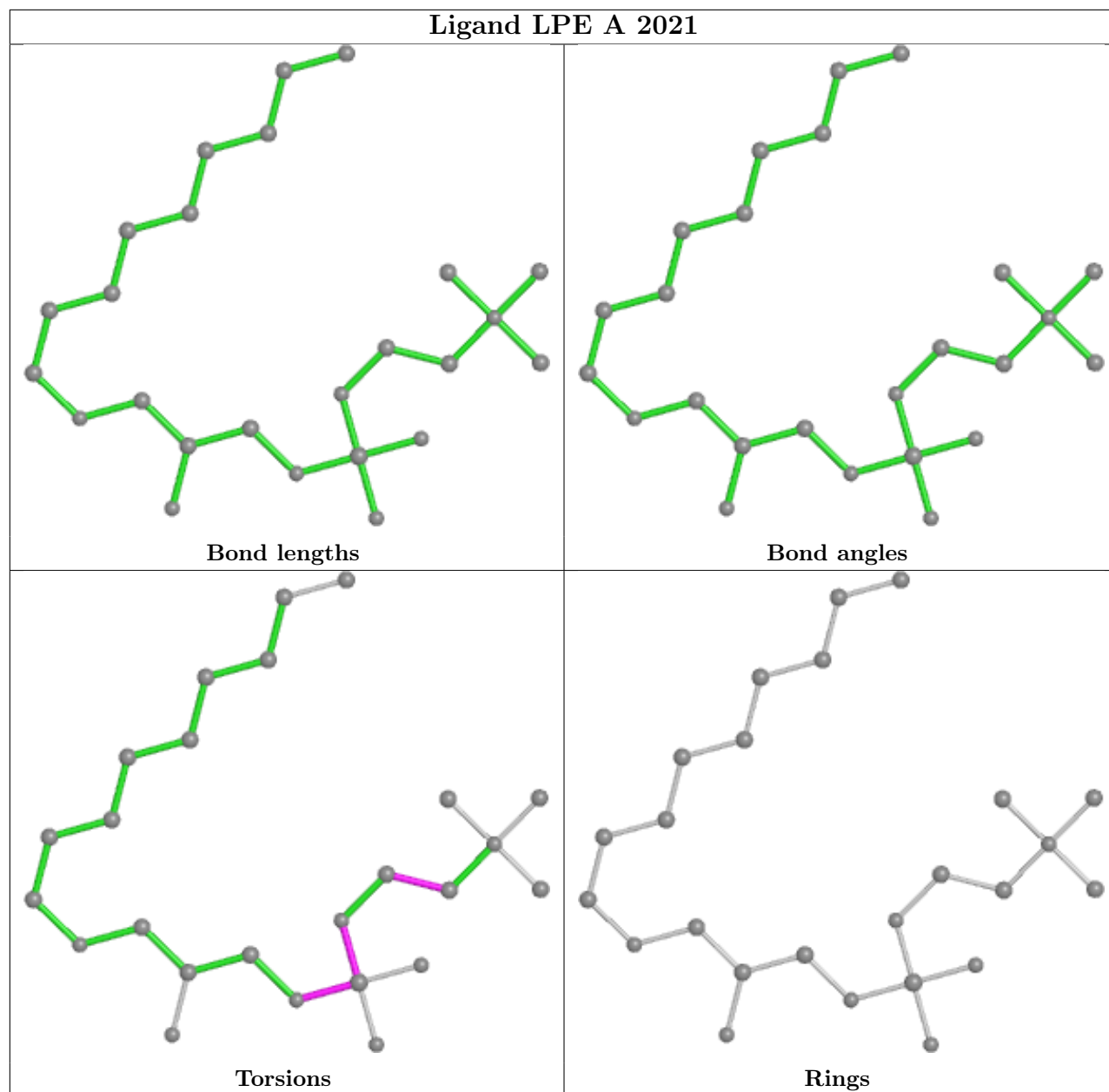


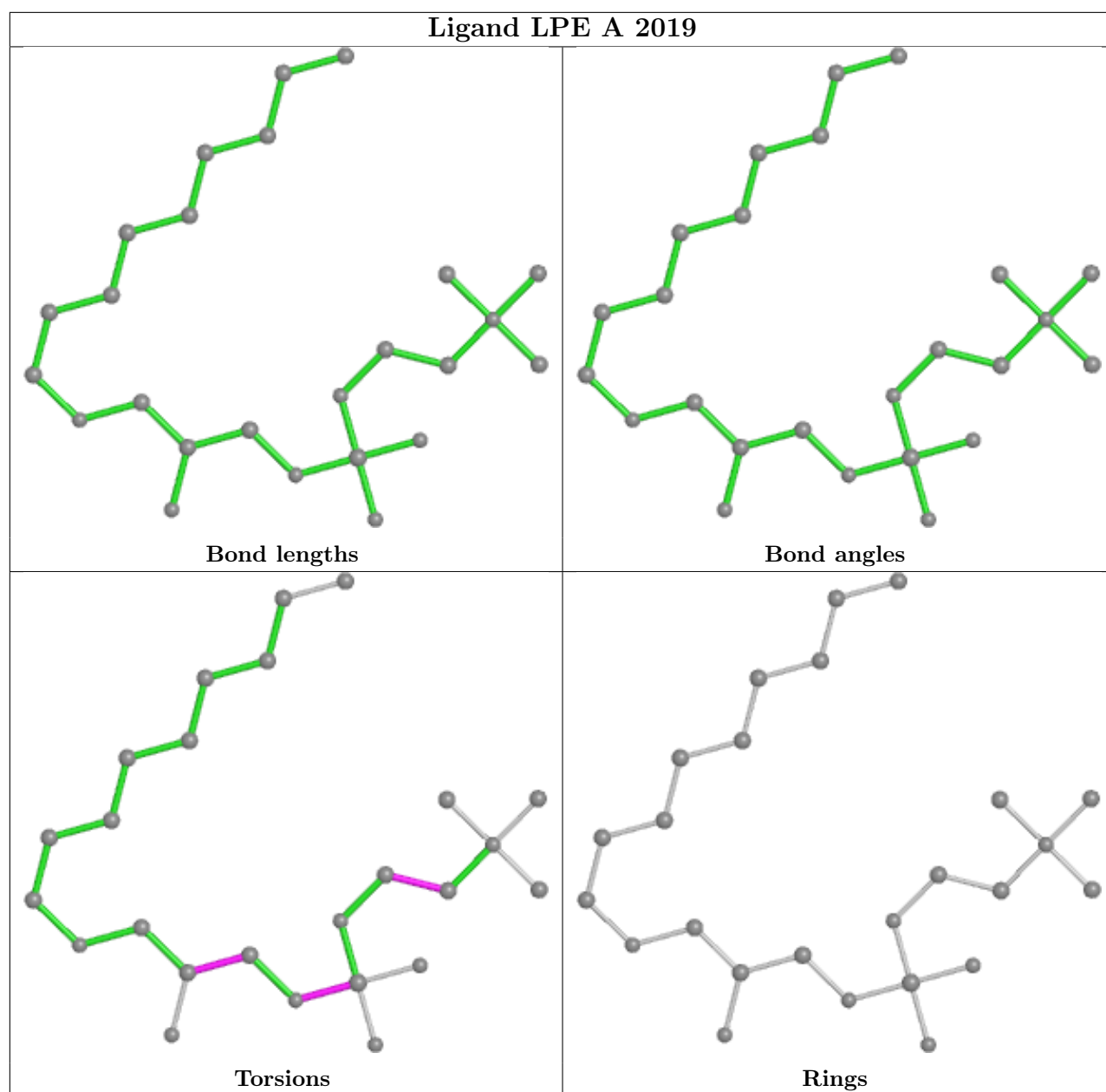


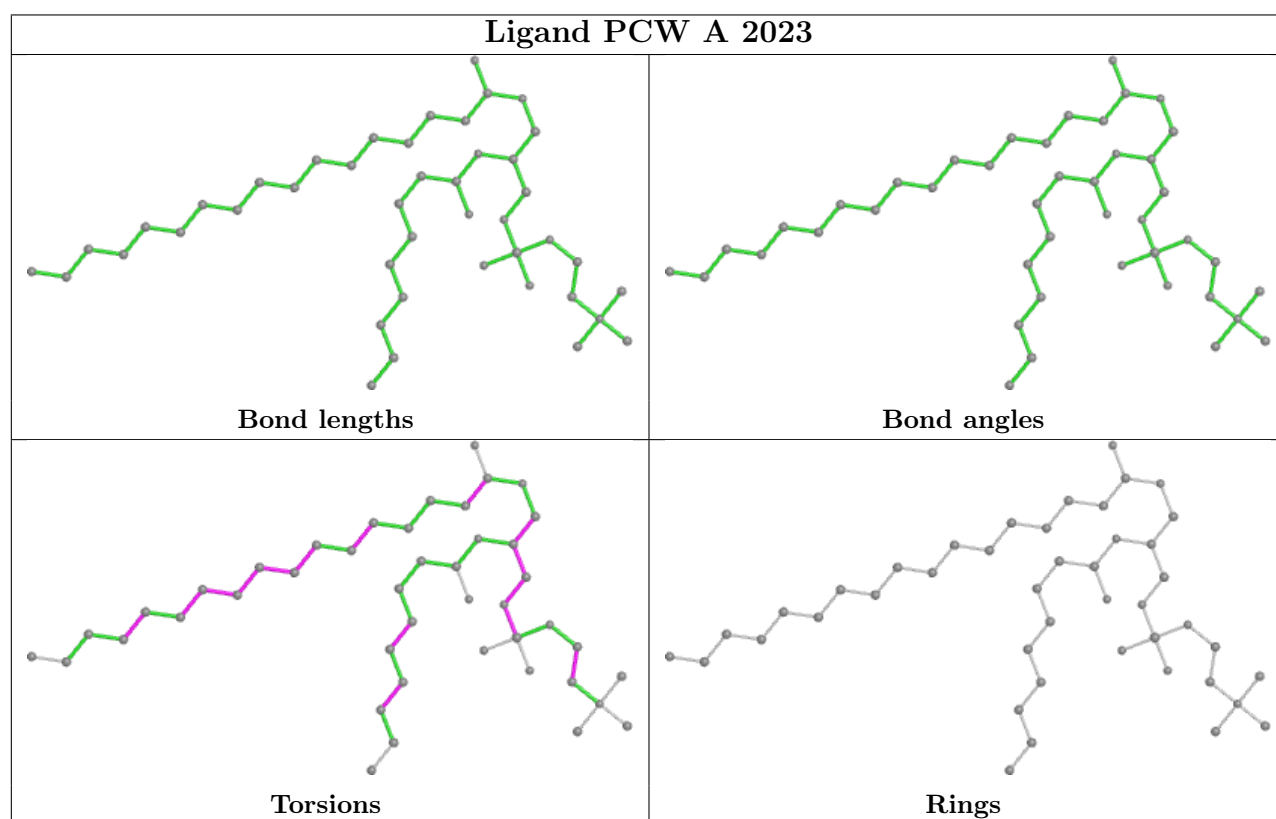
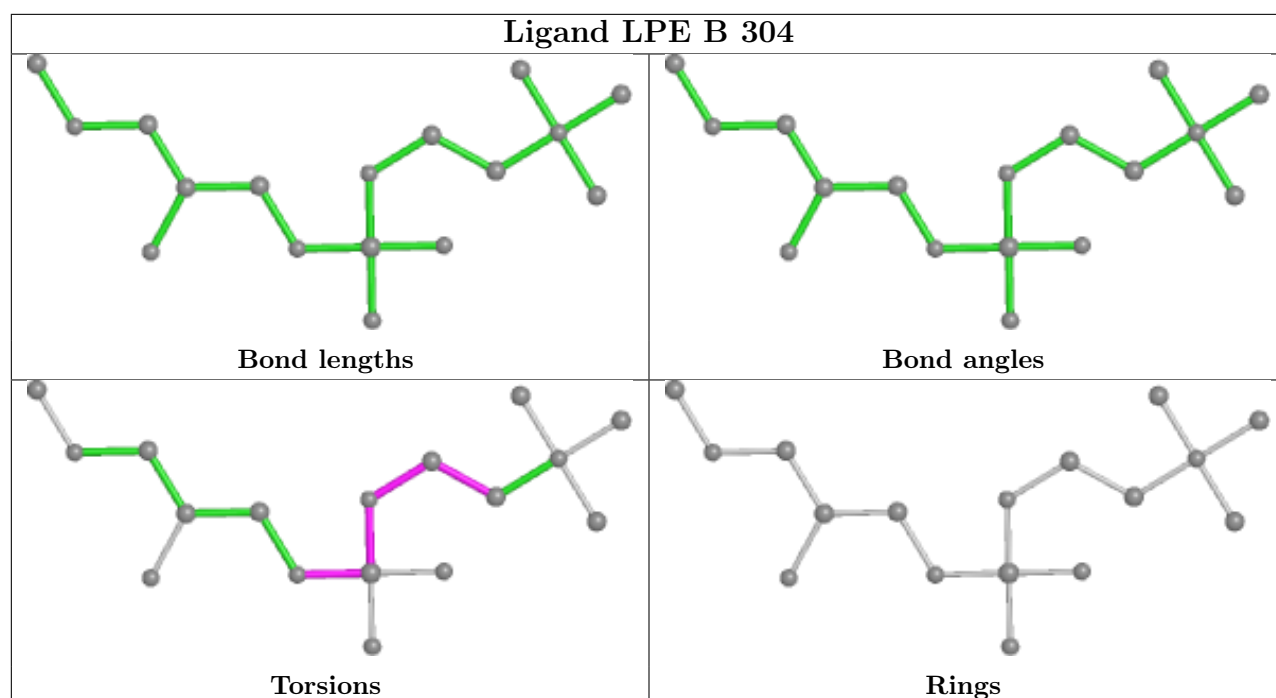


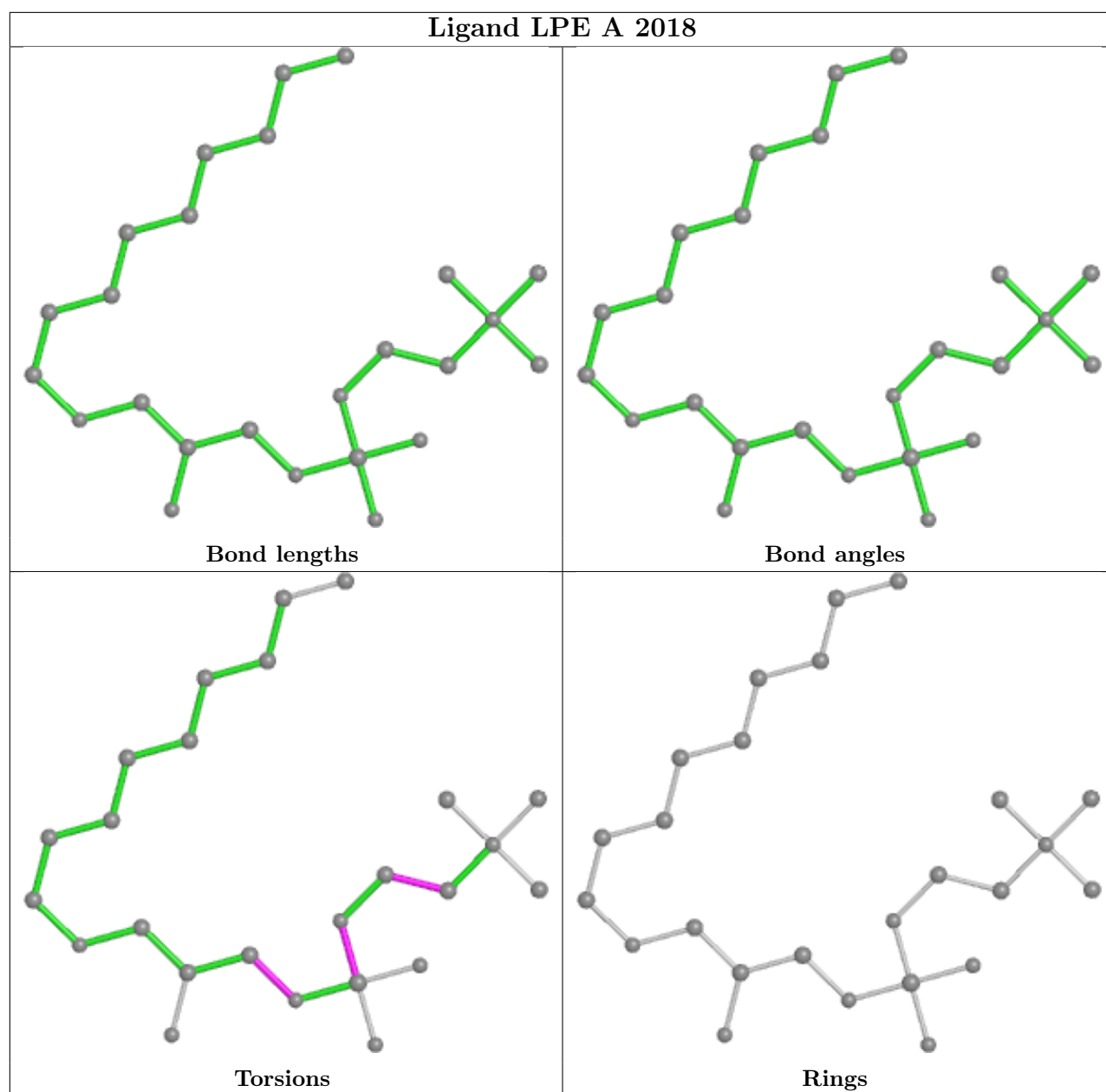




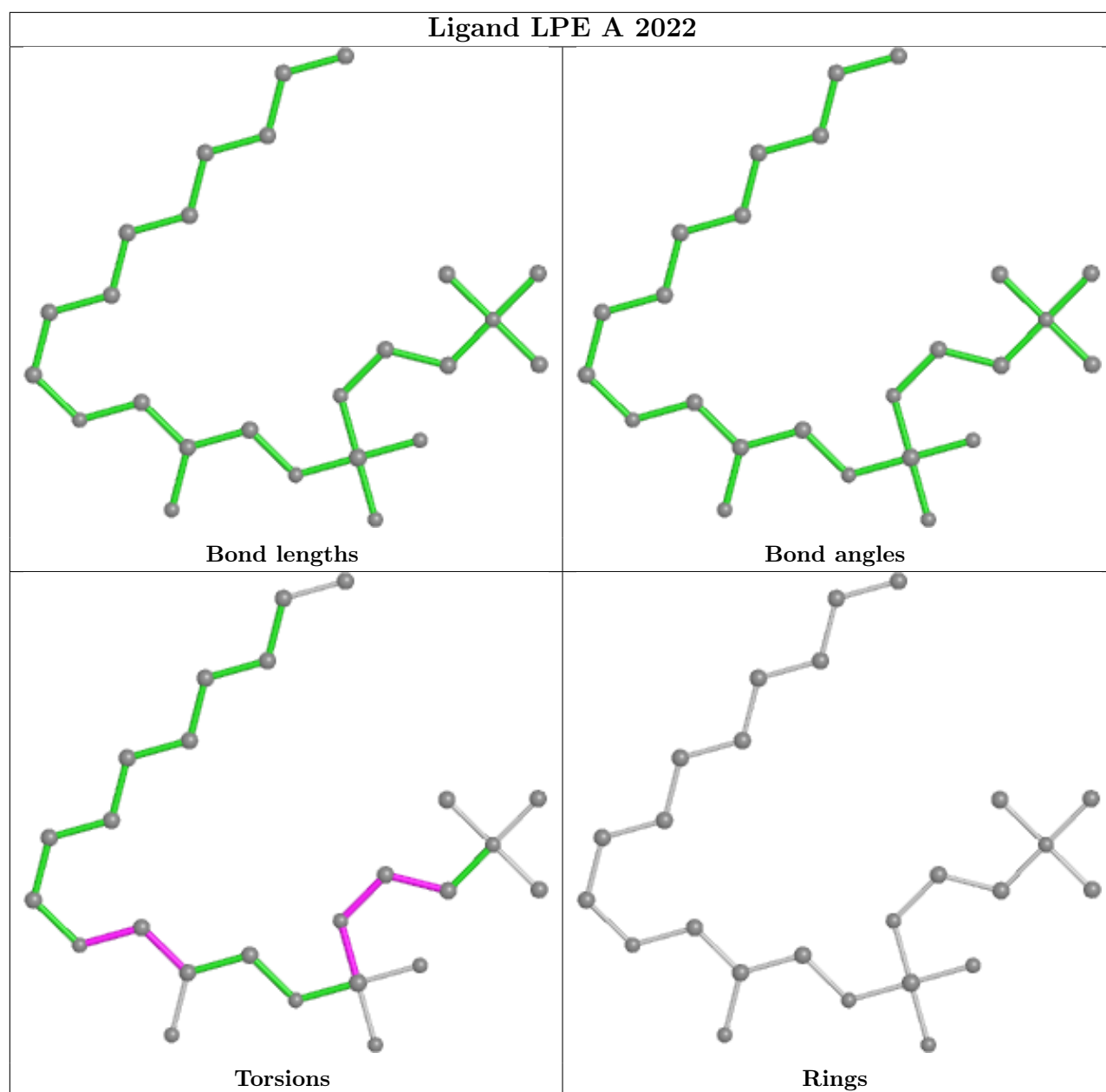


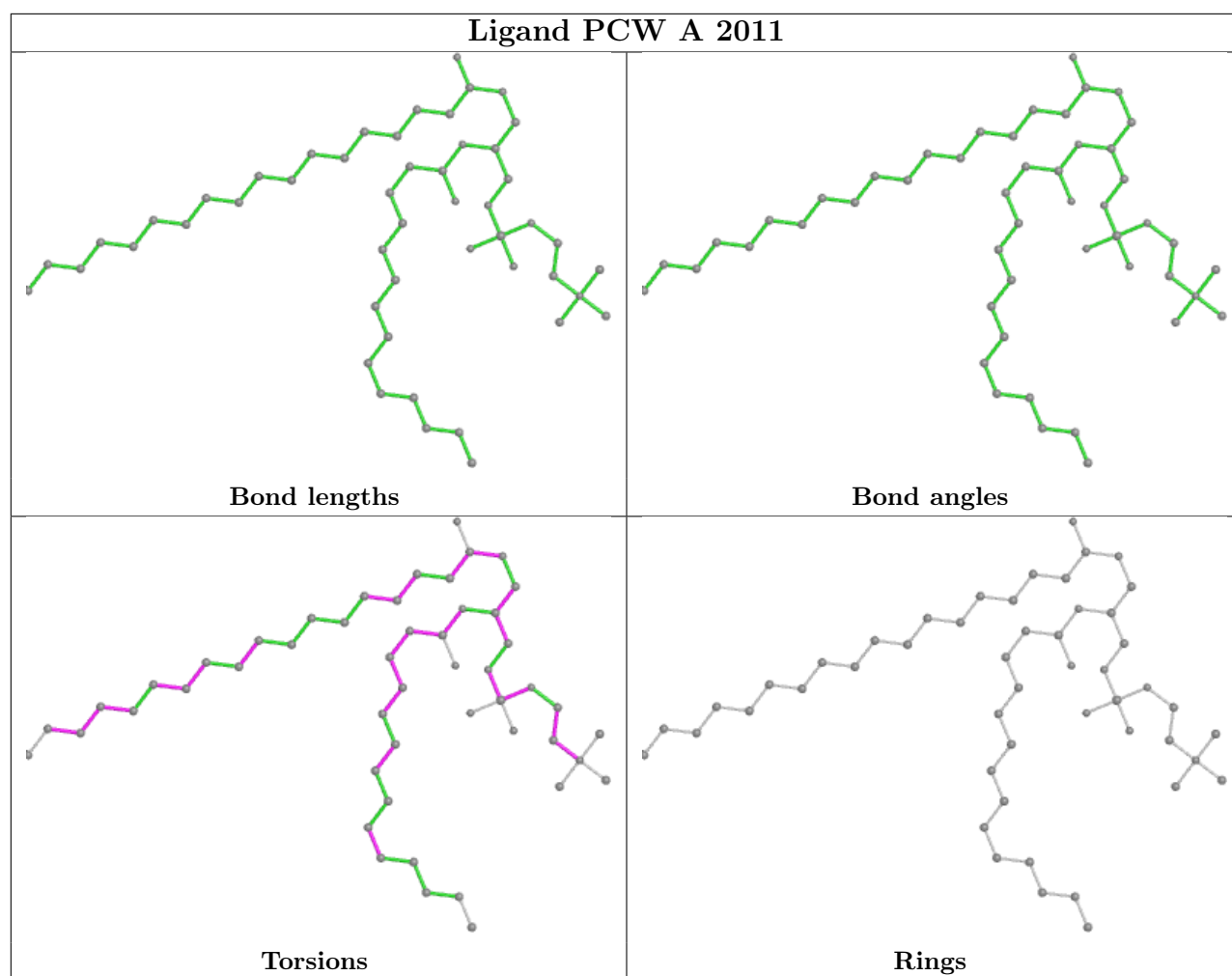


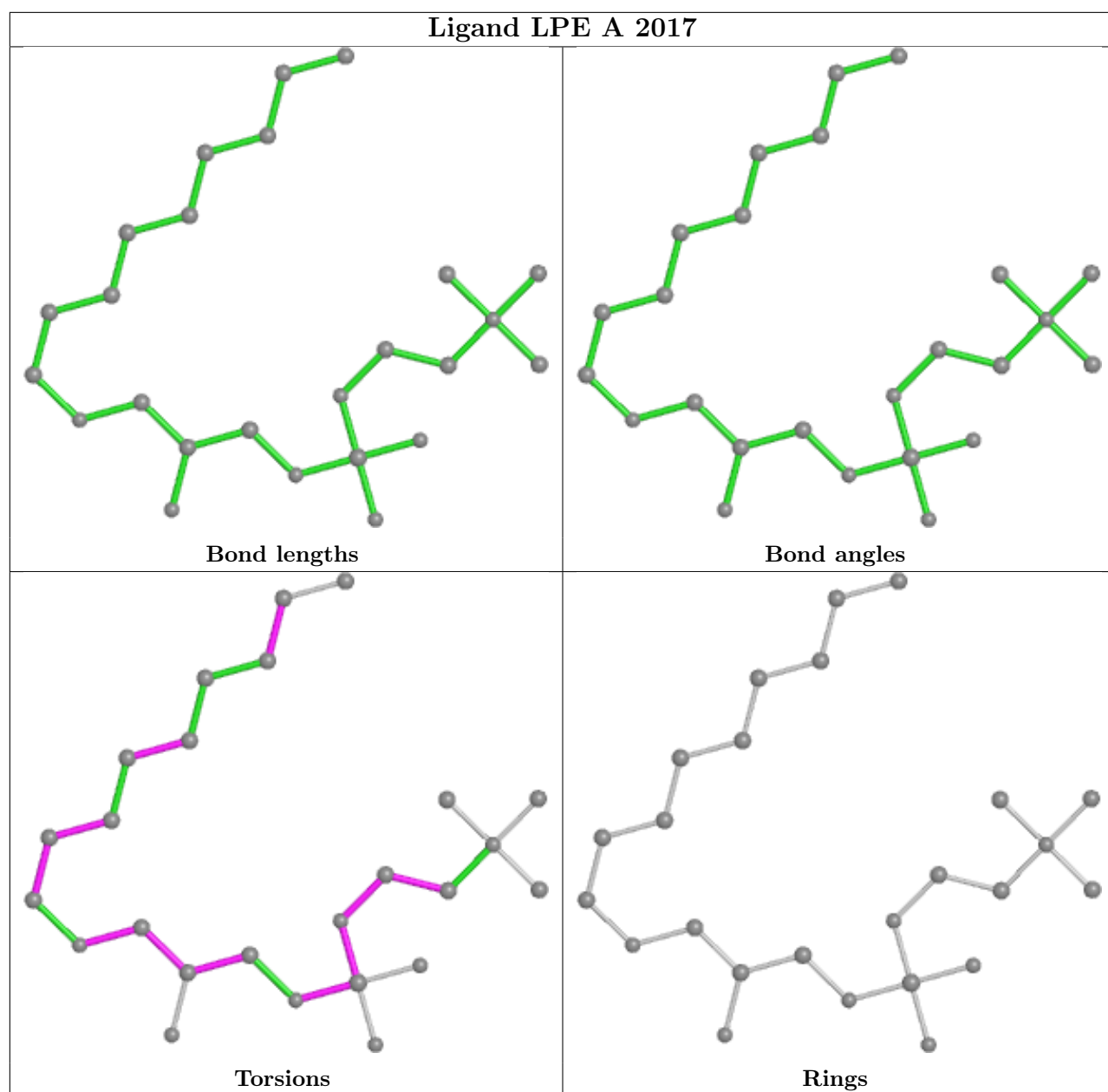


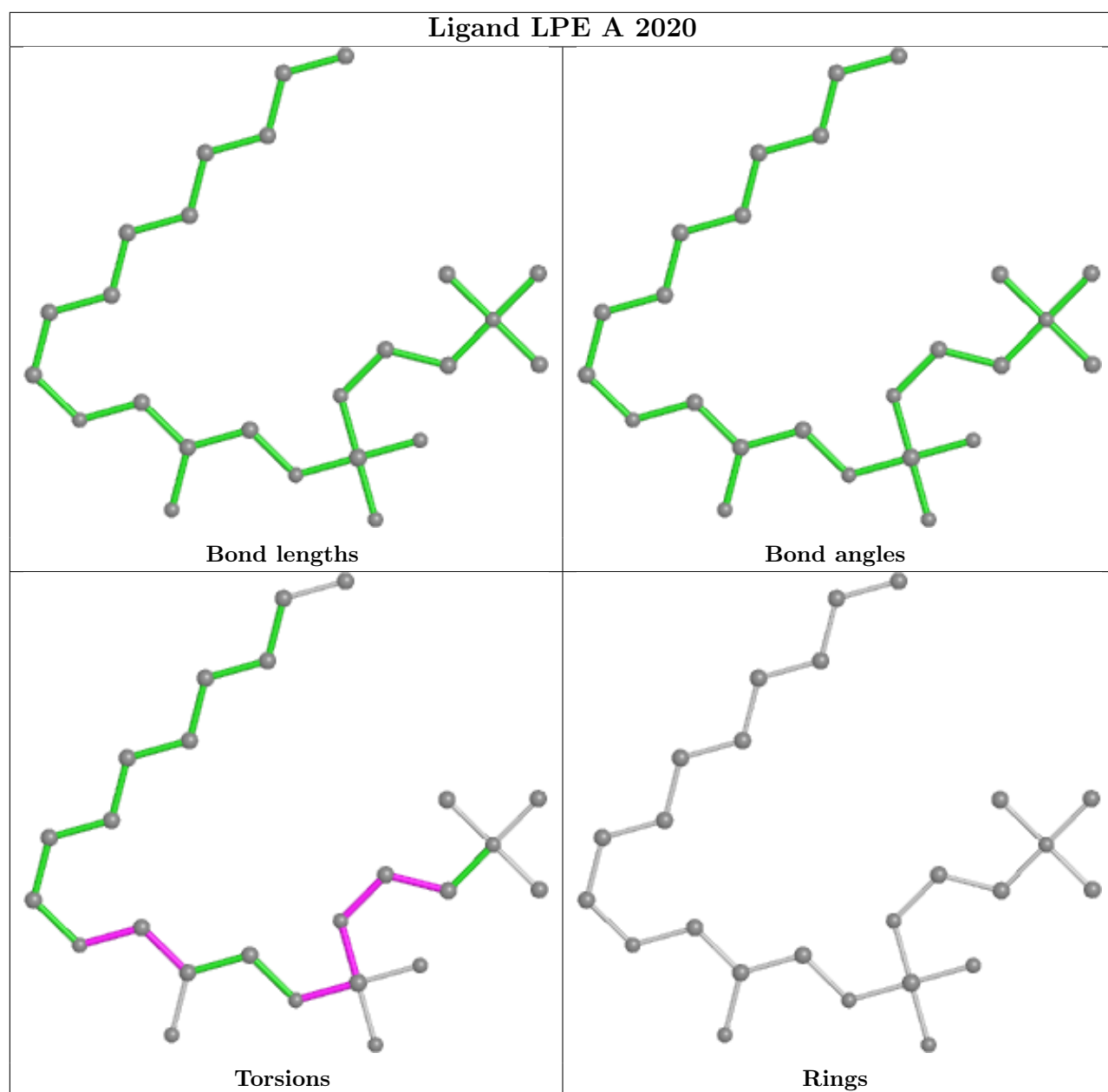


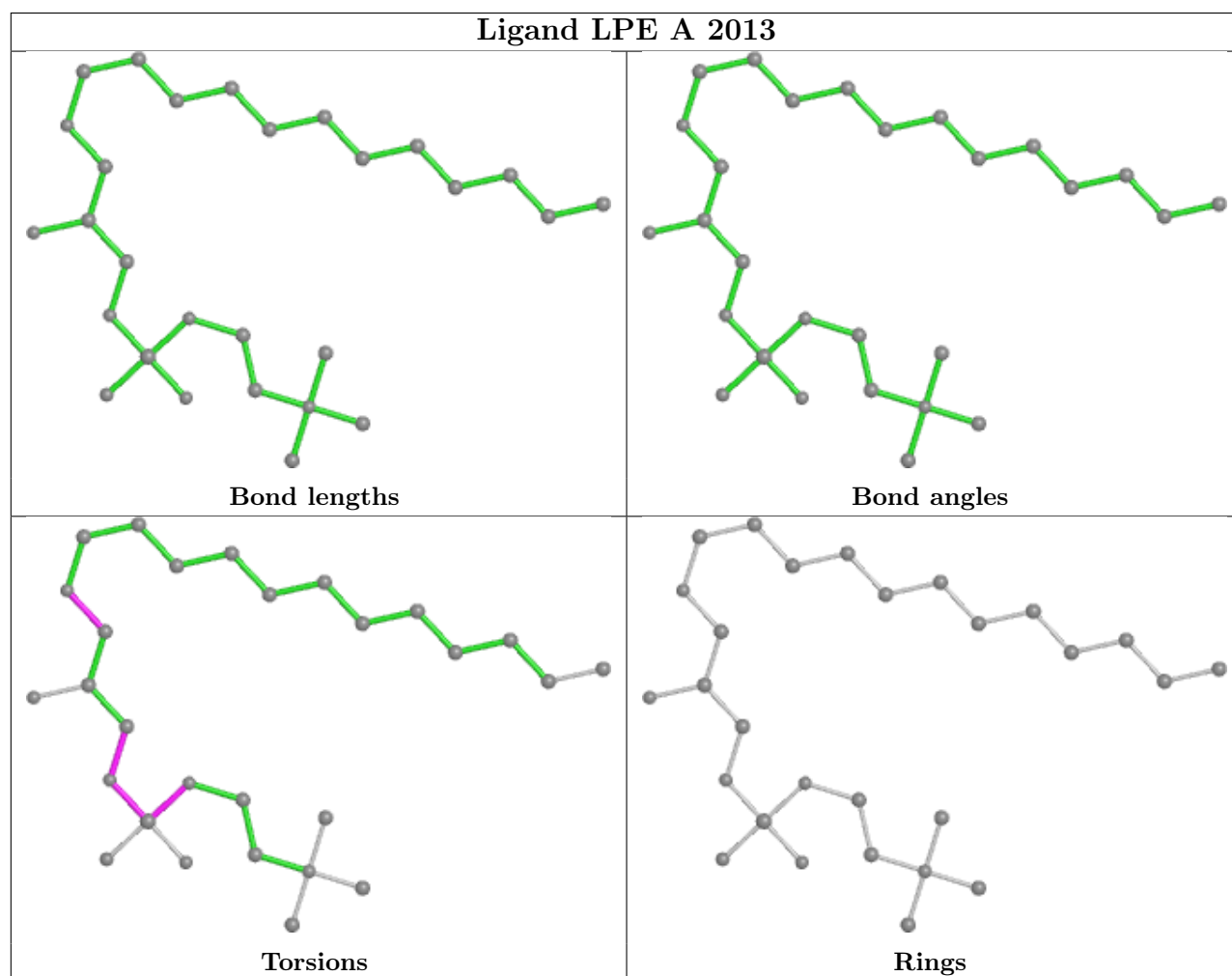
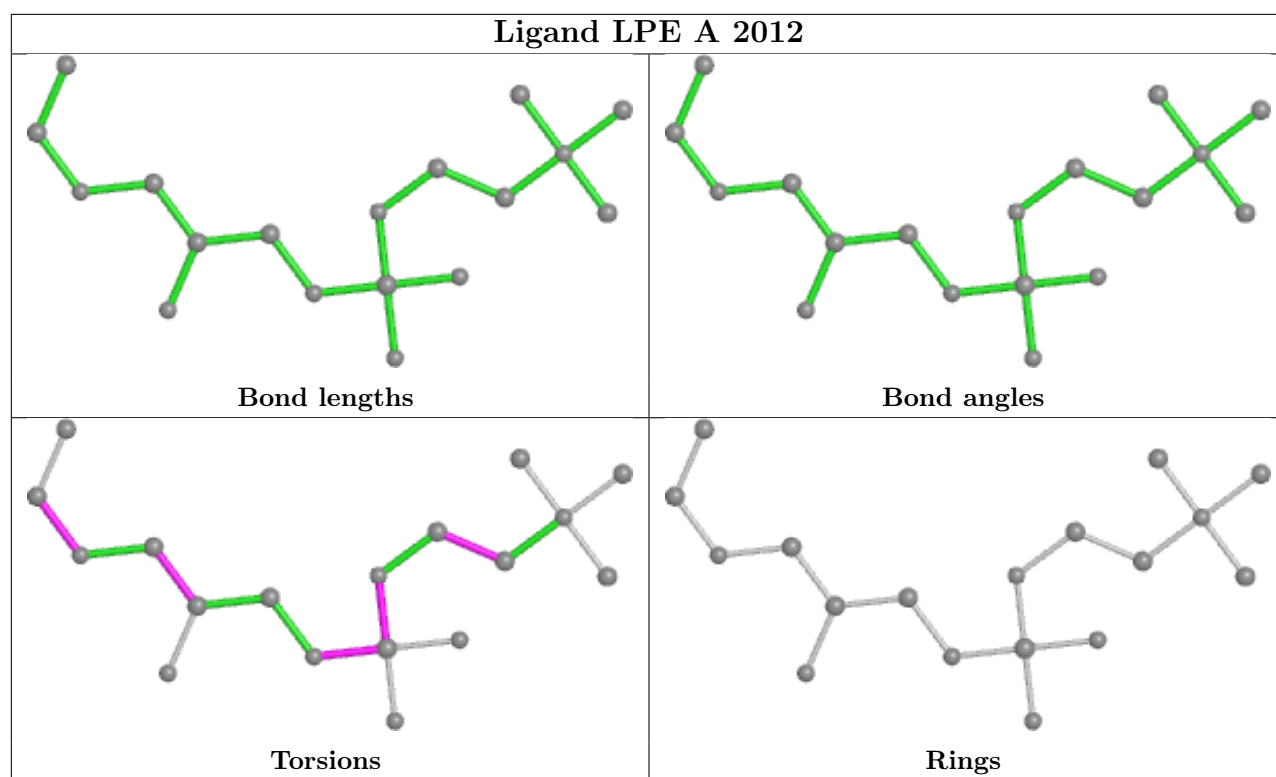


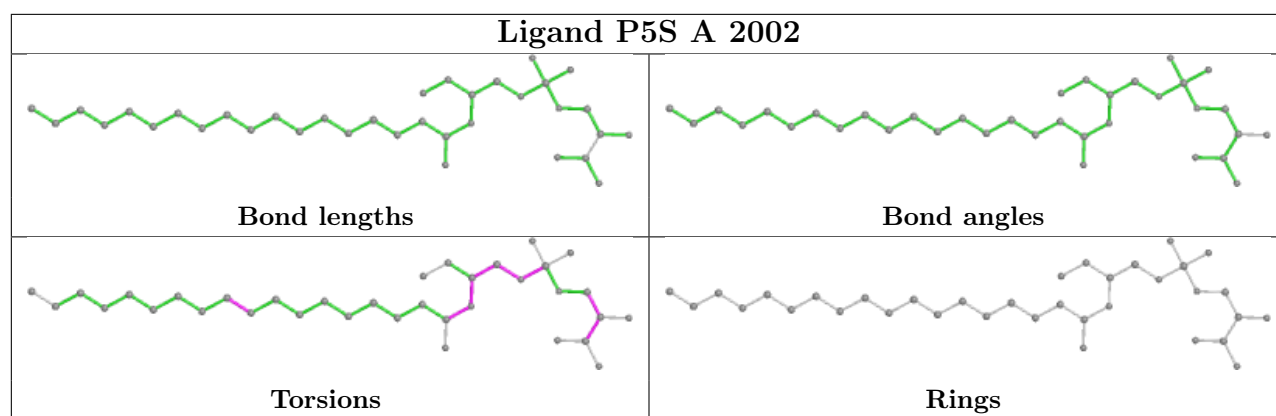












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

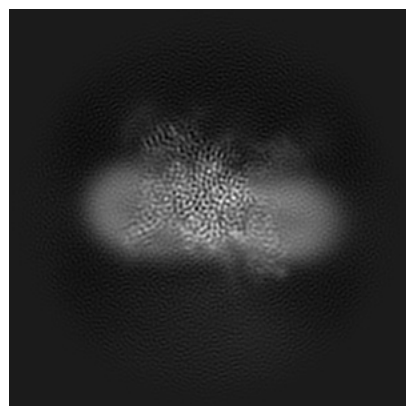
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35197. These allow visual inspection of the internal detail of the map and identification of artifacts.

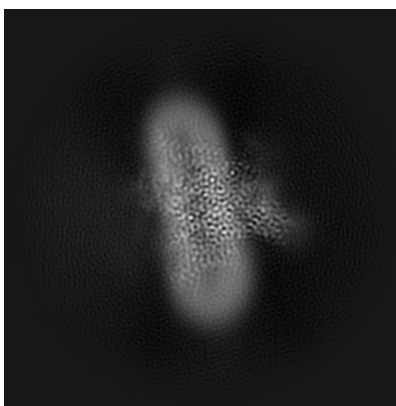
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

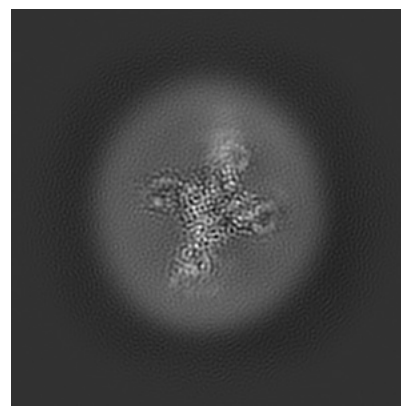
#### 6.1.1 Primary map



X

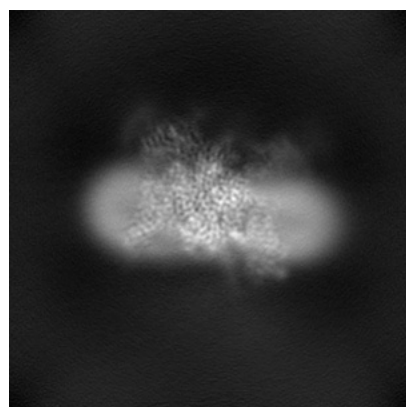


Y

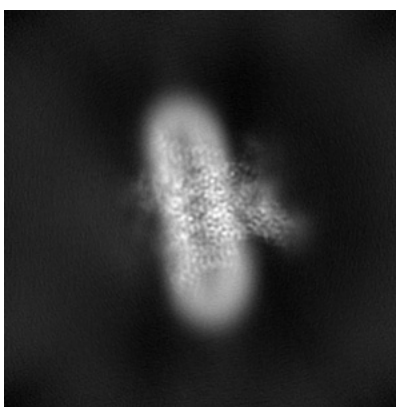


Z

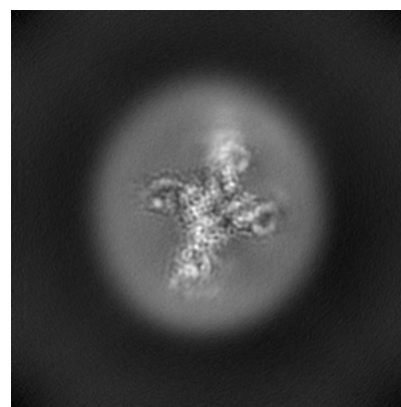
#### 6.1.2 Raw map



X



Y

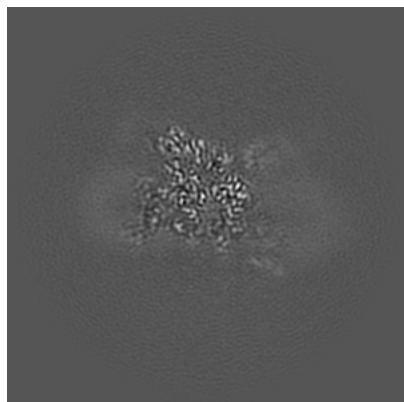


Z

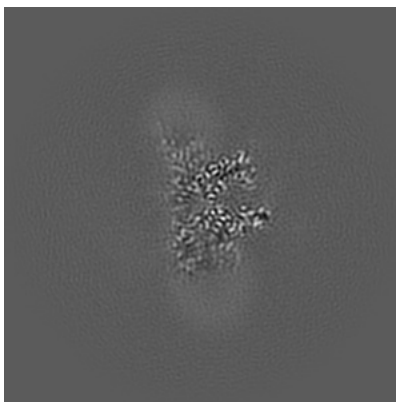
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

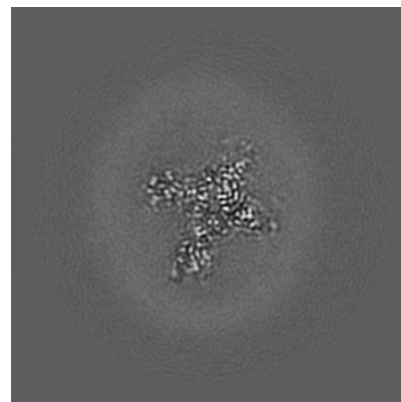
### 6.2.1 Primary map



X Index: 128

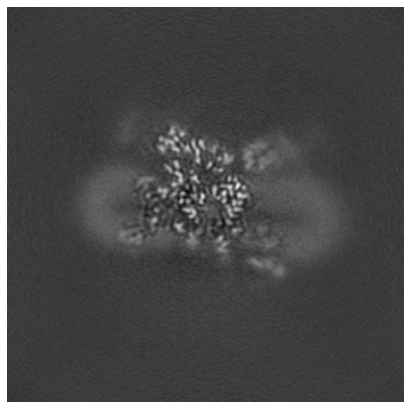


Y Index: 128

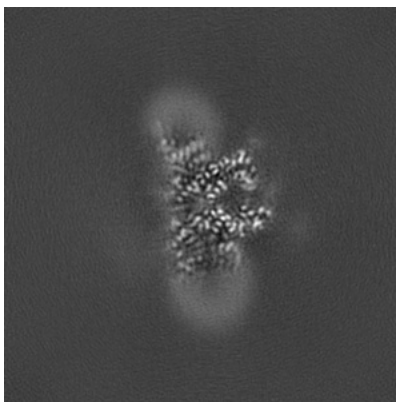


Z Index: 128

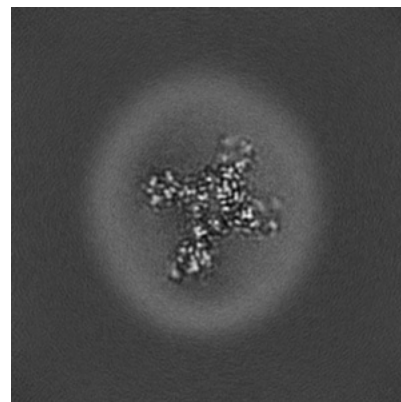
### 6.2.2 Raw map



X Index: 128



Y Index: 128



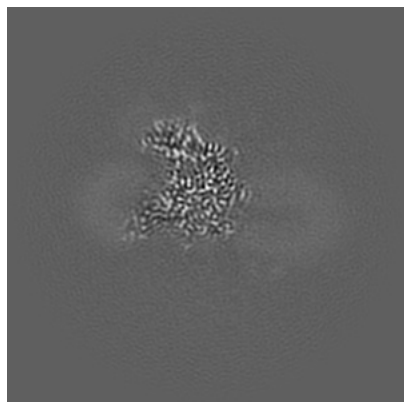
Z Index: 128

The images above show central slices of the map in three orthogonal directions.

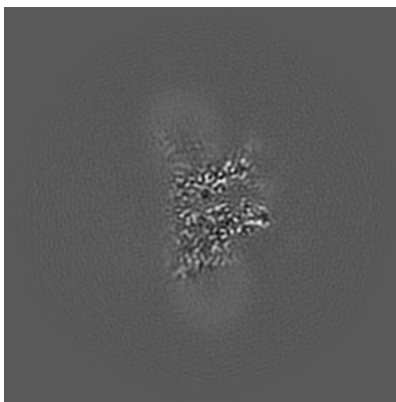


## 6.3 Largest variance slices [i](#)

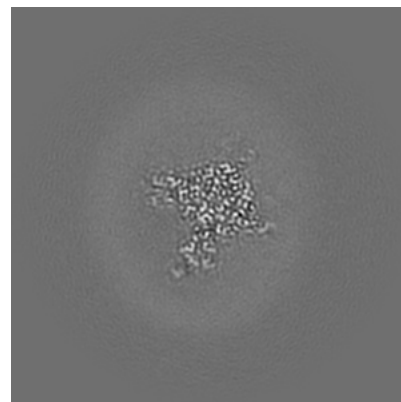
### 6.3.1 Primary map



X Index: 120

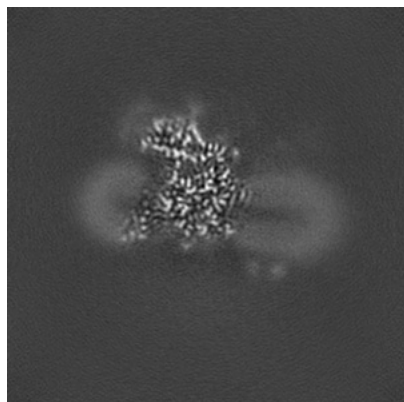


Y Index: 132

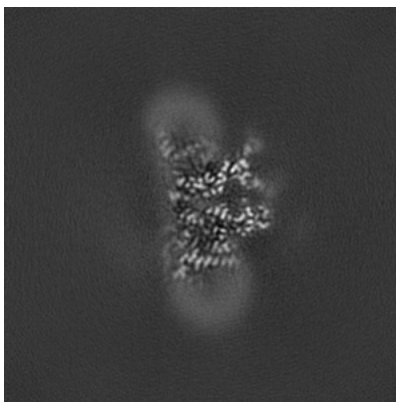


Z Index: 134

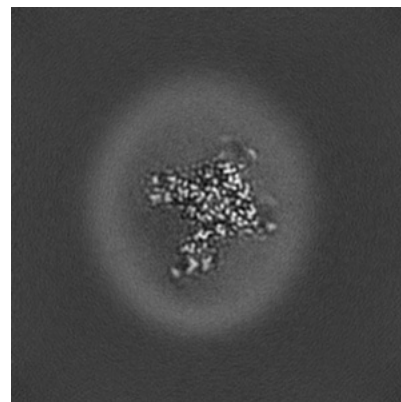
### 6.3.2 Raw map



X Index: 120



Y Index: 131

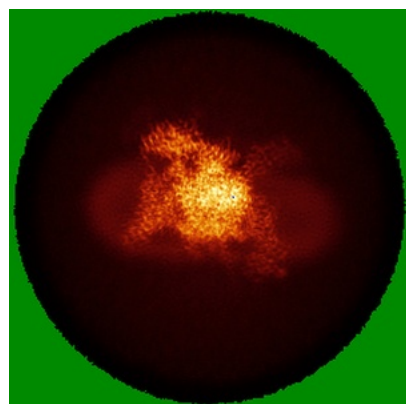


Z Index: 133

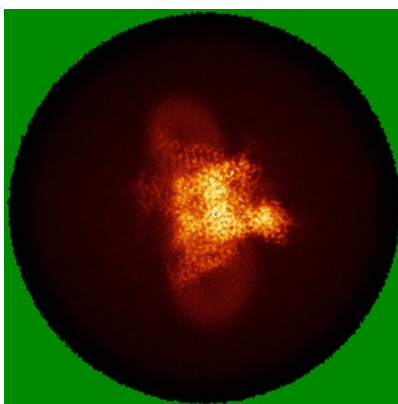
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

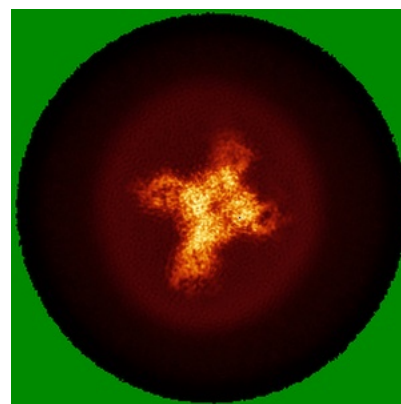
### 6.4.1 Primary map



X

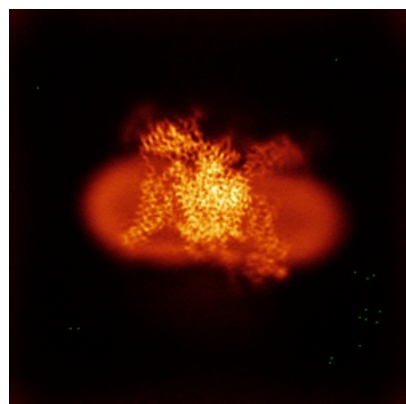


Y

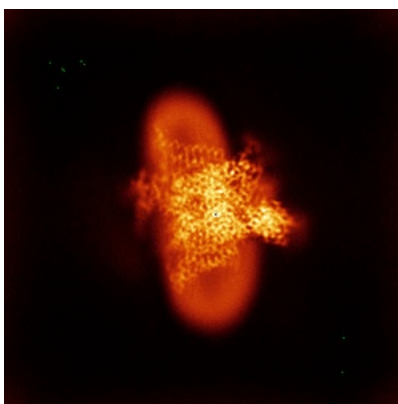


Z

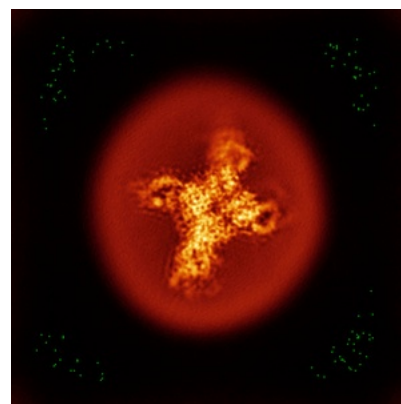
### 6.4.2 Raw map



X



Y

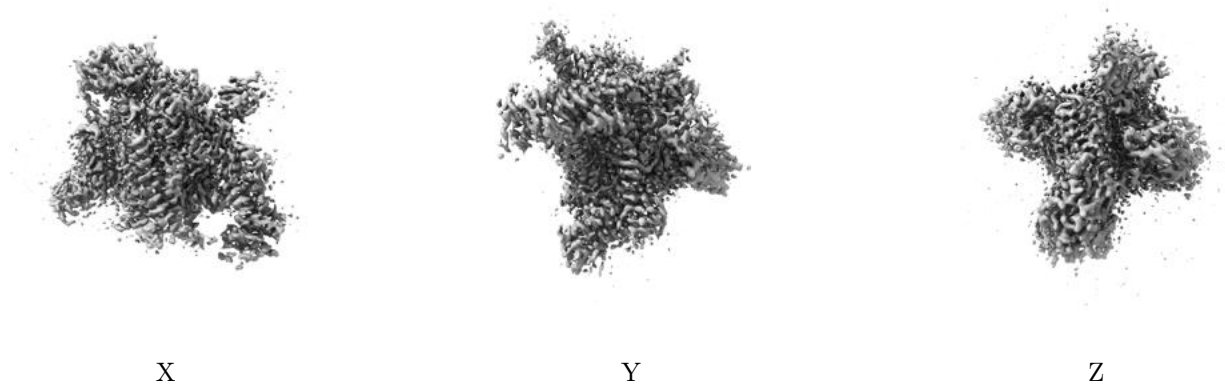


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

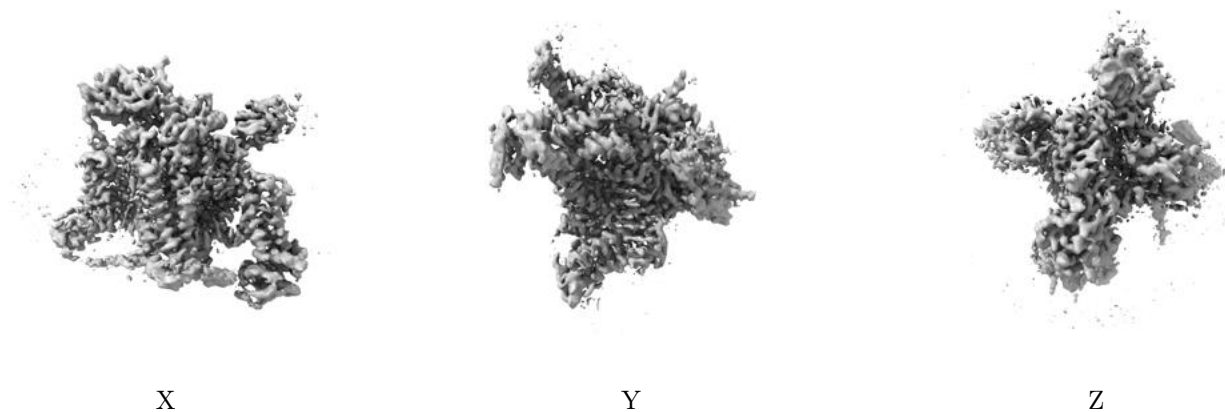
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.35. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

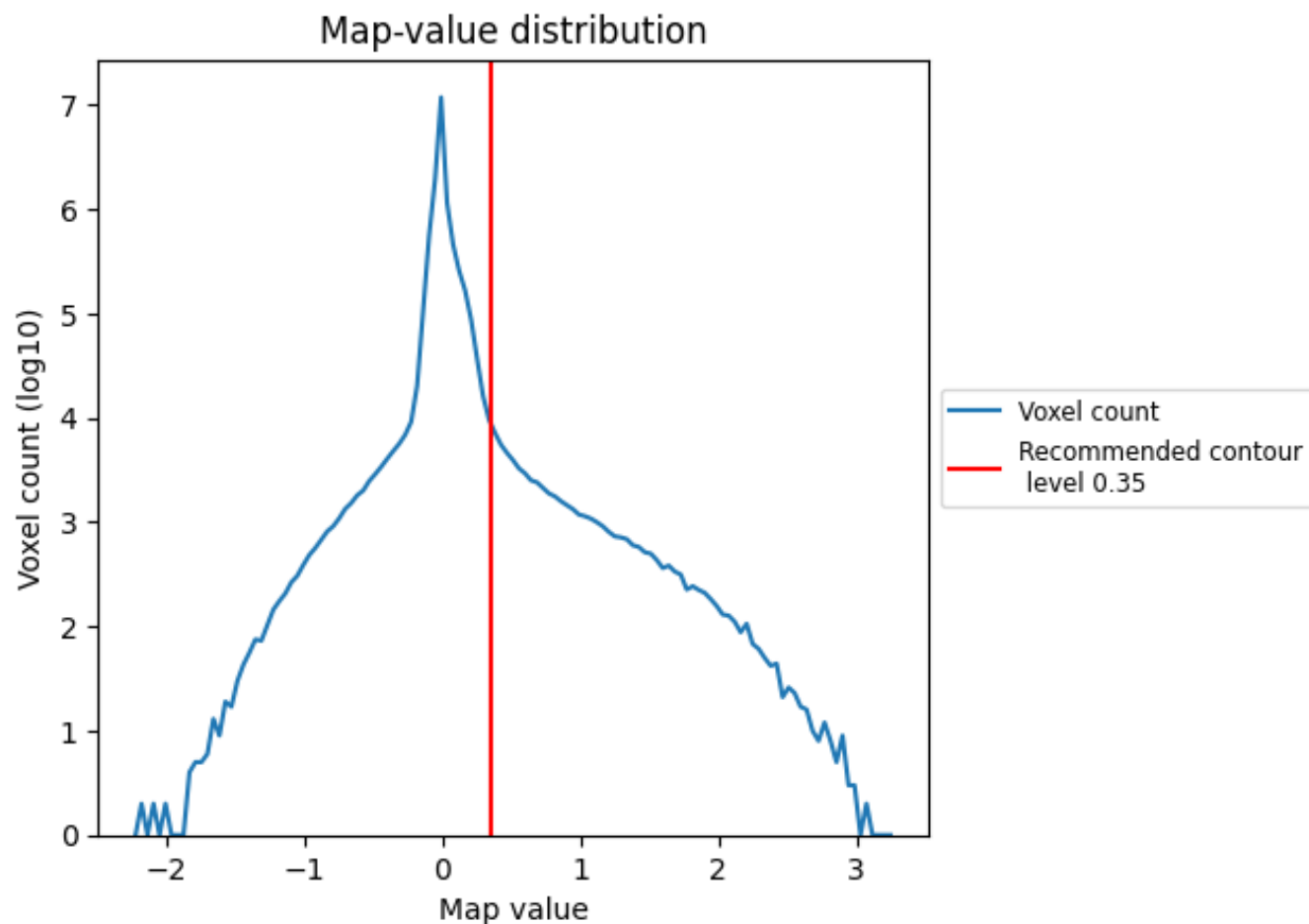
## 6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis [i](#)

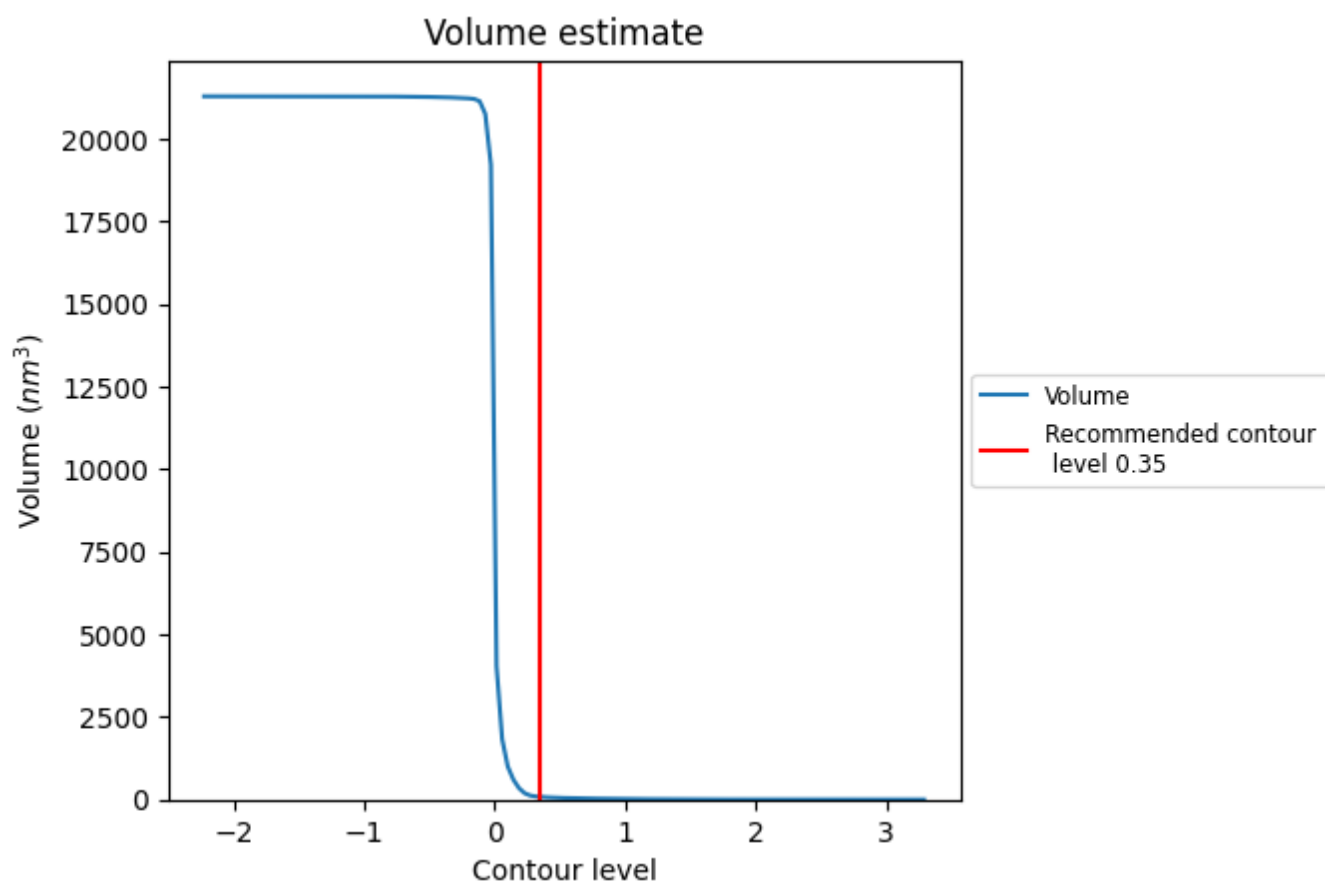
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

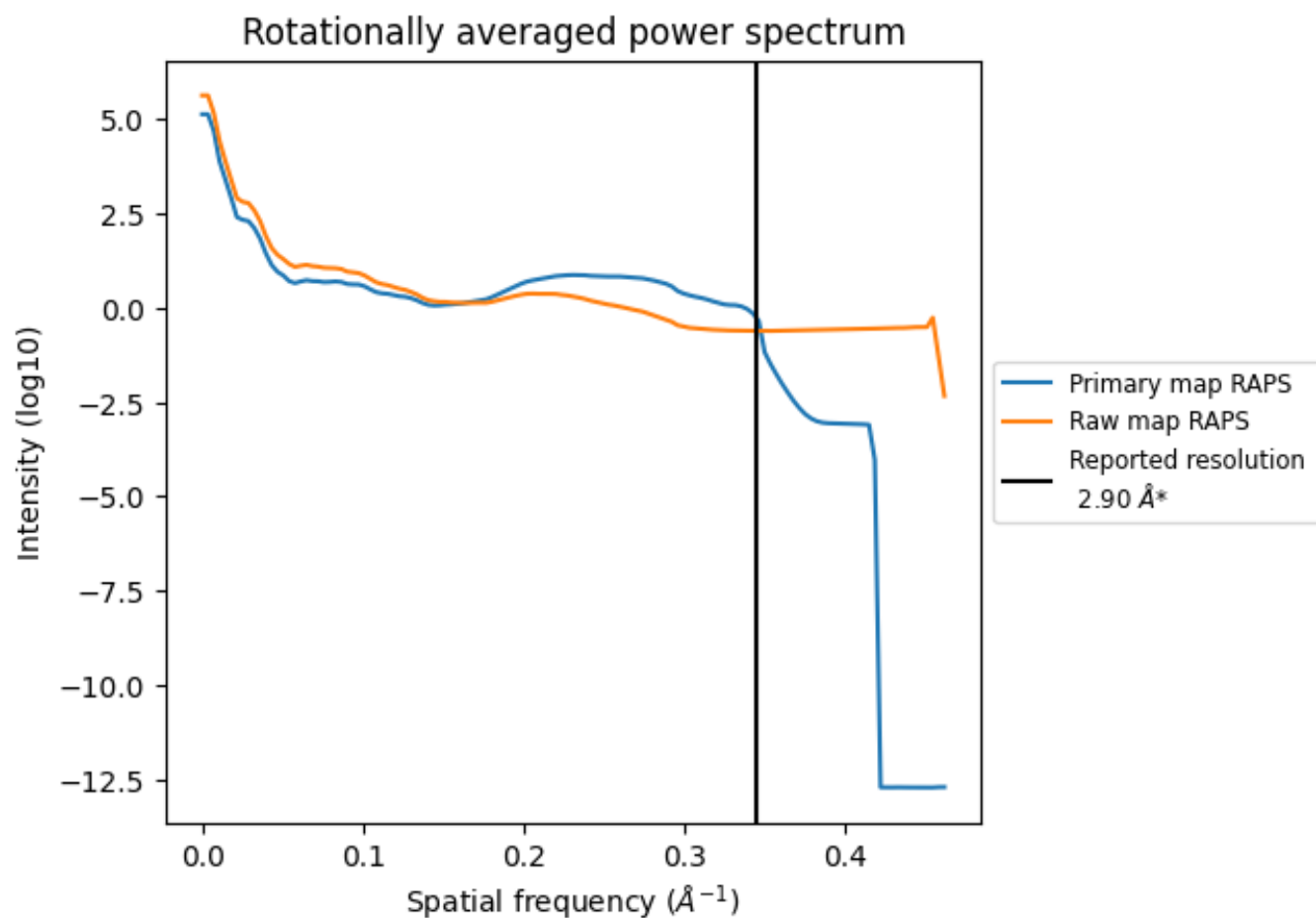
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 81 nm<sup>3</sup>; this corresponds to an approximate mass of 73 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ

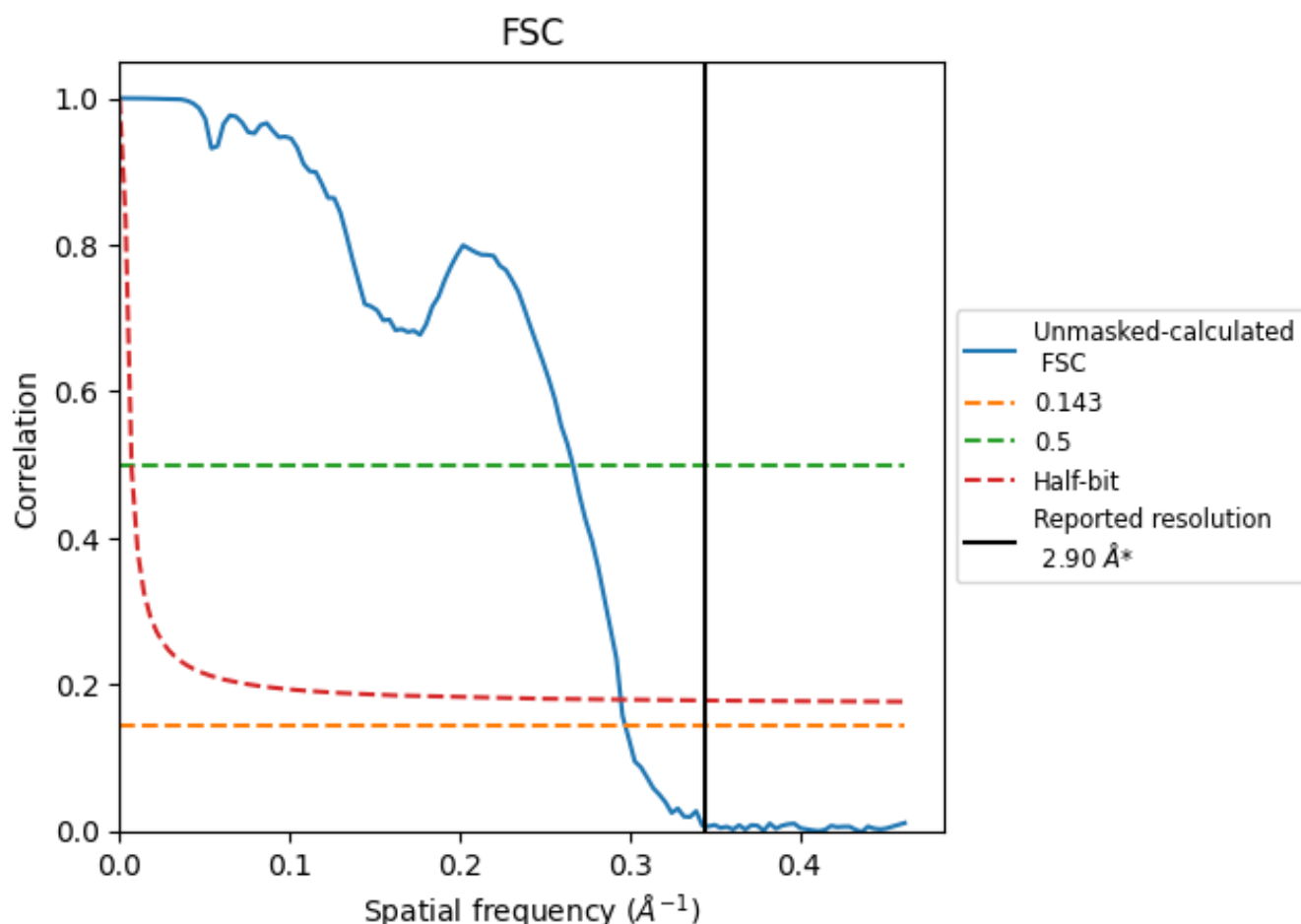


\*Reported resolution corresponds to spatial frequency of 0.345 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.345 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.36	3.75	3.39

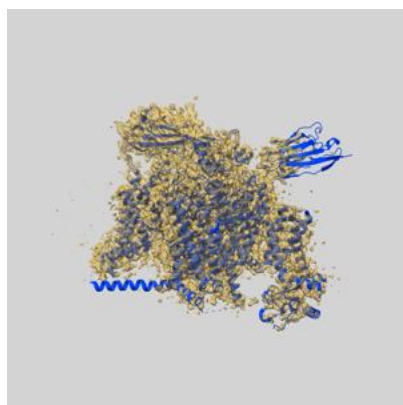
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.36 differs from the reported value 2.9 by more than 10 %



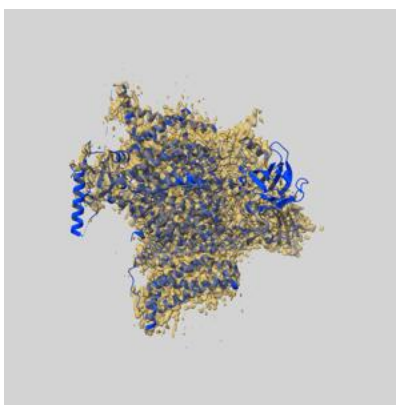
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-35197 and PDB model 8I5X. Per-residue inclusion information can be found in section 3 on page 11.

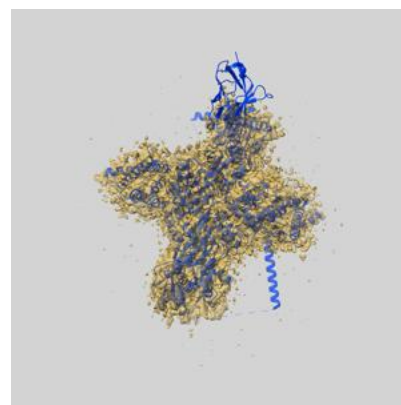
### 9.1 Map-model overlay [i](#)



X



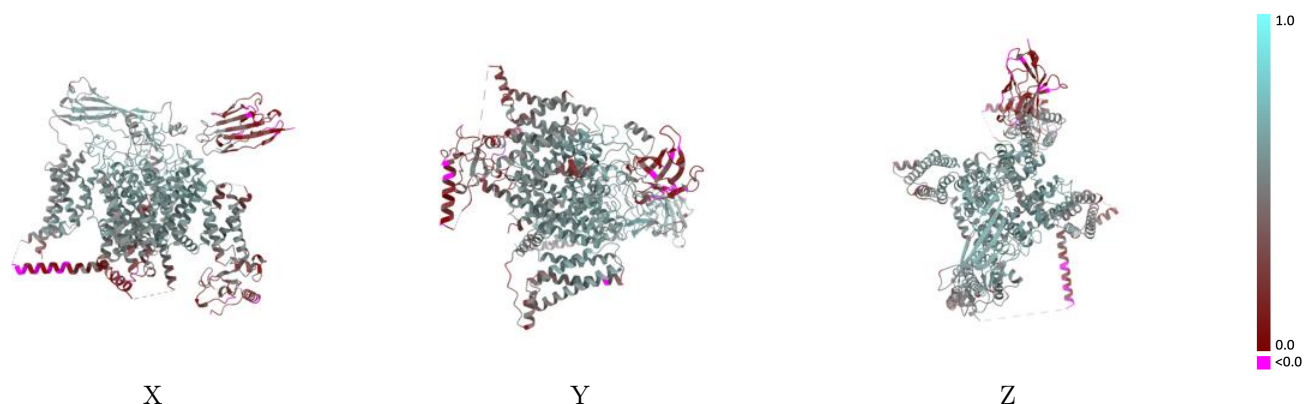
Y



Z

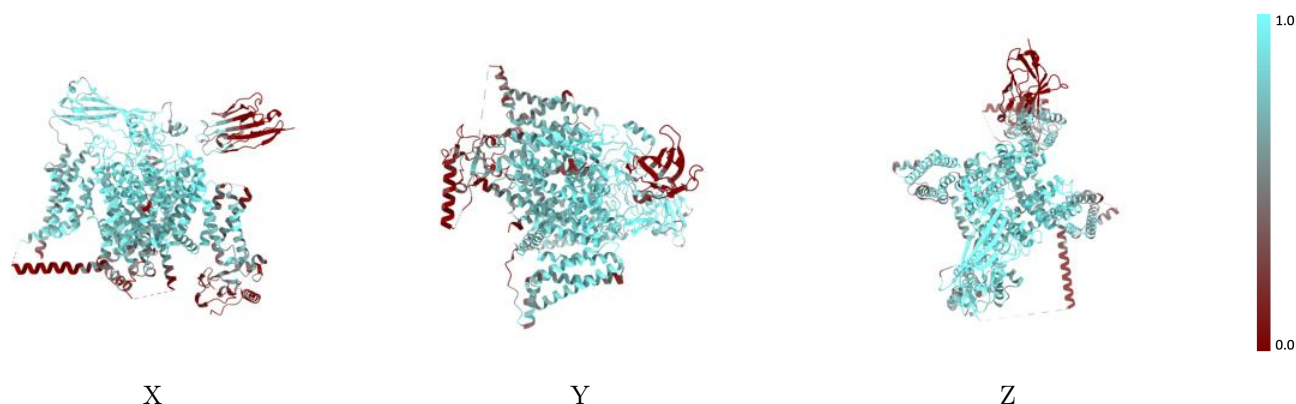
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [i](#)



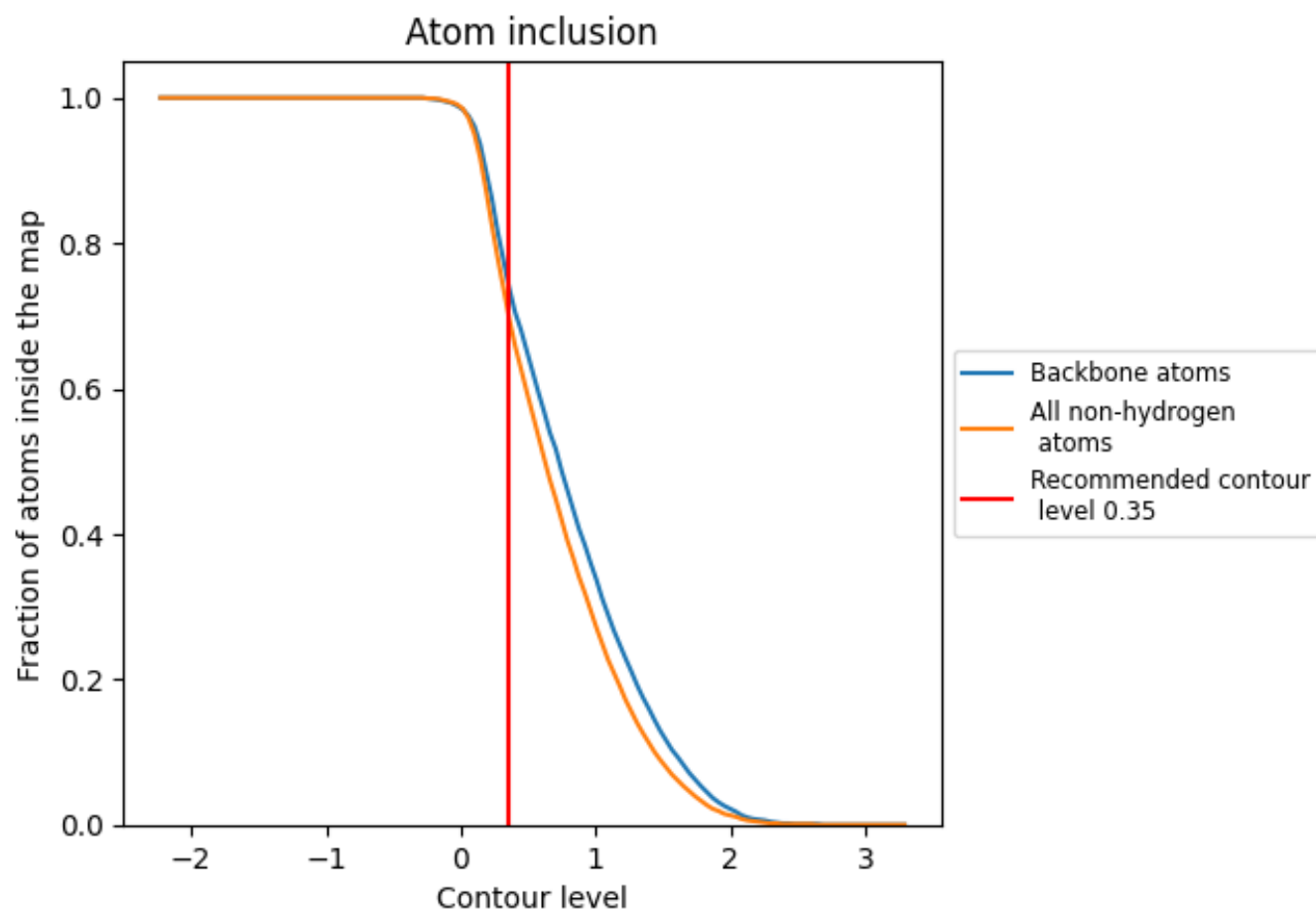
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.35).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 70% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.7040</div>	<div><div></div>0.4770</div>
A	<div><div></div>0.7340</div>	<div><div></div>0.4940</div>
B	<div><div></div>0.8130</div>	<div><div></div>0.5220</div>
C	<div><div></div>0.1960</div>	<div><div></div>0.2160</div>
D	<div><div></div>0.4640</div>	<div><div></div>0.3370</div>
E	<div><div></div>0.6070</div>	<div><div></div>0.4210</div>
F	<div><div></div>0.8930</div>	<div><div></div>0.5410</div>

1.0

0.0

<0.0