



Full wwPDB EM Validation Report ⓘ

Jun 29, 2023 – 06:19 PM EDT

PDB ID : 8G1A
EMDB ID : EMD-29665
Title : Cryo-EM structure of Nav1.7 with CBD
Authors : Fan, X.; Huang, J.; Yan, N.
Deposited on : 2023-02-01
Resolution : 2.80 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

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.dev50
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.33

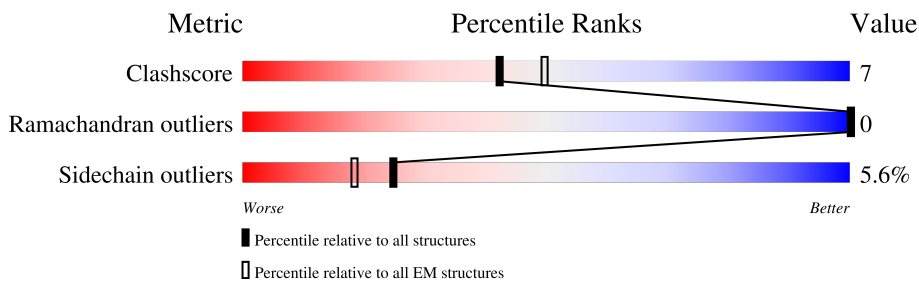
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 ≥ 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	1988	
2	B	218	
3	C	215	
4	D	2	
4	E	2	

2 Entry composition i

There are 11 unique types of molecules in this entry. The entry contains 13725 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
			Total	C	N	O	S		
1	A	1282	10366	6869	1631	1788	78	1	0

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	119	983	617	172	183	11	3	0

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



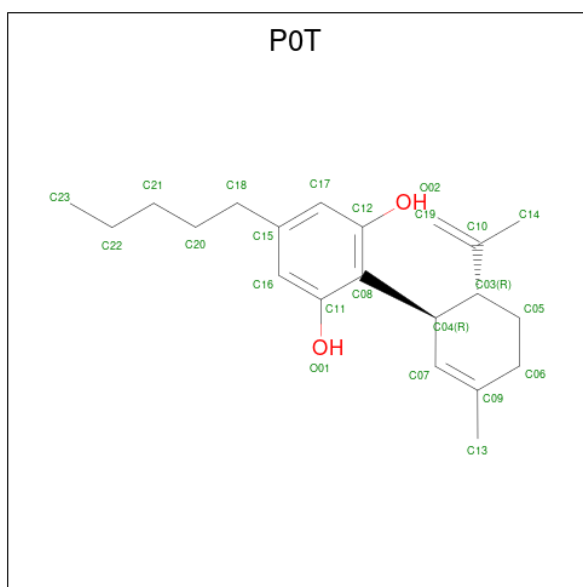
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	D	2	28	16	2	10	0	0
4	E	2	28	16	2	10	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



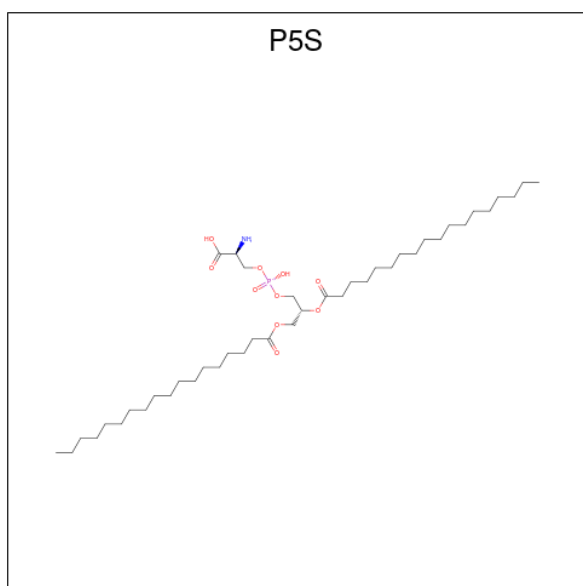
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 6 is cannabidiol (three-letter code: POT) (formula: $C_{21}H_{30}O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
6	A	1	Total	C	O	0
			23	21	2	
6	A	1	Total	C	O	0
			23	21	2	

- Molecule 7 is O-[(R)-{[(2R)-2,3-bis(octadecanoyloxy)propyl]oxy}(hydroxy)phosphoryl]-L-serine (three-letter code: P5S) (formula: $C_{42}H_{82}NO_{10}P$).



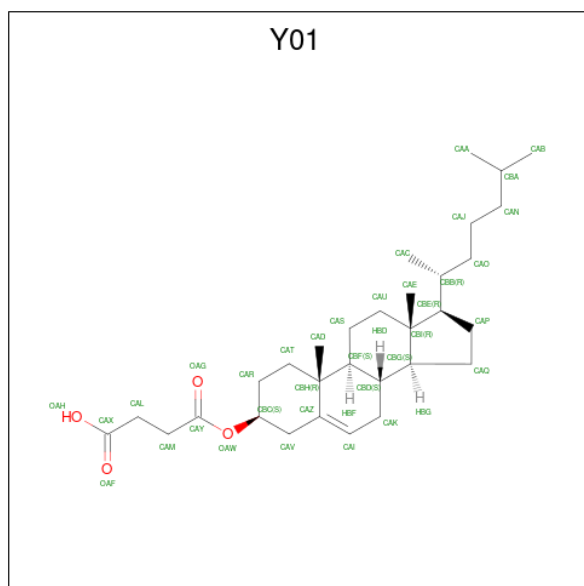
Mol	Chain	Residues	Atoms					AltConf
7	A	1	Total	C	N	O	P	0
			35	24	1	9	1	

Continued on next page...

Continued from previous page...

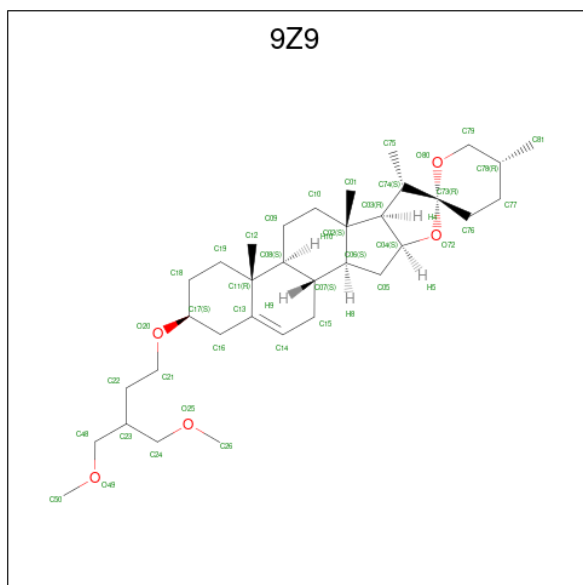
Mol	Chain	Residues	Atoms				AltConf	
			Total	C	N	O		P
7	A	1	41	31	1	8	1	0

- Molecule 8 is CHOLESTEROL HEMISUCCINATE (three-letter code: Y01) (formula: $C_{31}H_{50}O_4$).



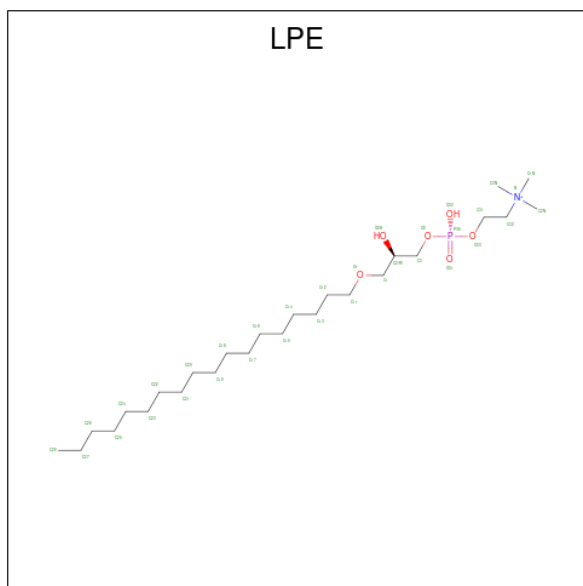
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
8	A	1	35	31	4	0
8	A	1	35	31	4	0
8	A	1	35	31	4	0
8	A	1	35	31	4	0
8	A	1	35	31	4	0

- Molecule 9 is (3beta,14beta,17beta,25R)-3-[4-methoxy-3-(methoxymethyl)butoxy]spirost-5-en (three-letter code: 9Z9) (formula: $C_{34}H_{56}O_5$).



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

- Molecule 10 is 1-O-OCTADECYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: LPE) (formula: $C_{26}H_{57}NO_6P$).



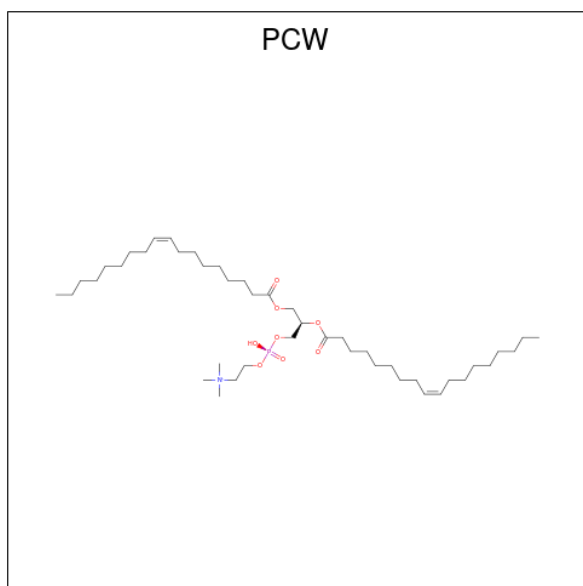
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
10	A	1	25	17	1	6	1	0
10	A	1	25	17	1	6	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
10	A	1	Total 20	12	1	6	1	0
10	A	1	Total 22	14	1	6	1	0
10	A	1	Total 28	20	1	6	1	0
10	A	1	Total 25	17	1	6	1	0
10	A	1	Total 25	17	1	6	1	0
10	A	1	Total 25	17	1	6	1	0
10	A	1	Total 25	17	1	6	1	0
10	A	1	Total 25	17	1	6	1	0
10	A	1	Total 17	9	1	6	1	0
10	B	1	Total 17	9	1	6	1	0
10	B	1	Total 17	9	1	6	1	0

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

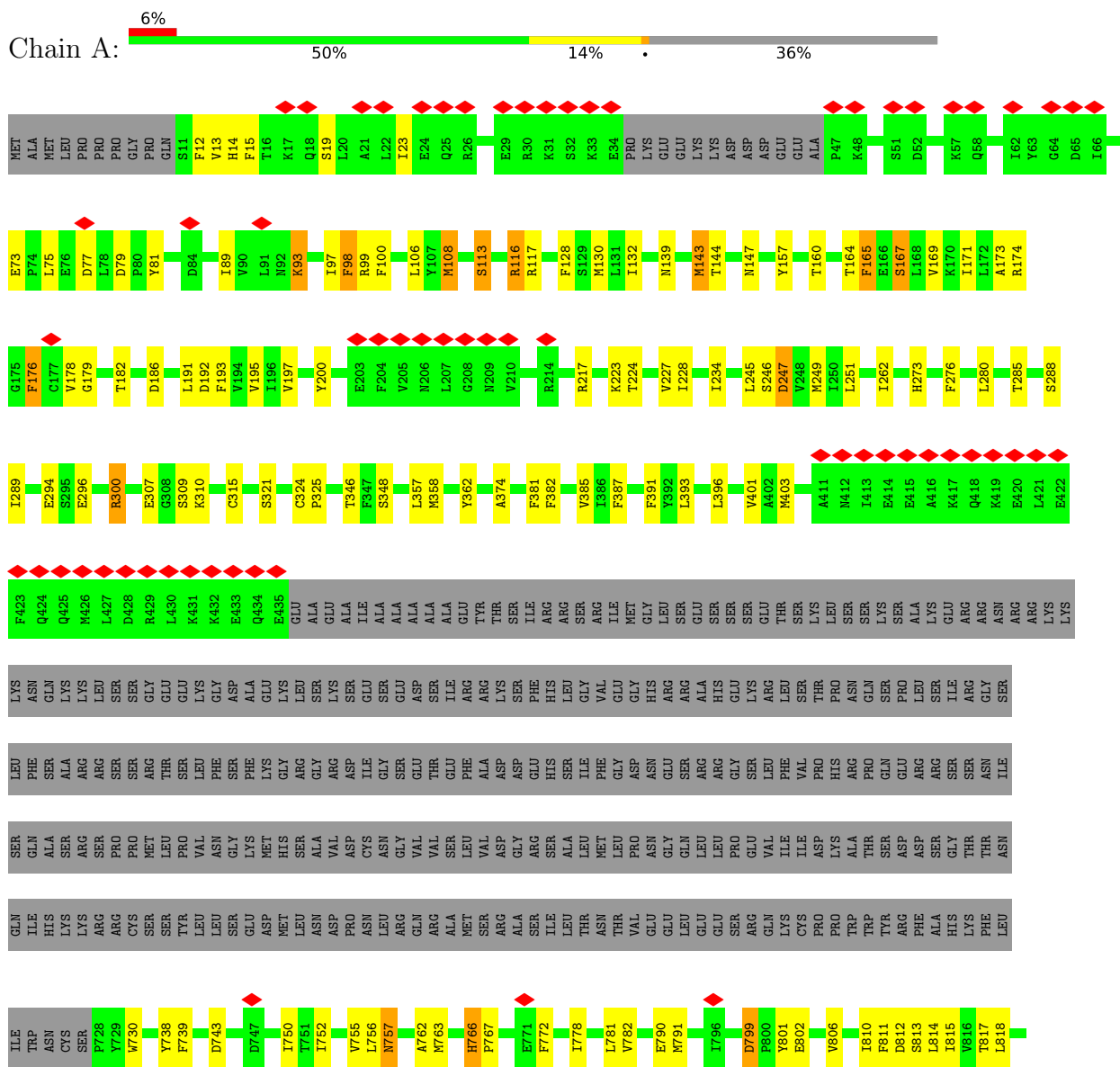


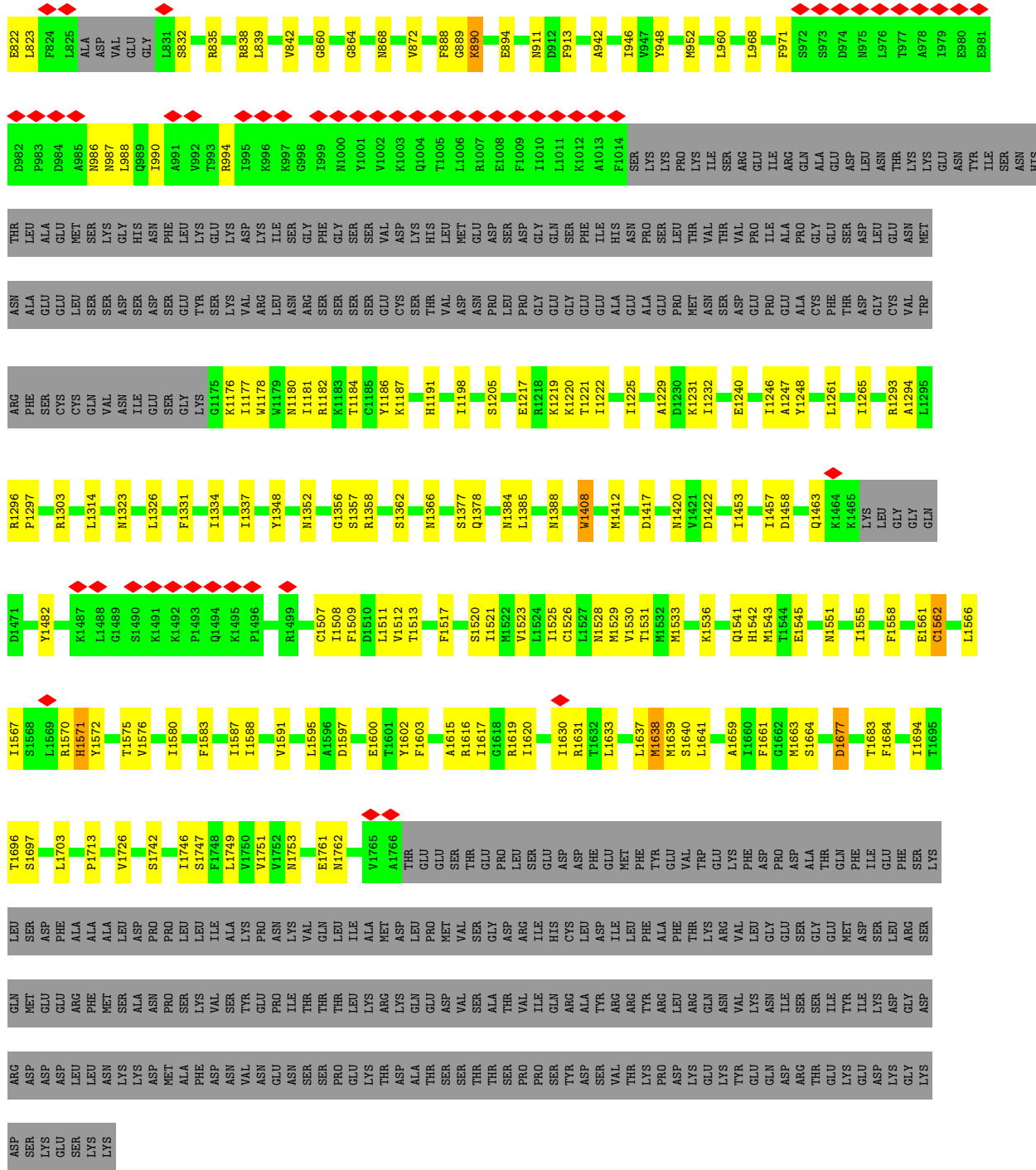
Mol	Chain	Residues	Atoms					AltConf
11	A	1	Total	C	N	O	P	0
			53	43	1	8	1	
11	A	1	Total	C	N	O	P	0
			47	37	1	8	1	
11	A	1	Total	C	N	O	P	0
			44	34	1	8	1	
11	A	1	Total	C	N	O	P	0
			44	34	1	8	1	

3 Residue-property plots

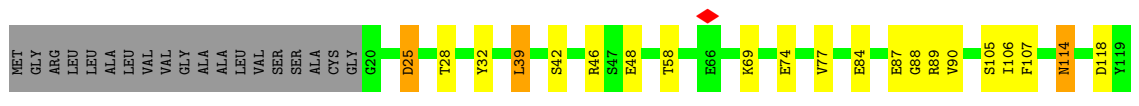
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

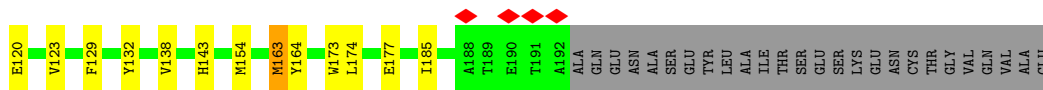
- Molecule 1: Sodium channel protein type 9 subunit alpha



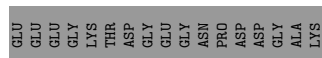
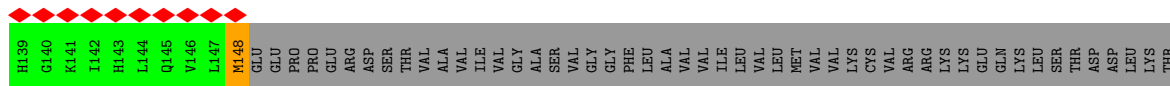
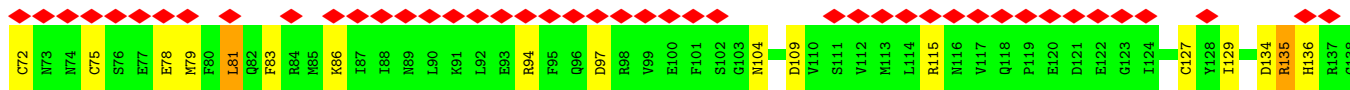
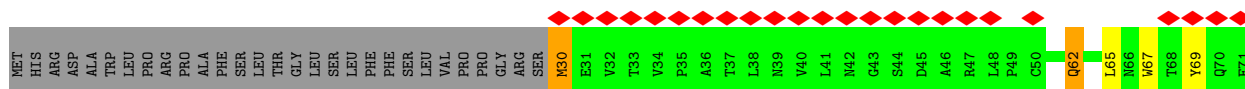
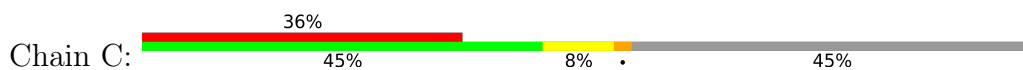


- Molecule 2: Sodium channel subunit beta-1





• 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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	488974	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)	1200	Depositor
Maximum defocus (nm)	1400	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.804	Depositor
Minimum map value	-2.301	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.064	Depositor
Recommended contour level	0.35	Depositor
Map size (\AA)	356.47998, 356.47998, 356.47998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.114, 1.114, 1.114	Depositor

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: 9Z9, P0T, PCW, Y01, P5S, NAG, 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	0.26	0/10616	0.48	0/14376
2	B	0.26	0/1442	0.50	0/1949
3	C	0.27	0/1014	0.55	0/1370
All	All	0.26	0/13072	0.49	0/17695

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	10366	0	10604	167	0
2	B	1416	0	1380	22	0
3	C	983	0	952	13	0
4	D	28	0	25	1	0
4	E	28	0	25	0	0
5	A	42	0	39	0	0
5	B	42	0	39	0	0
6	A	46	0	0	0	0
7	A	76	0	96	2	0
8	A	175	0	245	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	A	39	0	0	0	0
10	A	262	0	356	1	0
10	B	34	0	38	3	0
11	A	188	0	263	0	0
All	All	13725	0	14062	201	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (201) 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:1463:GLN:N	1:A:1463:GLN:OE1	2.19	0.76
3:C:104:ASN:N	3:C:109:ASP:O	2.28	0.67
1:A:1182:ARG:NH2	1:A:1248:TYR:O	2.28	0.66
1:A:1575:THR:HG22	1:A:1575:THR:O	1.96	0.65
1:A:1526:CYS:O	1:A:1530:VAL:HG23	1.98	0.64
1:A:1358:ARG:NH2	1:A:1417:ASP:OD2	2.30	0.64
2:B:28:THR:HG22	2:B:143:HIS:O	1.96	0.64
1:A:1591:VAL:O	1:A:1595:LEU:HD13	1.98	0.64
1:A:234:ILE:HG21	1:A:872:VAL:HG21	1.80	0.64
1:A:167:SER:O	1:A:171:ILE:HD12	1.98	0.63
1:A:757:ASN:OD1	1:A:838:ARG:NH2	2.32	0.63
1:A:357:LEU:HD21	1:A:385:VAL:HG11	1.82	0.62
1:A:224:THR:HG23	1:A:228:ILE:CD1	2.29	0.62
1:A:401:VAL:HG21	1:A:960:LEU:HD21	1.82	0.60
1:A:1385:LEU:O	1:A:1388:ASN:ND2	2.33	0.60
1:A:1659:ALA:O	1:A:1663:MET:HG3	2.02	0.60
2:B:58:THR:HG22	2:B:69:LYS:HA	1.85	0.59
1:A:781:LEU:HD11	1:A:823:LEU:HD13	1.85	0.59
1:A:224:THR:CG2	1:A:228:ILE:HD12	2.33	0.58
1:A:73:GLU:OE1	1:A:117:ARG:NH1	2.36	0.58
1:A:813:SER:O	1:A:817:THR:HG23	2.03	0.58
1:A:1726:VAL:HG12	1:A:1726:VAL:O	2.03	0.58
1:A:89:ILE:HD11	1:A:97:ILE:HB	1.86	0.58
1:A:811:PHE:CE1	1:A:815:ILE:HD11	2.39	0.57
1:A:889:GLY:O	1:A:911:ASN:ND2	2.37	0.57
1:A:262:ILE:HD11	1:A:1617:ILE:HD13	1.85	0.57
1:A:396:LEU:HD22	1:A:1633:LEU:CD2	2.35	0.57
1:A:358:MET:HE1	1:A:393:LEU:HD12	1.85	0.57
1:A:860:GLY:O	1:A:864:GLY:N	2.38	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1580:ILE:HD12	1:A:1580:ILE:H	1.70	0.56
1:A:1512:VAL:HG12	1:A:1517:PHE:CD2	2.40	0.56
1:A:986:ASN:OD1	1:A:988:LEU:N	2.37	0.56
1:A:251:LEU:HD23	1:A:1630:ILE:CG1	2.36	0.55
1:A:224:THR:HG23	1:A:228:ILE:HD11	1.87	0.55
1:A:1507:CYS:O	1:A:1511:LEU:HG	2.06	0.55
1:A:294:GLU:N	1:A:294:GLU:OE1	2.40	0.55
2:B:90:VAL:HG21	2:B:106:ILE:HD12	1.88	0.55
1:A:1482:TYR:OH	1:A:1761:GLU:OE2	2.20	0.54
1:A:307:GLU:HA	1:A:307:GLU:OE1	2.08	0.54
1:A:1570:ARG:O	1:A:1571:HIS:CD2	2.61	0.54
1:A:89:ILE:HD12	1:A:98:PHE:O	2.07	0.54
1:A:276:PHE:HZ	1:A:289:ILE:HD13	1.73	0.54
1:A:130:MET:HA	1:A:130:MET:HE2	1.89	0.53
3:C:72:CYS:SG	3:C:75:CYS:N	2.82	0.53
1:A:346:THR:HG22	1:A:348:SER:H	1.72	0.53
2:B:25:ASP:N	2:B:25:ASP:OD1	2.39	0.53
1:A:251:LEU:HD23	1:A:1630:ILE:HG13	1.90	0.53
1:A:1377:SER:OG	1:A:1378:GLN:N	2.41	0.53
1:A:1521:ILE:O	1:A:1525:ILE:HG13	2.09	0.53
1:A:839:LEU:HD21	1:A:1337:ILE:HG21	1.90	0.53
1:A:1694:ILE:HG21	1:A:1703:LEU:HD12	1.91	0.52
3:C:134:ASP:OD1	3:C:135:ARG:N	2.42	0.52
1:A:1576:VAL:O	1:A:1580:ILE:HD12	2.09	0.52
1:A:814:LEU:O	1:A:818:LEU:HD13	2.09	0.52
1:A:1749:LEU:O	1:A:1753:ASN:OD1	2.27	0.52
1:A:1509:PHE:O	1:A:1513:THR:HG22	2.09	0.52
1:A:1638:MET:HA	1:A:1641:LEU:HD23	1.92	0.51
1:A:321:SER:OG	1:A:374:ALA:O	2.28	0.51
1:A:1205:SER:O	1:A:1296:ARG:NH1	2.43	0.51
1:A:1588:ILE:HD13	1:A:1615:ALA:HB1	1.93	0.51
1:A:1219:LYS:HD2	1:A:1222:ILE:HD12	1.93	0.51
1:A:128:PHE:O	1:A:132:ILE:HG13	2.11	0.51
1:A:157:TYR:O	1:A:160:THR:HG22	2.11	0.50
1:A:1747:SER:O	1:A:1751:VAL:HG23	2.11	0.50
1:A:822:GLU:OE2	1:A:835:ARG:NE	2.45	0.50
2:B:174:LEU:HD13	10:B:305:LPE:H12	1.93	0.50
1:A:1366:ASN:HB2	1:A:1422:ASP:O	2.12	0.50
1:A:357:LEU:HD21	1:A:385:VAL:CG1	2.42	0.50
1:A:762:ALA:HB2	1:A:1337:ILE:HD11	1.94	0.50
1:A:1694:ILE:HG21	1:A:1703:LEU:CD1	2.43	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:CYS:HB2	1:A:325:PRO:CD	2.41	0.49
1:A:108:MET:N	1:A:108:MET:SD	2.86	0.49
1:A:750:ILE:HD11	1:A:790:GLU:HG3	1.95	0.48
1:A:948:TYR:O	1:A:952:MET:HG3	2.13	0.48
1:A:192:ASP:OD1	1:A:192:ASP:C	2.52	0.48
1:A:223:LYS:O	1:A:227:VAL:HG12	2.13	0.48
1:A:763:MET:O	1:A:763:MET:HG3	2.13	0.48
3:C:134:ASP:OD1	3:C:136:HIS:N	2.45	0.48
1:A:868:ASN:O	1:A:872:VAL:HG23	2.13	0.48
1:A:381:PHE:O	1:A:385:VAL:HG12	2.14	0.48
1:A:1575:THR:O	1:A:1575:THR:CG2	2.61	0.48
1:A:1261:LEU:O	1:A:1265:ILE:HG13	2.14	0.48
1:A:191:LEU:O	1:A:195:VAL:HG22	2.14	0.48
1:A:799:ASP:HB2	1:A:802:GLU:HB2	1.96	0.48
2:B:87:GLU:OE2	2:B:88:GLY:N	2.47	0.48
1:A:300:ARG:NH2	1:A:309:SER:O	2.47	0.47
1:A:193:PHE:O	1:A:197:VAL:HG13	2.14	0.47
1:A:285:THR:O	1:A:289:ILE:HD12	2.13	0.47
1:A:986:ASN:OD1	1:A:987:ASN:N	2.47	0.47
1:A:1177:ILE:O	1:A:1181:ILE:HG23	2.14	0.47
1:A:1408:TRP:CE3	1:A:1412:MET:CE	2.97	0.47
1:A:1458:ASP:N	1:A:1458:ASP:OD1	2.48	0.47
1:A:990:ILE:O	1:A:994:ARG:HG2	2.15	0.47
1:A:106:LEU:O	1:A:108:MET:SD	2.73	0.46
1:A:1567:ILE:C	1:A:1567:ILE:HD12	2.35	0.46
1:A:1508:ILE:HG21	1:A:1567:ILE:HD11	1.98	0.46
1:A:113:SER:O	1:A:117:ARG:HG3	2.16	0.46
1:A:1198:ILE:HG21	1:A:1303:ARG:HH12	1.80	0.46
1:A:1229:ALA:HA	1:A:1232:ILE:HD12	1.97	0.46
1:A:273:HIS:HB3	1:A:315:CYS:HB3	1.97	0.46
1:A:1529:MET:O	1:A:1533:MET:HG3	2.16	0.46
2:B:39:LEU:HA	2:B:105:SER:OG	2.15	0.46
1:A:1683:THR:HG22	1:A:1684:PHE:N	2.31	0.46
1:A:116:ARG:NH2	1:A:173:ALA:O	2.49	0.45
1:A:1696:THR:O	1:A:1697:SER:HB2	2.16	0.45
2:B:46:ARG:NE	2:B:48:GLU:OE2	2.43	0.45
2:B:177:GLU:OE1	10:B:305:LPE:H3N2	2.16	0.45
1:A:1742:SER:O	1:A:1746:ILE:HG13	2.16	0.45
1:A:165:PHE:O	1:A:165:PHE:CG	2.69	0.45
1:A:1453:ILE:O	1:A:1457:ILE:HG13	2.17	0.45
3:C:97:ASP:O	3:C:115:ARG:NH2	2.47	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:LEU:C	1:A:251:LEU:HD13	2.37	0.45
2:B:118:ASP:OD1	2:B:143:HIS:ND1	2.50	0.45
3:C:79:MET:HE1	3:C:81:LEU:O	2.17	0.45
1:A:164:THR:O	1:A:165:PHE:HB3	2.15	0.45
1:A:811:PHE:CZ	1:A:815:ILE:HD11	2.52	0.45
1:A:139:ASN:O	1:A:143:MET:HG3	2.16	0.45
1:A:1587:ILE:O	1:A:1591:VAL:HG23	2.17	0.45
1:A:147:ASN:CG	1:A:147:ASN:O	2.55	0.44
1:A:247:ASP:OD1	1:A:247:ASP:N	2.50	0.44
1:A:1186:TYR:HA	1:A:1247:ALA:HB1	1.98	0.44
2:B:84:GLU:OE1	2:B:84:GLU:N	2.46	0.44
1:A:1221:THR:O	1:A:1225:ILE:HD13	2.17	0.44
3:C:69:TYR:O	3:C:78:GLU:N	2.49	0.44
1:A:224:THR:HG22	1:A:228:ILE:HD12	1.99	0.44
1:A:1326:LEU:HD13	8:A:2008:Y01:HAQ2	1.98	0.44
1:A:1677:ASP:OD2	2:B:46:ARG:NH2	2.50	0.44
2:B:123:VAL:HG12	2:B:138:VAL:HB	2.00	0.44
1:A:79:ASP:OD1	1:A:81:TYR:CD2	2.70	0.44
1:A:1571:HIS:CD2	1:A:1571:HIS:C	2.91	0.44
1:A:1638:MET:HG3	1:A:1639:MET:HE2	1.99	0.44
1:A:1617:ILE:O	1:A:1620:ILE:HG12	2.18	0.44
1:A:743:ASP:OD1	1:A:743:ASP:N	2.42	0.43
2:B:129:PHE:HB2	2:B:132:TYR:HB3	1.99	0.43
1:A:280:LEU:HD12	1:A:280:LEU:O	2.18	0.43
1:A:968:LEU:C	1:A:968:LEU:HD23	2.38	0.43
3:C:129:ILE:HD12	3:C:129:ILE:N	2.33	0.43
3:C:148:MET:SD	3:C:148:MET:N	2.92	0.43
1:A:13:VAL:HG12	1:A:14[A]:HIS:N	2.33	0.43
1:A:1352:ASN:O	1:A:1356:GLY:N	2.47	0.43
2:B:114:ASN:N	2:B:114:ASN:OD1	2.52	0.43
1:A:382:PHE:HA	1:A:385:VAL:HG12	2.01	0.43
1:A:75:LEU:HB2	1:A:89:ILE:HG23	2.01	0.43
1:A:1528:ASN:HA	1:A:1531:THR:HG22	2.01	0.43
1:A:1637:LEU:O	1:A:1641:LEU:HD22	2.19	0.43
4:D:2:NAG:H3	4:D:2:NAG:H82	2.01	0.43
1:A:1558:PHE:HA	1:A:1561:GLU:HG2	2.00	0.43
1:A:755:VAL:HG13	8:A:2008:Y01:HAN2	2.01	0.42
1:A:1180:ASN:O	1:A:1184:THR:HG23	2.18	0.42
1:A:1631:ARG:NH1	7:A:2019:P5S:O16	2.51	0.42
1:A:1551:ASN:O	1:A:1555:ILE:HD12	2.19	0.42
1:A:1762:ASN:OD1	1:A:1762:ASN:C	2.57	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:VAL:HG12	1:A:14[B]:HIS:N	2.34	0.42
1:A:387:PHE:O	1:A:391:PHE:HB3	2.19	0.42
1:A:766:HIS:HB3	1:A:767:PRO:HD3	2.01	0.42
1:A:894:GLU:HA	1:A:894:GLU:OE1	2.20	0.42
2:B:90:VAL:HA	2:B:107:PHE:O	2.18	0.42
1:A:1314:LEU:C	1:A:1314:LEU:HD23	2.40	0.42
1:A:251:LEU:HD23	1:A:1630:ILE:HG12	2.01	0.42
1:A:1184:THR:HG22	2:B:185:ILE:HG12	2.01	0.42
1:A:1566:LEU:HD11	1:A:1583:PHE:HE1	1.85	0.42
3:C:30:MET:HB3	3:C:136:HIS:ND1	2.34	0.42
3:C:65:LEU:HB3	3:C:83:PHE:HB3	2.02	0.42
1:A:1661:PHE:CE1	10:A:2016:LPE:H2N1	2.54	0.42
1:A:1521:ILE:HD12	1:A:1561:GLU:OE2	2.20	0.42
2:B:58:THR:OG1	2:B:120:GLU:HB2	2.20	0.42
1:A:1294:ALA:O	1:A:1297:PRO:HD2	2.20	0.41
2:B:173:TRP:CE3	10:B:305:LPE:H31	2.55	0.41
1:A:93:LYS:HD2	1:A:93:LYS:O	2.20	0.41
1:A:179:GLY:H	1:A:182:THR:HG21	1.86	0.41
1:A:224:THR:CG2	1:A:228:ILE:CD1	2.94	0.41
1:A:812:ASP:HA	1:A:815:ILE:HD12	2.02	0.41
3:C:62:GLN:OE1	3:C:62:GLN:N	2.54	0.41
1:A:1182:ARG:HG2	1:A:1246:ILE:O	2.20	0.41
1:A:245:LEU:HD21	1:A:401:VAL:HG12	2.01	0.41
1:A:806:VAL:O	1:A:810:ILE:HG23	2.21	0.41
1:A:942:ALA:O	1:A:946:ILE:HG13	2.21	0.41
1:A:1541:GLN:O	1:A:1545:GLU:HG3	2.21	0.41
1:A:842:VAL:HG11	1:A:1334:ILE:HD11	2.02	0.41
1:A:1178:TRP:NE1	1:A:1182:ARG:HD2	2.36	0.41
1:A:1187:LYS:HZ3	1:A:1187:LYS:CB	2.34	0.41
1:A:98:PHE:HB2	1:A:100:PHE:HE1	1.85	0.41
1:A:752:ILE:O	1:A:756:LEU:HG	2.20	0.41
1:A:832:SER:O	1:A:832:SER:OG	2.38	0.41
1:A:890:LYS:O	1:A:894:GLU:HG2	2.21	0.41
1:A:1520:SER:O	1:A:1523:VAL:HG12	2.21	0.41
1:A:165:PHE:O	1:A:169:VAL:HG23	2.21	0.41
1:A:778:ILE:O	1:A:782:VAL:HG23	2.20	0.41
7:A:2019:P5S:C38	7:A:2019:P5S:C17	2.99	0.41
1:A:1232:ILE:HD11	2:B:163:MET:HB2	2.03	0.40
1:A:106:LEU:HD21	1:A:176:PHE:HB2	2.03	0.40
1:A:106:LEU:H	1:A:178:VAL:HG21	1.87	0.40
1:A:144:THR:HG23	1:A:913:PHE:CG	2.56	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1217:GLU:O	1:A:1220:LYS:HE2	2.21	0.40
1:A:1348:TYR:CE1	1:A:1384:ASN:HB2	2.56	0.40
1:A:19:SER:O	1:A:23:ILE:HD12	2.22	0.40
2:B:74:GLU:O	2:B:77:VAL:HG12	2.22	0.40
1:A:77:ASP:OD1	1:A:99:ARG:NH1	2.54	0.40
1:A:1561:GLU:HG3	1:A:1562:CYS:N	2.37	0.40
2:B:163:MET:HG3	2:B:164:TYR:N	2.36	0.40
3:C:127:CYS:SG	3:C:129:ILE:HD11	2.62	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	1271/1988 (64%)	1211 (95%)	60 (5%)	0	100	100
2	B	171/218 (78%)	169 (99%)	2 (1%)	0	100	100
3	C	120/215 (56%)	116 (97%)	4 (3%)	0	100	100
All	All	1562/2421 (64%)	1496 (96%)	66 (4%)	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	1148/1778 (65%)	1084 (94%)	64 (6%)	21	51
2	B	157/190 (83%)	149 (95%)	8 (5%)	24	55
3	C	115/193 (60%)	107 (93%)	8 (7%)	15	40
All	All	1420/2161 (66%)	1340 (94%)	80 (6%)	25	51

All (80) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	PHE
1	A	15	PHE
1	A	93	LYS
1	A	98	PHE
1	A	108	MET
1	A	113	SER
1	A	116	ARG
1	A	143	MET
1	A	165	PHE
1	A	167	SER
1	A	174	ARG
1	A	176	PHE
1	A	186	ASP
1	A	200	TYR
1	A	217	ARG
1	A	246	SER
1	A	247	ASP
1	A	249	MET
1	A	288	SER
1	A	296	GLU
1	A	300	ARG
1	A	310	LYS
1	A	362	TYR
1	A	403	MET
1	A	730	TRP
1	A	738	TYR
1	A	739	PHE
1	A	757	ASN
1	A	766	HIS
1	A	772	PHE
1	A	791	MET
1	A	799	ASP
1	A	801	TYR
1	A	888	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	890	LYS
1	A	971	PHE
1	A	1176	LYS
1	A	1191	HIS
1	A	1231	LYS
1	A	1240	GLU
1	A	1293	ARG
1	A	1323	ASN
1	A	1331	PHE
1	A	1357	SER
1	A	1362	SER
1	A	1408	TRP
1	A	1420	ASN
1	A	1536	LYS
1	A	1542	HIS
1	A	1543	MET
1	A	1562	CYS
1	A	1571	HIS
1	A	1572	TYR
1	A	1597	ASP
1	A	1600	GLU
1	A	1602	TYR
1	A	1603	PHE
1	A	1616	ARG
1	A	1619	ARG
1	A	1638	MET
1	A	1640	SER
1	A	1664	SER
1	A	1677	ASP
1	A	1713	PRO
2	B	25	ASP
2	B	32	TYR
2	B	39	LEU
2	B	42	SER
2	B	89	ARG
2	B	114	ASN
2	B	154	MET
2	B	163	MET
3	C	30	MET
3	C	62	GLN
3	C	67	TRP
3	C	81	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	C	86	LYS
3	C	94	ARG
3	C	135	ARG
3	C	148	MET

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	1571	HIS
3	C	131	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

4 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	1,4	14,14,15	0.34	0	17,19,21	0.87	0
4	NAG	D	2	4	14,14,15	0.46	0	17,19,21	1.03	2 (11%)
4	NAG	E	1	4,2	14,14,15	0.30	0	17,19,21	1.07	1 (5%)
4	NAG	E	2	4	14,14,15	0.30	0	17,19,21	0.69	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	1,4	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	3/6/23/26	0/1/1/1
4	NAG	E	1	4,2	-	0/6/23/26	0/1/1/1
4	NAG	E	2	4	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	1	NAG	C1-O5-C5	3.68	117.17	112.19
4	D	2	NAG	C8-C7-N2	2.30	119.99	116.10
4	D	2	NAG	O5-C1-C2	-2.01	108.11	111.29

There are no chirality outliers.

All (3) torsion outliers are listed below:

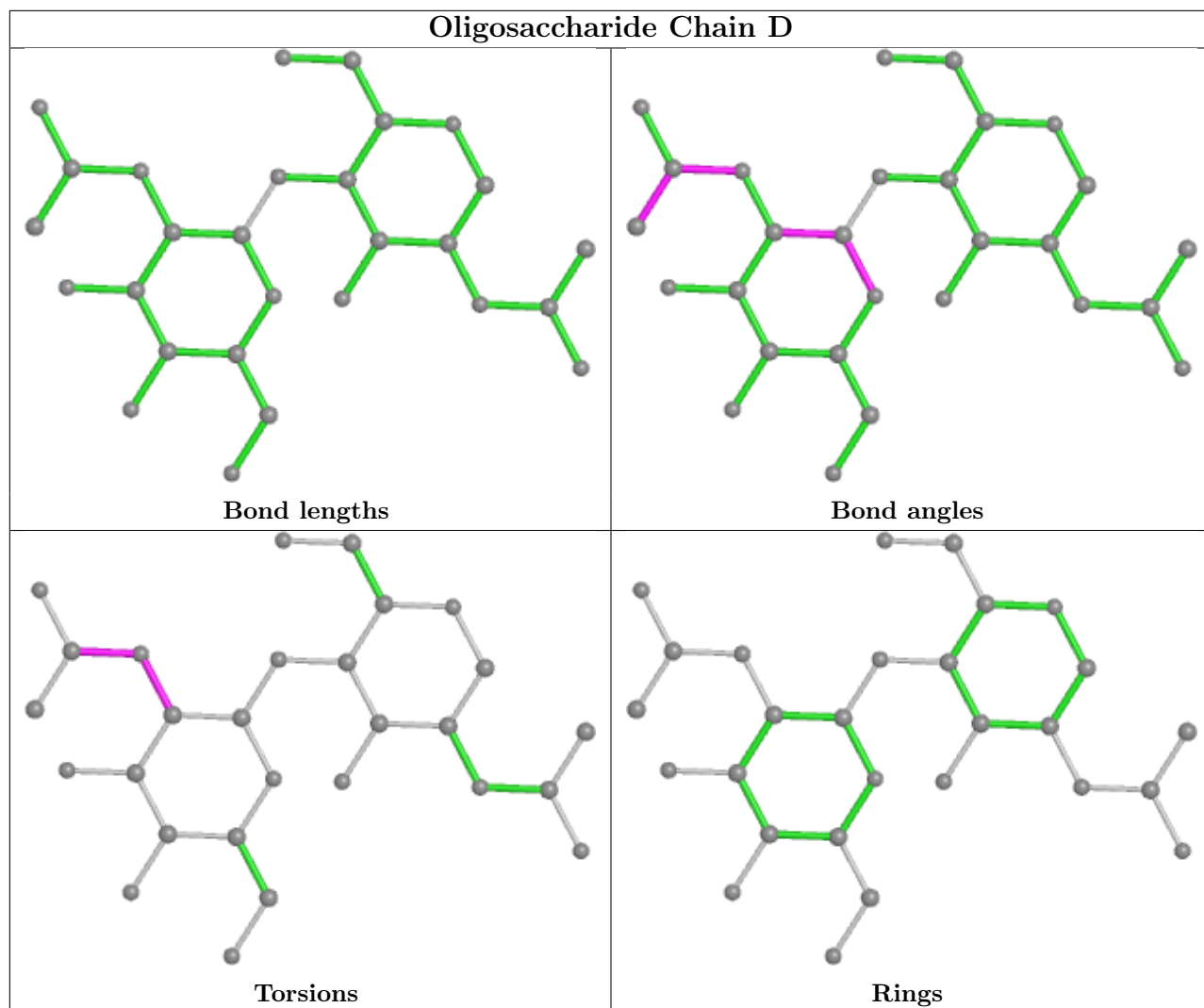
Mol	Chain	Res	Type	Atoms
4	D	2	NAG	C8-C7-N2-C2
4	D	2	NAG	O7-C7-N2-C2
4	D	2	NAG	C1-C2-N2-C7

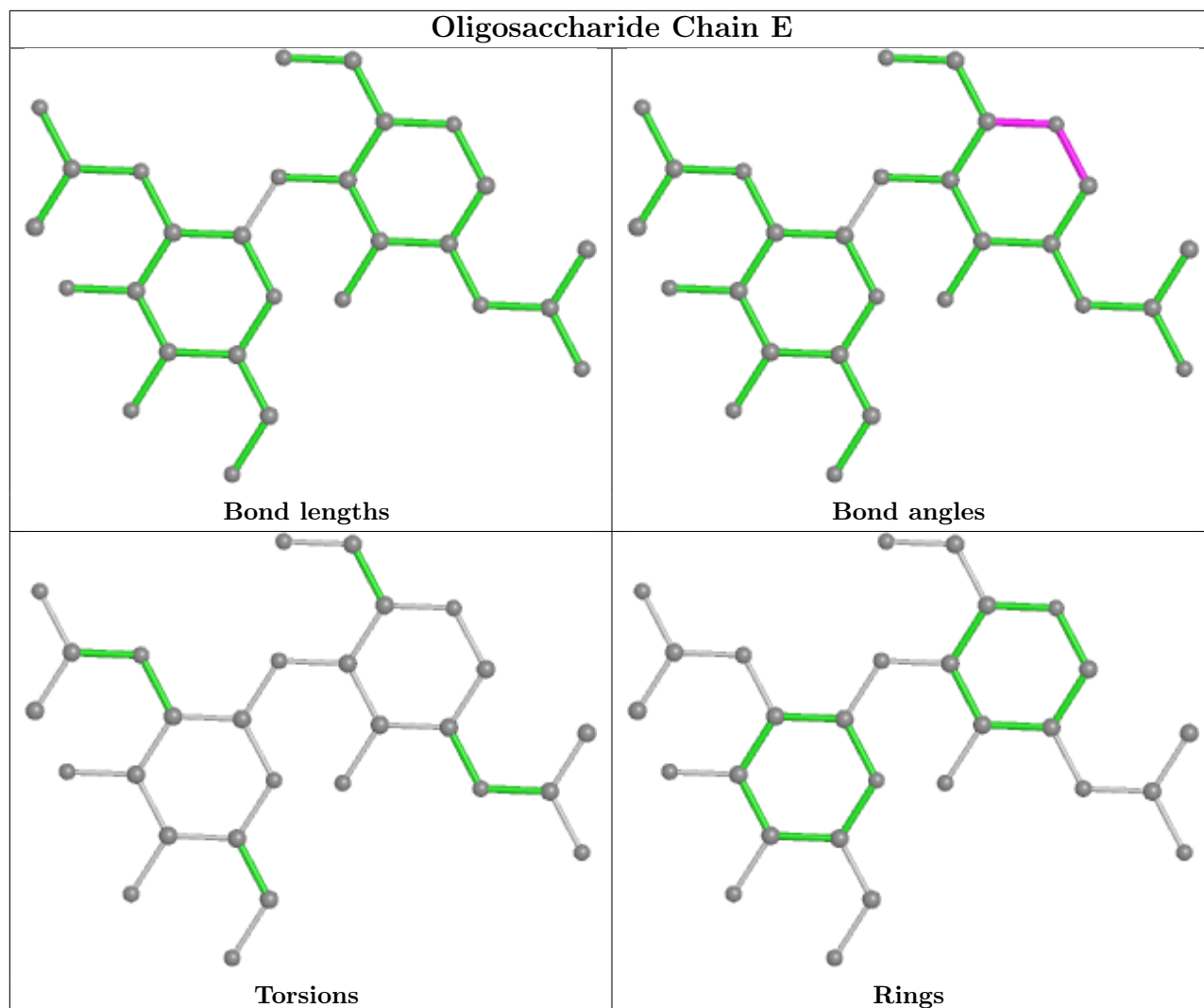
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	2	NAG	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 oligosaccharide.





5.6 Ligand geometry [i](#)

33 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	$\# Z > 2$
6	P0T	A	2005	-	24,24,24	0.22	0	27,33,33	1.19	2 (7%)
5	NAG	A	2001	1	14,14,15	0.32	0	17,19,21	0.54	0
8	Y01	A	2007	-	38,38,38	0.45	0	57,57,57	0.49	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	LPE	B	304	-	16,16,33	0.34	0	20,22,39	0.42	0
5	NAG	B	303	2	14,14,15	0.30	0	17,19,21	0.72	0
8	Y01	A	2028	-	38,38,38	0.45	0	57,57,57	0.47	0
8	Y01	A	2010	-	38,38,38	0.46	0	57,57,57	0.56	0
10	LPE	A	2022	-	24,24,33	0.29	0	28,30,39	0.40	0
5	NAG	A	2003	1	14,14,15	0.30	0	17,19,21	0.56	0
7	P5S	A	2006	-	33,34,53	0.45	0	36,40,60	0.58	0
11	PCW	A	2020	-	43,43,53	0.31	0	49,51,61	0.47	1 (2%)
10	LPE	A	2024	-	24,24,33	0.28	0	28,30,39	0.34	0
5	NAG	A	2002	1	14,14,15	0.39	0	17,19,21	2.17	4 (23%)
7	P5S	A	2019	-	40,40,53	0.30	0	43,45,60	0.35	0
10	LPE	A	2016	-	21,21,33	0.31	0	25,27,39	0.46	0
10	LPE	A	2023	-	24,24,33	0.29	0	28,30,39	0.35	0
11	PCW	A	2015	-	52,52,53	0.31	0	58,60,61	0.32	0
5	NAG	B	302	2	14,14,15	0.31	0	17,19,21	0.79	1 (5%)
10	LPE	A	2013	-	24,24,33	0.31	0	25,27,39	0.41	0
10	LPE	A	2017	-	27,27,33	0.26	0	31,33,39	0.35	0
10	LPE	B	305	-	16,16,33	0.35	0	20,22,39	0.40	0
11	PCW	A	2027	-	43,43,53	0.31	0	49,51,61	0.32	0
8	Y01	A	2011	-	38,38,38	0.44	0	57,57,57	0.54	0
10	LPE	A	2021	-	24,24,33	0.27	0	28,30,39	0.38	0
5	NAG	B	301	2	14,14,15	0.27	0	17,19,21	0.63	0
10	LPE	A	2014	-	19,19,33	0.31	0	23,25,39	0.39	0
10	LPE	A	2012	-	24,24,33	0.28	0	28,30,39	0.37	0
11	PCW	A	2018	-	46,46,53	0.32	0	52,54,61	0.39	0
8	Y01	A	2008	-	38,38,38	0.45	0	57,57,57	0.51	0
10	LPE	A	2025	-	24,24,33	0.27	0	28,30,39	0.36	0
9	9Z9	A	2009	-	44,44,44	0.26	0	66,68,68	0.43	0
6	P0T	A	2004	-	24,24,24	0.19	0	27,33,33	0.48	0
10	LPE	A	2026	-	16,16,33	0.34	0	20,22,39	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
6	P0T	A	2005	-	-	1/13/26/26	0/2/2/2
5	NAG	A	2001	1	-	1/6/23/26	0/1/1/1
8	Y01	A	2007	-	-	2/19/77/77	0/4/4/4
10	LPE	B	304	-	-	1/17/17/34	-
5	NAG	B	303	2	-	1/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	Y01	A	2028	-	-	0/19/77/77	0/4/4/4
8	Y01	A	2010	-	-	2/19/77/77	0/4/4/4
10	LPE	A	2022	-	-	7/25/25/34	-
5	NAG	A	2003	1	-	1/6/23/26	0/1/1/1
7	P5S	A	2006	-	-	9/39/39/59	-
11	PCW	A	2020	-	-	4/47/47/57	-
10	LPE	A	2024	-	-	5/25/25/34	-
5	NAG	A	2002	1	-	0/6/23/26	0/1/1/1
7	P5S	A	2019	-	-	2/44/44/59	-
10	LPE	A	2016	-	-	9/22/22/34	-
10	LPE	A	2023	-	-	4/25/25/34	-
11	PCW	A	2015	-	-	10/56/56/57	-
5	NAG	B	302	2	-	0/6/23/26	0/1/1/1
10	LPE	A	2013	-	-	5/25/25/34	-
10	LPE	A	2017	-	-	6/28/28/34	-
10	LPE	B	305	-	-	7/17/17/34	-
11	PCW	A	2027	-	-	4/47/47/57	-
8	Y01	A	2011	-	-	9/19/77/77	0/4/4/4
10	LPE	A	2021	-	-	7/25/25/34	-
5	NAG	B	301	2	-	0/6/23/26	0/1/1/1
10	LPE	A	2014	-	-	4/20/20/34	-
10	LPE	A	2012	-	-	5/25/25/34	-
11	PCW	A	2018	-	-	8/50/50/57	-
8	Y01	A	2008	-	-	5/19/77/77	0/4/4/4
10	LPE	A	2025	-	-	7/25/25/34	-
9	9Z9	A	2009	-	-	0/12/100/100	0/6/6/6
6	P0T	A	2004	-	-	5/13/26/26	0/2/2/2
10	LPE	A	2026	-	-	4/17/17/34	-

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	2002	NAG	C1-O5-C5	5.66	119.86	112.19
5	A	2002	NAG	O5-C1-C2	4.48	118.36	111.29
6	A	2005	P0T	C04-C07-C09	-4.45	117.00	124.68
6	A	2005	P0T	C06-C09-C07	-3.25	118.96	121.57

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	2002	NAG	C4-C3-C2	-3.19	106.35	111.02
5	A	2002	NAG	C3-C4-C5	-2.94	104.99	110.24
5	B	302	NAG	C1-O5-C5	2.48	115.55	112.19
11	A	2020	PCW	O2-C31-C32	2.21	116.27	111.50

There are no chirality outliers.

All (135) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	2006	P5S	C-CA-CB-OG
7	A	2006	P5S	N-CA-CB-OG
10	A	2013	LPE	C31-O33-P-O31
10	A	2013	LPE	C32-C31-O33-P
10	A	2016	LPE	C31-O33-P-O3
10	A	2016	LPE	C31-O33-P-O31
10	A	2021	LPE	O1-C1-C2-C3
10	A	2021	LPE	C31-O33-P-O32
10	A	2021	LPE	C32-C31-O33-P
10	A	2022	LPE	C2-C3-O3-P
10	A	2022	LPE	C3-O3-P-O32
10	A	2025	LPE	C31-O33-P-O31
10	A	2025	LPE	C32-C31-O33-P
10	A	2026	LPE	C31-O33-P-O31
10	B	305	LPE	C2-C3-O3-P
10	B	305	LPE	C3-O3-P-O31
10	B	305	LPE	C32-C31-O33-P
11	A	2020	PCW	C2-C1-O3P-P
11	A	2027	PCW	C1-O3P-P-O2P
10	A	2021	LPE	O1-C1-C2-O2H
8	A	2008	Y01	CAJ-CAO-CBB-CBE
6	A	2004	P0T	C15-C18-C20-C21
10	A	2021	LPE	C2-C1-O1-C11
7	A	2006	P5S	C3-O16-P12-OG
10	A	2021	LPE	C31-O33-P-O3
10	A	2022	LPE	C3-O3-P-O33
8	A	2008	Y01	CAJ-CAO-CBB-CAC
7	A	2006	P5S	OXT-C-CA-N
5	A	2001	NAG	O5-C5-C6-O6
10	A	2016	LPE	C2-C1-O1-C11
8	A	2007	Y01	CAR-CBC-OAW-CAY
6	A	2005	P0T	C15-C18-C20-C21
8	A	2007	Y01	CAV-CBC-OAW-CAY

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
10	A	2025	LPE	O1-C1-C2-C3
10	A	2012	LPE	C3-O3-P-O33
10	A	2025	LPE	C31-O33-P-O3
11	A	2027	PCW	C1-O3P-P-O4P
10	A	2026	LPE	C2-C1-O1-C11
7	A	2006	P5S	O-C-CA-N
10	A	2012	LPE	C2-C3-O3-P
10	A	2023	LPE	C2-C3-O3-P
10	A	2014	LPE	C2-C3-O3-P
10	A	2025	LPE	C2-C1-O1-C11
8	A	2008	Y01	CAR-CBC-OAW-CAY
8	A	2011	Y01	CAJ-CAN-CBA-CAB
8	A	2011	Y01	CAO-CBB-CBE-CBI
10	A	2026	LPE	C31-O33-P-O3
7	A	2006	P5S	C3-O16-P12-O13
10	A	2012	LPE	C32-C31-O33-P
10	A	2016	LPE	C32-C31-O33-P
10	A	2023	LPE	C32-C31-O33-P
10	A	2016	LPE	C12-C11-O1-C1
10	A	2023	LPE	C2-C1-O1-C11
10	A	2012	LPE	O33-C31-C32-N
10	A	2014	LPE	O33-C31-C32-N
10	A	2016	LPE	O33-C31-C32-N
10	A	2021	LPE	O33-C31-C32-N
10	A	2022	LPE	O33-C31-C32-N
10	A	2023	LPE	O33-C31-C32-N
10	A	2024	LPE	O33-C31-C32-N
10	A	2025	LPE	O33-C31-C32-N
10	B	305	LPE	O33-C31-C32-N
11	A	2027	PCW	O4P-C4-C5-N
8	A	2011	Y01	CAC-CBB-CBE-CBI
8	A	2011	Y01	CAO-CBB-CBE-CAP
11	A	2015	PCW	C2-C1-O3P-P
8	A	2011	Y01	CAJ-CAN-CBA-CAA
10	A	2013	LPE	C31-O33-P-O3
10	A	2014	LPE	C31-O33-P-O3
10	A	2016	LPE	C3-O3-P-O33
10	A	2017	LPE	C3-O3-P-O33
10	A	2017	LPE	C31-O33-P-O3
10	A	2022	LPE	C31-O33-P-O3
10	A	2024	LPE	C3-O3-P-O33
10	A	2024	LPE	C31-O33-P-O3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
10	A	2026	LPE	C3-O3-P-O33
10	B	304	LPE	C31-O33-P-O3
10	B	305	LPE	C3-O3-P-O33
10	B	305	LPE	C31-O33-P-O3
11	A	2018	PCW	C1-O3P-P-O4P
11	A	2018	PCW	C4-O4P-P-O3P
11	A	2020	PCW	C1-O3P-P-O4P
10	A	2022	LPE	C12-C11-O1-C1
8	A	2008	Y01	CAV-CBC-OAW-CAY
7	A	2019	P5S	C27-C28-C29-C30
8	A	2010	Y01	CAR-CBC-OAW-CAY
11	A	2027	PCW	O2-C2-C3-O3
10	A	2017	LPE	C2-C3-O3-P
11	A	2018	PCW	C19-C20-C21-C22
5	B	303	NAG	O5-C5-C6-O6
10	A	2017	LPE	O1-C1-C2-C3
11	A	2015	PCW	C37-C38-C39-C40
8	A	2011	Y01	CAM-CAL-CAX-OAF
11	A	2015	PCW	C32-C33-C34-C35
10	A	2013	LPE	C14-C15-C16-C17
11	A	2015	PCW	C31-C32-C33-C34
8	A	2010	Y01	CAV-CBC-OAW-CAY
8	A	2011	Y01	CAM-CAL-CAX-OAH
10	A	2016	LPE	C12-C13-C14-C15
11	A	2015	PCW	C2-C3-O3-C11
6	A	2004	P0T	C17-C15-C18-C20
7	A	2019	P5S	N-CA-CB-OG
6	A	2004	P0T	C16-C15-C18-C20
11	A	2015	PCW	O31-C31-O2-C2
6	A	2004	P0T	C05-C03-C10-C14
11	A	2015	PCW	C17-C18-C19-C20
11	A	2015	PCW	C19-C20-C21-C22
11	A	2015	PCW	C39-C40-C41-C42
10	A	2013	LPE	C13-C14-C15-C16
11	A	2018	PCW	C17-C18-C19-C20
8	A	2011	Y01	CAO-CAJ-CAN-CBA
6	A	2004	P0T	C04-C03-C10-C19
11	A	2018	PCW	O2-C31-C32-C33
10	A	2012	LPE	C12-C11-O1-C1
7	A	2006	P5S	CA-CB-OG-P12
10	A	2025	LPE	O1-C1-C2-O2H
11	A	2015	PCW	C32-C31-O2-C2

Continued on next page...

Continued from previous page...

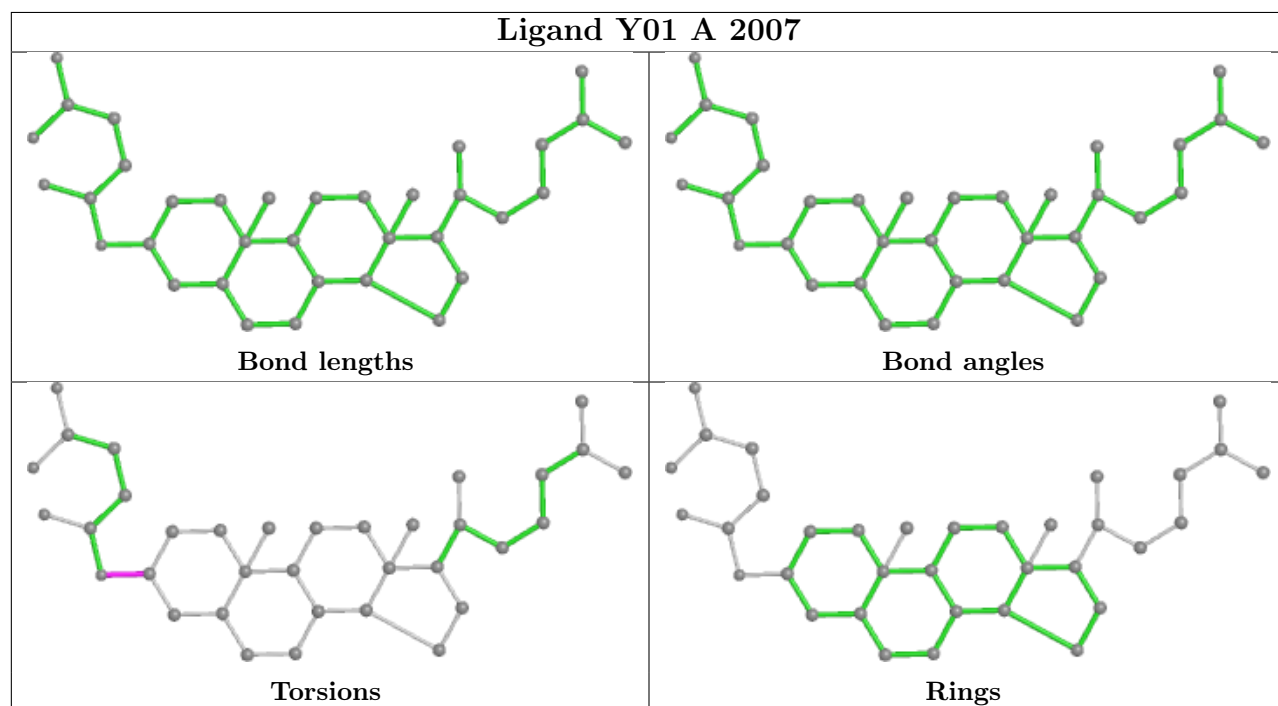
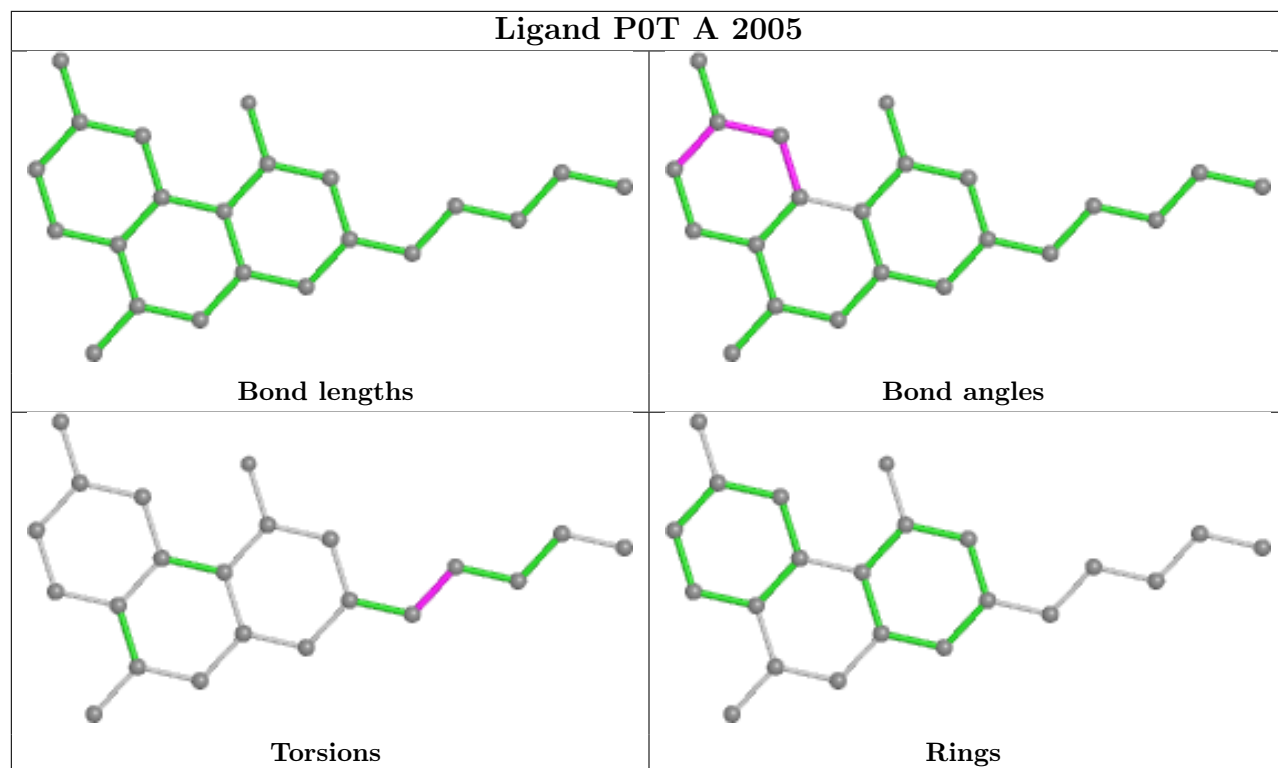
Mol	Chain	Res	Type	Atoms
7	A	2006	P5S	OXT-C-CA-CB
8	A	2011	Y01	CAC-CBB-CBE-CAP
5	A	2003	NAG	C3-C2-N2-C7
11	A	2020	PCW	O31-C31-O2-C2
10	A	2014	LPE	C31-O33-P-O31
10	A	2016	LPE	C3-O3-P-O31
10	A	2017	LPE	C3-O3-P-O31
10	A	2017	LPE	C31-O33-P-O31
10	A	2022	LPE	C31-O33-P-O31
10	A	2024	LPE	C3-O3-P-O31
10	A	2024	LPE	C31-O33-P-O31
10	B	305	LPE	C31-O33-P-O31
11	A	2018	PCW	C1-O3P-P-O2P
11	A	2020	PCW	C1-O3P-P-O2P
8	A	2008	Y01	CAN-CAJ-CAO-CBB
11	A	2018	PCW	C35-C36-C37-C38
11	A	2018	PCW	O31-C31-C32-C33
7	A	2006	P5S	O37-C38-C39-C40

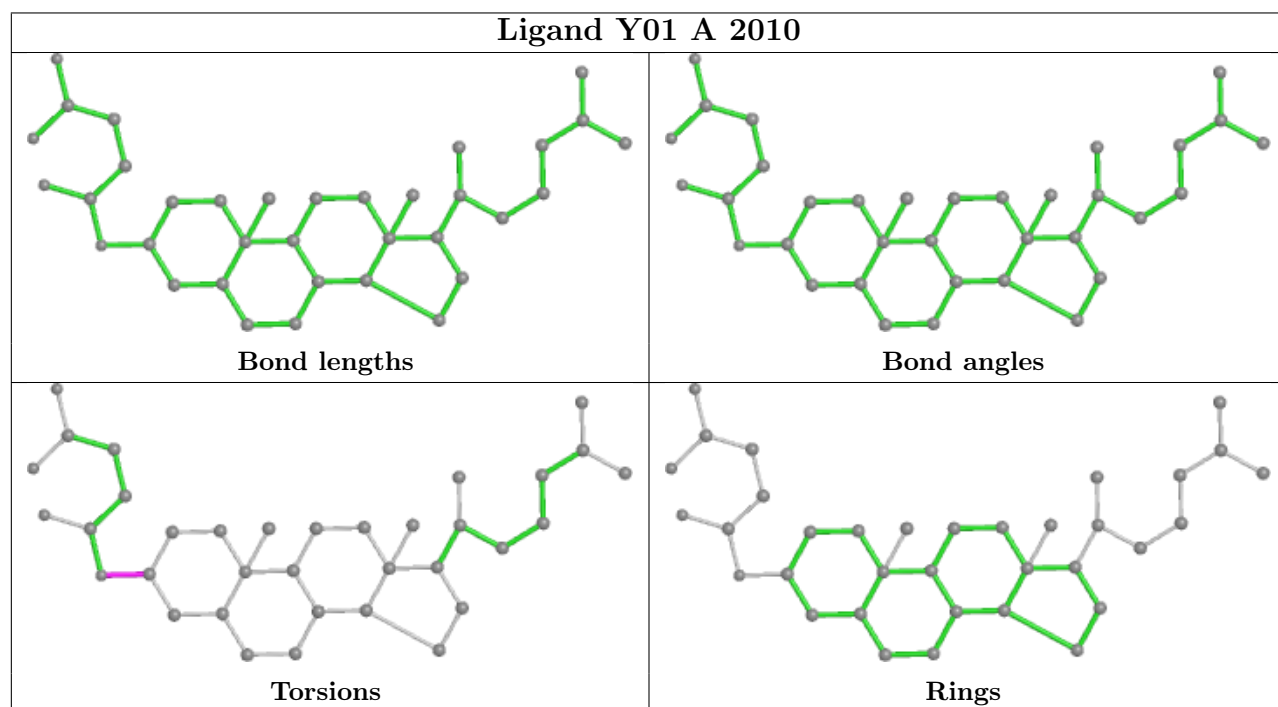
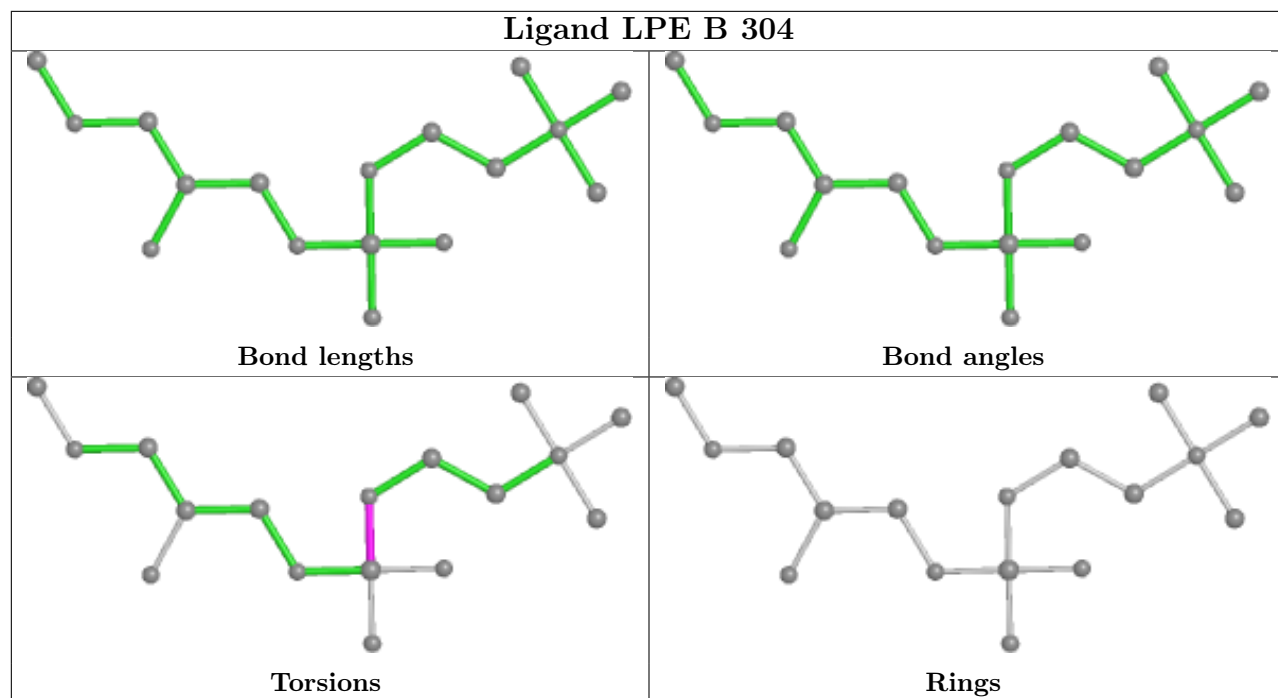
There are no ring outliers.

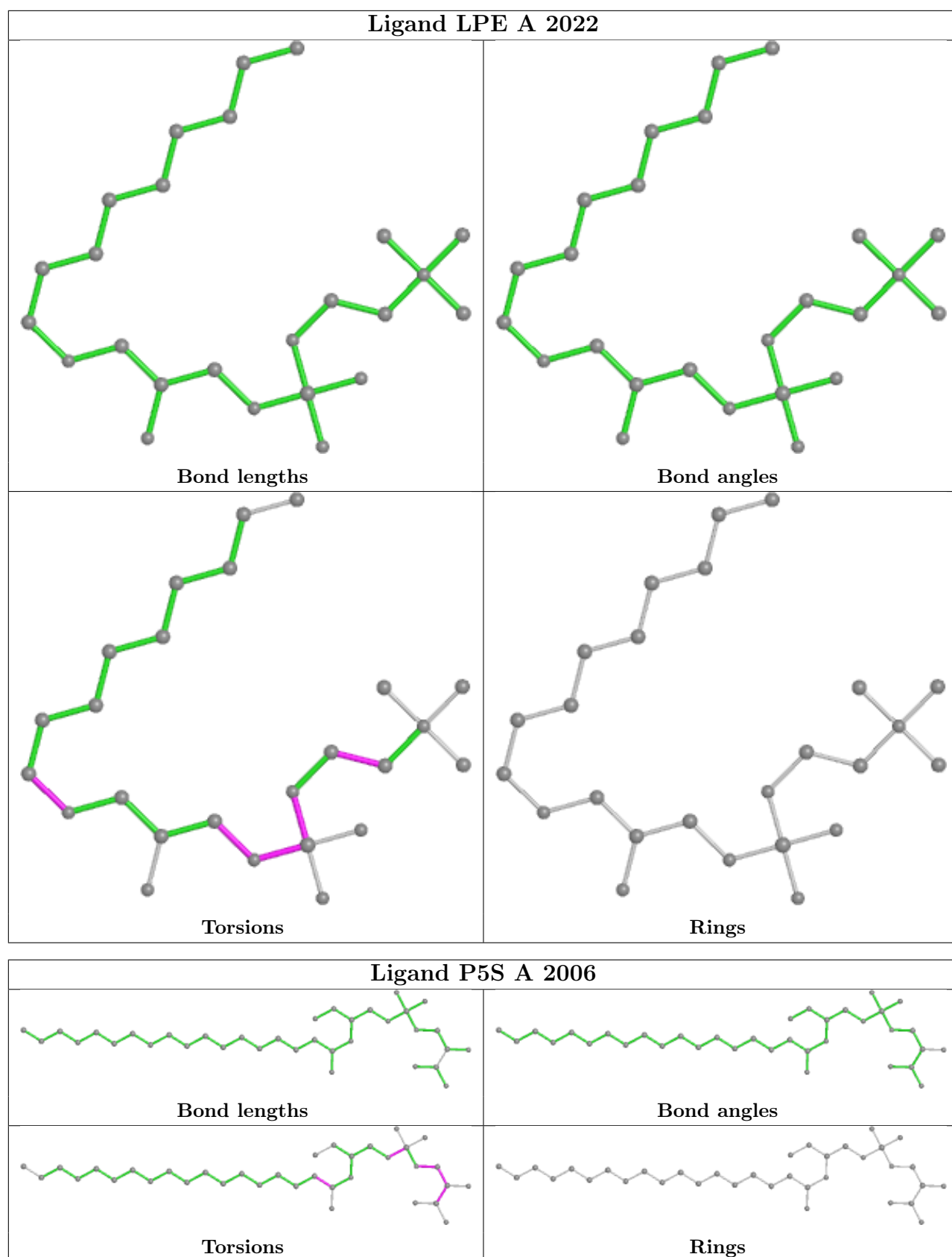
4 monomers are involved in 8 short contacts:

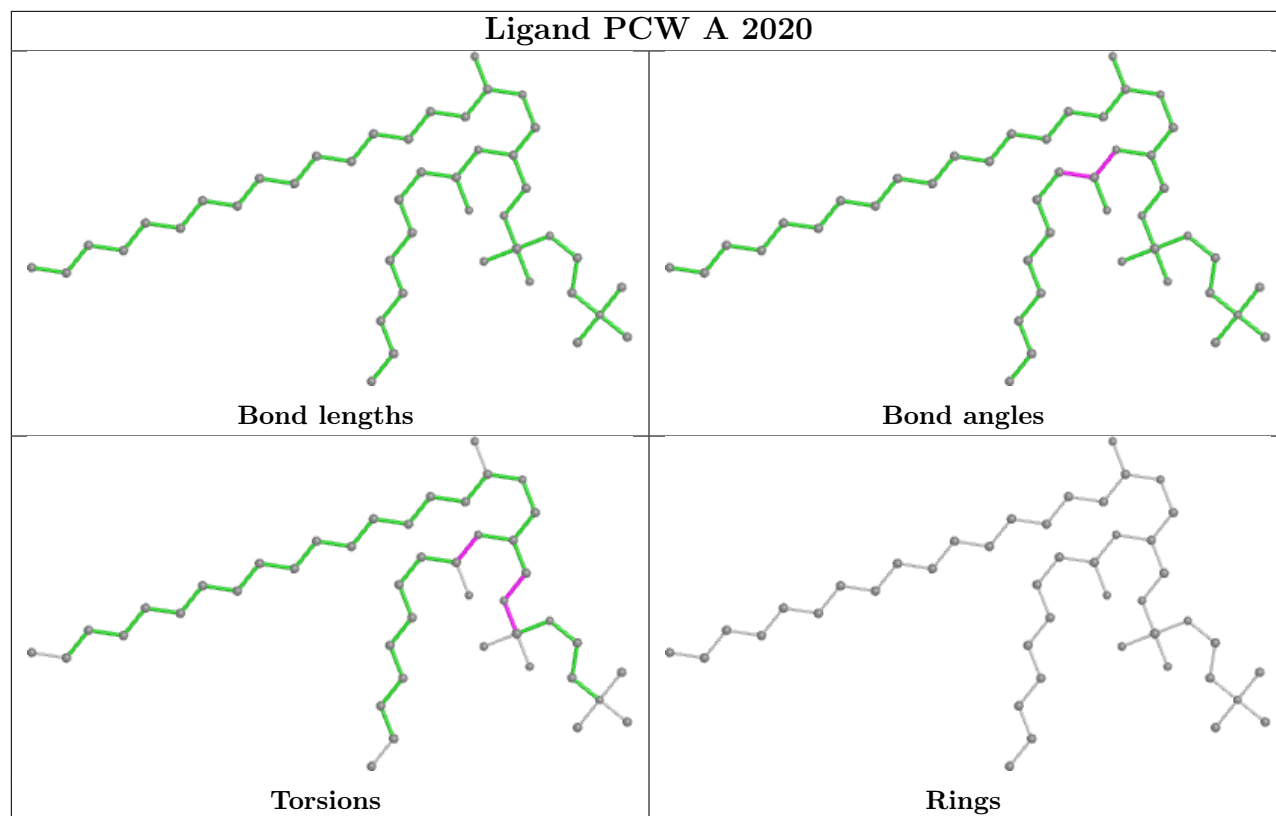
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	2019	P5S	2	0
10	A	2016	LPE	1	0
10	B	305	LPE	3	0
8	A	2008	Y01	2	0

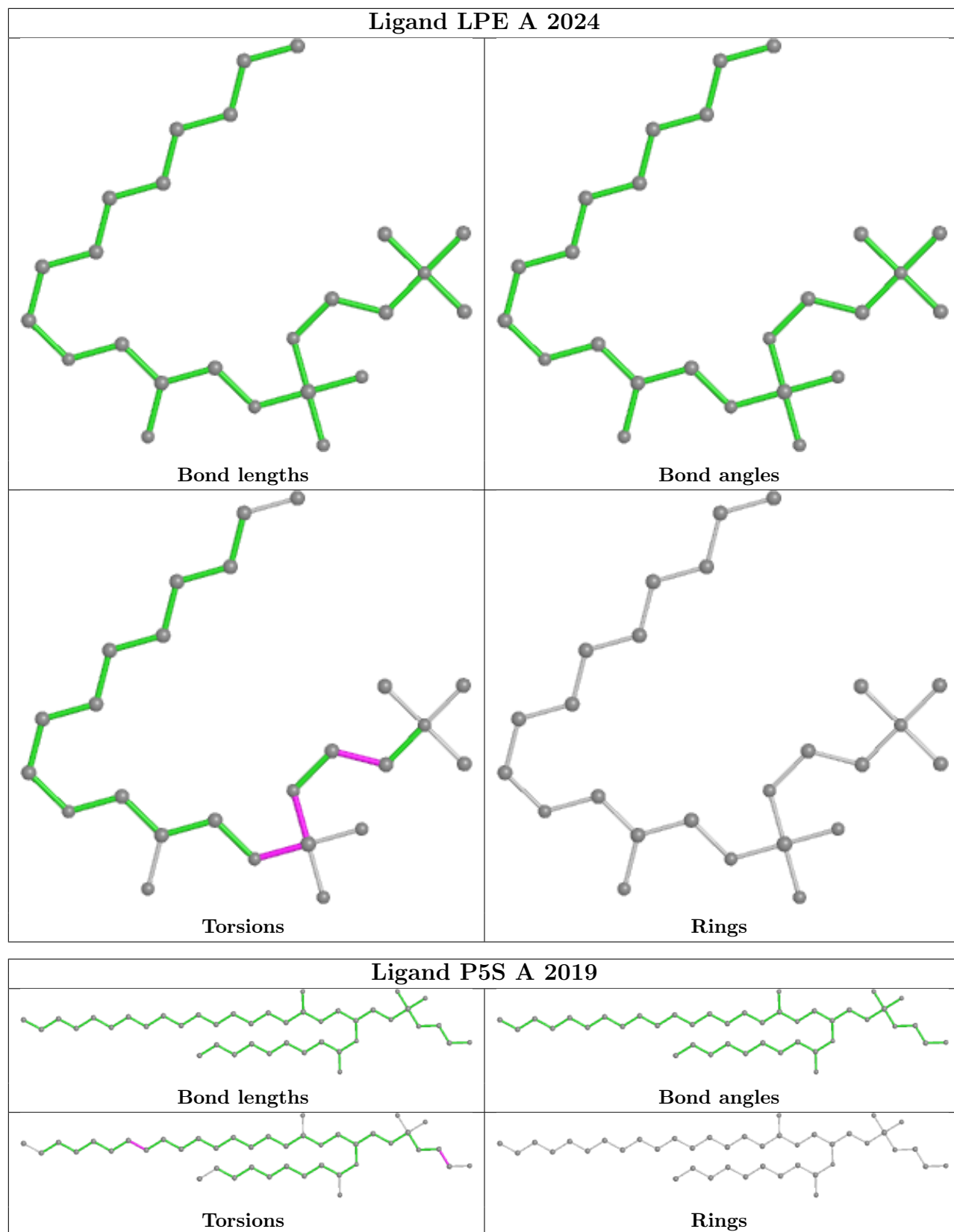
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

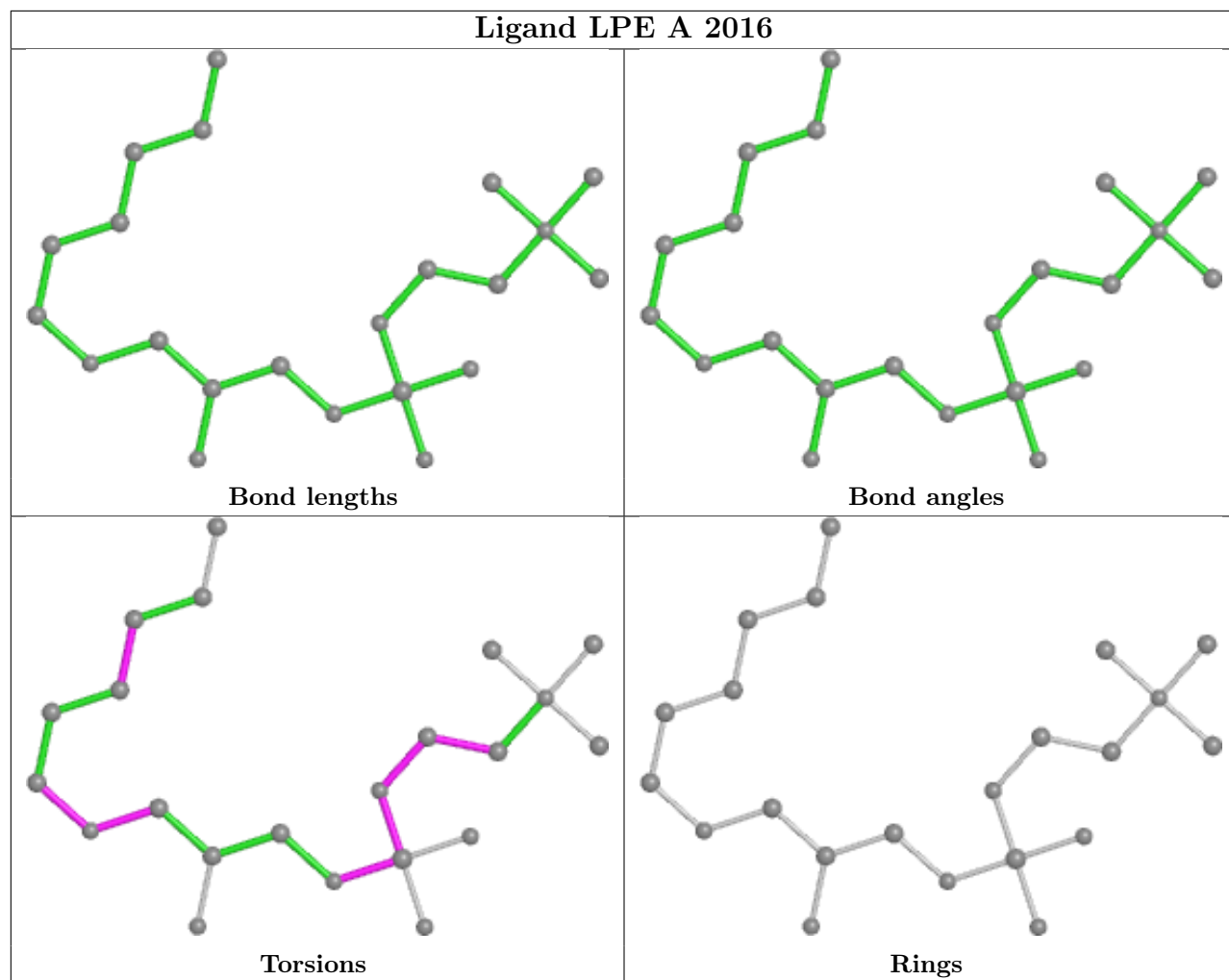


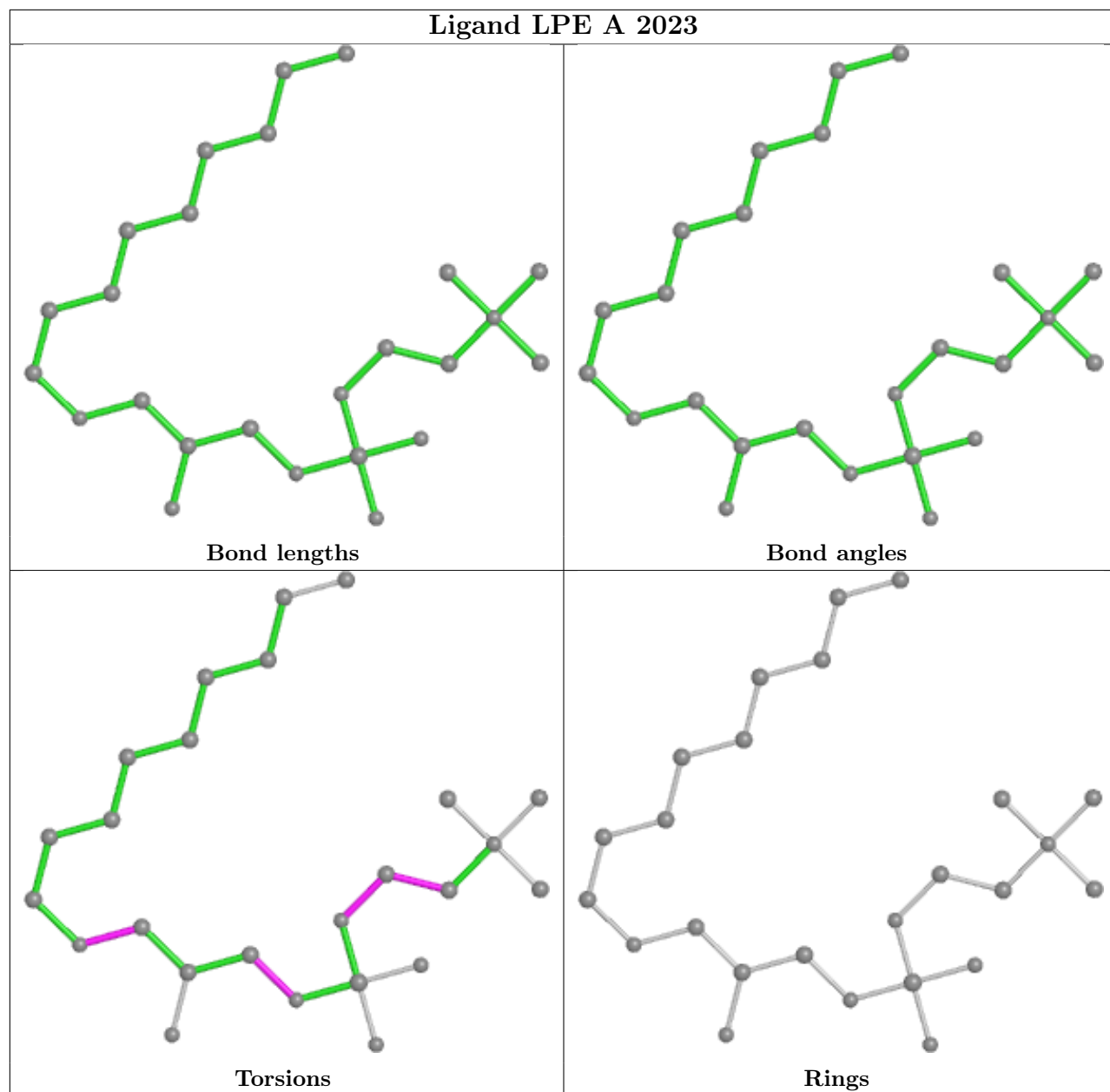


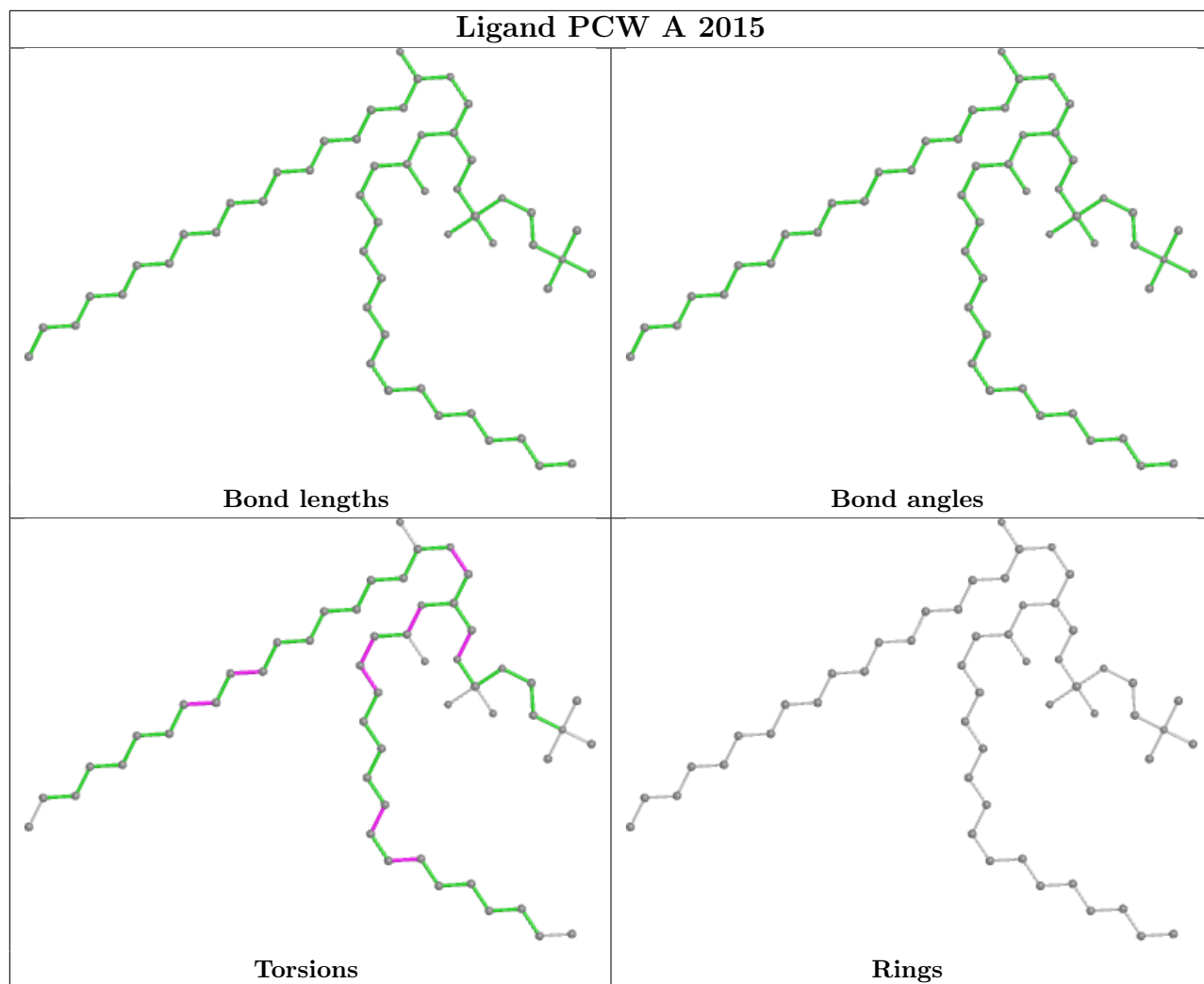


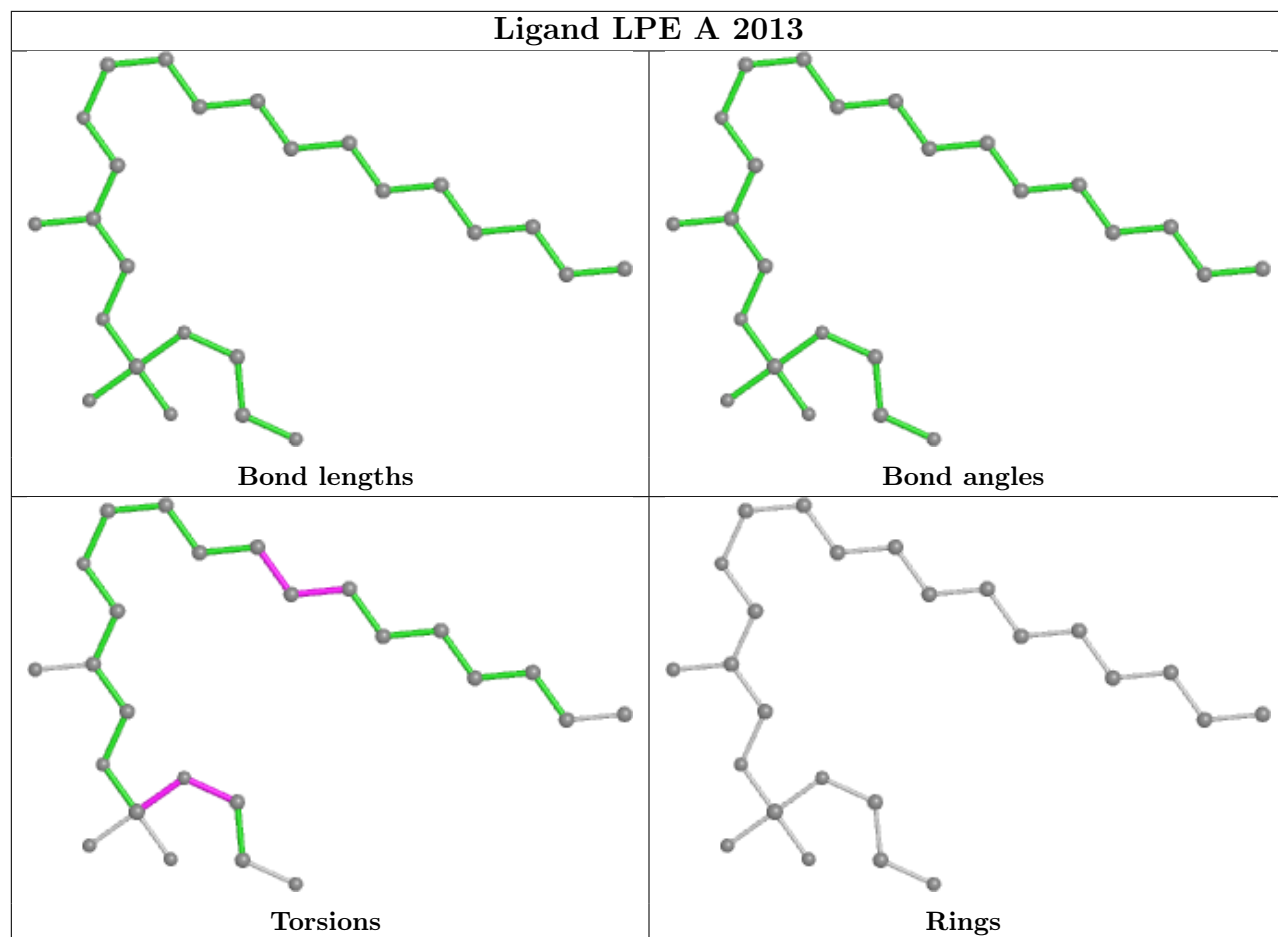


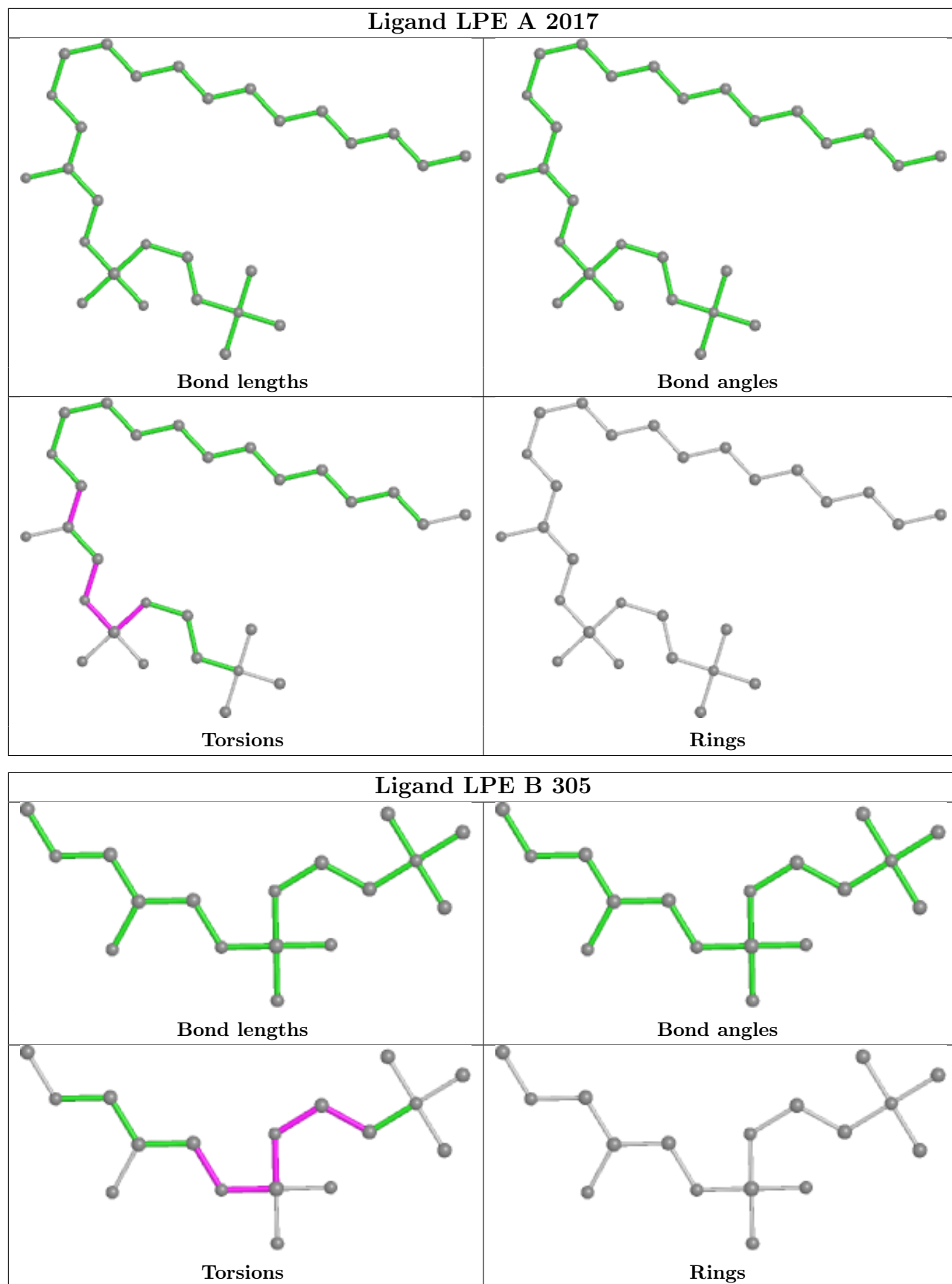


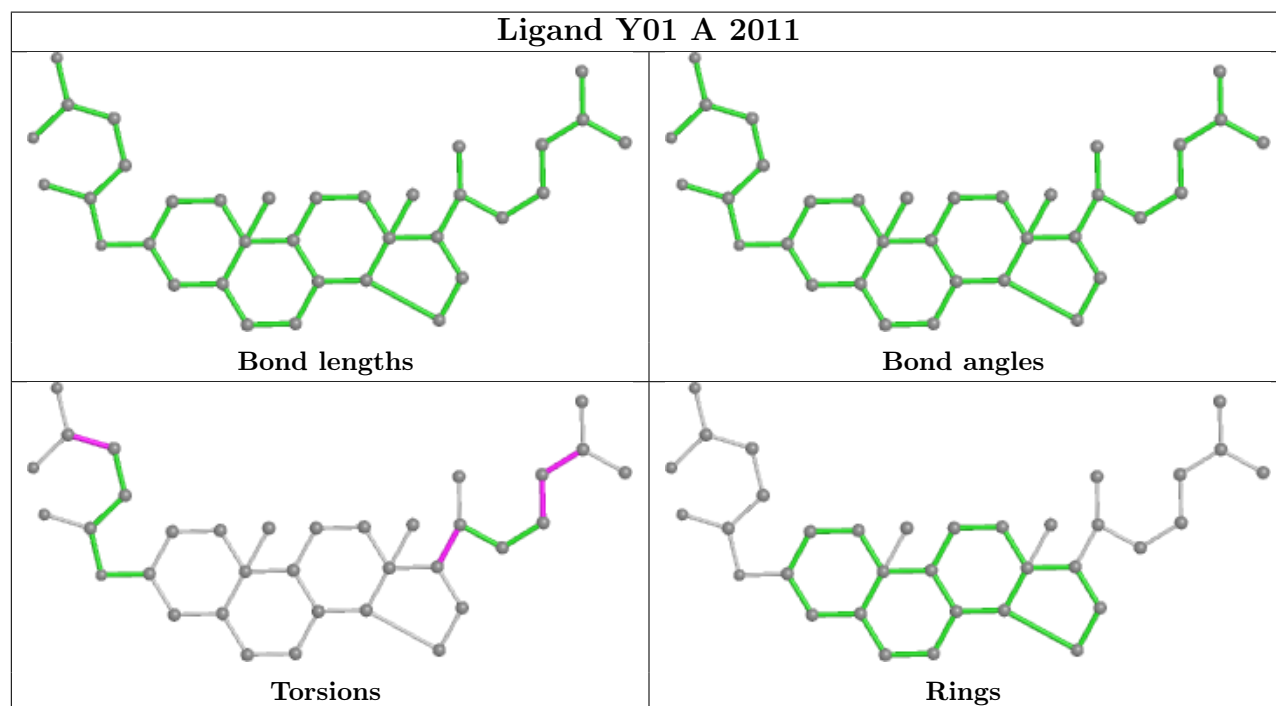
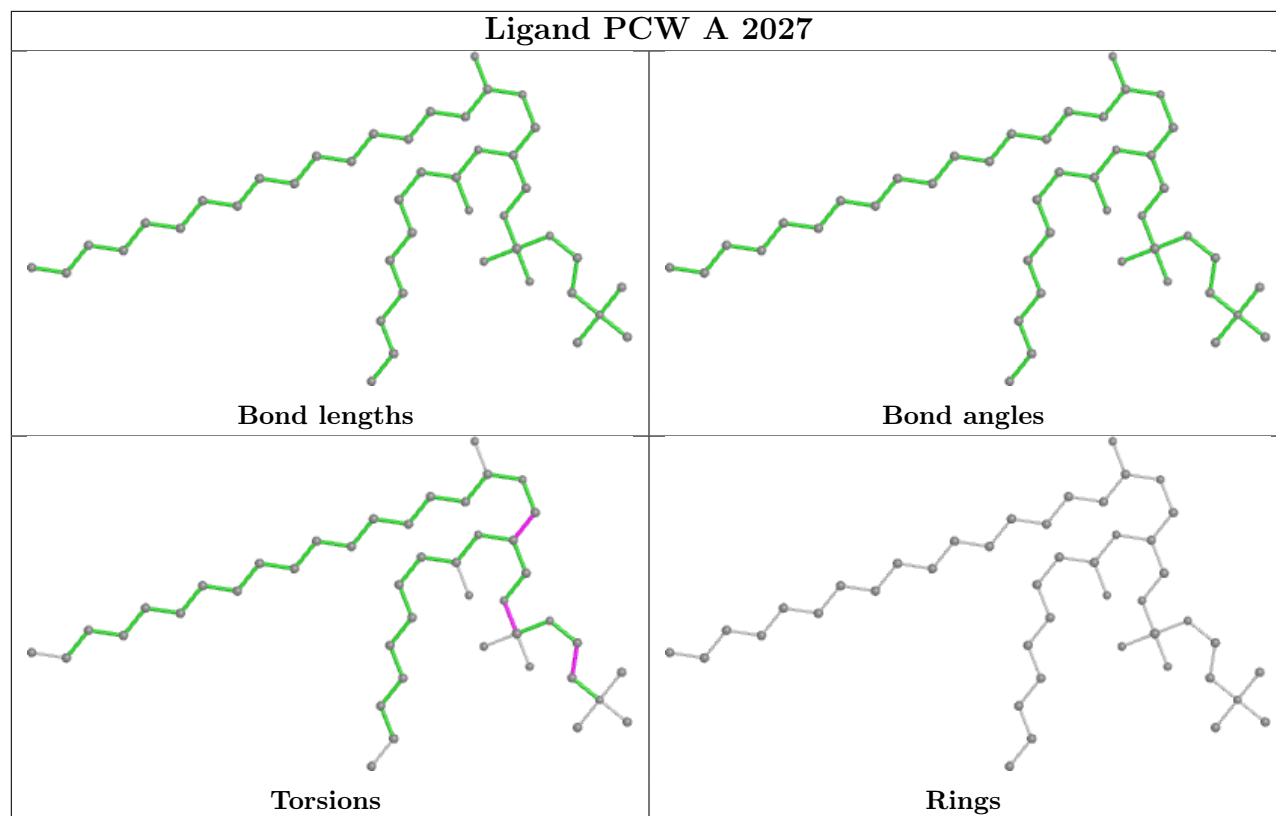


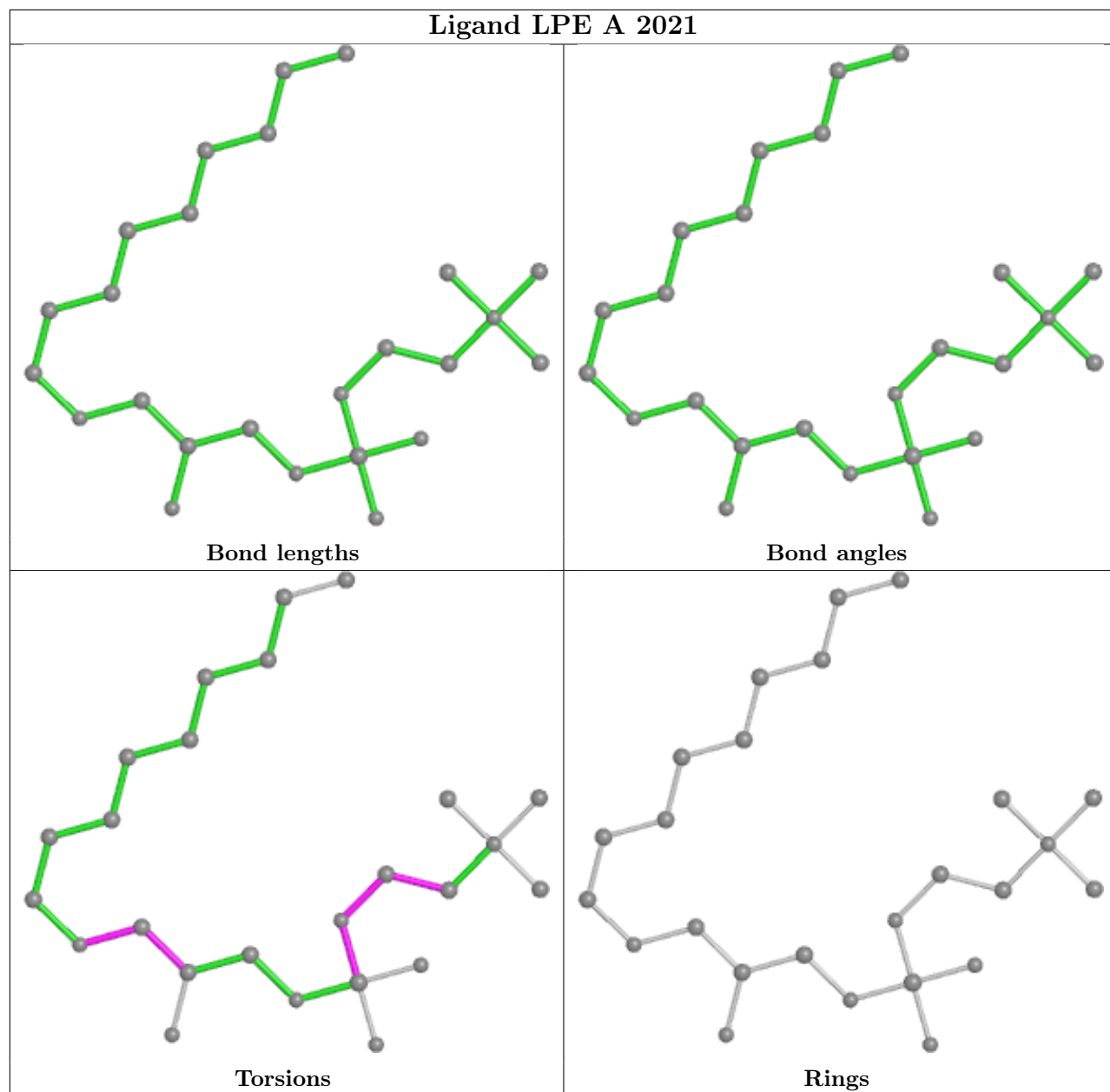


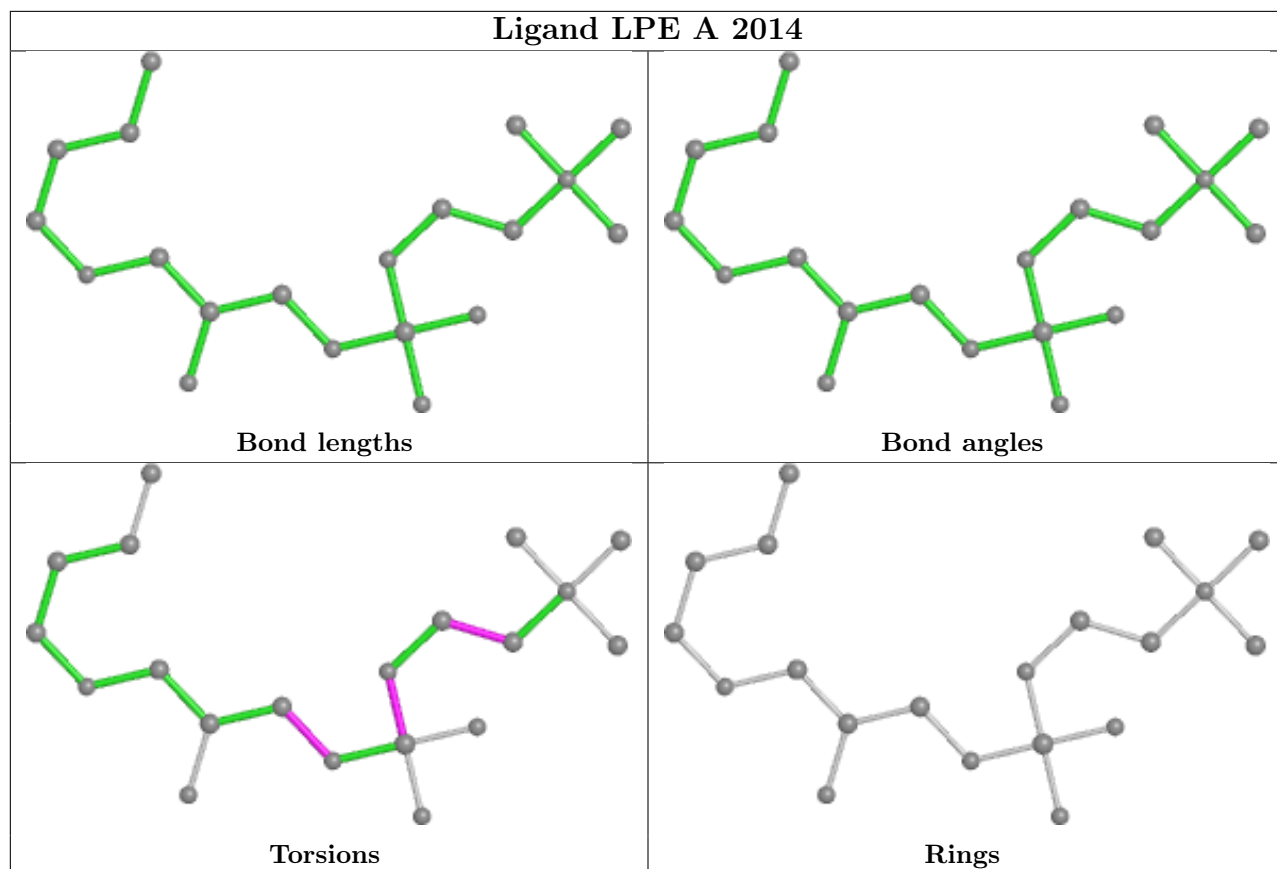


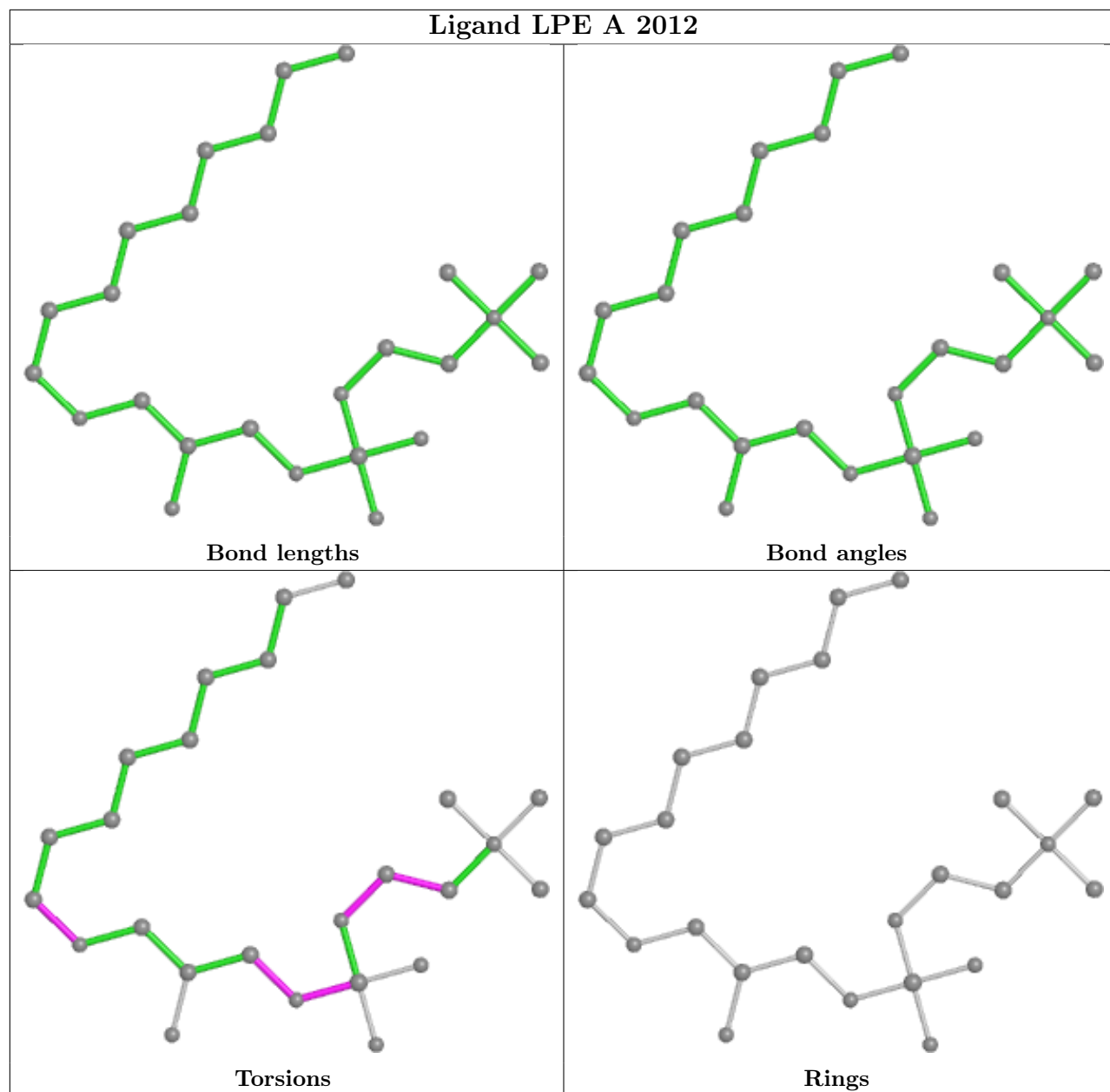


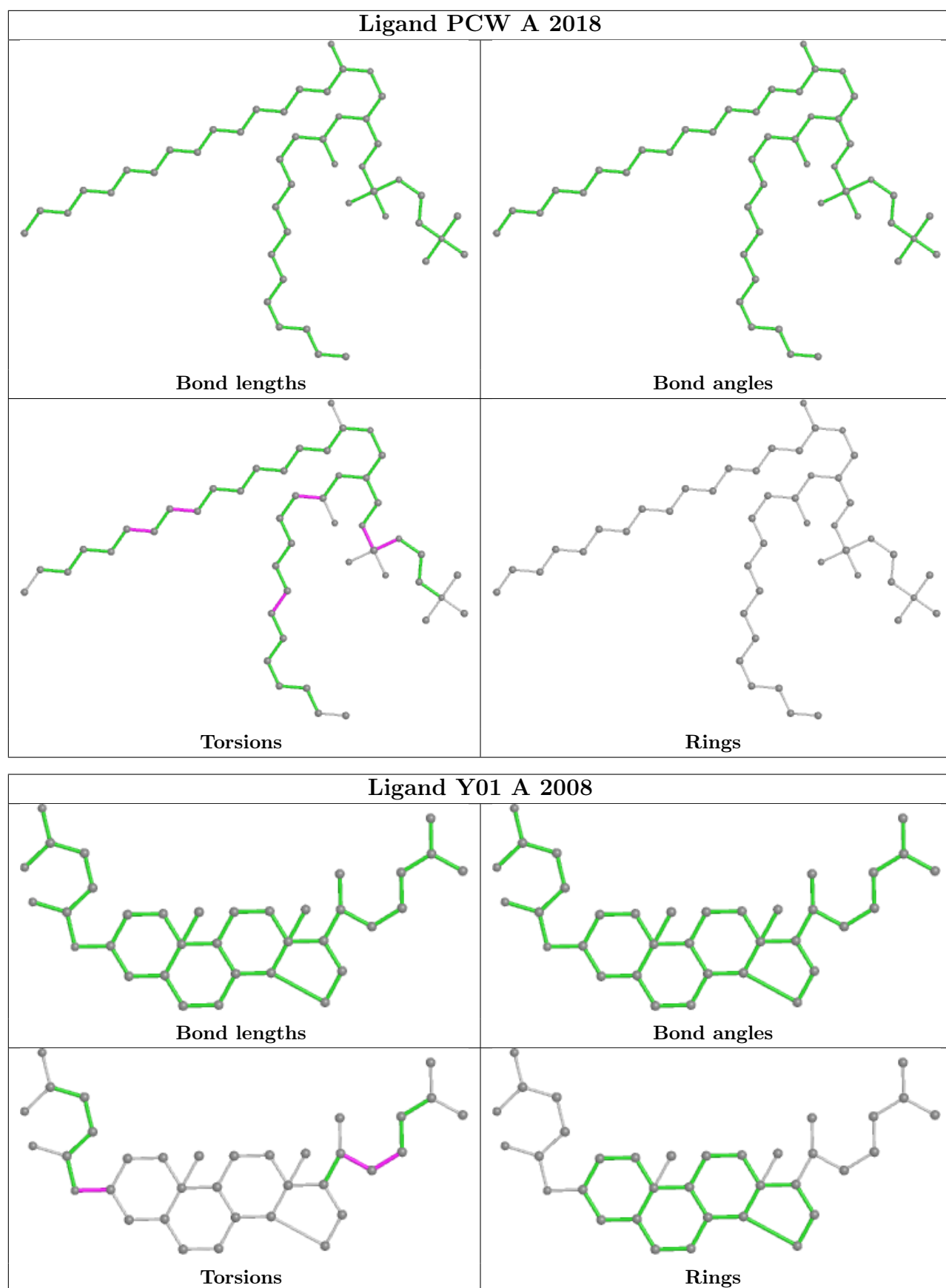


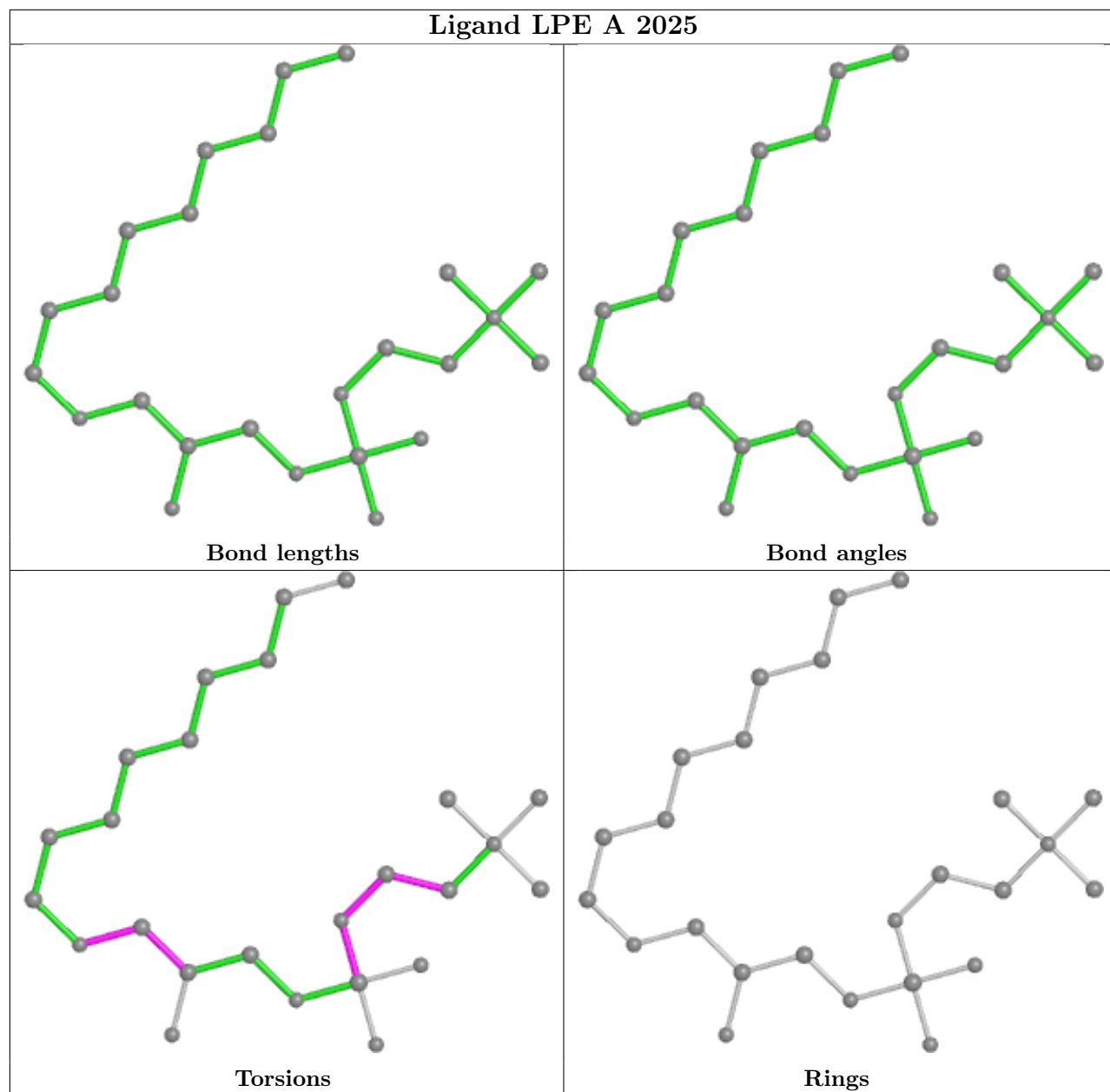


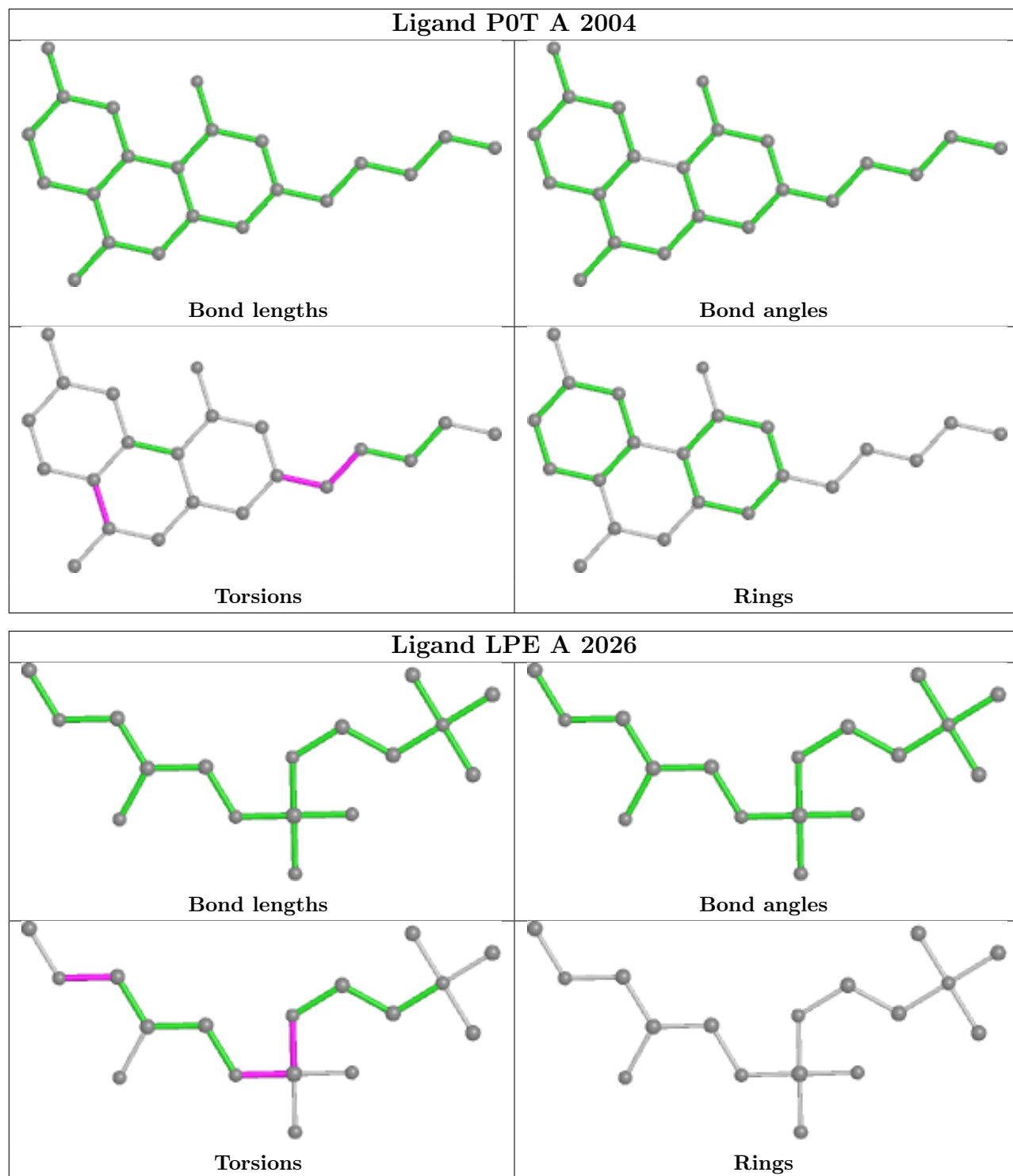












5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

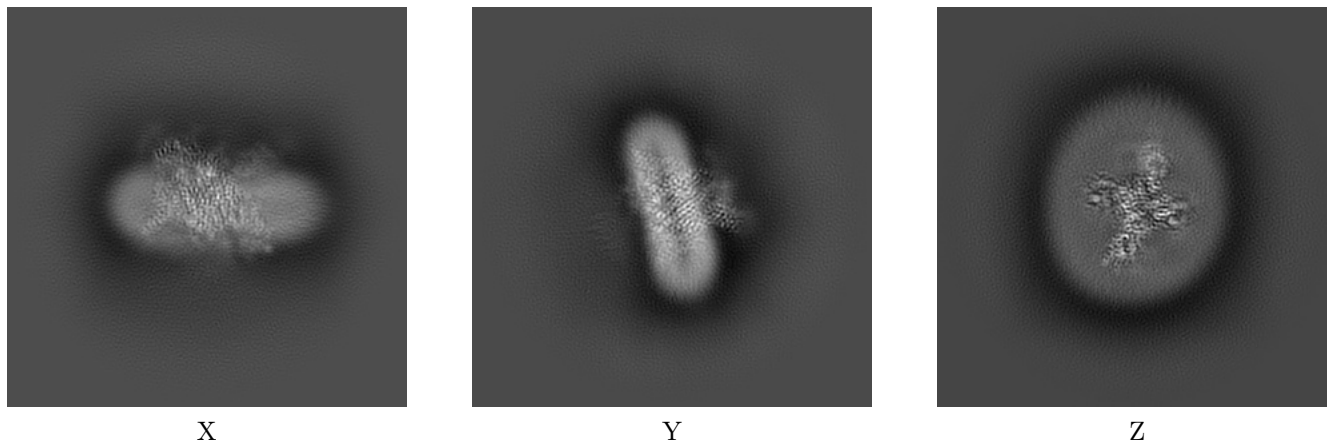
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29665. These allow visual inspection of the internal detail of the map and identification of artifacts.

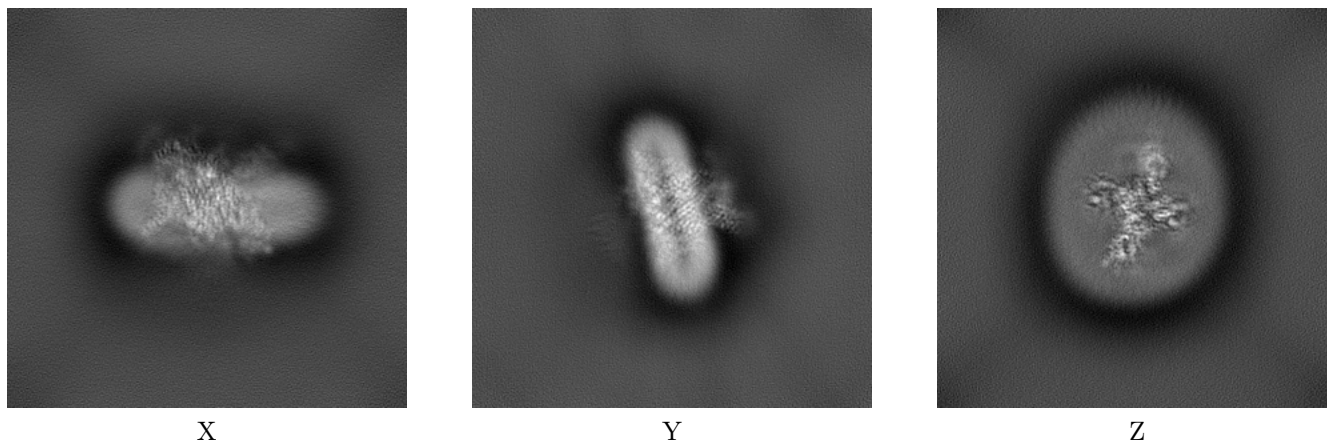
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



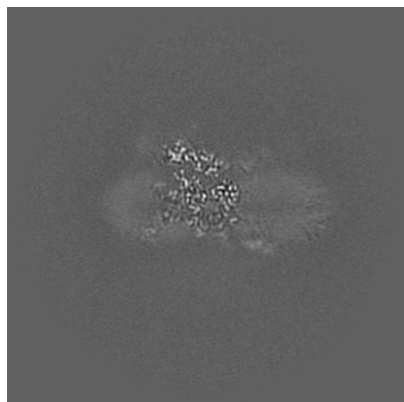
6.1.2 Raw map



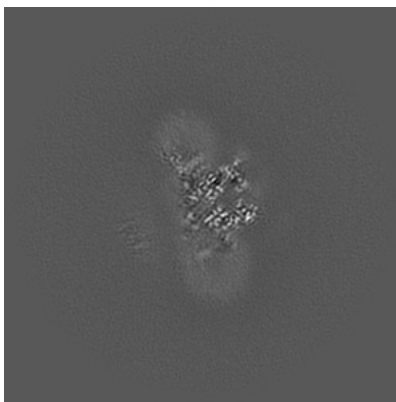
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

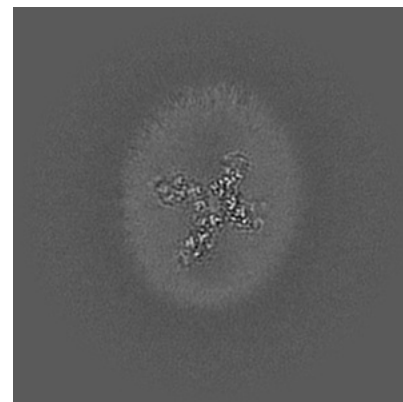
6.2.1 Primary map



X Index: 160

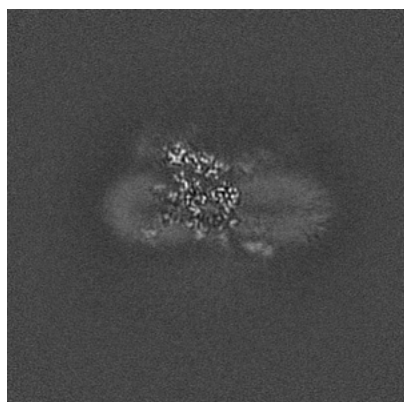


Y Index: 160

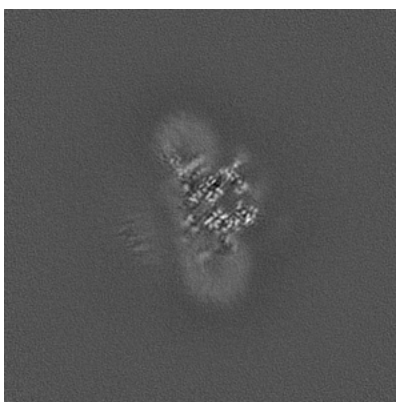


Z Index: 160

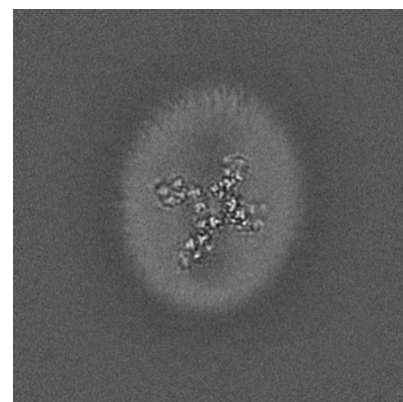
6.2.2 Raw map



X Index: 160



Y Index: 160

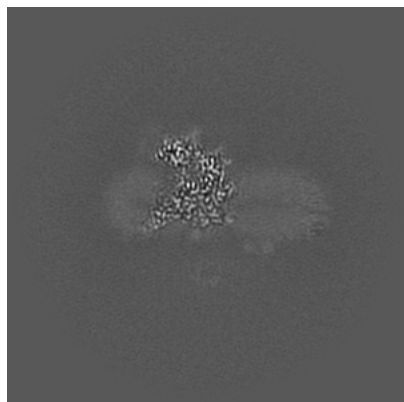


Z Index: 160

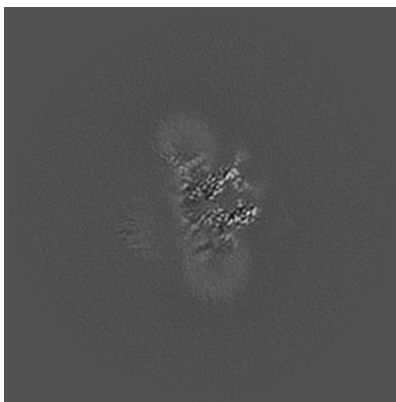
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

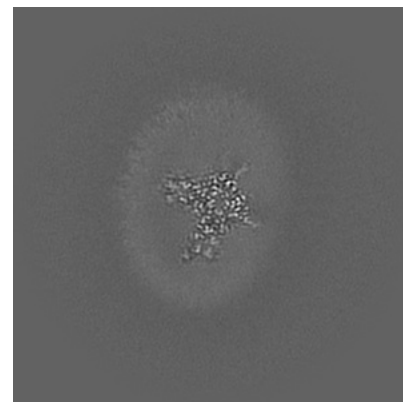
6.3.1 Primary map



X Index: 152

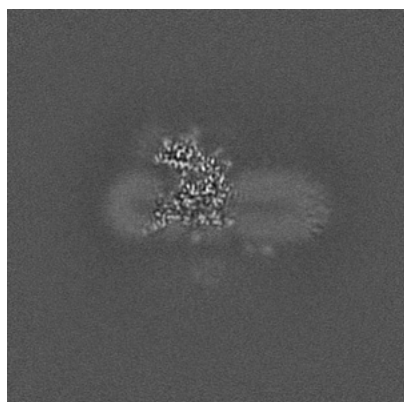


Y Index: 161

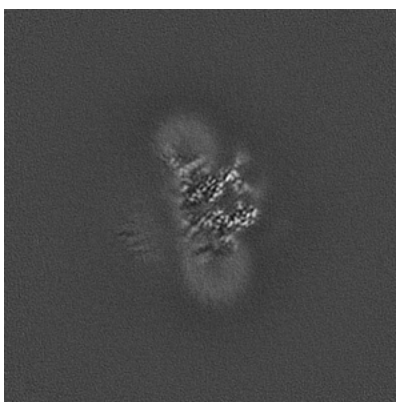


Z Index: 171

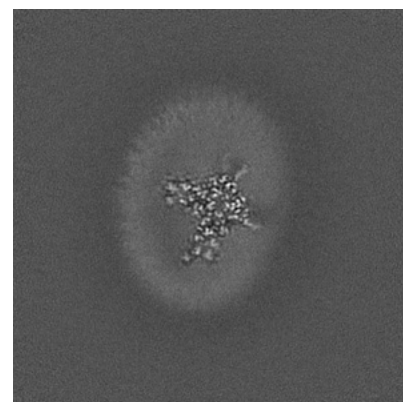
6.3.2 Raw map



X Index: 153



Y Index: 161

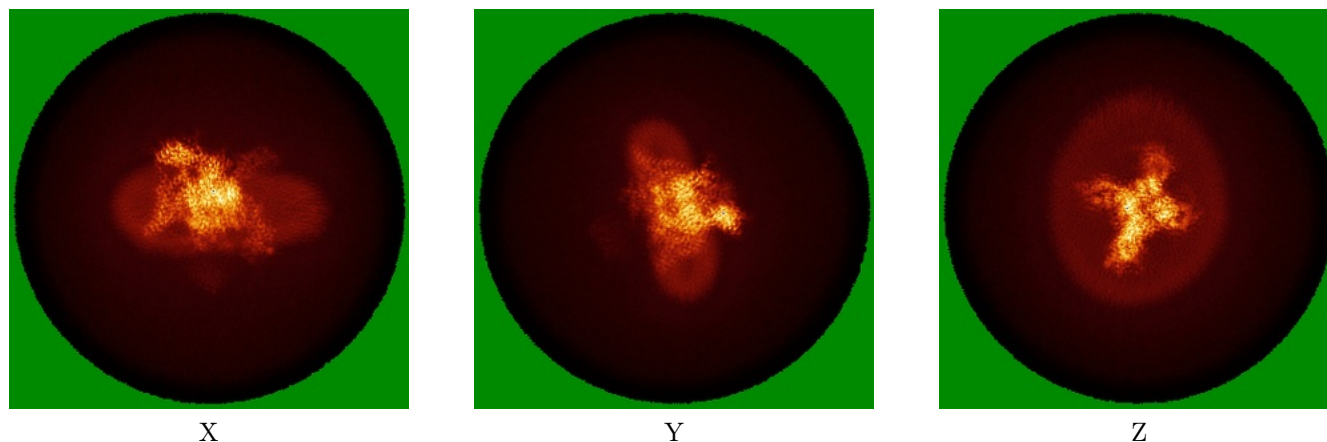


Z Index: 171

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

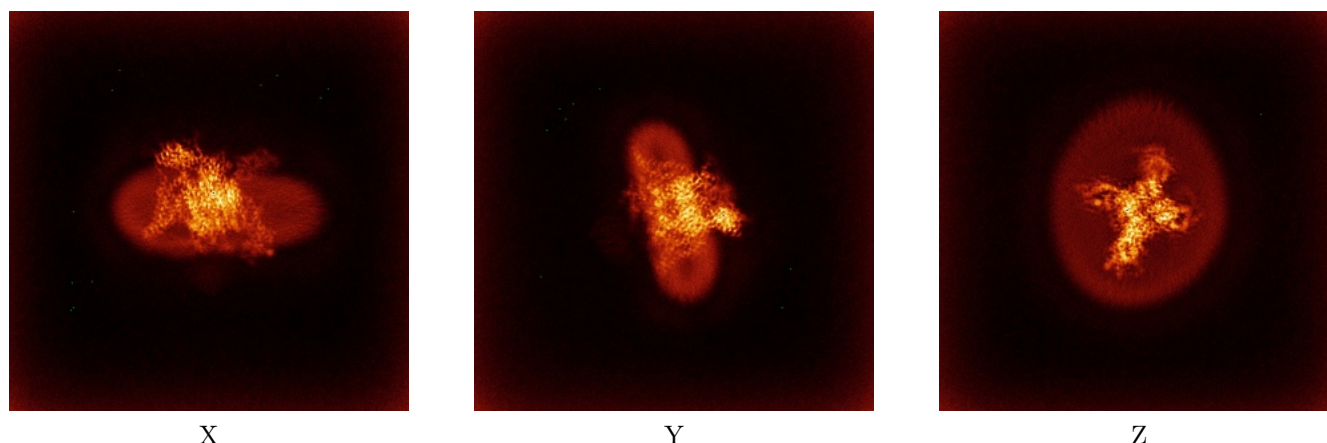


X

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.

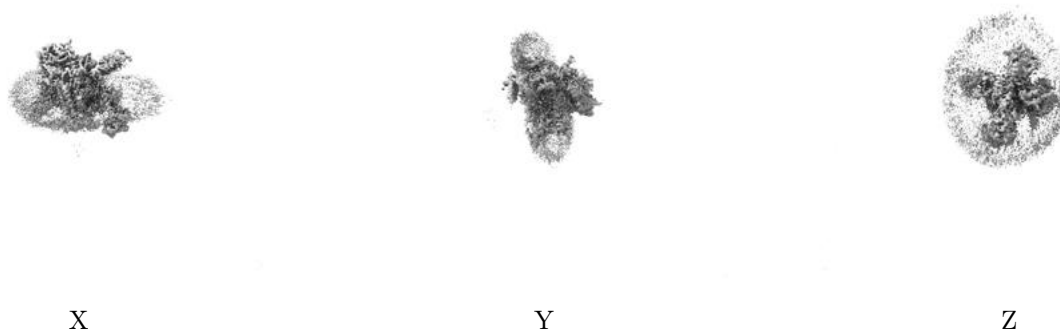
6.5 Orthogonal surface views [i](#)

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.

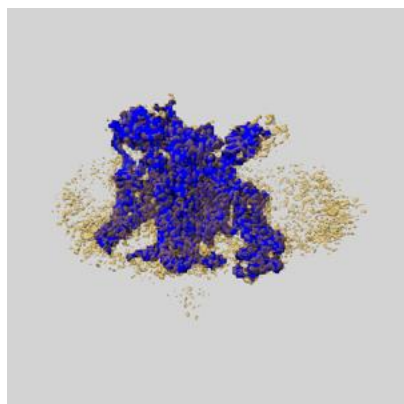
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

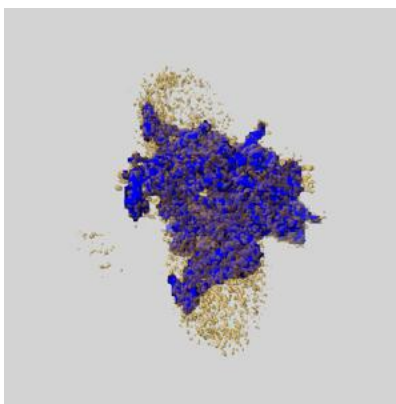
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

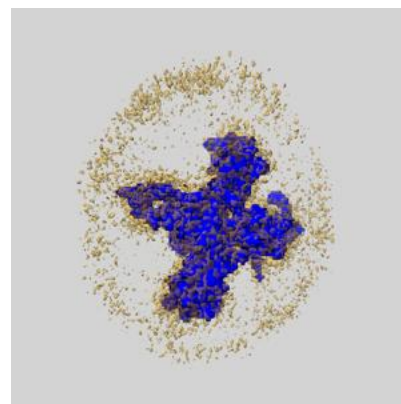
6.6.1 emd_29665_msk_1.map [i](#)



X



Y

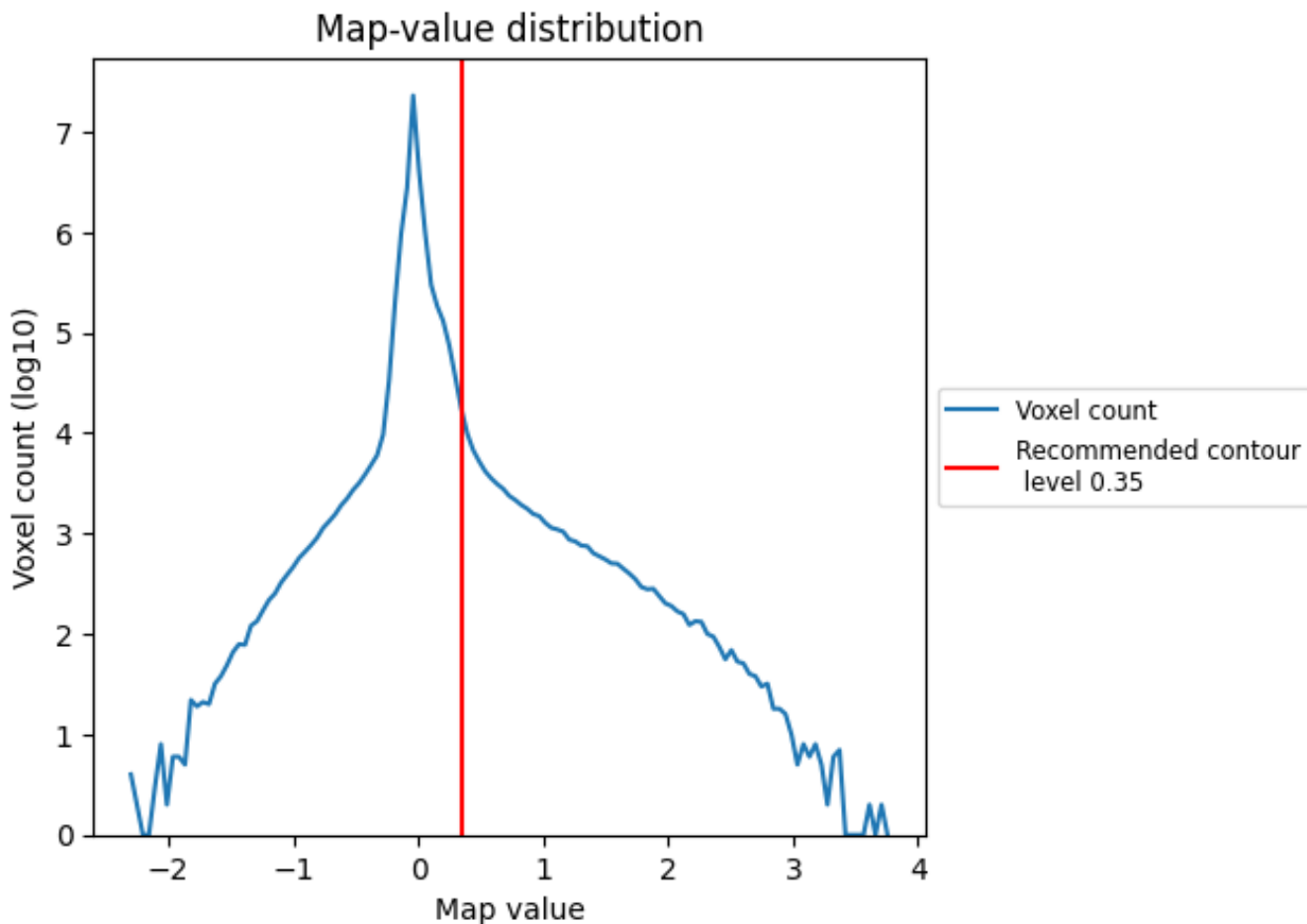


Z

7 Map analysis [i](#)

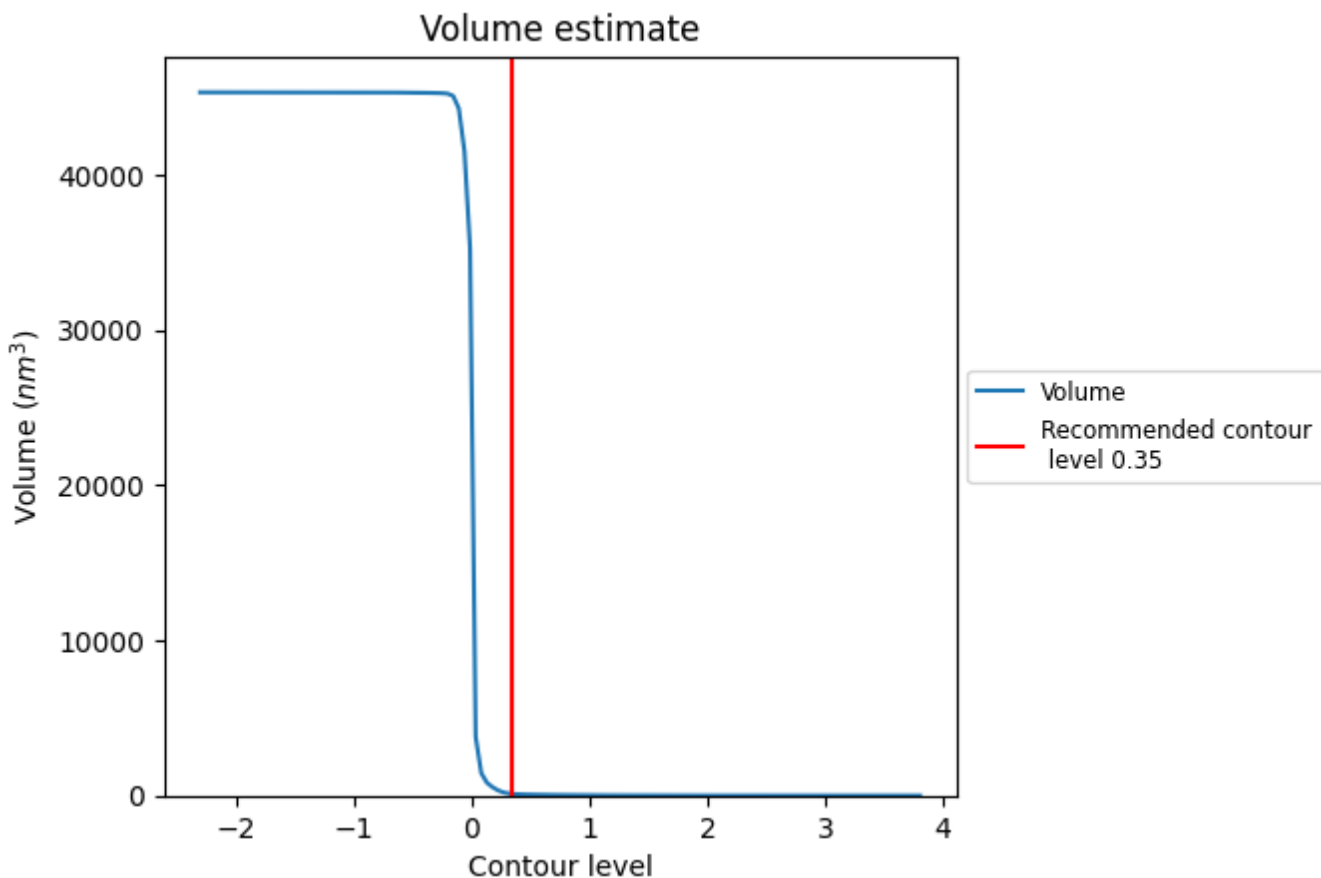
This section contains the results of statistical analysis of the map.

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.

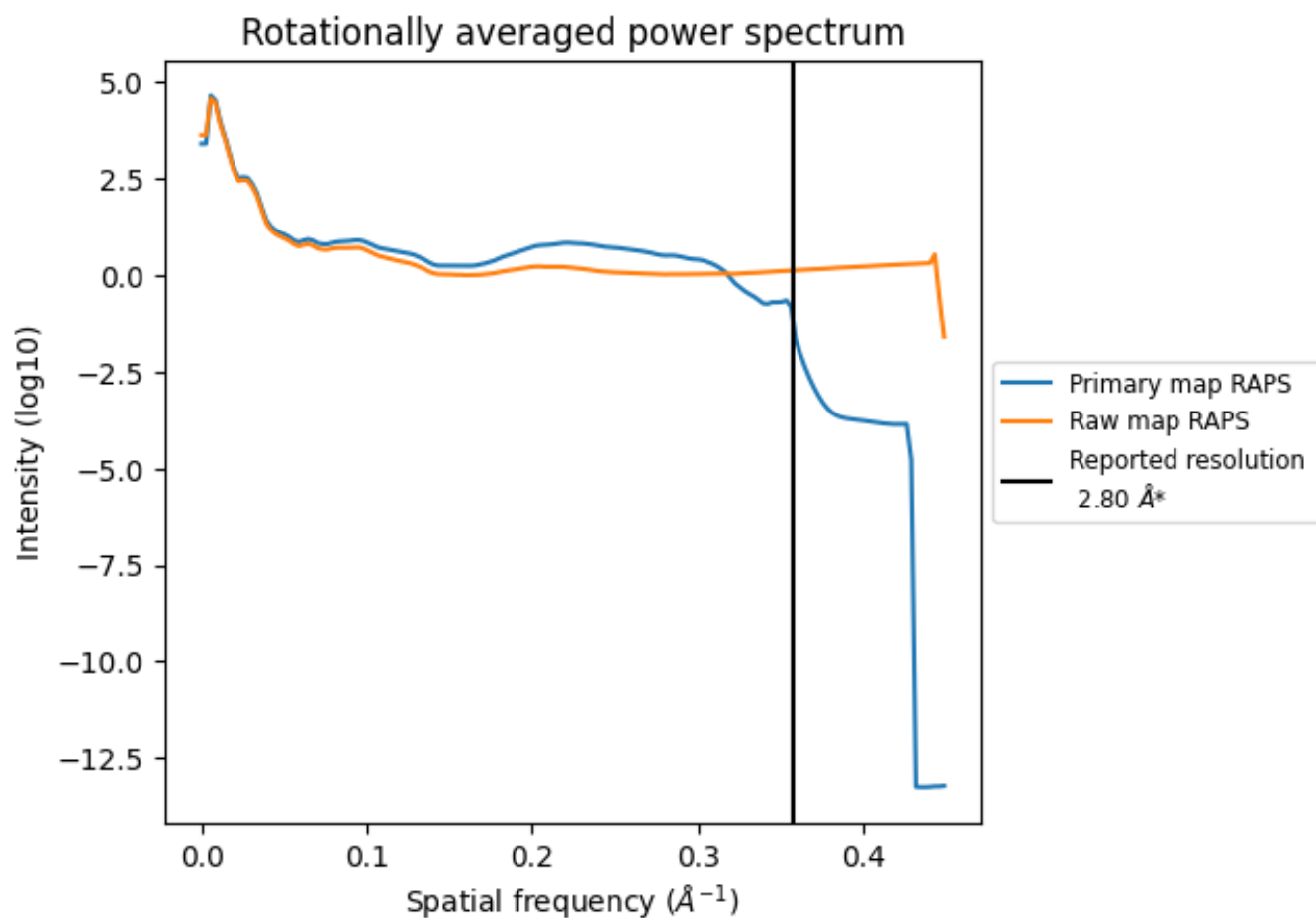
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 108 nm^3 ; this corresponds to an approximate mass of 97 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 [i](#)

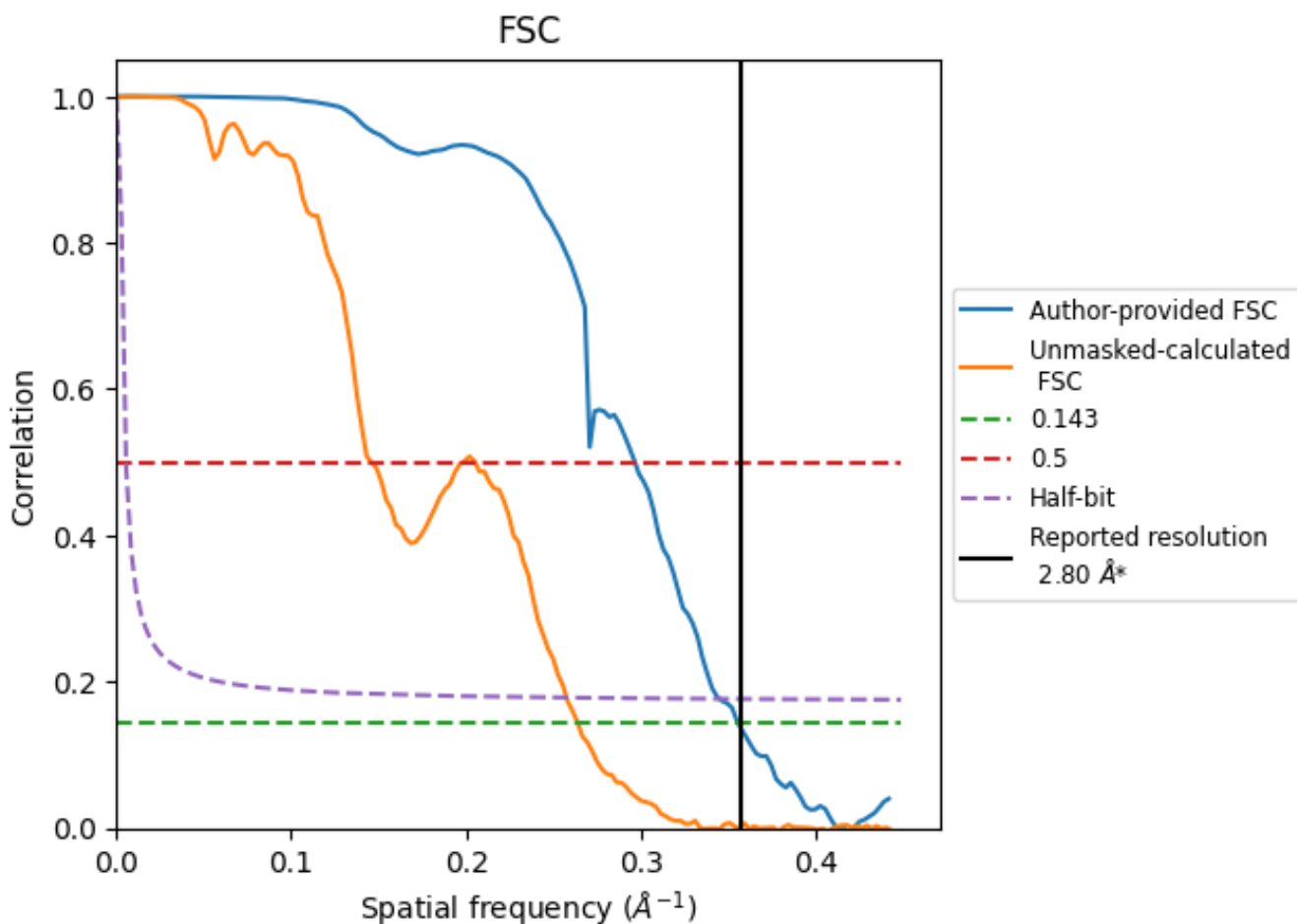


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

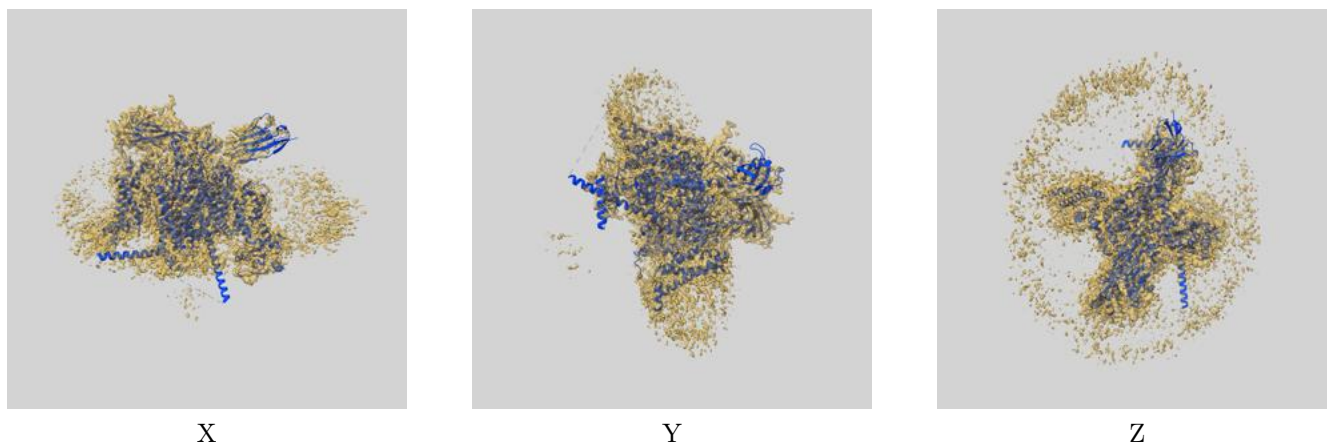
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.81	3.37	2.90
Unmasked-calculated*	3.79	6.86	3.89

*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 3.79 differs from the reported value 2.8 by more than 10 %

9 Map-model fit [i](#)

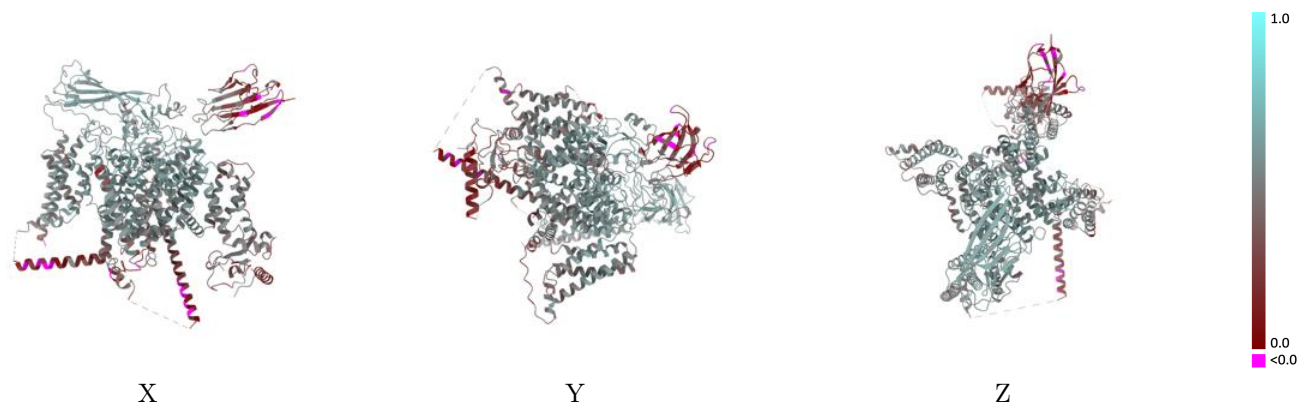
This section contains information regarding the fit between EMDB map EMD-29665 and PDB model 8G1A. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



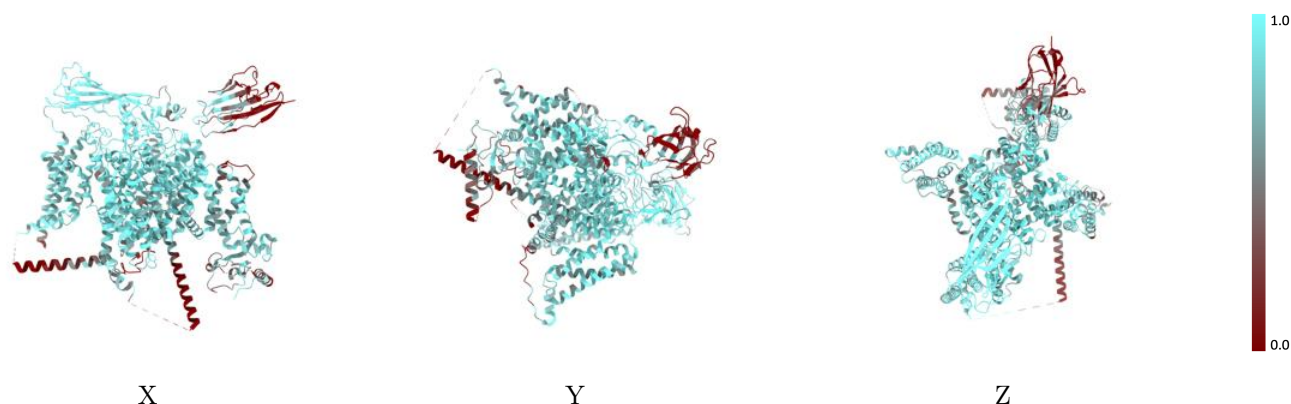
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



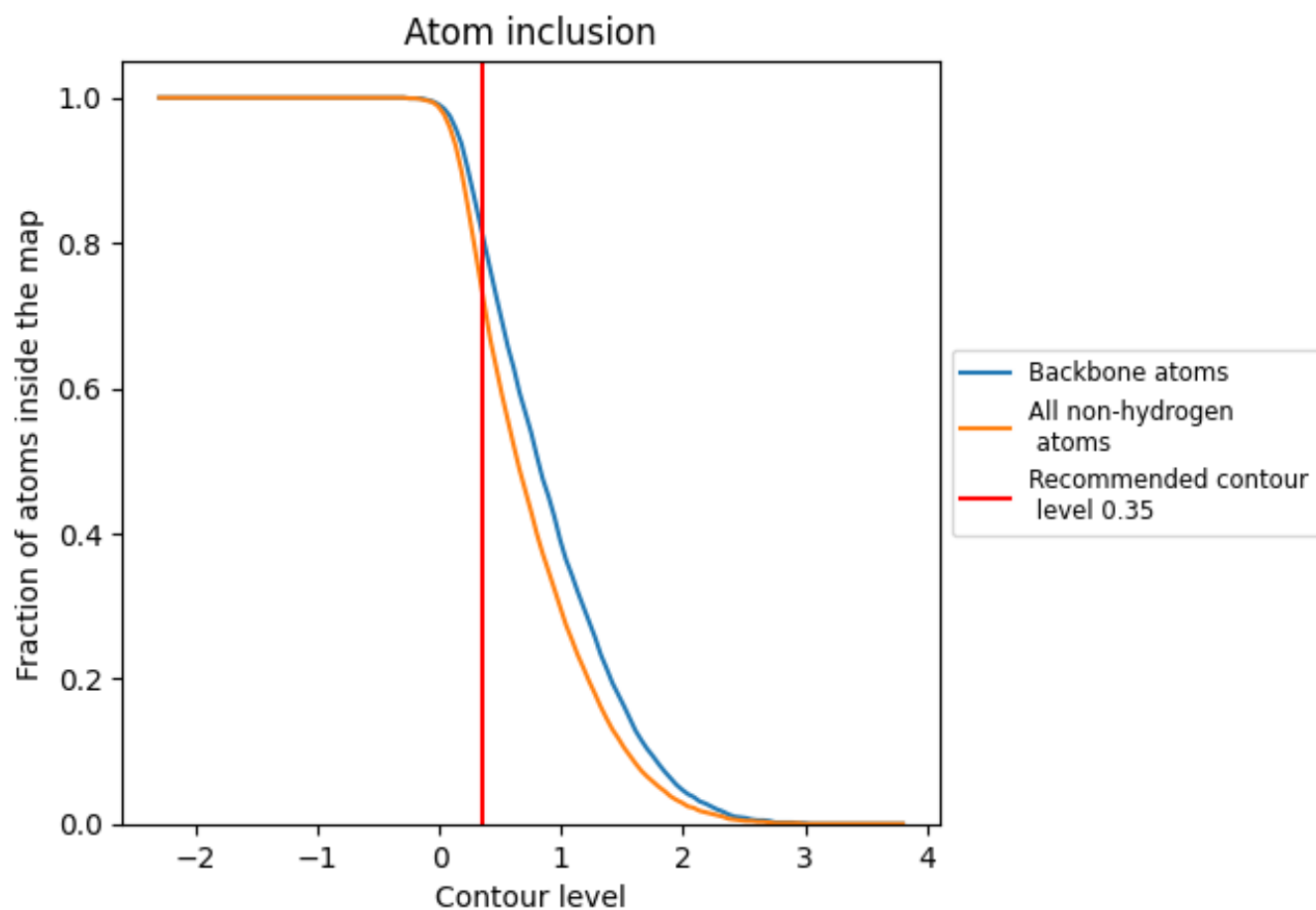
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 81% of all backbone atoms, 73% 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	 0.7320	 0.4720
A	 0.7510	 0.4800
B	 0.8460	 0.5310
C	 0.3380	 0.2860
D	 0.7500	 0.4610
E	 0.8930	 0.5110

