



Full wwPDB EM Validation Report ⓘ

Nov 10, 2024 – 01:48 PM EST

PDB ID : 9CUI
EMDB ID : EMD-45934
Title : Structure of human full-length ancestral TRPV6 channel in Calmodulin-bound state
Authors : Neuberger, A.; Nadezhdin, K.D.; Sobolevsky, A.I.
Deposited on : 2024-07-26
Resolution : 3.42 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.dev113
Mogul : 2022.3.0, CSD as543be (2022)
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

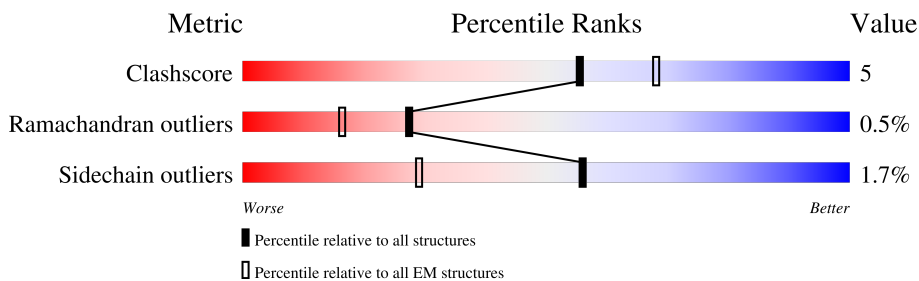
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.42 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 ≥ 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	765	
1	B	765	
1	C	765	
1	D	765	
2	E	149	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 22713 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 Transient receptor potential cation channel subfamily V member 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	612	4916	3176	834	868	38	0	0
1	B	620	4991	3220	854	879	38	0	0
1	C	653	5286	3400	922	926	38	0	0
1	D	617	4972	3213	847	874	38	0	0

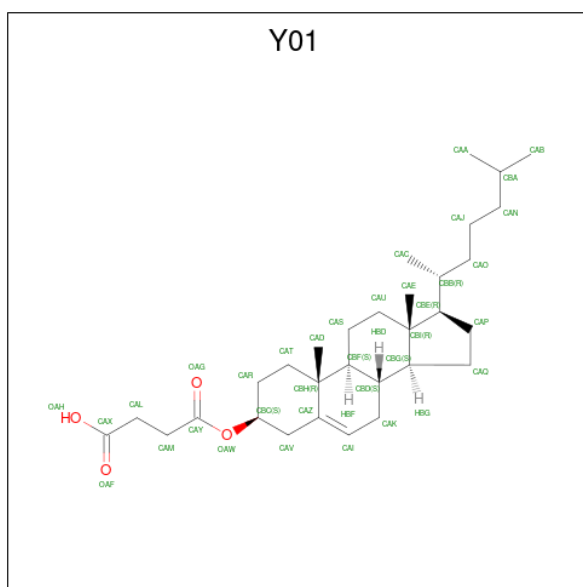
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	157	ARG	CYS	variant	UNP Q9H1D0
A	378	VAL	MET	variant	UNP Q9H1D0
A	681	THR	MET	variant	UNP Q9H1D0
B	157	ARG	CYS	variant	UNP Q9H1D0
B	378	VAL	MET	variant	UNP Q9H1D0
B	681	THR	MET	variant	UNP Q9H1D0
C	157	ARG	CYS	variant	UNP Q9H1D0
C	378	VAL	MET	variant	UNP Q9H1D0
C	681	THR	MET	variant	UNP Q9H1D0
D	157	ARG	CYS	variant	UNP Q9H1D0
D	378	VAL	MET	variant	UNP Q9H1D0
D	681	THR	MET	variant	UNP Q9H1D0

- Molecule 2 is a protein called Calmodulin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	148	1165	714	188	254	9	0	0

- Molecule 3 is CHOLESTEROL HEMISUCCINATE (three-letter code: Y01) (formula: C₃₁H₅₀O₄).



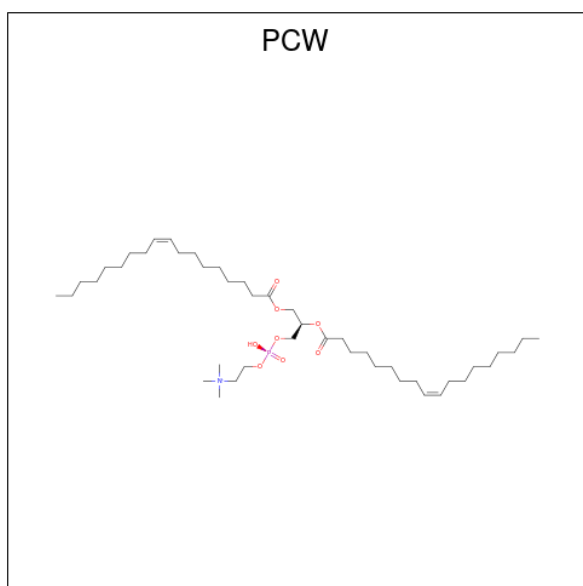
Mol	Chain	Residues	Atoms			AltConf
3	A	1	Total	C	O	0
			35	31	4	
3	A	1	Total	C	O	0
			35	31	4	
3	B	1	Total	C	O	0
			35	31	4	
3	B	1	Total	C	O	0
			35	31	4	
3	B	1	Total	C	O	0
			35	31	4	
3	C	1	Total	C	O	0
			35	31	4	
3	C	1	Total	C	O	0
			35	31	4	
3	D	1	Total	C	O	0
			35	31	4	

- Molecule 4 is CHOLESTEROL (three-letter code: CLR) (formula: C₂₇H₄₆O).



Mol	Chain	Residues	Atoms			AltConf
4	A	1	Total	C	O	0
			28	27	1	
4	B	1	Total	C	O	0
			28	27	1	
4	C	1	Total	C	O	0
			28	27	1	
4	D	1	Total	C	O	0
			28	27	1	

- Molecule 5 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PCW) (formula: $C_{44}H_{85}NO_8P$).



Mol	Chain	Residues	Atoms					AltConf
5	A	1	Total	C	N	O	P	0
			51	41	1	8	1	
5	A	1	Total	C				0
			16	16				
5	A	1	Total	C				0
			16	16				
5	A	1	Total	C				0
			11	11				
5	A	1	Total	C				0
			8	8				
5	A	1	Total	C				0
			8	8				
5	A	1	Total	C				0
			16	16				
5	A	1	Total	C				0
			13	13				
5	A	1	Total	C	N	O	P	0
			43	33	1	8	1	
5	A	1	Total	C	N	O	P	0
			51	41	1	8	1	
5	A	1	Total	C				0
			8	8				
5	A	1	Total	C				0
			15	15				
5	B	1	Total	C				0
			15	15				
5	B	1	Total	C	N	O	P	0
			51	41	1	8	1	
5	B	1	Total	C				0
			16	16				
5	B	1	Total	C				0
			11	11				
5	B	1	Total	C				0
			8	8				
5	B	1	Total	C				0
			16	16				
5	B	1	Total	C				0
			13	13				
5	B	1	Total	C	N	O	P	0
			43	33	1	8	1	
5	B	1	Total	C	N	O	P	0
			51	41	1	8	1	
5	C	1	Total	C				0
			15	15				

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Mol	Chain	Residues	Atoms	AltConf
5	C	1	Total C 16 16	0
5	C	1	Total C N O P 51 41 1 8 1	0
5	C	1	Total C 16 16	0
5	C	1	Total C 11 11	0
5	C	1	Total C 8 8	0
5	C	1	Total C 16 16	0
5	C	1	Total C 13 13	0
5	C	1	Total C N O P 43 33 1 8 1	0
5	C	1	Total C N O P 51 41 1 8 1	0
5	D	1	Total C 13 13	0
5	D	1	Total C N O P 43 33 1 8 1	0
5	D	1	Total C N O P 51 41 1 8 1	0
5	D	1	Total C 15 15	0
5	D	1	Total C 16 16	0
5	D	1	Total C N O P 51 41 1 8 1	0
5	D	1	Total C 16 16	0
5	D	1	Total C 16 16	0
5	D	1	Total C 11 11	0
5	D	1	Total C 8 8	0
5	D	1	Total C 8 8	0
5	D	1	Total C 16 16	0

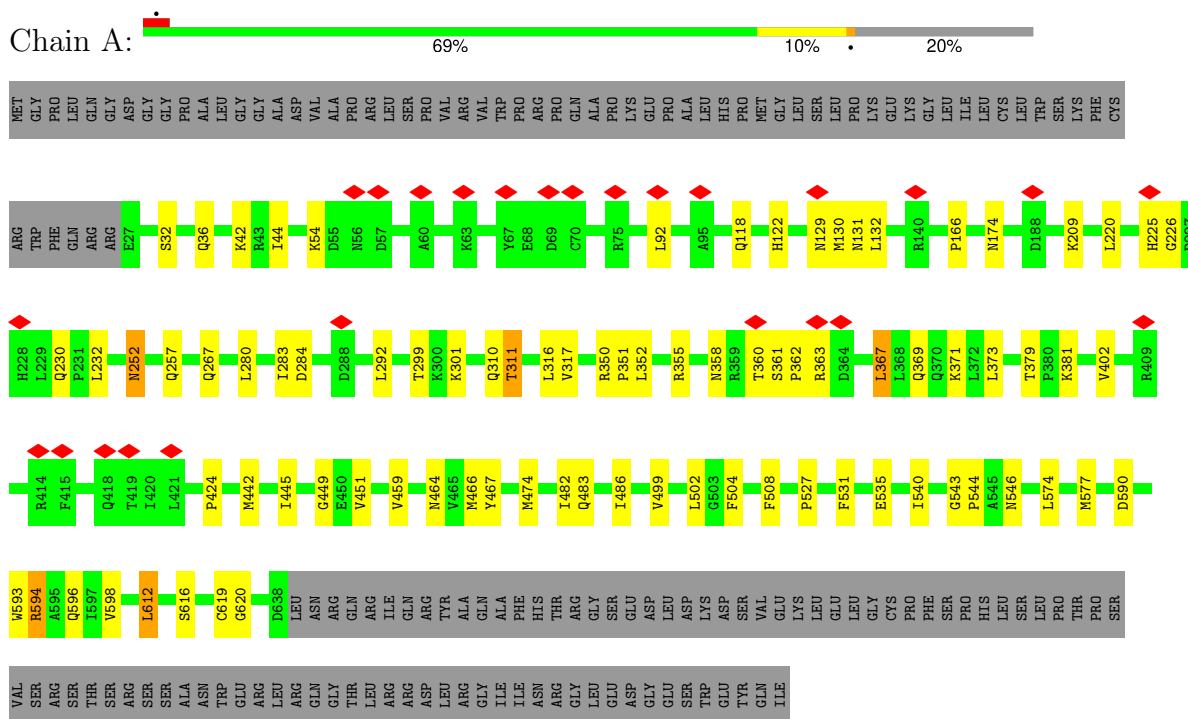
- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
6	A	2	Total 2	Ca 2	0
6	B	1	Total 1	Ca 1	0
6	E	4	Total 4	Ca 4	0

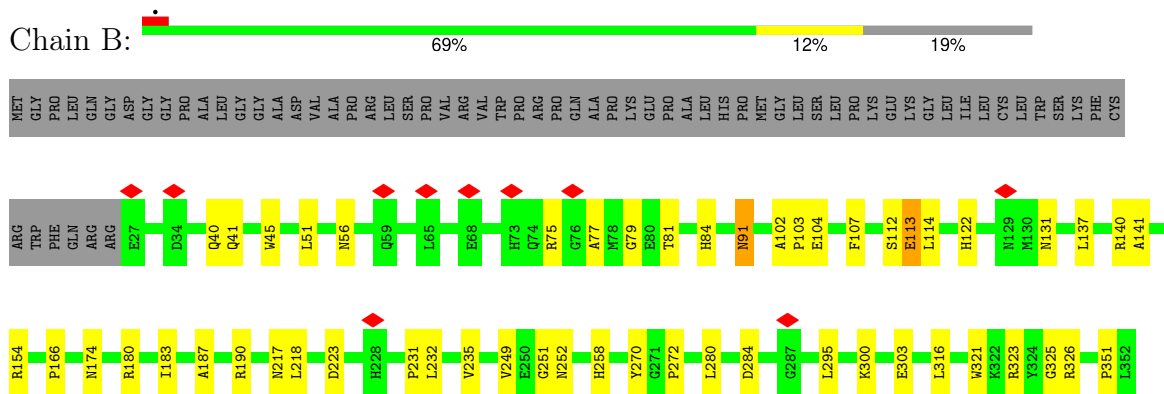
3 Residue-property plots

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: Transient receptor potential cation channel subfamily V member 6

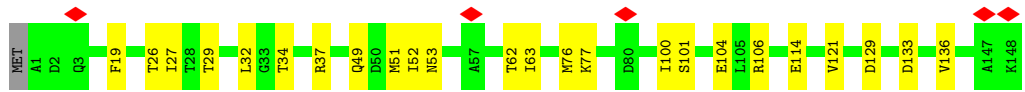


- Molecule 1: Transient receptor potential cation channel subfamily V member 6



• Molecule 2: Calmodulin-1

Chain E:  83% 16%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	232058	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	55	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.351	Depositor
Minimum map value	-2.180	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.103	Depositor
Recommended contour level	0.326	Depositor
Map size (\AA)	273.152, 273.152, 273.152	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.067, 1.067, 1.067	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: CLR, Y01, CA, PCW

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	0.30	0/5029	0.56	2/6824 (0.0%)
1	B	0.30	0/5104	0.59	1/6923 (0.0%)
1	C	0.31	0/5406	0.58	1/7326 (0.0%)
1	D	0.30	0/5088	0.57	2/6903 (0.0%)
2	E	0.26	0/1177	0.52	0/1580
All	All	0.30	0/21804	0.57	6/29556 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	5
1	C	0	1
1	D	0	4
All	All	0	11

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	367	LEU	CA-CB-CG	7.48	132.51	115.30
1	A	612	LEU	CA-CB-CG	6.19	129.54	115.30
1	D	367	LEU	CB-CG-CD1	5.49	120.33	111.00
1	A	367	LEU	CA-CB-CG	5.47	127.87	115.30
1	C	367	LEU	CA-CB-CG	5.19	127.24	115.30
1	D	612	LEU	CA-CB-CG	5.10	127.03	115.30

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	230	GLN	Peptide
1	B	102	ALA	Peptide
1	B	113	GLU	Peptide
1	B	223	ASP	Peptide
1	B	231	PRO	Peptide
1	B	361	SER	Peptide
1	C	357	ASN	Peptide
1	D	230	GLN	Peptide
1	D	361	SER	Peptide
1	D	565	ILE	Peptide
1	D	612	LEU	Peptide

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	4916	0	4972	47	0
1	B	4991	0	5055	54	0
1	C	5286	0	5342	55	0
1	D	4972	0	5025	40	0
2	E	1165	0	1096	13	0
3	A	70	0	98	6	0
3	B	105	0	147	10	0
3	C	70	0	98	3	0
3	D	35	0	49	3	0
4	A	28	0	46	5	0
4	B	28	0	46	5	0
4	C	28	0	46	5	0
4	D	28	0	46	4	0
5	A	256	0	380	8	0
5	B	224	0	330	8	0
5	C	240	0	356	7	0
5	D	264	0	394	7	0
6	A	2	0	0	0	0
6	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	E	4	0	0	0	0
All	All	22713	0	23526	220	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 5.

All (220) 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:B:426:HIS:CE1	3:B:803:Y01:HAL1	2.29	0.67
1:A:351:PRO:HB2	1:A:373:LEU:HB2	1.81	0.63
2:E:101:SER:H	2:E:104:GLU:HB2	1.65	0.62
1:A:531:PHE:HB2	3:B:801:Y01:HAS1	1.81	0.62
1:D:130:MET:HB3	1:D:132:LEU:H	1.65	0.61
2:E:29:THR:HG22	2:E:52:ILE:HG13	1.84	0.60
1:B:443:ARG:HD2	5:B:810:PCW:H212	1.84	0.60
1:B:81:THR:H	1:B:84:HIS:HD2	1.48	0.59
1:B:280:LEU:HD11	1:B:316:LEU:HD22	1.84	0.59
1:B:367:LEU:HG	1:C:549:VAL:HG11	1.84	0.59
1:D:382:ASP:OD1	1:D:385:ARG:NH2	2.36	0.59
1:B:180:ARG:HE	1:B:218:LEU:HD11	1.68	0.58
1:D:353:LYS:HB3	1:D:373:LEU:HD12	1.87	0.57
1:A:474:MET:O	1:B:492:ARG:NH2	2.37	0.57
1:C:565:ILE:HA	1:C:569:LEU:HB3	1.87	0.56
1:A:32:SER:O	1:A:36:GLN:NE2	2.38	0.56
1:C:245:LYS:HG2	1:C:292:LEU:HD12	1.87	0.56
1:C:402:VAL:HG23	1:C:403:GLU:HG3	1.86	0.56
1:A:467:TYR:CE2	3:A:801:Y01:HAR2	2.40	0.56
1:D:81:THR:HG23	1:D:83:LEU:H	1.70	0.56
1:C:489:ASP:OD1	1:C:492:ARG:NH2	2.38	0.56
1:B:367:LEU:HD22	1:C:516:ASP:HB3	1.88	0.56
1:C:486:ILE:HG13	4:C:804:CLR:C19	2.36	0.56
1:C:210:THR:O	1:C:214:GLN:NE2	2.39	0.55
1:A:350:ARG:HH22	1:A:451:VAL:HG12	1.71	0.55
2:E:49:GLN:NE2	2:E:53:ASN:OD1	2.39	0.55
1:A:574:LEU:HA	1:A:577:MET:HG2	1.89	0.54
4:C:804:CLR:H181	1:D:565:ILE:HD11	1.89	0.54
1:C:389:GLU:HB3	5:C:810:PCW:H231	1.89	0.54
1:C:697:ARG:NH1	2:E:114:GLU:OE1	2.40	0.54
1:B:251:GLY:HA3	1:B:303:GLU:HG3	1.89	0.54
1:C:267:GLN:HE21	1:C:277:LEU:HD22	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:317:VAL:HG11	1:C:598:VAL:HG22	1.89	0.54
1:B:520:LEU:HD21	1:B:544:PRO:HB3	1.90	0.54
1:C:119:THR:HG23	1:C:121:LEU:H	1.73	0.54
2:E:100:ILE:HG22	2:E:136:VAL:HB	1.90	0.54
1:B:556:SER:CB	3:B:801:Y01:HBC	2.37	0.53
1:C:466:MET:SD	4:C:804:CLR:H6	2.48	0.53
1:D:209:LYS:HE3	1:D:252:ASN:HD22	1.74	0.53
1:A:527:PRO:HB3	3:B:801:Y01:HAD1	1.90	0.53
1:B:367:LEU:HD13	1:C:516:ASP:H	1.74	0.53
1:B:553:PHE:HD1	3:B:801:Y01:HAM1	1.74	0.52
1:C:405:PRO:HA	1:C:408:PHE:HB2	1.91	0.52
1:A:257:GLN:NE2	1:A:310:GLN:OE1	2.43	0.52
1:B:379:THR:HG22	1:B:381:LYS:H	1.74	0.52
1:B:632:ARG:NH1	1:C:34:ASP:OD1	2.40	0.52
1:A:535:GLU:HG2	1:A:540:ILE:HD11	1.91	0.52
1:B:45:TRP:HA	1:B:51:LEU:HD12	1.91	0.52
1:D:402:VAL:HG23	1:D:403:GLU:HG2	1.91	0.52
1:D:564:ILE:HG23	1:D:568:LEU:HD23	1.92	0.52
1:A:619:CYS:SG	1:A:620:GLY:N	2.82	0.52
1:C:40:GLN:NE2	1:C:80:GLU:OE2	2.43	0.52
1:D:33:ARG:HG2	1:D:114:LEU:HD21	1.92	0.51
1:B:190:ARG:HG2	1:B:232:LEU:HD11	1.91	0.51
1:B:486:ILE:CD1	4:B:804:CLR:H191	2.41	0.51
1:C:619:CYS:SG	1:C:620:GLY:N	2.84	0.51
1:A:352:LEU:HD11	1:B:514:THR:HB	1.92	0.51
1:A:44:ILE:HG21	1:A:54:LYS:HD2	1.94	0.50
1:B:183:ILE:HD13	1:B:187:ALA:HB3	1.93	0.50
1:C:137:LEU:HD23	1:C:141:ALA:HB3	1.92	0.50
1:A:482:ILE:HG23	1:B:569:LEU:HD21	1.93	0.50
1:D:92:LEU:HD11	1:D:131:ASN:HB2	1.92	0.50
1:A:449:GLY:HA3	5:A:806:PCW:H142	1.94	0.50
1:B:508:PHE:HE1	1:B:558:THR:HG23	1.76	0.49
1:A:42:LYS:HD2	1:D:623:TYR:HA	1.94	0.49
1:C:102:ALA:HB3	1:C:105:LEU:HD22	1.94	0.49
1:D:411:GLY:HA3	1:D:415:PHE:HB3	1.94	0.49
1:D:488:GLY:O	1:D:492:ARG:NE	2.44	0.49
1:A:424:PRO:HD2	4:A:802:CLR:H21	1.94	0.49
1:B:112:SER:OG	1:B:113:GLU:N	2.45	0.49
1:B:623:TYR:HA	1:C:42:LYS:HD3	1.94	0.49
1:C:373:LEU:HD13	1:C:376:ALA:HB3	1.93	0.49
1:B:137:LEU:HD23	1:B:141:ALA:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:470:ARG:NH1	1:C:596:GLN:OE1	2.45	0.49
5:B:806:PCW:H262	5:B:806:PCW:H231	1.65	0.49
1:B:351:PRO:HB2	1:B:373:LEU:HD12	1.95	0.48
1:A:361:SER:O	1:A:363:ARG:N	2.47	0.48
1:A:593:TRP:HD1	1:A:596:GLN:HE21	1.62	0.48
1:B:370:GLN:O	1:C:514:THR:OG1	2.31	0.48
1:B:486:ILE:HD13	4:B:804:CLR:H191	1.94	0.48
1:D:129:ASN:HA	1:D:178:ILE:HD11	1.95	0.48
1:D:418:GLN:O	1:D:422:GLY:N	2.46	0.48
1:B:56:ASN:OD1	1:B:91:ASN:ND2	2.47	0.48
1:A:504:PHE:O	1:A:508:PHE:N	2.45	0.48
1:C:236:PRO:HB2	1:C:240:GLY:HA2	1.94	0.48
1:D:228:HIS:HB3	1:D:231:PRO:HG3	1.95	0.48
1:D:424:PRO:HD2	4:D:807:CLR:H21	1.94	0.48
1:C:353:LYS:O	1:C:371:LYS:N	2.39	0.47
1:C:621:ARG:NE	1:C:627:ASP:OD1	2.47	0.47
5:A:812:PCW:H72	5:A:812:PCW:H12	1.97	0.47
1:C:266:THR:HA	1:C:276:THR:HA	1.97	0.47
1:D:572:ASN:HD22	1:D:575:ILE:HD12	1.80	0.47
1:A:92:LEU:HD21	1:A:131:ASN:HB2	1.95	0.47
1:A:317:VAL:HG11	1:A:598:VAL:HG22	1.97	0.47
1:C:244:PHE:HA	1:C:259:LEU:HD13	1.97	0.47
1:C:467:TYR:CE2	3:C:803:Y01:HAR2	2.50	0.47
5:C:806:PCW:H341	5:C:806:PCW:H371	1.70	0.47
4:A:802:CLR:H222	4:A:802:CLR:H162	1.68	0.47
1:D:402:VAL:HG21	3:D:806:Y01:HAK1	1.97	0.47
1:B:284:ASP:OD2	1:B:616:SER:OG	2.33	0.47
1:A:267:GLN:HE21	1:B:41:GLN:HG3	1.80	0.46
1:B:232:LEU:HA	1:B:235:VAL:HG12	1.96	0.46
1:A:118:GLN:NE2	1:D:270:TYR:OH	2.47	0.46
1:B:323:ARG:HH12	1:C:31:GLN:HE21	1.63	0.46
1:B:467:TYR:CE1	3:B:803:Y01:HAM2	2.49	0.46
1:C:466:MET:HG3	1:D:499:VAL:HG11	1.97	0.46
2:E:129:ASP:OD2	2:E:133:ASP:N	2.48	0.46
1:A:486:ILE:HG13	4:A:802:CLR:H191	1.98	0.46
1:B:356:THR:H	1:B:371:LYS:HE2	1.80	0.46
3:B:805:Y01:HAO1	3:B:805:Y01:HAP1	1.54	0.46
5:B:808:PCW:H141	5:C:802:PCW:H132	1.98	0.46
1:C:150:THR:HB	1:C:157:ARG:HH12	1.80	0.46
1:D:621:ARG:NH1	1:D:627:ASP:OD1	2.49	0.46
4:B:804:CLR:H211	4:B:804:CLR:H232	1.72	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:302:ARG:HG3	1:C:305:ARG:HH11	1.80	0.45
1:D:359:ARG:HD2	1:D:363:ARG:HE	1.81	0.45
1:C:143:VAL:HG12	1:C:166:PRO:HG2	1.98	0.45
5:D:809:PCW:H152	5:D:809:PCW:H181	1.72	0.45
1:B:107:PHE:HZ	1:B:140:ARG:HG3	1.81	0.45
1:B:353:LYS:HD3	1:B:373:LEU:HD23	1.98	0.45
1:D:137:LEU:HD23	1:D:141:ALA:HB3	1.97	0.45
1:B:272:PRO:HB2	1:B:636:ARG:HG3	1.98	0.45
4:C:804:CLR:H232	4:C:804:CLR:H263	1.77	0.45
1:B:270:TYR:OH	1:C:118:GLN:NE2	2.50	0.45
1:C:646:ARG:HH21	2:E:77:LYS:HD3	1.82	0.45
5:C:801:PCW:H241	5:C:801:PCW:H212	1.86	0.45
5:C:806:PCW:H161	5:D:804:PCW:H20	1.99	0.45
2:E:19:PHE:HZ	2:E:32:LEU:HG	1.82	0.45
3:D:806:Y01:HAC3	3:D:806:Y01:HAJ1	1.74	0.45
1:A:590:ASP:O	1:A:594:ARG:NE	2.43	0.45
1:C:106:VAL:HG12	1:C:136:LEU:HD22	1.98	0.45
1:D:239:GLN:HG3	1:D:241:LEU:HD23	1.98	0.45
3:A:814:Y01:HAP1	3:A:814:Y01:HAO2	1.22	0.44
1:A:486:ILE:HD11	1:B:569:LEU:HD22	1.99	0.44
1:B:425:PHE:HB2	3:B:803:Y01:HAM1	2.00	0.44
3:A:814:Y01:HAO1	5:D:808:PCW:H282	1.99	0.44
1:C:280:LEU:HD21	1:C:316:LEU:HD13	1.99	0.44
5:A:815:PCW:H241	5:D:808:PCW:H172	2.00	0.44
3:B:805:Y01:HAL2	1:C:553:PHE:HD1	1.82	0.44
2:E:106:ARG:HG2	2:E:121:VAL:HG21	1.98	0.44
4:B:804:CLR:H162	4:B:804:CLR:H221	1.53	0.44
5:D:808:PCW:H132	5:D:808:PCW:H162	1.90	0.44
1:B:480:ILE:HD13	1:B:592:LEU:HB3	2.00	0.43
5:B:806:PCW:H151	5:B:806:PCW:H181	1.74	0.43
1:D:122:HIS:CD2	1:D:166:PRO:HG3	2.52	0.43
1:A:130:MET:HB3	1:A:132:LEU:H	1.82	0.43
1:A:225:HIS:CD2	1:A:226:GLY:H	2.36	0.43
1:A:358:ASN:HB3	1:A:360:THR:HG23	2.00	0.43
1:B:40:GLN:HB3	1:B:77:ALA:HB3	2.00	0.43
5:B:806:PCW:H182	5:B:806:PCW:H212	1.75	0.43
2:E:34:THR:HA	2:E:37:ARG:HH21	1.83	0.43
1:C:350:ARG:HH22	1:C:451:VAL:HG12	1.84	0.43
1:D:535:GLU:HB3	1:D:541:ILE:HG12	2.00	0.43
3:D:806:Y01:HAO2	3:D:806:Y01:HAP1	1.64	0.43
1:A:209:LYS:HG3	1:A:252:ASN:HD21	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:502:LEU:HD21	5:A:803:PCW:H221	2.01	0.43
1:C:295:LEU:O	1:C:299:THR:OG1	2.28	0.43
1:D:80:GLU:HG3	1:D:85:ILE:HD11	2.00	0.43
1:A:299:THR:HG22	1:A:301:LYS:H	1.84	0.43
5:A:803:PCW:H161	5:B:802:PCW:H20	2.01	0.43
1:D:483:GLN:HB2	4:D:807:CLR:O1	2.18	0.43
5:D:804:PCW:H20	5:D:804:PCW:H171	1.85	0.43
1:A:466:MET:HG3	1:B:499:VAL:HG11	2.01	0.43
1:D:81:THR:HG22	1:D:84:HIS:CD2	2.53	0.43
1:B:122:HIS:CD2	1:B:166:PRO:HG3	2.54	0.42
1:C:154:ARG:HH12	1:C:205:LEU:HD22	1.83	0.42
1:D:520:LEU:HG	1:D:522:HIS:HD2	1.83	0.42
2:E:26:THR:HB	2:E:62:THR:HB	2.00	0.42
1:B:75:ARG:NH2	1:B:79:GLY:O	2.53	0.42
1:B:326:ARG:HD3	5:B:812:PCW:H31	2.01	0.42
1:B:217:ASN:HD21	1:B:258:HIS:CE1	2.38	0.42
1:B:321:TRP:HA	1:B:325:GLY:HA3	2.01	0.42
1:C:404:VAL:O	1:C:408:PHE:N	2.44	0.42
1:A:499:VAL:HG11	1:D:466:MET:HG3	2.01	0.42
1:A:459:VAL:HG21	4:A:802:CLR:H241	2.01	0.42
1:C:279:ASP:OD2	1:C:628:ARG:NH2	2.53	0.42
5:C:813:PCW:H20	5:C:813:PCW:H171	1.84	0.42
1:D:553:PHE:HZ	5:D:804:PCW:H172	1.84	0.42
4:C:804:CLR:H222	4:C:804:CLR:H162	1.73	0.42
5:C:808:PCW:H211	5:C:808:PCW:H182	1.80	0.42
1:D:248:GLY:HA2	1:D:307:ILE:HD13	2.02	0.42
1:D:459:VAL:HG21	4:D:807:CLR:H241	2.02	0.42
1:A:284:ASP:OD1	1:A:616:SER:OG	2.38	0.42
1:B:355:ARG:NH2	1:B:361:SER:OG	2.53	0.42
1:C:45:TRP:HA	1:C:51:LEU:HD12	2.02	0.42
1:C:486:ILE:HD11	1:D:569:LEU:HD22	2.01	0.42
1:B:483:GLN:HB3	4:B:804:CLR:O1	2.20	0.41
5:A:810:PCW:H172	5:A:811:PCW:H42	2.03	0.41
1:C:639:LEU:HA	1:C:639:LEU:HD12	1.80	0.41
1:A:402:VAL:HG21	3:A:801:Y01:HAK1	2.02	0.41
1:A:483:GLN:HB2	4:A:802:CLR:O1	2.20	0.41
5:A:804:PCW:H152	5:A:804:PCW:H182	1.87	0.41
1:B:355:ARG:HA	1:B:371:LYS:HE2	2.01	0.41
1:C:686:ARG:HE	1:C:688:THR:HB	1.85	0.41
1:D:486:ILE:HG21	4:D:807:CLR:H193	2.01	0.41
1:A:122:HIS:CD2	1:A:166:PRO:HG3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:220:LEU:HD23	1:A:232:LEU:HD23	2.03	0.41
1:A:543:GLY:HA2	1:A:544:PRO:HD3	1.87	0.41
3:B:805:Y01:HAE2	3:B:805:Y01:HBB	1.92	0.41
5:B:806:PCW:H132	5:B:806:PCW:H162	1.73	0.41
1:A:280:LEU:HD21	1:A:316:LEU:HD13	2.03	0.41
1:A:283:ILE:HA	1:A:292:LEU:HB3	2.02	0.41
1:C:221:SER:O	1:C:224:ARG:NH1	2.54	0.41
1:C:391:VAL:HG13	3:C:803:Y01:HAA2	2.03	0.41
1:C:404:VAL:HA	1:C:407:ILE:HG22	2.03	0.41
3:C:805:Y01:CAJ	3:C:805:Y01:HAP1	2.44	0.41
1:C:653:THR:HG22	2:E:51:MET:HG2	2.02	0.41
2:E:27:ILE:HB	2:E:63:ILE:HB	2.02	0.41
5:A:812:PCW:H162	5:A:812:PCW:H131	1.76	0.41
3:A:814:Y01:HAC2	3:A:814:Y01:HAJ1	1.77	0.41
1:C:353:LYS:HE2	1:C:353:LYS:HB3	1.95	0.41
1:D:297:ILE:HD12	1:D:297:ILE:HA	1.96	0.41
1:D:269:THR:HG23	1:D:274:THR:HG22	2.03	0.41
3:A:801:Y01:HAC3	3:A:801:Y01:HAJ1	1.71	0.40
1:A:442:MET:HA	1:A:445:ILE:HG22	2.03	0.40
1:B:249:VAL:HG22	1:B:295:LEU:HB3	2.03	0.40
1:D:418:GLN:HA	1:D:421:LEU:HB2	2.04	0.40
1:B:404:VAL:HA	1:B:407:ILE:HG12	2.04	0.40
1:A:355:ARG:HD2	1:A:369:GLN:HA	2.03	0.40
1:A:379:THR:HG23	1:A:381:LYS:H	1.85	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	610/765 (80%)	547 (90%)	60 (10%)	3 (0%)	25 55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	618/765 (81%)	539 (87%)	75 (12%)	4 (1%)	22	51
1	C	649/765 (85%)	566 (87%)	80 (12%)	3 (0%)	25	55
1	D	615/765 (80%)	543 (88%)	68 (11%)	4 (1%)	19	48
2	E	146/149 (98%)	131 (90%)	15 (10%)	0	100	100
All	All	2638/3209 (82%)	2326 (88%)	298 (11%)	14 (0%)	27	55

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	371	LYS
1	B	114	LEU
1	B	104	GLU
1	B	639	LEU
1	C	114	LEU
1	C	357	ASN
1	D	566	ALA
1	C	302	ARG
1	D	231	PRO
1	D	360	THR
1	A	311	THR
1	A	362	PRO
1	B	103	PRO
1	D	287	GLY

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	531/662 (80%)	522 (98%)	9 (2%)	56	74
1	B	539/662 (81%)	527 (98%)	12 (2%)	47	68
1	C	568/662 (86%)	560 (99%)	8 (1%)	62	77
1	D	536/662 (81%)	526 (98%)	10 (2%)	52	71
2	E	126/127 (99%)	125 (99%)	1 (1%)	79	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2300/2775 (83%)	2260 (98%)	40 (2%)	56 74

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	129	ASN
1	A	174	ASN
1	A	252	ASN
1	A	311	THR
1	A	367	LEU
1	A	464	ASN
1	A	546	ASN
1	A	594	ARG
1	A	612	LEU
1	B	91	ASN
1	B	131	ASN
1	B	154	ARG
1	B	174	ASN
1	B	252	ASN
1	B	300	LYS
1	B	365	ASN
1	B	367	LEU
1	B	414	ARG
1	B	485	MET
1	B	546	ASN
1	B	646	ARG
1	C	26	ARG
1	C	140	ARG
1	C	154	ARG
1	C	174	ASN
1	C	358	ASN
1	C	363	ARG
1	C	367	LEU
1	C	546	ASN
1	D	26	ARG
1	D	54	LYS
1	D	129	ASN
1	D	300	LYS
1	D	365	ASN
1	D	367	LEU
1	D	409	ARG
1	D	414	ARG

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Mol	Chain	Res	Type
1	D	546	ASN
1	D	594	ARG
2	E	76	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (42) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	GLN
1	A	73	HIS
1	A	84	HIS
1	A	118	GLN
1	A	129	ASN
1	A	174	ASN
1	A	197	ASN
1	A	206	GLN
1	A	225	HIS
1	A	230	GLN
1	A	252	ASN
1	A	267	GLN
1	A	572	ASN
1	B	56	ASN
1	B	84	HIS
1	B	91	ASN
1	B	118	GLN
1	B	131	ASN
1	B	174	ASN
1	B	206	GLN
1	B	217	ASN
1	B	252	ASN
1	B	365	ASN
1	B	426	HIS
1	B	582	HIS
1	C	31	GLN
1	C	118	GLN
1	C	174	ASN
1	C	252	ASN
1	C	267	GLN
1	C	358	ASN
1	C	546	ASN
1	C	572	ASN
1	D	31	GLN
1	D	84	HIS

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Mol	Chain	Res	Type
1	D	118	GLN
1	D	129	ASN
1	D	252	ASN
1	D	365	ASN
1	D	464	ASN
1	D	522	HIS
1	D	572	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](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 62 ligands modelled in this entry, 7 are monoatomic - leaving 55 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	PCW	D	808	-	50,50,53	1.31	6 (12%)	56,58,61	0.99	3 (5%)
5	PCW	C	809	-	7,7,53	0.92	0	6,6,61	0.29	0
5	PCW	A	811	-	42,42,53	1.42	7 (16%)	48,50,61	1.01	3 (6%)
3	Y01	A	801	-	38,38,38	0.54	0	57,57,57	0.63	0
3	Y01	A	814	-	38,38,38	0.53	0	57,57,57	0.79	2 (3%)
4	CLR	A	802	-	31,31,31	0.38	0	48,48,48	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	PCW	B	809	-	7,7,53	0.92	0	6,6,61	0.29	0
5	PCW	C	807	-	15,15,53	1.51	2 (13%)	14,14,61	0.69	0
5	PCW	D	802	-	42,42,53	1.42	7 (16%)	48,50,61	1.01	3 (6%)
5	PCW	B	802	-	14,14,53	0.87	0	13,13,61	0.36	0
5	PCW	B	807	-	15,15,53	1.51	2 (13%)	14,14,61	0.70	0
5	PCW	A	809	-	15,15,53	1.53	2 (13%)	14,14,61	0.73	0
5	PCW	C	806	-	50,50,53	1.33	6 (12%)	56,58,61	0.97	3 (5%)
4	CLR	D	807	-	31,31,31	0.38	0	48,48,48	0.57	0
5	PCW	D	803	-	50,50,53	1.34	6 (12%)	56,58,61	0.93	3 (5%)
3	Y01	C	805	-	38,38,38	0.54	0	57,57,57	0.95	4 (7%)
5	PCW	B	808	-	10,10,53	0.95	0	9,9,61	0.45	0
5	PCW	D	811	-	10,10,53	0.95	0	9,9,61	0.43	0
5	PCW	C	811	-	12,12,53	0.85	0	11,11,61	0.34	0
5	PCW	B	810	-	15,15,53	1.51	2 (13%)	14,14,61	0.69	0
4	CLR	B	804	-	31,31,31	0.41	0	48,48,48	0.81	0
5	PCW	A	806	-	10,10,53	0.95	0	9,9,61	0.49	0
5	PCW	A	803	-	50,50,53	1.34	6 (12%)	56,58,61	0.96	3 (5%)
5	PCW	C	813	-	50,50,53	1.33	7 (14%)	56,58,61	0.95	3 (5%)
5	PCW	A	808	-	7,7,53	0.92	0	6,6,61	0.31	0
5	PCW	D	814	-	15,15,53	1.53	2 (13%)	14,14,61	0.69	0
5	PCW	A	812	-	50,50,53	1.34	7 (14%)	56,58,61	0.91	3 (5%)
3	Y01	B	805	-	38,38,38	0.53	0	57,57,57	0.78	1 (1%)
4	CLR	C	804	-	31,31,31	0.45	0	48,48,48	0.71	0
5	PCW	D	812	-	7,7,53	0.90	0	6,6,61	0.34	0
3	Y01	C	803	-	38,38,38	0.54	0	57,57,57	0.73	0
5	PCW	C	801	-	14,14,53	0.87	0	13,13,61	0.41	0
5	PCW	B	806	-	50,50,53	1.33	6 (12%)	56,58,61	0.93	3 (5%)
5	PCW	D	813	-	7,7,53	0.92	0	6,6,61	0.27	0
5	PCW	D	810	-	15,15,53	1.53	2 (13%)	14,14,61	0.69	0
5	PCW	A	807	-	7,7,53	0.90	0	6,6,61	0.34	0
5	PCW	B	813	-	50,50,53	1.34	6 (12%)	56,58,61	0.94	3 (5%)
5	PCW	C	802	-	15,15,53	1.52	2 (13%)	14,14,61	0.70	0
5	PCW	D	801	-	12,12,53	0.85	0	11,11,61	0.34	0
3	Y01	B	801	-	38,38,38	0.51	0	57,57,57	0.97	5 (8%)
5	PCW	C	812	-	42,42,53	1.40	6 (14%)	48,50,61	0.99	3 (6%)
5	PCW	B	812	-	42,42,53	1.43	7 (16%)	48,50,61	0.98	3 (6%)
5	PCW	C	808	-	10,10,53	0.95	0	9,9,61	0.43	0
5	PCW	A	805	-	15,15,53	1.52	2 (13%)	14,14,61	0.67	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	PCW	A	804	-	15,15,53	1.49	2 (13%)	14,14,61	0.72	0
5	PCW	B	811	-	12,12,53	0.82	0	11,11,61	0.40	0
5	PCW	D	809	-	15,15,53	1.52	2 (13%)	14,14,61	0.70	0
5	PCW	A	813	-	7,7,53	0.91	0	6,6,61	0.30	0
3	Y01	D	806	-	38,38,38	0.51	0	57,57,57	0.72	0
3	Y01	B	803	-	38,38,38	0.52	0	57,57,57	0.70	1 (1%)
5	PCW	A	815	-	14,14,53	0.88	0	13,13,61	0.33	0
5	PCW	D	805	-	15,15,53	1.52	2 (13%)	14,14,61	0.68	0
5	PCW	D	804	-	14,14,53	0.88	0	13,13,61	0.35	0
5	PCW	A	810	-	12,12,53	0.84	0	11,11,61	0.40	0
5	PCW	C	810	-	15,15,53	1.52	2 (13%)	14,14,61	0.67	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
5	PCW	D	808	-	-	24/54/54/57	-
5	PCW	C	809	-	-	2/5/5/57	-
5	PCW	A	811	-	-	22/46/46/57	-
3	Y01	A	801	-	-	10/19/77/77	0/4/4/4
3	Y01	A	814	-	-	14/19/77/77	0/4/4/4
4	CLR	A	802	-	-	5/10/68/68	0/4/4/4
5	PCW	B	809	-	-	2/5/5/57	-
5	PCW	C	807	-	-	9/13/13/57	-
5	PCW	D	802	-	-	20/46/46/57	-
5	PCW	B	802	-	-	6/12/12/57	-
5	PCW	B	807	-	-	10/13/13/57	-
5	PCW	A	809	-	-	8/13/13/57	-
5	PCW	C	806	-	-	29/54/54/57	-
4	CLR	D	807	-	-	7/10/68/68	0/4/4/4
5	PCW	D	803	-	-	24/54/54/57	-
3	Y01	C	805	-	-	12/19/77/77	0/4/4/4
5	PCW	B	808	-	-	4/8/8/57	-
5	PCW	D	811	-	-	4/8/8/57	-
5	PCW	C	811	-	-	4/10/10/57	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PCW	B	810	-	-	8/13/13/57	-
4	CLR	B	804	-	-	8/10/68/68	0/4/4/4
5	PCW	A	806	-	-	3/8/8/57	-
5	PCW	A	803	-	-	23/54/54/57	-
5	PCW	C	813	-	-	28/54/54/57	-
5	PCW	A	808	-	-	1/5/5/57	-
5	PCW	D	814	-	-	6/13/13/57	-
5	PCW	A	812	-	-	24/54/54/57	-
3	Y01	B	805	-	-	14/19/77/77	0/4/4/4
4	CLR	C	804	-	-	7/10/68/68	0/4/4/4
5	PCW	D	812	-	-	3/5/5/57	-
3	Y01	C	803	-	-	9/19/77/77	0/4/4/4
5	PCW	C	801	-	-	6/12/12/57	-
5	PCW	B	806	-	-	24/54/54/57	-
5	PCW	D	813	-	-	2/5/5/57	-
5	PCW	D	810	-	-	11/13/13/57	-
5	PCW	A	807	-	-	2/5/5/57	-
5	PCW	B	813	-	-	29/54/54/57	-
5	PCW	C	802	-	-	9/13/13/57	-
5	PCW	D	801	-	-	5/10/10/57	-
3	Y01	B	801	-	-	6/19/77/77	0/4/4/4
5	PCW	C	812	-	-	20/46/46/57	-
5	PCW	B	812	-	-	18/46/46/57	-
5	PCW	C	808	-	-	1/8/8/57	-
5	PCW	A	805	-	-	5/13/13/57	-
5	PCW	A	804	-	-	6/13/13/57	-
5	PCW	B	811	-	-	4/10/10/57	-
5	PCW	D	809	-	-	7/13/13/57	-
5	PCW	A	813	-	-	1/5/5/57	-
3	Y01	D	806	-	-	10/19/77/77	0/4/4/4
3	Y01	B	803	-	-	14/19/77/77	0/4/4/4
5	PCW	A	815	-	-	7/12/12/57	-
5	PCW	D	805	-	-	6/13/13/57	-
5	PCW	D	804	-	-	6/12/12/57	-
5	PCW	A	810	-	-	4/10/10/57	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PCW	C	810	-	-	8/13/13/57	-

All (101) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	810	PCW	C20-C19	4.15	1.55	1.31
5	A	809	PCW	C20-C19	4.15	1.55	1.31
5	D	809	PCW	C20-C19	4.14	1.55	1.31
5	D	810	PCW	C20-C19	4.14	1.55	1.31
5	D	814	PCW	C20-C19	4.13	1.55	1.31
5	D	805	PCW	C20-C19	4.13	1.55	1.31
5	A	805	PCW	C20-C19	4.12	1.55	1.31
5	C	802	PCW	C20-C19	4.12	1.55	1.31
5	A	804	PCW	C20-C19	4.11	1.55	1.31
5	B	810	PCW	C20-C19	4.11	1.55	1.31
5	C	807	PCW	C20-C19	4.11	1.55	1.31
5	B	807	PCW	C20-C19	4.11	1.55	1.31
5	B	812	PCW	O3-C11	3.87	1.44	1.33
5	A	812	PCW	O3-C11	3.80	1.44	1.33
5	C	813	PCW	O3-C11	3.80	1.44	1.33
5	A	803	PCW	O3-C11	3.79	1.44	1.33
5	B	806	PCW	O3-C11	3.77	1.44	1.33
5	D	803	PCW	O3-C11	3.76	1.44	1.33
5	B	813	PCW	O3-C11	3.75	1.44	1.33
5	D	802	PCW	O3-C11	3.75	1.44	1.33
5	A	811	PCW	O3-C11	3.74	1.44	1.33
5	C	806	PCW	O3-C11	3.72	1.44	1.33
5	D	808	PCW	O3-C11	3.70	1.44	1.33
5	C	812	PCW	O3-C11	3.67	1.44	1.33
5	C	806	PCW	O2-C31	3.51	1.44	1.34
5	A	812	PCW	O2-C31	3.48	1.44	1.34
5	B	813	PCW	O2-C31	3.48	1.44	1.34
5	B	812	PCW	O2-C31	3.43	1.44	1.34
5	A	811	PCW	O2-C31	3.43	1.44	1.34
5	D	802	PCW	O2-C31	3.39	1.43	1.34
5	D	803	PCW	O2-C31	3.38	1.43	1.34
5	A	803	PCW	O2-C31	3.38	1.43	1.34
5	C	813	PCW	O2-C31	3.35	1.43	1.34
5	D	808	PCW	O2-C31	3.33	1.43	1.34
5	C	812	PCW	O2-C31	3.32	1.43	1.34
5	B	806	PCW	O2-C31	3.29	1.43	1.34
5	A	803	PCW	O2-C2	-3.08	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	806	PCW	O2-C2	-3.01	1.39	1.46
5	D	808	PCW	O2-C2	-3.01	1.39	1.46
5	C	812	PCW	O2-C2	-3.00	1.39	1.46
5	B	812	PCW	O2-C2	-2.96	1.39	1.46
5	C	813	PCW	O2-C2	-2.95	1.39	1.46
5	A	812	PCW	O2-C2	-2.94	1.39	1.46
5	D	802	PCW	O2-C2	-2.94	1.39	1.46
5	B	813	PCW	O2-C2	-2.92	1.39	1.46
5	A	811	PCW	O2-C2	-2.91	1.39	1.46
5	D	803	PCW	O2-C2	-2.90	1.39	1.46
5	C	806	PCW	O2-C2	-2.89	1.39	1.46
5	C	807	PCW	C18-C19	-2.72	1.35	1.50
5	B	807	PCW	C18-C19	-2.72	1.35	1.50
5	C	802	PCW	C18-C19	-2.71	1.35	1.50
5	B	810	PCW	C18-C19	-2.70	1.35	1.50
5	D	810	PCW	C18-C19	-2.70	1.35	1.50
5	D	814	PCW	C18-C19	-2.69	1.35	1.50
5	A	804	PCW	C18-C19	-2.69	1.35	1.50
5	D	809	PCW	C18-C19	-2.68	1.35	1.50
5	D	805	PCW	C18-C19	-2.68	1.35	1.50
5	A	805	PCW	C18-C19	-2.68	1.35	1.50
5	A	809	PCW	C18-C19	-2.68	1.35	1.50
5	C	810	PCW	C18-C19	-2.67	1.35	1.50
5	B	813	PCW	P-O3P	2.52	1.69	1.59
5	B	812	PCW	P-O3P	2.49	1.69	1.59
5	A	803	PCW	P-O3P	2.49	1.69	1.59
5	D	802	PCW	P-O3P	2.47	1.69	1.59
5	A	811	PCW	P-O3P	2.46	1.69	1.59
5	A	812	PCW	P-O3P	2.46	1.69	1.59
5	D	803	PCW	P-O3P	2.45	1.69	1.59
5	B	812	PCW	P-O4P	2.44	1.69	1.59
5	A	812	PCW	P-O4P	2.44	1.68	1.59
5	B	813	PCW	P-O4P	2.44	1.68	1.59
5	C	813	PCW	P-O3P	2.43	1.68	1.59
5	A	811	PCW	P-O4P	2.43	1.68	1.59
5	A	803	PCW	P-O4P	2.42	1.68	1.59
5	D	803	PCW	P-O4P	2.42	1.68	1.59
5	C	806	PCW	P-O3P	2.41	1.68	1.59
5	B	806	PCW	P-O4P	2.41	1.68	1.59
5	D	802	PCW	P-O4P	2.39	1.68	1.59
5	C	813	PCW	P-O4P	2.39	1.68	1.59
5	C	806	PCW	P-O4P	2.39	1.68	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	812	PCW	P-O4P	2.39	1.68	1.59
5	C	812	PCW	P-O3P	2.39	1.68	1.59
5	D	808	PCW	P-O4P	2.38	1.68	1.59
5	B	806	PCW	P-O3P	2.37	1.68	1.59
5	D	808	PCW	P-O3P	2.35	1.68	1.59
5	C	806	PCW	C12-C11	2.30	1.57	1.50
5	D	803	PCW	C12-C11	2.26	1.57	1.50
5	A	811	PCW	C12-C11	2.25	1.57	1.50
5	B	812	PCW	C12-C11	2.25	1.57	1.50
5	A	803	PCW	C12-C11	2.24	1.57	1.50
5	D	808	PCW	C12-C11	2.24	1.57	1.50
5	B	813	PCW	C12-C11	2.24	1.57	1.50
5	A	812	PCW	C12-C11	2.23	1.57	1.50
5	D	802	PCW	C12-C11	2.21	1.57	1.50
5	B	806	PCW	C12-C11	2.20	1.57	1.50
5	C	812	PCW	C12-C11	2.20	1.57	1.50
5	C	813	PCW	C12-C11	2.17	1.57	1.50
5	A	811	PCW	C32-C31	2.06	1.56	1.50
5	A	812	PCW	C32-C31	2.04	1.56	1.50
5	B	812	PCW	C32-C31	2.04	1.56	1.50
5	D	802	PCW	C32-C31	2.03	1.56	1.50
5	C	813	PCW	C32-C31	2.02	1.56	1.50

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	808	PCW	O2-C31-C32	4.22	120.61	111.48
5	A	803	PCW	O2-C31-C32	4.21	120.59	111.48
5	C	806	PCW	O2-C31-C32	4.16	120.48	111.48
5	D	802	PCW	O2-C31-C32	4.06	120.26	111.48
5	A	811	PCW	O2-C31-C32	3.99	120.12	111.48
5	D	803	PCW	O2-C31-C32	3.99	120.10	111.48
5	B	812	PCW	O2-C31-C32	3.93	119.98	111.48
5	C	813	PCW	O2-C31-C32	3.81	119.73	111.48
5	B	806	PCW	O2-C31-C32	3.80	119.71	111.48
5	B	813	PCW	O2-C31-C32	3.79	119.69	111.48
5	A	812	PCW	O2-C31-C32	3.78	119.67	111.48
5	C	812	PCW	O2-C31-C32	3.65	119.38	111.48
3	C	805	Y01	CAP-CAQ-CBG	-3.41	98.48	105.14
5	C	813	PCW	O3-C11-C12	2.81	120.39	111.83
5	B	813	PCW	O3-C11-C12	2.78	120.30	111.83
5	B	806	PCW	O3-C11-C12	2.77	120.27	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	803	Y01	CAL-CAM-CAY	2.74	121.56	113.44
5	D	803	PCW	O3-C11-C12	2.73	120.17	111.83
5	B	813	PCW	C7-N-C5	2.69	120.61	109.91
5	C	806	PCW	O3-C11-C12	2.68	120.01	111.83
5	B	812	PCW	O3-C11-C12	2.63	119.87	111.83
5	A	812	PCW	O3-C11-C12	2.63	119.84	111.83
5	C	812	PCW	O3-C11-C12	2.61	119.80	111.83
5	D	802	PCW	O3-C11-C12	2.59	119.72	111.83
5	A	811	PCW	O3-C11-C12	2.58	119.70	111.83
5	D	808	PCW	O3-C11-C12	2.57	119.68	111.83
5	A	803	PCW	O3-C11-C12	2.57	119.66	111.83
3	C	805	Y01	CBG-CBI-CBE	2.50	102.97	100.10
3	C	805	Y01	CBF-CBD-CBG	-2.48	105.84	109.09
3	B	801	Y01	CAR-CBC-CAV	-2.46	107.56	110.97
3	C	805	Y01	CAU-CBI-CBG	-2.45	103.58	107.25
5	D	808	PCW	C7-N-C5	2.39	119.42	109.91
5	A	812	PCW	C7-N-C5	2.37	119.35	109.91
5	B	806	PCW	C7-N-C5	2.36	119.27	109.91
5	D	802	PCW	C7-N-C5	2.35	119.25	109.91
5	C	813	PCW	C7-N-C5	2.35	119.24	109.91
5	A	811	PCW	C7-N-C5	2.33	119.19	109.91
5	C	812	PCW	C7-N-C5	2.32	119.13	109.91
5	A	803	PCW	C7-N-C5	2.28	118.98	109.91
5	C	806	PCW	C7-N-C5	2.23	118.76	109.91
5	D	803	PCW	C7-N-C5	2.17	118.55	109.91
3	A	814	Y01	CAP-CAQ-CBG	-2.17	100.90	105.14
5	B	812	PCW	C7-N-C5	2.16	118.51	109.91
3	B	805	Y01	OAW-CBC-CAR	2.15	113.45	108.37
3	B	801	Y01	CAT-CBH-CAZ	2.15	112.44	108.74
3	B	801	Y01	CAT-CBH-CBF	-2.11	105.94	108.74
3	A	814	Y01	CBG-CBI-CBE	2.06	102.47	100.10
3	B	801	Y01	CBG-CBI-CBE	2.02	102.42	100.10
3	B	801	Y01	CAR-CAT-CBH	2.02	117.08	112.78

There are no chirality outliers.

All (561) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	814	Y01	CAM-CAY-OAW-CBC
3	B	803	Y01	CAO-CBB-CBE-CAP
3	B	803	Y01	CAO-CBB-CBE-CBI
3	B	803	Y01	CAC-CBB-CBE-CBI

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Mol	Chain	Res	Type	Atoms
3	B	805	Y01	CAR-CBC-OAW-CAY
3	C	803	Y01	CAC-CBB-CBE-CBI
3	C	805	Y01	CAM-CAY-OAW-CBC
4	B	804	CLR	C13-C17-C20-C21
5	A	803	PCW	O4P-C4-C5-N
5	A	803	PCW	C32-C31-O2-C2
5	A	803	PCW	C4-O4P-P-O3P
5	A	811	PCW	C32-C31-O2-C2
5	A	811	PCW	C4-O4P-P-O3P
5	A	812	PCW	C4-O4P-P-O2P
5	A	812	PCW	C4-O4P-P-O3P
5	B	806	PCW	C1-O3P-P-O1P
5	B	806	PCW	C4-O4P-P-O1P
5	B	806	PCW	C4-O4P-P-O3P
5	B	812	PCW	O31-C31-O2-C2
5	B	813	PCW	C1-O3P-P-O2P
5	B	813	PCW	C1-O3P-P-O4P
5	B	813	PCW	C4-O4P-P-O2P
5	B	813	PCW	C4-O4P-P-O3P
5	C	806	PCW	C1-O3P-P-O1P
5	C	806	PCW	C4-O4P-P-O1P
5	C	806	PCW	C4-O4P-P-O2P
5	C	806	PCW	C4-O4P-P-O3P
5	C	812	PCW	C1-O3P-P-O1P
5	C	812	PCW	C1-O3P-P-O2P
5	C	812	PCW	C1-O3P-P-O4P
5	C	813	PCW	O4P-C4-C5-N
5	C	813	PCW	C32-C31-O2-C2
5	C	813	PCW	C1-O3P-P-O1P
5	C	813	PCW	C1-O3P-P-O2P
5	C	813	PCW	C1-O3P-P-O4P
5	D	802	PCW	O4P-C4-C5-N
5	D	802	PCW	C1-O3P-P-O1P
5	D	802	PCW	C1-O3P-P-O4P
5	D	802	PCW	C4-O4P-P-O1P
5	D	802	PCW	C4-O4P-P-O3P
5	D	803	PCW	O4P-C4-C5-N
5	D	803	PCW	C4-O4P-P-O1P
5	D	803	PCW	C4-O4P-P-O2P
5	D	803	PCW	C4-O4P-P-O3P
5	D	805	PCW	C18-C19-C20-C21
5	D	808	PCW	O4P-C4-C5-N

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Mol	Chain	Res	Type	Atoms
5	D	808	PCW	C1-O3P-P-O4P
5	D	808	PCW	C4-O4P-P-O2P
5	A	812	PCW	O11-C11-O3-C3
5	B	813	PCW	O11-C11-O3-C3
5	C	813	PCW	O11-C11-O3-C3
3	B	801	Y01	CAO-CAJ-CAN-CBA
3	B	801	Y01	CAV-CBC-OAW-CAY
5	A	812	PCW	C12-C11-O3-C3
5	B	813	PCW	C12-C11-O3-C3
5	C	813	PCW	C12-C11-O3-C3
5	A	803	PCW	O11-C11-O3-C3
5	A	811	PCW	O11-C11-O3-C3
5	C	812	PCW	O11-C11-O3-C3
5	D	803	PCW	O11-C11-O3-C3
5	D	808	PCW	O11-C11-O3-C3
3	A	814	Y01	CAC-CBB-CBE-CAP
3	B	803	Y01	CAC-CBB-CBE-CAP
3	B	805	Y01	CAC-CBB-CBE-CAP
3	C	803	Y01	CAC-CBB-CBE-CAP
4	B	804	CLR	C16-C17-C20-C21
3	A	814	Y01	CAC-CBB-CBE-CBI
3	B	805	Y01	CAC-CBB-CBE-CBI
4	C	804	CLR	C13-C17-C20-C21
4	D	807	CLR	C13-C17-C20-C21
4	B	804	CLR	C16-C17-C20-C22
4	C	804	CLR	C13-C17-C20-C22
3	A	814	Y01	OAG-CAY-OAW-CBC
5	A	803	PCW	O31-C31-O2-C2
5	A	811	PCW	O31-C31-O2-C2
5	C	813	PCW	O31-C31-O2-C2
5	A	803	PCW	C12-C11-O3-C3
5	C	812	PCW	C12-C11-O3-C3
5	D	803	PCW	C12-C11-O3-C3
5	B	812	PCW	C32-C31-O2-C2
3	C	803	Y01	CAJ-CAO-CBB-CAC
3	D	806	Y01	CAC-CBB-CBE-CAP
4	C	804	CLR	C16-C17-C20-C21
4	D	807	CLR	C16-C17-C20-C21
3	A	814	Y01	CAO-CBB-CBE-CAP
3	C	803	Y01	CAO-CBB-CBE-CAP
3	D	806	Y01	CAO-CBB-CBE-CAP
3	A	801	Y01	CAO-CBB-CBE-CBI

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Mol	Chain	Res	Type	Atoms
3	A	814	Y01	CAO-CBB-CBE-CBI
3	B	805	Y01	CAO-CBB-CBE-CBI
3	C	803	Y01	CAO-CBB-CBE-CBI
4	B	804	CLR	C13-C17-C20-C22
4	D	807	CLR	C13-C17-C20-C22
3	B	805	Y01	CAX-CAL-CAM-CAY
5	A	811	PCW	C12-C11-O3-C3
5	D	808	PCW	C12-C11-O3-C3
3	A	814	Y01	CAJ-CAO-CBB-CAC
4	D	807	CLR	C21-C20-C22-C23
3	C	805	Y01	OAG-CAY-OAW-CBC
3	A	801	Y01	CAC-CBB-CBE-CBI
3	D	806	Y01	CAO-CBB-CBE-CBI
5	C	806	PCW	C12-C11-O3-C3
5	C	806	PCW	O11-C11-O3-C3
3	D	806	Y01	CAC-CBB-CBE-CBI
4	D	807	CLR	C16-C17-C20-C22
3	C	803	Y01	CAJ-CAO-CBB-CBE
5	B	806	PCW	C23-C24-C25-C26
3	A	801	Y01	CAJ-CAO-CBB-CAC
3	B	803	Y01	CAJ-CAO-CBB-CAC
3	A	814	Y01	CAJ-CAO-CBB-CBE
5	B	806	PCW	C33-C34-C35-C36
4	B	804	CLR	C21-C20-C22-C23
3	A	801	Y01	CAC-CBB-CBE-CAP
5	B	813	PCW	C4-C5-N-C7
5	B	813	PCW	C4-C5-N-C8
3	B	805	Y01	CAO-CBB-CBE-CAP
4	C	804	CLR	C16-C17-C20-C22
3	C	805	Y01	CAJ-CAO-CBB-CBE
5	C	812	PCW	C32-C31-O2-C2
5	C	813	PCW	C31-C32-C33-C34
3	D	806	Y01	CAJ-CAO-CBB-CAC
3	D	806	Y01	CAN-CAJ-CAO-CBB
5	B	810	PCW	C18-C19-C20-C21
4	D	807	CLR	C17-C20-C22-C23
3	C	805	Y01	CAX-CAL-CAM-CAY
5	A	811	PCW	C11-C12-C13-C14
5	C	809	PCW	C15-C16-C17-C18
5	B	813	PCW	C11-C12-C13-C14
5	C	812	PCW	C31-C32-C33-C34
3	C	805	Y01	CAJ-CAO-CBB-CAC

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Mol	Chain	Res	Type	Atoms
3	C	803	Y01	CAN-CAJ-CAO-CBB
5	A	812	PCW	C31-C32-C33-C34
5	B	806	PCW	C11-C12-C13-C14
5	D	808	PCW	C31-C32-C33-C34
3	A	801	Y01	CAO-CAJ-CAN-CBA
5	B	813	PCW	C31-C32-C33-C34
5	D	803	PCW	C11-C12-C13-C14
3	A	814	Y01	CAO-CAJ-CAN-CBA
3	A	814	Y01	CAN-CAJ-CAO-CBB
5	C	802	PCW	C18-C19-C20-C21
3	D	806	Y01	CAX-CAL-CAM-CAY
3	B	803	Y01	CAN-CAJ-CAO-CBB
5	B	806	PCW	C12-C11-O3-C3
3	B	803	Y01	CAM-CAY-OAW-CBC
5	D	802	PCW	C32-C31-O2-C2
5	D	810	PCW	C15-C16-C17-C18
3	B	805	Y01	OAG-CAY-OAW-CBC
5	C	812	PCW	O31-C31-O2-C2
5	D	802	PCW	O31-C31-O2-C2
3	B	805	Y01	CAO-CAJ-CAN-CBA
3	B	801	Y01	CAM-CAY-OAW-CBC
3	B	805	Y01	CAM-CAY-OAW-CBC
5	B	806	PCW	C13-C14-C15-C16
3	B	801	Y01	OAG-CAY-OAW-CBC
3	B	803	Y01	OAG-CAY-OAW-CBC
5	B	806	PCW	O11-C11-O3-C3
3	A	801	Y01	CAO-CBB-CBE-CAP
3	B	805	Y01	CAJ-CAN-CBA-CAB
5	B	812	PCW	C31-C32-C33-C34
5	D	808	PCW	C33-C34-C35-C36
5	A	803	PCW	C14-C15-C16-C17
5	A	803	PCW	C35-C36-C37-C38
5	C	813	PCW	C34-C35-C36-C37
5	D	810	PCW	C22-C23-C24-C25
5	D	809	PCW	C21-C22-C23-C24
5	D	810	PCW	C12-C13-C14-C15
5	D	813	PCW	C13-C14-C15-C16
5	B	807	PCW	C13-C14-C15-C16
5	B	810	PCW	C21-C22-C23-C24
5	D	814	PCW	C12-C13-C14-C15
5	D	804	PCW	C14-C15-C16-C17
3	A	814	Y01	CAJ-CAN-CBA-CAB

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Mol	Chain	Res	Type	Atoms
5	A	812	PCW	C40-C41-C42-C43
5	A	806	PCW	C13-C14-C15-C16
5	B	812	PCW	C12-C13-C14-C15
5	B	813	PCW	C13-C14-C15-C16
5	C	810	PCW	C12-C13-C14-C15
5	C	810	PCW	C14-C15-C16-C17
5	B	806	PCW	C24-C25-C26-C27
5	C	813	PCW	C33-C34-C35-C36
4	A	802	CLR	C13-C17-C20-C22
5	A	812	PCW	C41-C42-C43-C44
5	B	802	PCW	C21-C22-C23-C24
5	B	812	PCW	C12-C11-O3-C3
5	C	810	PCW	C21-C22-C23-C24
5	C	813	PCW	C14-C15-C16-C17
5	A	812	PCW	C35-C36-C37-C38
5	B	802	PCW	C15-C16-C17-C18
5	B	812	PCW	C15-C16-C17-C18
5	B	812	PCW	C34-C35-C36-C37
5	C	802	PCW	C14-C15-C16-C17
5	C	802	PCW	C22-C23-C24-C25
5	C	806	PCW	C35-C36-C37-C38
5	D	802	PCW	C15-C16-C17-C18
5	B	813	PCW	C4-C5-N-C6
5	A	807	PCW	C13-C14-C15-C16
5	A	807	PCW	C15-C16-C17-C18
5	A	812	PCW	C33-C34-C35-C36
3	B	803	Y01	CAJ-CAN-CBA-CAA
3	C	805	Y01	CAJ-CAN-CBA-CAA
5	B	806	PCW	C32-C31-O2-C2
5	D	808	PCW	C32-C31-O2-C2
5	C	802	PCW	C20-C21-C22-C23
5	C	806	PCW	C40-C41-C42-C43
5	A	805	PCW	C18-C19-C20-C21
5	D	802	PCW	C12-C13-C14-C15
5	D	803	PCW	C15-C16-C17-C18
5	A	811	PCW	C13-C14-C15-C16
5	B	806	PCW	C15-C16-C17-C18
5	D	803	PCW	C13-C14-C15-C16
5	D	803	PCW	C32-C33-C34-C35
5	A	811	PCW	C33-C34-C35-C36
5	B	809	PCW	C13-C14-C15-C16
3	B	805	Y01	CAJ-CAN-CBA-CAA

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Mol	Chain	Res	Type	Atoms
5	B	806	PCW	C12-C13-C14-C15
5	C	813	PCW	C35-C36-C37-C38
5	A	808	PCW	C15-C16-C17-C18
5	B	806	PCW	C31-C32-C33-C34
5	B	813	PCW	C19-C20-C21-C22
4	A	802	CLR	C16-C17-C20-C21
4	A	802	CLR	C13-C17-C20-C21
3	A	801	Y01	CAM-CAY-OAW-CBC
5	D	803	PCW	C32-C31-O2-C2
5	B	812	PCW	O11-C11-O3-C3
5	A	803	PCW	C11-C12-C13-C14
5	A	815	PCW	C21-C22-C23-C24
5	B	806	PCW	C36-C37-C38-C39
5	B	808	PCW	C16-C17-C18-C19
5	B	813	PCW	C20-C21-C22-C23
5	C	807	PCW	C20-C21-C22-C23
5	C	812	PCW	C16-C17-C18-C19
5	D	808	PCW	C36-C37-C38-C39
4	A	802	CLR	C22-C23-C24-C25
5	B	812	PCW	C33-C34-C35-C36
5	D	803	PCW	C35-C36-C37-C38
3	A	801	Y01	CAN-CAJ-CAO-CBB
5	A	809	PCW	C12-C13-C14-C15
5	C	806	PCW	C31-C32-C33-C34
5	D	803	PCW	C31-C32-C33-C34
5	A	811	PCW	C36-C37-C38-C39
5	D	804	PCW	C20-C21-C22-C23
5	B	809	PCW	C15-C16-C17-C18
5	B	807	PCW	C14-C15-C16-C17
5	B	812	PCW	C32-C33-C34-C35
5	D	804	PCW	C21-C22-C23-C24
5	B	811	PCW	C17-C18-C19-C20
5	C	801	PCW	C19-C20-C21-C22
5	C	806	PCW	C37-C38-C39-C40
5	C	810	PCW	C19-C20-C21-C22
5	D	809	PCW	C19-C20-C21-C22
5	B	808	PCW	C13-C14-C15-C16
5	C	806	PCW	C14-C15-C16-C17
5	C	813	PCW	C21-C22-C23-C24
4	C	804	CLR	C22-C23-C24-C25
5	C	806	PCW	C32-C33-C34-C35
5	C	806	PCW	C34-C35-C36-C37

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Mol	Chain	Res	Type	Atoms
5	B	810	PCW	C12-C13-C14-C15
5	D	803	PCW	C39-C40-C41-C42
5	D	808	PCW	C23-C24-C25-C26
5	A	803	PCW	C40-C41-C42-C43
5	B	813	PCW	C36-C37-C38-C39
5	C	813	PCW	C20-C21-C22-C23
5	D	802	PCW	C36-C37-C38-C39
5	A	812	PCW	O3P-C1-C2-C3
5	B	813	PCW	O3P-C1-C2-C3
5	D	802	PCW	O3P-C1-C2-C3
5	B	806	PCW	O31-C31-O2-C2
5	D	808	PCW	O31-C31-O2-C2
5	C	806	PCW	C32-C31-O2-C2
5	B	810	PCW	C13-C14-C15-C16
5	C	806	PCW	C17-C18-C19-C20
5	C	806	PCW	C1-C2-C3-O3
5	D	808	PCW	C1-C2-C3-O3
5	A	804	PCW	C16-C17-C18-C19
5	B	812	PCW	C36-C37-C38-C39
5	C	806	PCW	C16-C17-C18-C19
5	C	810	PCW	C20-C21-C22-C23
5	D	814	PCW	C16-C17-C18-C19
5	A	809	PCW	C22-C23-C24-C25
5	D	803	PCW	C22-C23-C24-C25
5	A	803	PCW	C34-C35-C36-C37
3	B	805	Y01	CAN-CAJ-CAO-CBB
5	A	812	PCW	C11-C12-C13-C14
5	B	811	PCW	C19-C20-C21-C22
5	D	803	PCW	C37-C38-C39-C40
5	C	802	PCW	C15-C16-C17-C18
5	C	812	PCW	C20-C21-C22-C23
5	D	802	PCW	C20-C21-C22-C23
5	A	811	PCW	C15-C16-C17-C18
5	B	807	PCW	C21-C22-C23-C24
5	C	806	PCW	C15-C16-C17-C18
5	C	812	PCW	C32-C33-C34-C35
5	A	812	PCW	C36-C37-C38-C39
5	C	811	PCW	C16-C17-C18-C19
5	D	810	PCW	C16-C17-C18-C19
5	B	811	PCW	C15-C16-C17-C18
3	C	805	Y01	CAC-CBB-CBE-CAP
5	D	808	PCW	O3P-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
4	C	804	CLR	C21-C20-C22-C23
4	A	802	CLR	C16-C17-C20-C22
5	B	811	PCW	C24-C25-C26-C27
3	B	801	Y01	CAJ-CAN-CBA-CAB
5	C	812	PCW	C15-C16-C17-C18
5	D	811	PCW	C15-C16-C17-C18
5	C	811	PCW	C15-C16-C17-C18
5	D	808	PCW	C15-C16-C17-C18
5	B	813	PCW	O2-C2-C3-O3
5	C	812	PCW	O2-C2-C3-O3
5	D	802	PCW	C35-C36-C37-C38
5	B	813	PCW	C42-C43-C44-C45
5	A	815	PCW	C13-C14-C15-C16
5	A	809	PCW	C14-C15-C16-C17
5	A	812	PCW	C19-C20-C21-C22
5	C	807	PCW	C19-C20-C21-C22
5	D	803	PCW	O31-C31-O2-C2
5	C	807	PCW	C16-C17-C18-C19
5	D	808	PCW	C14-C15-C16-C17
5	D	801	PCW	C15-C16-C17-C18
5	B	810	PCW	C23-C24-C25-C26
5	A	803	PCW	C33-C34-C35-C36
5	A	806	PCW	C15-C16-C17-C18
5	D	802	PCW	C14-C15-C16-C17
3	A	801	Y01	OAG-CAY-OAW-CBC
5	C	802	PCW	C19-C20-C21-C22
5	D	805	PCW	C22-C23-C24-C25
5	B	813	PCW	C2-C1-O3P-P
5	B	812	PCW	C14-C15-C16-C17
5	A	810	PCW	C15-C16-C17-C18
5	D	808	PCW	O3P-C1-C2-C3
5	D	810	PCW	C23-C24-C25-C26
3	A	814	Y01	CAJ-CAN-CBA-CAA
5	B	810	PCW	C22-C23-C24-C25
5	C	801	PCW	C14-C15-C16-C17
5	A	811	PCW	C32-C33-C34-C35
5	A	812	PCW	C13-C14-C15-C16
5	D	811	PCW	C13-C14-C15-C16
5	A	812	PCW	C15-C16-C17-C18
5	B	808	PCW	C15-C16-C17-C18
3	B	801	Y01	CAJ-CAN-CBA-CAA
5	C	807	PCW	C12-C13-C14-C15

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Mol	Chain	Res	Type	Atoms
3	C	805	Y01	CAC-CBB-CBE-CBI
3	C	805	Y01	CAJ-CAN-CBA-CAB
5	A	803	PCW	O3P-C1-C2-O2
5	A	812	PCW	O3P-C1-C2-O2
5	D	802	PCW	O3P-C1-C2-O2
5	A	804	PCW	C23-C24-C25-C26
5	A	809	PCW	C18-C19-C20-C21
5	D	814	PCW	C21-C22-C23-C24
3	C	805	Y01	CAN-CAJ-CAO-CBB
5	D	803	PCW	C33-C34-C35-C36
5	D	812	PCW	C15-C16-C17-C18
5	A	815	PCW	C22-C23-C24-C25
3	B	803	Y01	CAJ-CAN-CBA-CAB
5	C	807	PCW	C15-C16-C17-C18
5	D	810	PCW	C14-C15-C16-C17
5	C	813	PCW	C17-C18-C19-C20
5	D	805	PCW	C19-C20-C21-C22
5	A	803	PCW	C12-C13-C14-C15
5	A	811	PCW	C35-C36-C37-C38
3	C	805	Y01	CAO-CBB-CBE-CBI
5	A	806	PCW	C19-C20-C21-C22
5	D	802	PCW	C39-C40-C41-C42
5	B	807	PCW	C15-C16-C17-C18
5	C	807	PCW	C13-C14-C15-C16
4	D	807	CLR	C22-C23-C24-C25
5	B	813	PCW	C25-C26-C27-C28
5	A	803	PCW	C31-C32-C33-C34
5	C	806	PCW	O31-C31-O2-C2
5	D	814	PCW	C13-C14-C15-C16
5	C	813	PCW	C36-C37-C38-C39
5	D	801	PCW	C16-C17-C18-C19
3	C	805	Y01	CAO-CBB-CBE-CAP
5	A	809	PCW	C23-C24-C25-C26
5	C	802	PCW	C21-C22-C23-C24
5	C	813	PCW	C19-C20-C21-C22
5	D	804	PCW	C17-C18-C19-C20
5	B	807	PCW	C18-C19-C20-C21
5	A	811	PCW	C16-C17-C18-C19
5	B	807	PCW	C20-C21-C22-C23
5	C	806	PCW	O2-C2-C3-O3
5	C	813	PCW	O2-C2-C3-O3
4	C	804	CLR	C23-C24-C25-C26

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Mol	Chain	Res	Type	Atoms
5	B	806	PCW	C14-C15-C16-C17
5	A	811	PCW	O4P-C4-C5-N
5	B	806	PCW	O4P-C4-C5-N
5	B	812	PCW	O4P-C4-C5-N
5	C	806	PCW	O4P-C4-C5-N
5	C	812	PCW	O4P-C4-C5-N
5	A	809	PCW	C21-C22-C23-C24
5	C	810	PCW	C16-C17-C18-C19
5	A	803	PCW	C21-C22-C23-C24
5	D	808	PCW	C34-C35-C36-C37
5	C	806	PCW	C41-C42-C43-C44
5	D	810	PCW	C21-C22-C23-C24
5	A	811	PCW	C37-C38-C39-C40
5	B	807	PCW	C11-C12-C13-C14
5	D	801	PCW	C21-C22-C23-C24
5	B	802	PCW	C13-C14-C15-C16
5	B	813	PCW	C15-C16-C17-C18
5	B	813	PCW	O3P-C1-C2-O2
5	C	812	PCW	C36-C37-C38-C39
5	C	813	PCW	C13-C14-C15-C16
5	A	811	PCW	O2-C2-C3-O3
5	D	808	PCW	O2-C2-C3-O3
5	B	812	PCW	C13-C14-C15-C16
5	B	813	PCW	C1-C2-C3-O3
5	C	813	PCW	C1-C2-C3-O3
5	D	804	PCW	C15-C16-C17-C18
5	D	803	PCW	C25-C26-C27-C28
5	A	811	PCW	C4-O4P-P-O2P
5	A	812	PCW	C1-O3P-P-O1P
5	A	812	PCW	C1-O3P-P-O2P
5	A	812	PCW	C1-O3P-P-O4P
5	A	812	PCW	C4-O4P-P-O1P
5	B	806	PCW	C1-O3P-P-O2P
5	B	806	PCW	C1-O3P-P-O4P
5	B	813	PCW	C1-O3P-P-O1P
5	C	806	PCW	C1-O3P-P-O4P
5	D	802	PCW	C1-O3P-P-O2P
5	D	808	PCW	C1-O3P-P-O2P
5	D	802	PCW	C33-C34-C35-C36
5	D	803	PCW	C2-C1-O3P-P
5	B	806	PCW	C22-C23-C24-C25
5	B	806	PCW	C35-C36-C37-C38

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Mol	Chain	Res	Type	Atoms
5	C	801	PCW	C15-C16-C17-C18
5	A	805	PCW	C14-C15-C16-C17
5	D	801	PCW	C22-C23-C24-C25
5	D	802	PCW	C19-C20-C21-C22
5	C	806	PCW	C12-C13-C14-C15
5	A	812	PCW	C16-C17-C18-C19
5	C	813	PCW	C15-C16-C17-C18
5	A	811	PCW	C39-C40-C41-C42
5	B	812	PCW	C39-C40-C41-C42
5	C	812	PCW	C39-C40-C41-C42
5	C	801	PCW	C20-C21-C22-C23
5	A	811	PCW	C1-C2-C3-O3
5	C	812	PCW	C1-C2-C3-O3
5	B	807	PCW	C22-C23-C24-C25
4	B	804	CLR	C23-C24-C25-C26
5	A	815	PCW	C20-C21-C22-C23
5	D	803	PCW	C36-C37-C38-C39
5	D	810	PCW	C20-C21-C22-C23
5	A	810	PCW	C24-C25-C26-C27
5	C	801	PCW	C21-C22-C23-C24
5	A	815	PCW	C23-C24-C25-C26
5	D	805	PCW	C13-C14-C15-C16
5	C	802	PCW	C16-C17-C18-C19
5	A	804	PCW	C19-C20-C21-C22
5	A	812	PCW	C17-C18-C19-C20
5	D	804	PCW	C19-C20-C21-C22
5	C	806	PCW	C23-C24-C25-C26
5	D	810	PCW	C13-C14-C15-C16
5	A	803	PCW	C41-C42-C43-C44
3	D	806	Y01	CAM-CAL-CAX-OAH
5	A	810	PCW	C16-C17-C18-C19
5	A	815	PCW	C24-C25-C26-C27
5	B	813	PCW	C12-C13-C14-C15
5	D	809	PCW	C15-C16-C17-C18
3	D	806	Y01	CAM-CAL-CAX-OAF
5	C	813	PCW	C12-C13-C14-C15
5	C	812	PCW	C34-C35-C36-C37
5	A	809	PCW	C11-C12-C13-C14
5	B	806	PCW	C40-C41-C42-C43
5	C	806	PCW	C36-C37-C38-C39
5	D	805	PCW	C23-C24-C25-C26
5	A	803	PCW	C23-C24-C25-C26

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Mol	Chain	Res	Type	Atoms
3	B	803	Y01	CAM-CAL-CAX-OAF
5	A	811	PCW	C19-C20-C21-C22
5	B	802	PCW	C17-C18-C19-C20
5	B	807	PCW	C19-C20-C21-C22
5	D	813	PCW	C15-C16-C17-C18
4	B	804	CLR	C20-C22-C23-C24
5	C	811	PCW	C19-C20-C21-C22
5	C	813	PCW	C39-C40-C41-C42
5	B	810	PCW	C14-C15-C16-C17
5	A	805	PCW	C19-C20-C21-C22
5	B	813	PCW	C24-C25-C26-C27
3	A	814	Y01	CAM-CAL-CAX-OAH
5	B	812	PCW	C2-C1-O3P-P
5	D	808	PCW	C2-C1-O3P-P
5	A	812	PCW	C22-C23-C24-C25
3	B	803	Y01	CAM-CAL-CAX-OAH
5	C	801	PCW	C23-C24-C25-C26
5	C	809	PCW	C13-C14-C15-C16
5	B	812	PCW	C19-C20-C21-C22
5	D	803	PCW	C17-C18-C19-C20
3	C	803	Y01	CAM-CAL-CAX-OAH
5	D	803	PCW	O3P-C1-C2-C3
5	B	808	PCW	C17-C18-C19-C20
5	C	812	PCW	C19-C20-C21-C22
5	D	801	PCW	C17-C18-C19-C20
3	A	814	Y01	CAM-CAL-CAX-OAF
5	D	808	PCW	C13-C14-C15-C16
5	A	813	PCW	C12-C13-C14-C15
5	A	804	PCW	C13-C14-C15-C16
5	D	810	PCW	C19-C20-C21-C22
5	D	814	PCW	C18-C19-C20-C21
4	B	804	CLR	C22-C23-C24-C25
5	A	810	PCW	C17-C18-C19-C20
5	A	803	PCW	C25-C26-C27-C28
5	C	807	PCW	C18-C19-C20-C21
5	B	806	PCW	C39-C40-C41-C42
5	C	813	PCW	O3P-C1-C2-O2
5	C	806	PCW	C21-C22-C23-C24
5	C	808	PCW	C15-C16-C17-C18
5	A	803	PCW	C39-C40-C41-C42
5	B	812	PCW	C37-C38-C39-C40
5	C	812	PCW	C17-C18-C19-C20

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Mol	Chain	Res	Type	Atoms
5	A	803	PCW	C42-C43-C44-C45
5	C	806	PCW	C19-C20-C21-C22
5	D	808	PCW	C39-C40-C41-C42
5	D	812	PCW	C14-C15-C16-C17
5	A	803	PCW	O3P-C1-C2-C3
5	C	813	PCW	O3P-C1-C2-C3
3	C	803	Y01	CAM-CAL-CAX-OAF
3	D	806	Y01	CAJ-CAN-CBA-CAB
5	A	803	PCW	C19-C20-C21-C22
5	D	808	PCW	C19-C20-C21-C22
5	A	812	PCW	C37-C38-C39-C40
5	A	815	PCW	C17-C18-C19-C20
5	C	807	PCW	C21-C22-C23-C24
5	C	810	PCW	C23-C24-C25-C26
3	B	803	Y01	CAL-CAM-CAY-OAW
5	D	812	PCW	C12-C13-C14-C15
5	B	802	PCW	C23-C24-C25-C26
5	B	813	PCW	C41-C42-C43-C44
5	A	811	PCW	O3-C11-C12-C13
5	B	813	PCW	C22-C23-C24-C25
3	A	801	Y01	CAX-CAL-CAM-CAY
5	A	805	PCW	C15-C16-C17-C18
5	C	811	PCW	C24-C25-C26-C27
5	C	813	PCW	O2-C31-C32-C33
5	D	808	PCW	C21-C22-C23-C24
5	B	813	PCW	C40-C41-C42-C43
5	A	804	PCW	C15-C16-C17-C18
3	B	805	Y01	CAL-CAM-CAY-OAW
5	D	811	PCW	C19-C20-C21-C22
5	D	809	PCW	C12-C13-C14-C15
5	D	809	PCW	C23-C24-C25-C26
5	D	811	PCW	C17-C18-C19-C20
5	D	802	PCW	C13-C14-C15-C16
3	B	805	Y01	CAL-CAM-CAY-OAG
5	A	804	PCW	C17-C18-C19-C20
5	A	805	PCW	C17-C18-C19-C20
5	A	809	PCW	C17-C18-C19-C20
5	B	807	PCW	C17-C18-C19-C20
5	B	810	PCW	C17-C18-C19-C20
5	C	802	PCW	C17-C18-C19-C20
5	C	807	PCW	C17-C18-C19-C20
5	C	810	PCW	C17-C18-C19-C20

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Mol	Chain	Res	Type	Atoms
5	D	805	PCW	C17-C18-C19-C20
5	D	809	PCW	C17-C18-C19-C20
5	D	810	PCW	C17-C18-C19-C20
5	D	814	PCW	C17-C18-C19-C20
5	D	809	PCW	C13-C14-C15-C16
5	A	811	PCW	O11-C11-C12-C13
5	C	813	PCW	O31-C31-C32-C33
5	C	806	PCW	O3-C11-C12-C13
3	B	803	Y01	CAL-CAM-CAY-OAG
5	B	802	PCW	C16-C17-C18-C19
5	D	803	PCW	C24-C25-C26-C27

There are no ring outliers.

33 monomers are involved in 66 short contacts:

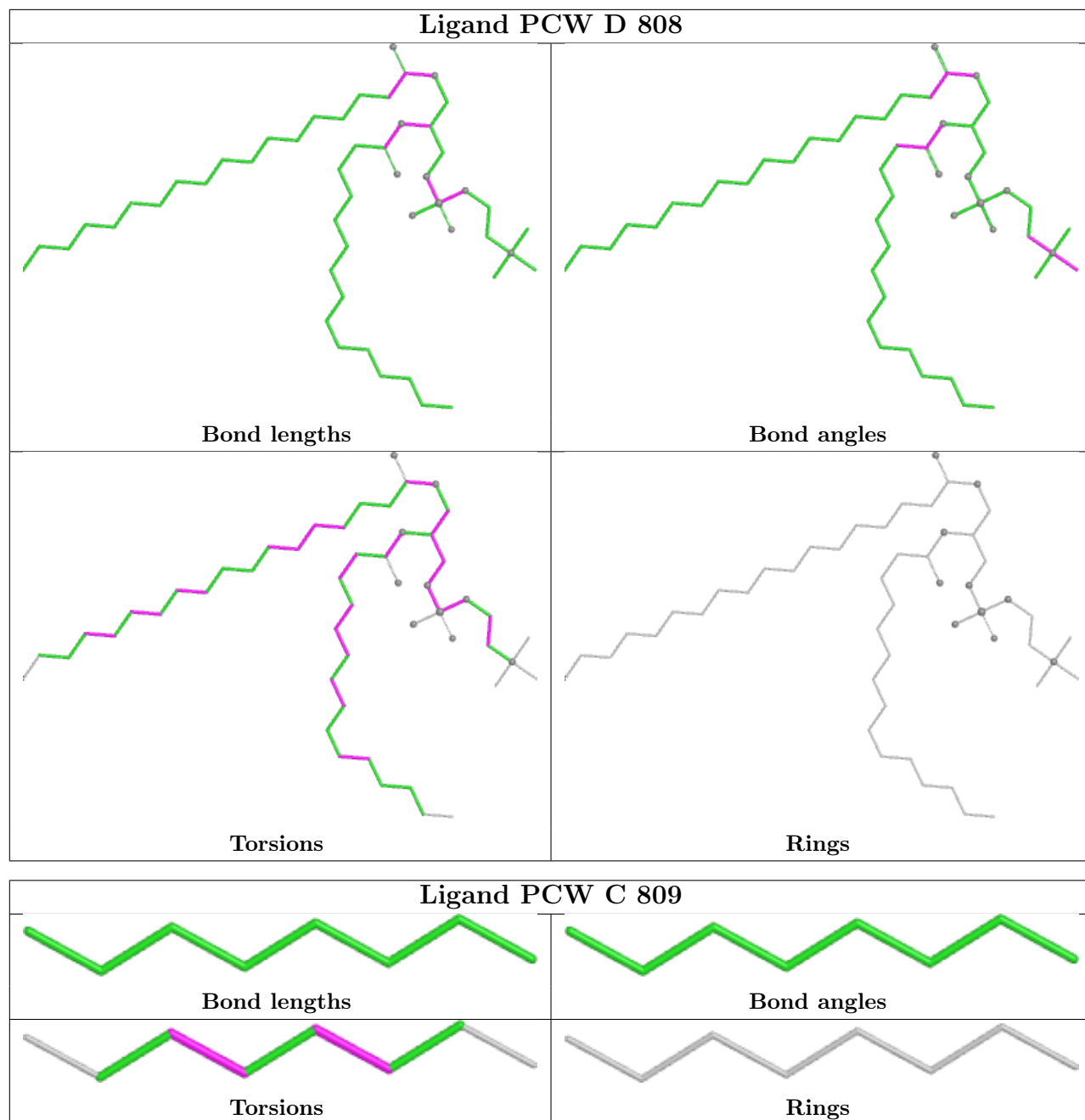
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	808	PCW	3	0
5	A	811	PCW	1	0
3	A	801	Y01	3	0
3	A	814	Y01	3	0
4	A	802	CLR	5	0
5	B	802	PCW	1	0
5	C	806	PCW	2	0
4	D	807	CLR	4	0
3	C	805	Y01	1	0
5	B	808	PCW	1	0
5	B	810	PCW	1	0
4	B	804	CLR	5	0
5	A	806	PCW	1	0
5	A	803	PCW	2	0
5	C	813	PCW	1	0
5	A	812	PCW	2	0
3	B	805	Y01	3	0
4	C	804	CLR	5	0
3	C	803	Y01	2	0
5	C	801	PCW	1	0
5	B	806	PCW	4	0
5	C	802	PCW	1	0
3	B	801	Y01	4	0
5	B	812	PCW	1	0
5	C	808	PCW	1	0
5	A	804	PCW	1	0

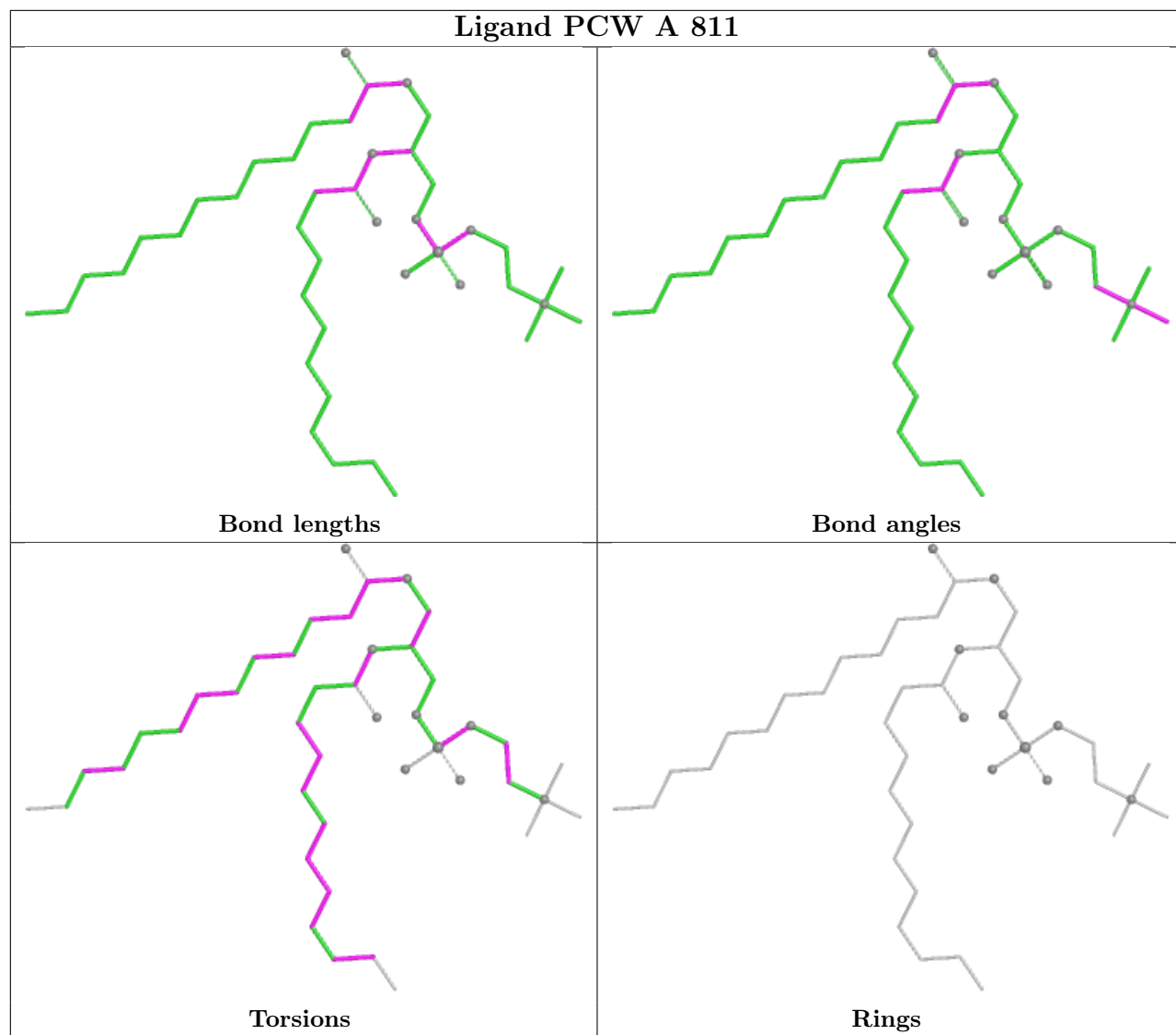
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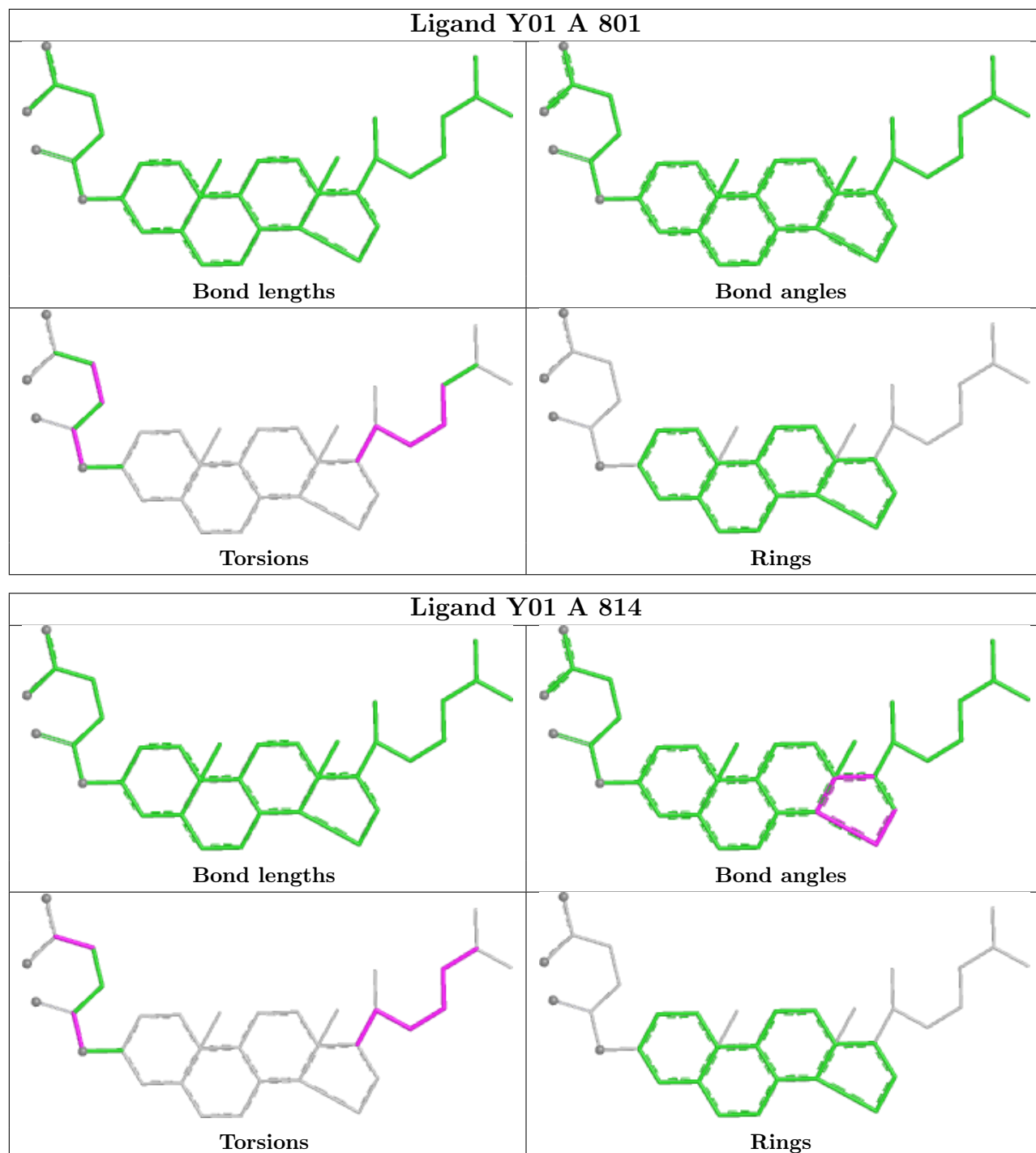
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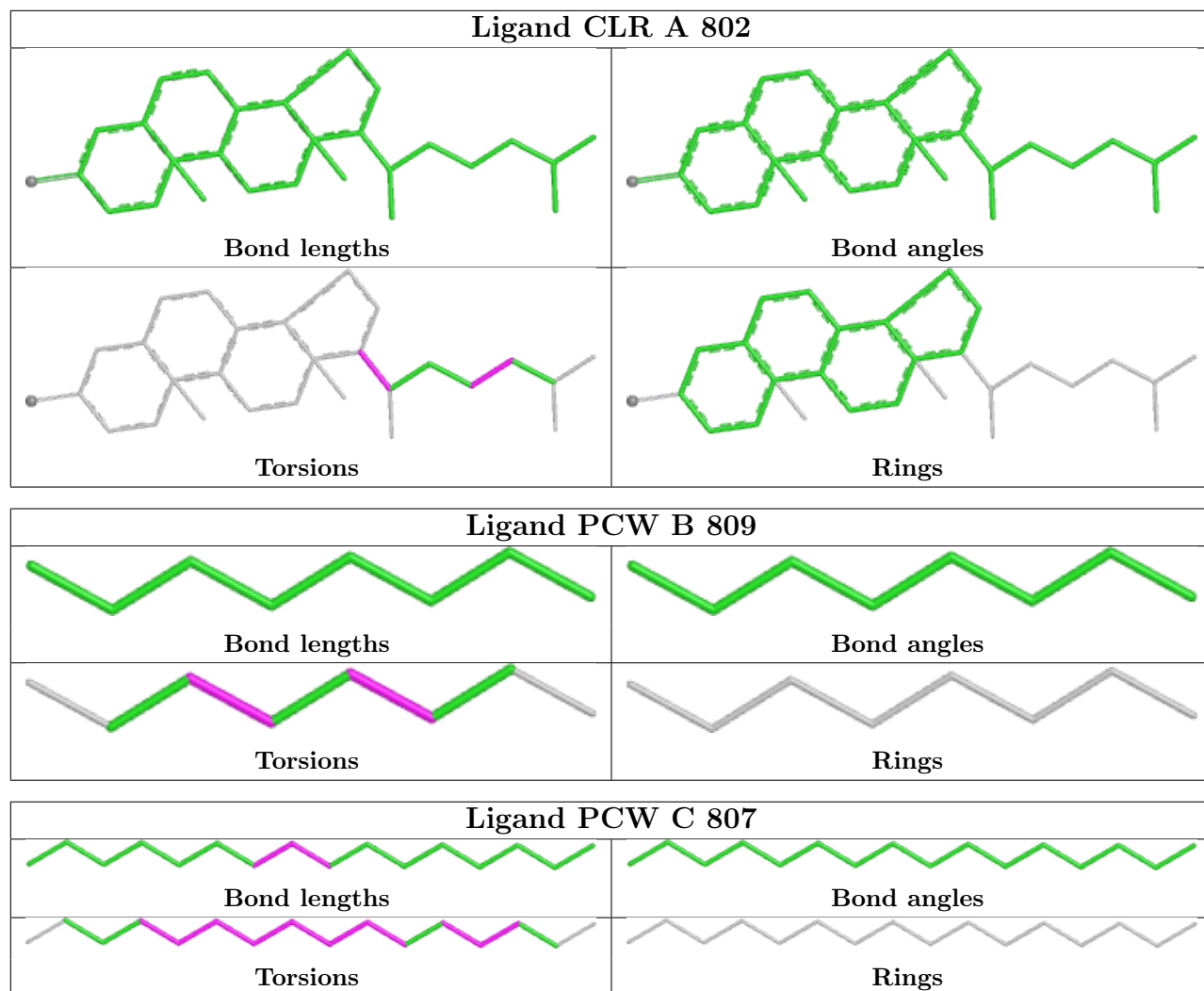
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	809	PCW	1	0
3	D	806	Y01	3	0
3	B	803	Y01	3	0
5	A	815	PCW	1	0
5	D	804	PCW	3	0
5	A	810	PCW	1	0
5	C	810	PCW	1	0

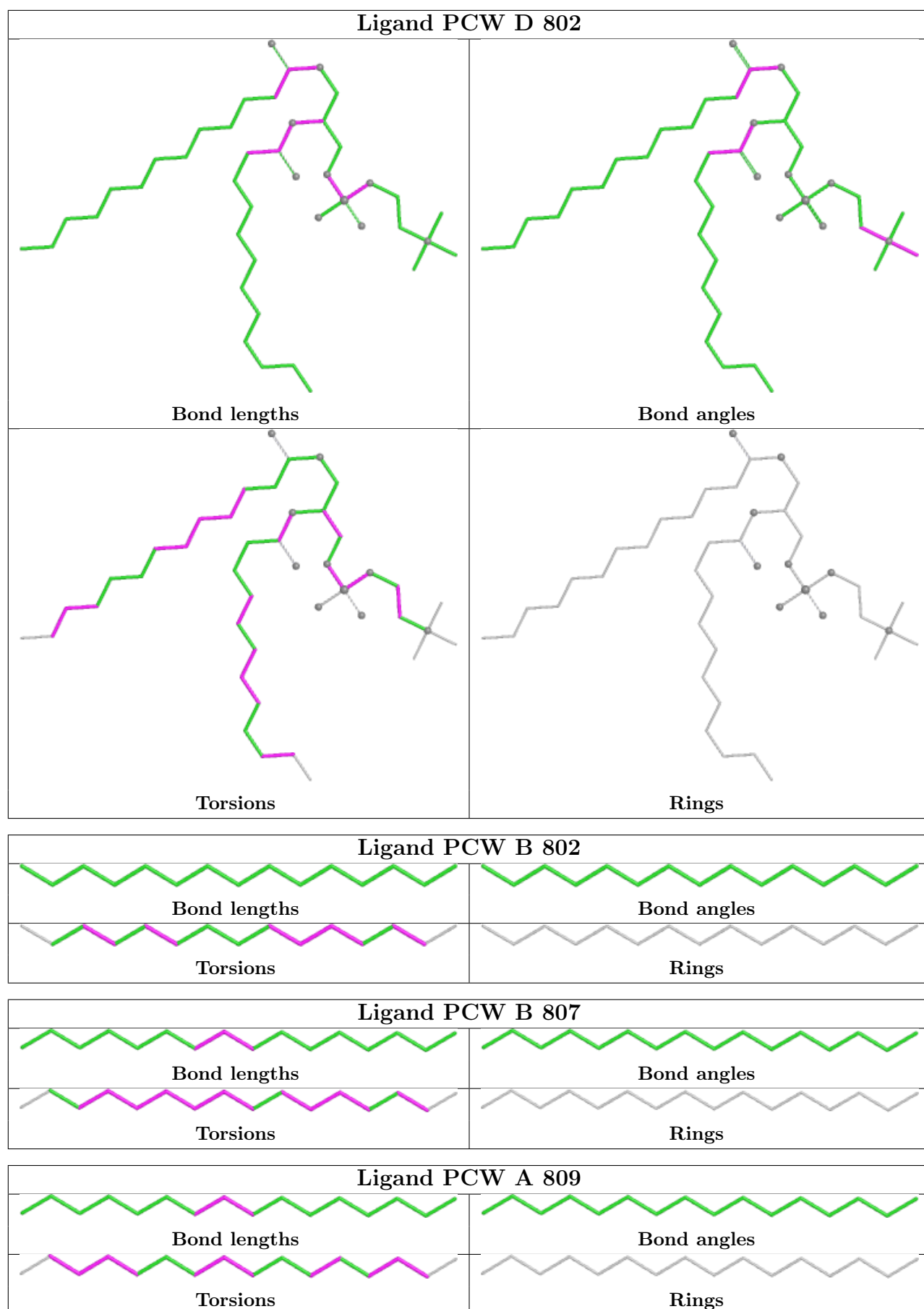
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

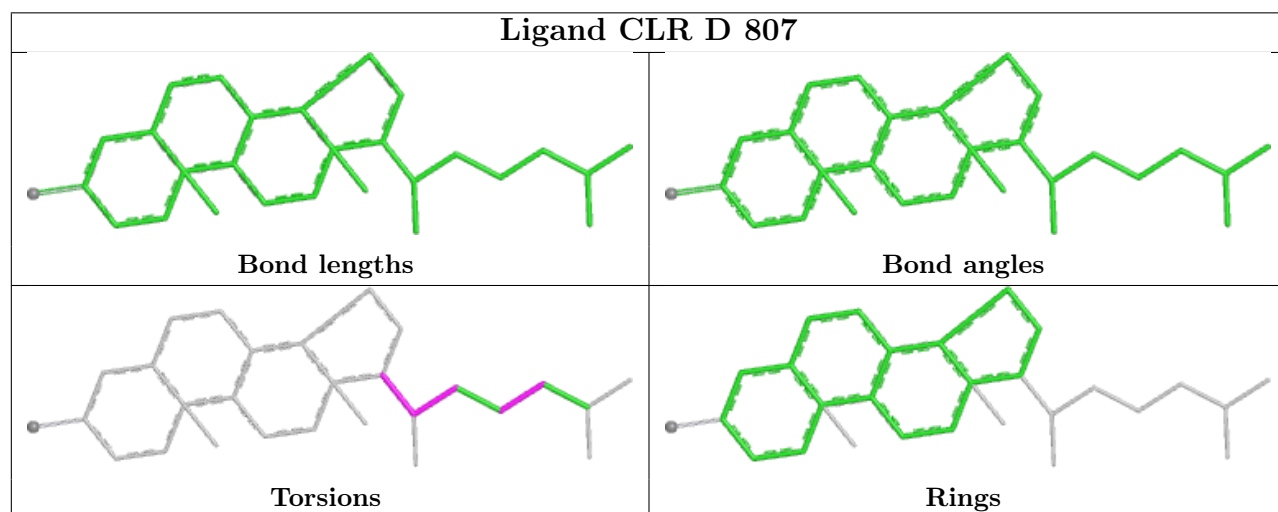
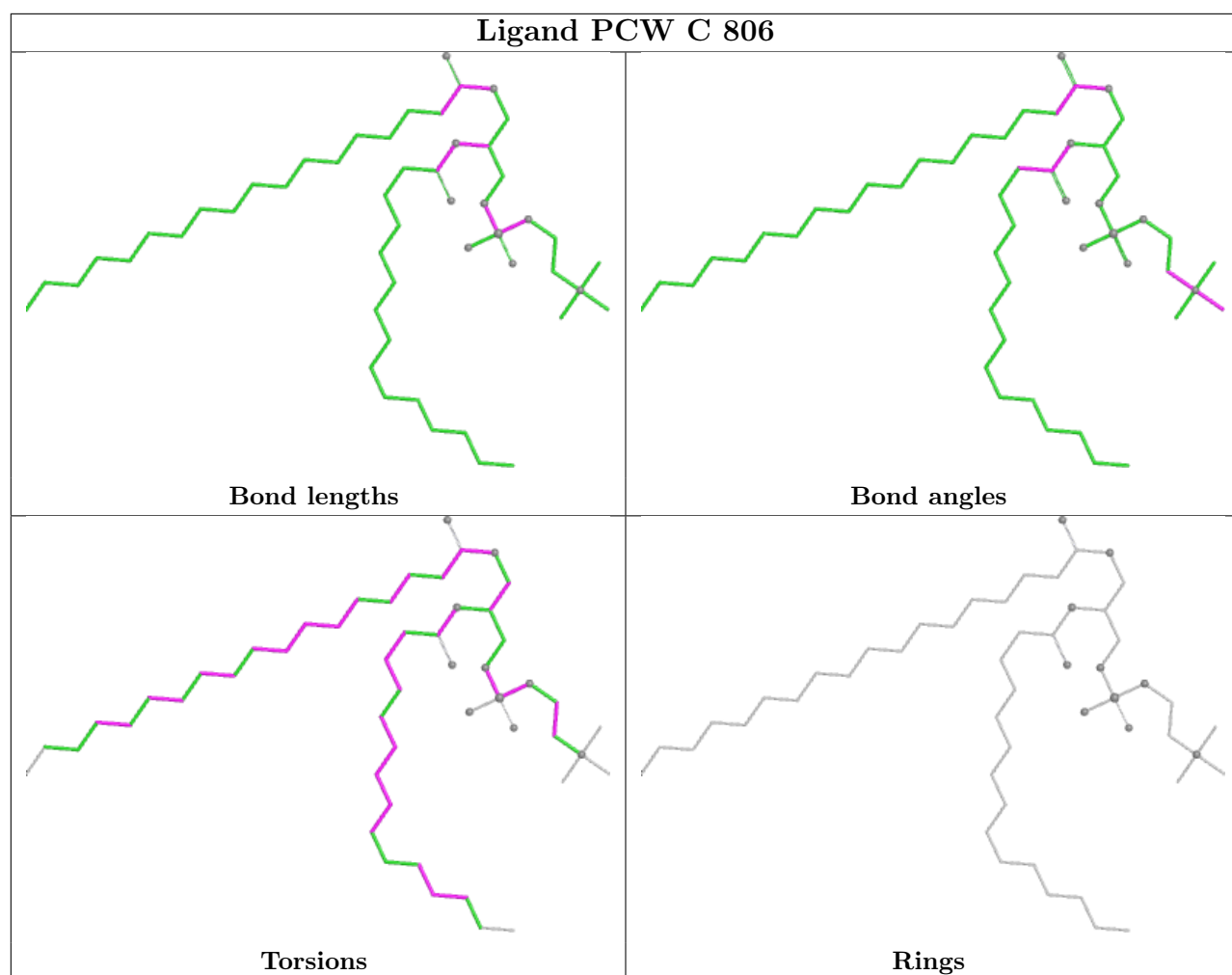


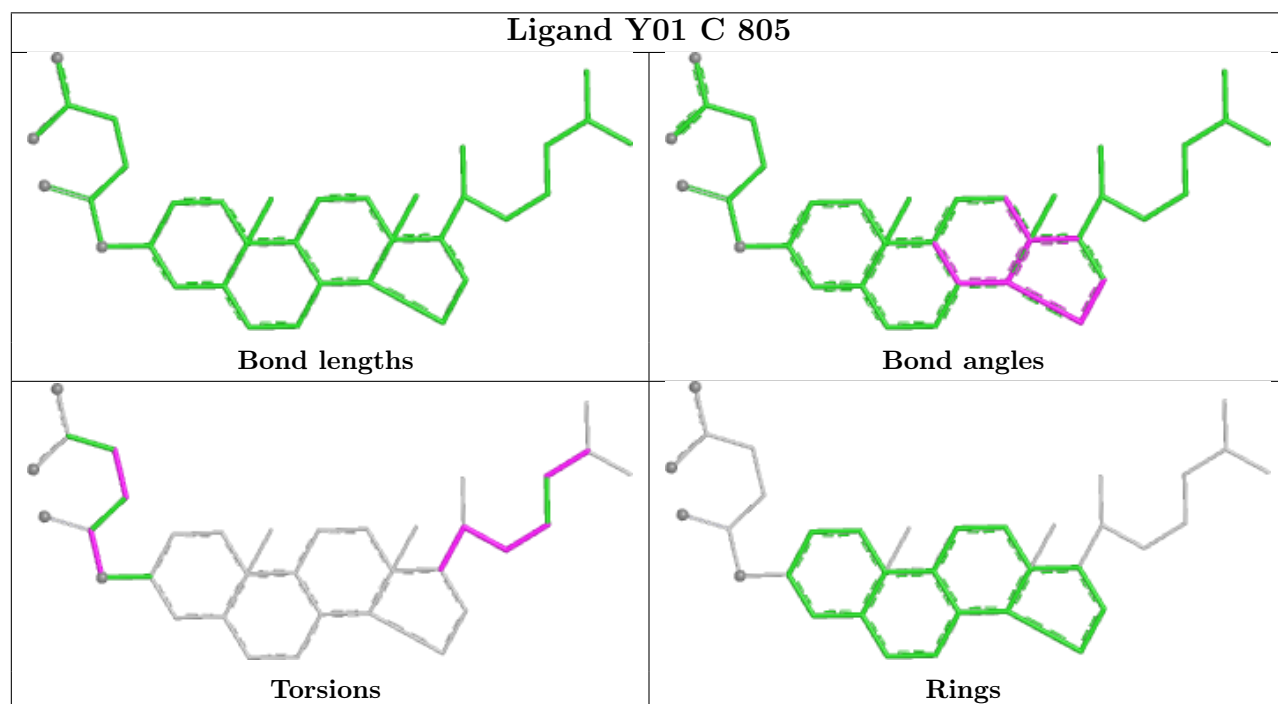
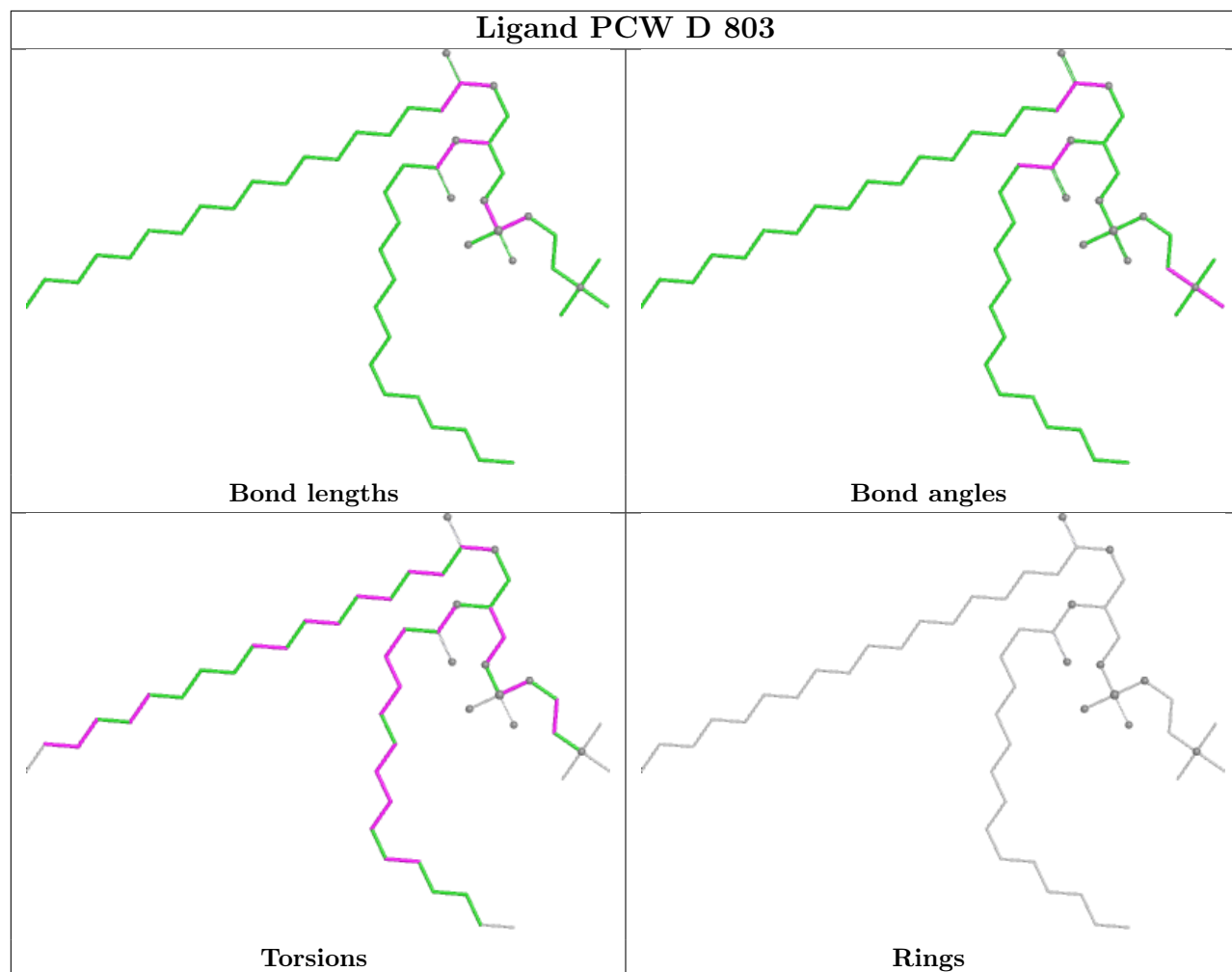


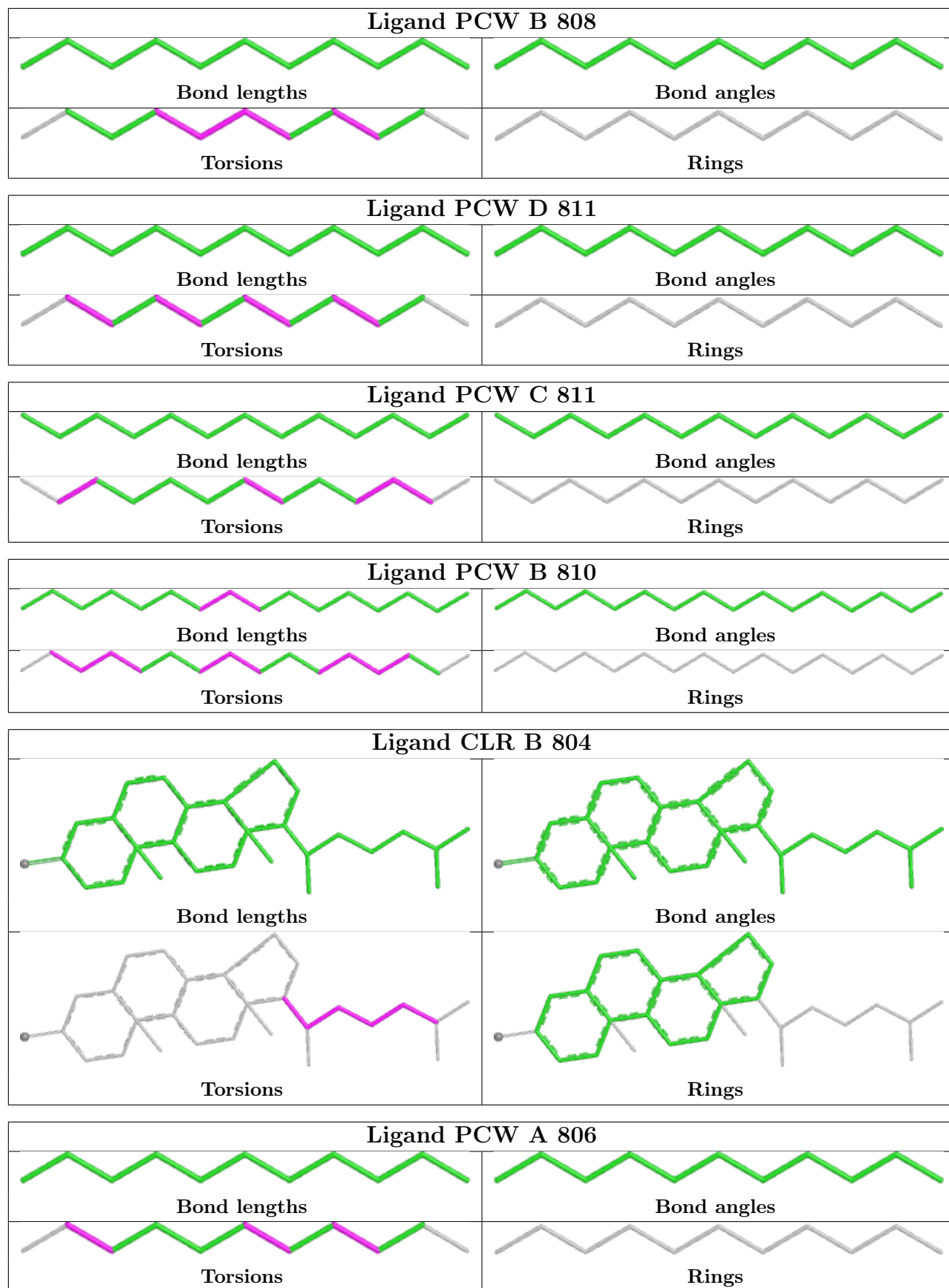


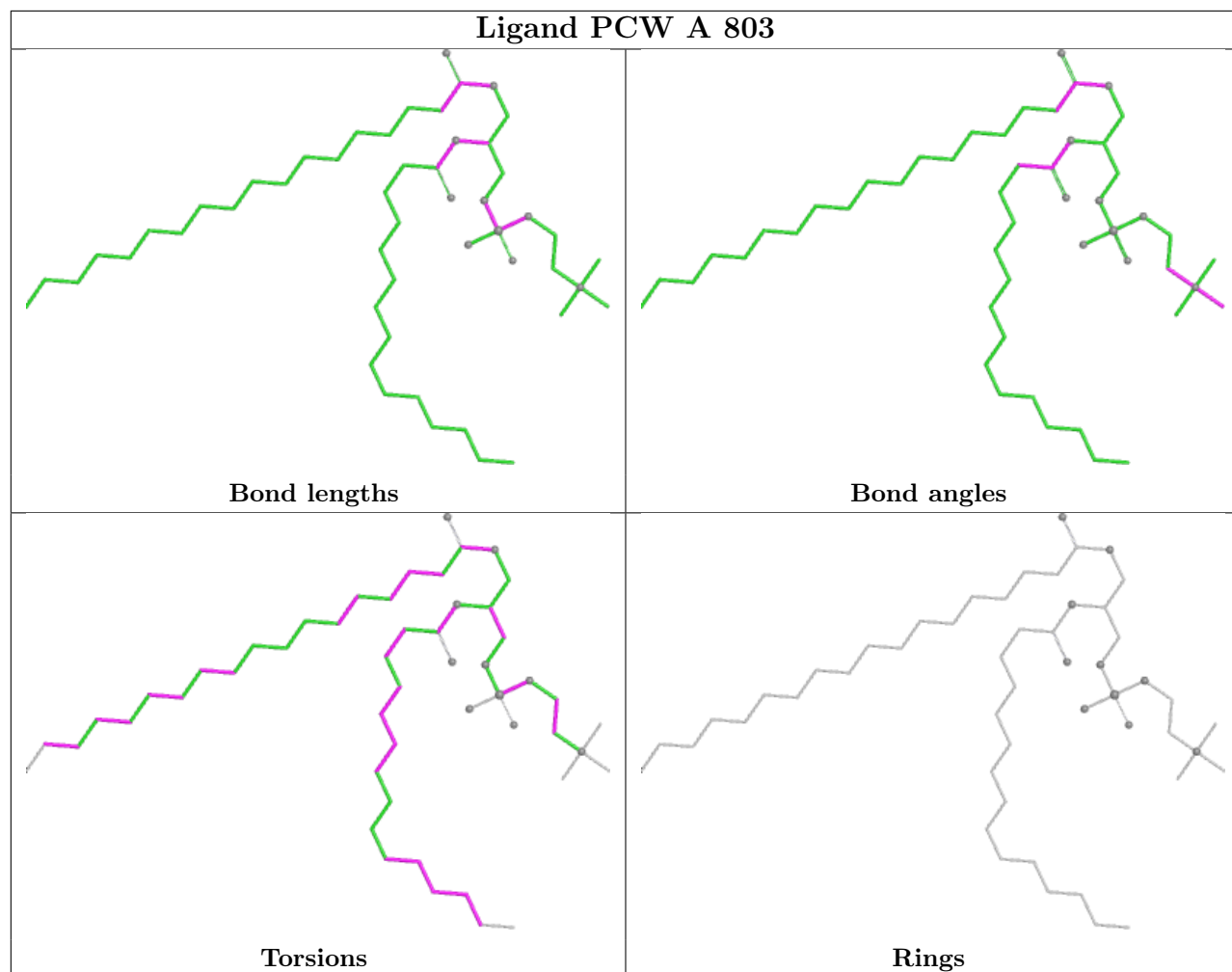


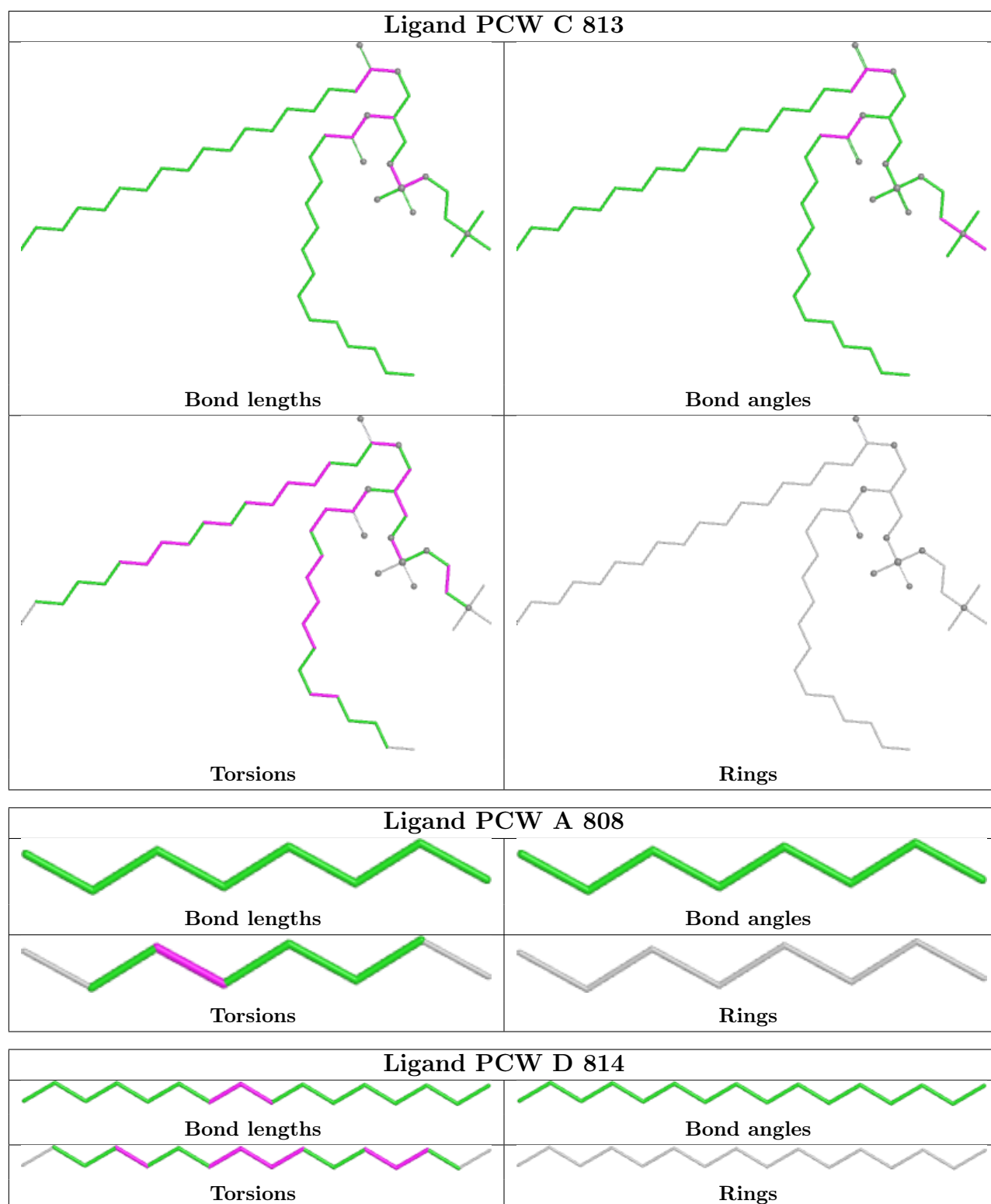


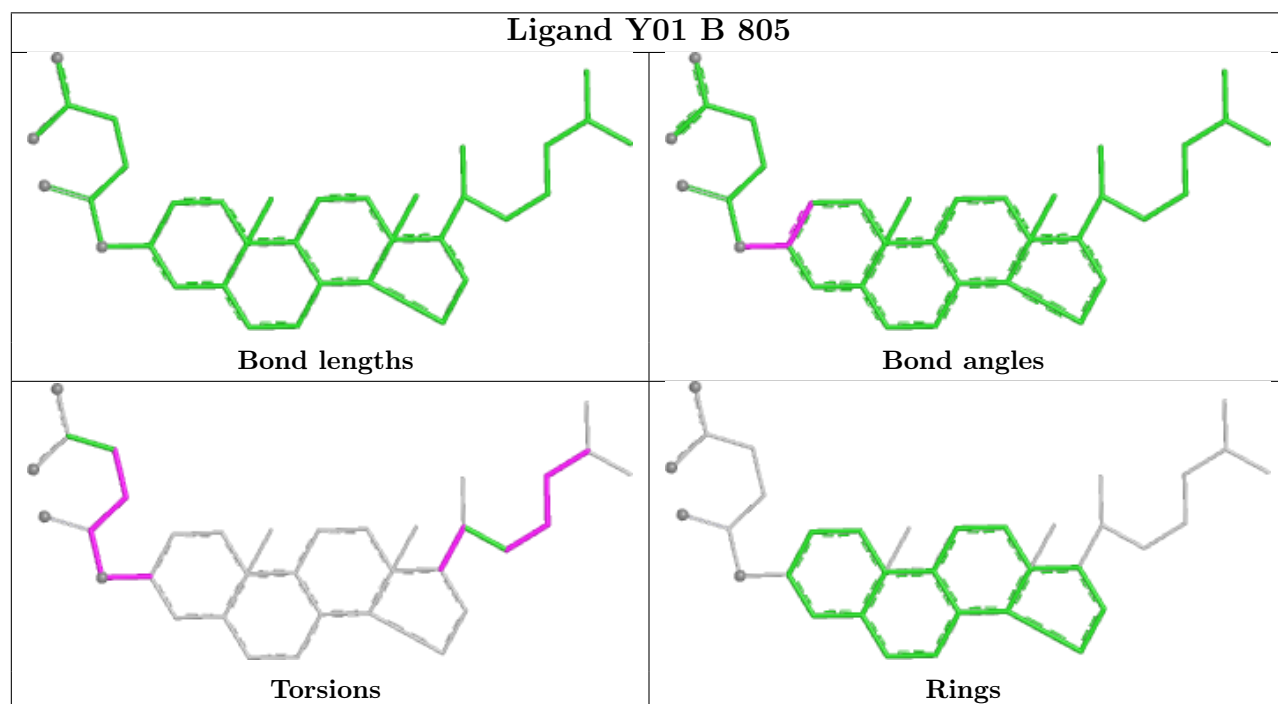
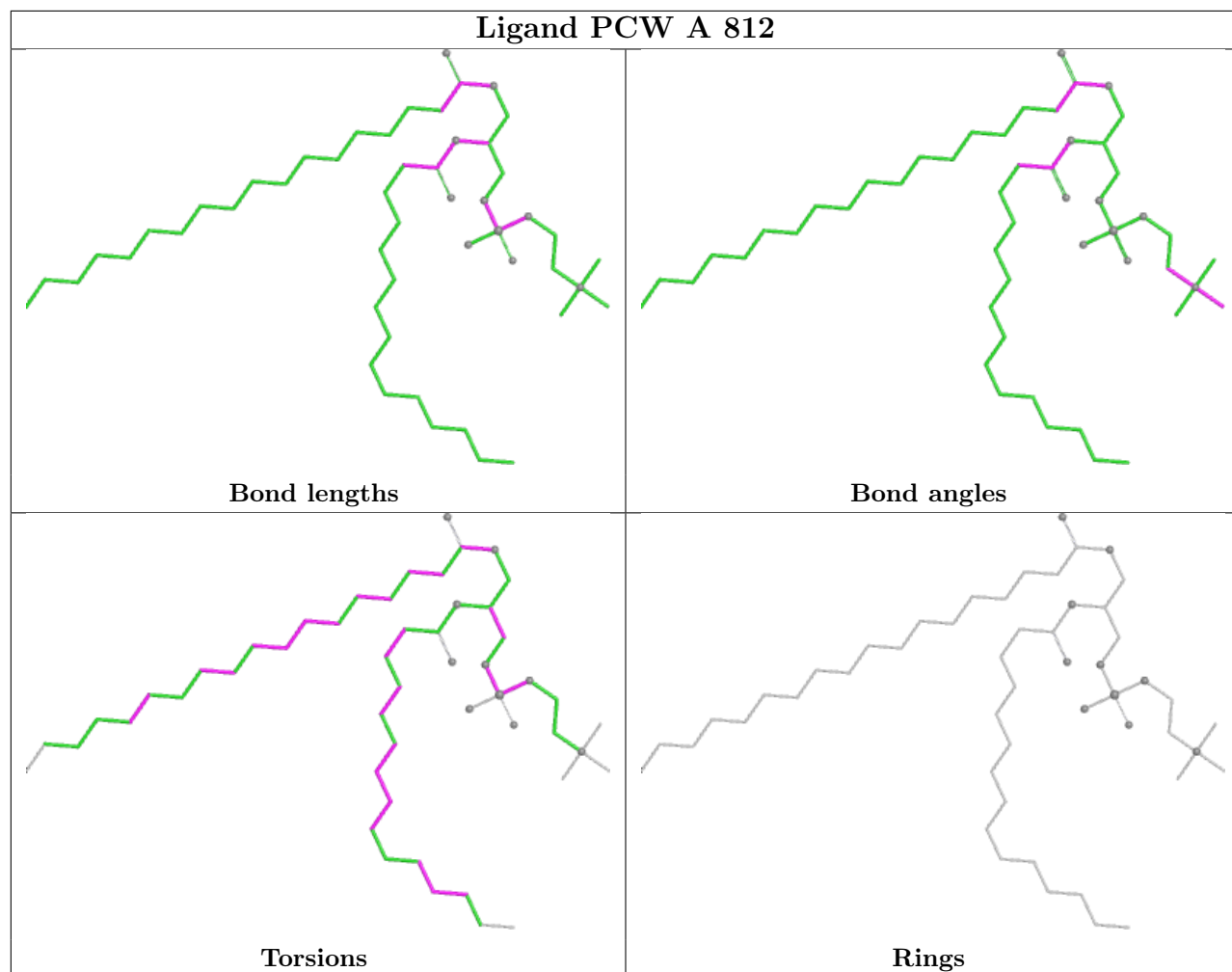


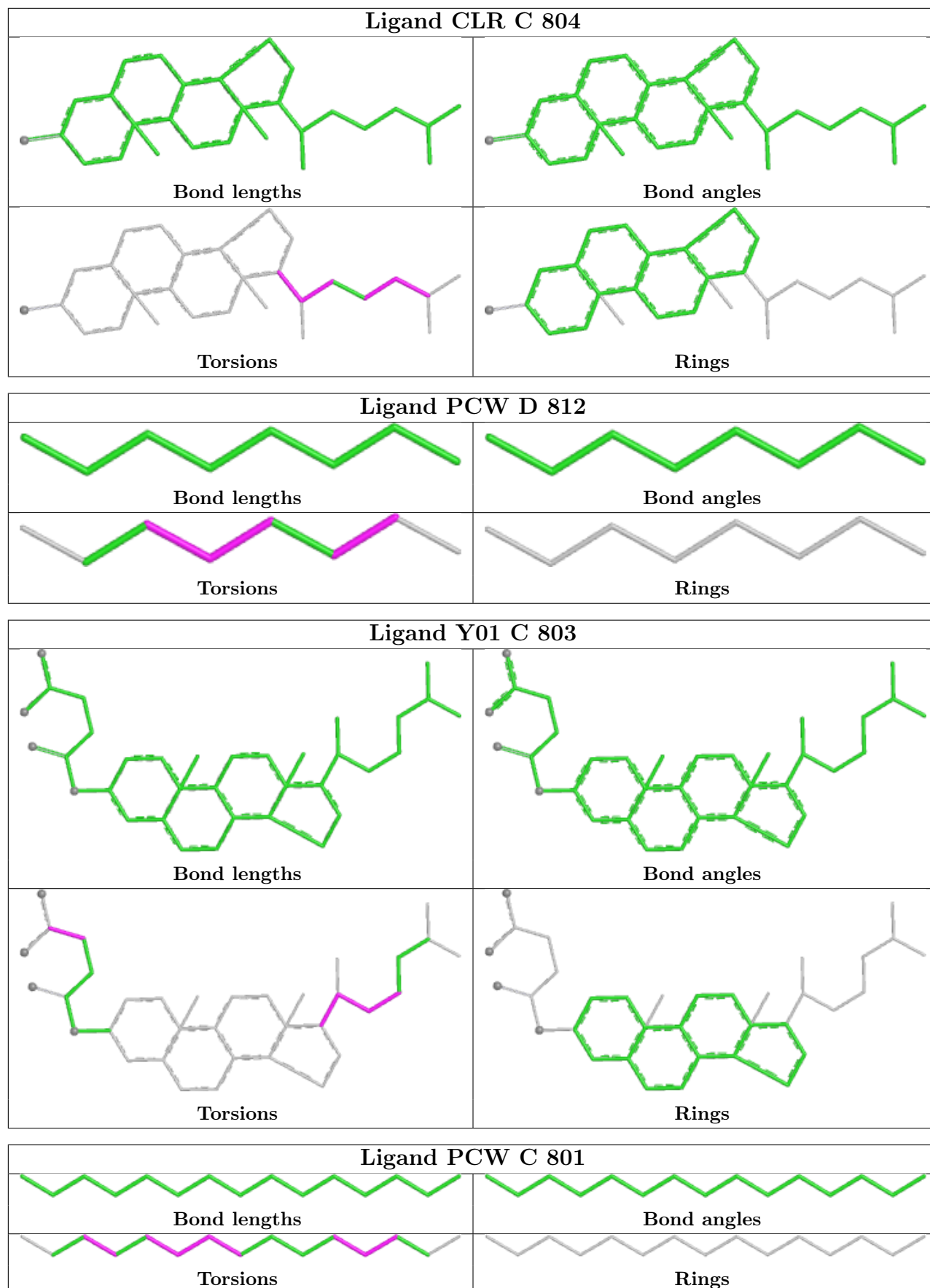


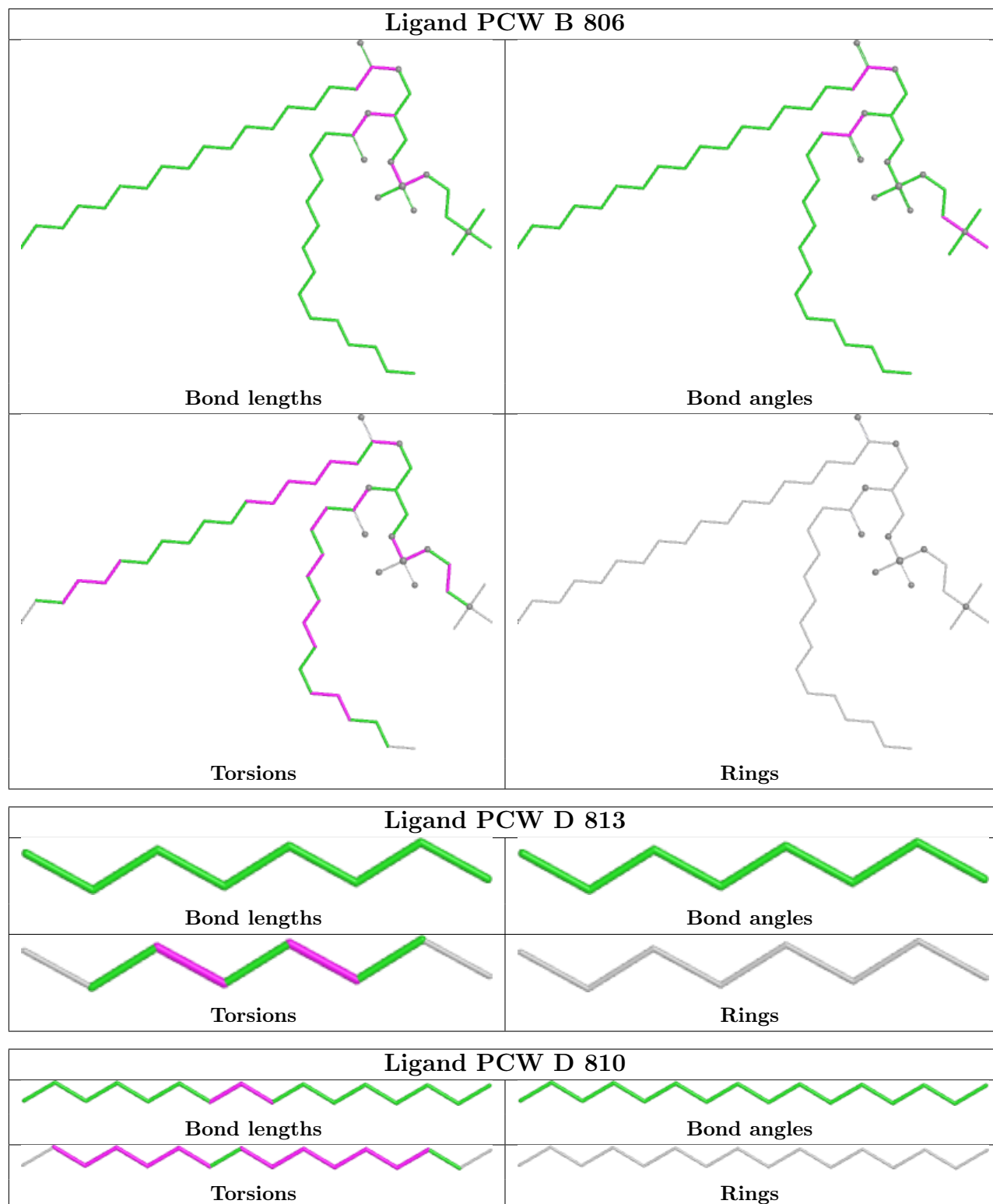


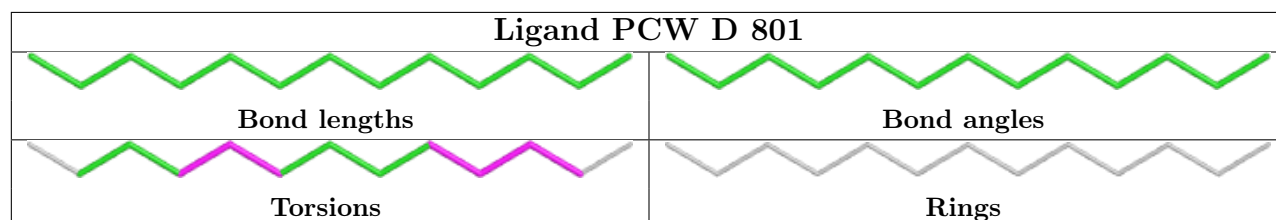
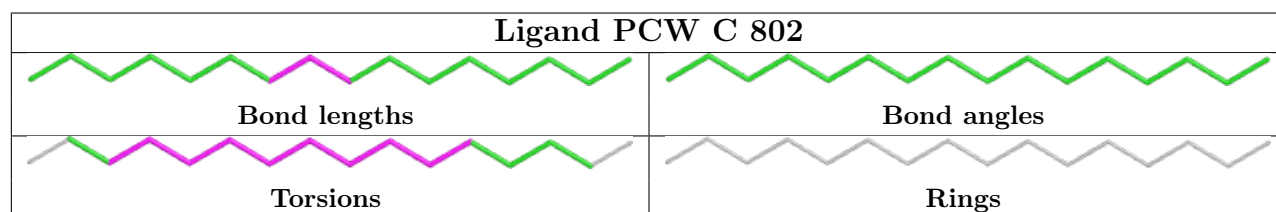
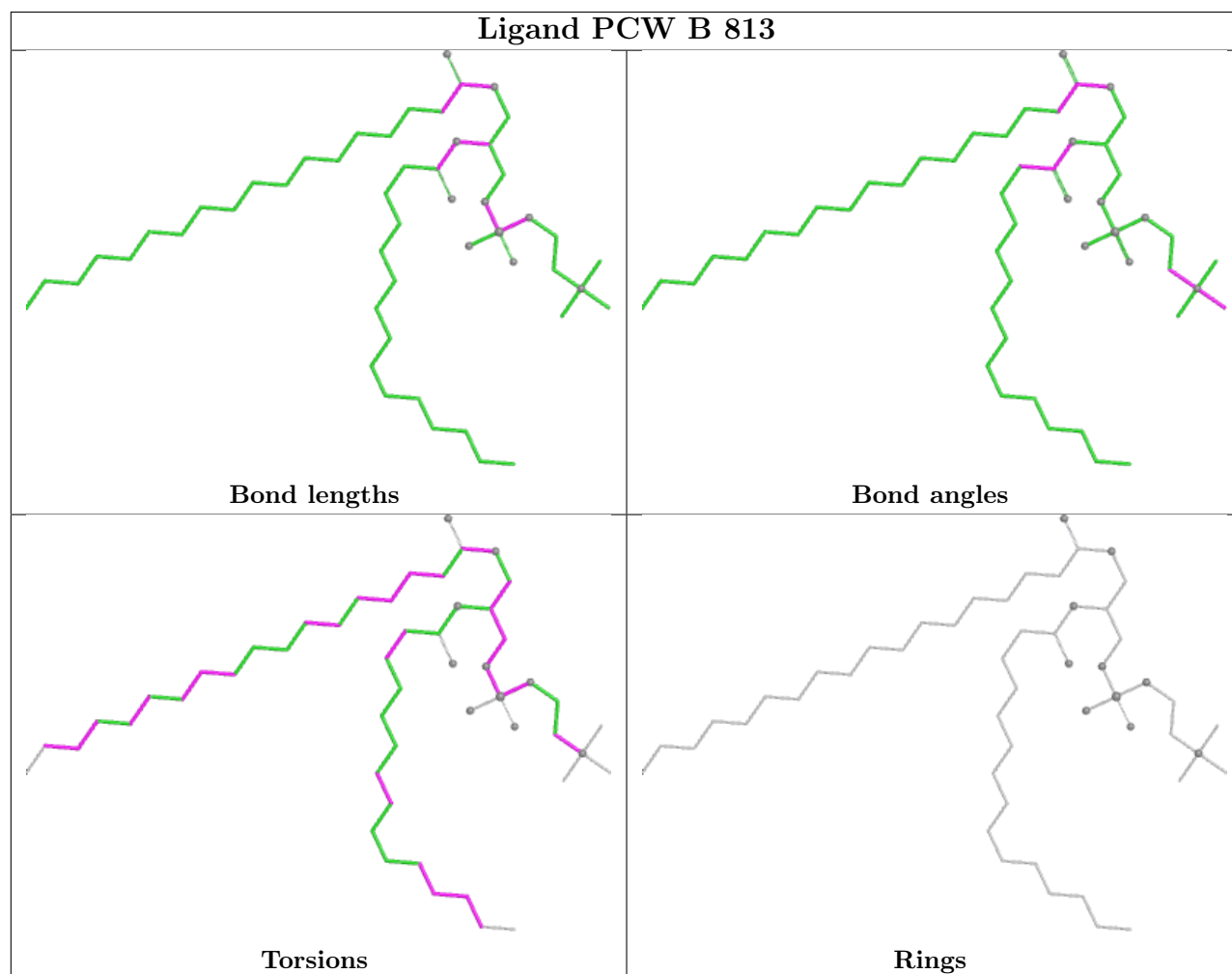
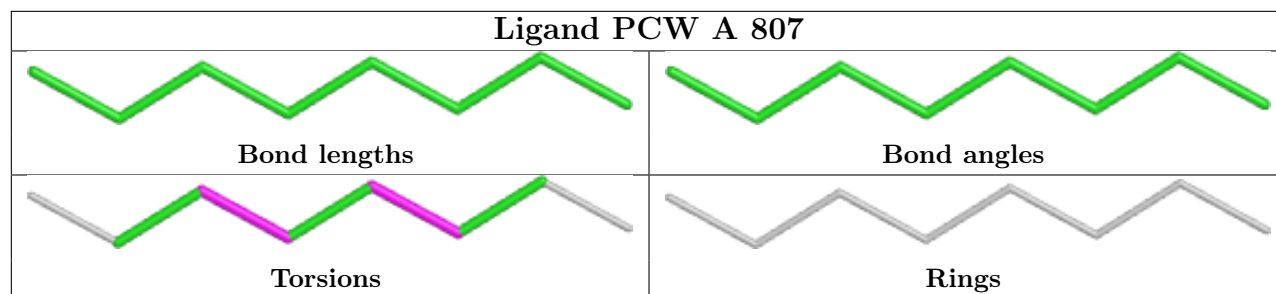


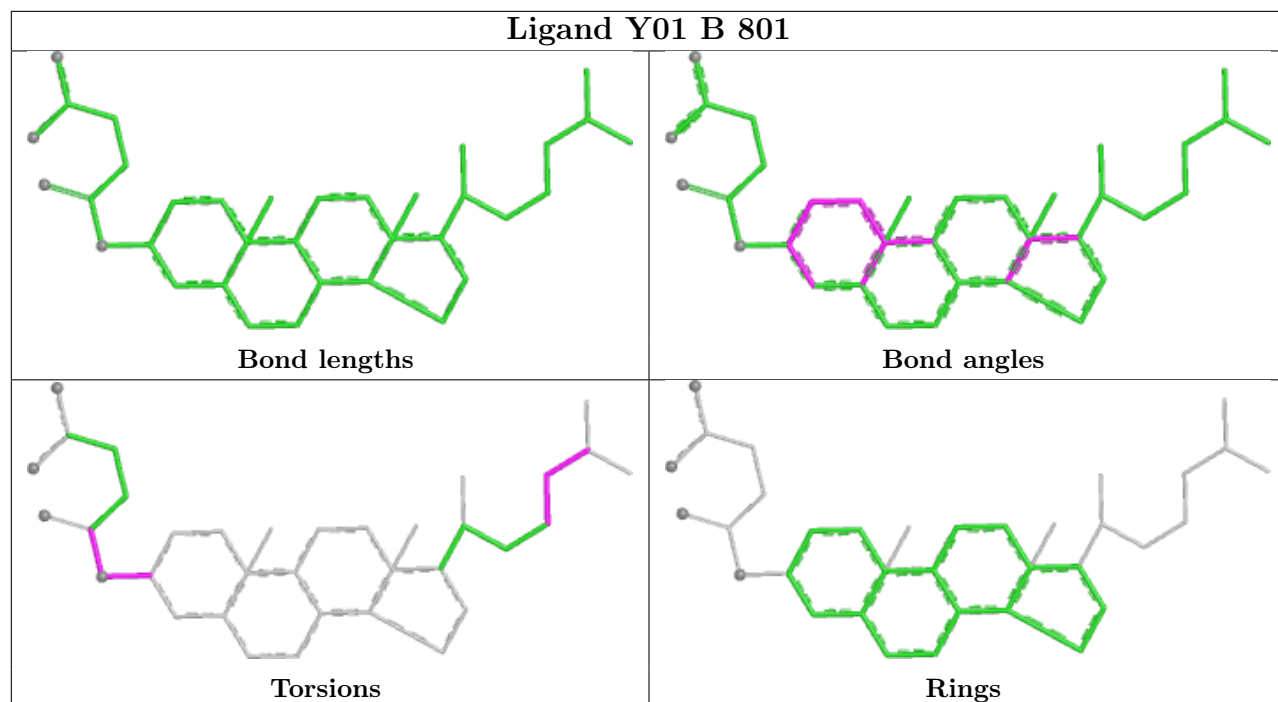


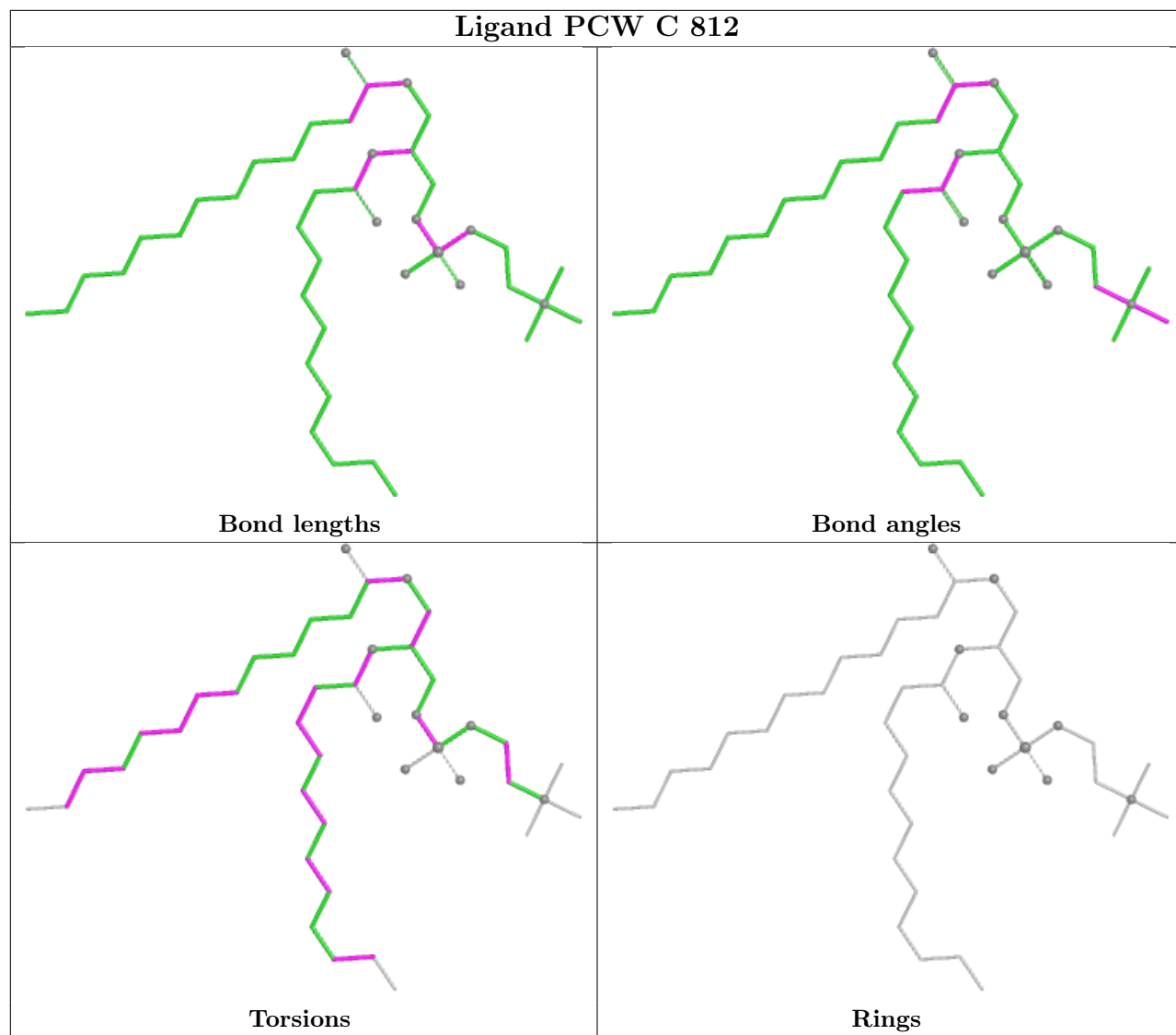


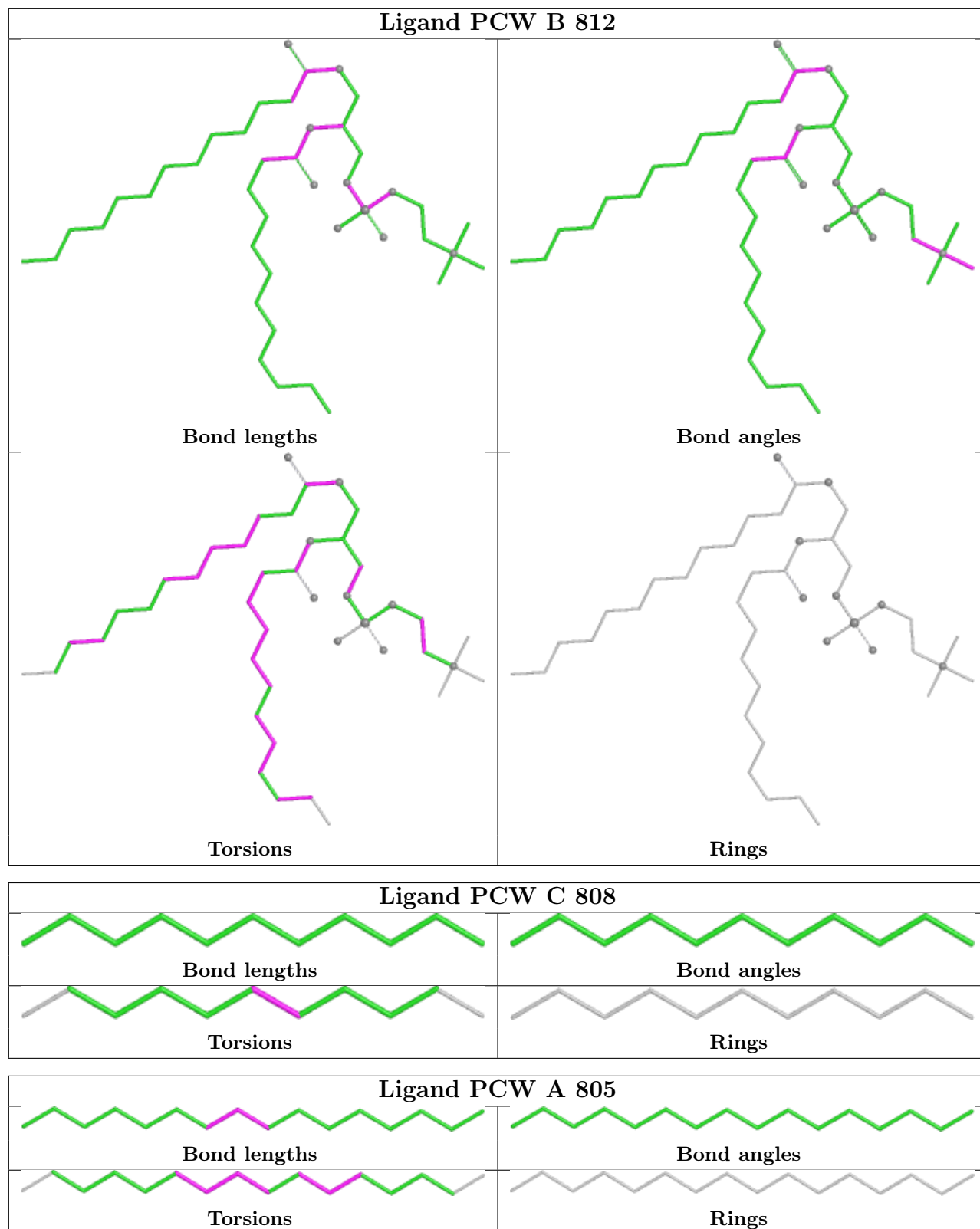


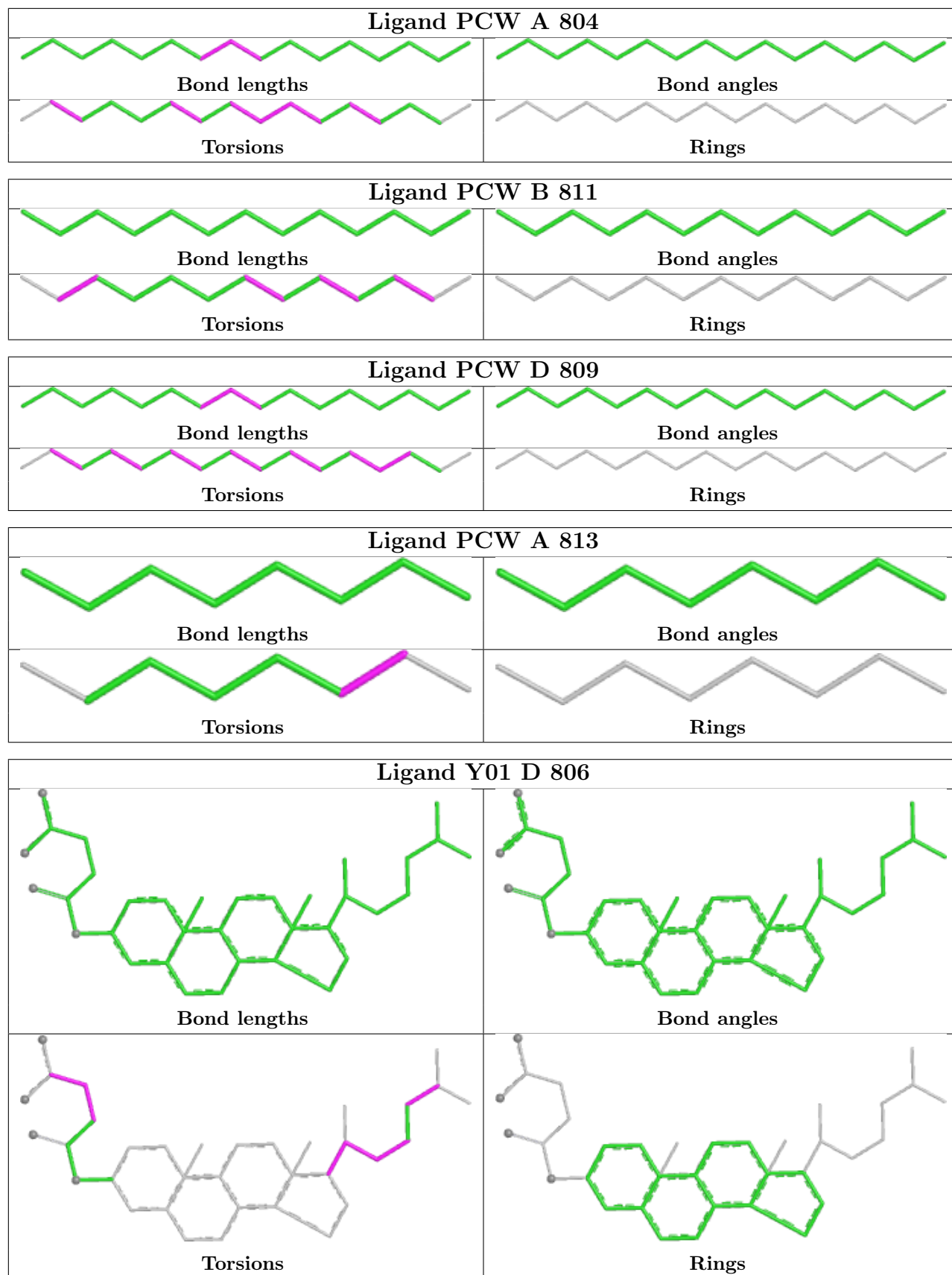


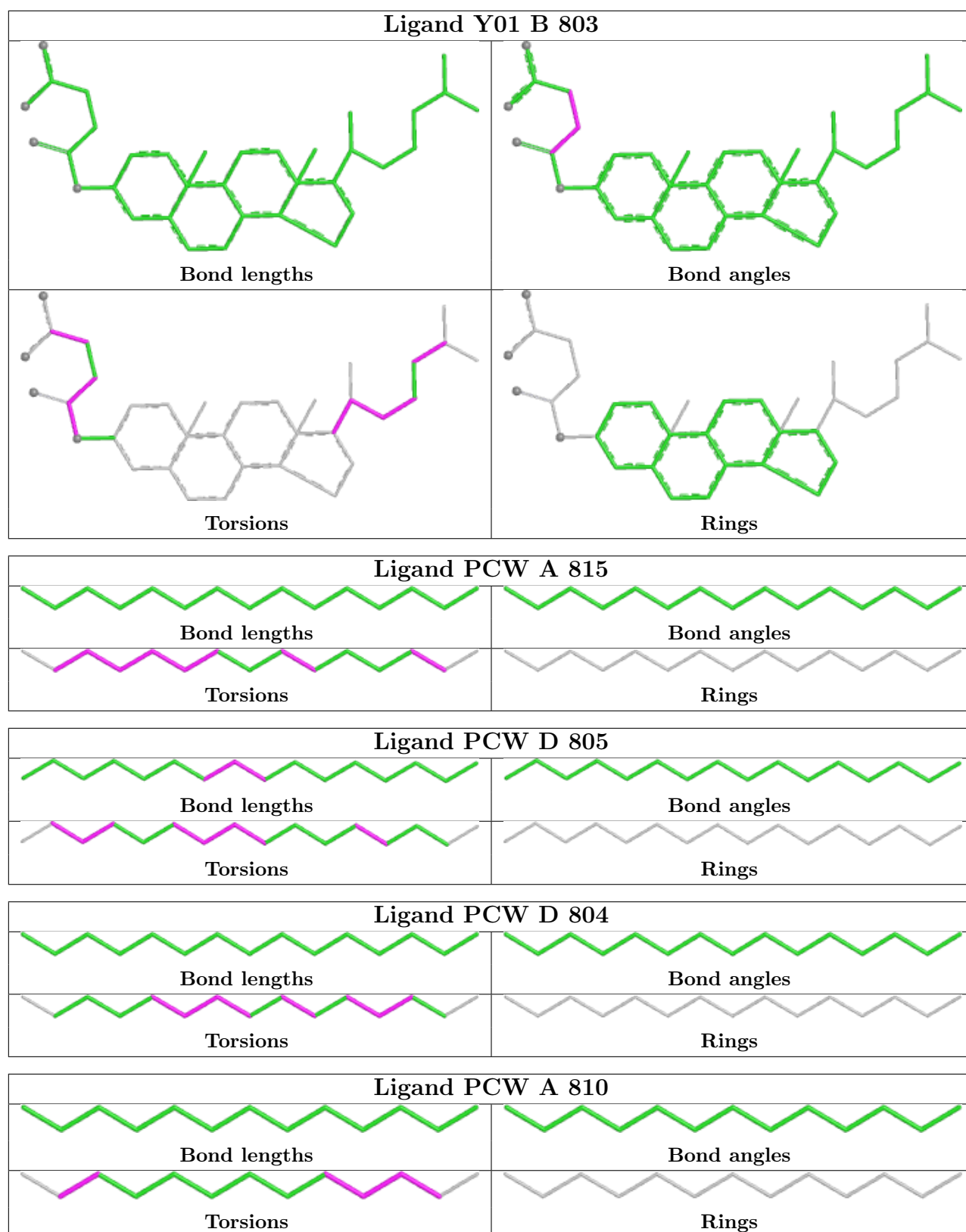


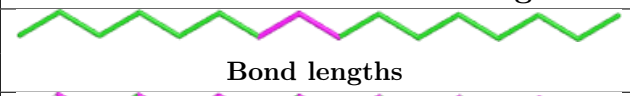













Ligand PCW C 810	
 <p>Bond lengths</p>	 <p>Bond angles</p>
 <p>Torsions</p>	 <p>Rings</p>

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.

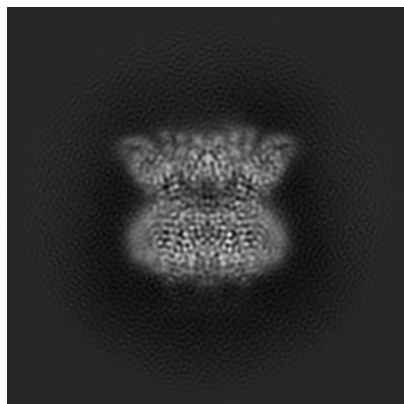
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45934. These allow visual inspection of the internal detail of the map and identification of artifacts.

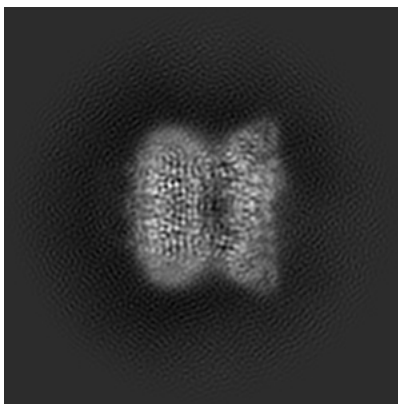
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

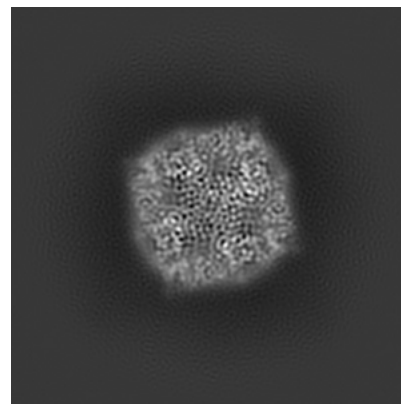
6.1.1 Primary map



X

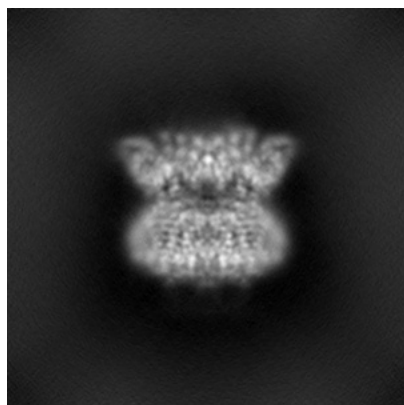


Y

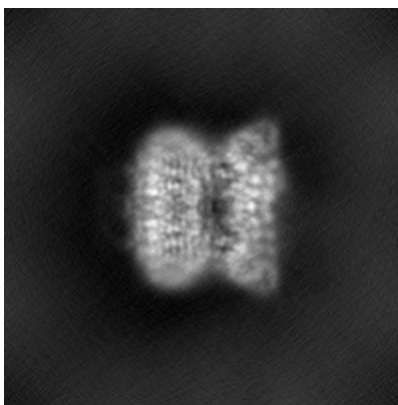


Z

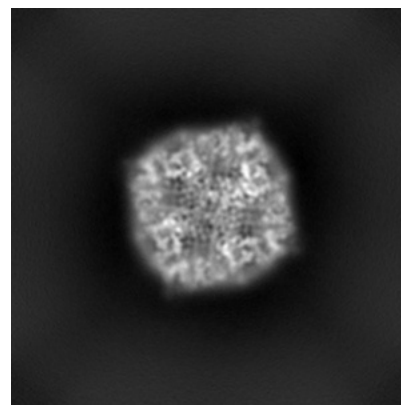
6.1.2 Raw map



X



Y

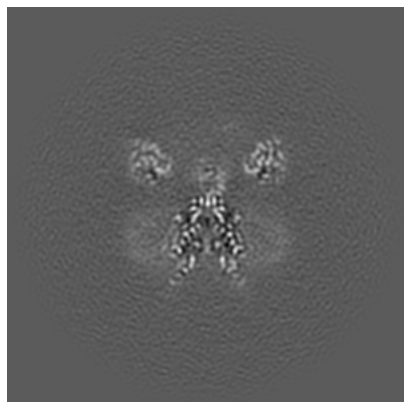


Z

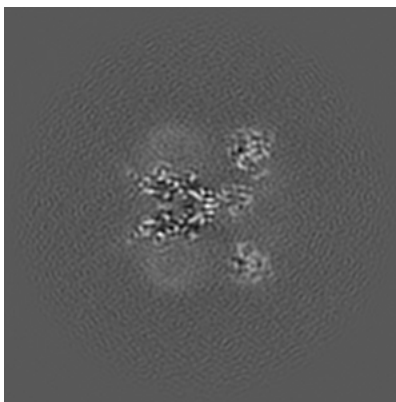
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

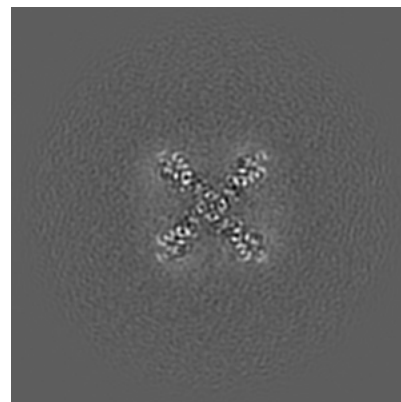
6.2.1 Primary map



X Index: 128

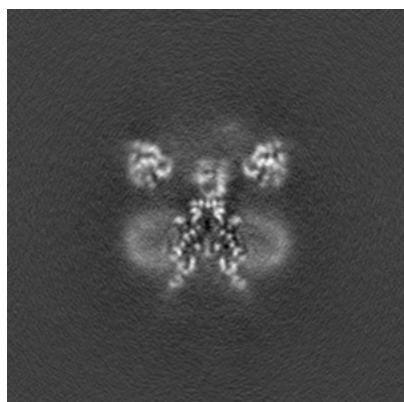


Y Index: 128

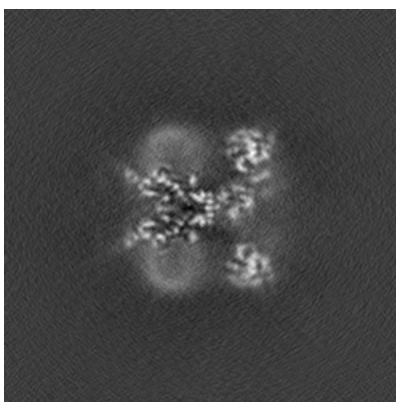


Z Index: 128

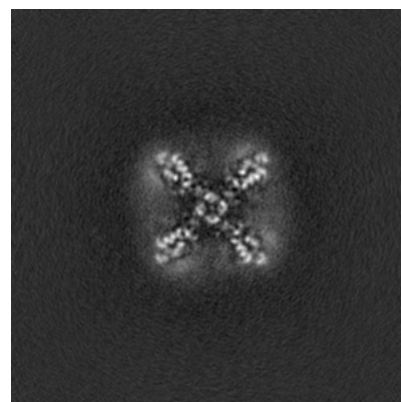
6.2.2 Raw map



X Index: 128



Y Index: 128

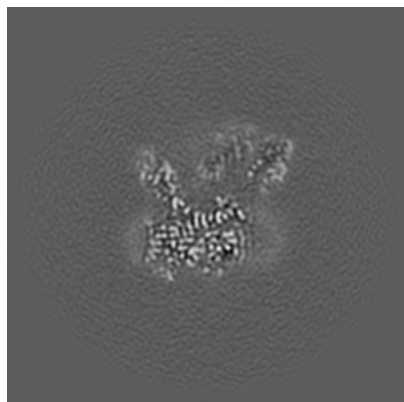


Z Index: 128

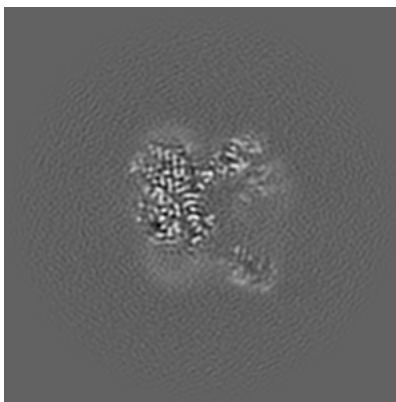
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

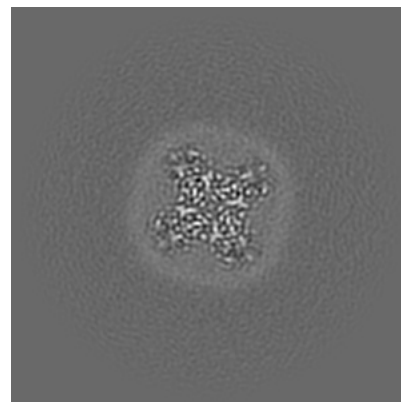
6.3.1 Primary map



X Index: 142

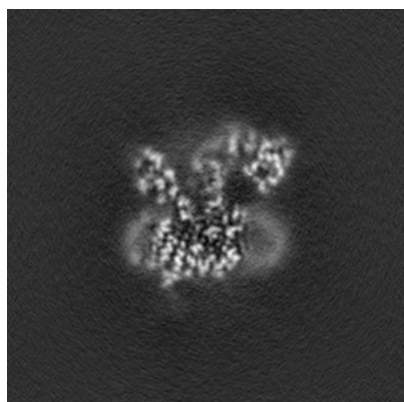


Y Index: 142

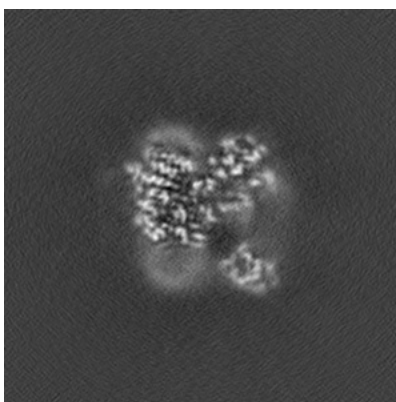


Z Index: 102

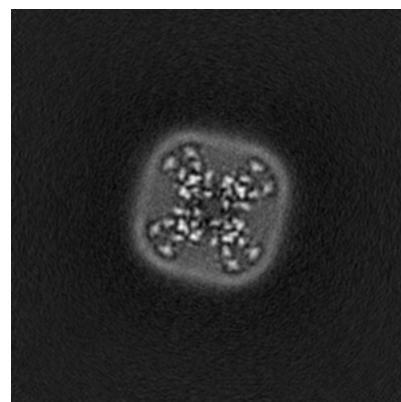
6.3.2 Raw map



X Index: 138



Y Index: 138

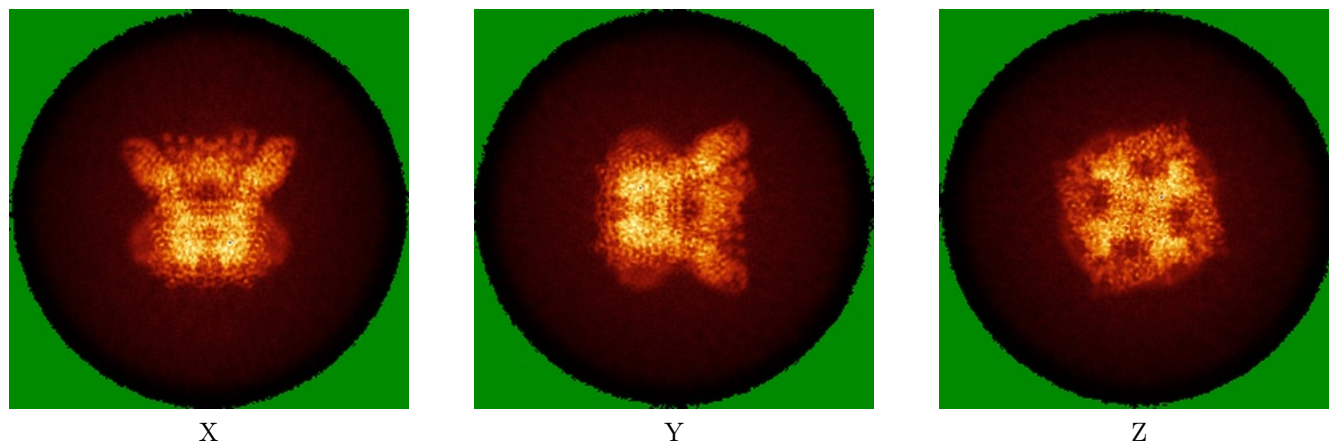


Z Index: 96

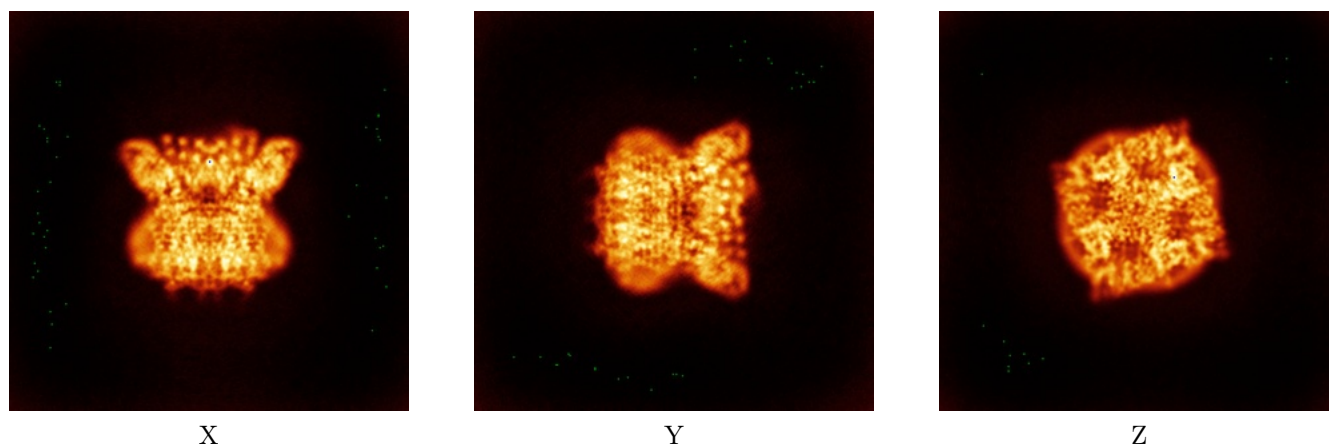
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



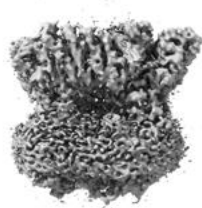
6.4.2 Raw map



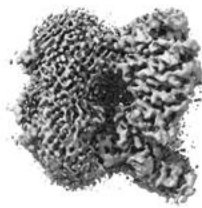
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

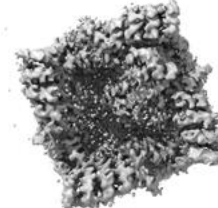
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.326. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

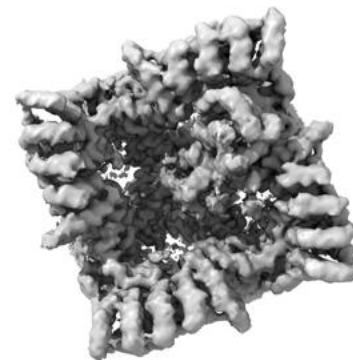
6.5.2 Raw map



X



Y



Z

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.

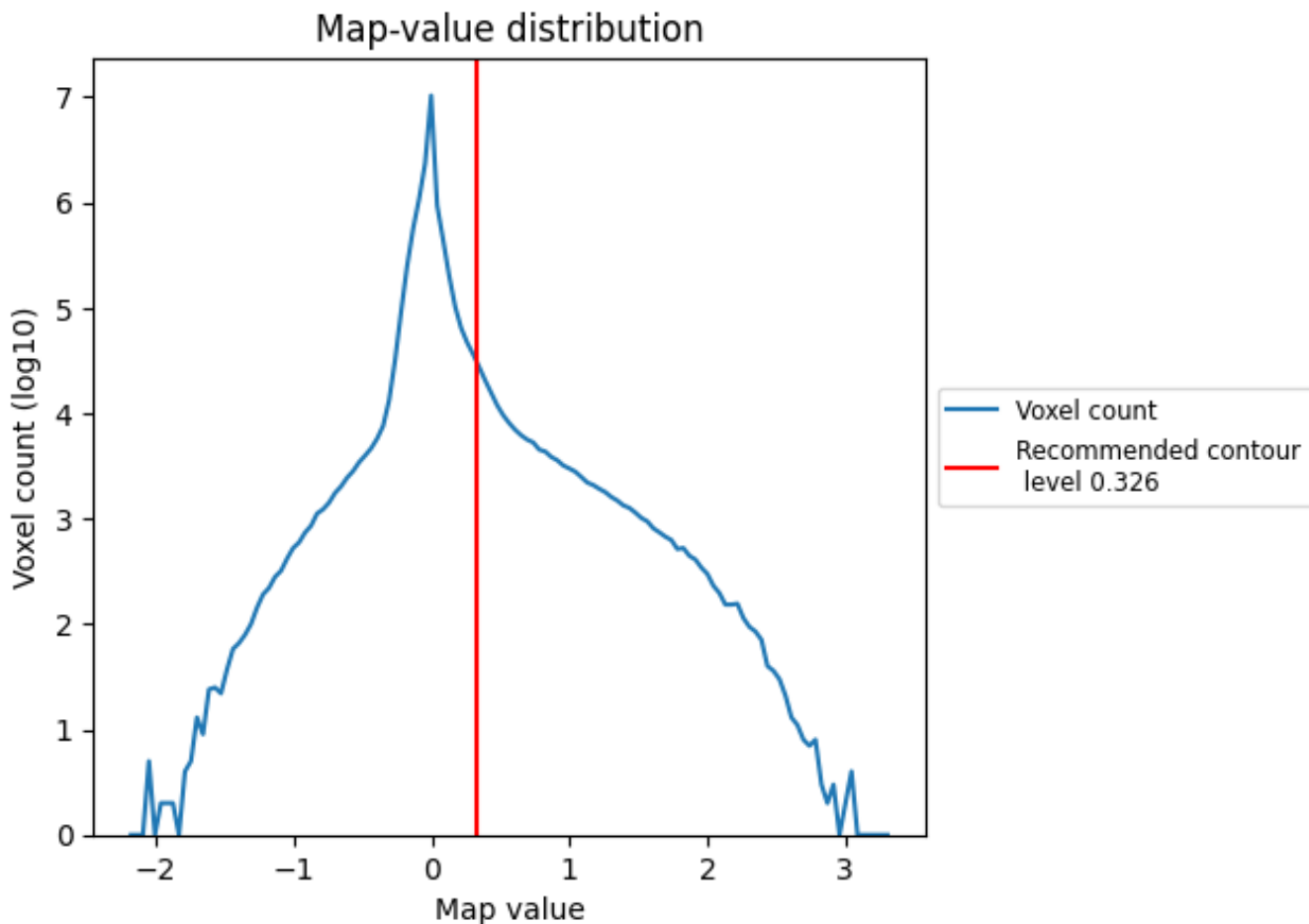
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

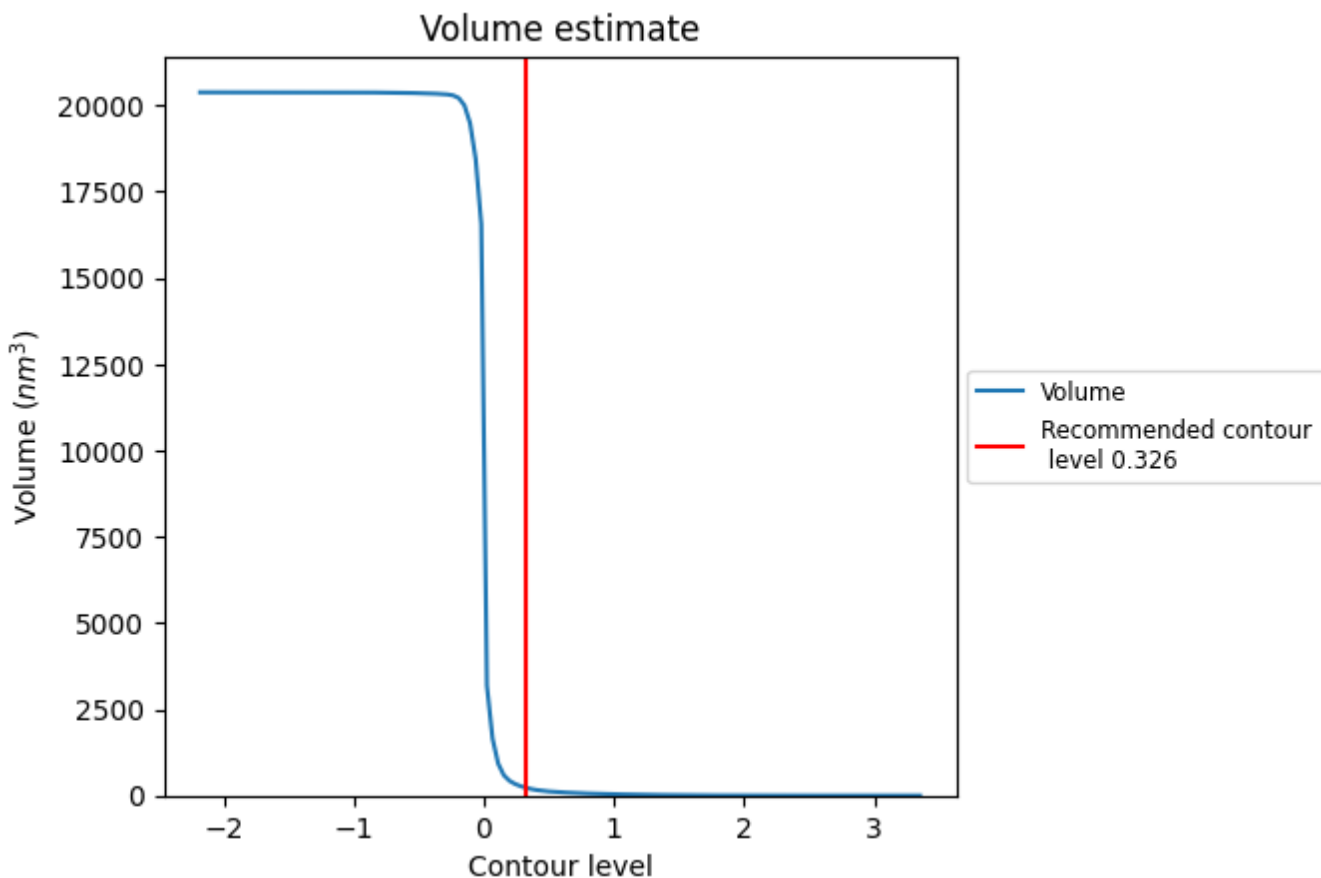
This section contains the results of statistical analysis of the map.

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.

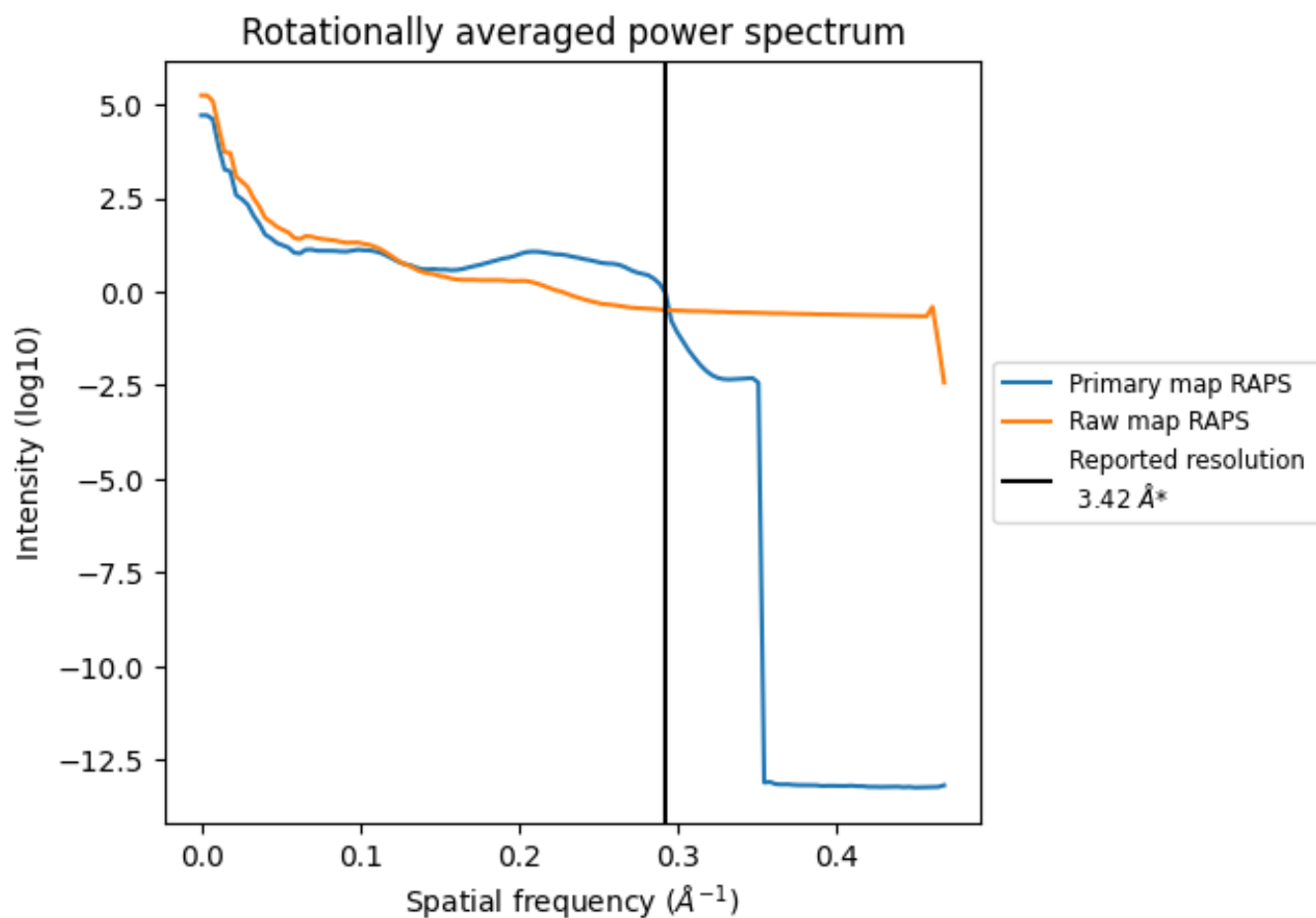
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 223 nm³; this corresponds to an approximate mass of 202 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

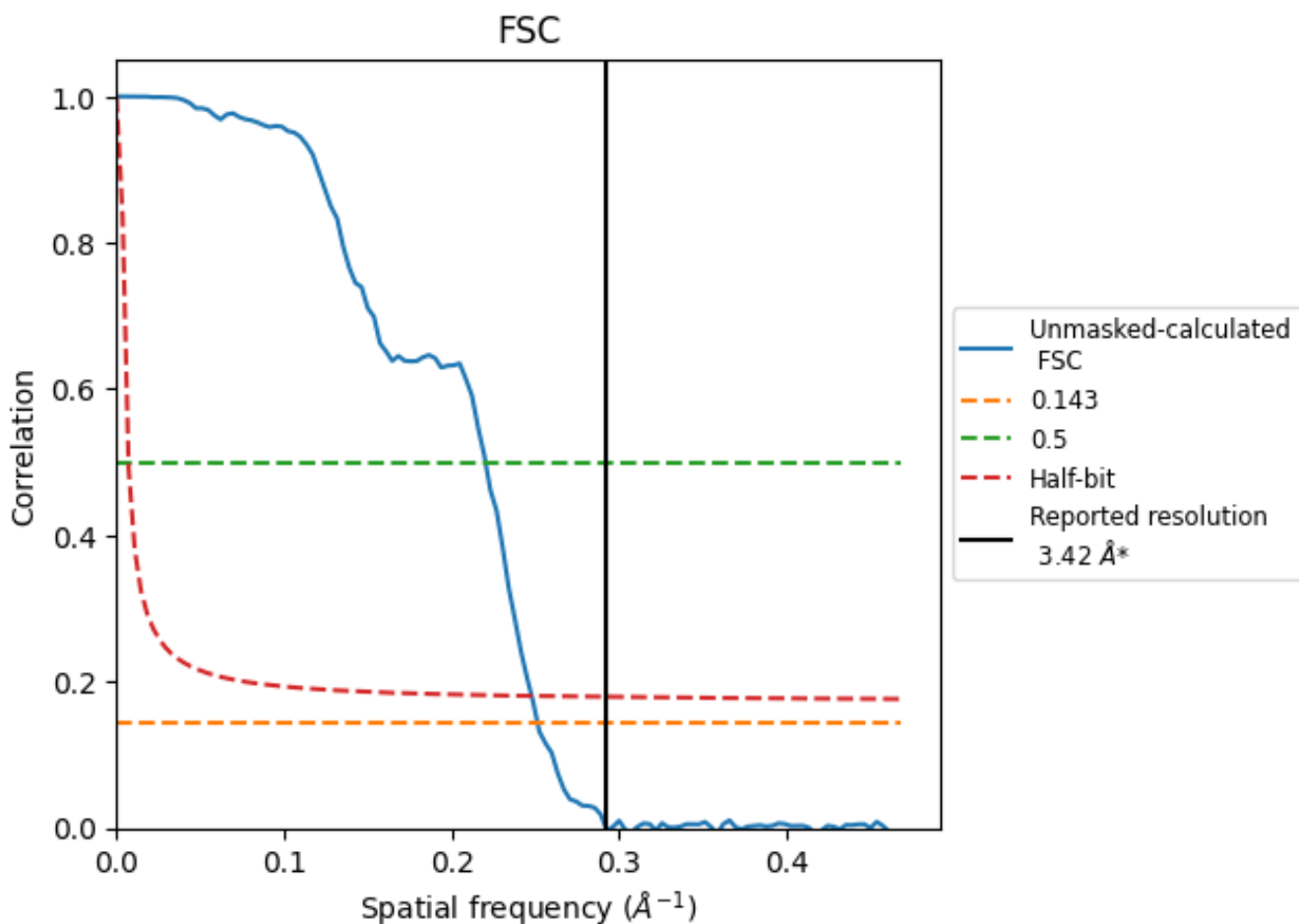


*Reported resolution corresponds to spatial frequency of 0.292 Å⁻¹

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 0.292 Å⁻¹

8.2 Resolution estimates [i](#)

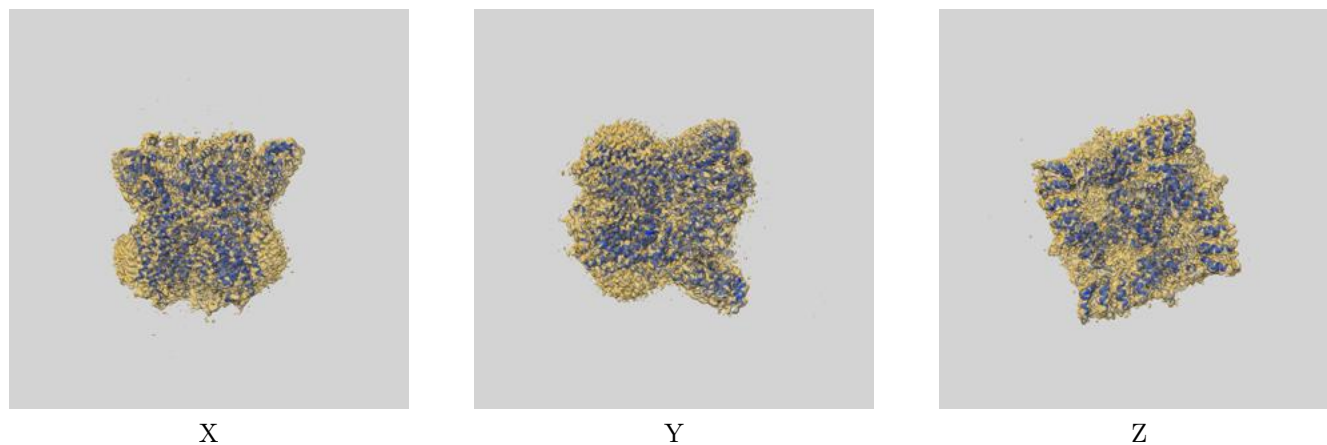
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.42	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.97	4.54	4.03

*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 3.97 differs from the reported value 3.42 by more than 10 %

9 Map-model fit [i](#)

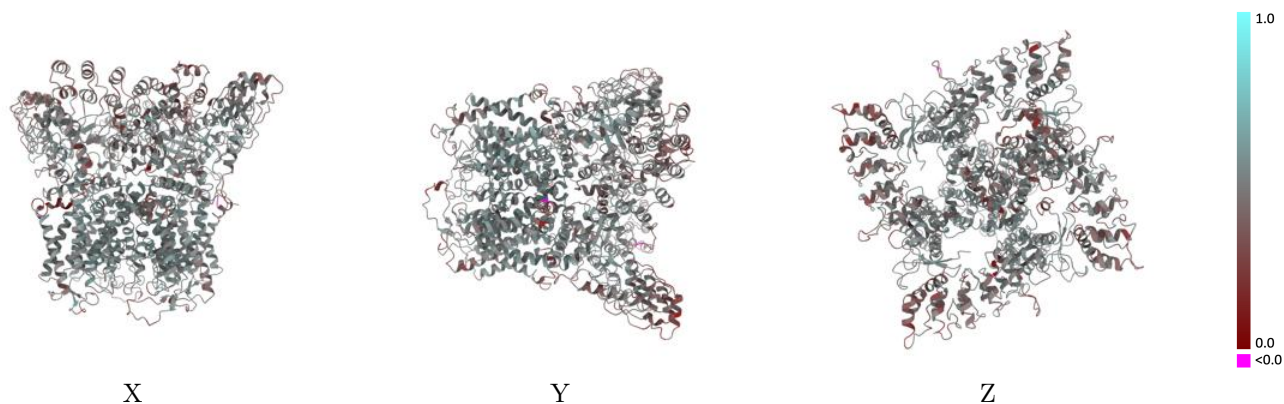
This section contains information regarding the fit between EMDB map EMD-45934 and PDB model 9CUI. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)



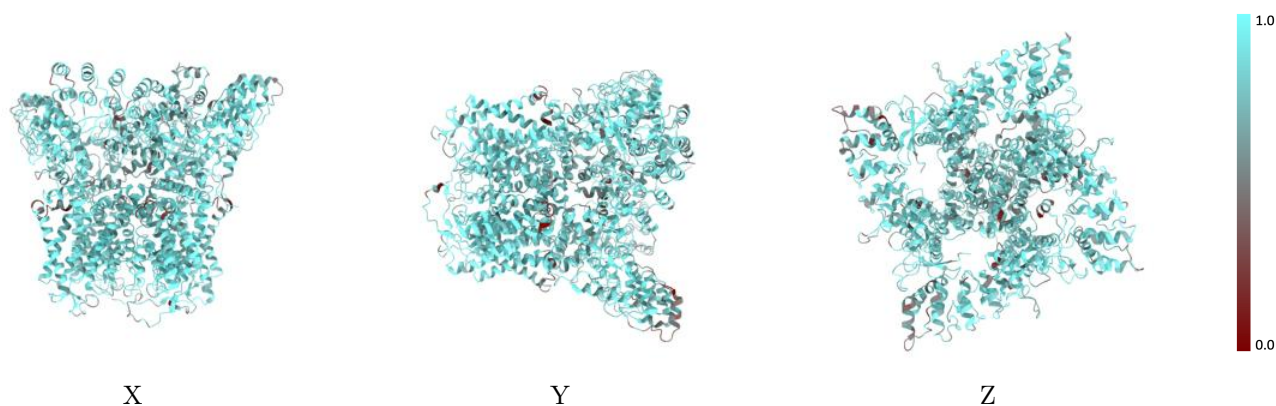
The images above show the 3D surface view of the map at the recommended contour level 0.326 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



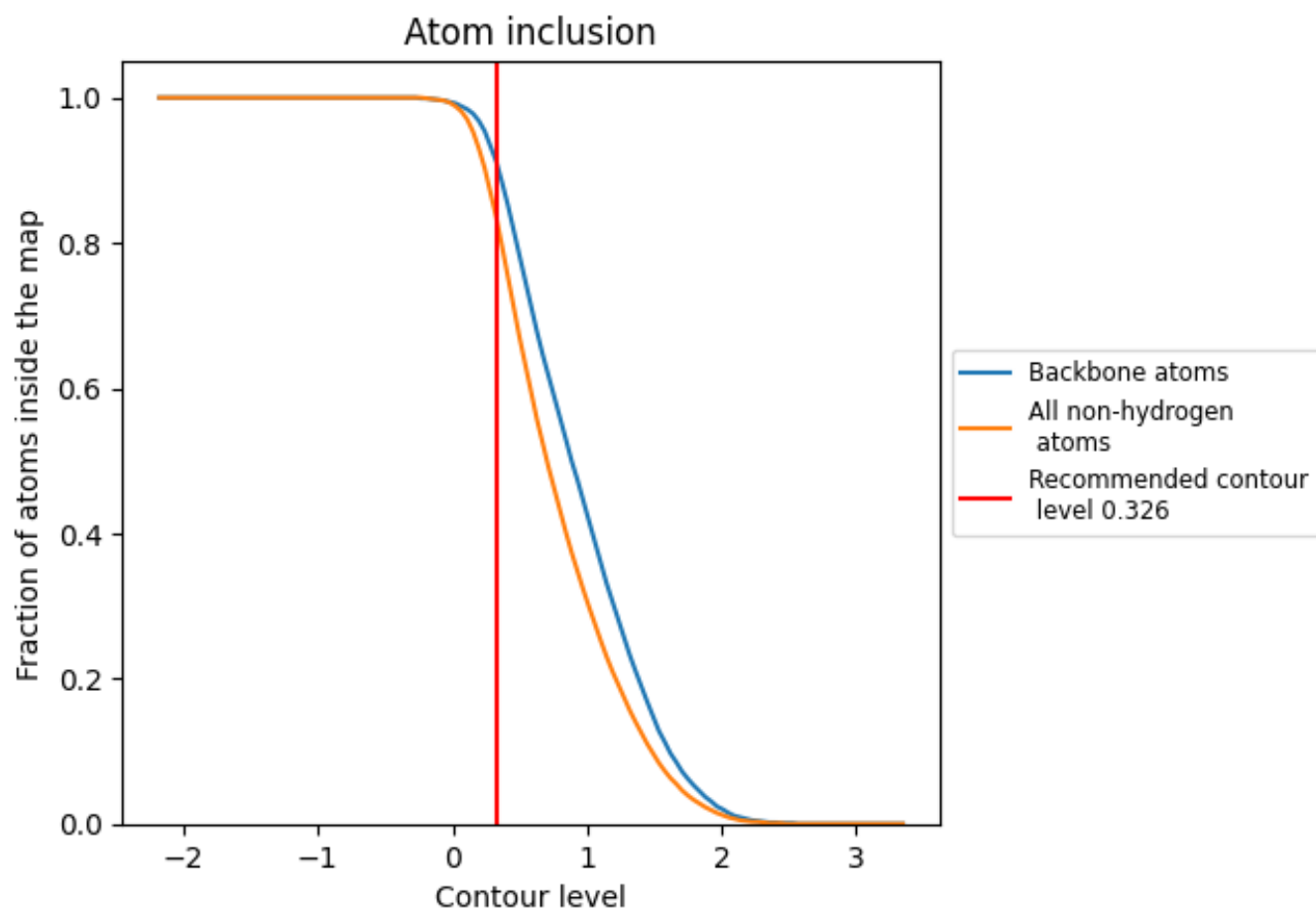
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.326).













9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 84% 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 (0.326) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8350	 0.4680
A	 0.8320	 0.4680
B	 0.8340	 0.4690
C	 0.8380	 0.4680
D	 0.8580	 0.4820
E	 0.7410	 0.4070

