



## Full wwPDB EM Validation Report ⓘ

Nov 19, 2022 – 05:48 PM EST

PDB ID : 7LR0  
EMDB ID : EMD-23493  
Title : Structure of squirrel TRPV1 in complex with capsaicin  
Authors : Neuberger, A.; Nadezhdin, K.D.; Sobolevsky, A.I.  
Deposited on : 2021-02-15  
Resolution : 3.81 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43  
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) : 2.31.2

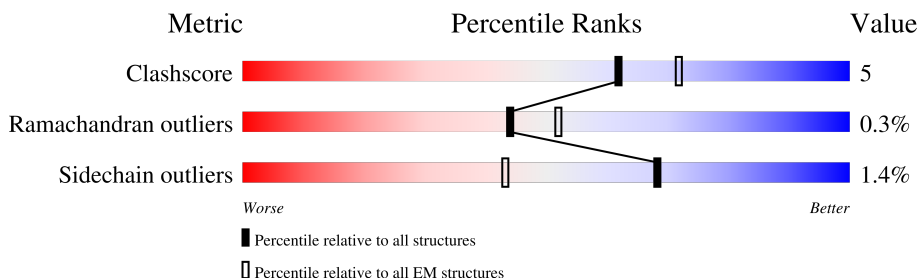
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.81 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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	844	<div> <div>17%</div> <div>67%</div> <div>10%</div> <div>23%</div> </div>
1	B	844	<div> <div>17%</div> <div>66%</div> <div>10%</div> <div>23%</div> </div>
1	C	844	<div> <div>17%</div> <div>66%</div> <div>10%</div> <div>23%</div> </div>
1	D	844	<div> <div>18%</div> <div>67%</div> <div>10%</div> <div>23%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 44069 atoms, of which 22156 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.

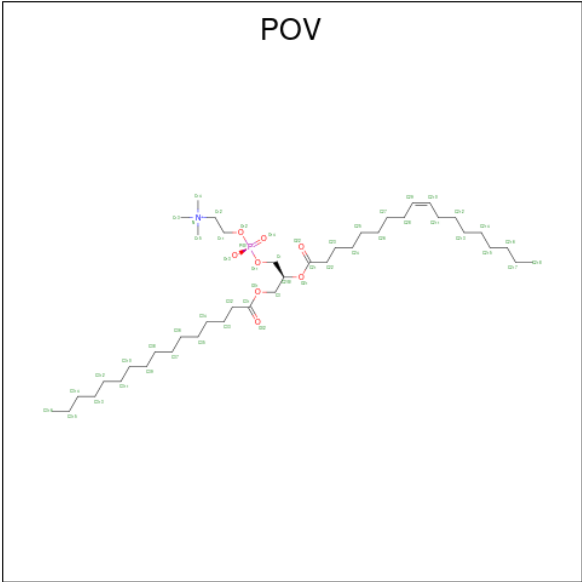
- Molecule 1 is a protein called Osm-9-like TRP channel 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	646	Total 10445	C 3378	H 5234	N 854	O 948	S 31	0	0
1	B	646	Total 10445	C 3378	H 5234	N 854	O 948	S 31	0	0
1	C	646	Total 10445	C 3378	H 5234	N 854	O 948	S 31	0	0
1	D	646	Total 10445	C 3378	H 5234	N 854	O 948	S 31	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	841	LEU	-	expression tag	UNP I3LZN5
A	842	PRO	-	expression tag	UNP I3LZN5
A	843	VAL	-	expression tag	UNP I3LZN5
A	844	ARG	-	expression tag	UNP I3LZN5
B	841	LEU	-	expression tag	UNP I3LZN5
B	842	PRO	-	expression tag	UNP I3LZN5
B	843	VAL	-	expression tag	UNP I3LZN5
B	844	ARG	-	expression tag	UNP I3LZN5
C	841	LEU	-	expression tag	UNP I3LZN5
C	842	PRO	-	expression tag	UNP I3LZN5
C	843	VAL	-	expression tag	UNP I3LZN5
C	844	ARG	-	expression tag	UNP I3LZN5
D	841	LEU	-	expression tag	UNP I3LZN5
D	842	PRO	-	expression tag	UNP I3LZN5
D	843	VAL	-	expression tag	UNP I3LZN5
D	844	ARG	-	expression tag	UNP I3LZN5

- Molecule 2 is (2S)-3-(hexadecanoyloxy)-2-[(9Z)-octadec-9-enoyloxy]propyl 2-(trimethylamm onio)ethyl phosphate (three-letter code: POV) (formula: C<sub>42</sub>H<sub>82</sub>NO<sub>8</sub>P).



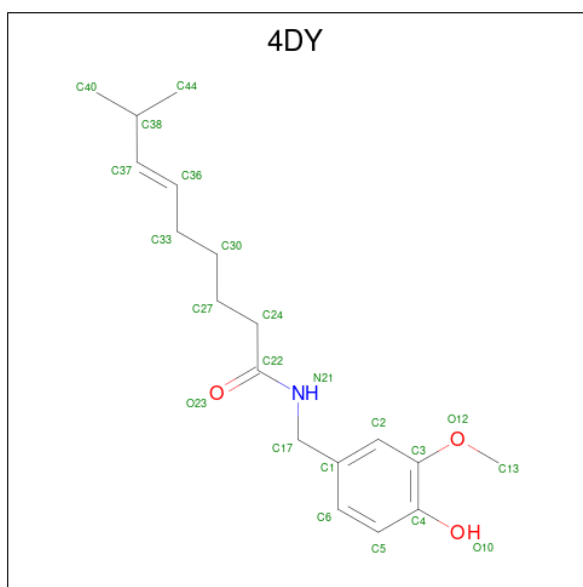
Mol	Chain	Residues	Atoms						AltConf
2	A	1	Total	C	H	N	O	P	0
			620	229	331	6	48	6	
2	A	1	Total	C	H	N	O	P	0
			620	229	331	6	48	6	
2	A	1	Total	C	H	N	O	P	0
			620	229	331	6	48	6	
2	A	1	Total	C	H	N	O	P	0
			620	229	331	6	48	6	
2	A	1	Total	C	H	N	O	P	0
			620	229	331	6	48	6	
2	A	1	Total	C	H	N	O	P	0
			620	229	331	6	48	6	
2	A	1	Total	C	H	N	O	P	0
			620	229	331	6	48	6	
2	B	1	Total	C	H	N	O	P	0
			523	195	278	5	40	5	
2	B	1	Total	C	H	N	O	P	0
			523	195	278	5	40	5	
2	B	1	Total	C	H	N	O	P	0
			523	195	278	5	40	5	
2	B	1	Total	C	H	N	O	P	0
			523	195	278	5	40	5	
2	B	1	Total	C	H	N	O	P	0
			523	195	278	5	40	5	

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Mol	Chain	Residues	Atoms						AltConf
2	B	1	Total	C	H	N	O	P	0
			523	195	278	5	40	5	
2	C	1	Total	C	H	N	O	P	0
			523	195	278	5	40	5	
2	C	1	Total	C	H	N	O	P	0
			523	195	278	5	40	5	
2	C	1	Total	C	H	N	O	P	0
			523	195	278	5	40	5	
2	C	1	Total	C	H	N	O	P	0
			523	195	278	5	40	5	
2	C	1	Total	C	H	N	O	P	0
			523	195	278	5	40	5	
2	C	1	Total	C	H	N	O	P	0
			523	195	278	5	40	5	
2	D	1	Total	C	H	N	O	P	0
			426	161	225	4	32	4	
2	D	1	Total	C	H	N	O	P	0
			426	161	225	4	32	4	
2	D	1	Total	C	H	N	O	P	0
			426	161	225	4	32	4	
2	D	1	Total	C	H	N	O	P	0
			426	161	225	4	32	4	
2	D	1	Total	C	H	N	O	P	0
			426	161	225	4	32	4	

- Molecule 3 is (6E)-N-(4-hydroxy-3-methoxybenzyl)-8-methylnon-6-enamide (three-letter code: 4DY) (formula: C<sub>18</sub>H<sub>27</sub>NO<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	H	N	O	0
			49	18	27	1	3	
3	B	1	Total	C	H	N	O	0
			49	18	27	1	3	
3	C	1	Total	C	H	N	O	0
			49	18	27	1	3	
3	D	1	Total	C	H	N	O	0
			49	18	27	1	3	

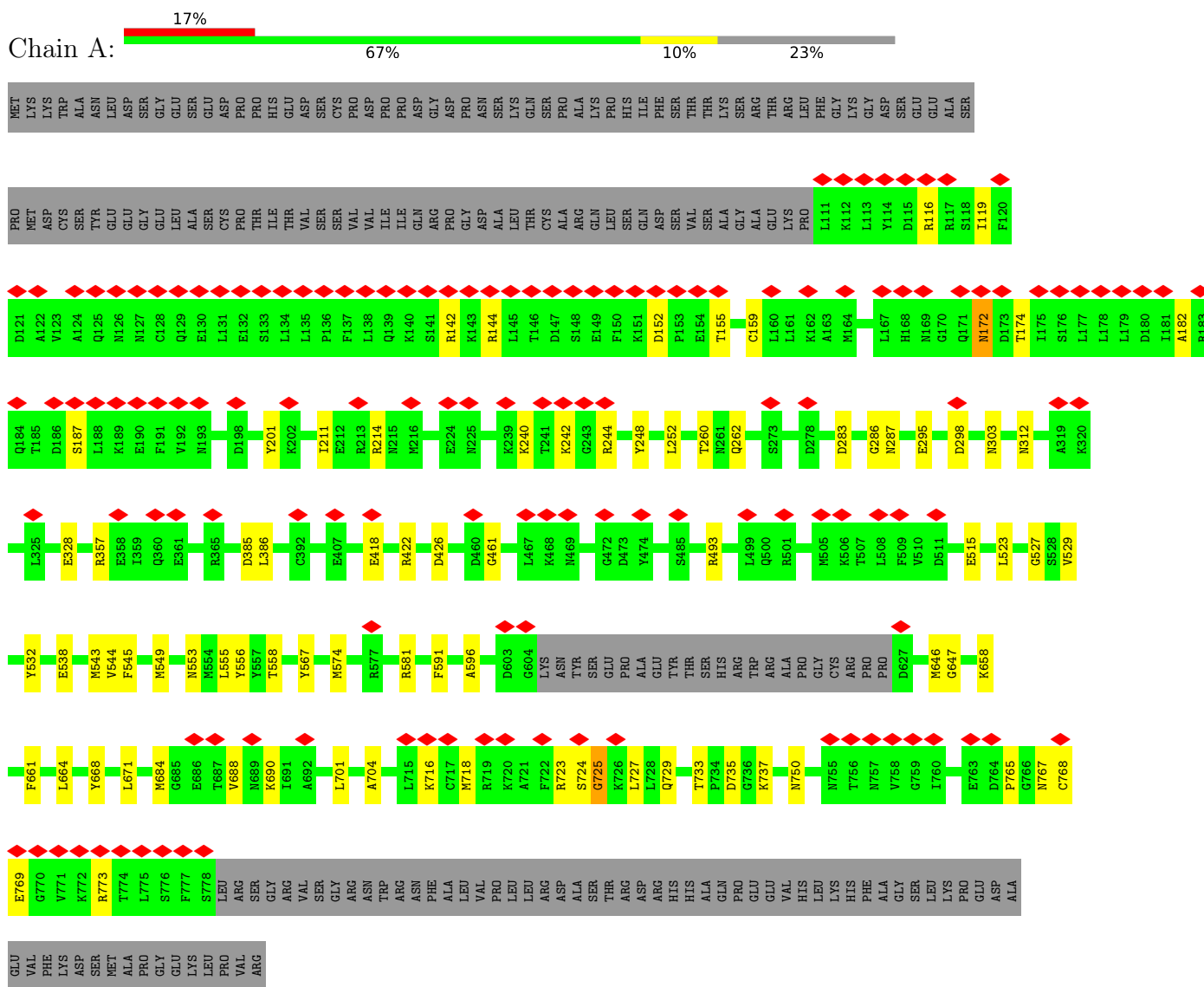
- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total	Na	0
			1	1	

### 3 Residue-property plots

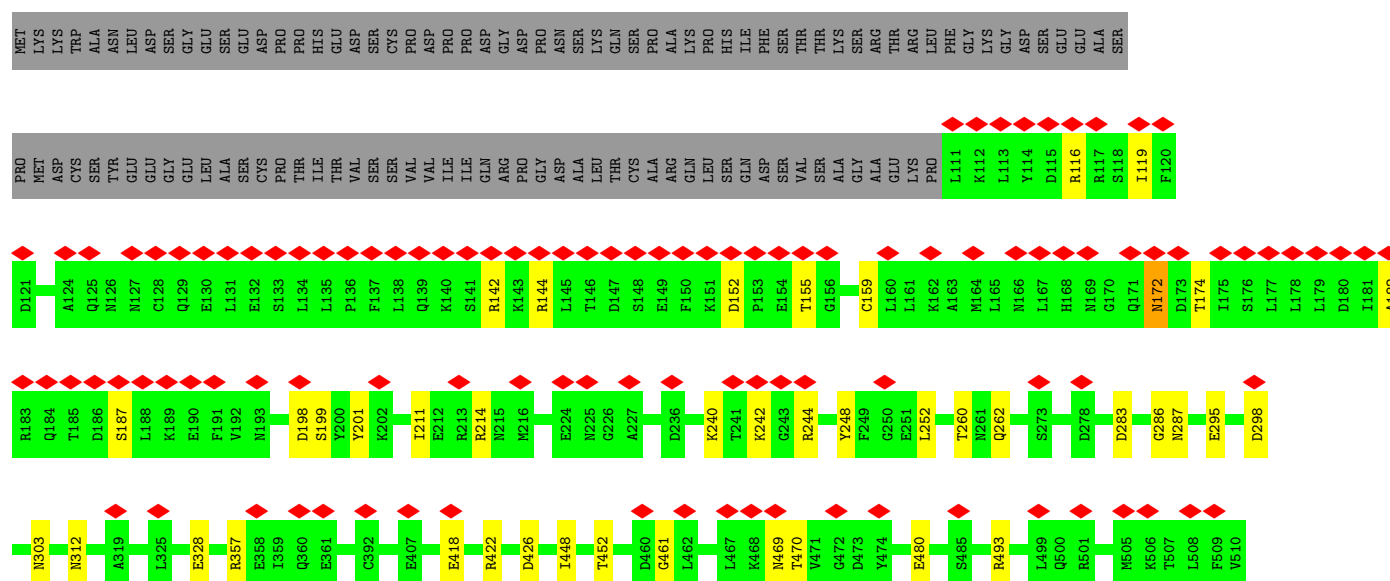
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Osm-9-like TRP channel 1



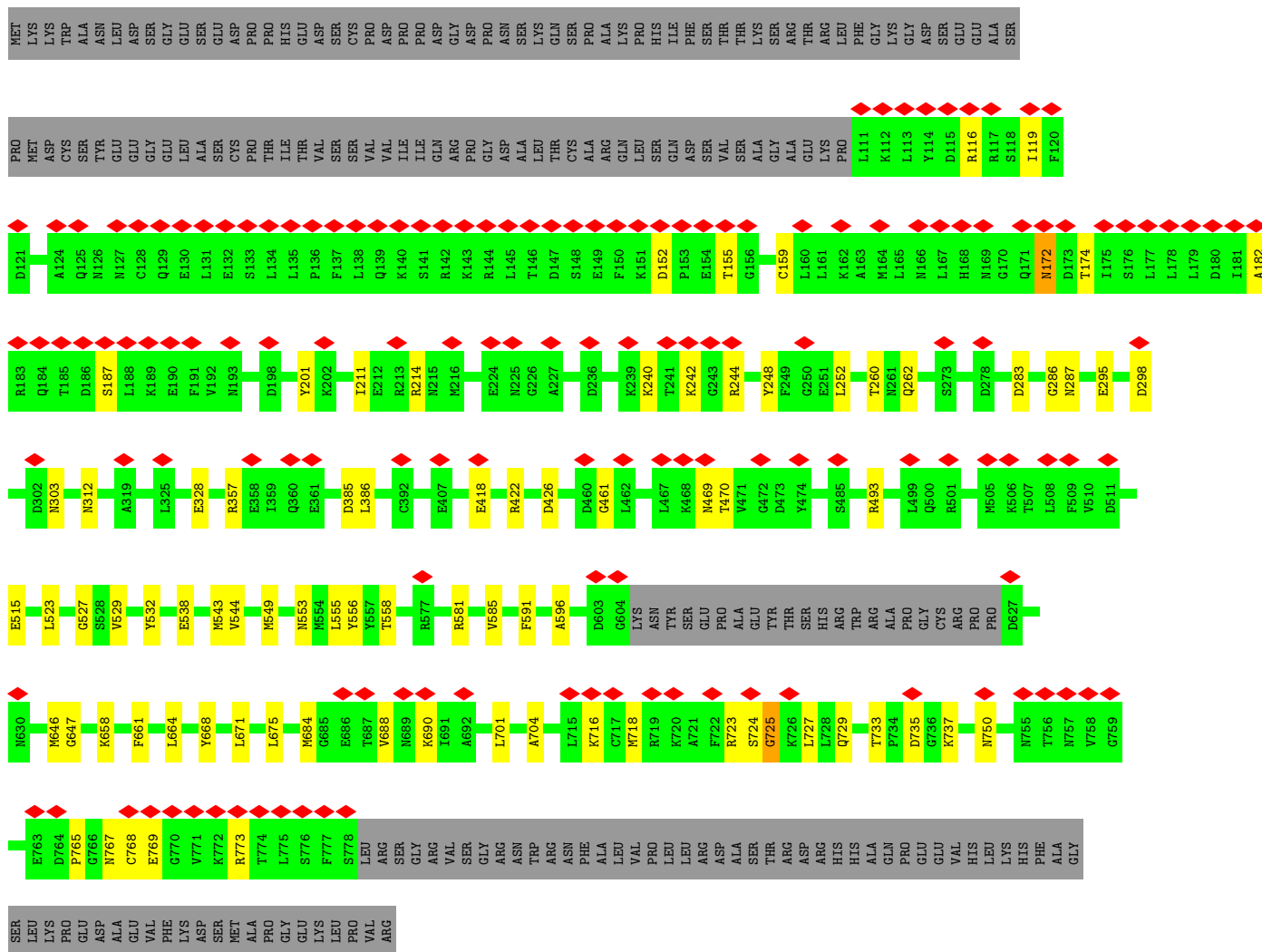
#### • Molecule 1: Osm-9-like TRP channel 1







- Molecule 1: Osm-9-like TRP channel 1



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	62014	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	58.5	Depositor
Minimum defocus (nm)	-1000	Depositor
Maximum defocus (nm)	-2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.034	Depositor
Minimum map value	-1.568	Depositor
Average map value	0.015	Depositor
Map value standard deviation	0.095	Depositor
Recommended contour level	0.395	Depositor
Map size ( $\text{\AA}$ )	212.48, 212.48, 212.48	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.83, 0.83, 0.83	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: POV, NA, 4DY

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	0.60	0/5325	0.63	2/7204 (0.0%)
1	B	0.60	0/5325	0.63	2/7204 (0.0%)
1	C	0.60	0/5325	0.63	2/7204 (0.0%)
1	D	0.60	0/5325	0.63	2/7204 (0.0%)
All	All	0.60	0/21300	0.63	8/28816 (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	1
1	C	0	1
1	D	0	1
All	All	0	4

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	581	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	D	581	ARG	NE-CZ-NH1	5.40	123.00	120.30
1	D	252	LEU	CA-CB-CG	5.39	127.69	115.30
1	A	252	LEU	CA-CB-CG	5.36	127.63	115.30
1	B	252	LEU	CA-CB-CG	5.36	127.62	115.30
1	A	581	ARG	NE-CZ-NH1	5.35	122.98	120.30
1	C	252	LEU	CA-CB-CG	5.35	127.61	115.30
1	B	581	ARG	NE-CZ-NH1	5.33	122.96	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	725	GLY	Peptide
1	B	725	GLY	Peptide
1	C	725	GLY	Peptide
1	D	725	GLY	Peptide

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5211	5234	5238	51	0
1	B	5211	5234	5238	54	0
1	C	5211	5234	5238	54	0
1	D	5211	5234	5238	49	0
2	A	289	331	423	9	0
2	B	245	278	360	9	0
2	C	245	278	360	10	0
2	D	201	225	297	9	0
3	A	22	27	0	4	0
3	B	22	27	0	3	0
3	C	22	27	0	3	0
3	D	22	27	0	3	0
4	A	1	0	0	0	0
All	All	21913	22156	22392	200	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 (200) 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:240:LYS:NZ	1:A:295:GLU:OE2	2.18	0.77
1:D:240:LYS:NZ	1:D:295:GLU:OE2	2.18	0.77
1:B:240:LYS:NZ	1:B:295:GLU:OE2	2.18	0.76
1:C:240:LYS:NZ	1:C:295:GLU:OE2	2.18	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:733:THR:OG1	1:C:735:ASP:OD1	2.05	0.75
1:B:733:THR:OG1	1:B:735:ASP:OD1	2.05	0.72
1:D:733:THR:OG1	1:D:735:ASP:OD1	2.05	0.72
1:A:733:THR:OG1	1:A:735:ASP:OD1	2.05	0.71
1:A:298:ASP:OD1	1:A:303:ASN:ND2	2.23	0.71
1:C:298:ASP:OD1	1:C:303:ASN:ND2	2.23	0.70
1:D:298:ASP:OD1	1:D:303:ASN:ND2	2.23	0.70
1:B:298:ASP:OD1	1:B:303:ASN:ND2	2.23	0.70
1:A:765:PRO:O	1:B:201:TYR:OH	2.06	0.70
1:B:549:MET:O	1:B:553:ASN:N	2.24	0.69
1:A:549:MET:O	1:A:553:ASN:N	2.24	0.69
1:C:549:MET:O	1:C:553:ASN:N	2.24	0.69
1:D:549:MET:O	1:D:553:ASN:N	2.24	0.69
1:B:283:ASP:OD1	1:B:286:GLY:N	2.26	0.69
1:D:283:ASP:OD1	1:D:286:GLY:N	2.26	0.69
1:A:283:ASP:OD1	1:A:286:GLY:N	2.26	0.69
1:C:283:ASP:OD1	1:C:286:GLY:N	2.26	0.69
1:A:244:ARG:NH2	1:D:767:ASN:O	2.25	0.69
1:D:729:GLN:OE1	1:D:773:ARG:NH1	2.27	0.68
1:A:767:ASN:O	1:B:244:ARG:NH2	2.27	0.68
1:C:729:GLN:OE1	1:C:773:ARG:NH1	2.27	0.68
1:A:729:GLN:OE1	1:A:773:ARG:NH1	2.27	0.67
1:B:729:GLN:OE1	1:B:773:ARG:NH1	2.27	0.67
1:A:201:TYR:OH	1:D:765:PRO:O	2.12	0.66
1:B:765:PRO:O	1:C:201:TYR:OH	2.12	0.66
1:D:172:ASN:ND2	1:D:174:THR:OG1	2.30	0.64
1:B:172:ASN:ND2	1:B:174:THR:OG1	2.30	0.64
1:C:172:ASN:ND2	1:C:174:THR:OG1	2.30	0.64
1:B:211:ILE:O	1:B:262:GLN:NE2	2.32	0.63
1:A:172:ASN:ND2	1:A:174:THR:OG1	2.30	0.63
2:A:907:POV:H35A	1:B:591:PHE:HZ	1.64	0.63
1:C:765:PRO:O	1:D:201:TYR:OH	2.13	0.62
2:B:907:POV:H35A	1:C:591:PHE:HZ	1.64	0.62
2:C:907:POV:H35A	1:D:591:PHE:HZ	1.63	0.62
2:D:902:POV:H33A	2:D:902:POV:H13A	1.82	0.62
2:C:908:POV:H13A	2:C:908:POV:H33A	1.82	0.61
1:A:591:PHE:HZ	2:D:901:POV:H35A	1.64	0.61
1:C:211:ILE:O	1:C:262:GLN:NE2	2.31	0.61
2:A:908:POV:H33A	2:A:908:POV:H13A	1.82	0.61
1:A:647:GLY:N	1:D:646:MET:SD	2.75	0.60
1:B:767:ASN:O	1:C:244:ARG:NH2	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:767:ASN:O	1:D:244:ARG:NH2	2.36	0.58
1:B:735:ASP:OD2	1:B:737:LYS:NZ	2.36	0.58
2:B:908:POV:H33A	2:B:908:POV:H13A	1.85	0.58
1:A:211:ILE:O	1:A:262:GLN:NE2	2.32	0.58
1:D:211:ILE:O	1:D:262:GLN:NE2	2.31	0.58
1:C:248:TYR:OH	1:C:283:ASP:OD2	2.21	0.58
1:C:735:ASP:OD2	1:C:737:LYS:NZ	2.36	0.58
1:D:735:ASP:OD2	1:D:737:LYS:NZ	2.36	0.57
1:A:248:TYR:OH	1:A:283:ASP:OD2	2.21	0.57
1:A:646:MET:SD	1:B:647:GLY:N	2.78	0.57
1:A:735:ASP:OD2	1:A:737:LYS:NZ	2.36	0.57
1:D:515:GLU:OE1	2:D:905:POV:H13	2.05	0.57
1:D:248:TYR:OH	1:D:283:ASP:OD2	2.21	0.57
1:B:515:GLU:OE1	2:B:904:POV:H13	2.05	0.56
1:C:515:GLU:OE1	2:C:904:POV:H13	2.05	0.56
1:A:515:GLU:OE1	2:A:904:POV:H13	2.05	0.56
1:B:248:TYR:OH	1:B:283:ASP:OD2	2.22	0.56
1:B:646:MET:SD	1:C:647:GLY:N	2.79	0.56
1:B:768:CYS:SG	1:B:769:GLU:N	2.79	0.56
1:A:768:CYS:SG	1:A:769:GLU:N	2.79	0.55
1:A:664:LEU:HD23	3:D:904:4DY:C44	2.36	0.55
1:D:768:CYS:SG	1:D:769:GLU:N	2.79	0.54
1:C:768:CYS:SG	1:C:769:GLU:N	2.79	0.54
3:C:903:4DY:C27	1:D:671:LEU:HD11	2.38	0.54
1:D:152:ASP:OD2	1:D:155:THR:OG1	2.25	0.54
1:C:646:MET:SD	1:D:647:GLY:N	2.80	0.54
1:A:671:LEU:HD11	3:D:904:4DY:C27	2.38	0.52
1:C:493:ARG:HE	2:C:904:POV:H13B	1.74	0.52
1:D:493:ARG:HE	2:D:905:POV:H13B	1.74	0.52
1:B:493:ARG:HE	2:B:904:POV:H13B	1.74	0.52
2:B:904:POV:H23A	2:B:904:POV:H3A	1.92	0.52
1:A:493:ARG:HE	2:A:904:POV:H13B	1.74	0.52
1:C:448:ILE:O	1:C:452:THR:OG1	2.19	0.51
2:D:905:POV:H23A	2:D:905:POV:H3A	1.92	0.51
1:B:529:VAL:HG23	2:B:906:POV:H214	1.92	0.51
1:C:529:VAL:HG23	2:C:906:POV:H214	1.93	0.51
1:D:523:LEU:O	1:D:527:GLY:N	2.42	0.51
2:A:904:POV:H23A	2:A:904:POV:H3A	1.93	0.51
1:B:426:ASP:OD2	1:B:723:ARG:NH2	2.44	0.50
3:B:903:4DY:C27	1:C:671:LEU:HD11	2.40	0.50
1:D:426:ASP:OD2	1:D:723:ARG:NH2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:426:ASP:OD2	1:A:723:ARG:NH2	2.44	0.50
2:C:904:POV:H23A	2:C:904:POV:H3A	1.94	0.50
1:D:529:VAL:HG23	2:D:907:POV:H214	1.93	0.50
1:B:152:ASP:OD2	1:B:155:THR:OG1	2.25	0.50
1:B:523:LEU:O	1:B:527:GLY:N	2.43	0.50
1:A:328:GLU:OE2	1:A:357:ARG:NH2	2.44	0.49
1:A:523:LEU:O	1:A:527:GLY:N	2.43	0.49
1:A:556:TYR:HB2	3:A:903:4DY:C13	2.43	0.49
1:B:448:ILE:O	1:B:452:THR:OG1	2.19	0.49
1:C:426:ASP:OD2	1:C:723:ARG:NH2	2.44	0.49
1:A:538:GLU:N	1:A:538:GLU:OE1	2.46	0.49
1:C:523:LEU:O	1:C:527:GLY:N	2.43	0.49
1:D:538:GLU:N	1:D:538:GLU:OE1	2.46	0.49
1:A:529:VAL:HG23	2:A:906:POV:H214	1.95	0.49
1:A:545:PHE:HD1	3:A:903:4DY:C40	2.26	0.49
1:B:538:GLU:OE1	1:B:538:GLU:N	2.46	0.48
1:A:283:ASP:OD1	1:A:287:ASN:N	2.46	0.48
1:B:283:ASP:OD1	1:B:287:ASN:N	2.47	0.48
1:C:283:ASP:OD1	1:C:287:ASN:N	2.46	0.48
1:A:152:ASP:OD2	1:A:155:THR:OG1	2.25	0.48
1:D:119:ILE:HG21	1:D:159:CYS:SG	2.54	0.48
1:A:119:ILE:HG21	1:A:159:CYS:SG	2.54	0.48
1:B:418:GLU:OE2	1:B:422:ARG:NH1	2.43	0.48
1:B:328:GLU:OE2	1:B:357:ARG:NH2	2.44	0.48
1:D:283:ASP:OD1	1:D:287:ASN:N	2.47	0.48
3:A:903:4DY:C27	1:B:671:LEU:HD11	2.44	0.47
1:B:119:ILE:HG21	1:B:159:CYS:SG	2.54	0.47
1:B:555:LEU:O	1:B:558:THR:HG22	2.15	0.47
1:C:418:GLU:OE2	1:C:422:ARG:NH1	2.43	0.47
1:C:538:GLU:N	1:C:538:GLU:OE1	2.46	0.47
1:D:214:ARG:NH2	1:D:260:THR:O	2.47	0.47
1:C:119:ILE:HG21	1:C:159:CYS:SG	2.54	0.47
1:A:555:LEU:O	1:A:558:THR:HG22	2.15	0.47
1:D:385:ASP:OD1	1:D:386:LEU:N	2.46	0.46
1:B:214:ARG:NH2	1:B:260:THR:O	2.48	0.46
3:C:903:4DY:C44	1:D:664:LEU:HD23	2.45	0.46
1:D:555:LEU:O	1:D:558:THR:HG22	2.15	0.46
1:A:544:VAL:HG13	1:B:596:ALA:HB1	1.98	0.46
1:A:182:ALA:HB1	1:A:187:SER:O	2.16	0.46
1:B:182:ALA:HB1	1:B:187:SER:O	2.16	0.46
1:D:556:TYR:HB2	3:D:904:4DY:C13	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:328:GLU:OE2	1:C:357:ARG:NH2	2.44	0.46
1:D:182:ALA:HB1	1:D:187:SER:O	2.16	0.46
1:C:152:ASP:OD2	1:C:155:THR:OG1	2.25	0.46
1:D:684:MET:O	1:D:688:VAL:HG12	2.16	0.46
1:C:555:LEU:O	1:C:558:THR:HG22	2.15	0.46
1:A:385:ASP:OD1	1:A:386:LEU:N	2.46	0.45
1:C:684:MET:O	1:C:688:VAL:HG12	2.16	0.45
1:D:328:GLU:OE2	1:D:357:ARG:NH2	2.44	0.45
1:A:142:ARG:O	1:A:144:ARG:NH1	2.46	0.45
1:B:684:MET:O	1:B:688:VAL:HG12	2.16	0.45
1:C:556:TYR:HB2	3:C:903:4DY:C13	2.46	0.45
1:A:418:GLU:OE2	1:A:422:ARG:NH1	2.43	0.45
1:B:544:VAL:HG13	1:C:596:ALA:HB1	1.99	0.45
1:D:664:LEU:O	1:D:668:TYR:N	2.50	0.45
2:A:904:POV:H24A	2:A:904:POV:H27	1.73	0.45
3:B:903:4DY:C44	1:C:664:LEU:HD23	2.47	0.45
1:C:142:ARG:O	1:C:144:ARG:NH1	2.46	0.45
1:C:182:ALA:HB1	1:C:187:SER:O	2.16	0.45
1:D:701:LEU:O	1:D:704:ALA:N	2.50	0.45
1:C:567:TYR:OH	1:D:675:LEU:O	2.34	0.45
1:B:725:GLY:O	1:B:727:LEU:N	2.50	0.44
1:A:684:MET:O	1:A:688:VAL:HG12	2.16	0.44
1:A:725:GLY:O	1:A:727:LEU:N	2.50	0.44
1:D:725:GLY:O	1:D:727:LEU:N	2.50	0.44
1:A:701:LEU:O	1:A:704:ALA:N	2.50	0.44
1:B:701:LEU:O	1:B:704:ALA:N	2.50	0.44
1:C:664:LEU:O	1:C:668:TYR:N	2.50	0.44
1:C:725:GLY:O	1:C:727:LEU:N	2.50	0.44
1:B:567:TYR:OH	1:C:675:LEU:O	2.35	0.44
1:B:532:TYR:CD2	2:B:906:POV:H21B	2.53	0.44
1:C:532:TYR:CD2	2:C:906:POV:H21B	2.53	0.44
1:B:469:ASN:O	1:B:470:THR:OG1	2.33	0.44
1:C:198:ASP:OD1	1:C:199:SER:N	2.50	0.43
1:C:214:ARG:NH2	1:C:260:THR:O	2.48	0.43
2:D:905:POV:H24A	2:D:905:POV:H27	1.71	0.43
1:B:664:LEU:O	1:B:668:TYR:N	2.50	0.43
1:B:198:ASP:OD1	1:B:199:SER:N	2.50	0.43
1:B:556:TYR:HB2	3:B:903:4DY:C13	2.48	0.43
1:A:214:ARG:NH2	1:A:260:THR:O	2.48	0.43
1:A:664:LEU:O	1:A:668:TYR:N	2.50	0.43
1:D:418:GLU:OE2	1:D:422:ARG:NH1	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:214:ARG:HG2	1:B:262:GLN:HE21	1.84	0.43
3:A:903:4DY:C44	1:B:664:LEU:HD23	2.49	0.43
1:A:214:ARG:HG2	1:A:262:GLN:HE21	1.84	0.43
2:C:904:POV:H27	2:C:904:POV:H24A	1.75	0.43
1:C:543:MET:SD	2:C:906:POV:H21G	2.59	0.43
1:C:544:VAL:HG13	1:D:596:ALA:HB1	2.00	0.43
1:C:701:LEU:O	1:C:704:ALA:N	2.50	0.43
1:D:214:ARG:HG2	1:D:262:GLN:HE21	1.84	0.43
1:D:532:TYR:CD2	2:D:907:POV:H21B	2.54	0.42
1:D:543:MET:SD	2:D:907:POV:H21G	2.59	0.42
1:A:543:MET:SD	2:A:906:POV:H21G	2.58	0.42
1:A:574:MET:CE	1:B:678:ASN:HD21	2.32	0.42
1:B:543:MET:SD	2:B:906:POV:H21G	2.59	0.42
1:B:142:ARG:O	1:B:144:ARG:NH1	2.46	0.42
2:B:904:POV:H24A	2:B:904:POV:H27	1.75	0.42
1:A:658:LYS:O	1:A:661:PHE:N	2.53	0.42
1:C:658:LYS:O	1:C:661:PHE:N	2.53	0.42
1:D:469:ASN:O	1:D:470:THR:OG1	2.33	0.41
1:A:567:TYR:OH	1:B:675:LEU:O	2.38	0.41
1:C:214:ARG:HG2	1:C:262:GLN:HE21	1.84	0.41
1:D:658:LYS:O	1:D:661:PHE:N	2.53	0.41
1:B:260:THR:O	1:B:260:THR:HG22	2.21	0.41
1:A:260:THR:O	1:A:260:THR:HG22	2.21	0.41
1:C:469:ASN:O	1:C:470:THR:OG1	2.33	0.41
1:B:256:LEU:O	1:B:260:THR:OG1	2.25	0.41
1:C:480:GLU:OE1	2:C:906:POV:H21F	2.21	0.41
1:C:586:TYR:HH	1:C:643:THR:HG1	1.69	0.41
1:A:596:ALA:HB1	1:D:544:VAL:HG13	2.03	0.41
1:A:532:TYR:CD2	2:A:906:POV:H21B	2.56	0.40
1:D:585:VAL:HG11	1:D:675:LEU:HD11	2.04	0.40
1:B:332:ASN:OD1	1:B:336:LEU:N	2.55	0.40
1:C:260:THR:O	1:C:260:THR:HG22	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	642/844 (76%)	568 (88%)	72 (11%)	2 (0%)	41	74
1	B	642/844 (76%)	567 (88%)	73 (11%)	2 (0%)	41	74
1	C	642/844 (76%)	567 (88%)	73 (11%)	2 (0%)	41	74
1	D	642/844 (76%)	566 (88%)	74 (12%)	2 (0%)	41	74
All	All	2568/3376 (76%)	2268 (88%)	292 (11%)	8 (0%)	44	74

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	724	SER
1	B	724	SER
1	C	724	SER
1	D	724	SER
1	A	461	GLY
1	B	461	GLY
1	C	461	GLY
1	D	461	GLY

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	572/742 (77%)	564 (99%)	8 (1%)	67	81
1	B	572/742 (77%)	564 (99%)	8 (1%)	67	81
1	C	572/742 (77%)	564 (99%)	8 (1%)	67	81
1	D	572/742 (77%)	564 (99%)	8 (1%)	67	81
All	All	2288/2968 (77%)	2256 (99%)	32 (1%)	68	81

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	116	ARG
1	A	172	ASN
1	A	242	LYS
1	A	312	ASN
1	A	690	LYS
1	A	716	LYS
1	A	718	MET
1	A	750	ASN
1	B	116	ARG
1	B	172	ASN
1	B	242	LYS
1	B	312	ASN
1	B	690	LYS
1	B	716	LYS
1	B	718	MET
1	B	750	ASN
1	C	116	ARG
1	C	172	ASN
1	C	242	LYS
1	C	312	ASN
1	C	690	LYS
1	C	716	LYS
1	C	718	MET
1	C	750	ASN
1	D	116	ARG
1	D	172	ASN
1	D	242	LYS
1	D	312	ASN
1	D	690	LYS
1	D	716	LYS
1	D	718	MET
1	D	750	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	ASN
1	A	291	HIS
1	A	303	ASN
1	A	312	ASN
1	A	469	ASN
1	A	750	ASN
1	B	172	ASN

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Mol	Chain	Res	Type
1	B	291	HIS
1	B	303	ASN
1	B	312	ASN
1	B	469	ASN
1	B	750	ASN
1	C	172	ASN
1	C	291	HIS
1	C	303	ASN
1	C	312	ASN
1	C	469	ASN
1	C	750	ASN
1	D	172	ASN
1	D	291	HIS
1	D	303	ASN
1	D	312	ASN
1	D	469	ASN
1	D	750	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 33 ligands modelled in this entry, 1 is monoatomic - leaving 32 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
2	POV	D	903	-	46,46,51	0.98	4 (8%)	52,54,59	0.98	1 (1%)
2	POV	B	908	-	51,51,51	0.95	3 (5%)	57,59,59	0.91	1 (1%)
2	POV	D	905	-	32,32,51	1.13	3 (9%)	38,40,59	1.19	3 (7%)
2	POV	D	902	-	51,51,51	0.95	4 (7%)	57,59,59	0.91	2 (3%)
2	POV	A	907	-	42,42,51	1.03	4 (9%)	48,50,59	1.09	2 (4%)
2	POV	B	904	-	32,32,51	1.14	3 (9%)	38,40,59	1.18	3 (7%)
2	POV	B	906	-	9,9,51	0.37	0	8,8,59	0.89	0
2	POV	C	901	-	43,43,51	1.05	4 (9%)	49,51,59	0.87	2 (4%)
2	POV	A	902	-	46,46,51	0.97	4 (8%)	52,54,59	0.96	1 (1%)
2	POV	B	901	-	43,43,51	1.05	4 (9%)	49,51,59	0.86	2 (4%)
2	POV	A	909	-	43,43,51	1.05	4 (9%)	49,51,59	0.86	2 (4%)
2	POV	C	902	-	46,46,51	0.97	4 (8%)	52,54,59	0.97	1 (1%)
2	POV	D	901	-	42,42,51	1.03	4 (9%)	48,50,59	1.09	2 (4%)
2	POV	D	907	-	9,9,51	0.37	0	8,8,59	0.89	0
2	POV	A	901	-	43,43,51	1.05	4 (9%)	49,51,59	0.86	2 (4%)
3	4DY	C	903	-	22,22,22	0.32	0	27,27,27	0.34	0
2	POV	C	908	-	51,51,51	0.95	4 (7%)	57,59,59	0.91	1 (1%)
2	POV	C	906	-	9,9,51	0.37	0	8,8,59	0.89	0
3	4DY	D	904	-	22,22,22	0.31	0	27,27,27	0.34	0
2	POV	D	906	-	15,15,51	0.32	0	14,14,59	0.71	0
2	POV	C	905	-	15,15,51	0.32	0	14,14,59	0.71	0
3	4DY	B	903	-	22,22,22	0.31	0	27,27,27	0.34	0
2	POV	C	907	-	42,42,51	1.03	4 (9%)	48,50,59	1.09	2 (4%)
2	POV	B	905	-	15,15,51	0.32	0	14,14,59	0.70	0
2	POV	B	902	-	46,46,51	0.97	4 (8%)	52,54,59	0.97	1 (1%)
3	4DY	A	903	-	22,22,22	0.30	0	27,27,27	0.35	0
2	POV	A	908	-	51,51,51	0.95	4 (7%)	57,59,59	0.91	1 (1%)
2	POV	A	904	-	32,32,51	1.13	3 (9%)	38,40,59	1.20	3 (7%)
2	POV	A	906	-	9,9,51	0.37	0	8,8,59	0.88	0
2	POV	C	904	-	32,32,51	1.13	3 (9%)	38,40,59	1.19	3 (7%)
2	POV	A	905	-	15,15,51	0.32	0	14,14,59	0.70	0
2	POV	B	907	-	42,42,51	1.04	4 (9%)	48,50,59	1.08	2 (4%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	POV	D	903	-	-	23/50/50/55	-
2	POV	B	908	-	-	21/55/55/55	-
2	POV	D	905	-	-	18/36/36/55	-
2	POV	D	902	-	-	22/55/55/55	-
2	POV	A	907	-	-	28/46/46/55	-
2	POV	B	904	-	-	18/36/36/55	-
2	POV	B	906	-	-	4/7/7/55	-
2	POV	C	901	-	-	18/47/47/55	-
2	POV	A	902	-	-	23/50/50/55	-
2	POV	B	901	-	-	18/47/47/55	-
2	POV	A	909	-	-	17/47/47/55	-
2	POV	C	902	-	-	23/50/50/55	-
2	POV	D	901	-	-	32/46/46/55	-
2	POV	D	907	-	-	4/7/7/55	-
2	POV	A	901	-	-	18/47/47/55	-
3	4DY	C	903	-	-	7/16/16/16	0/1/1/1
2	POV	C	908	-	-	22/55/55/55	-
2	POV	C	906	-	-	4/7/7/55	-
3	4DY	D	904	-	-	7/16/16/16	0/1/1/1
2	POV	D	906	-	-	8/13/13/55	-
2	POV	C	905	-	-	8/13/13/55	-
3	4DY	B	903	-	-	7/16/16/16	0/1/1/1
2	POV	C	907	-	-	28/46/46/55	-
2	POV	B	905	-	-	8/13/13/55	-
2	POV	B	902	-	-	23/50/50/55	-
3	4DY	A	903	-	-	7/16/16/16	0/1/1/1
2	POV	A	908	-	-	22/55/55/55	-
2	POV	A	904	-	-	18/36/36/55	-
2	POV	A	906	-	-	4/7/7/55	-
2	POV	C	904	-	-	18/36/36/55	-
2	POV	A	905	-	-	8/13/13/55	-
2	POV	B	907	-	-	28/46/46/55	-

All (75) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	909	POV	O31-C31	2.67	1.41	1.33
2	A	901	POV	O31-C31	2.64	1.41	1.33
2	A	901	POV	O21-C2	-2.63	1.40	1.46
2	B	901	POV	O31-C31	2.62	1.41	1.33
2	A	909	POV	O21-C2	-2.61	1.40	1.46
2	B	901	POV	O21-C2	-2.59	1.40	1.46
2	C	901	POV	O21-C2	-2.59	1.40	1.46
2	C	901	POV	O31-C31	2.57	1.40	1.33
2	D	903	POV	O21-C2	-2.56	1.40	1.46
2	B	907	POV	O21-C2	-2.56	1.40	1.46
2	A	908	POV	O21-C2	-2.54	1.40	1.46
2	A	907	POV	O21-C2	-2.54	1.40	1.46
2	D	902	POV	O21-C2	-2.54	1.40	1.46
2	C	902	POV	O21-C2	-2.53	1.40	1.46
2	A	902	POV	O21-C2	-2.53	1.40	1.46
2	C	907	POV	O21-C2	-2.52	1.40	1.46
2	C	908	POV	O21-C2	-2.52	1.40	1.46
2	D	901	POV	O21-C2	-2.52	1.40	1.46
2	B	902	POV	O21-C2	-2.51	1.40	1.46
2	B	908	POV	O21-C2	-2.51	1.40	1.46
2	B	907	POV	O31-C31	2.50	1.40	1.33
2	D	901	POV	O31-C31	2.47	1.40	1.33
2	B	908	POV	O31-C31	2.46	1.40	1.33
2	C	907	POV	O31-C31	2.45	1.40	1.33
2	A	904	POV	O21-C2	-2.45	1.40	1.46
2	A	907	POV	O31-C31	2.45	1.40	1.33
2	D	905	POV	O21-C2	-2.45	1.40	1.46
2	B	904	POV	O21-C2	-2.44	1.40	1.46
2	C	908	POV	O31-C31	2.43	1.40	1.33
2	C	904	POV	O21-C2	-2.42	1.40	1.46
2	D	902	POV	O31-C31	2.41	1.40	1.33
2	A	908	POV	O31-C31	2.41	1.40	1.33
2	C	902	POV	O31-C31	2.37	1.40	1.33
2	B	902	POV	O31-C31	2.34	1.40	1.33
2	A	902	POV	O31-C31	2.33	1.40	1.33
2	D	903	POV	O31-C31	2.30	1.40	1.33
2	A	901	POV	O21-C21	2.27	1.40	1.34
2	C	901	POV	O21-C21	2.26	1.40	1.34
2	B	904	POV	O31-C31	2.26	1.39	1.33
2	C	904	POV	O31-C31	2.24	1.39	1.33
2	D	905	POV	O31-C31	2.24	1.39	1.33
2	A	904	POV	O31-C31	2.24	1.39	1.33
2	B	901	POV	O21-C21	2.23	1.40	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	909	POV	O21-C21	2.20	1.40	1.34
2	B	902	POV	O31-C3	-2.20	1.40	1.45
2	D	903	POV	O31-C3	-2.19	1.40	1.45
2	B	907	POV	O21-C21	2.19	1.40	1.34
2	B	904	POV	O31-C3	-2.19	1.40	1.45
2	D	905	POV	O31-C3	-2.17	1.40	1.45
2	B	908	POV	O21-C21	2.17	1.40	1.34
2	A	907	POV	O21-C21	2.17	1.40	1.34
2	C	907	POV	O21-C21	2.17	1.40	1.34
2	D	901	POV	O21-C21	2.16	1.40	1.34
2	A	902	POV	O31-C3	-2.16	1.40	1.45
2	C	904	POV	O31-C3	-2.16	1.40	1.45
2	D	902	POV	O21-C21	2.16	1.40	1.34
2	C	908	POV	O21-C21	2.16	1.40	1.34
2	A	908	POV	O21-C21	2.15	1.40	1.34
2	C	907	POV	O31-C3	-2.15	1.40	1.45
2	A	904	POV	O31-C3	-2.14	1.40	1.45
2	B	907	POV	O31-C3	-2.13	1.40	1.45
2	D	903	POV	O21-C21	2.13	1.40	1.34
2	A	907	POV	O31-C3	-2.13	1.40	1.45
2	A	902	POV	O21-C21	2.13	1.40	1.34
2	B	902	POV	O21-C21	2.12	1.40	1.34
2	D	901	POV	O31-C3	-2.11	1.40	1.45
2	C	902	POV	O21-C21	2.11	1.40	1.34
2	C	902	POV	O31-C3	-2.10	1.40	1.45
2	C	908	POV	O31-C3	-2.07	1.40	1.45
2	D	902	POV	O31-C3	-2.07	1.40	1.45
2	A	908	POV	O31-C3	-2.06	1.40	1.45
2	B	901	POV	O31-C3	-2.05	1.40	1.45
2	C	901	POV	O31-C3	-2.05	1.40	1.45
2	A	901	POV	O31-C3	-2.03	1.40	1.45
2	A	909	POV	O31-C3	-2.01	1.40	1.45

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	901	POV	O21-C21-C22	4.39	120.96	111.50
2	C	907	POV	O21-C21-C22	4.34	120.86	111.50
2	B	907	POV	O21-C21-C22	4.34	120.85	111.50
2	A	907	POV	O21-C21-C22	4.32	120.81	111.50
2	C	908	POV	O21-C21-C22	3.97	120.05	111.50
2	A	908	POV	O21-C21-C22	3.94	119.98	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	902	POV	O21-C21-C22	3.92	119.95	111.50
2	D	903	POV	O21-C21-C22	3.91	119.92	111.50
2	B	902	POV	O21-C21-C22	3.88	119.86	111.50
2	B	908	POV	O21-C21-C22	3.84	119.77	111.50
2	C	902	POV	O21-C21-C22	3.82	119.72	111.50
2	A	902	POV	O21-C21-C22	3.80	119.69	111.50
2	B	904	POV	O21-C21-C22	3.31	118.63	111.50
2	D	905	POV	O21-C21-C22	3.29	118.59	111.50
2	C	904	POV	O21-C21-C22	3.26	118.54	111.50
2	A	904	POV	O21-C21-C22	3.26	118.53	111.50
2	A	909	POV	O21-C21-C22	3.20	118.40	111.50
2	C	901	POV	O21-C21-C22	3.18	118.35	111.50
2	B	901	POV	O21-C21-C22	3.16	118.32	111.50
2	A	901	POV	O21-C21-C22	3.15	118.30	111.50
2	C	907	POV	O31-C31-C32	2.77	120.61	111.91
2	A	907	POV	O31-C31-C32	2.77	120.61	111.91
2	A	904	POV	C15-N-C14	2.71	115.93	108.97
2	B	907	POV	O31-C31-C32	2.70	120.38	111.91
2	D	901	POV	O31-C31-C32	2.69	120.35	111.91
2	D	905	POV	C15-N-C14	2.63	115.73	108.97
2	C	904	POV	C15-N-C14	2.62	115.71	108.97
2	B	904	POV	C15-N-C14	2.62	115.71	108.97
2	C	901	POV	O31-C31-C32	2.51	119.78	111.91
2	B	901	POV	O31-C31-C32	2.50	119.75	111.91
2	A	904	POV	O31-C31-C32	2.48	119.68	111.91
2	C	904	POV	O31-C31-C32	2.47	119.66	111.91
2	A	901	POV	O31-C31-C32	2.45	119.58	111.91
2	D	905	POV	O31-C31-C32	2.42	119.50	111.91
2	B	904	POV	O31-C31-C32	2.39	119.42	111.91
2	A	909	POV	O31-C31-C32	2.33	119.20	111.91
2	D	902	POV	C2-O21-C21	-2.01	112.85	117.79

There are no chirality outliers.

All (514) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	POV	C1-O11-P-O12
2	A	901	POV	C1-O11-P-O13
2	A	901	POV	C1-O11-P-O14
2	A	902	POV	C11-O12-P-O13
2	A	902	POV	C11-O12-P-O14
2	A	904	POV	C1-O11-P-O14

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Mol	Chain	Res	Type	Atoms
2	A	904	POV	C11-O12-P-O13
2	A	904	POV	C11-O12-P-O14
2	A	904	POV	O12-C11-C12-N
2	A	907	POV	C1-O11-P-O12
2	A	907	POV	C1-O11-P-O13
2	A	907	POV	C1-O11-P-O14
2	A	907	POV	C11-O12-P-O13
2	A	907	POV	O12-C11-C12-N
2	A	907	POV	C22-C21-O21-C2
2	A	907	POV	O22-C21-O21-C2
2	A	908	POV	O12-C11-C12-N
2	A	908	POV	C210-C211-C212-C213
2	A	908	POV	C22-C21-O21-C2
2	A	909	POV	C1-O11-P-O12
2	A	909	POV	C1-O11-P-O13
2	A	909	POV	C1-O11-P-O14
2	B	901	POV	C1-O11-P-O12
2	B	901	POV	C1-O11-P-O13
2	B	901	POV	C1-O11-P-O14
2	B	902	POV	C11-O12-P-O13
2	B	902	POV	C11-O12-P-O14
2	B	904	POV	C11-O12-P-O13
2	B	904	POV	C11-O12-P-O14
2	B	904	POV	O12-C11-C12-N
2	B	907	POV	C1-O11-P-O12
2	B	907	POV	C1-O11-P-O13
2	B	907	POV	C1-O11-P-O14
2	B	907	POV	C11-O12-P-O13
2	B	907	POV	O12-C11-C12-N
2	B	907	POV	C22-C21-O21-C2
2	B	907	POV	O22-C21-O21-C2
2	B	908	POV	O12-C11-C12-N
2	B	908	POV	C210-C211-C212-C213
2	B	908	POV	C22-C21-O21-C2
2	C	901	POV	C1-O11-P-O12
2	C	901	POV	C1-O11-P-O13
2	C	901	POV	C1-O11-P-O14
2	C	902	POV	C11-O12-P-O13
2	C	902	POV	C11-O12-P-O14
2	C	904	POV	C1-O11-P-O14
2	C	904	POV	C11-O12-P-O13
2	C	904	POV	C11-O12-P-O14

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Mol	Chain	Res	Type	Atoms
2	C	904	POV	O12-C11-C12-N
2	C	907	POV	C1-O11-P-O12
2	C	907	POV	C1-O11-P-O13
2	C	907	POV	C1-O11-P-O14
2	C	907	POV	C11-O12-P-O13
2	C	907	POV	O12-C11-C12-N
2	C	907	POV	C22-C21-O21-C2
2	C	907	POV	O22-C21-O21-C2
2	C	908	POV	O12-C11-C12-N
2	C	908	POV	C210-C211-C212-C213
2	C	908	POV	C22-C21-O21-C2
2	D	901	POV	C1-O11-P-O12
2	D	901	POV	C1-O11-P-O13
2	D	901	POV	C11-O12-P-O13
2	D	901	POV	O12-C11-C12-N
2	D	901	POV	O22-C21-O21-C2
2	D	902	POV	O12-C11-C12-N
2	D	902	POV	C210-C211-C212-C213
2	D	902	POV	C22-C21-O21-C2
2	D	903	POV	C11-O12-P-O13
2	D	903	POV	C11-O12-P-O14
2	D	905	POV	C11-O12-P-O13
2	D	905	POV	C11-O12-P-O14
2	D	905	POV	O12-C11-C12-N
3	A	903	4DY	C33-C36-C37-C38
3	A	903	4DY	C24-C22-N21-C17
3	B	903	4DY	C33-C36-C37-C38
3	B	903	4DY	C24-C22-N21-C17
3	C	903	4DY	C33-C36-C37-C38
3	C	903	4DY	C24-C22-N21-C17
3	D	904	4DY	C33-C36-C37-C38
3	D	904	4DY	C24-C22-N21-C17
3	A	903	4DY	O23-C22-N21-C17
3	B	903	4DY	O23-C22-N21-C17
3	C	903	4DY	O23-C22-N21-C17
3	D	904	4DY	O23-C22-N21-C17
2	A	904	POV	O32-C31-O31-C3
2	B	904	POV	O32-C31-O31-C3
2	C	904	POV	O32-C31-O31-C3
2	D	905	POV	O32-C31-O31-C3
2	A	908	POV	O22-C21-O21-C2
2	B	902	POV	O22-C21-O21-C2

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Mol	Chain	Res	Type	Atoms
2	B	908	POV	O22-C21-O21-C2
2	C	908	POV	O22-C21-O21-C2
2	D	902	POV	O22-C21-O21-C2
2	D	903	POV	O22-C21-O21-C2
2	D	901	POV	C22-C21-O21-C2
2	D	903	POV	C22-C21-O21-C2
2	A	904	POV	C32-C31-O31-C3
2	B	904	POV	C32-C31-O31-C3
2	C	904	POV	C32-C31-O31-C3
2	D	905	POV	C32-C31-O31-C3
2	A	902	POV	O22-C21-O21-C2
3	B	903	4DY	C4-C3-O12-C13
3	A	903	4DY	C4-C3-O12-C13
3	C	903	4DY	C4-C3-O12-C13
3	D	904	4DY	C4-C3-O12-C13
2	A	902	POV	C22-C21-O21-C2
2	B	902	POV	C22-C21-O21-C2
2	C	902	POV	C22-C21-O21-C2
2	C	902	POV	O22-C21-O21-C2
3	A	903	4DY	C2-C3-O12-C13
3	B	903	4DY	C2-C3-O12-C13
3	C	903	4DY	C2-C3-O12-C13
3	D	904	4DY	C2-C3-O12-C13
2	A	902	POV	C11-C12-N-C13
2	B	902	POV	C11-C12-N-C13
2	C	902	POV	C11-C12-N-C13
2	D	903	POV	C11-C12-N-C13
2	A	908	POV	C22-C23-C24-C25
2	D	902	POV	C22-C23-C24-C25
2	C	908	POV	C22-C23-C24-C25
2	B	908	POV	C22-C23-C24-C25
2	A	907	POV	C21-C22-C23-C24
2	B	907	POV	C21-C22-C23-C24
2	C	907	POV	C21-C22-C23-C24
2	D	901	POV	C21-C22-C23-C24
2	A	904	POV	C21-C22-C23-C24
2	B	904	POV	C21-C22-C23-C24
2	C	904	POV	C21-C22-C23-C24
2	C	908	POV	C21-C22-C23-C24
2	D	905	POV	C21-C22-C23-C24
2	A	902	POV	C11-O12-P-O11
2	A	904	POV	C1-O11-P-O12

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Mol	Chain	Res	Type	Atoms
2	A	904	POV	C11-O12-P-O11
2	A	907	POV	C11-O12-P-O11
2	B	902	POV	C11-O12-P-O11
2	B	904	POV	C1-O11-P-O12
2	B	904	POV	C11-O12-P-O11
2	B	907	POV	C11-O12-P-O11
2	C	902	POV	C11-O12-P-O11
2	C	904	POV	C1-O11-P-O12
2	C	904	POV	C11-O12-P-O11
2	C	907	POV	C11-O12-P-O11
2	D	901	POV	C11-O12-P-O11
2	D	903	POV	C11-O12-P-O11
2	D	905	POV	C1-O11-P-O12
2	D	905	POV	C11-O12-P-O11
2	A	908	POV	C21-C22-C23-C24
2	D	902	POV	C21-C22-C23-C24
2	A	904	POV	O22-C21-O21-C2
2	B	904	POV	O22-C21-O21-C2
2	C	904	POV	O22-C21-O21-C2
2	D	905	POV	O22-C21-O21-C2
2	D	901	POV	C11-C12-N-C15
2	D	902	POV	C36-C37-C38-C39
2	A	904	POV	C22-C21-O21-C2
2	B	904	POV	C22-C21-O21-C2
2	C	904	POV	C22-C21-O21-C2
2	D	905	POV	C22-C21-O21-C2
2	A	901	POV	C34-C35-C36-C37
2	A	902	POV	C214-C215-C216-C217
2	A	908	POV	C36-C37-C38-C39
2	A	909	POV	C34-C35-C36-C37
2	B	902	POV	C214-C215-C216-C217
2	C	902	POV	C214-C215-C216-C217
2	D	903	POV	C214-C215-C216-C217
2	B	901	POV	C34-C35-C36-C37
2	C	901	POV	C34-C35-C36-C37
2	B	908	POV	C36-C37-C38-C39
2	C	908	POV	C36-C37-C38-C39
2	D	902	POV	C310-C311-C312-C313
2	D	903	POV	C31-C32-C33-C34
2	B	902	POV	C25-C26-C27-C28
2	C	902	POV	C25-C26-C27-C28
2	A	902	POV	C25-C26-C27-C28

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Mol	Chain	Res	Type	Atoms
2	D	903	POV	C25-C26-C27-C28
2	B	908	POV	C21-C22-C23-C24
2	A	905	POV	C25-C26-C27-C28
2	A	908	POV	C310-C311-C312-C313
2	B	905	POV	C25-C26-C27-C28
2	B	908	POV	C310-C311-C312-C313
2	C	905	POV	C25-C26-C27-C28
2	C	908	POV	C310-C311-C312-C313
2	D	906	POV	C25-C26-C27-C28
3	A	903	4DY	C24-C27-C30-C33
3	B	903	4DY	C24-C27-C30-C33
3	C	903	4DY	C24-C27-C30-C33
3	D	904	4DY	C24-C27-C30-C33
2	A	906	POV	C210-C211-C212-C213
2	A	907	POV	C26-C27-C28-C29
2	B	905	POV	C26-C27-C28-C29
2	B	907	POV	C26-C27-C28-C29
2	C	905	POV	C26-C27-C28-C29
2	C	907	POV	C26-C27-C28-C29
2	C	908	POV	C26-C27-C28-C29
2	D	901	POV	C26-C27-C28-C29
2	D	906	POV	C26-C27-C28-C29
2	B	902	POV	C31-C32-C33-C34
2	B	908	POV	C31-C32-C33-C34
2	D	902	POV	C31-C32-C33-C34
2	C	901	POV	C32-C33-C34-C35
2	A	902	POV	C11-C12-N-C14
2	A	902	POV	C11-C12-N-C15
2	B	902	POV	C11-C12-N-C14
2	B	902	POV	C11-C12-N-C15
2	C	902	POV	C11-C12-N-C14
2	C	902	POV	C11-C12-N-C15
2	D	901	POV	C11-C12-N-C13
2	D	903	POV	C11-C12-N-C15
2	A	901	POV	C32-C33-C34-C35
2	A	909	POV	C32-C33-C34-C35
2	B	901	POV	C32-C33-C34-C35
2	A	902	POV	C37-C38-C39-C310
2	A	907	POV	C23-C24-C25-C26
2	C	902	POV	C37-C38-C39-C310
2	D	903	POV	C37-C38-C39-C310
2	D	905	POV	C22-C23-C24-C25

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Mol	Chain	Res	Type	Atoms
2	B	902	POV	C37-C38-C39-C310
2	C	907	POV	C23-C24-C25-C26
2	B	907	POV	C23-C24-C25-C26
2	A	904	POV	C22-C23-C24-C25
2	D	901	POV	C23-C24-C25-C26
2	A	908	POV	C31-C32-C33-C34
2	B	904	POV	C22-C23-C24-C25
2	C	904	POV	C22-C23-C24-C25
2	A	902	POV	C31-C32-C33-C34
2	C	904	POV	C31-C32-C33-C34
2	A	902	POV	C26-C27-C28-C29
2	A	905	POV	C26-C27-C28-C29
2	B	902	POV	C26-C27-C28-C29
2	B	906	POV	C210-C211-C212-C213
2	B	908	POV	C26-C27-C28-C29
2	C	902	POV	C26-C27-C28-C29
2	C	906	POV	C210-C211-C212-C213
2	D	903	POV	C26-C27-C28-C29
2	D	907	POV	C210-C211-C212-C213
2	A	907	POV	C211-C212-C213-C214
2	C	907	POV	C211-C212-C213-C214
2	D	901	POV	C211-C212-C213-C214
2	B	907	POV	C211-C212-C213-C214
2	B	907	POV	C212-C213-C214-C215
2	C	907	POV	C212-C213-C214-C215
2	D	901	POV	C212-C213-C214-C215
2	C	902	POV	C34-C35-C36-C37
2	D	903	POV	C11-C12-N-C14
2	C	908	POV	C31-C32-C33-C34
2	A	907	POV	C212-C213-C214-C215
2	D	903	POV	C34-C35-C36-C37
2	A	907	POV	C32-C31-O31-C3
2	A	902	POV	C34-C35-C36-C37
2	C	908	POV	C212-C213-C214-C215
2	A	908	POV	C26-C27-C28-C29
2	D	901	POV	C210-C211-C212-C213
2	C	907	POV	C32-C31-O31-C3
2	D	901	POV	C32-C31-O31-C3
2	B	902	POV	C34-C35-C36-C37
2	C	902	POV	C31-C32-C33-C34
2	A	908	POV	C212-C213-C214-C215
2	B	907	POV	C32-C31-O31-C3

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Mol	Chain	Res	Type	Atoms
2	B	908	POV	C212-C213-C214-C215
2	B	902	POV	C211-C212-C213-C214
2	B	907	POV	C11-C12-N-C15
2	C	907	POV	C11-C12-N-C15
2	D	901	POV	C11-C12-N-C14
2	A	902	POV	C211-C212-C213-C214
2	C	902	POV	C211-C212-C213-C214
2	A	905	POV	C210-C211-C212-C213
2	A	907	POV	C210-C211-C212-C213
2	B	905	POV	C210-C211-C212-C213
2	B	907	POV	C210-C211-C212-C213
2	C	905	POV	C210-C211-C212-C213
2	C	907	POV	C210-C211-C212-C213
2	D	906	POV	C210-C211-C212-C213
2	A	905	POV	C213-C214-C215-C216
2	B	905	POV	C213-C214-C215-C216
2	C	905	POV	C213-C214-C215-C216
2	D	903	POV	C211-C212-C213-C214
2	D	906	POV	C213-C214-C215-C216
2	A	907	POV	O32-C31-O31-C3
2	C	907	POV	O32-C31-O31-C3
2	B	907	POV	C33-C34-C35-C36
2	D	902	POV	C26-C27-C28-C29
2	D	902	POV	C212-C213-C214-C215
2	D	901	POV	O32-C31-O31-C3
2	A	908	POV	C1-C2-C3-O31
2	B	908	POV	C1-C2-C3-O31
2	C	908	POV	C1-C2-C3-O31
2	D	902	POV	C1-C2-C3-O31
2	A	907	POV	C34-C35-C36-C37
2	C	907	POV	C34-C35-C36-C37
2	D	902	POV	C312-C313-C314-C315
2	D	901	POV	C34-C35-C36-C37
2	A	904	POV	C31-C32-C33-C34
2	B	904	POV	C31-C32-C33-C34
2	D	905	POV	C31-C32-C33-C34
2	B	901	POV	C210-C211-C212-C213
2	B	907	POV	O32-C31-O31-C3
2	B	907	POV	C34-C35-C36-C37
2	A	908	POV	C312-C313-C314-C315
2	A	906	POV	C212-C213-C214-C215
2	C	908	POV	C312-C313-C314-C315

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Mol	Chain	Res	Type	Atoms
2	B	908	POV	C312-C313-C314-C315
2	A	909	POV	C210-C211-C212-C213
2	C	901	POV	C210-C211-C212-C213
2	B	907	POV	O21-C2-C3-O31
2	C	907	POV	O21-C2-C3-O31
2	D	901	POV	O21-C2-C3-O31
2	C	907	POV	C33-C34-C35-C36
2	A	907	POV	C33-C34-C35-C36
2	D	907	POV	C212-C213-C214-C215
2	B	901	POV	C23-C24-C25-C26
2	D	901	POV	C33-C34-C35-C36
2	C	901	POV	C23-C24-C25-C26
2	A	909	POV	C23-C24-C25-C26
2	B	906	POV	C212-C213-C214-C215
2	C	906	POV	C212-C213-C214-C215
2	C	901	POV	C211-C212-C213-C214
2	A	909	POV	C211-C212-C213-C214
2	B	901	POV	C211-C212-C213-C214
2	A	902	POV	C33-C34-C35-C36
2	D	903	POV	C33-C34-C35-C36
2	A	901	POV	C211-C212-C213-C214
2	A	901	POV	C23-C24-C25-C26
2	B	902	POV	C33-C34-C35-C36
2	C	902	POV	C33-C34-C35-C36
2	A	901	POV	C210-C211-C212-C213
2	A	907	POV	C11-C12-N-C15
2	B	907	POV	C11-C12-N-C13
2	B	907	POV	C11-C12-N-C14
2	A	907	POV	O21-C2-C3-O31
2	A	909	POV	O21-C2-C3-O31
2	A	904	POV	C2-C1-O11-P
2	B	904	POV	C2-C1-O11-P
2	C	904	POV	C2-C1-O11-P
2	D	905	POV	C2-C1-O11-P
2	A	907	POV	C11-C12-N-C13
2	C	907	POV	C11-C12-N-C13
2	C	907	POV	C11-C12-N-C14
2	A	908	POV	O11-C1-C2-C3
2	C	908	POV	O11-C1-C2-C3
2	A	901	POV	C35-C36-C37-C38
2	A	909	POV	C1-C2-C3-O31
2	B	908	POV	O21-C2-C3-O31

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Mol	Chain	Res	Type	Atoms
2	A	901	POV	C22-C23-C24-C25
2	B	901	POV	C35-C36-C37-C38
2	A	907	POV	C11-C12-N-C14
2	A	909	POV	C22-C23-C24-C25
2	A	902	POV	C21-C22-C23-C24
2	B	901	POV	C22-C23-C24-C25
2	C	901	POV	C35-C36-C37-C38
2	C	901	POV	C22-C23-C24-C25
2	A	901	POV	C33-C34-C35-C36
2	D	906	POV	C23-C24-C25-C26
2	A	909	POV	C35-C36-C37-C38
2	B	901	POV	C33-C34-C35-C36
2	C	905	POV	C23-C24-C25-C26
2	A	901	POV	C11-O12-P-O11
2	B	901	POV	C11-O12-P-O11
2	C	901	POV	C11-O12-P-O11
2	C	901	POV	C33-C34-C35-C36
2	A	907	POV	C11-O12-P-O14
2	B	904	POV	C1-O11-P-O14
2	B	907	POV	C11-O12-P-O14
2	C	907	POV	C11-O12-P-O14
2	D	901	POV	C1-O11-P-O14
2	D	901	POV	C11-O12-P-O14
2	D	905	POV	C1-O11-P-O14
2	B	906	POV	C215-C216-C217-C218
2	D	902	POV	O11-C1-C2-C3
2	A	906	POV	C213-C214-C215-C216
2	A	909	POV	C33-C34-C35-C36
2	A	902	POV	C311-C310-C39-C38
2	C	902	POV	C311-C310-C39-C38
2	C	906	POV	C215-C216-C217-C218
2	B	905	POV	C23-C24-C25-C26
2	D	903	POV	C311-C310-C39-C38
2	B	902	POV	C311-C310-C39-C38
2	D	907	POV	C215-C216-C217-C218
2	A	905	POV	C23-C24-C25-C26
2	A	902	POV	O12-C11-C12-N
2	B	902	POV	O12-C11-C12-N
2	C	902	POV	O12-C11-C12-N
2	C	907	POV	C1-C2-C3-O31
2	D	901	POV	C1-C2-C3-O31
2	D	903	POV	O12-C11-C12-N

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Mol	Chain	Res	Type	Atoms
2	A	908	POV	O21-C2-C3-O31
2	C	908	POV	O21-C2-C3-O31
2	D	902	POV	O21-C2-C3-O31
2	B	905	POV	C211-C212-C213-C214
2	C	902	POV	C21-C22-C23-C24
2	A	904	POV	C3-C2-O21-C21
2	B	904	POV	C3-C2-O21-C21
2	C	904	POV	C3-C2-O21-C21
2	D	905	POV	C3-C2-O21-C21
2	C	905	POV	C211-C212-C213-C214
2	A	908	POV	O11-C1-C2-O21
2	C	908	POV	O11-C1-C2-O21
2	D	906	POV	C211-C212-C213-C214
2	A	908	POV	C11-O12-P-O11
2	A	909	POV	C11-O12-P-O11
2	B	908	POV	C11-O12-P-O11
2	C	908	POV	C11-O12-P-O11
2	D	902	POV	C11-O12-P-O11
2	B	907	POV	C1-C2-C3-O31
2	A	906	POV	C215-C216-C217-C218
2	A	905	POV	C211-C212-C213-C214
2	D	903	POV	C23-C24-C25-C26
2	C	906	POV	C213-C214-C215-C216
2	D	907	POV	C213-C214-C215-C216
2	B	902	POV	C21-C22-C23-C24
2	D	902	POV	C24-C25-C26-C27
2	B	906	POV	C213-C214-C215-C216
2	D	901	POV	C214-C215-C216-C217
2	B	901	POV	O21-C2-C3-O31
2	C	901	POV	O21-C2-C3-O31
2	B	902	POV	C23-C24-C25-C26
2	A	908	POV	C24-C25-C26-C27
2	A	907	POV	C214-C215-C216-C217
2	A	901	POV	C1-C2-C3-O31
2	A	907	POV	C1-C2-C3-O31
2	B	907	POV	C214-C215-C216-C217
2	D	901	POV	C213-C214-C215-C216
2	C	907	POV	C214-C215-C216-C217
2	A	907	POV	C213-C214-C215-C216
2	C	907	POV	C213-C214-C215-C216
2	A	902	POV	O11-C1-C2-C3
2	B	902	POV	O11-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
2	C	902	POV	O11-C1-C2-C3
2	D	903	POV	O11-C1-C2-C3
2	C	902	POV	C23-C24-C25-C26
2	B	907	POV	C213-C214-C215-C216
2	B	908	POV	C24-C25-C26-C27
2	C	908	POV	C24-C25-C26-C27
2	A	901	POV	O21-C2-C3-O31
2	A	902	POV	C23-C24-C25-C26
2	B	907	POV	C32-C33-C34-C35
2	C	908	POV	C214-C215-C216-C217
2	B	908	POV	C214-C215-C216-C217
2	A	908	POV	C214-C215-C216-C217
2	B	901	POV	O32-C31-O31-C3
2	D	902	POV	O11-C1-C2-O21
2	D	901	POV	C32-C33-C34-C35
2	D	903	POV	C21-C22-C23-C24
2	B	908	POV	O21-C21-C22-C23
2	D	905	POV	O31-C31-C32-C33
2	C	902	POV	C29-C210-C211-C212
2	A	907	POV	C32-C33-C34-C35
2	B	904	POV	O31-C31-C32-C33
2	C	908	POV	O21-C21-C22-C23
2	A	908	POV	O21-C21-C22-C23
2	B	902	POV	C29-C210-C211-C212
2	D	903	POV	C29-C210-C211-C212
2	C	901	POV	O32-C31-O31-C3
2	C	907	POV	C32-C33-C34-C35
2	A	909	POV	O21-C21-C22-C23
2	B	901	POV	O21-C21-C22-C23
2	C	904	POV	O31-C31-C32-C33
2	D	902	POV	O21-C21-C22-C23
2	A	902	POV	C29-C210-C211-C212
2	A	901	POV	O21-C21-C22-C23
2	A	904	POV	O31-C31-C32-C33
2	C	901	POV	O21-C21-C22-C23
2	B	901	POV	C32-C31-O31-C3
2	D	905	POV	C27-C28-C29-C210
3	A	903	4DY	C30-C33-C36-C37
3	B	903	4DY	C30-C33-C36-C37
3	C	903	4DY	C30-C33-C36-C37
3	D	904	4DY	C30-C33-C36-C37
2	D	902	POV	C214-C215-C216-C217

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Mol	Chain	Res	Type	Atoms
2	A	902	POV	C27-C28-C29-C210
2	A	904	POV	C27-C28-C29-C210
2	C	902	POV	C27-C28-C29-C210
2	A	901	POV	O22-C21-C22-C23
2	C	904	POV	C27-C28-C29-C210
2	D	903	POV	C27-C28-C29-C210
2	B	908	POV	O22-C21-C22-C23
2	D	902	POV	O22-C21-C22-C23
2	D	905	POV	O32-C31-C32-C33
2	B	904	POV	O32-C31-C32-C33
2	C	904	POV	O32-C31-C32-C33
2	B	908	POV	C23-C24-C25-C26
2	C	901	POV	C25-C26-C27-C28
2	A	908	POV	O22-C21-C22-C23
2	A	905	POV	C27-C28-C29-C210
2	B	902	POV	C27-C28-C29-C210
2	B	904	POV	C27-C28-C29-C210
2	C	901	POV	C32-C31-O31-C3
2	A	909	POV	O22-C21-C22-C23
2	C	908	POV	O22-C21-C22-C23
2	A	904	POV	O32-C31-C32-C33
2	B	901	POV	C25-C26-C27-C28
2	A	908	POV	C11-O12-P-O14
2	B	908	POV	C11-O12-P-O14
2	C	908	POV	C11-O12-P-O14
2	D	902	POV	C11-O12-P-O14
2	A	909	POV	C25-C26-C27-C28
2	A	907	POV	O31-C31-C32-C33
2	C	901	POV	O22-C21-C22-C23
2	D	901	POV	C12-C11-O12-P
2	A	901	POV	O32-C31-O31-C3
2	B	901	POV	O22-C21-C22-C23
2	B	905	POV	C27-C28-C29-C210
2	D	901	POV	O31-C31-C32-C33
2	C	907	POV	O31-C31-C32-C33
2	B	907	POV	O31-C31-C32-C33
2	C	905	POV	C27-C28-C29-C210
2	D	906	POV	C27-C28-C29-C210
2	A	905	POV	C212-C213-C214-C215
2	C	905	POV	C212-C213-C214-C215
2	D	906	POV	C212-C213-C214-C215
2	B	905	POV	C212-C213-C214-C215

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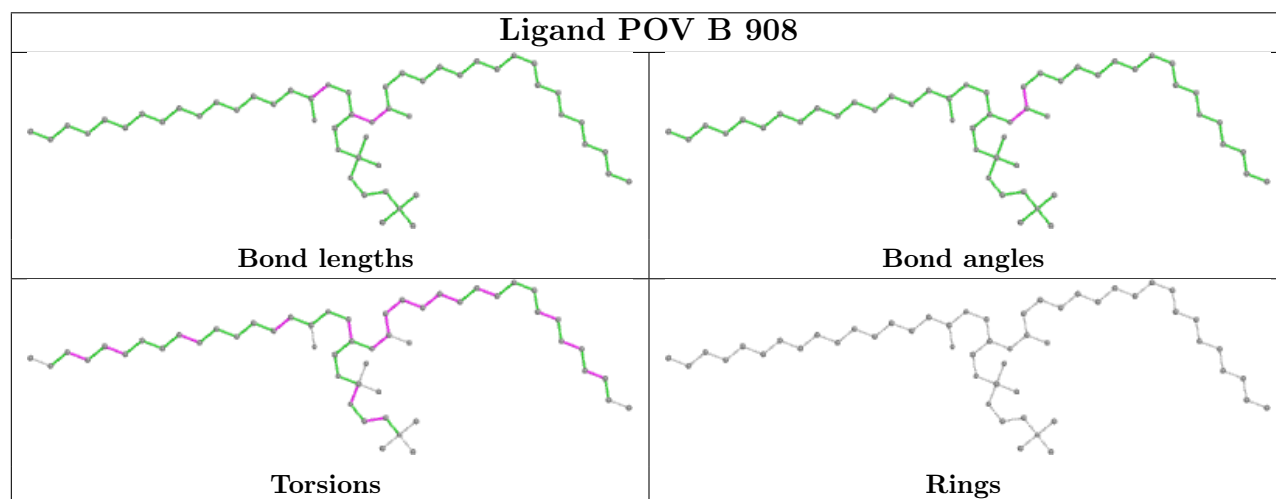
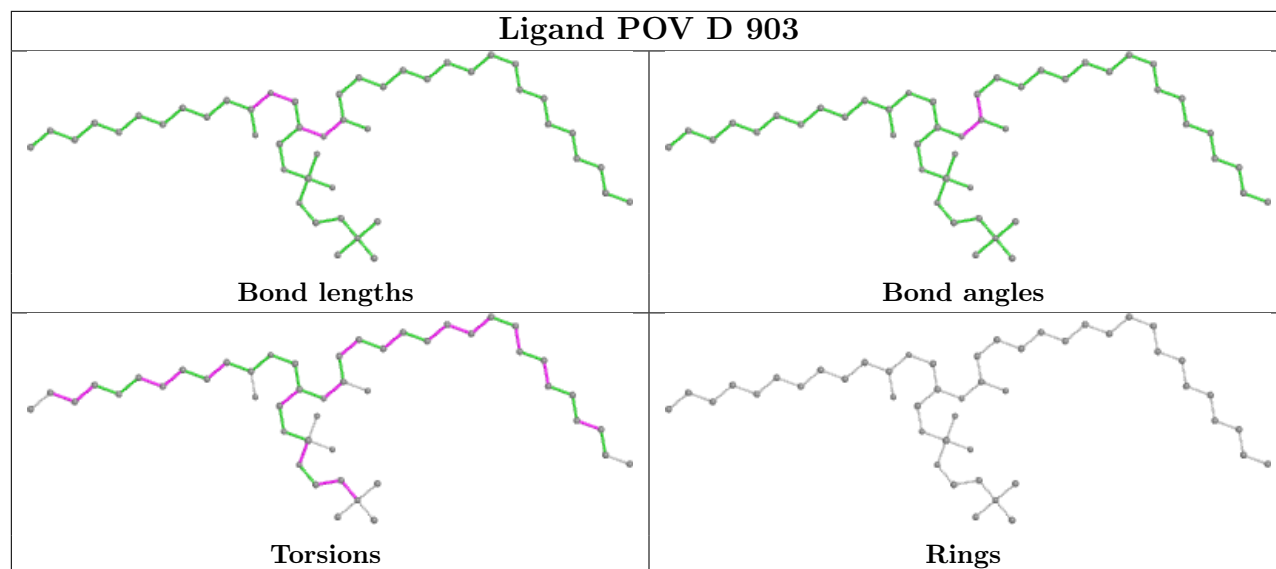
Mol	Chain	Res	Type	Atoms
2	A	901	POV	C27-C28-C29-C210
2	D	901	POV	C29-C210-C211-C212
2	D	901	POV	O32-C31-C32-C33
2	D	901	POV	O21-C21-C22-C23

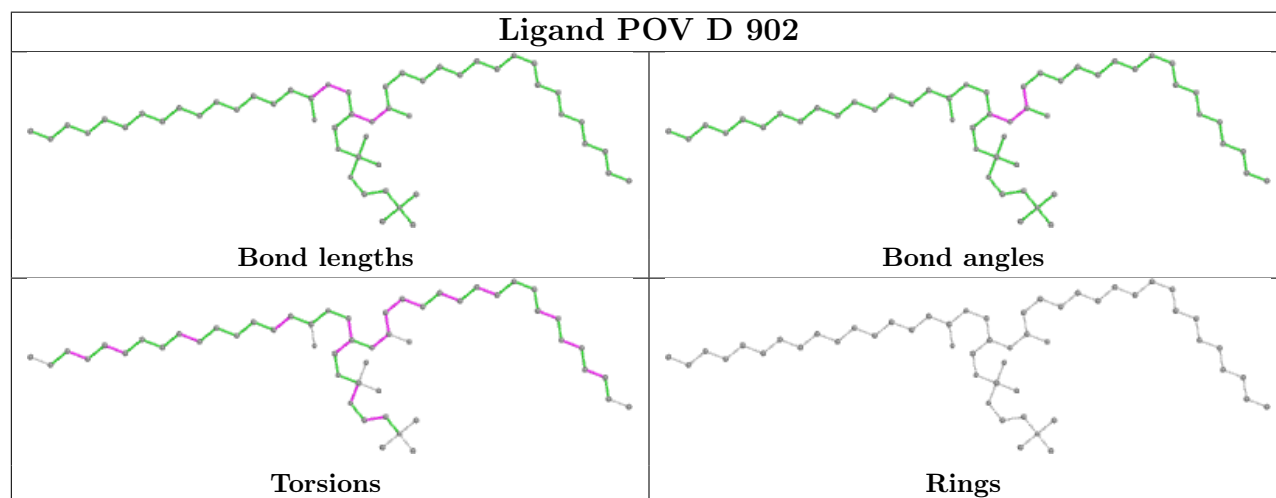
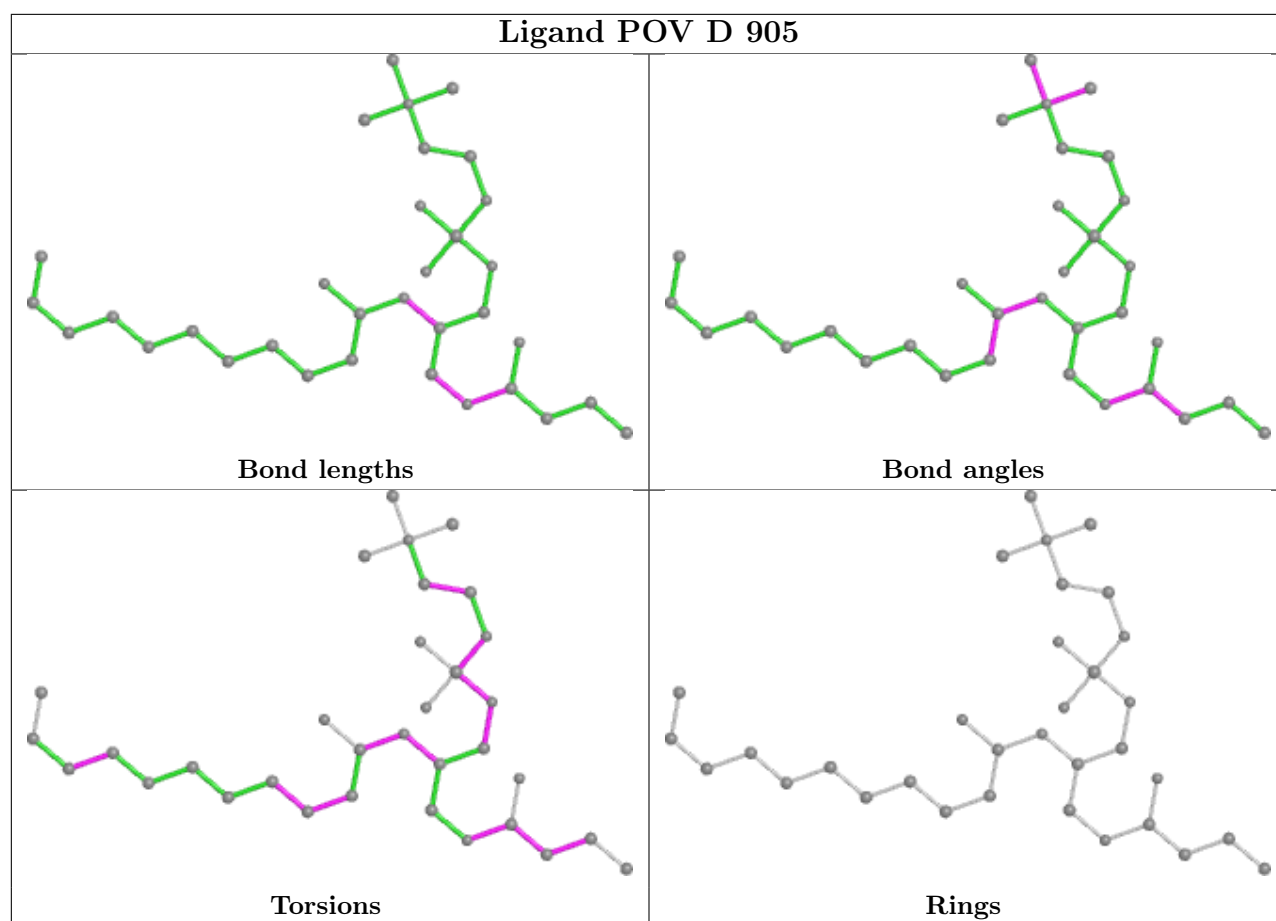
There are no ring outliers.

20 monomers are involved in 50 short contacts:

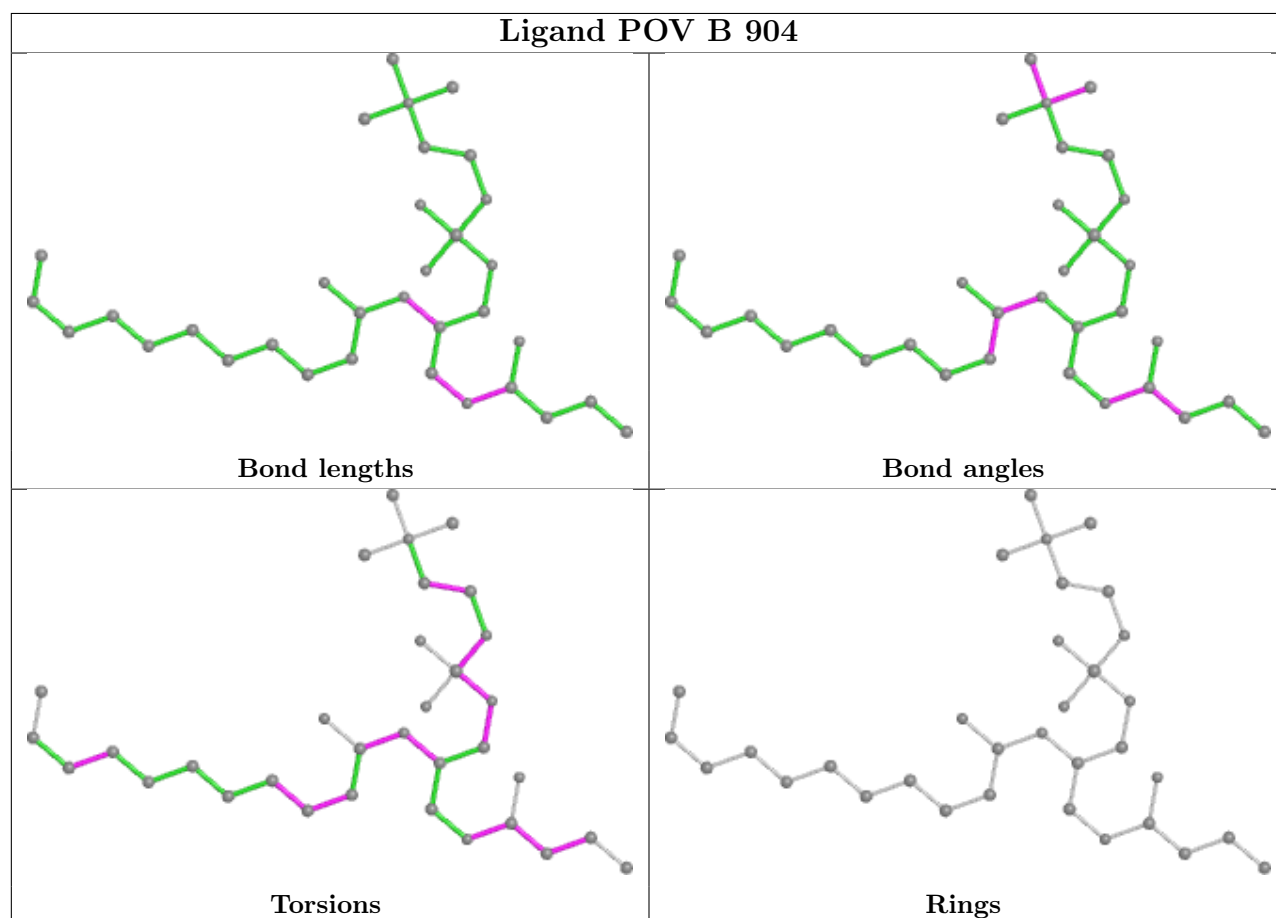
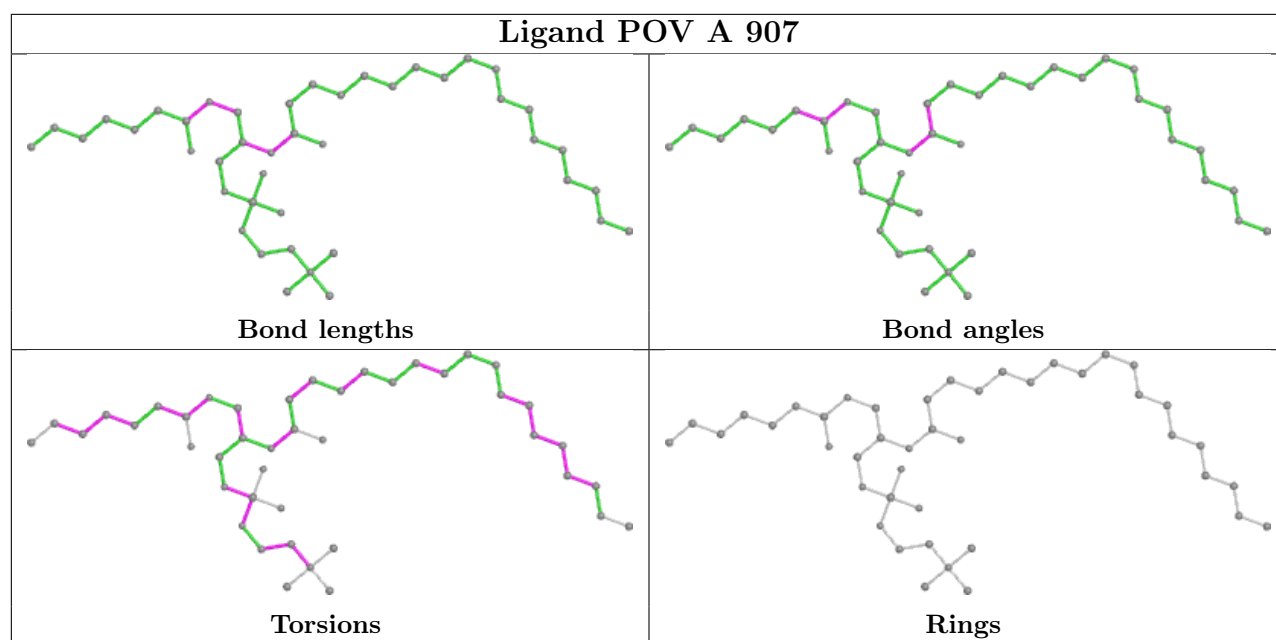
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	908	POV	1	0
2	D	905	POV	4	0
2	D	902	POV	1	0
2	A	907	POV	1	0
2	B	904	POV	4	0
2	B	906	POV	3	0
2	D	901	POV	1	0
2	D	907	POV	3	0
3	C	903	4DY	3	0
2	C	908	POV	1	0
2	C	906	POV	4	0
3	D	904	4DY	3	0
3	B	903	4DY	3	0
2	C	907	POV	1	0
3	A	903	4DY	4	0
2	A	908	POV	1	0
2	A	904	POV	4	0
2	A	906	POV	3	0
2	C	904	POV	4	0
2	B	907	POV	1	0

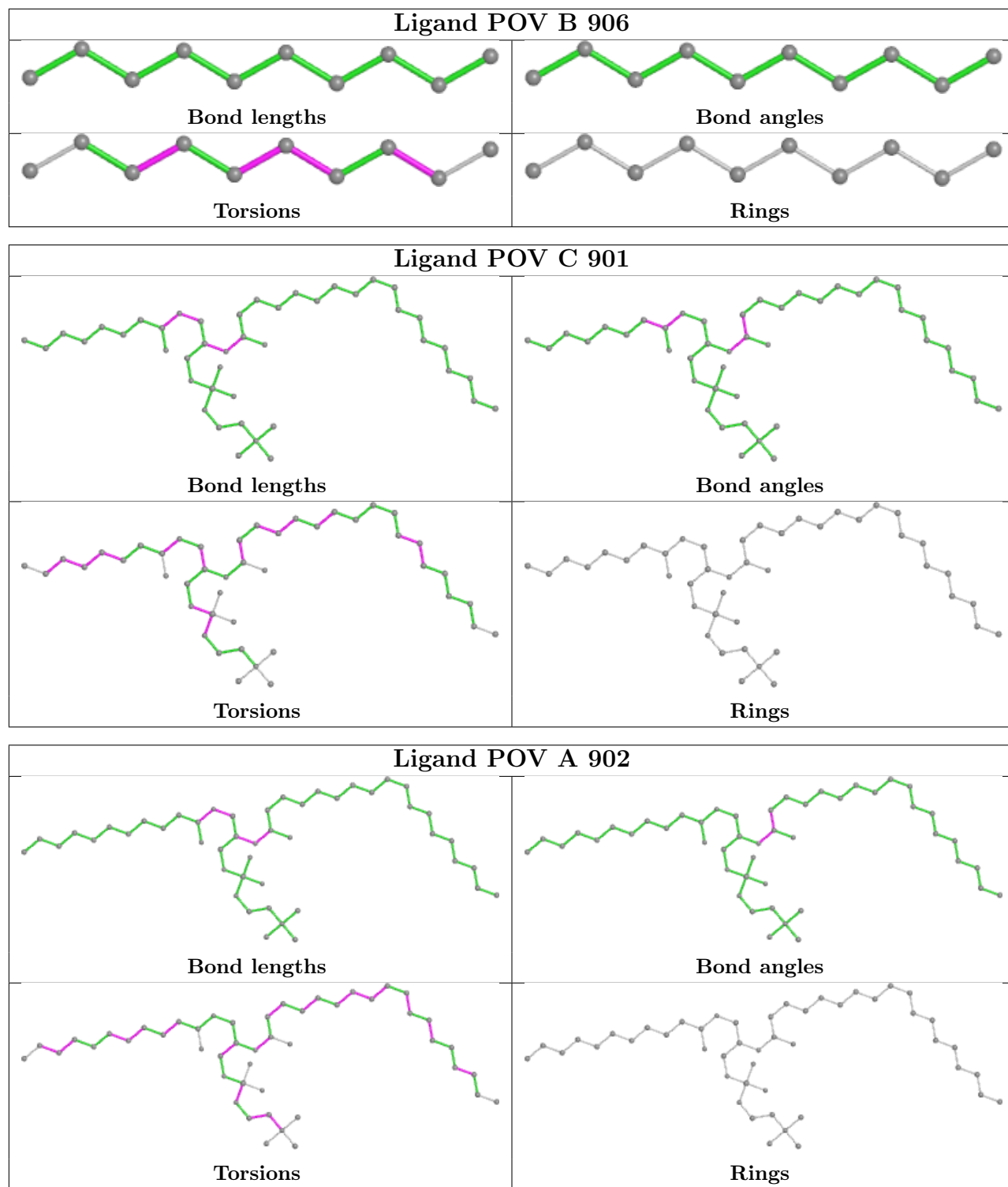
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

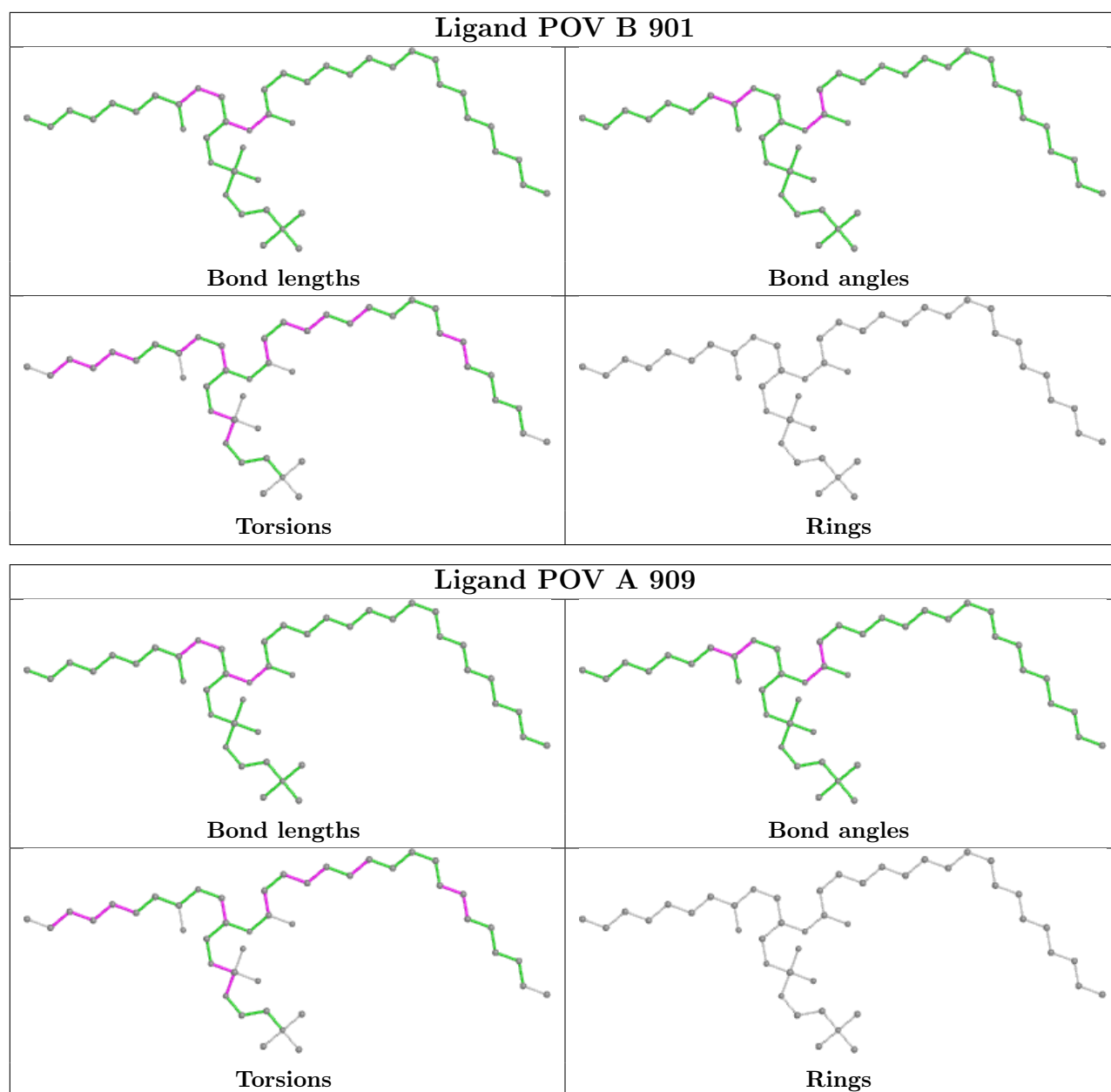


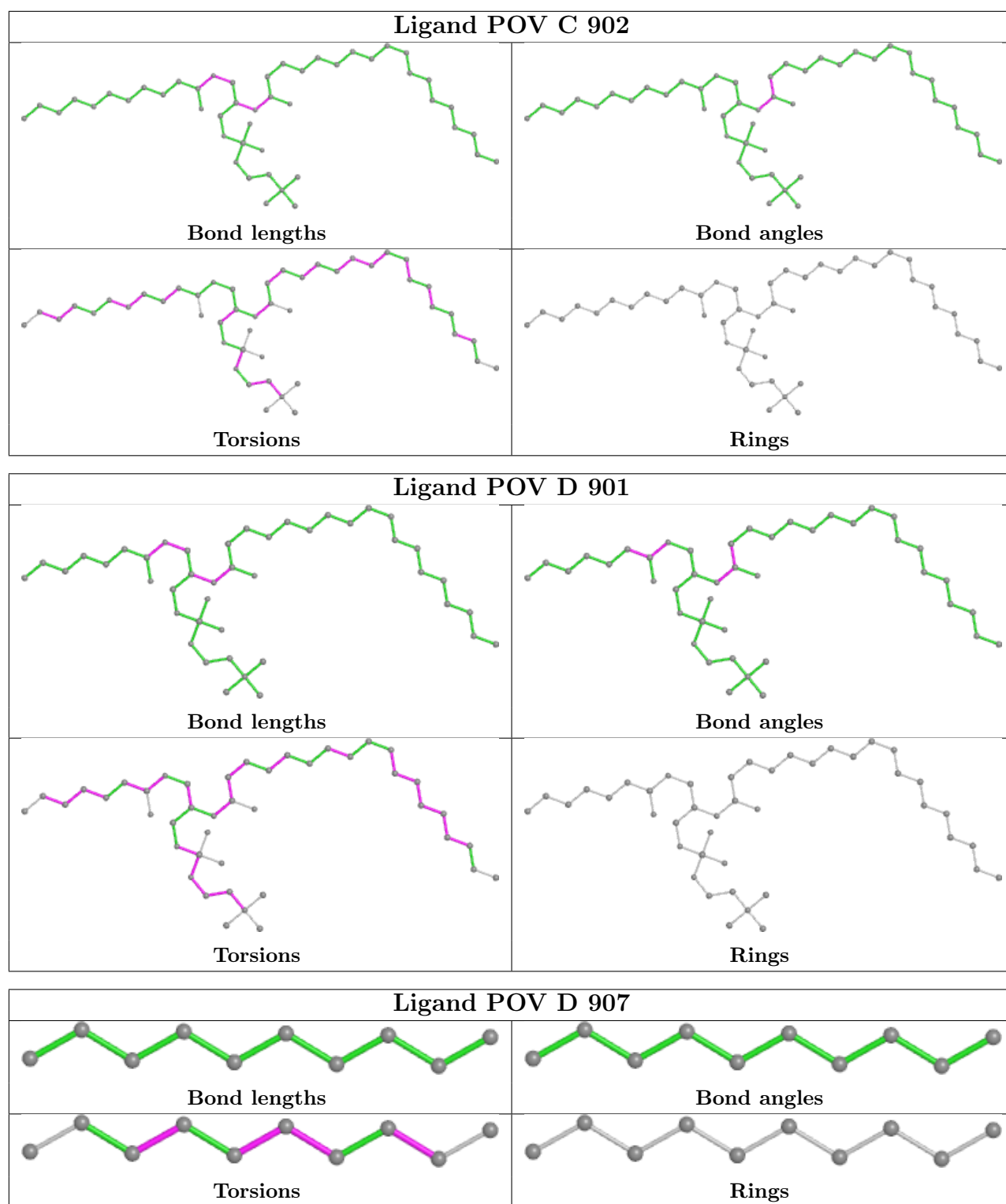


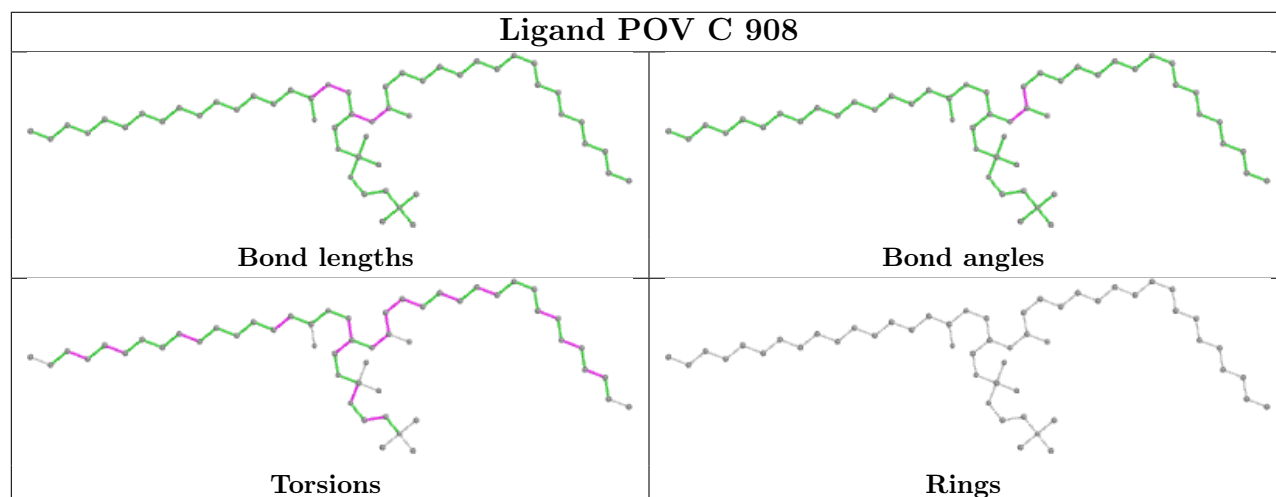
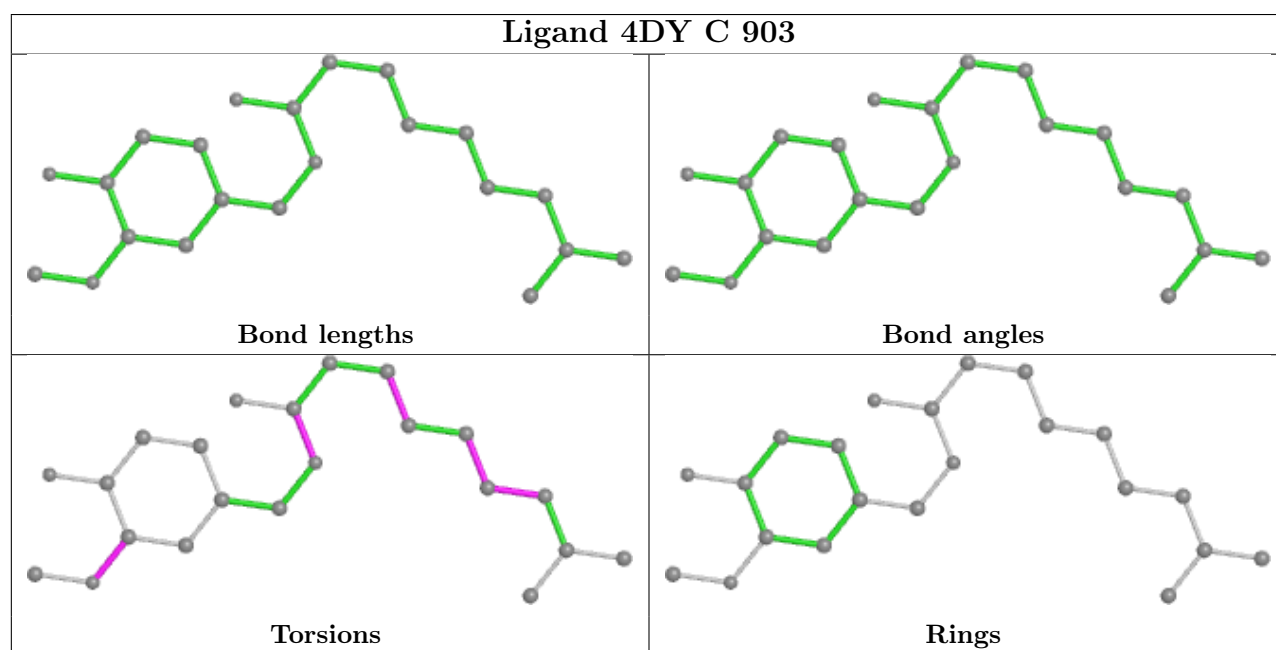
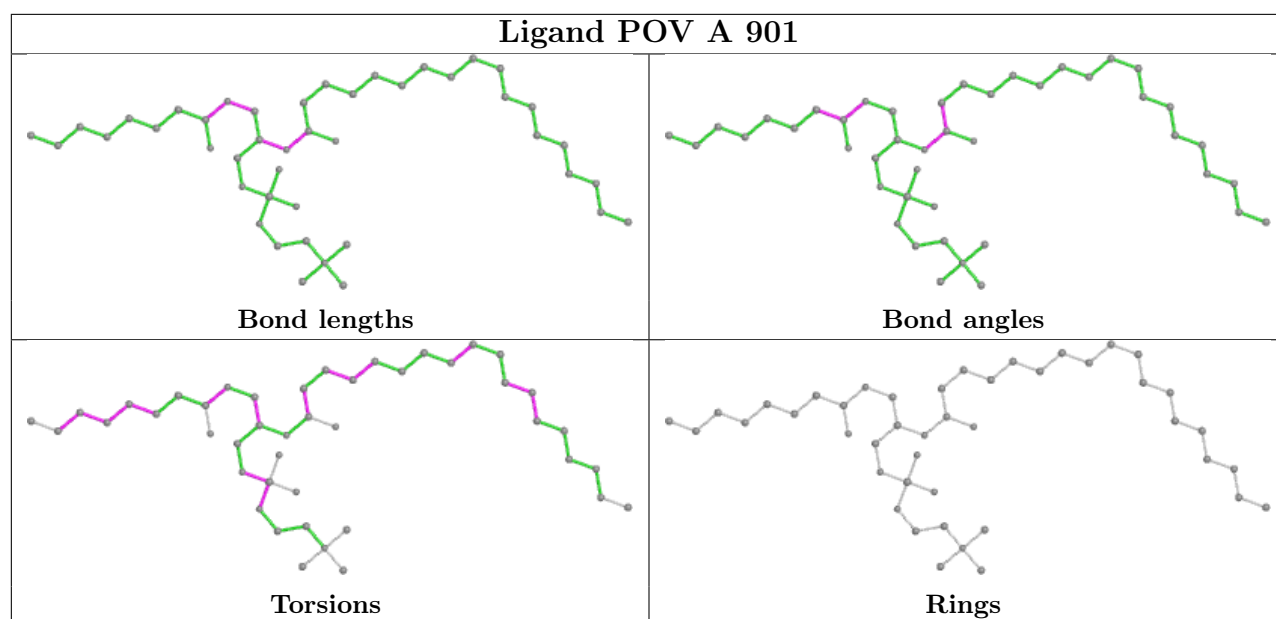


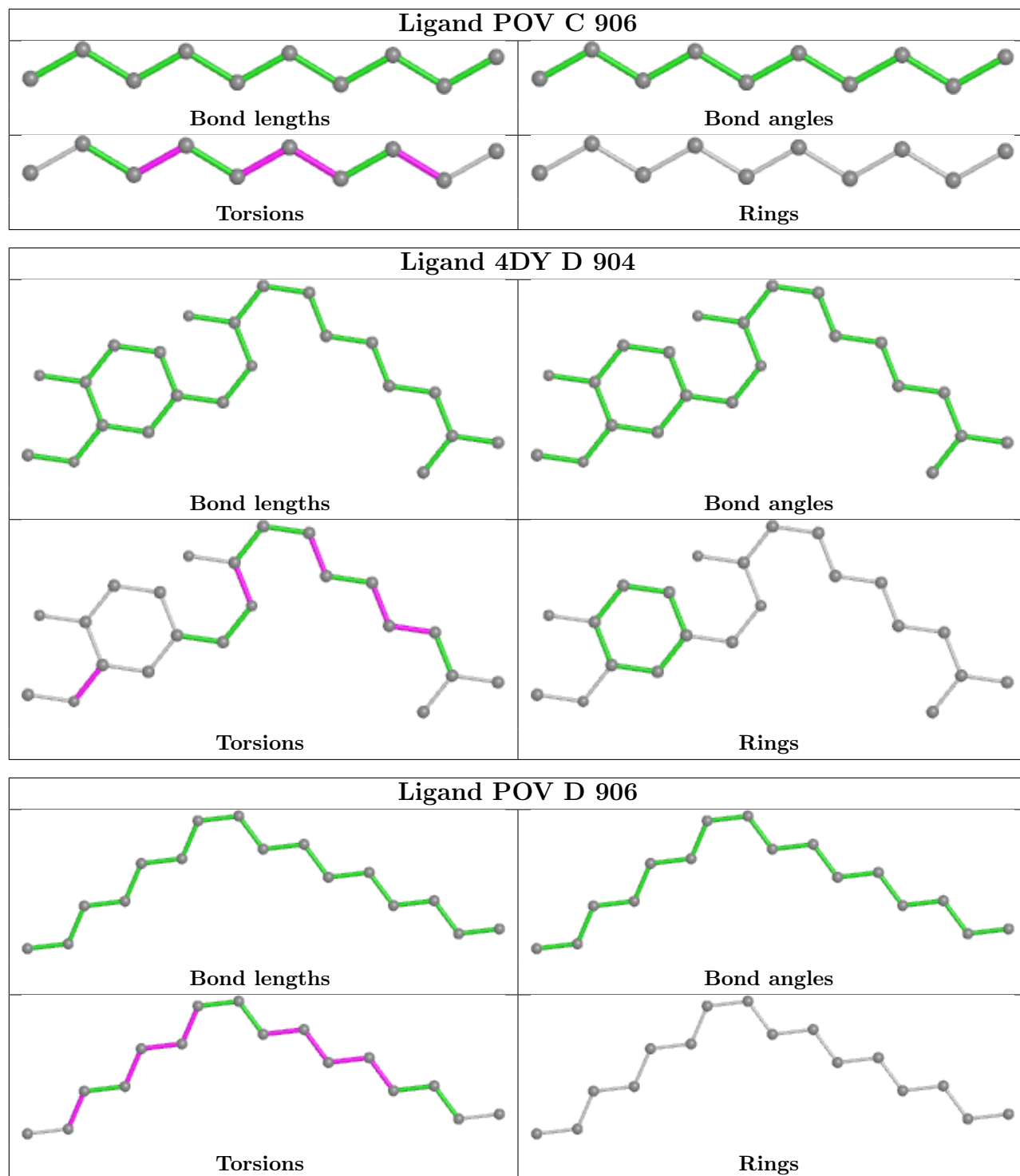


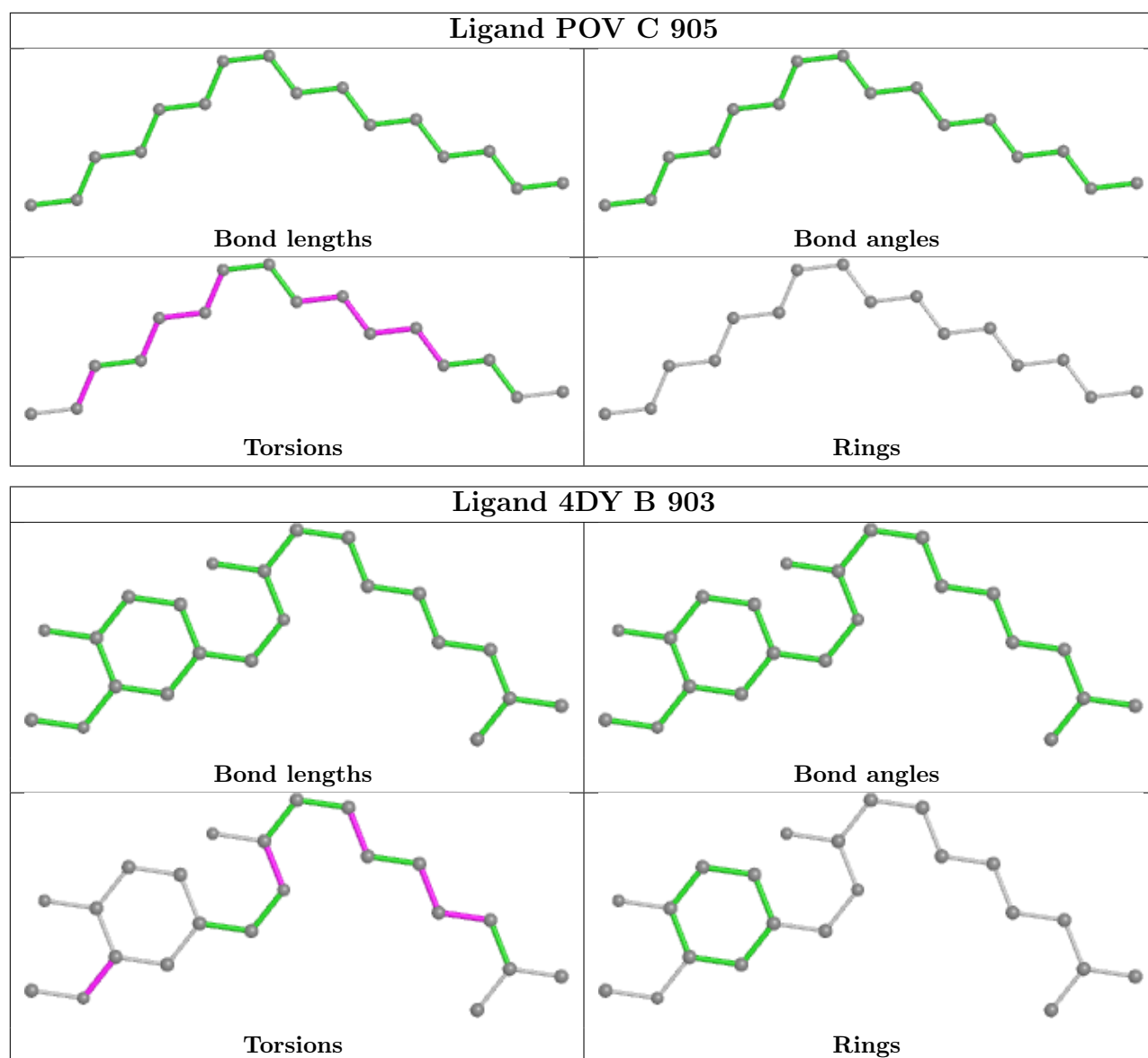


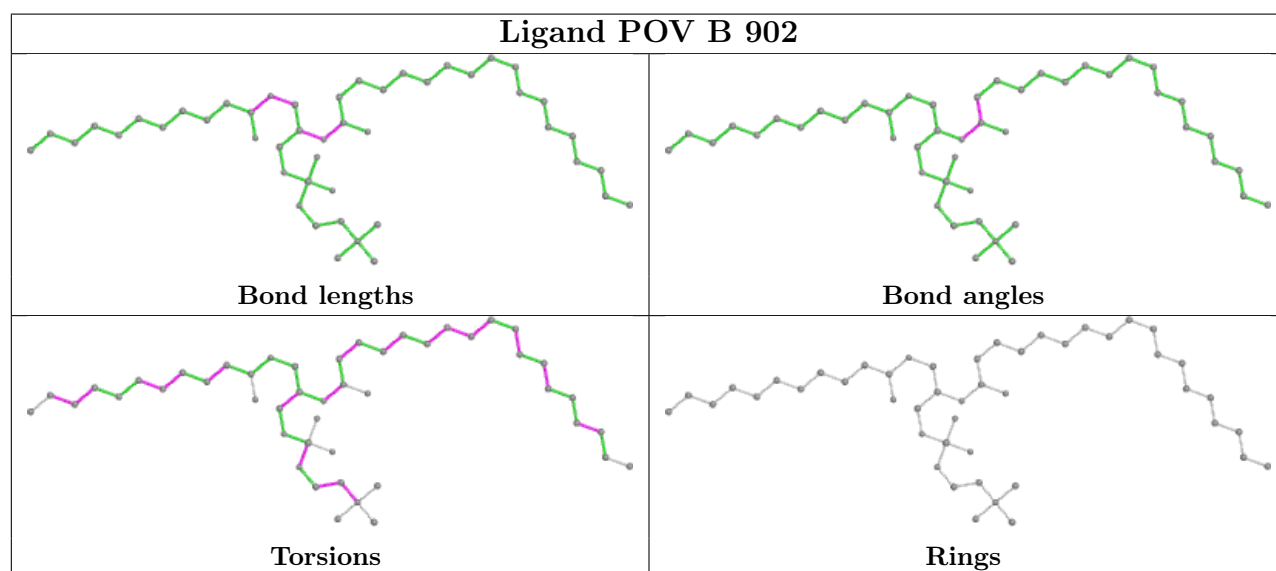
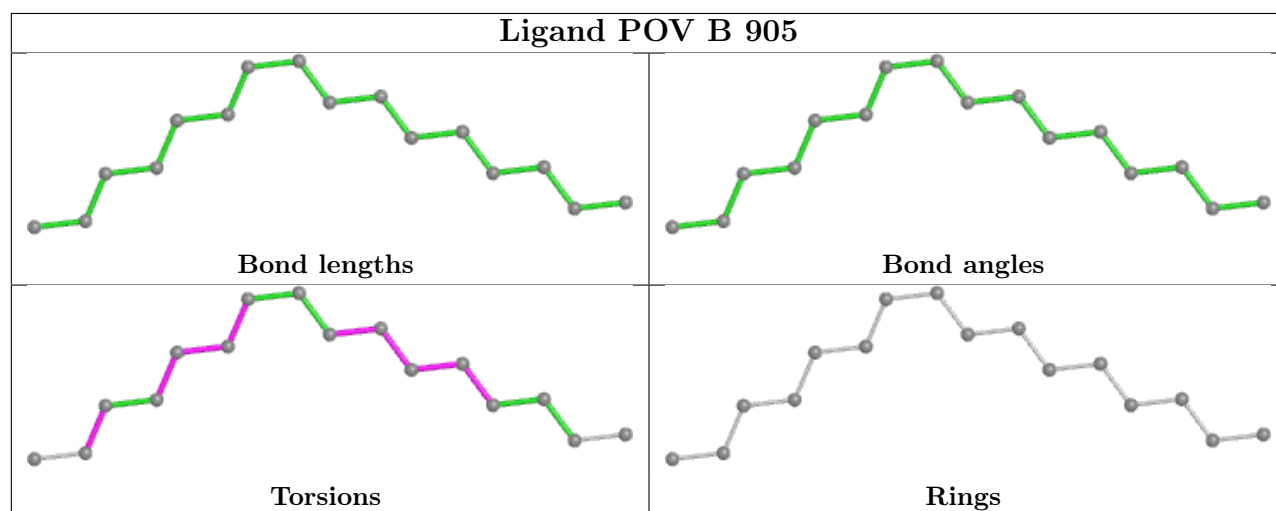
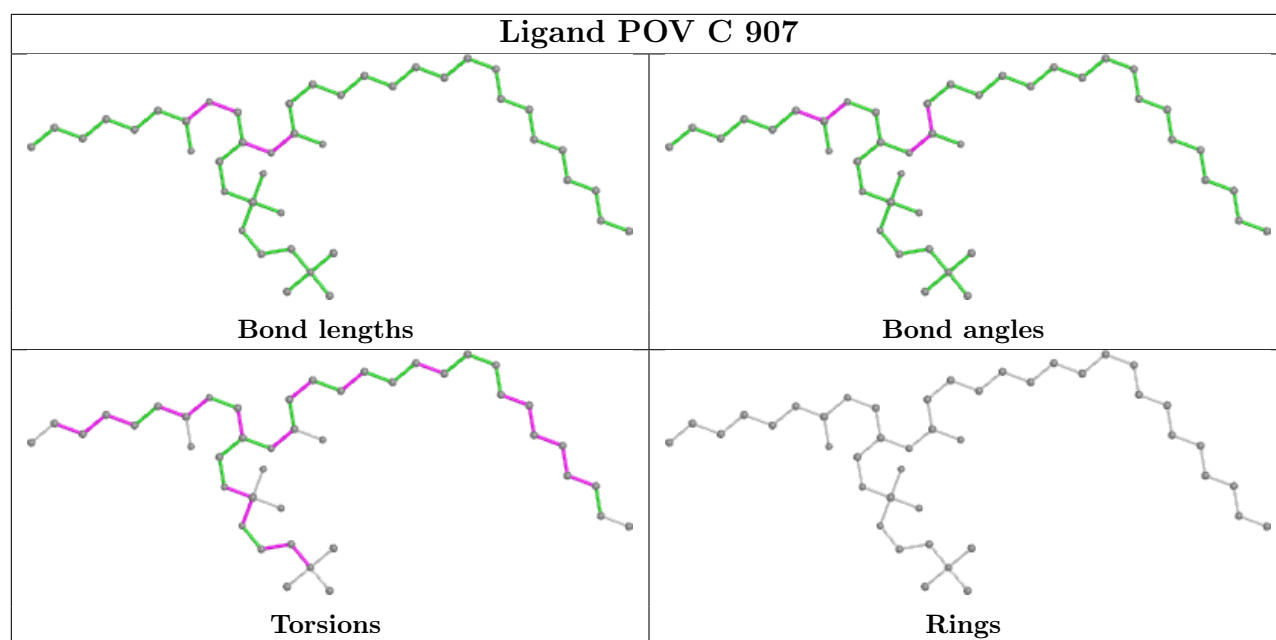




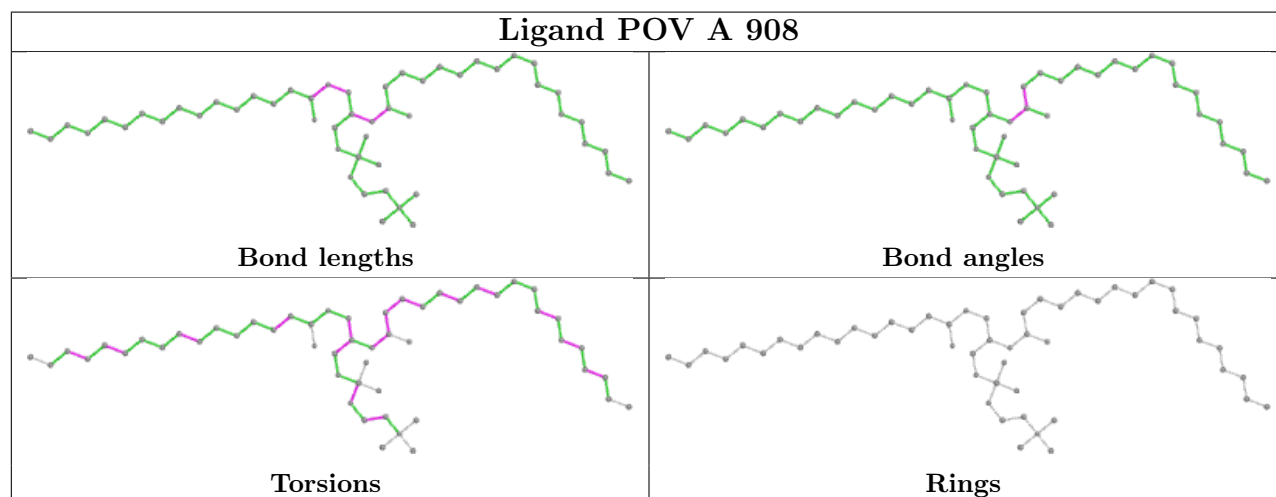
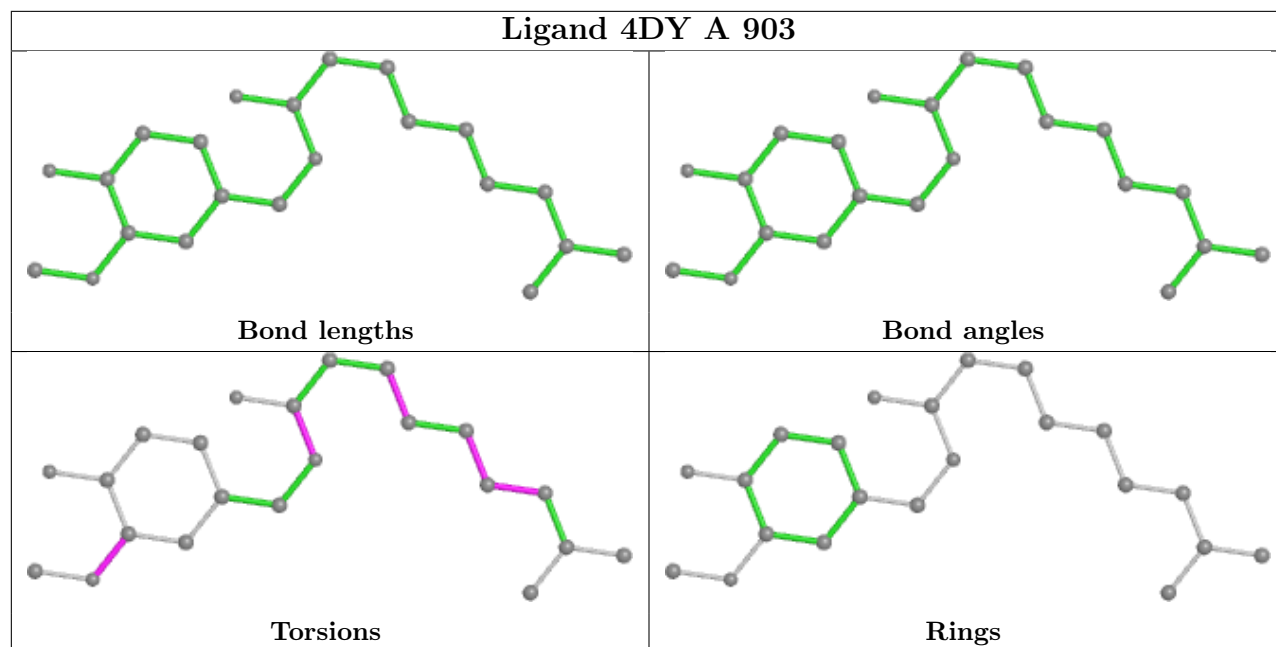


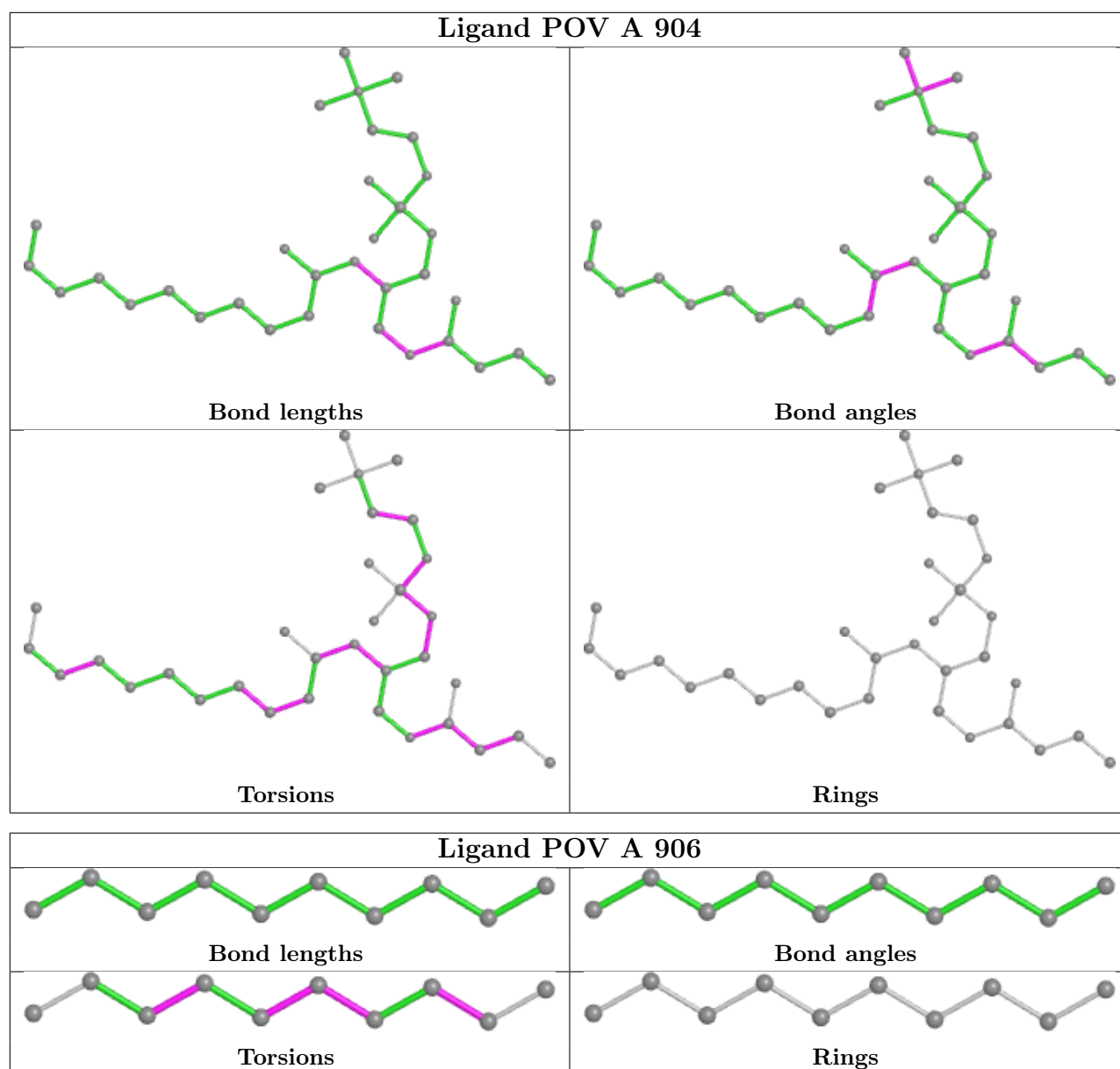


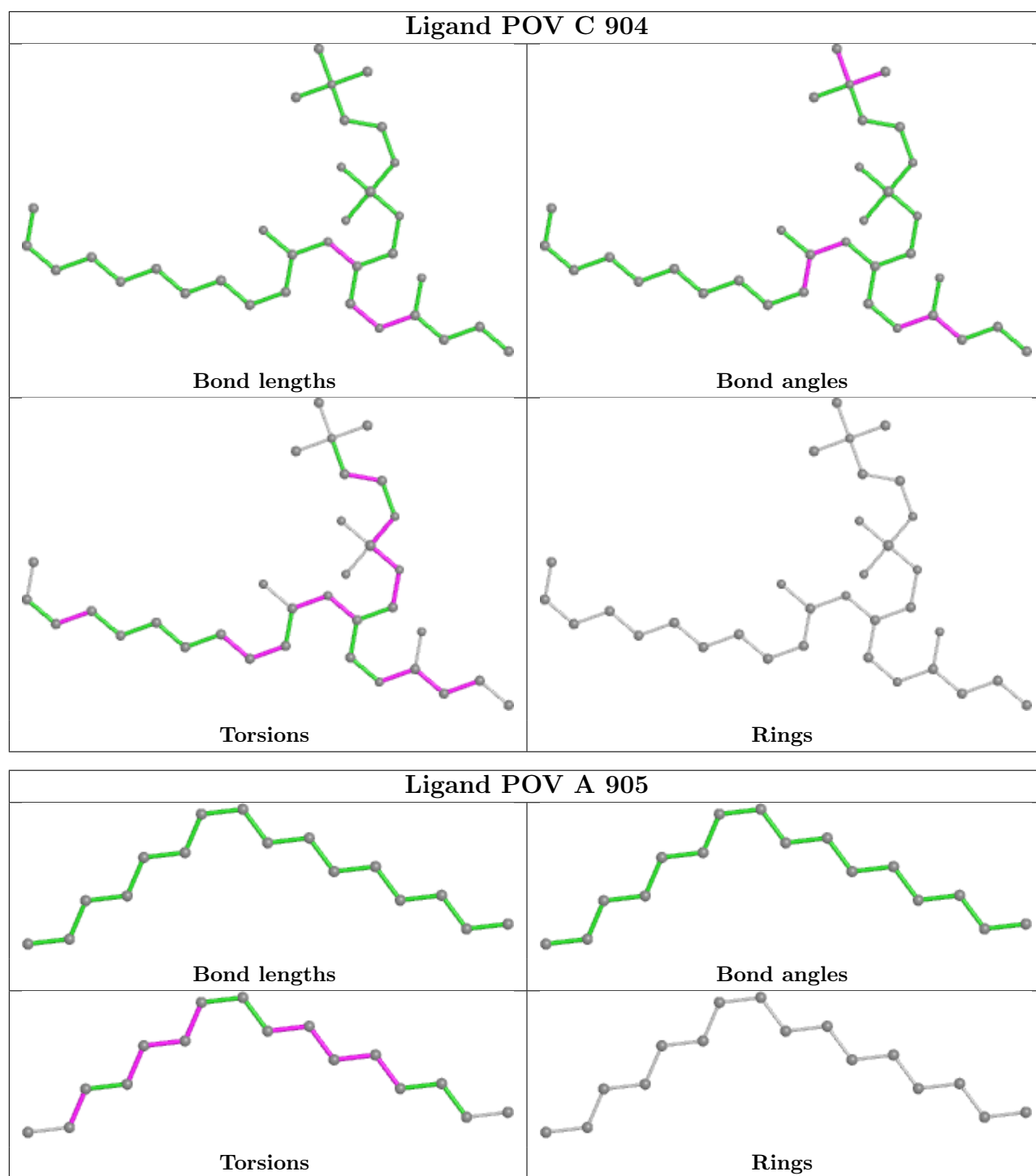


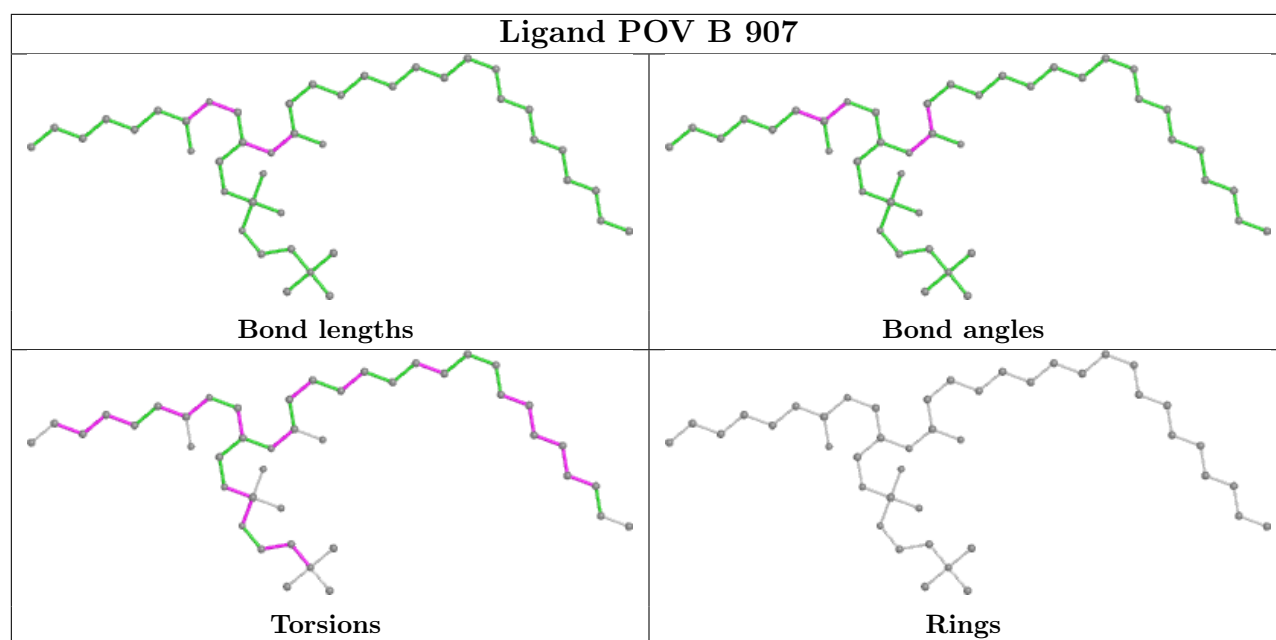












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

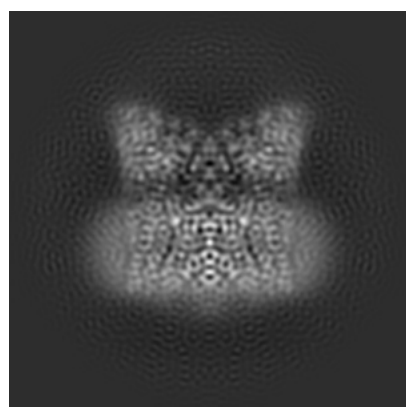
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23493. These allow visual inspection of the internal detail of the map and identification of artifacts.

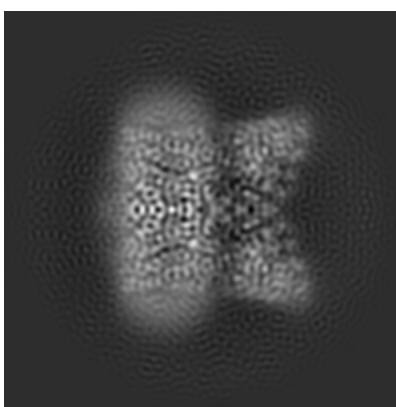
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

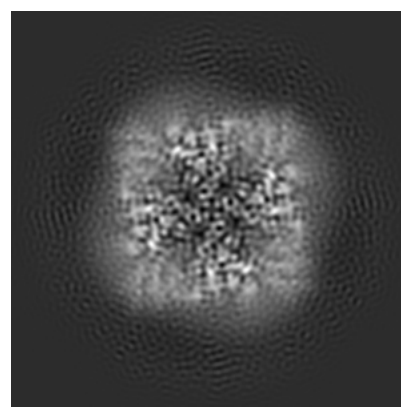
#### 6.1.1 Primary map



X



Y

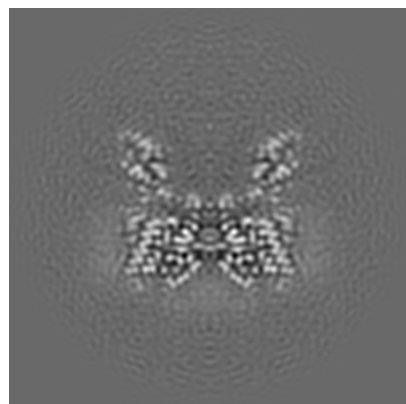


Z

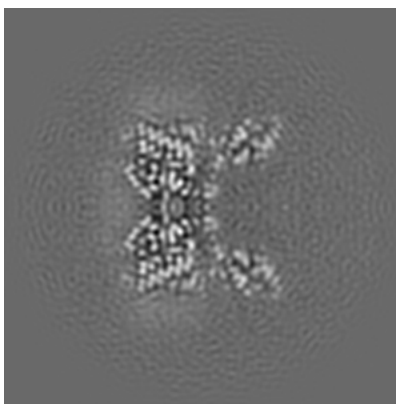
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

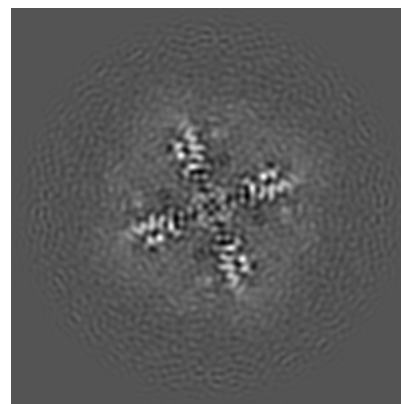
#### 6.2.1 Primary map



X Index: 128



Y Index: 128

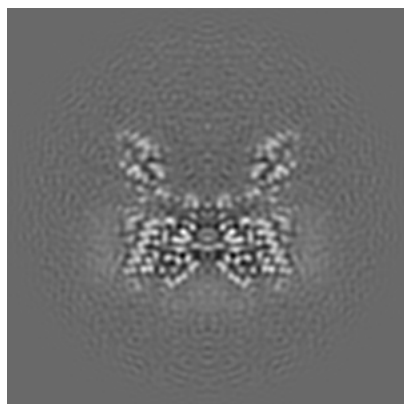


Z Index: 128

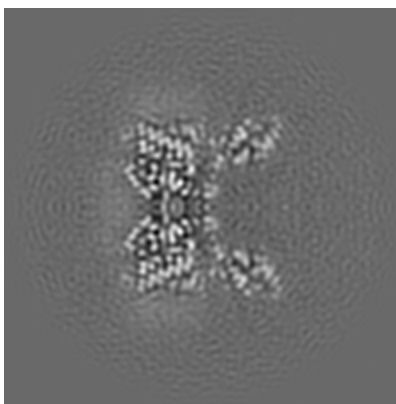
The images above show central slices of the map in three orthogonal directions.

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

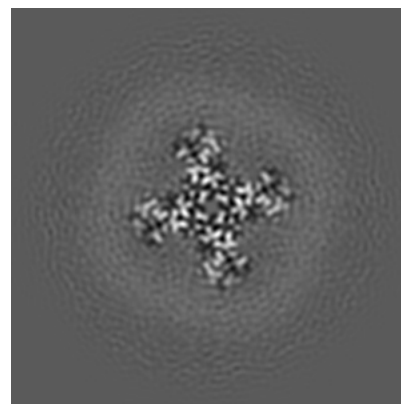
### 6.3.1 Primary map



X Index: 128



Y Index: 128

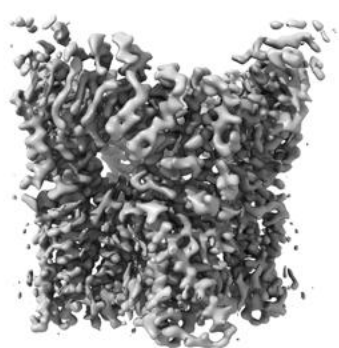


Z Index: 100

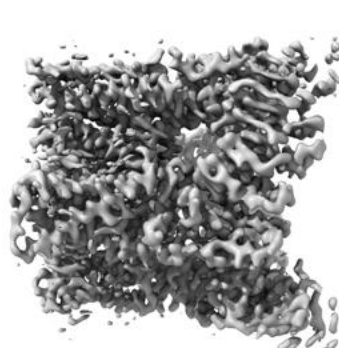
The images above show the largest variance slices of the map in three orthogonal directions.

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

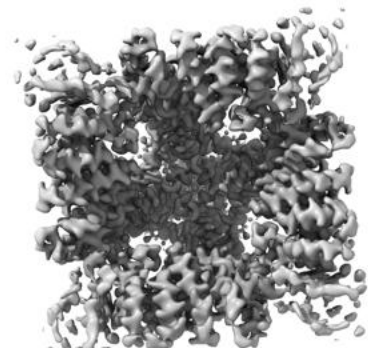
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.395. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

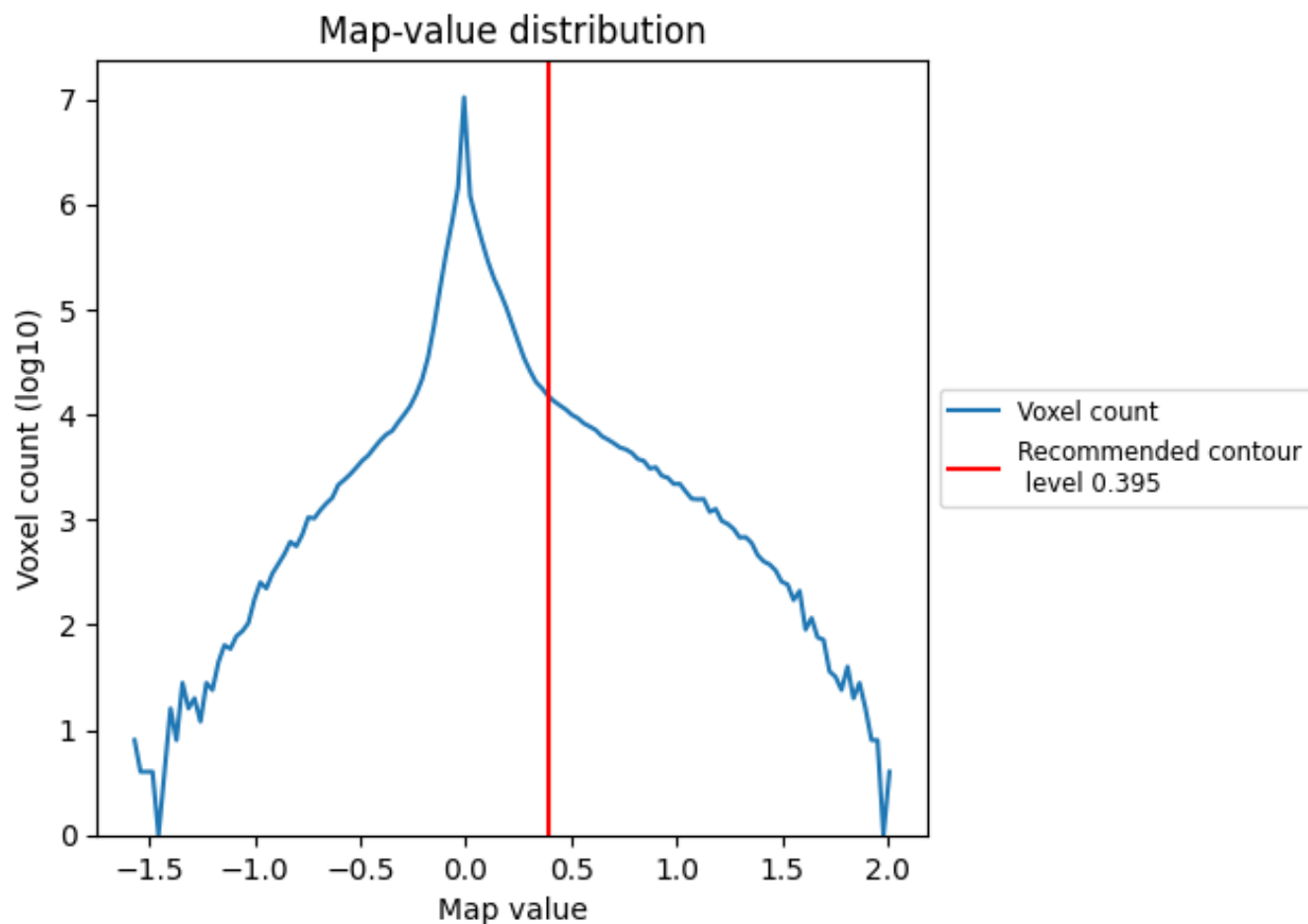
## 6.5 Mask visualisation

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.

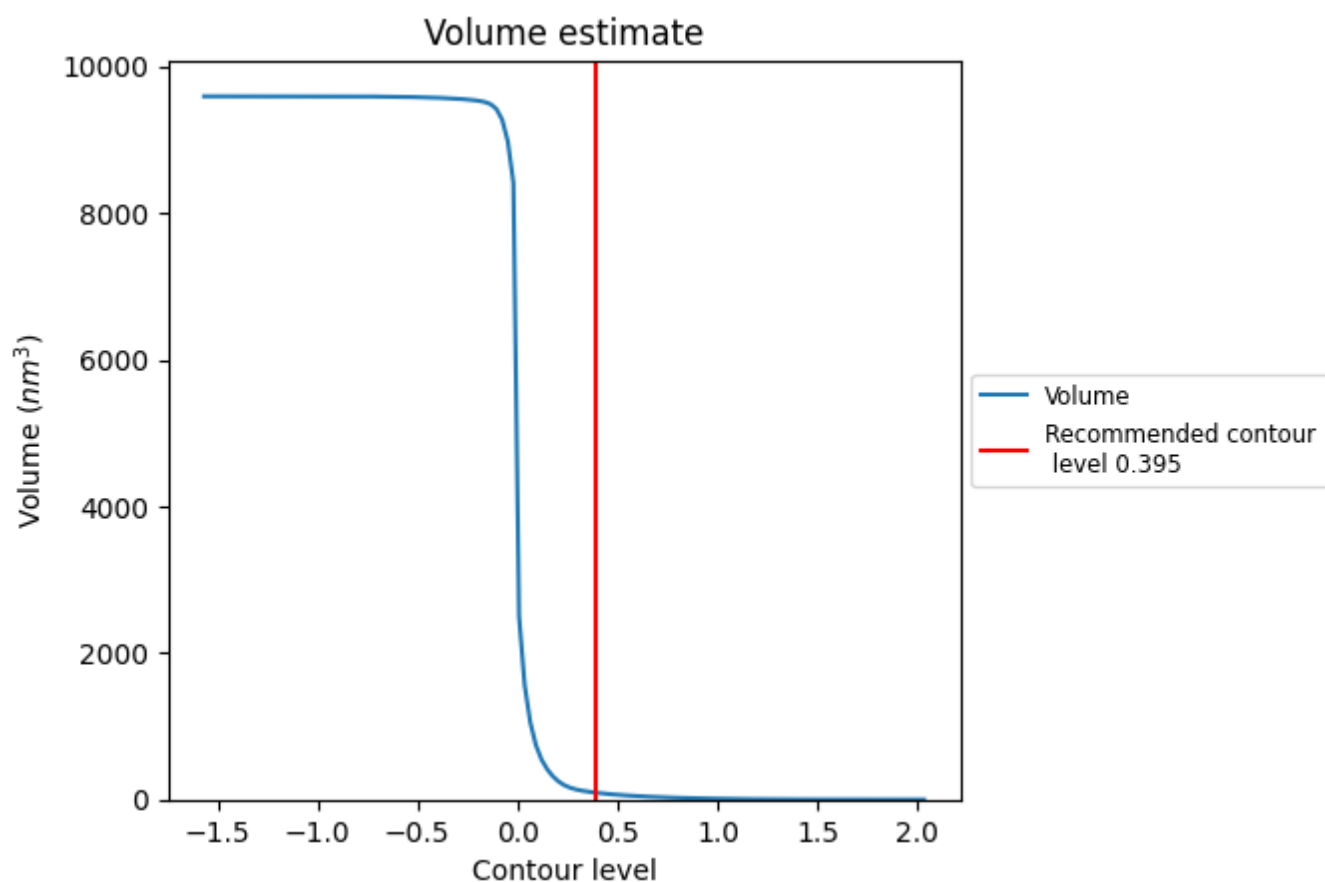
### 7.1 Map-value distribution [i](#)



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.



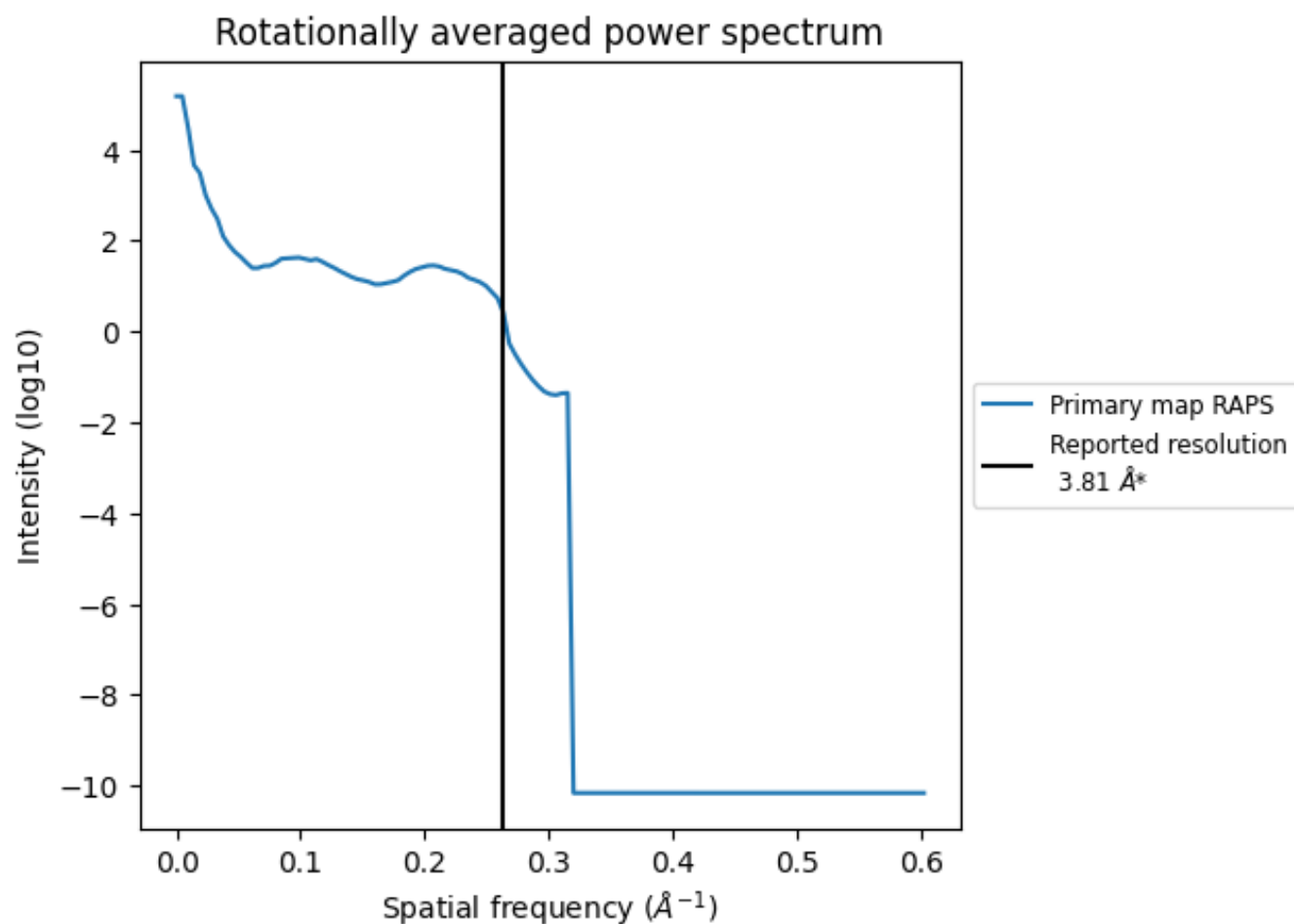
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 93 nm<sup>3</sup>; this corresponds to an approximate mass of 84 kDa.

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

### 7.3 Rotationally averaged power spectrum ⓘ



\*Reported resolution corresponds to spatial frequency of 0.262 Å<sup>-1</sup>

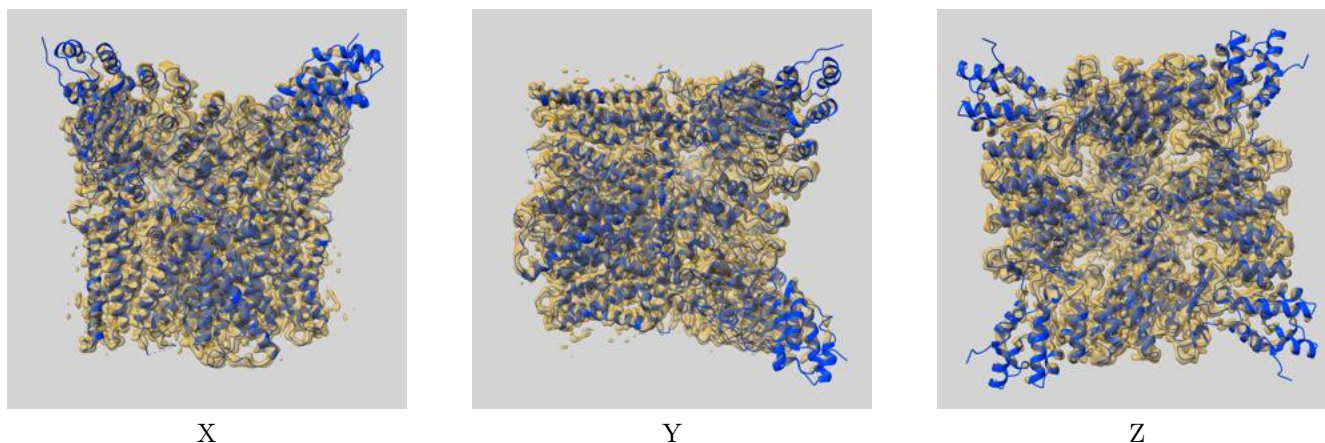
## 8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

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

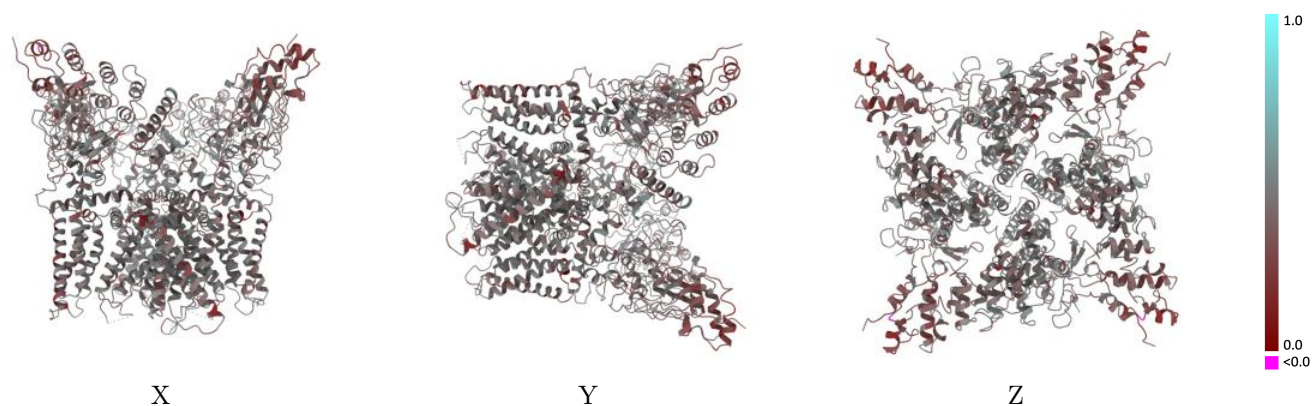
This section contains information regarding the fit between EMDB map EMD-23493 and PDB model 7LR0. Per-residue inclusion information can be found in section [3](#) on page [7](#).

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



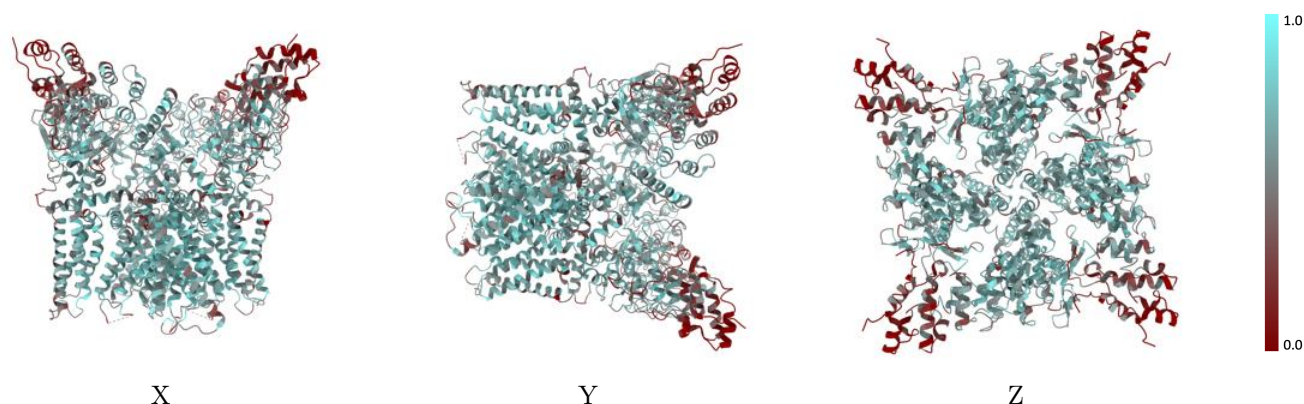
The images above show the 3D surface view of the map at the recommended contour level 0.395 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



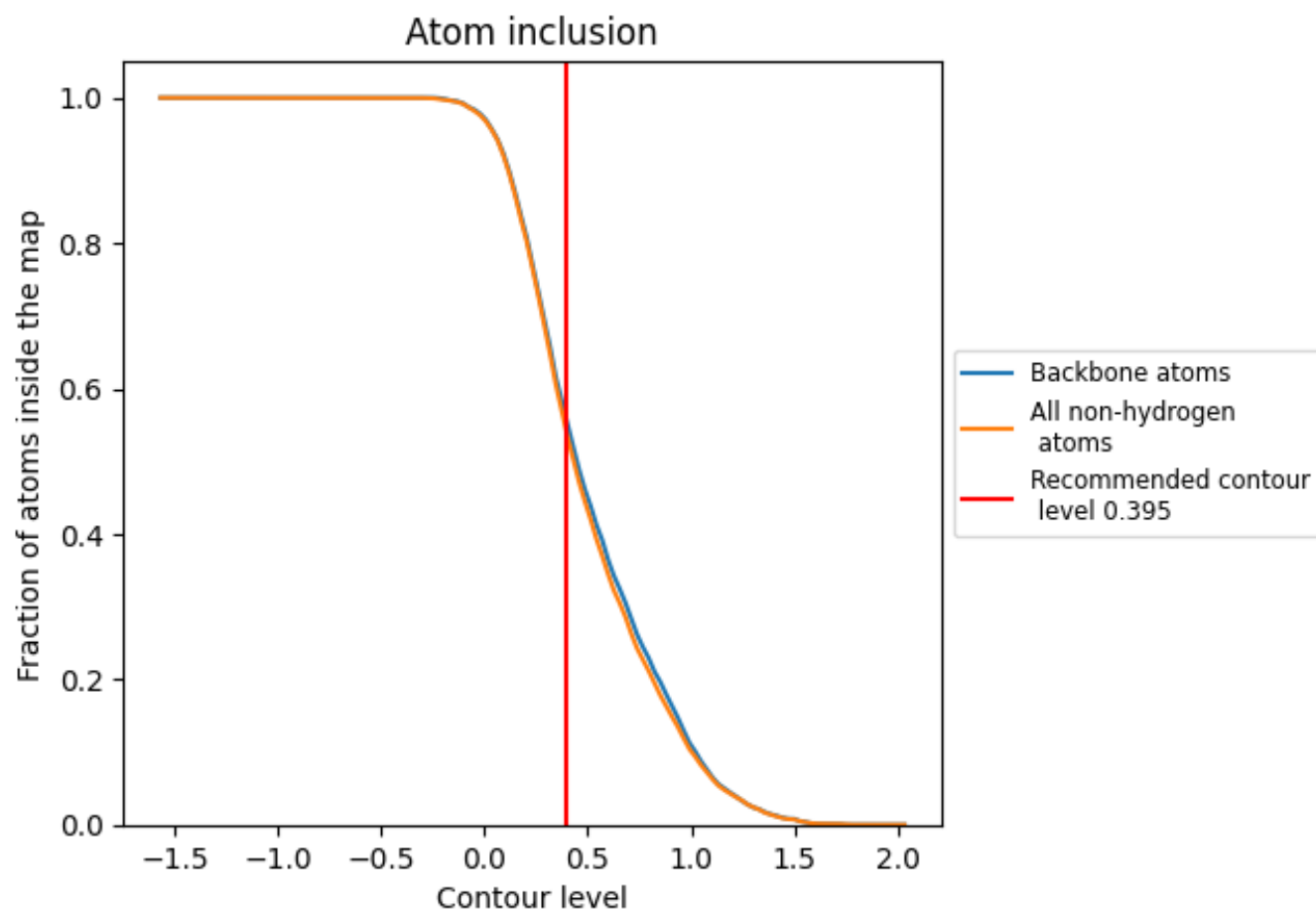
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.395).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 56% of all backbone atoms, 54% 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 (0.395) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5425	<div></div> 0.4180
A	<div></div> 0.5515	<div></div> 0.4190
B	<div></div> 0.5527	<div></div> 0.4190
C	<div></div> 0.5511	<div></div> 0.4180
D	<div></div> 0.5498	<div></div> 0.4160

