



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 10:30 AM UTC

PDB ID : 9Z9B / pdb_00009z9b
EMDB ID : EMD-73900
Title : Gated state sheep connexin-50 in DMPC nanodiscs at neutral pH
Authors : Jarodsky, J.M.; Myers, J.B.; Reichow, S.L.
Deposited on : 2025-11-18
Resolution : 2.70 Å (reported)
Based on initial model : 7jjp

This is a wwPDB EM Validation Summary 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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

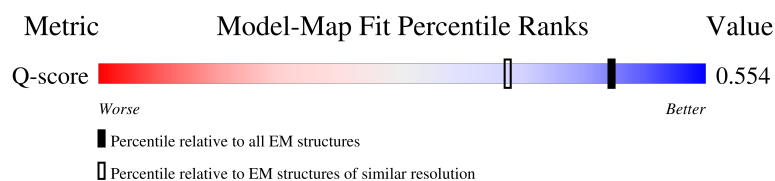
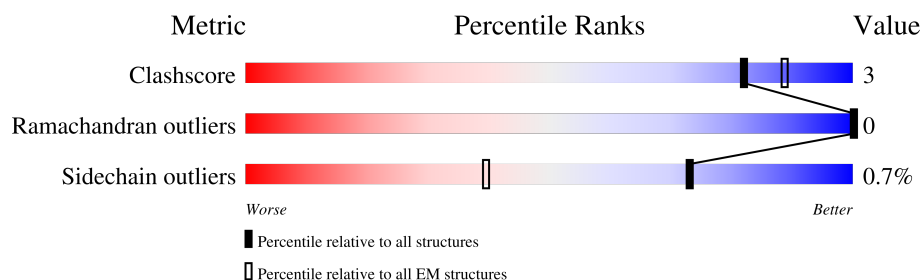
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10327 (2.20 - 3.20)

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	440	
1	B	440	
1	C	440	
1	D	440	

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Mol	Chain	Length	Quality of chain
1	E	440	 39% 58%
1	F	440	 39% 58%
1	G	440	 39% 58%
1	H	440	 40% 58%
1	I	440	 40% 58%
1	J	440	 40% 58%
1	K	440	 40% 58%
1	L	440	 39% 58%

2 Entry composition

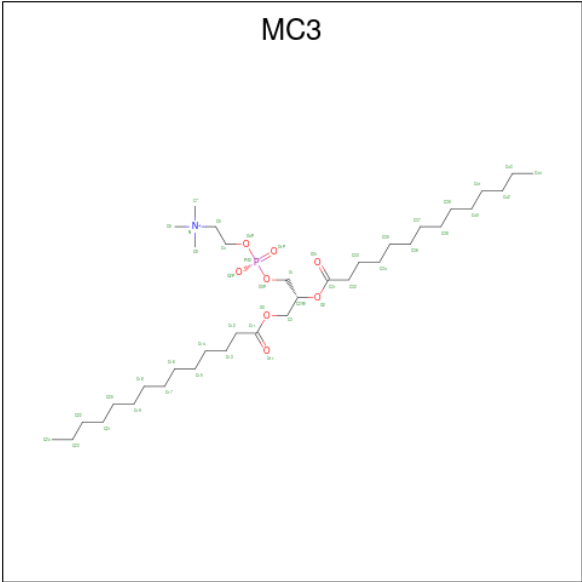
There are 2 unique types of molecules in this entry. The entry contains 40392 atoms, of which 20772 are hydrogens and 0 are deuteriums.

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 Gap junction alpha-8 protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	184	Total	C	H	N	O	S	0	0
			2815	951	1379	235	241	9		
1	B	184	Total	C	H	N	O	S	0	0
			2815	951	1379	235	241	9		
1	C	184	Total	C	H	N	O	S	0	0
			2815	951	1379	235	241	9		
1	D	184	Total	C	H	N	O	S	0	0
			2815	951	1379	235	241	9		
1	E	184	Total	C	H	N	O	S	0	0
			2815	951	1379	235	241	9		
1	F	184	Total	C	H	N	O	S	0	0
			2815	951	1379	235	241	9		
1	G	184	Total	C	H	N	O	S	0	0
			2815	951	1379	235	241	9		
1	H	184	Total	C	H	N	O	S	0	0
			2815	951	1379	235	241	9		
1	I	184	Total	C	H	N	O	S	0	0
			2815	951	1379	235	241	9		
1	J	184	Total	C	H	N	O	S	0	0
			2815	951	1379	235	241	9		
1	K	184	Total	C	H	N	O	S	0	0
			2815	951	1379	235	241	9		
1	L	184	Total	C	H	N	O	S	0	0
			2815	951	1379	235	241	9		

- Molecule 2 is 1,2-DIMYRISTOYL-RAC-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: MC3) (formula: C₃₆H₇₂NO₈P).



Mol	Chain	Residues	Atoms			AltConf
2	A	1	Total	C	H	0
			36	12	24	
2	A	1	Total	C	H	0
			39	13	26	
2	A	1	Total	C	H	0
			39	13	26	
2	A	1	Total	C	H	0
			30	10	20	
2	A	1	Total	C	H	0
			39	13	26	
2	A	1	Total	C	H	0
			18	6	12	
2	A	1	Total	C	H	0
			27	9	18	
2	A	1	Total	C	H	0
			33	11	22	
2	A	1	Total	C	H	0
			24	8	16	
2	A	1	Total	C	H	0
			39	13	26	
2	A	1	Total	C	H	0
			33	11	22	
2	A	1	Total	C	H	0
			36	12	24	
2	A	1	Total	C	H	0
			24	8	16	
2	A	1	Total	C	H	0
			30	10	20	

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Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	H	O	P	0
			61	19	33	8	1	
2	A	1	Total	C	H	O	P	0
			43	13	21	8	1	
2	B	1	Total	C	H			0
			36	12	24			
2	B	1	Total	C	H			0
			39	13	26			
2	B	1	Total	C	H			0
			39	13	26			
2	B	1	Total	C	H			0
			30	10	20			
2	B	1	Total	C	H			0
			39	13	26			
2	B	1	Total	C	H			0
			18	6	12			
2	B	1	Total	C	H			0
			27	9	18			
2	B	1	Total	C	H			0
			33	11	22			
2	B	1	Total	C	H			0
			24	8	16			
2	B	1	Total	C	H			0
			39	13	26			
2	B	1	Total	C	H			0
			33	11	22			
2	B	1	Total	C	H			0
			36	12	24			
2	B	1	Total	C	H			0
			24	8	16			
2	B	1	Total	C	H			0
			30	10	20			
2	B	1	Total	C	H	O	P	0
			61	19	33	8	1	
2	B	1	Total	C	H	O	P	0
			43	13	21	8	1	
2	C	1	Total	C	H			0
			36	12	24			
2	C	1	Total	C	H			0
			39	13	26			
2	C	1	Total	C	H			0
			39	13	26			

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Mol	Chain	Residues	Atoms					AltConf
2	C	1	Total 30	C 10	H 20			0
2	C	1	Total 39	C 13	H 26			0
2	C	1	Total 18	C 6	H 12			0
2	C	1	Total 27	C 9	H 18			0
2	C	1	Total 33	C 11	H 22			0
2	C	1	Total 24	C 8	H 16			0
2	C	1	Total 39	C 13	H 26			0
2	C	1	Total 33	C 11	H 22			0
2	C	1	Total 36	C 12	H 24			0
2	C	1	Total 24	C 8	H 16			0
2	C	1	Total 30	C 10	H 20			0
2	C	1	Total 61	C 19	H 33	O 8	P 1	0
2	C	1	Total 43	C 13	H 21	O 8	P 1	0
2	D	1	Total 36	C 12	H 24			0
2	D	1	Total 39	C 13	H 26			0
2	D	1	Total 39	C 13	H 26			0
2	D	1	Total 30	C 10	H 20			0
2	D	1	Total 39	C 13	H 26			0
2	D	1	Total 18	C 6	H 12			0
2	D	1	Total 27	C 9	H 18			0
2	D	1	Total 33	C 11	H 22			0

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Mol	Chain	Residues	Atoms					AltConf
2	D	1	Total	C	H			0
			24	8	16			
2	D	1	Total	C	H			0
			39	13	26			
2	D	1	Total	C	H			0
			33	11	22			
2	D	1	Total	C	H			0
			36	12	24			
2	D	1	Total	C	H			0
			24	8	16			
2	D	1	Total	C	H			0
			30	10	20			
2	D	1	Total	C	H	O	P	0
			61	19	33	8	1	
2	D	1	Total	C	H	O	P	0
			43	13	21	8	1	
2	E	1	Total	C	H			0
			36	12	24			
2	E	1	Total	C	H			0
			39	13	26			
2	E	1	Total	C	H			0
			39	13	26			
2	E	1	Total	C	H			0
			30	10	20			
2	E	1	Total	C	H			0
			39	13	26			
2	E	1	Total	C	H			0
			18	6	12			
2	E	1	Total	C	H			0
			27	9	18			
2	E	1	Total	C	H			0
			33	11	22			
2	E	1	Total	C	H			0
			24	8	16			
2	E	1	Total	C	H			0
			39	13	26			
2	E	1	Total	C	H			0
			33	11	22			
2	E	1	Total	C	H			0
			36	12	24			
2	E	1	Total	C	H			0
			24	8	16			

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Mol	Chain	Residues	Atoms					AltConf
2	E	1	Total	C	H			0
			30	10	20			
2	E	1	Total	C	H	O	P	0
			61	19	33	8	1	
2	E	1	Total	C	H	O	P	0
			43	13	21	8	1	
2	F	1	Total	C	H			0
			39	13	26			
2	F	1	Total	C	H			0
			33	11	22			
2	F	1	Total	C	H			0
			36	12	24			
2	F	1	Total	C	H			0
			24	8	16			
2	F	1	Total	C	H			0
			30	10	20			
2	F	1	Total	C	H	O	P	0
			61	19	33	8	1	
2	F	1	Total	C	H	O	P	0
			43	13	21	8	1	
2	F	1	Total	C	H			0
			36	12	24			
2	F	1	Total	C	H			0
			39	13	26			
2	F	1	Total	C	H			0
			39	13	26			
2	F	1	Total	C	H			0
			30	10	20			
2	F	1	Total	C	H			0
			39	13	26			
2	F	1	Total	C	H			0
			18	6	12			
2	F	1	Total	C	H			0
			27	9	18			
2	F	1	Total	C	H			0
			33	11	22			
2	F	1	Total	C	H			0
			24	8	16			
2	G	1	Total	C	H			0
			36	12	24			
2	G	1	Total	C	H			0
			39	13	26			

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Mol	Chain	Residues	Atoms					AltConf
2	G	1	Total	C	H			0
			39	13	26			
2	G	1	Total	C	H			0
			30	10	20			
2	G	1	Total	C	H			0
			39	13	26			
2	G	1	Total	C	H			0
			18	6	12			
2	G	1	Total	C	H			0
			27	9	18			
2	G	1	Total	C	H			0
			33	11	22			
2	G	1	Total	C	H	O	P	0
			61	19	33	8	1	
2	G	1	Total	C	H			0
			24	8	16			
2	G	1	Total	C	H			0
			39	13	26			
2	G	1	Total	C	H			0
			33	11	22			
2	G	1	Total	C	H			0
			36	12	24			
2	G	1	Total	C	H			0
			24	8	16			
2	G	1	Total	C	H			0
			30	10	20			
2	G	1	Total	C	H	O	P	0
			61	19	33	8	1	
2	G	1	Total	C	H	O	P	0
			43	13	21	8	1	
2	H	1	Total	C	H			0
			36	12	24			
2	H	1	Total	C	H			0
			39	13	26			
2	H	1	Total	C	H			0
			39	13	26			
2	H	1	Total	C	H			0
			30	10	20			
2	H	1	Total	C	H			0
			39	13	26			
2	H	1	Total	C	H			0
			18	6	12			

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Mol	Chain	Residues	Atoms					AltConf
2	H	1	Total	C	H			0
			27	9	18			
2	H	1	Total	C	H			0
			33	11	22			
2	H	1	Total	C	H			0
			24	8	16			
2	H	1	Total	C	H			0
			39	13	26			
2	H	1	Total	C	H			0
			33	11	22			
2	H	1	Total	C	H			0
			36	12	24			
2	H	1	Total	C	H			0
			24	8	16			
2	H	1	Total	C	H			0
			30	10	20			
2	H	1	Total	C	H	O	P	0
			61	19	33	8	1	
2	H	1	Total	C	H	O	P	0
			43	13	21	8	1	
2	I	1	Total	C	H			0
			36	12	24			
2	I	1	Total	C	H			0
			39	13	26			
2	I	1	Total	C	H			0
			39	13	26			
2	I	1	Total	C	H			0
			30	10	20			
2	I	1	Total	C	H			0
			39	13	26			
2	I	1	Total	C	H			0
			18	6	12			
2	I	1	Total	C	H			0
			27	9	18			
2	I	1	Total	C	H			0
			33	11	22			
2	I	1	Total	C	H			0
			24	8	16			
2	I	1	Total	C	H			0
			39	13	26			
2	I	1	Total	C	H			0
			33	11	22			

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Mol	Chain	Residues	Atoms					AltConf
2	I	1	Total	C	H			0
			36	12	24			
2	I	1	Total	C	H			0
			24	8	16			
2	I	1	Total	C	H			0
			30	10	20			
2	I	1	Total	C	H	O	P	0
			61	19	33	8	1	
2	I	1	Total	C	H	O	P	0
			43	13	21	8	1	
2	J	1	Total	C	H			0
			36	12	24			
2	J	1	Total	C	H			0
			39	13	26			
2	J	1	Total	C	H			0
			39	13	26			
2	J	1	Total	C	H			0
			30	10	20			
2	J	1	Total	C	H			0
			39	13	26			
2	J	1	Total	C	H			0
			18	6	12			
2	J	1	Total	C	H			0
			27	9	18			
2	J	1	Total	C	H			0
			33	11	22			
2	J	1	Total	C	H			0
			24	8	16			
2	J	1	Total	C	H			0
			39	13	26			
2	J	1	Total	C	H			0
			33	11	22			
2	J	1	Total	C	H			0
			36	12	24			
2	J	1	Total	C	H			0
			24	8	16			
2	J	1	Total	C	H			0
			30	10	20			
2	J	1	Total	C	H	O	P	0
			61	19	33	8	1	
2	J	1	Total	C	H	O	P	0
			43	13	21	8	1	

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Mol	Chain	Residues	Atoms					AltConf	
2	K	1	Total 36	C 12	H 24				0
2	K	1	Total 39	C 13	H 26				0
2	K	1	Total 39	C 13	H 26				0
2	K	1	Total 30	C 10	H 20				0
2	K	1	Total 39	C 13	H 26				0
2	K	1	Total 18	C 6	H 12				0
2	K	1	Total 27	C 9	H 18				0
2	K	1	Total 33	C 11	H 22				0
2	K	1	Total 24	C 8	H 16				0
2	K	1	Total 39	C 13	H 26				0
2	K	1	Total 33	C 11	H 22				0
2	K	1	Total 36	C 12	H 24				0
2	K	1	Total 24	C 8	H 16				0
2	K	1	Total 30	C 10	H 20				0
2	K	1	Total 61	C 19	H 33	O 8	P 1		0
2	K	1	Total 43	C 13	H 21	O 8	P 1		0
2	L	1	Total 39	C 13	H 26				0
2	L	1	Total 33	C 11	H 22				0
2	L	1	Total 36	C 12	H 24				0
2	L	1	Total 24	C 8	H 16				0
2	L	1	Total 30	C 10	H 20				0

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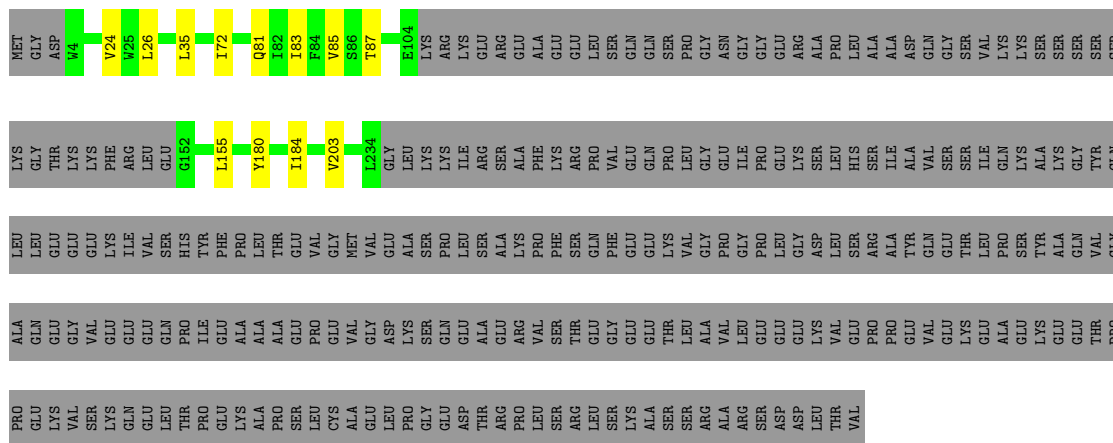
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Mol	Chain	Residues	Atoms					AltConf
2	L	1	Total 43	C 13	H 21	O 8	P 1	0
2	L	1	Total 36	C 12	H 24			0
2	L	1	Total 39	C 13	H 26			0
2	L	1	Total 39	C 13	H 26			0
2	L	1	Total 30	C 10	H 20			0
2	L	1	Total 39	C 13	H 26			0
2	L	1	Total 18	C 6	H 12			0
2	L	1	Total 27	C 9	H 18			0
2	L	1	Total 33	C 11	H 22			0
2	L	1	Total 24	C 8	H 16			0

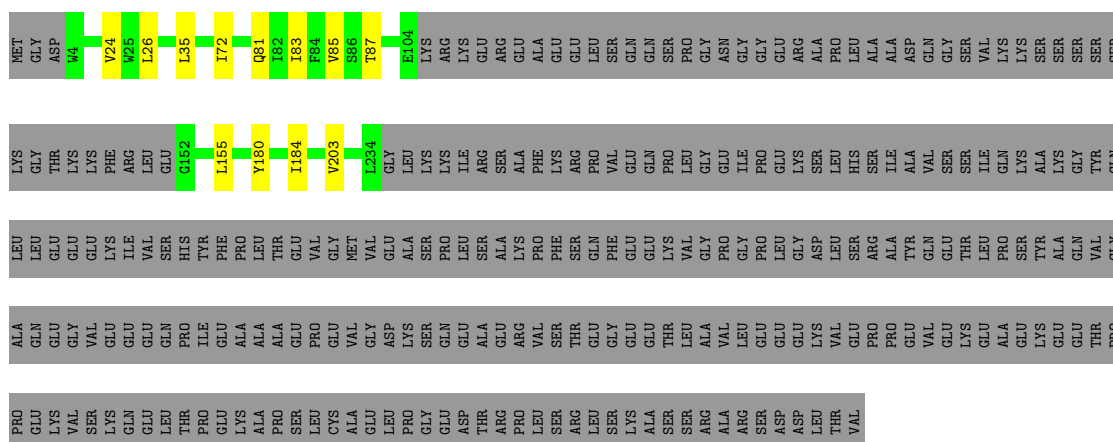
58%



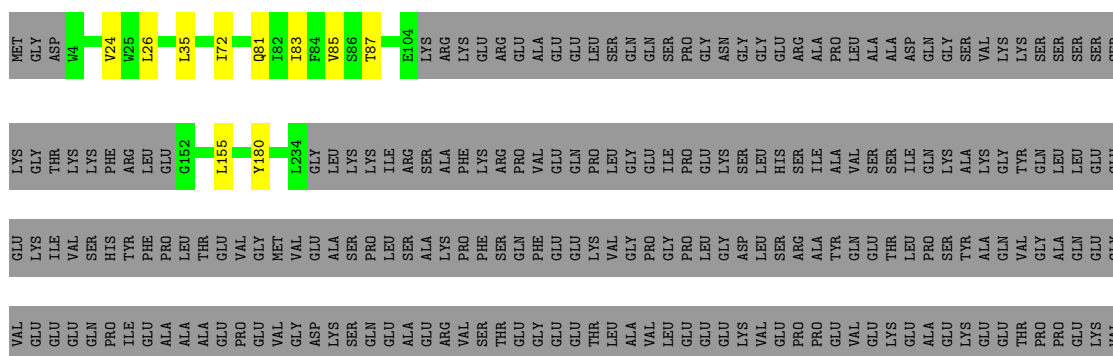
Chain F: 39% . 58%



Chain G: 39% 0% 58%



Chain H: 40% . 58%



SER	LYS	GLN	GLU	LEU	THR	PRO	GLU	LYS	ALA	PRO	SER	SER	CYS	ALA	GLU	LEU	PRO	GLY	GLU	ASP	THR	ARG	PRO	LYS	LEU	SER	ARG	SER	LYS	ALA	SER	SER	ASP	ASP	LEU	THR	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

● Molecule 1: Gap junction alpha-8 protein

Chain I:

40%

58%

MET	GLY	ASP	W4	V24	Q25	L26	L35	I72	Q81	I82	I83	F84	V85	S86	T87	E104	LYS	ARG	LYS	GLU	ARG	GLU	PRO	GLN	GLY	GLN	ARG	ALA	ARG	SER	PRO	GLY	ASN	GLY	GLY	GLU	GLU	ARG	ALA	PRO	LEU	VAL	ALA	SER	VAL	LYS	LYS	TYR	GLN	SER	SER	SER	SER	GLY
LYS	GLY	THR	LYS	PHE	ARG	LEU	G152	L155	Y180	L234	GLY	LEU	LYS	LYS	LYS	ILE	ARG	ALA	LYS	PRO	PHE	LYS	ARG	PRO	GLN	VAL	ALA	ILE	GLY	PRO	GLY	LYS	SER	HIS	GLY	GLU	GLU	ARG	ALA	PRO	LEU	VAL	SER	VAL	LYS	TYR	GLN	SER	SER	SER	GLY			
GLU	LYS	ILE	VAL	SER	HIS	TYR	PHE	PRO	GLY	VAL	MET	VAL	GLU	ALA	SER	PRO	GLY	VAL	GLN	ARG	VAL	PHE	SER	GLN	PHE	GLY	GLY	PRO	GLY	LEU	GLY	ASP	SER	SER	ARG	ALA	TYR	GLN	VAL	GLU	THR	LYS	THR	GLN	GLY	GLY	PRO	PRO	GLY	GLU	VAL			
VAL	GLU	GLU	GLU	GLN	PRO	ILE	GLY	ALA	PRO	ALA	VAL	GLY	ASP	LYS	SER	GLN	GLU	ALA	ARG	GLY	VAL	SER	THR	GLY	GLY	GLY	LYS	THR	LEU	VAL	SER	VAL	VAL	VAL	VAL	PRO	GLU	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL			
SER	LYS	GLN	GLU	LEU	THR	PRO	GLU	ALA	SER	LEU	CYS	ALA	GLU	LEU	PRO	GLY	ASP	THR	ARG	LYS	LEU	SER	ARG	LEU	LYS	ALA	ARG	ALA	ARG	SER	ASP	ASP	GLU	LYS	LEU	THR	VAL																	

● Molecule 1: Gap junction alpha-8 protein

Chain J:

40%

58%

SER	LYS	VAL	GLU	VAL	GLU	LYS	GLY	GLY	THR	LYS	GLY	ASP	MET
GLN	GLU	GLU	GLU	GLU	ILE	LYS	GLY	THR	LYS	GLY	ASP	W4	
LEU	GLN	GLN	SER	SER	VAL	LYS	PHE	LYS	LYS	PHE	W24	V25	
THR	PRO	ILE	THR	PRO	TYR	ARG	TYR	ARG	ARG	LEU	L26	Q25	
GLU	GLU	GLY	GLY	GLY	PHE	GLY	PHE	LEU	LEU	GLY	L35	I72	
LYS	ALA	ALA	ALA	ALA	PRO	GLY	PRO	GLY	GLY	GLY	Y180	Q81	
ALA	ALA	VAL	VAL	VAL	LEU	MET	VAL	VAL	GLY	G152	L35	I72	
PRO	PRO	ALA	GLU	GLU	THR	THR	THR	THR	L155	L155	I72	Q81	
SER	SER	GLU	GLU	PRO	GLY	VAL	VAL	GLY	GLY	Y180	I72	Q81	
LEU	CYS	GLY	GLY	GLY	GLY	GLY	VAL	VAL	GLY	Y180	I72	Q81	
ALA	ALA	VAL	VAL	VAL	MET	MET	VAL	VAL	GLY	Y180	I72	Q81	
GLU	GLU	GLY	ASP	GLY	VAL	VAL	VAL	VAL	GLY	L234	I72	Q81	
LEU	LEU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	L234	I72	Q81	
PRO	PRO	LYS	LYS	LYS	SER	SER	SER	ALA	LEU	F84	I72	Q81	
GLY	GLY	SER	SER	SER	SER	SER	SER	ALA	LEU	V85	I72	Q81	
GLU	GLU	GLN	GLY	GLN	PRO	PRO	PRO	LYS	LYS	S86	I72	Q81	
ASP	ASP	GLY	GLY	GLY	LEU	LEU	LEU	ILE	ILE	T87	I72	Q81	
THR	THR	ALA	ALA	ALA	SER	SER	SER	ARG	ARG	E104	I72	Q81	
ARG	ARG	GLU	GLU	GLU	LYS	LYS	LYS	ARG	ARG	LYS	I72	Q81	
ALA	ALA	VAL	VAL	VAL	PRO	PRO	PRO	ALA	ALA	ARG	I72	Q81	
ALA	ARG	LEU	LEU	LEU	GLY	GLY	GLY	PHE	PHE	LYS	I72	Q81	
ARG	SER	GLY	GLY	GLY	PHE	PHE	PHE	ARG	ARG	GLY	I72	Q81	
LEU	LEU	THR	THR	THR	GLN	GLN	GLN	ARG	ARG	GLY	I72	Q81	
SER	SER	LEU	LEU	LEU	VAL	VAL	VAL	LEU	LEU	SER	I72	Q81	
SER	SER	LEU	LEU	LEU	VAL	VAL	VAL	SER	SER	GLN	I72	Q81	
ARG	ARG	ALA	ALA	ALA	GLY	GLY	GLY	GLN	GLN	GLN	I72	Q81	
ALA	ARG	LEU	LEU	LEU	GLY	GLY	GLY	GLY	GLY	GLY	I72	Q81	
SER	SER	GLY	GLY	GLY	PRO	PRO	PRO	PRO	PRO	PRO	I72	Q81	
ASP	ASP	GLY	GLY	GLY	LEU	LEU	LEU	GLY	GLY	GLY	I72	Q81	
LEU	LEU	LYS	LYS	LYS	ASP	ASP	ASP	LYS	LYS	ASN	I72	Q81	
THR	THR	VAL	VAL	VAL	SER	SER	SER	SER	SER	GLY	I72	Q81	
VAL	VAL	VAL	VAL	VAL	LEU	LEU	LEU	LEU	LEU	GLY	I72	Q81	
		GLU	GLU	GLU	SER	SER	SER	HIS	GLY	GLY	I72	Q81	
		PRO	PRO	PRO	ARG	ARG	ARG	SER	ARG	ARG	I72	Q81	
		GLY	GLY	GLY	ALA	ALA	ALA	ILE	ILE	PRO	I72	Q81	
		PRO	PRO	PRO	ALA	ALA	ALA	ILE	ILE	ALA	I72	Q81	
		VAL	VAL	VAL	GLN	GLN	GLN	VAL	VAL	LEU	I72	Q81	
		GLY	GLY	GLY	GLY	GLY	GLY	SER	SER	ALA	I72	Q81	
		GLY	GLY	GLY	LEU	LEU	LEU	ILE	ILE	ALA	I72	Q81	
		ALA	ALA	ALA	PRO	PRO	PRO	GLN	GLN	GLN	I72	Q81	
		GLY	GLY	GLY	SER	SER	SER	LYS	LYS	GLY	I72	Q81	
		LYS	LYS	LYS	TYR	TYR	TYR	ALA	ALA	SER	I72	Q81	
		GLY	GLY	GLY	ALA	ALA	ALA	LYS	LYS	VAL	I72	Q81	
		GLY	GLY	GLY	GLN	GLN	GLN	GLY	GLY	LYS	I72	Q81	
		THR	THR	THR	VAL	VAL	VAL	TYR	TYR	LYS	I72	Q81	
		PRO	PRO	PRO	GLY	GLY	GLY	GLN	GLN	SER	I72	Q81	
		PRO	PRO	PRO	ALA	ALA	ALA	LEU	LEU	SER	I72	Q81	
		GLY	GLY	GLY	GLN	GLN	GLN	LEU	LEU	SER	I72	Q81	
		LYS	LYS	LYS	VAL	VAL	VAL	GLY	GLY	SER	I72	Q81	
		VAL	VAL	VAL	GLY	GLY	GLY	GLY	GLY	SER	I72	Q81	

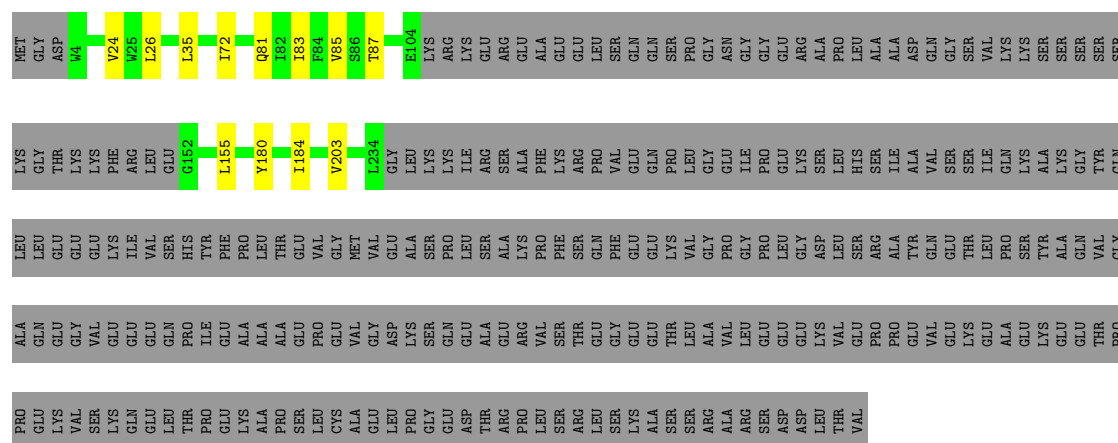
● Molecule 1: Gap junction alpha-8 protein

Chain K:

40%

58%

MET	GLY	ASP	W4	V24	Q25	L26	L35	I72	Q81	I82	I83	F84	V85	S86	T87	E104	LYS	ARG	LYS	GLU	ARG	GLU	PRO	GLN	GLY	GLN	ARG	ALA	ARG	SER	PRO	GLY	ASN	GLY	GLU	GLU	ARG	ALA	PRO	LEU	VAL	ALA	SER	VAL	LYS	LYS	SER	SER	SER	SER	GLY		
LYS	GLY	THR	LYS	PHE	ARG	LEU	G152	L155	Y180	L234	GLY	LEU	LYS	LYS	ILE	ARG	ALA	LYS	PRO	PHE	LYS	ARG	PRO	GLN	VAL	ALA	ILE	GLY	PRO	GLY	LYS	SER	HIS	GLY	GLU	GLU	ARG	ALA	TYR	GLN	VAL	GLY	TYR	LYS	TYR	LEU	LEU	GLU	GLY				
GLU	LYS	ILE	VAL	SER	HIS	TYR	PHE	PRO	GLY	VAL	MET	VAL	GLU	ALA	SER	PRO	GLY	VAL	GLN	ARG	VAL	PHE	SER	GLY	PHE	GLY	GLY	GLY	PRO	GLY	LEU	GLY	ASP	SER	SER	ARG	ALA	TYR	GLN	VAL	GLU	THR	LYS	THR	GLN	GLY	GLY	PRO	PRO	GLY	LYS	VAL	
VAL	GLU	GLU	GLU	GLN	PRO	ILE	GLY	ALA	PRO	ALA	GLY	ASP	LYS	SER	GLN	GLU	ALA	ARG	GLY	VAL	SER	THR	GLY	GLY	GLY	GLY	LYS	THR	LEU	VAL	SER	VAL	VAL	VAL	GLY	VAL																	
SER	LYS	GLN	GLU	LEU	THR	PRO	GLU	ALA	SER	LEU	CYS	ALA	GLU	LEU	PRO	GLY	ASP	THR	ARG	LYS	LEU	SER	ARG	LEU	LYS	ALA	ARG	ALA	ARG	SER	ASP	ASP	LEU	THR	VAL																		



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D6	Depositor
Number of particles used	15342	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.294	Depositor
Minimum map value	-0.962	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.04	Depositor
Map size ($\text{\AA}$)	315.648, 315.648, 315.648	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.822, 0.822, 0.822	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: MC3

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	0.13	0/1478	0.26	0/2020
1	B	0.14	0/1478	0.26	0/2020
1	C	0.14	0/1478	0.26	0/2020
1	D	0.14	0/1478	0.26	0/2020
1	E	0.14	0/1478	0.26	0/2020
1	F	0.14	0/1478	0.26	0/2020
1	G	0.14	0/1478	0.26	0/2020
1	H	0.14	0/1478	0.26	0/2020
1	I	0.14	0/1478	0.26	0/2020
1	J	0.14	0/1478	0.26	0/2020
1	K	0.14	0/1478	0.26	0/2020
1	L	0.14	0/1478	0.26	0/2020
All	All	0.14	0/17736	0.26	0/24240

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1436	1379	1378	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1436	1379	1378	10	0
1	C	1436	1379	1378	8	0
1	D	1436	1379	1378	9	0
1	E	1436	1379	1378	11	0
1	F	1436	1379	1378	11	0
1	G	1436	1379	1378	10	0
1	H	1436	1379	1378	8	0
1	I	1436	1379	1378	10	0
1	J	1436	1379	1378	8	0
1	K	1436	1379	1378	9	0
1	L	1436	1379	1378	11	0
2	A	199	352	309	2	0
2	B	199	352	309	3	0
2	C	199	352	309	2	0
2	D	199	352	309	2	0
2	E	199	352	309	3	0
2	F	199	352	309	3	0
2	G	227	385	338	4	0
2	H	199	352	309	2	0
2	I	199	352	309	3	0
2	J	199	352	309	2	0
2	K	199	352	309	2	0
2	L	171	319	280	1	0
All	All	19620	20772	20244	101	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 3.

The worst 5 of 101 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:35:LEU:HD12	1:B:83:ILE:HD11	1.82	0.60
1:E:35:LEU:HD11	2:F:516:MC3:H181	1.84	0.59
2:G:510:MC3:H181	1:L:35:LEU:HD11	1.85	0.58
1:H:35:LEU:HD11	2:I:509:MC3:H181	1.85	0.58
1:B:35:LEU:HD11	2:C:509:MC3:H181	1.85	0.58

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	180/440 (41%)	180 (100%)	0	0	100	100
1	B	180/440 (41%)	180 (100%)	0	0	100	100
1	C	180/440 (41%)	180 (100%)	0	0	100	100
1	D	180/440 (41%)	180 (100%)	0	0	100	100
1	E	180/440 (41%)	180 (100%)	0	0	100	100
1	F	180/440 (41%)	180 (100%)	0	0	100	100
1	G	180/440 (41%)	180 (100%)	0	0	100	100
1	H	180/440 (41%)	180 (100%)	0	0	100	100
1	I	180/440 (41%)	180 (100%)	0	0	100	100
1	J	180/440 (41%)	180 (100%)	0	0	100	100
1	K	180/440 (41%)	180 (100%)	0	0	100	100
1	L	180/440 (41%)	180 (100%)	0	0	100	100
All	All	2160/5280 (41%)	2160 (100%)	0	0	100	100

There are no Ramachandran outliers to report.

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	152/385 (40%)	151 (99%)	1 (1%)	76	90
1	B	152/385 (40%)	151 (99%)	1 (1%)	76	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	152/385 (40%)	151 (99%)	1 (1%)	76	90
1	D	152/385 (40%)	151 (99%)	1 (1%)	76	90
1	E	152/385 (40%)	151 (99%)	1 (1%)	76	90
1	F	152/385 (40%)	151 (99%)	1 (1%)	76	90
1	G	152/385 (40%)	151 (99%)	1 (1%)	76	90
1	H	152/385 (40%)	151 (99%)	1 (1%)	76	90
1	I	152/385 (40%)	151 (99%)	1 (1%)	76	90
1	J	152/385 (40%)	151 (99%)	1 (1%)	76	90
1	K	152/385 (40%)	151 (99%)	1 (1%)	76	90
1	L	152/385 (40%)	151 (99%)	1 (1%)	76	90
All	All	1824/4620 (40%)	1812 (99%)	12 (1%)	73	90

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	87	THR
1	I	87	THR
1	L	87	THR
1	J	87	THR
1	D	87	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	57	GLN
1	J	57	GLN
1	G	57	GLN
1	F	57	GLN
1	I	57	GLN

5.3.3 RNA ⓘ

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](#)

192 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	MC3	K	507	-	8,8,45	0.25	0	7,7,53	0.18	0
2	MC3	K	501	-	11,11,45	0.22	0	10,10,53	0.19	0
2	MC3	J	512	-	11,11,45	0.24	0	10,10,53	0.18	0
2	MC3	C	513	-	7,7,45	0.26	0	6,6,53	0.19	0
2	MC3	C	503	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	I	505	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	G	503	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	G	516	-	27,27,45	0.49	0	30,32,53	0.65	1 (3%)
2	MC3	D	502	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	H	505	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	A	507	-	8,8,45	0.25	0	7,7,53	0.19	0
2	MC3	A	514	-	9,9,45	0.23	0	8,8,53	0.18	0
2	MC3	H	510	-	12,12,45	0.21	0	11,11,53	0.21	0
2	MC3	I	515	-	27,27,45	0.49	0	30,32,53	0.65	1 (3%)
2	MC3	D	507	-	8,8,45	0.25	0	7,7,53	0.19	0
2	MC3	B	512	-	11,11,45	0.24	0	10,10,53	0.18	0
2	MC3	K	502	-	12,12,45	0.22	0	11,11,53	0.22	0
2	MC3	B	515	-	27,27,45	0.49	0	30,32,53	0.65	1 (3%)
2	MC3	C	508	-	10,10,45	0.23	0	9,9,53	0.22	0
2	MC3	K	508	-	10,10,45	0.23	0	9,9,53	0.22	0
2	MC3	H	513	-	7,7,45	0.26	0	6,6,53	0.19	0
2	MC3	F	509	-	12,12,45	0.22	0	11,11,53	0.22	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	G	517	-	21,21,45	0.55	0	24,26,53	0.67	1 (4%)
2	MC3	G	511	-	12,12,45	0.21	0	11,11,53	0.21	0
2	MC3	F	506	-	27,27,45	0.49	0	30,32,53	0.65	1 (3%)
2	MC3	C	509	-	7,7,45	0.55	0	6,6,53	0.39	0
2	MC3	F	507	-	21,21,45	0.55	0	24,26,53	0.67	1 (4%)
2	MC3	C	502	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	E	516	-	21,21,45	0.54	0	24,26,53	0.67	1 (4%)
2	MC3	E	502	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	J	511	-	10,10,45	0.24	0	9,9,53	0.18	0
2	MC3	J	509	-	7,7,45	0.56	0	6,6,53	0.39	0
2	MC3	L	511	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	B	508	-	10,10,45	0.23	0	9,9,53	0.22	0
2	MC3	D	516	-	21,21,45	0.55	0	24,26,53	0.67	1 (4%)
2	MC3	D	515	-	27,27,45	0.49	0	30,32,53	0.65	1 (3%)
2	MC3	C	512	-	11,11,45	0.24	0	10,10,53	0.18	0
2	MC3	F	513	-	5,5,45	0.27	0	4,4,53	0.17	0
2	MC3	J	515	-	27,27,45	0.49	0	30,32,53	0.65	1 (3%)
2	MC3	G	504	-	9,9,45	0.23	0	8,8,53	0.19	0
2	MC3	H	506	-	5,5,45	0.26	0	4,4,53	0.17	0
2	MC3	B	506	-	5,5,45	0.27	0	4,4,53	0.17	0
2	MC3	F	504	-	7,7,45	0.26	0	6,6,53	0.19	0
2	MC3	H	507	-	8,8,45	0.25	0	7,7,53	0.18	0
2	MC3	F	511	-	9,9,45	0.23	0	8,8,53	0.19	0
2	MC3	E	501	-	11,11,45	0.22	0	10,10,53	0.19	0
2	MC3	G	514	-	7,7,45	0.26	0	6,6,53	0.18	0
2	MC3	K	505	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	F	514	-	8,8,45	0.25	0	7,7,53	0.19	0
2	MC3	C	501	-	11,11,45	0.22	0	10,10,53	0.19	0
2	MC3	J	510	-	12,12,45	0.21	0	11,11,53	0.21	0
2	MC3	B	502	-	12,12,45	0.23	0	11,11,53	0.22	0
2	MC3	F	503	-	11,11,45	0.24	0	10,10,53	0.18	0
2	MC3	I	516	-	21,21,45	0.55	0	24,26,53	0.67	1 (4%)
2	MC3	L	510	-	9,9,45	0.23	0	8,8,53	0.19	0
2	MC3	B	507	-	8,8,45	0.25	0	7,7,53	0.19	0
2	MC3	D	501	-	11,11,45	0.22	0	10,10,53	0.19	0
2	MC3	F	516	-	7,7,45	0.56	0	6,6,53	0.38	0
2	MC3	H	514	-	9,9,45	0.24	0	8,8,53	0.19	0
2	MC3	J	501	-	11,11,45	0.22	0	10,10,53	0.19	0
2	MC3	A	515	-	27,27,45	0.49	0	30,32,53	0.65	1 (3%)
2	MC3	J	513	-	7,7,45	0.26	0	6,6,53	0.19	0
2	MC3	L	515	-	7,7,45	0.55	0	6,6,53	0.39	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	I	510	-	12,12,45	0.21	0	11,11,53	0.21	0
2	MC3	K	513	-	7,7,45	0.26	0	6,6,53	0.18	0
2	MC3	L	513	-	8,8,45	0.25	0	7,7,53	0.19	0
2	MC3	B	510	-	12,12,45	0.21	0	11,11,53	0.21	0
2	MC3	G	513	-	11,11,45	0.24	0	10,10,53	0.18	0
2	MC3	I	514	-	9,9,45	0.24	0	8,8,53	0.19	0
2	MC3	G	501	-	11,11,45	0.22	0	10,10,53	0.19	0
2	MC3	L	502	-	10,10,45	0.24	0	9,9,53	0.18	0
2	MC3	A	512	-	11,11,45	0.24	0	10,10,53	0.18	0
2	MC3	H	508	-	10,10,45	0.23	0	9,9,53	0.22	0
2	MC3	H	511	-	10,10,45	0.24	0	9,9,53	0.18	0
2	MC3	D	513	-	7,7,45	0.26	0	6,6,53	0.18	0
2	MC3	I	513	-	7,7,45	0.26	0	6,6,53	0.18	0
2	MC3	B	513	-	7,7,45	0.25	0	6,6,53	0.18	0
2	MC3	A	508	-	10,10,45	0.23	0	9,9,53	0.22	0
2	MC3	G	509	-	27,27,45	0.49	0	30,32,53	0.65	1 (3%)
2	MC3	K	514	-	9,9,45	0.24	0	8,8,53	0.19	0
2	MC3	H	503	-	12,12,45	0.22	0	11,11,53	0.22	0
2	MC3	D	511	-	10,10,45	0.24	0	9,9,53	0.18	0
2	MC3	A	503	-	12,12,45	0.22	0	11,11,53	0.22	0
2	MC3	J	508	-	10,10,45	0.23	0	9,9,53	0.22	0
2	MC3	G	512	-	10,10,45	0.23	0	9,9,53	0.17	0
2	MC3	A	516	-	21,21,45	0.54	0	24,26,53	0.67	1 (4%)
2	MC3	B	511	-	10,10,45	0.24	0	9,9,53	0.18	0
2	MC3	H	515	-	27,27,45	0.49	0	30,32,53	0.65	1 (3%)
2	MC3	E	507	-	8,8,45	0.25	0	7,7,53	0.19	0
2	MC3	B	516	-	21,21,45	0.55	0	24,26,53	0.67	1 (4%)
2	MC3	G	510	-	7,7,45	0.55	0	6,6,53	0.39	0
2	MC3	K	512	-	11,11,45	0.24	0	10,10,53	0.18	0
2	MC3	A	505	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	A	506	-	5,5,45	0.27	0	4,4,53	0.17	0
2	MC3	E	514	-	9,9,45	0.24	0	8,8,53	0.19	0
2	MC3	L	506	-	21,21,45	0.55	0	24,26,53	0.67	1 (4%)
2	MC3	L	503	-	11,11,45	0.24	0	10,10,53	0.18	0
2	MC3	K	506	-	5,5,45	0.26	0	4,4,53	0.17	0
2	MC3	K	511	-	10,10,45	0.24	0	9,9,53	0.18	0
2	MC3	H	502	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	A	502	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	I	506	-	5,5,45	0.26	0	4,4,53	0.17	0
2	MC3	E	512	-	11,11,45	0.24	0	10,10,53	0.18	0
2	MC3	D	506	-	5,5,45	0.26	0	4,4,53	0.17	0
2	MC3	H	509	-	7,7,45	0.56	0	6,6,53	0.38	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	E	511	-	10,10,45	0.23	0	9,9,53	0.18	0
2	MC3	F	501	-	12,12,45	0.21	0	11,11,53	0.21	0
2	MC3	E	510	-	12,12,45	0.21	0	11,11,53	0.21	0
2	MC3	I	511	-	10,10,45	0.24	0	9,9,53	0.18	0
2	MC3	F	512	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	J	507	-	8,8,45	0.25	0	7,7,53	0.19	0
2	MC3	F	515	-	10,10,45	0.23	0	9,9,53	0.22	0
2	MC3	K	509	-	7,7,45	0.55	0	6,6,53	0.38	0
2	MC3	F	508	-	11,11,45	0.22	0	10,10,53	0.19	0
2	MC3	D	510	-	12,12,45	0.21	0	11,11,53	0.21	0
2	MC3	E	504	-	9,9,45	0.23	0	8,8,53	0.19	0
2	MC3	F	505	-	9,9,45	0.24	0	8,8,53	0.19	0
2	MC3	E	505	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	G	506	-	5,5,45	0.27	0	4,4,53	0.17	0
2	MC3	L	514	-	10,10,45	0.23	0	9,9,53	0.22	0
2	MC3	C	505	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	H	501	-	11,11,45	0.22	0	10,10,53	0.19	0
2	MC3	G	505	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	I	503	-	12,12,45	0.22	0	11,11,53	0.22	0
2	MC3	H	516	-	21,21,45	0.55	0	24,26,53	0.67	1 (4%)
2	MC3	B	503	-	12,12,45	0.22	0	11,11,53	0.22	0
2	MC3	J	502	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	D	509	-	7,7,45	0.55	0	6,6,53	0.39	0
2	MC3	A	501	-	11,11,45	0.22	0	10,10,53	0.19	0
2	MC3	C	510	-	12,12,45	0.21	0	11,11,53	0.21	0
2	MC3	D	505	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	I	504	-	9,9,45	0.23	0	8,8,53	0.19	0
2	MC3	J	504	-	9,9,45	0.23	0	8,8,53	0.19	0
2	MC3	L	508	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	J	505	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	L	504	-	7,7,45	0.26	0	6,6,53	0.18	0
2	MC3	E	515	-	27,27,45	0.49	0	30,32,53	0.65	1 (3%)
2	MC3	G	508	-	10,10,45	0.23	0	9,9,53	0.22	0
2	MC3	B	504	-	9,9,45	0.23	0	8,8,53	0.19	0
2	MC3	J	516	-	21,21,45	0.55	0	24,26,53	0.67	1 (4%)
2	MC3	K	504	-	9,9,45	0.23	0	8,8,53	0.19	0
2	MC3	L	501	-	12,12,45	0.21	0	11,11,53	0.21	0
2	MC3	C	514	-	9,9,45	0.24	0	8,8,53	0.19	0
2	MC3	L	507	-	11,11,45	0.22	0	10,10,53	0.19	0
2	MC3	J	503	-	12,12,45	0.22	0	11,11,53	0.22	0
2	MC3	I	512	-	11,11,45	0.24	0	10,10,53	0.18	0
2	MC3	K	503	-	12,12,45	0.22	0	11,11,53	0.22	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	I	508	-	10,10,45	0.23	0	9,9,53	0.22	0
2	MC3	D	504	-	9,9,45	0.23	0	8,8,53	0.19	0
2	MC3	A	510	-	12,12,45	0.21	0	11,11,53	0.21	0
2	MC3	E	513	-	7,7,45	0.26	0	6,6,53	0.18	0
2	MC3	B	505	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	I	509	-	7,7,45	0.55	0	6,6,53	0.39	0
2	MC3	K	516	-	21,21,45	0.54	0	24,26,53	0.67	1 (4%)
2	MC3	A	511	-	10,10,45	0.24	0	9,9,53	0.18	0
2	MC3	I	502	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	A	513	-	7,7,45	0.26	0	6,6,53	0.19	0
2	MC3	E	509	-	7,7,45	0.56	0	6,6,53	0.38	0
2	MC3	E	503	-	12,12,45	0.22	0	11,11,53	0.21	0
2	MC3	G	515	-	9,9,45	0.23	0	8,8,53	0.19	0
2	MC3	H	512	-	11,11,45	0.24	0	10,10,53	0.18	0
2	MC3	L	512	-	5,5,45	0.27	0	4,4,53	0.17	0
2	MC3	E	506	-	5,5,45	0.26	0	4,4,53	0.17	0
2	MC3	D	503	-	12,12,45	0.22	0	11,11,53	0.22	0
2	MC3	C	504	-	9,9,45	0.23	0	8,8,53	0.19	0
2	MC3	C	506	-	5,5,45	0.26	0	4,4,53	0.17	0
2	MC3	D	512	-	11,11,45	0.24	0	10,10,53	0.18	0
2	MC3	B	514	-	9,9,45	0.23	0	8,8,53	0.19	0
2	MC3	G	507	-	8,8,45	0.25	0	7,7,53	0.19	0
2	MC3	D	514	-	9,9,45	0.23	0	8,8,53	0.19	0
2	MC3	E	508	-	10,10,45	0.23	0	9,9,53	0.22	0
2	MC3	H	504	-	9,9,45	0.24	0	8,8,53	0.20	0
2	MC3	J	506	-	5,5,45	0.26	0	4,4,53	0.17	0
2	MC3	C	516	-	21,21,45	0.55	0	24,26,53	0.67	1 (4%)
2	MC3	I	507	-	8,8,45	0.25	0	7,7,53	0.19	0
2	MC3	I	501	-	11,11,45	0.22	0	10,10,53	0.19	0
2	MC3	A	504	-	9,9,45	0.23	0	8,8,53	0.19	0
2	MC3	K	510	-	12,12,45	0.20	0	11,11,53	0.21	0
2	MC3	C	511	-	10,10,45	0.24	0	9,9,53	0.18	0
2	MC3	A	509	-	7,7,45	0.55	0	6,6,53	0.38	0
2	MC3	B	509	-	7,7,45	0.55	0	6,6,53	0.39	0
2	MC3	K	515	-	27,27,45	0.49	0	30,32,53	0.65	1 (3%)
2	MC3	C	507	-	8,8,45	0.25	0	7,7,53	0.18	0
2	MC3	B	501	-	11,11,45	0.22	0	10,10,53	0.19	0
2	MC3	D	508	-	10,10,45	0.23	0	9,9,53	0.22	0
2	MC3	L	509	-	12,12,45	0.22	0	11,11,53	0.22	0
2	MC3	F	510	-	12,12,45	0.22	0	11,11,53	0.22	0
2	MC3	C	515	-	27,27,45	0.49	0	30,32,53	0.65	1 (3%)
2	MC3	G	502	-	12,12,45	0.22	0	11,11,53	0.21	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	F	502	-	10,10,45	0.24	0	9,9,53	0.18	0
2	MC3	J	514	-	9,9,45	0.24	0	8,8,53	0.19	0
2	MC3	L	505	-	9,9,45	0.24	0	8,8,53	0.19	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	K	507	-	-	0/6/6/49	-
2	MC3	K	501	-	-	0/9/9/49	-
2	MC3	J	512	-	-	0/9/9/49	-
2	MC3	C	513	-	-	0/5/5/49	-
2	MC3	C	503	-	-	0/10/10/49	-
2	MC3	I	505	-	-	0/10/10/49	-
2	MC3	G	503	-	-	0/10/10/49	-
2	MC3	G	516	-	-	15/29/29/49	-
2	MC3	D	502	-	-	0/10/10/49	-
2	MC3	H	505	-	-	0/10/10/49	-
2	MC3	A	507	-	-	0/6/6/49	-
2	MC3	A	514	-	-	0/7/7/49	-
2	MC3	H	510	-	-	0/10/10/49	-
2	MC3	I	515	-	-	15/29/29/49	-
2	MC3	D	507	-	-	0/6/6/49	-
2	MC3	B	512	-	-	0/9/9/49	-
2	MC3	K	502	-	-	0/10/10/49	-
2	MC3	B	515	-	-	15/29/29/49	-
2	MC3	C	508	-	-	0/8/8/49	-
2	MC3	K	508	-	-	0/8/8/49	-
2	MC3	H	513	-	-	0/5/5/49	-
2	MC3	F	509	-	-	0/10/10/49	-
2	MC3	G	517	-	-	13/23/23/49	-
2	MC3	G	511	-	-	0/10/10/49	-
2	MC3	F	506	-	-	15/29/29/49	-
2	MC3	C	509	-	-	1/5/5/49	-
2	MC3	F	507	-	-	13/23/23/49	-
2	MC3	C	502	-	-	0/10/10/49	-
2	MC3	E	516	-	-	13/23/23/49	-
2	MC3	E	502	-	-	0/10/10/49	-
2	MC3	J	511	-	-	0/8/8/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	J	509	-	-	1/5/5/49	-
2	MC3	L	511	-	-	0/10/10/49	-
2	MC3	B	508	-	-	0/8/8/49	-
2	MC3	D	516	-	-	13/23/23/49	-
2	MC3	D	515	-	-	15/29/29/49	-
2	MC3	C	512	-	-	0/9/9/49	-
2	MC3	F	513	-	-	0/3/3/49	-
2	MC3	J	515	-	-	15/29/29/49	-
2	MC3	G	504	-	-	0/7/7/49	-
2	MC3	H	506	-	-	0/3/3/49	-
2	MC3	B	506	-	-	0/3/3/49	-
2	MC3	F	504	-	-	0/5/5/49	-
2	MC3	H	507	-	-	0/6/6/49	-
2	MC3	F	511	-	-	0/7/7/49	-
2	MC3	E	501	-	-	0/9/9/49	-
2	MC3	G	514	-	-	0/5/5/49	-
2	MC3	K	505	-	-	0/10/10/49	-
2	MC3	F	514	-	-	0/6/6/49	-
2	MC3	C	501	-	-	0/9/9/49	-
2	MC3	J	510	-	-	0/10/10/49	-
2	MC3	B	502	-	-	0/10/10/49	-
2	MC3	F	503	-	-	0/9/9/49	-
2	MC3	I	516	-	-	13/23/23/49	-
2	MC3	L	510	-	-	0/7/7/49	-
2	MC3	B	507	-	-	0/6/6/49	-
2	MC3	D	501	-	-	0/9/9/49	-
2	MC3	F	516	-	-	1/5/5/49	-
2	MC3	H	514	-	-	0/7/7/49	-
2	MC3	J	501	-	-	0/9/9/49	-
2	MC3	A	515	-	-	15/29/29/49	-
2	MC3	J	513	-	-	0/5/5/49	-
2	MC3	L	515	-	-	1/5/5/49	-
2	MC3	I	510	-	-	0/10/10/49	-
2	MC3	K	513	-	-	0/5/5/49	-
2	MC3	L	513	-	-	0/6/6/49	-
2	MC3	B	510	-	-	0/10/10/49	-
2	MC3	G	513	-	-	0/9/9/49	-
2	MC3	I	514	-	-	0/7/7/49	-
2	MC3	G	501	-	-	0/9/9/49	-
2	MC3	L	502	-	-	0/8/8/49	-
2	MC3	A	512	-	-	0/9/9/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	H	508	-	-	0/8/8/49	-
2	MC3	H	511	-	-	0/8/8/49	-
2	MC3	D	513	-	-	0/5/5/49	-
2	MC3	I	513	-	-	0/5/5/49	-
2	MC3	B	513	-	-	0/5/5/49	-
2	MC3	A	508	-	-	0/8/8/49	-
2	MC3	G	509	-	-	15/29/29/49	-
2	MC3	K	514	-	-	0/7/7/49	-
2	MC3	H	503	-	-	0/10/10/49	-
2	MC3	D	511	-	-	0/8/8/49	-
2	MC3	A	503	-	-	0/10/10/49	-
2	MC3	J	508	-	-	0/8/8/49	-
2	MC3	G	512	-	-	0/8/8/49	-
2	MC3	A	516	-	-	13/23/23/49	-
2	MC3	B	511	-	-	0/8/8/49	-
2	MC3	H	515	-	-	15/29/29/49	-
2	MC3	E	507	-	-	0/6/6/49	-
2	MC3	B	516	-	-	13/23/23/49	-
2	MC3	G	510	-	-	1/5/5/49	-
2	MC3	K	512	-	-	0/9/9/49	-
2	MC3	A	505	-	-	0/10/10/49	-
2	MC3	A	506	-	-	0/3/3/49	-
2	MC3	E	514	-	-	0/7/7/49	-
2	MC3	L	506	-	-	13/23/23/49	-
2	MC3	L	503	-	-	0/9/9/49	-
2	MC3	K	506	-	-	0/3/3/49	-
2	MC3	K	511	-	-	0/8/8/49	-
2	MC3	H	502	-	-	0/10/10/49	-
2	MC3	A	502	-	-	0/10/10/49	-
2	MC3	I	506	-	-	0/3/3/49	-
2	MC3	E	512	-	-	0/9/9/49	-
2	MC3	D	506	-	-	0/3/3/49	-
2	MC3	H	509	-	-	1/5/5/49	-
2	MC3	E	511	-	-	0/8/8/49	-
2	MC3	F	501	-	-	0/10/10/49	-
2	MC3	E	510	-	-	0/10/10/49	-
2	MC3	I	511	-	-	0/8/8/49	-
2	MC3	F	512	-	-	0/10/10/49	-
2	MC3	J	507	-	-	0/6/6/49	-
2	MC3	F	515	-	-	0/8/8/49	-
2	MC3	K	509	-	-	1/5/5/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	F	508	-	-	0/9/9/49	-
2	MC3	D	510	-	-	0/10/10/49	-
2	MC3	E	504	-	-	0/7/7/49	-
2	MC3	F	505	-	-	0/7/7/49	-
2	MC3	E	505	-	-	0/10/10/49	-
2	MC3	G	506	-	-	0/3/3/49	-
2	MC3	L	514	-	-	0/8/8/49	-
2	MC3	C	505	-	-	0/10/10/49	-
2	MC3	H	501	-	-	0/9/9/49	-
2	MC3	G	505	-	-	0/10/10/49	-
2	MC3	I	503	-	-	0/10/10/49	-
2	MC3	H	516	-	-	13/23/23/49	-
2	MC3	B	503	-	-	0/10/10/49	-
2	MC3	J	502	-	-	0/10/10/49	-
2	MC3	D	509	-	-	1/5/5/49	-
2	MC3	A	501	-	-	0/9/9/49	-
2	MC3	C	510	-	-	0/10/10/49	-
2	MC3	D	505	-	-	0/10/10/49	-
2	MC3	I	504	-	-	0/7/7/49	-
2	MC3	J	504	-	-	0/7/7/49	-
2	MC3	L	508	-	-	0/10/10/49	-
2	MC3	J	505	-	-	0/10/10/49	-
2	MC3	L	504	-	-	0/5/5/49	-
2	MC3	E	515	-	-	15/29/29/49	-
2	MC3	G	508	-	-	0/8/8/49	-
2	MC3	B	504	-	-	0/7/7/49	-
2	MC3	J	516	-	-	13/23/23/49	-
2	MC3	K	504	-	-	0/7/7/49	-
2	MC3	L	501	-	-	0/10/10/49	-
2	MC3	C	514	-	-	0/7/7/49	-
2	MC3	L	507	-	-	0/9/9/49	-
2	MC3	J	503	-	-	0/10/10/49	-
2	MC3	I	512	-	-	0/9/9/49	-
2	MC3	K	503	-	-	0/10/10/49	-
2	MC3	I	508	-	-	0/8/8/49	-
2	MC3	D	504	-	-	0/7/7/49	-
2	MC3	A	510	-	-	0/10/10/49	-
2	MC3	E	513	-	-	0/5/5/49	-
2	MC3	B	505	-	-	0/10/10/49	-
2	MC3	I	509	-	-	1/5/5/49	-
2	MC3	K	516	-	-	13/23/23/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	A	511	-	-	0/8/8/49	-
2	MC3	I	502	-	-	0/10/10/49	-
2	MC3	A	513	-	-	0/5/5/49	-
2	MC3	E	509	-	-	1/5/5/49	-
2	MC3	E	503	-	-	0/10/10/49	-
2	MC3	G	515	-	-	0/7/7/49	-
2	MC3	H	512	-	-	0/9/9/49	-
2	MC3	L	512	-	-	0/3/3/49	-
2	MC3	E	506	-	-	0/3/3/49	-
2	MC3	D	503	-	-	0/10/10/49	-
2	MC3	C	504	-	-	0/7/7/49	-
2	MC3	C	506	-	-	0/3/3/49	-
2	MC3	D	512	-	-	0/9/9/49	-
2	MC3	B	514	-	-	0/7/7/49	-
2	MC3	G	507	-	-	0/6/6/49	-
2	MC3	D	514	-	-	0/7/7/49	-
2	MC3	E	508	-	-	0/8/8/49	-
2	MC3	H	504	-	-	0/7/7/49	-
2	MC3	J	506	-	-	0/3/3/49	-
2	MC3	C	516	-	-	13/23/23/49	-
2	MC3	I	507	-	-	0/6/6/49	-
2	MC3	I	501	-	-	0/9/9/49	-
2	MC3	A	504	-	-	0/7/7/49	-
2	MC3	K	510	-	-	0/10/10/49	-
2	MC3	C	511	-	-	0/8/8/49	-
2	MC3	A	509	-	-	1/5/5/49	-
2	MC3	B	509	-	-	1/5/5/49	-
2	MC3	K	515	-	-	15/29/29/49	-
2	MC3	C	507	-	-	0/6/6/49	-
2	MC3	B	501	-	-	0/9/9/49	-
2	MC3	D	508	-	-	0/8/8/49	-
2	MC3	L	509	-	-	0/10/10/49	-
2	MC3	F	510	-	-	0/10/10/49	-
2	MC3	C	515	-	-	15/29/29/49	-
2	MC3	G	502	-	-	0/10/10/49	-
2	MC3	F	502	-	-	0/8/8/49	-
2	MC3	J	514	-	-	0/7/7/49	-
2	MC3	L	505	-	-	0/7/7/49	-

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	506	MC3	O2P-P-O1P	2.30	119.80	110.83
2	A	516	MC3	O2P-P-O1P	2.29	119.76	110.83
2	I	516	MC3	O2P-P-O1P	2.29	119.74	110.83
2	B	516	MC3	O2P-P-O1P	2.28	119.73	110.83
2	G	517	MC3	O2P-P-O1P	2.28	119.73	110.83

There are no chirality outliers.

5 of 348 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	515	MC3	C1-C2-O2-C31
2	A	515	MC3	C32-C31-O2-C2
2	A	515	MC3	C1-O3P-P-O2P
2	A	515	MC3	C1-O3P-P-O4P
2	A	516	MC3	C1-O3P-P-O2P

There are no ring outliers.

24 monomers are involved in 29 short contacts:

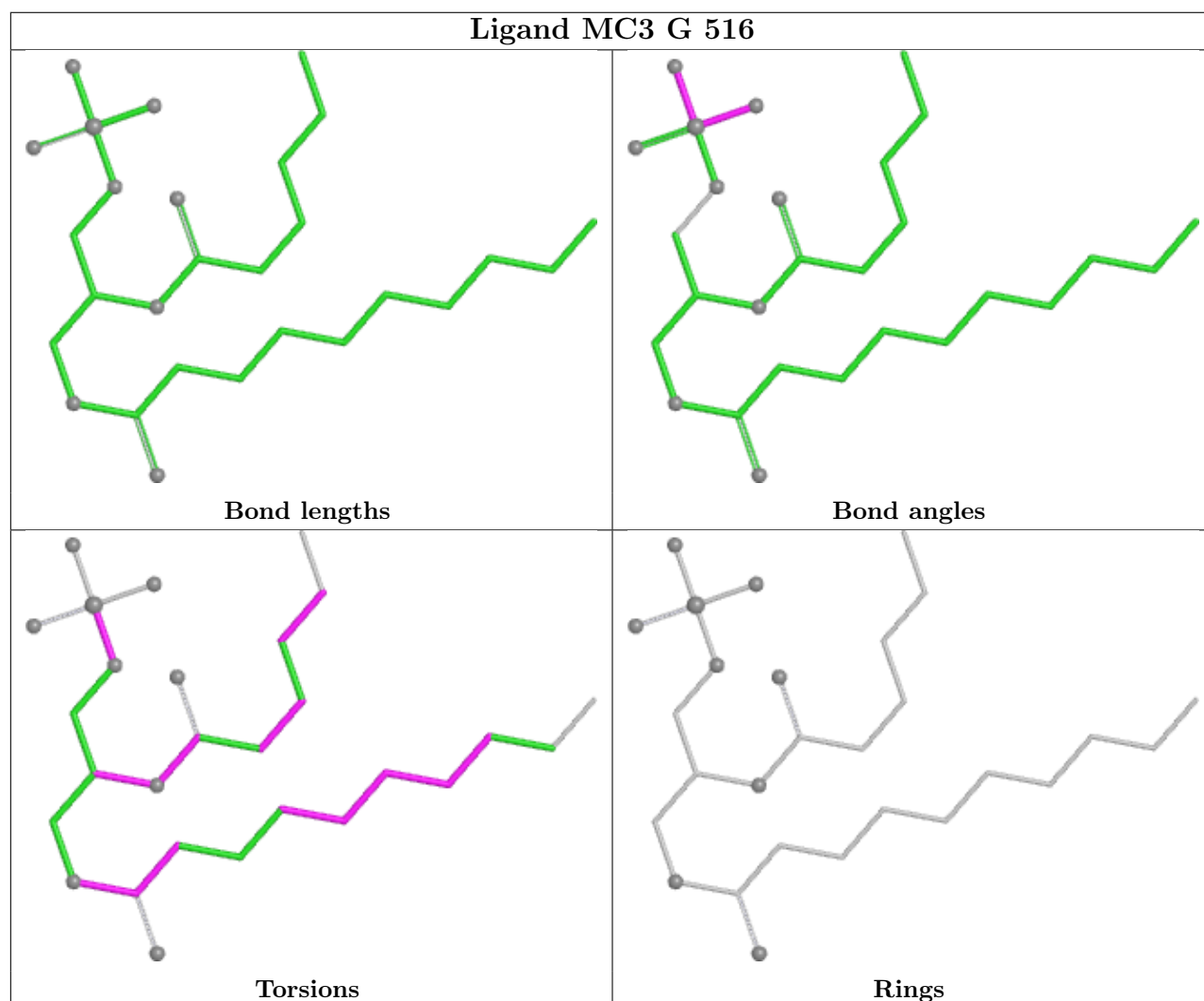
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	516	MC3	1	0
2	I	515	MC3	2	0
2	B	515	MC3	2	0
2	F	506	MC3	2	0
2	C	509	MC3	1	0
2	J	509	MC3	1	0
2	D	515	MC3	1	0
2	J	515	MC3	1	0
2	F	516	MC3	1	0
2	A	515	MC3	1	0
2	L	515	MC3	1	0
2	G	509	MC3	2	0
2	H	515	MC3	1	0
2	G	510	MC3	1	0
2	H	509	MC3	1	0
2	K	509	MC3	1	0
2	D	509	MC3	1	0
2	E	515	MC3	2	0
2	I	509	MC3	1	0
2	E	509	MC3	1	0
2	A	509	MC3	1	0
2	B	509	MC3	1	0

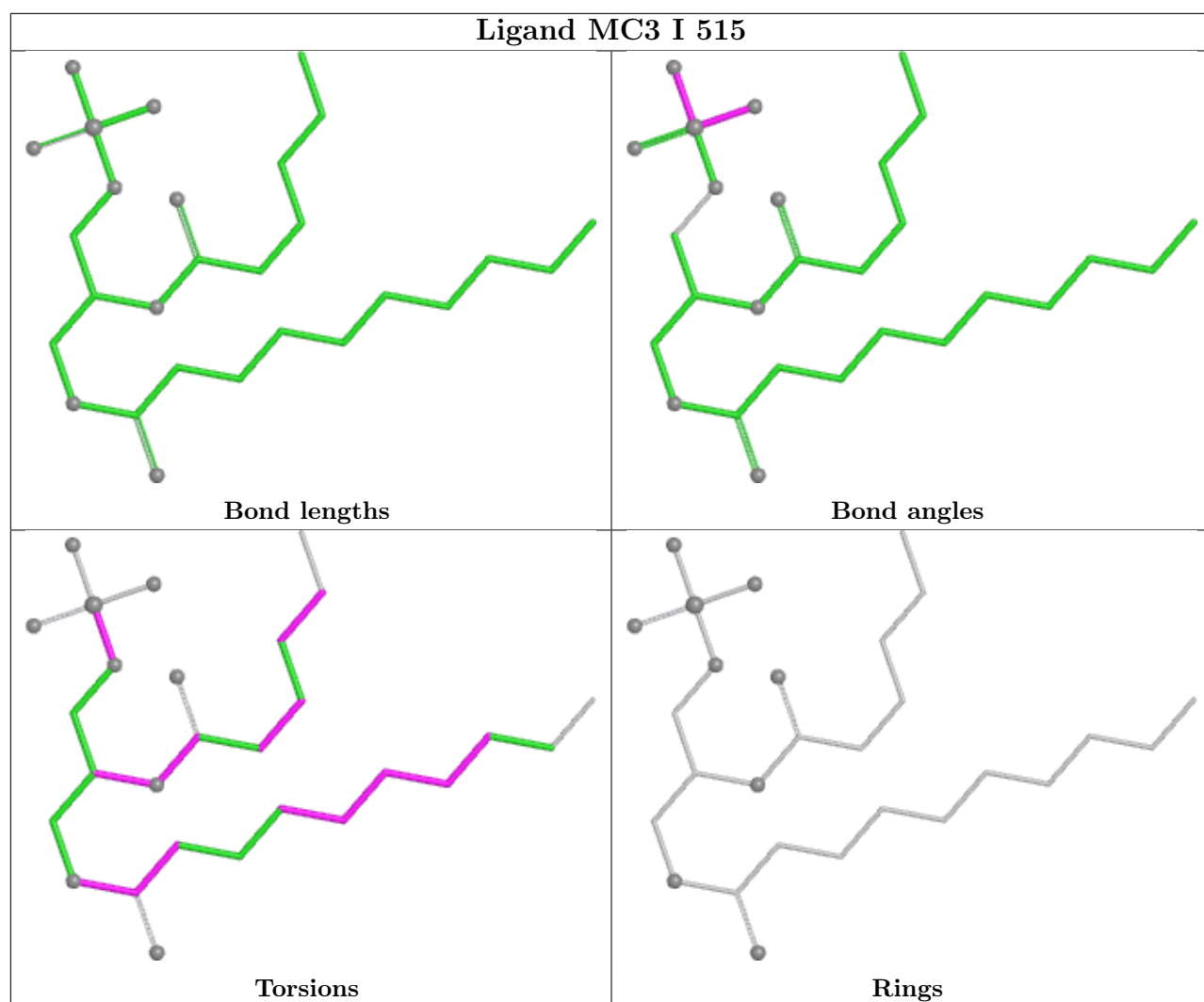
Continued on next page...

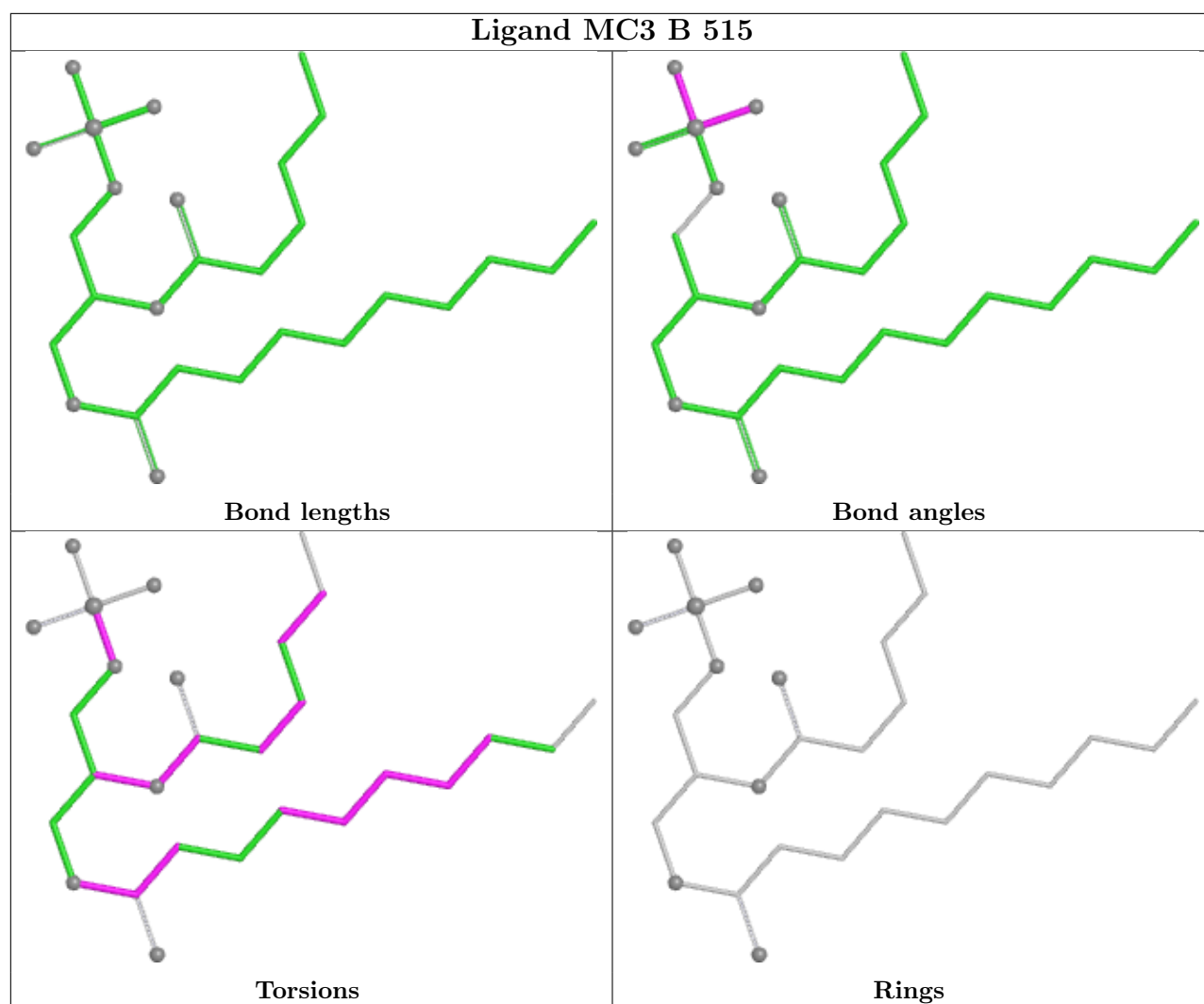
Continued from previous page...

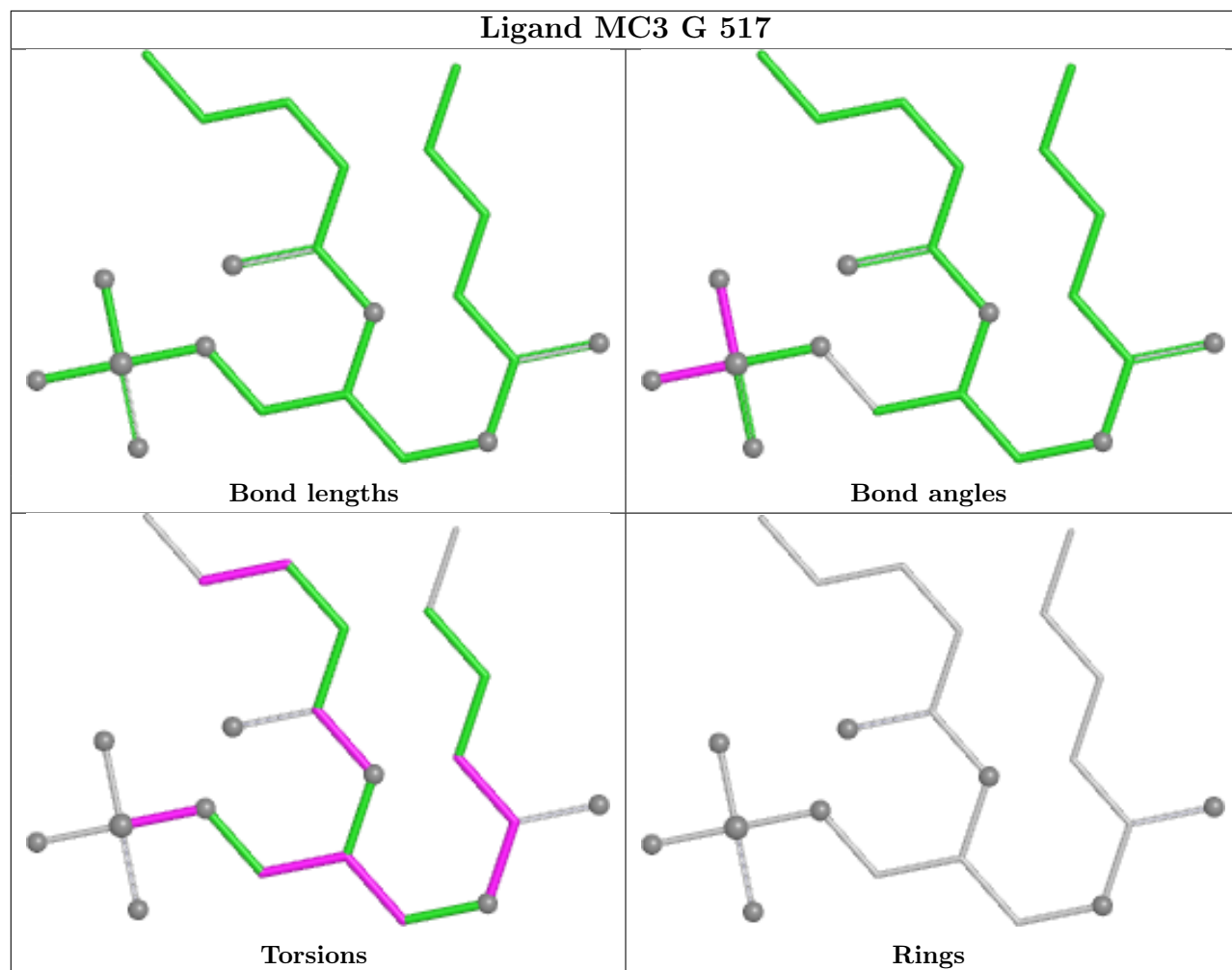
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	K	515	MC3	1	0
2	C	515	MC3	1	0

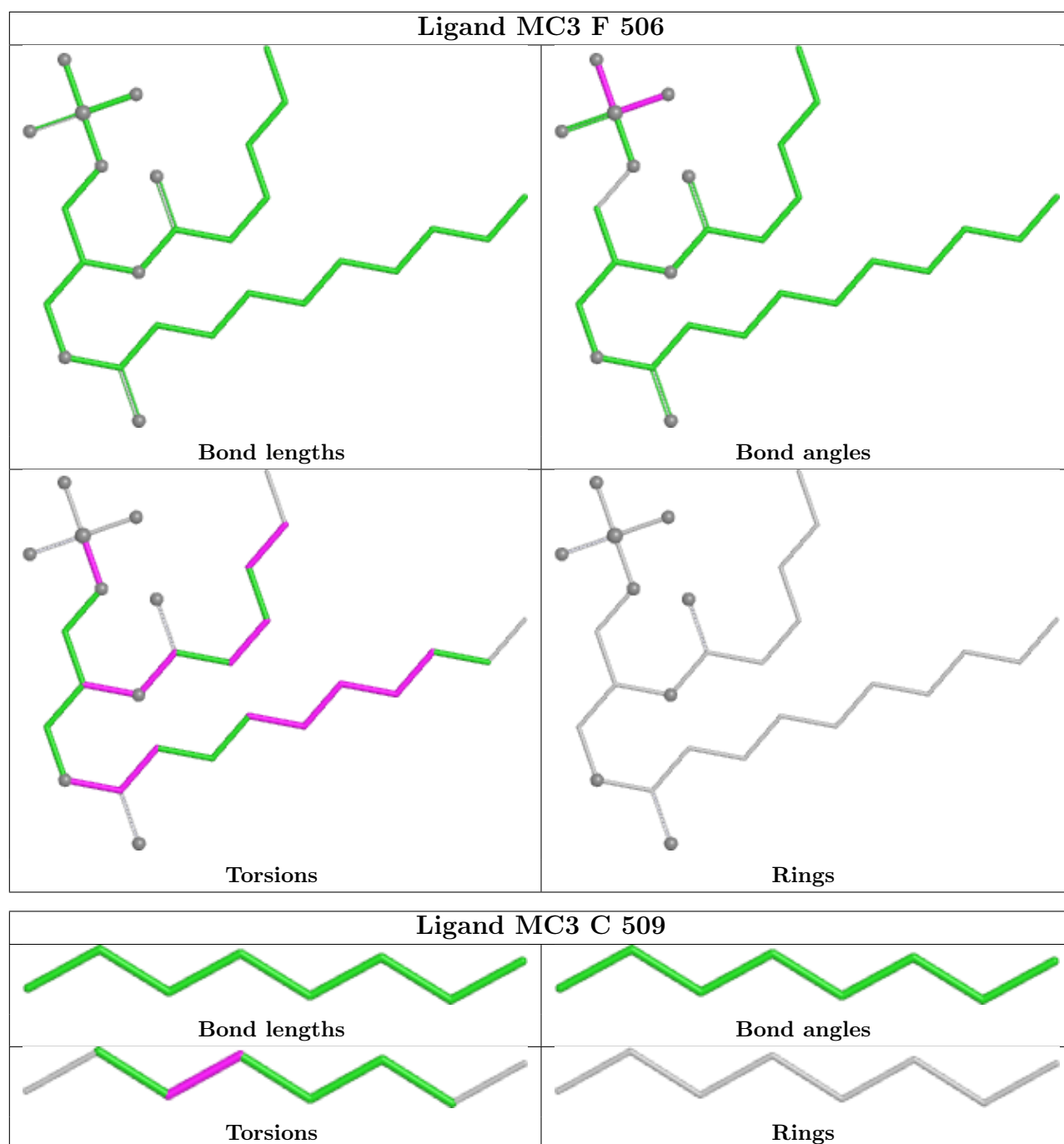
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

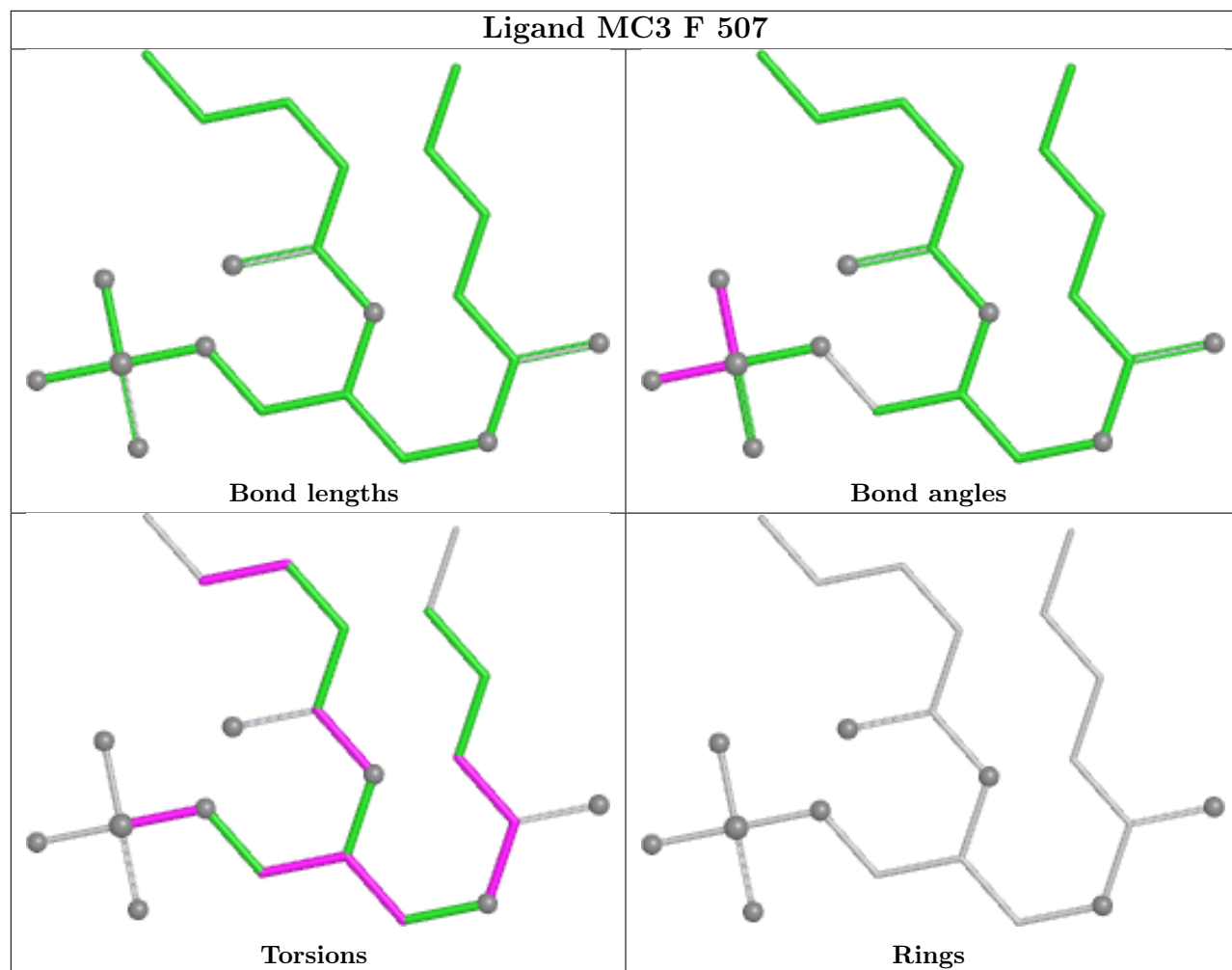


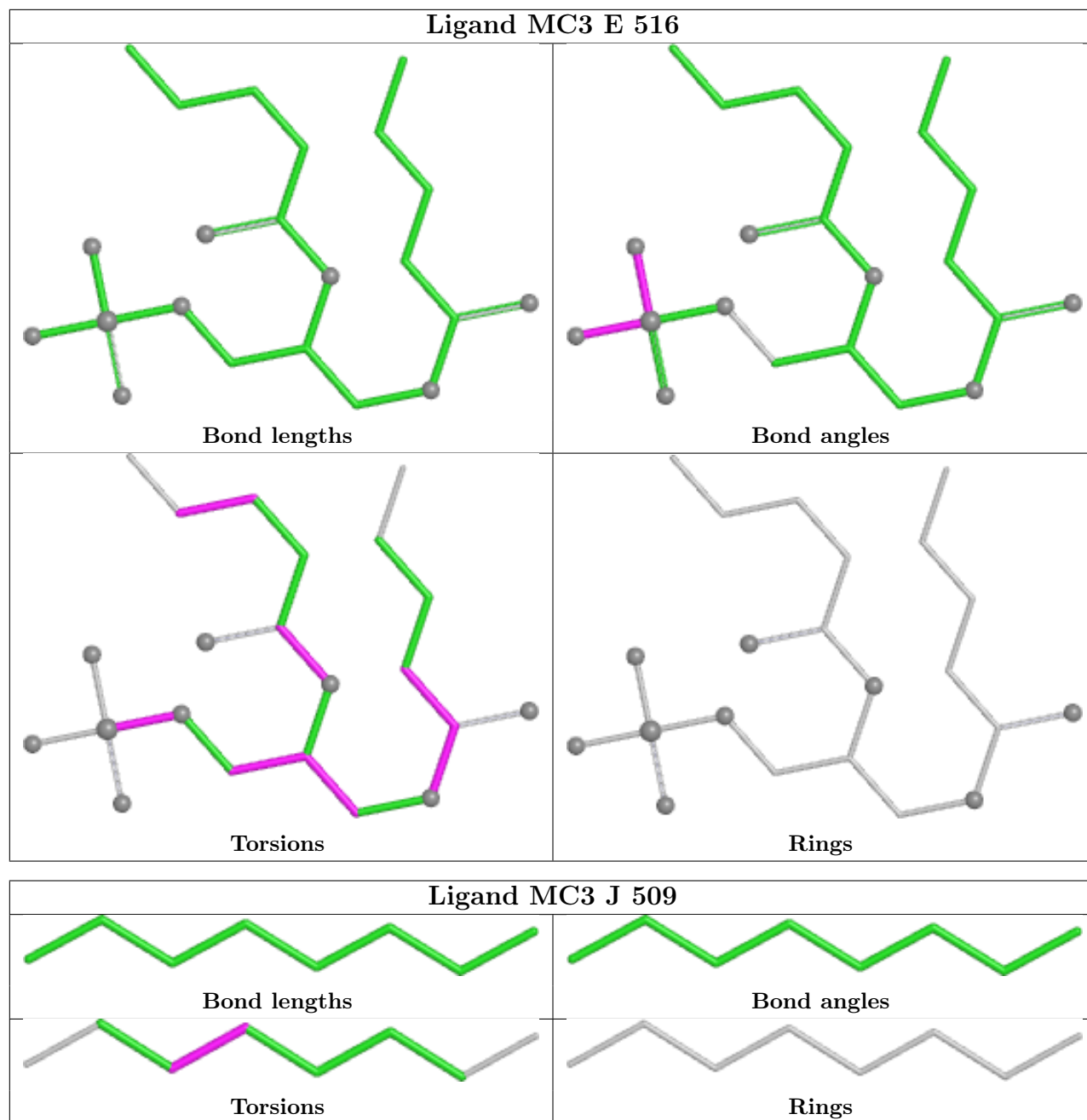


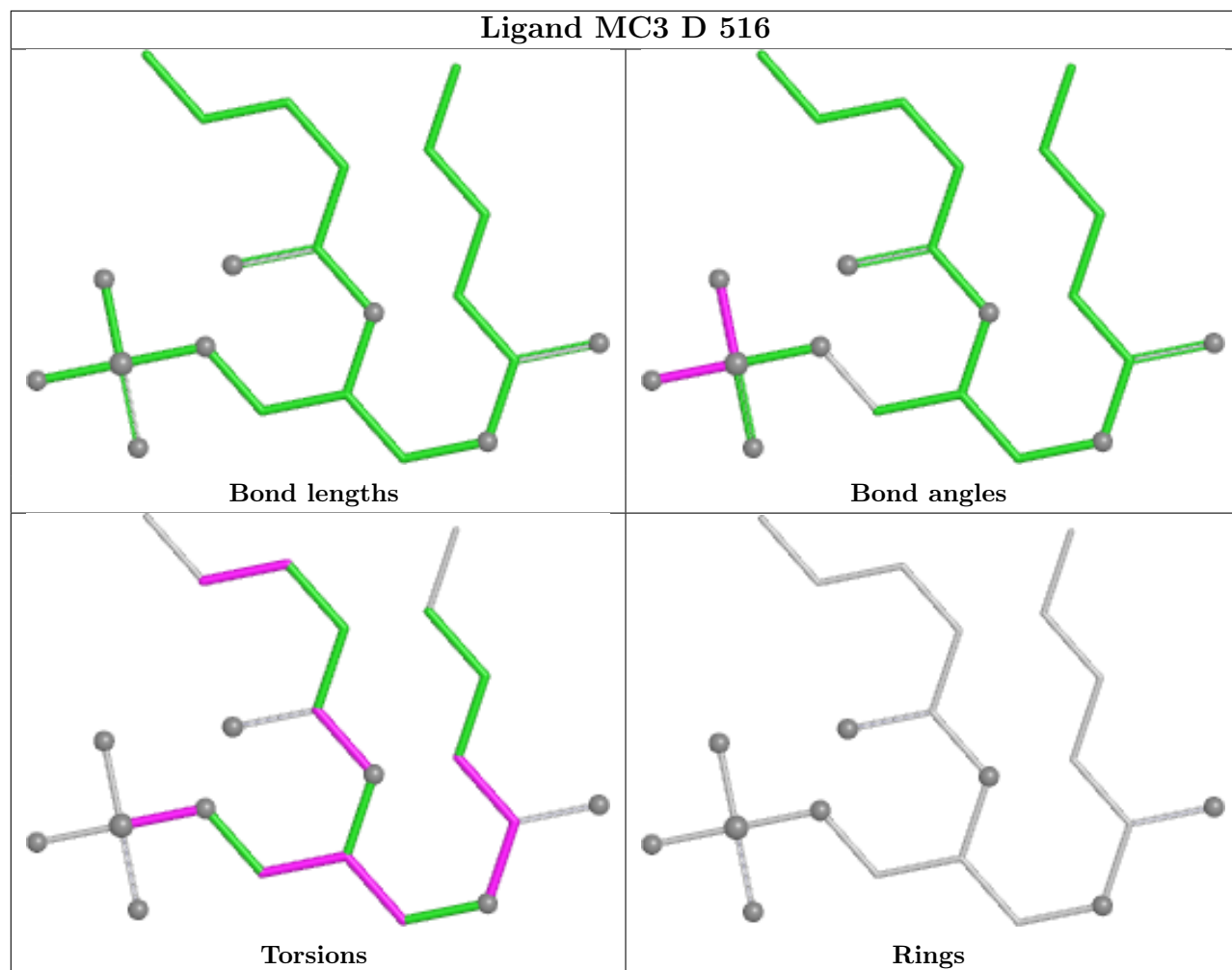


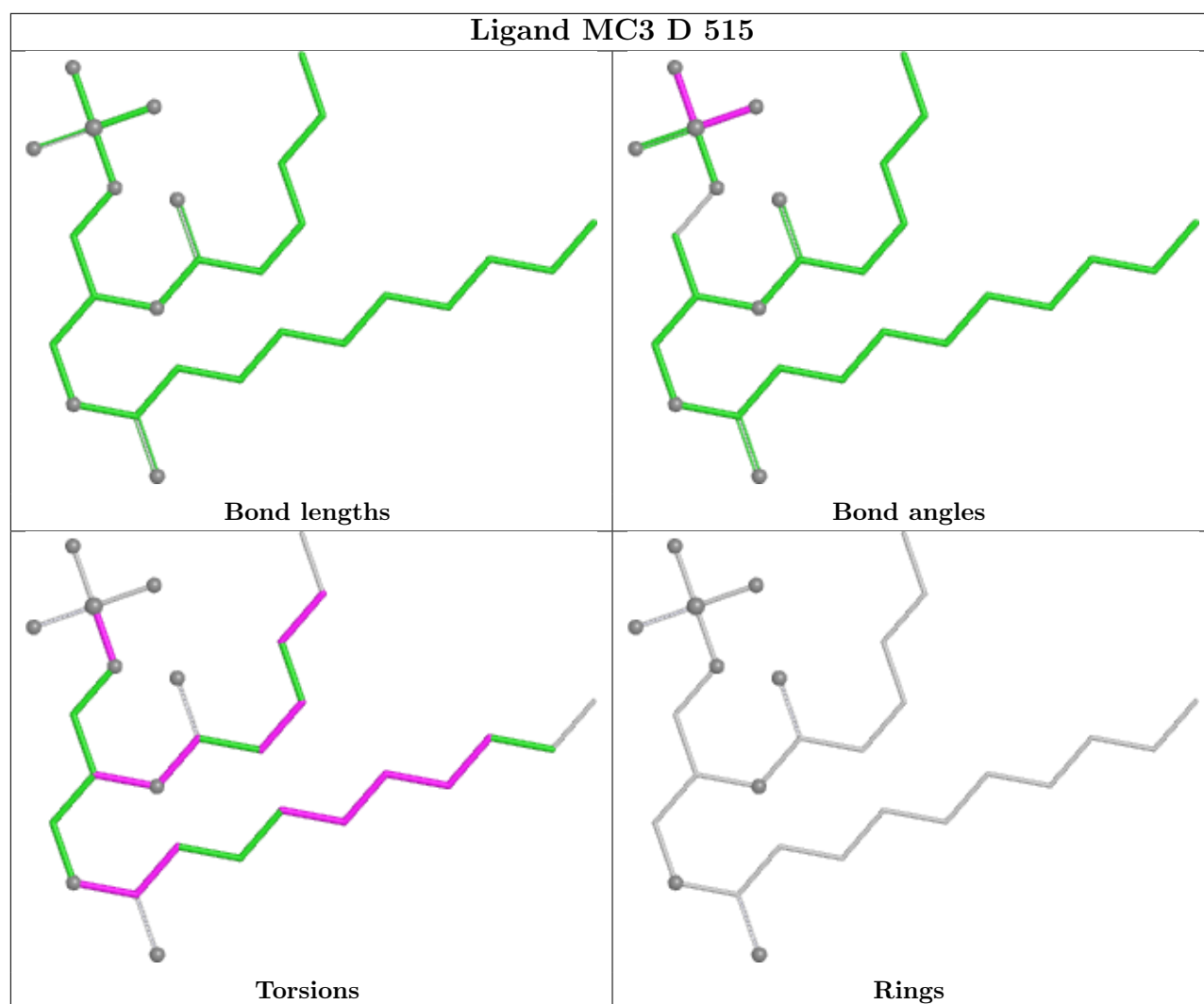


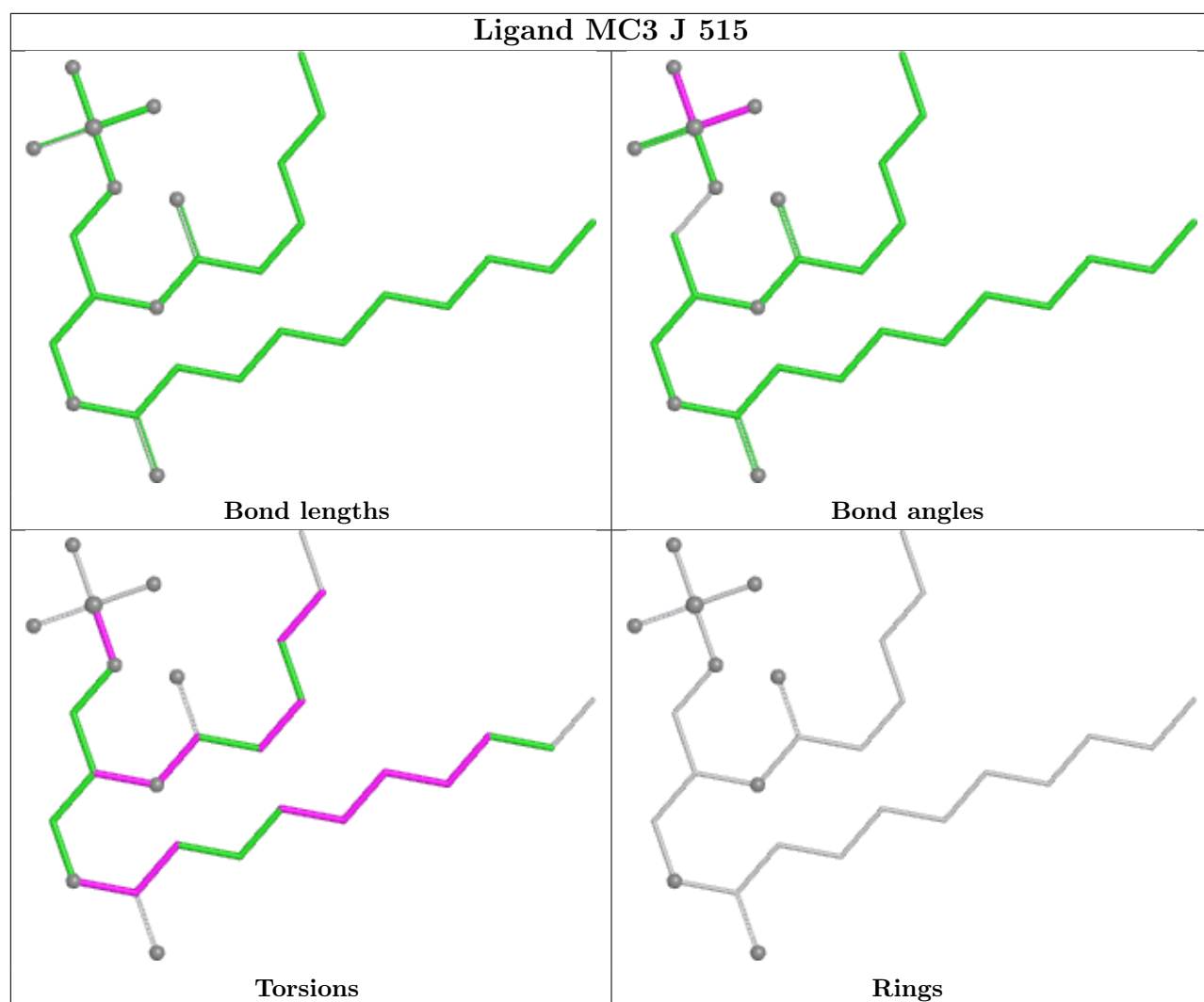


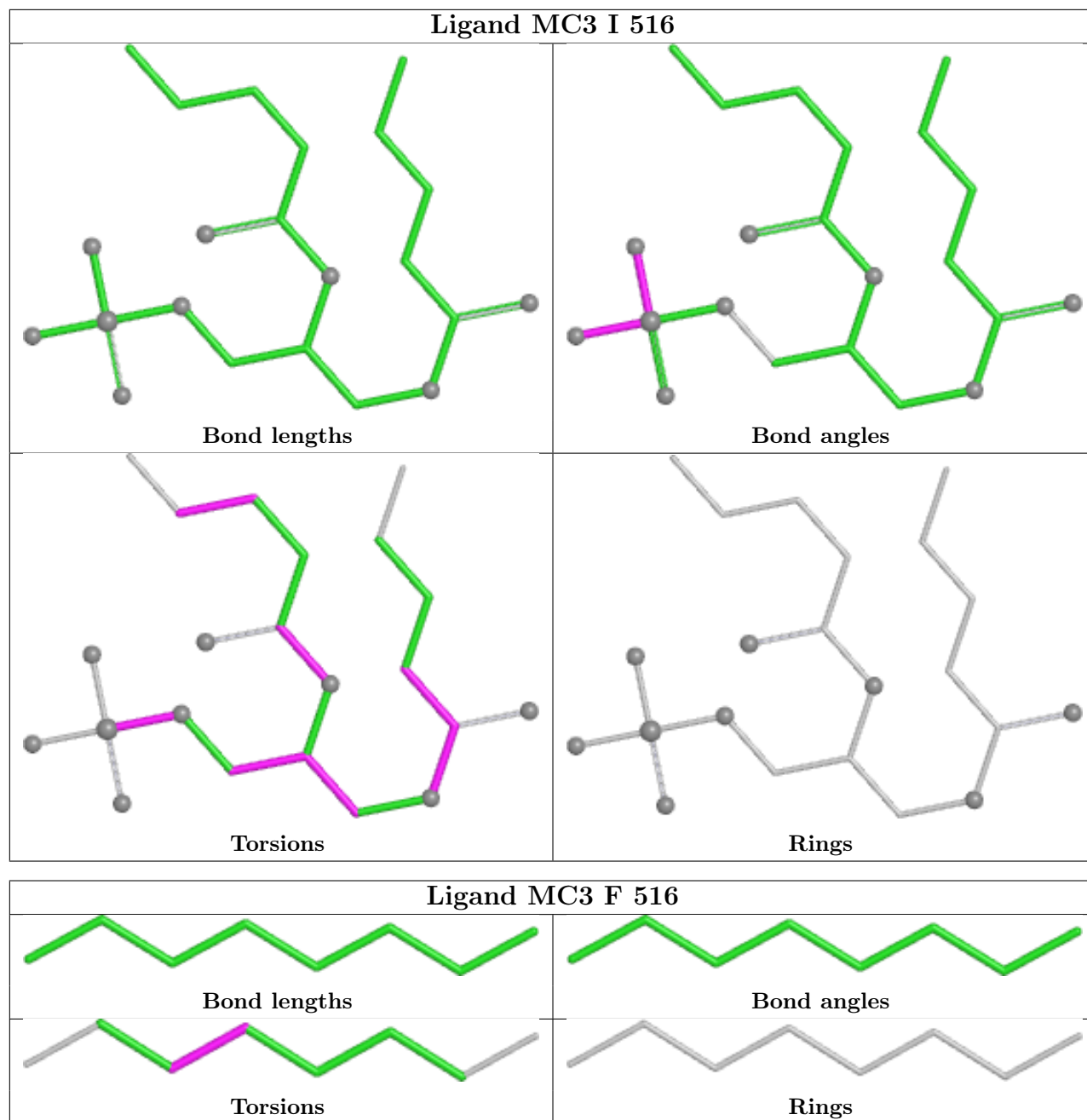


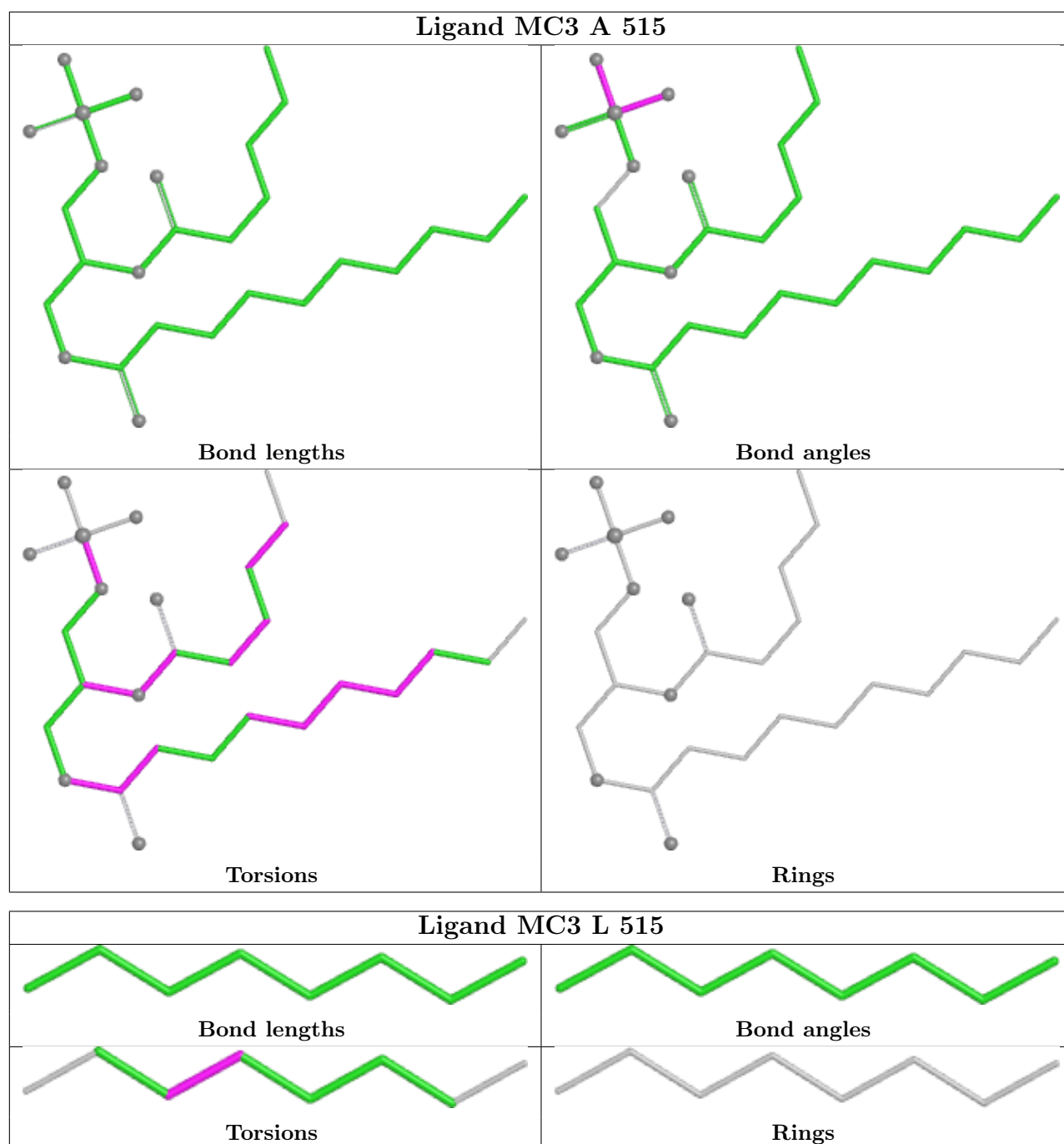


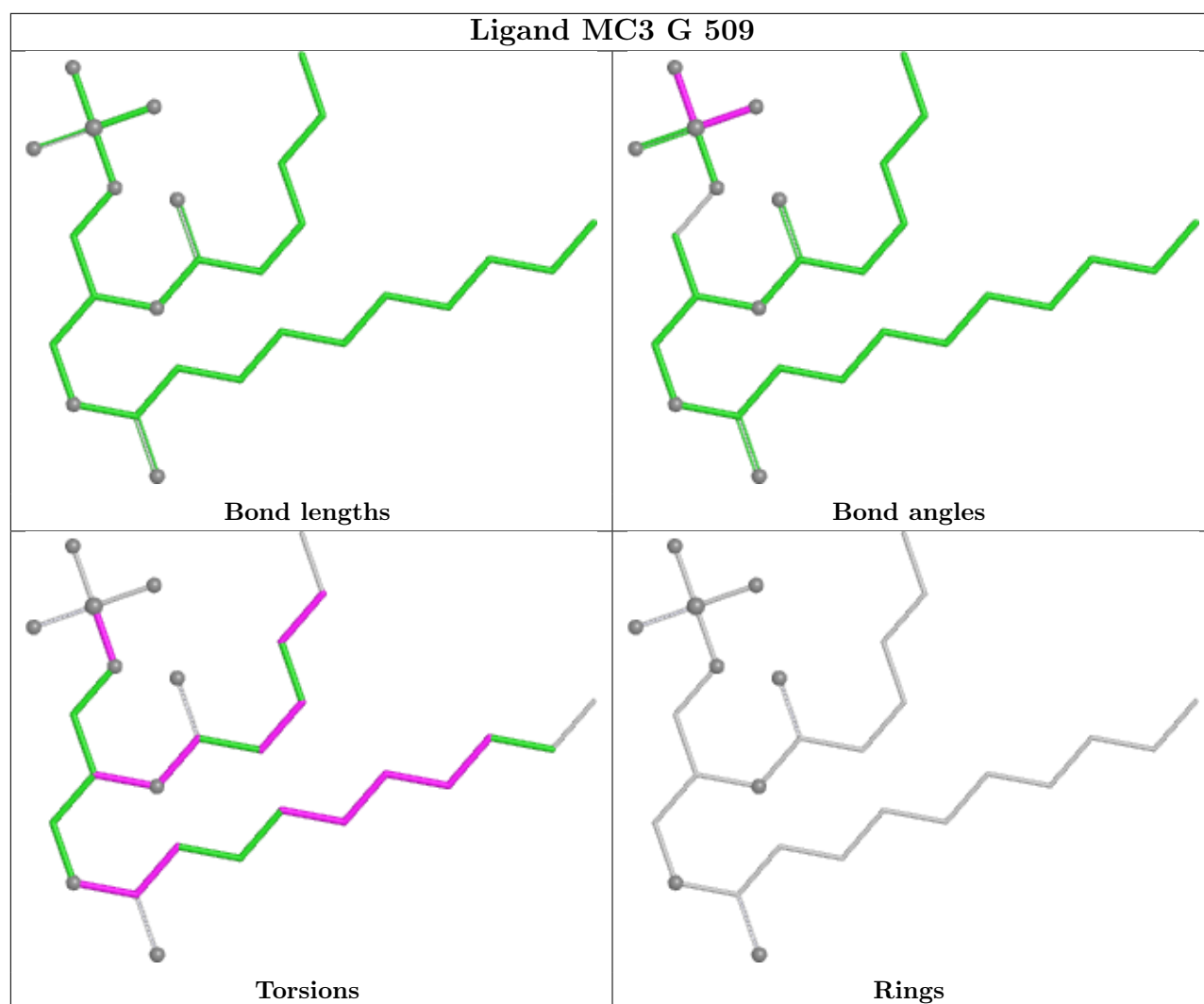


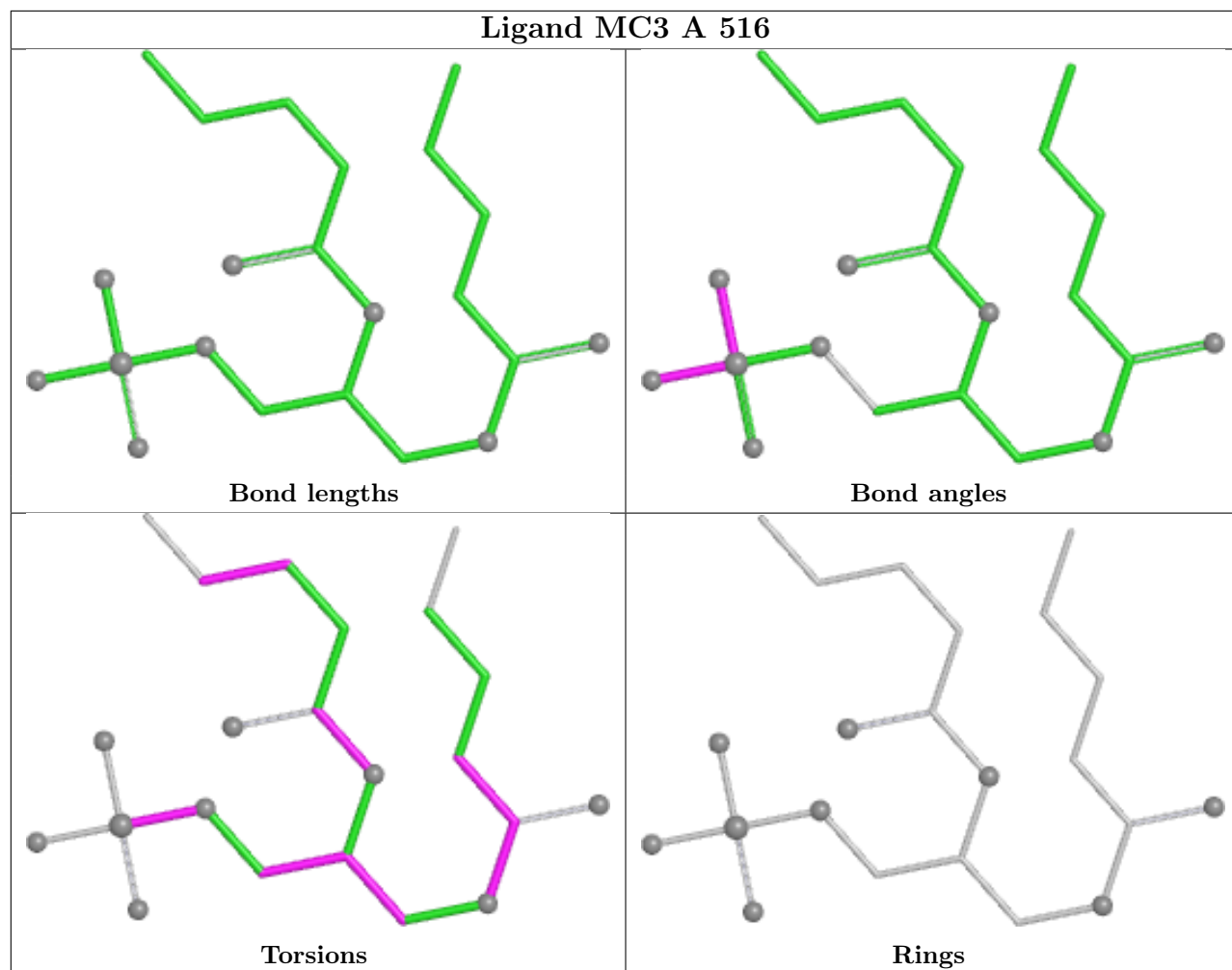


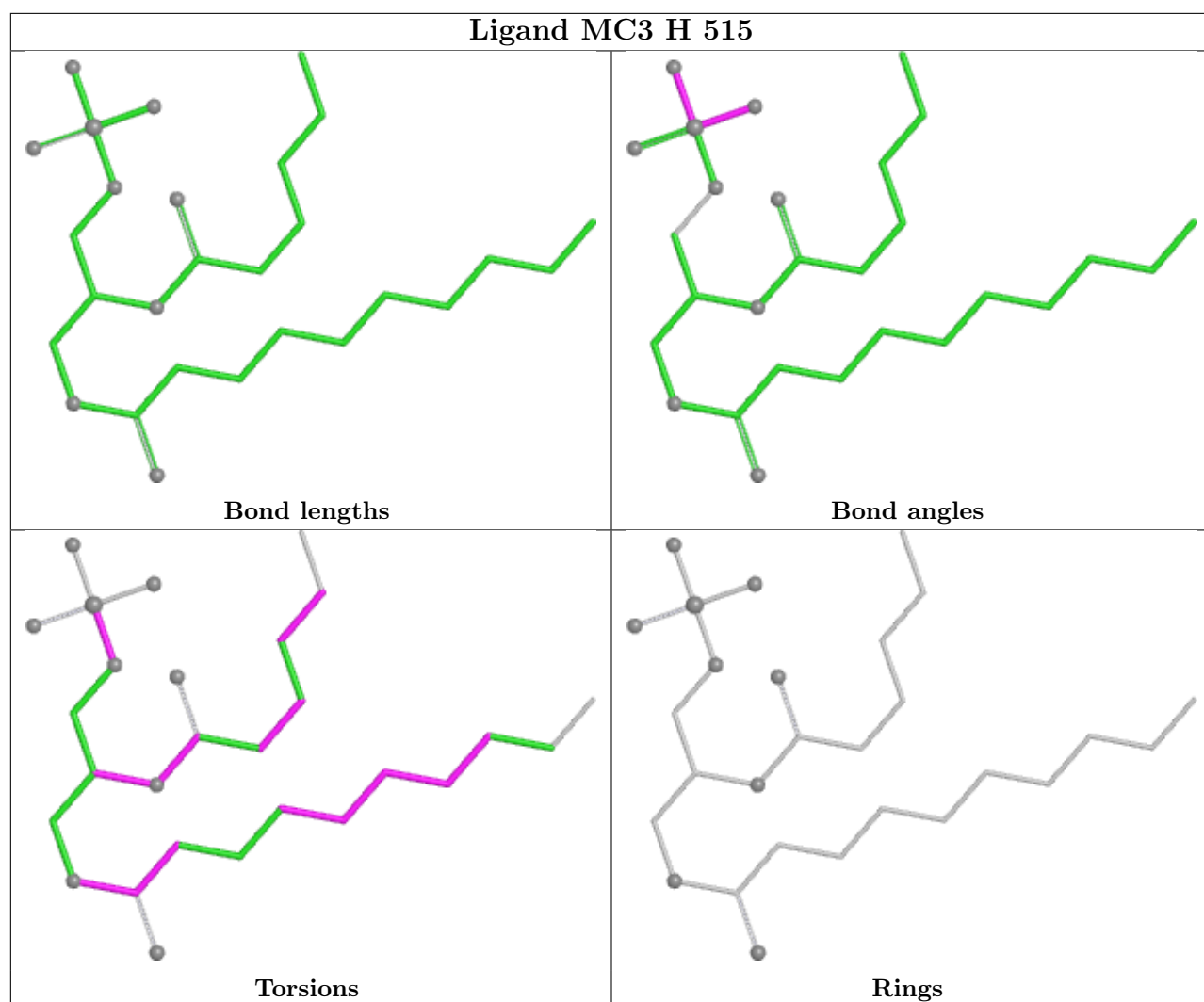


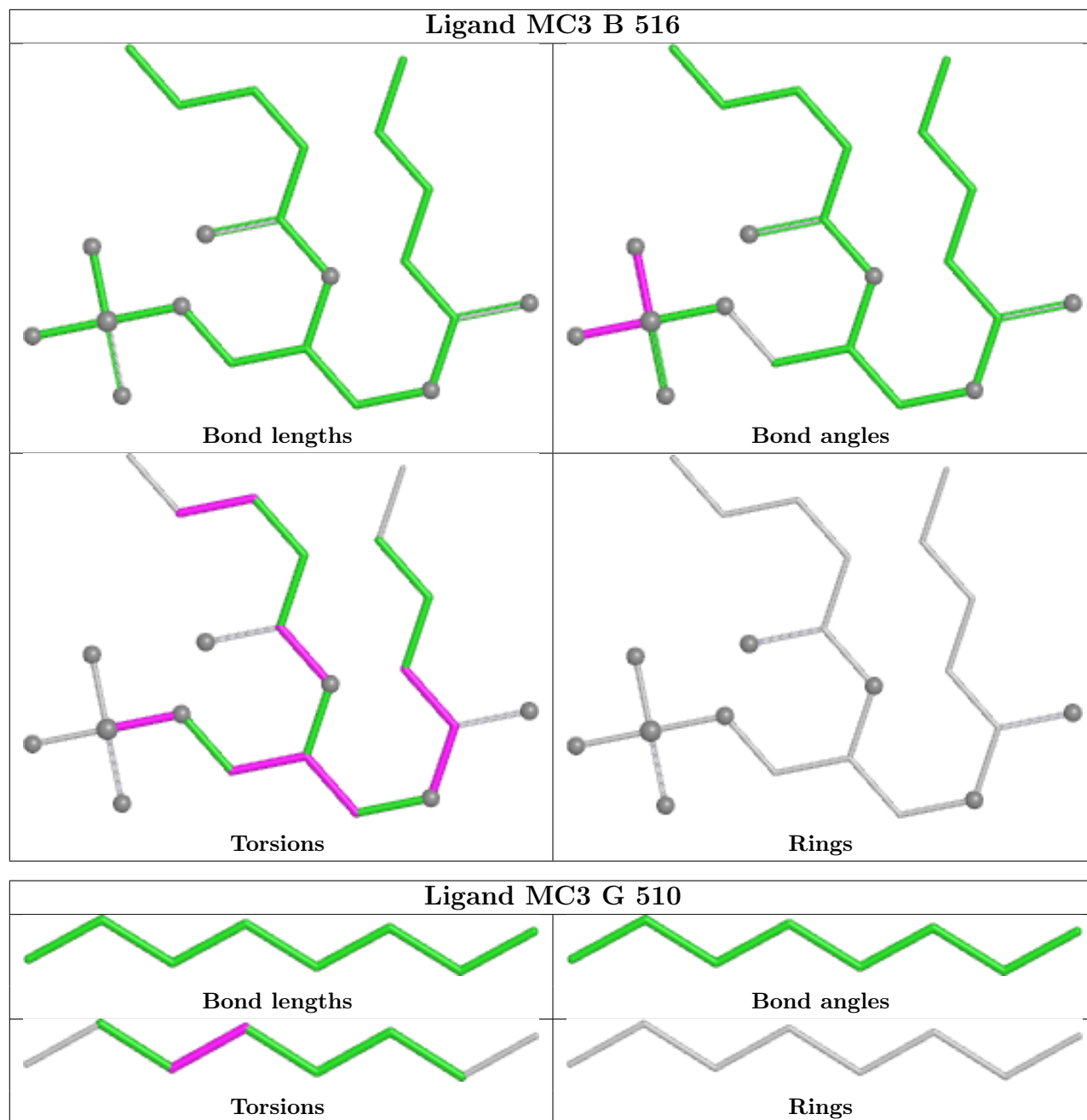


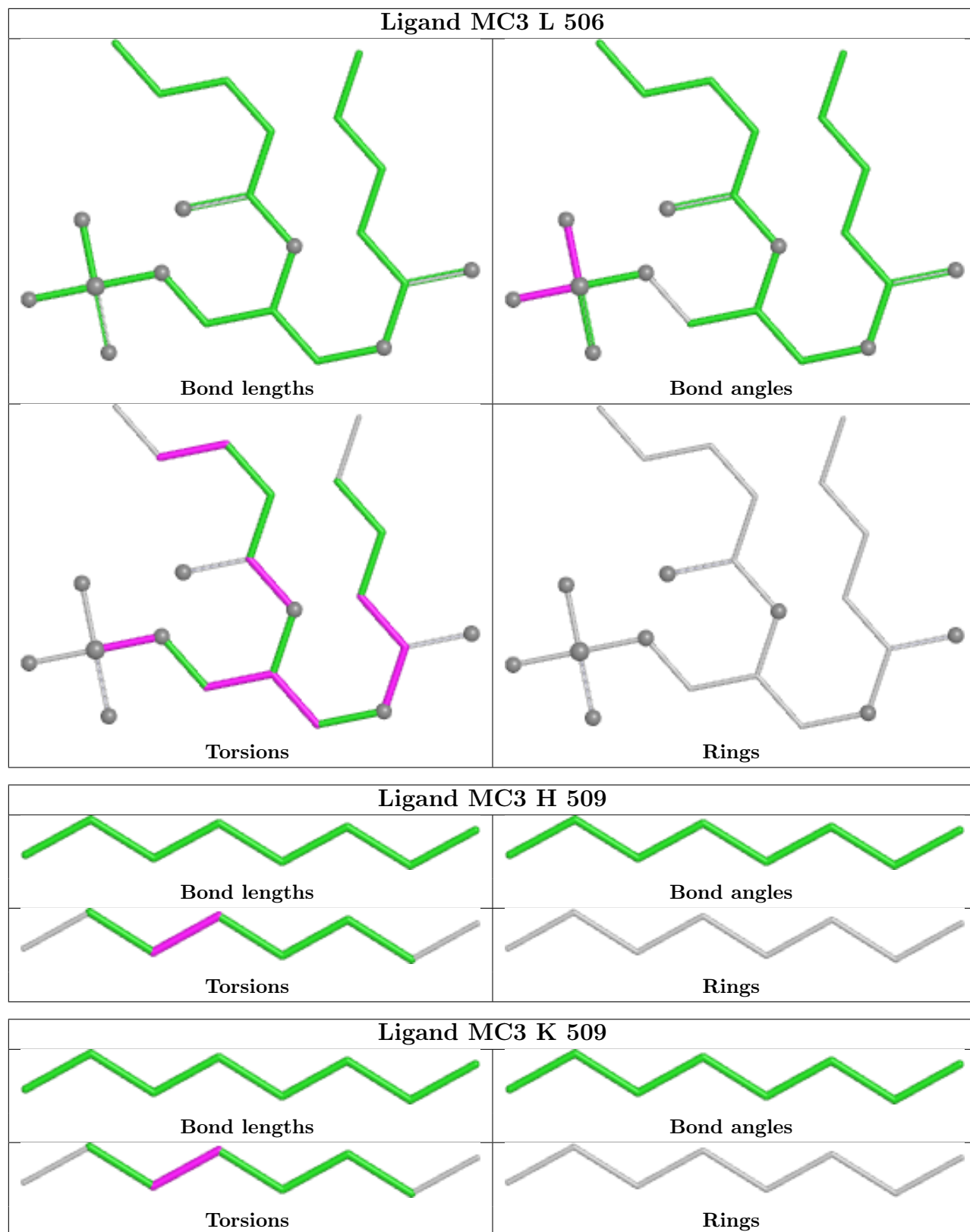


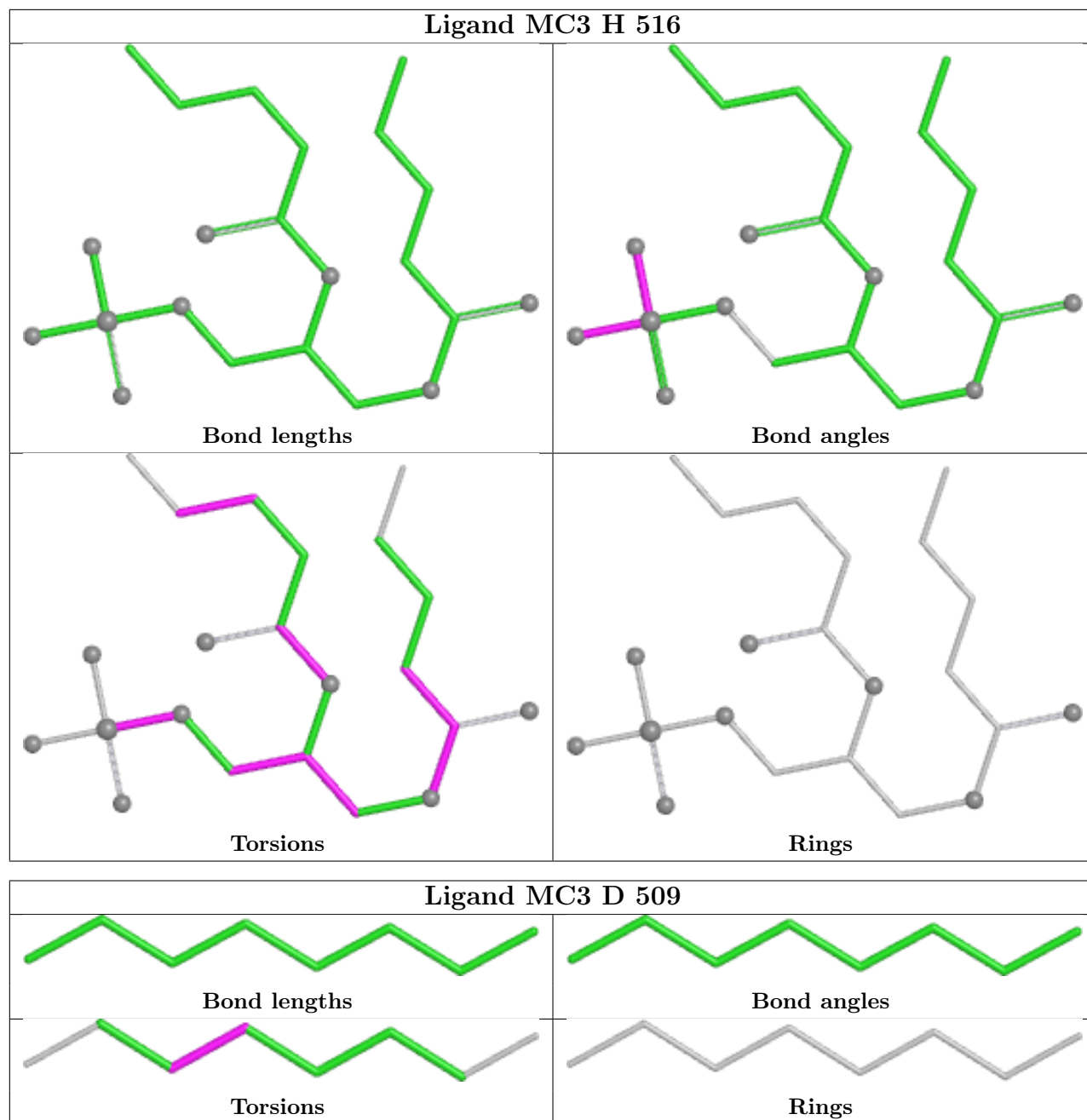


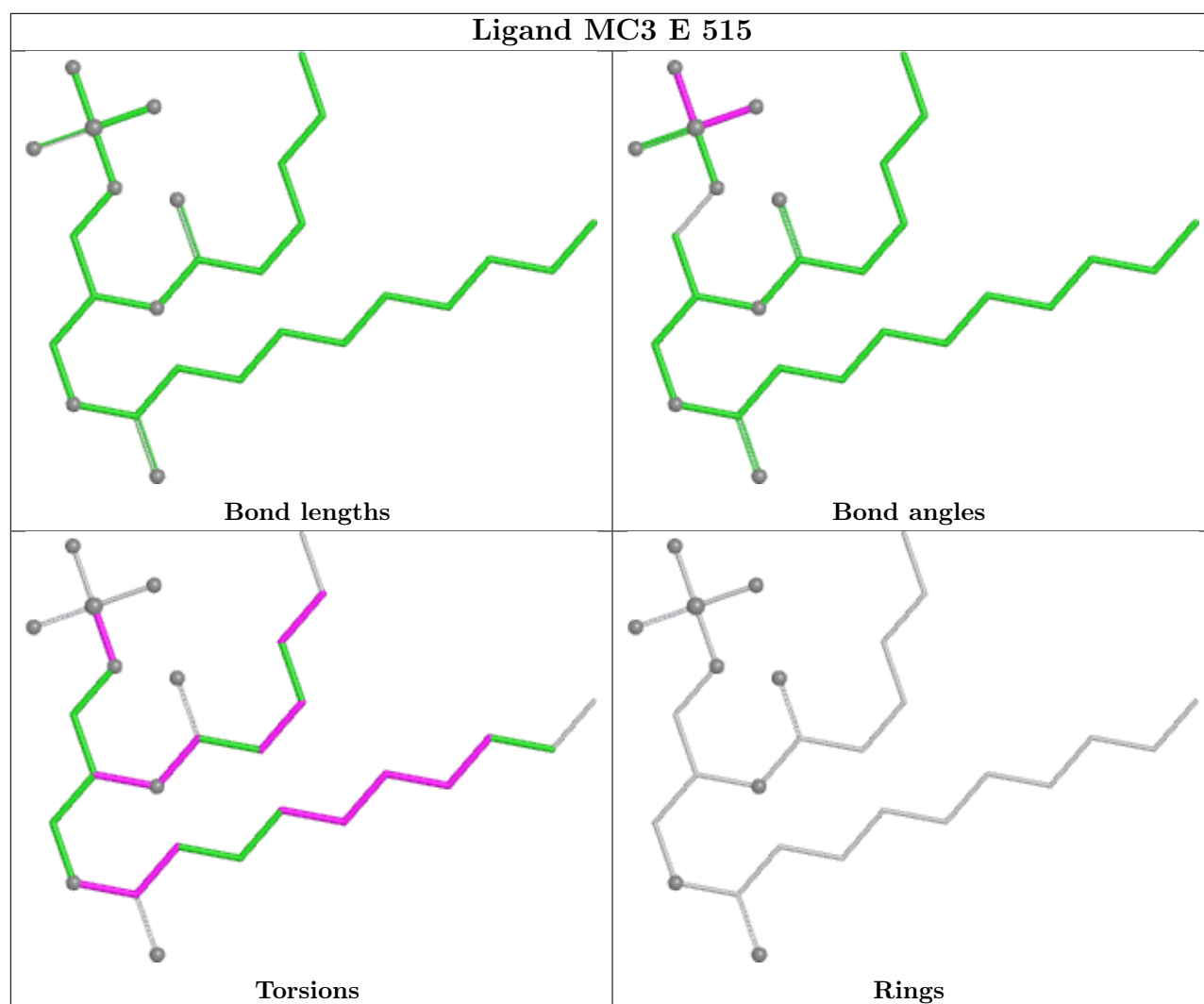


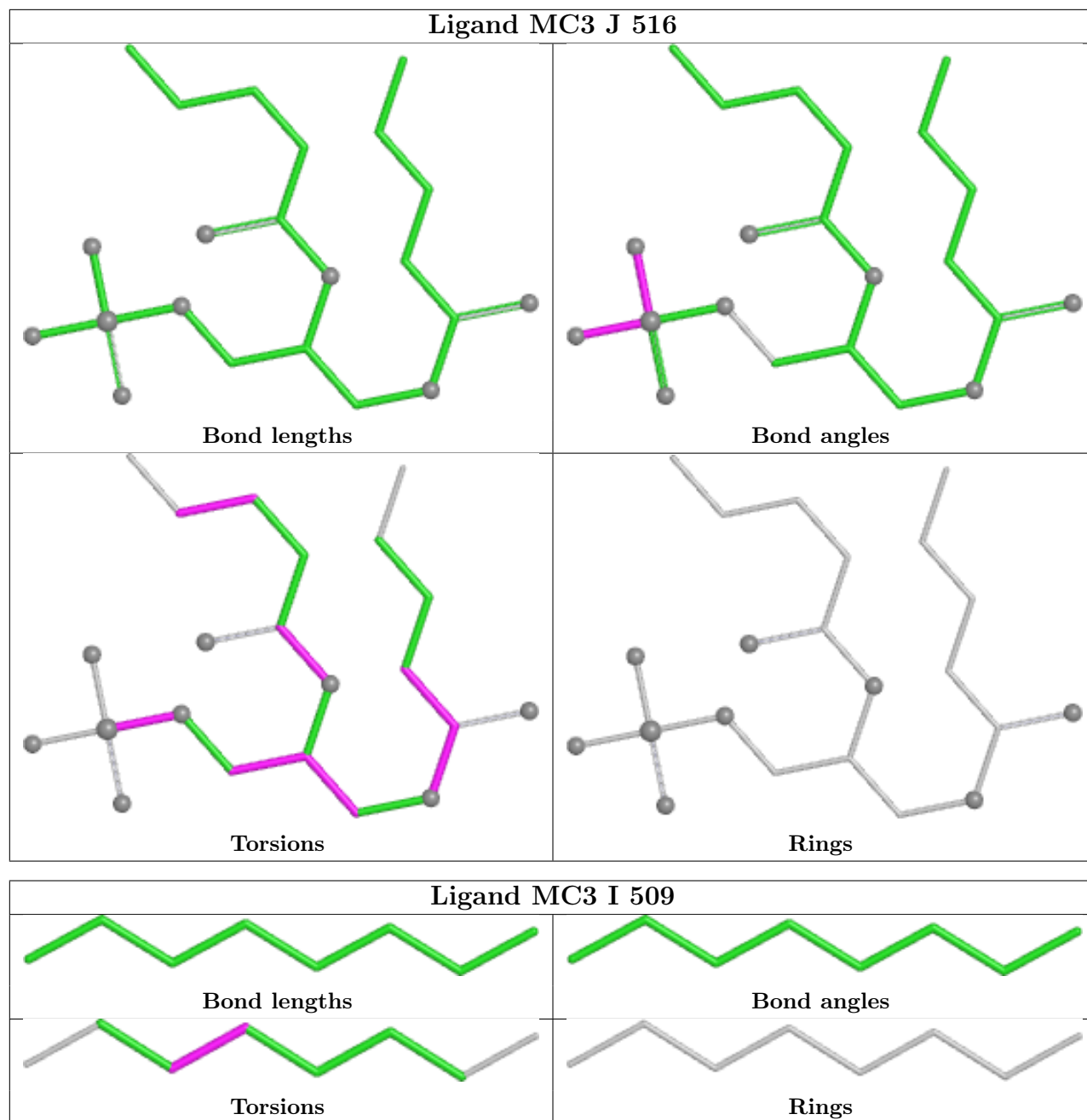


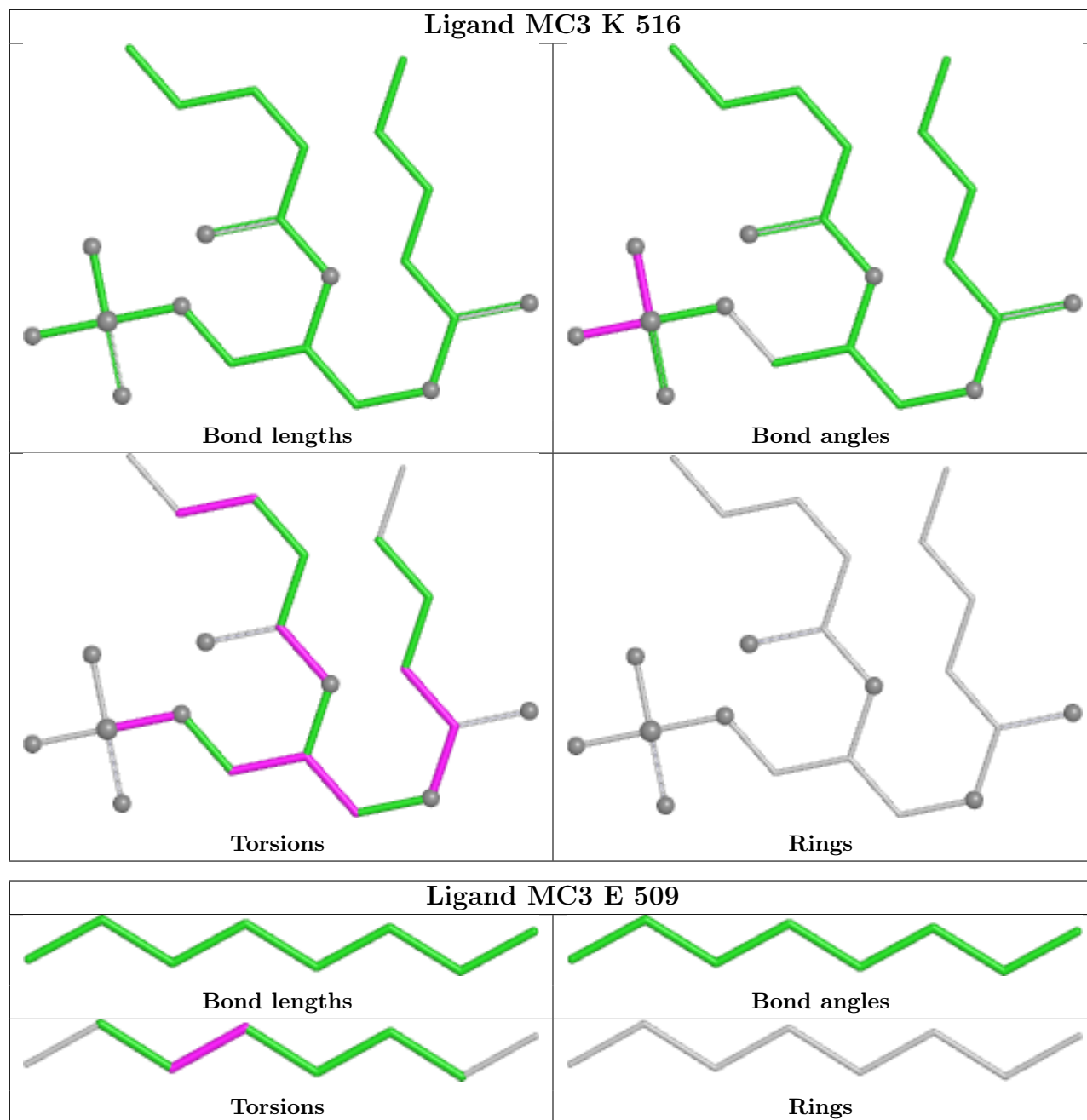


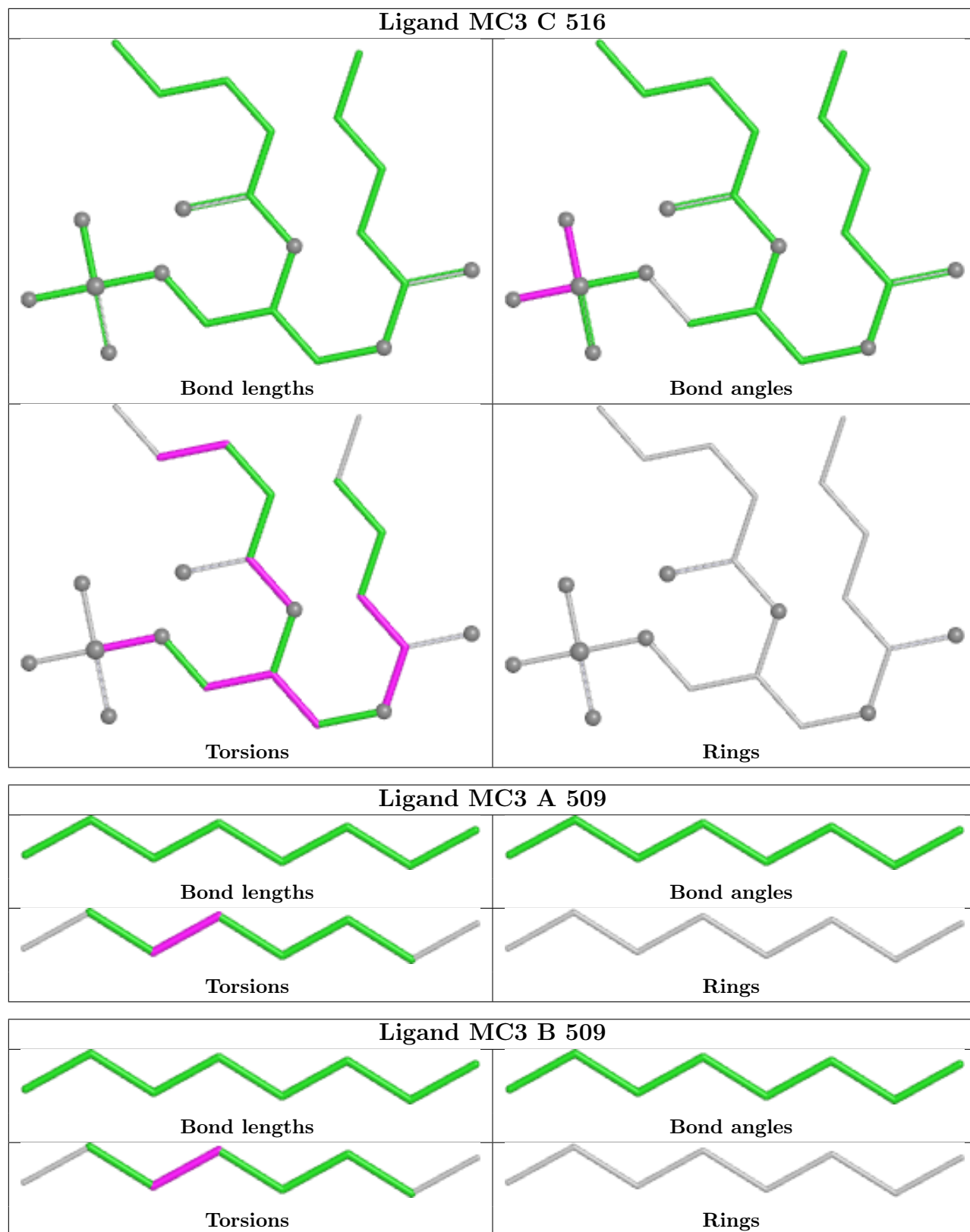


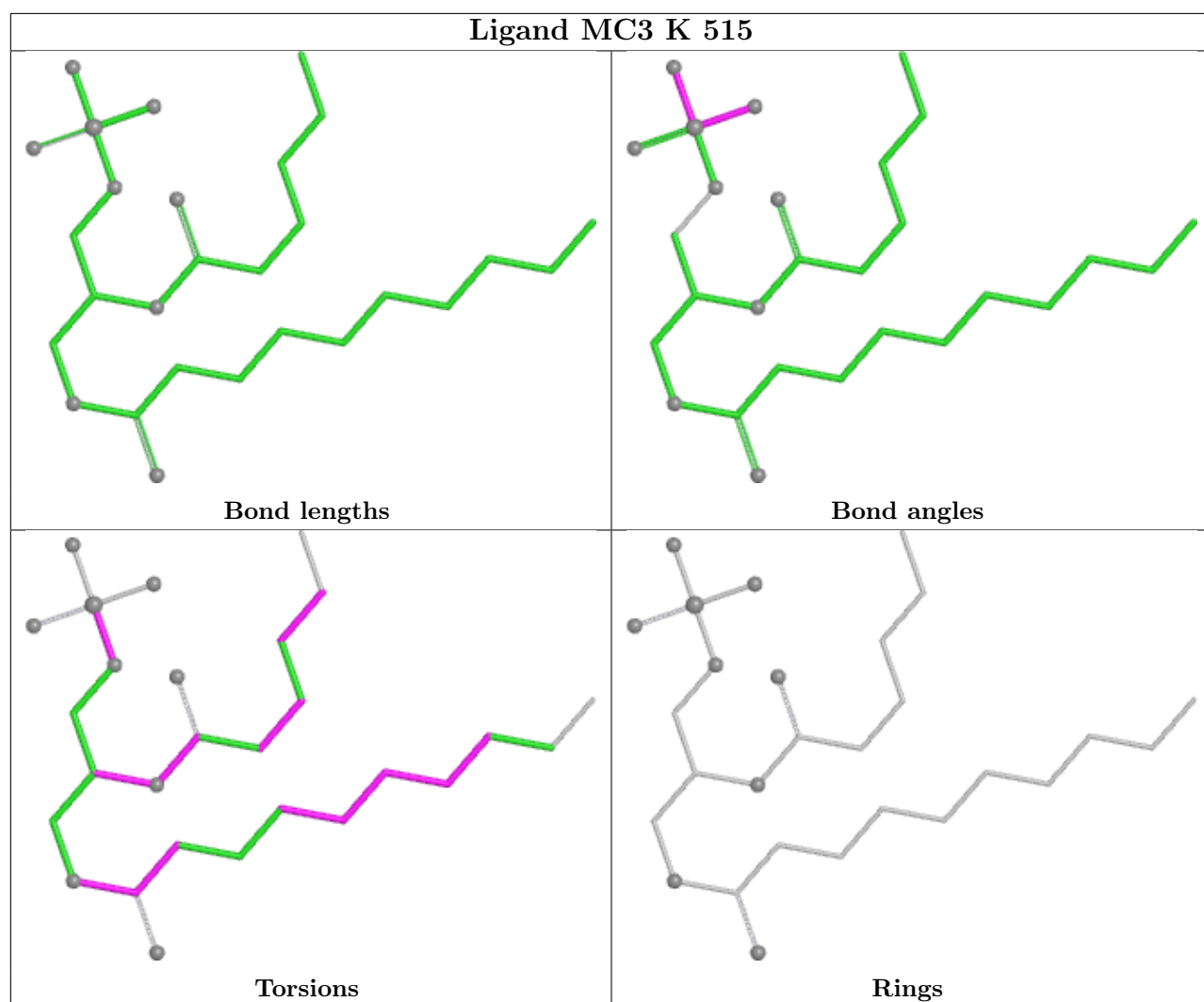


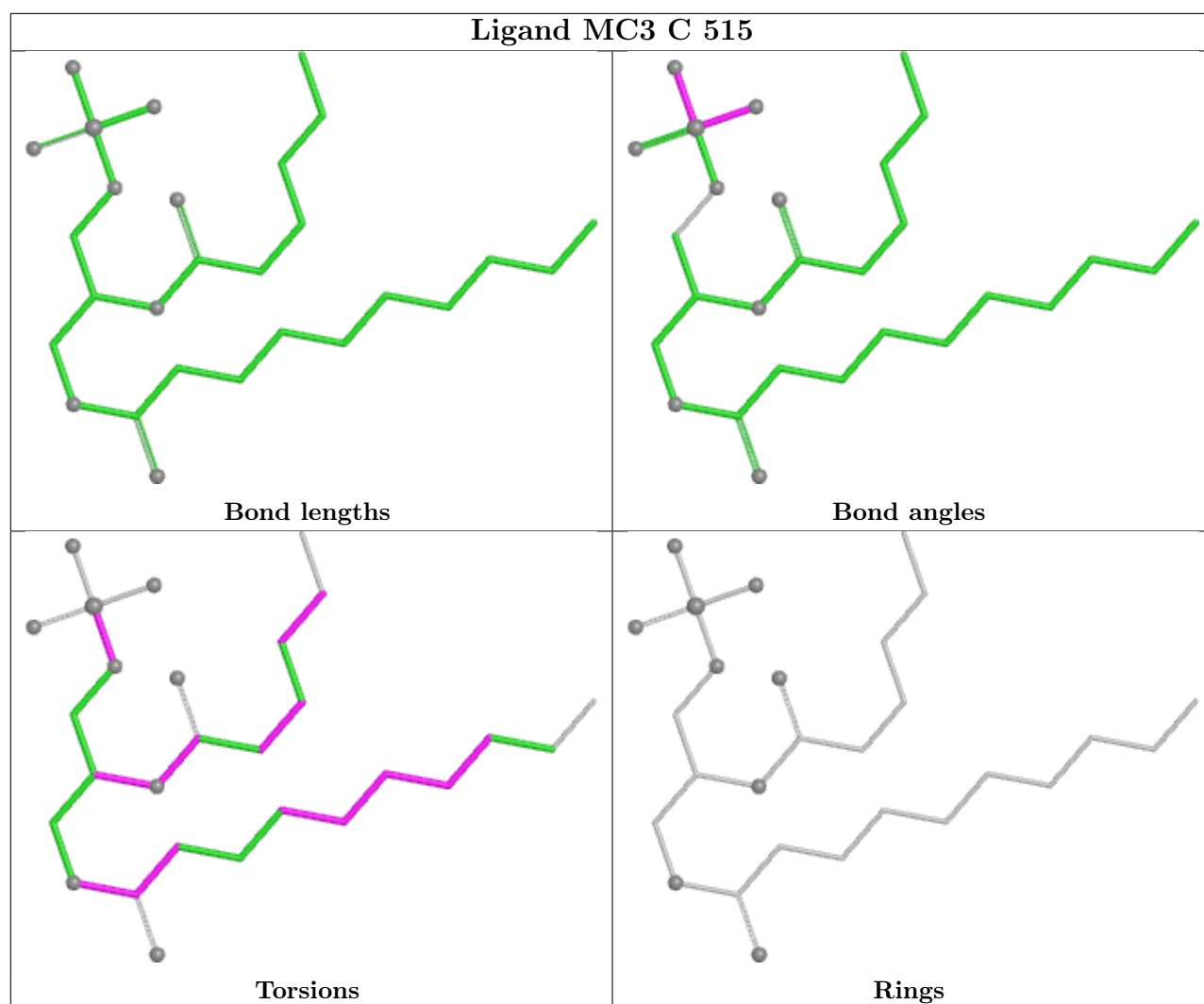












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

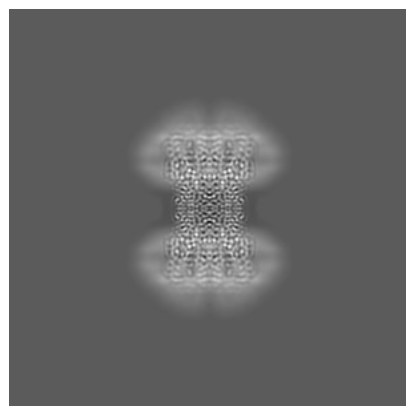
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73900. These allow visual inspection of the internal detail of the map and identification of artifacts.

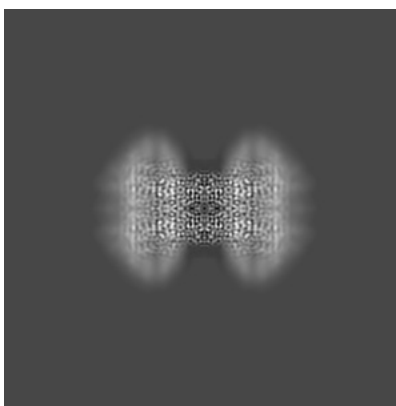
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

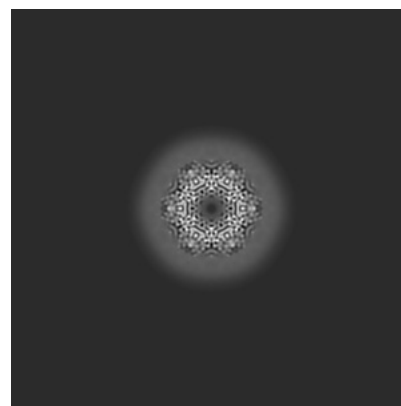
6.1.1 Primary map



X

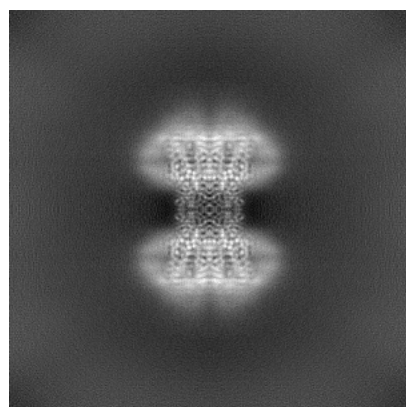


Y

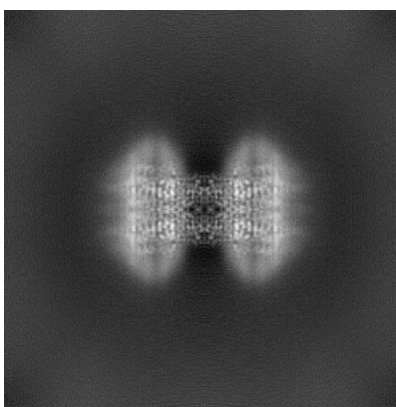


Z

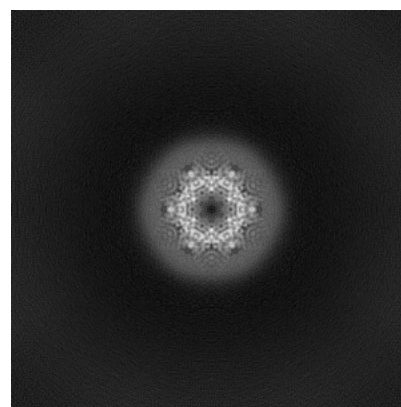
6.1.2 Raw map



X



Y

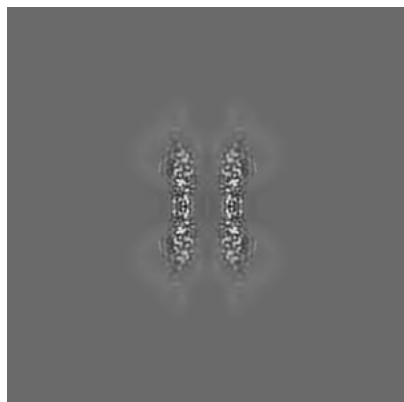


Z

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

6.2 Central slices [i](#)

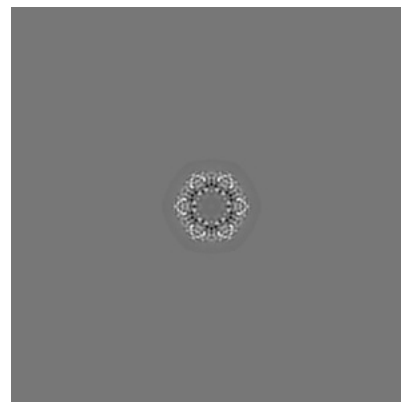
6.2.1 Primary map



X Index: 192

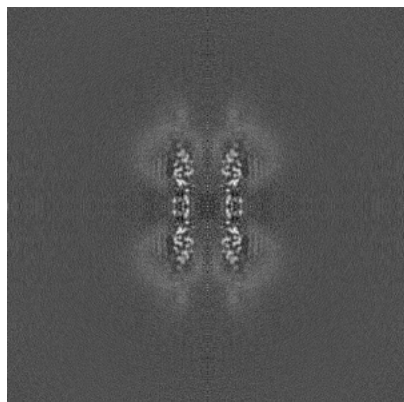


Y Index: 192

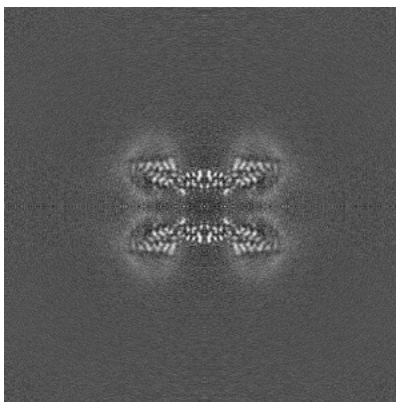


Z Index: 192

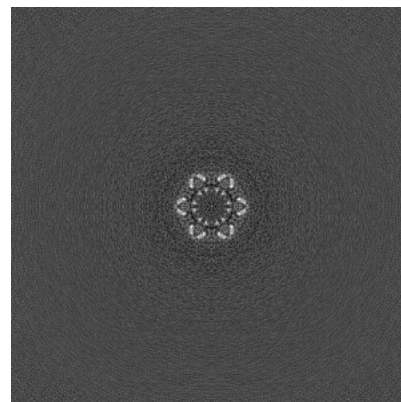
6.2.2 Raw map



X Index: 192



Y Index: 192



Z Index: 192

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

6.3 Largest variance slices [i](#)

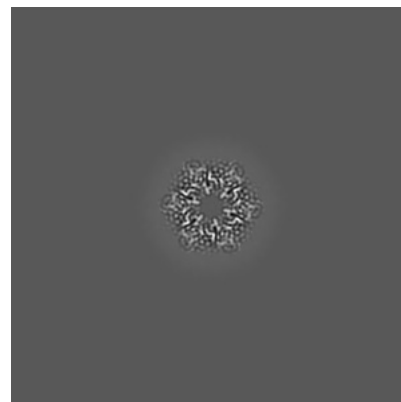
6.3.1 Primary map



X Index: 175

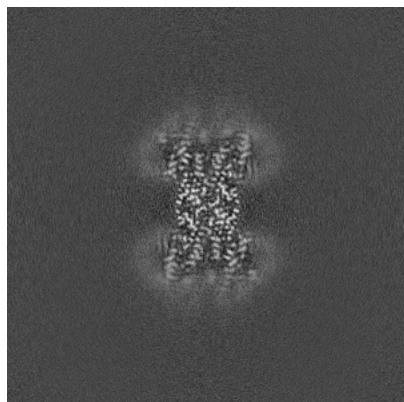


Y Index: 172

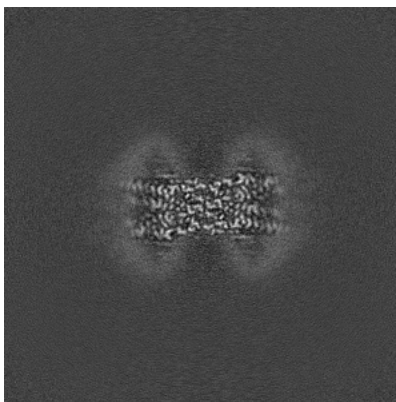


Z Index: 162

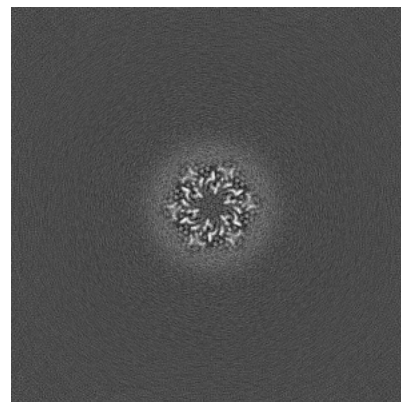
6.3.2 Raw map



X Index: 175



Y Index: 172

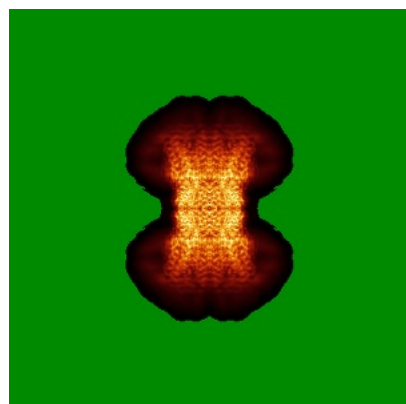


Z Index: 222

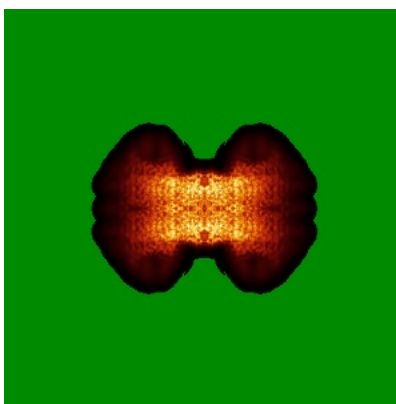
The images above show the largest variance slices of the map in three orthogonal directions.

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

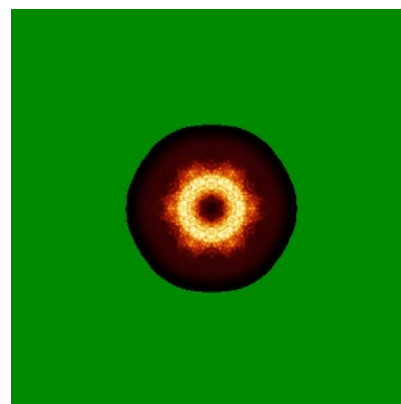
6.4.1 Primary map



X

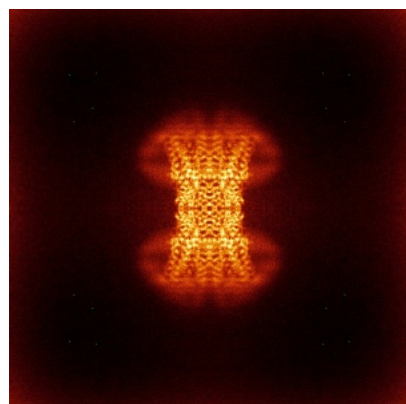


Y

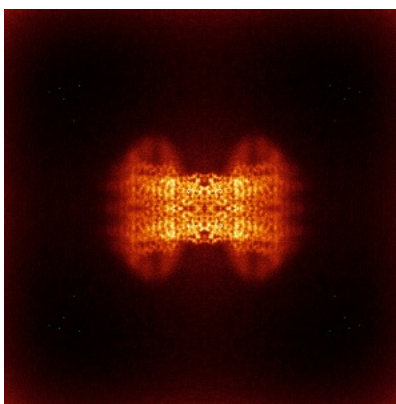


Z

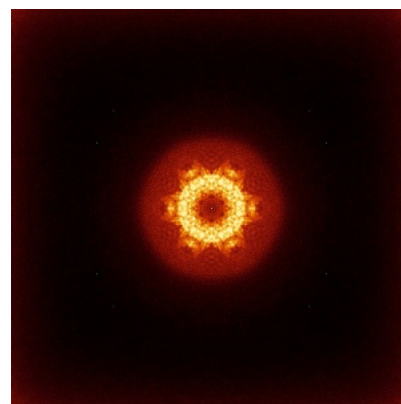
6.4.2 Raw map



X



Y

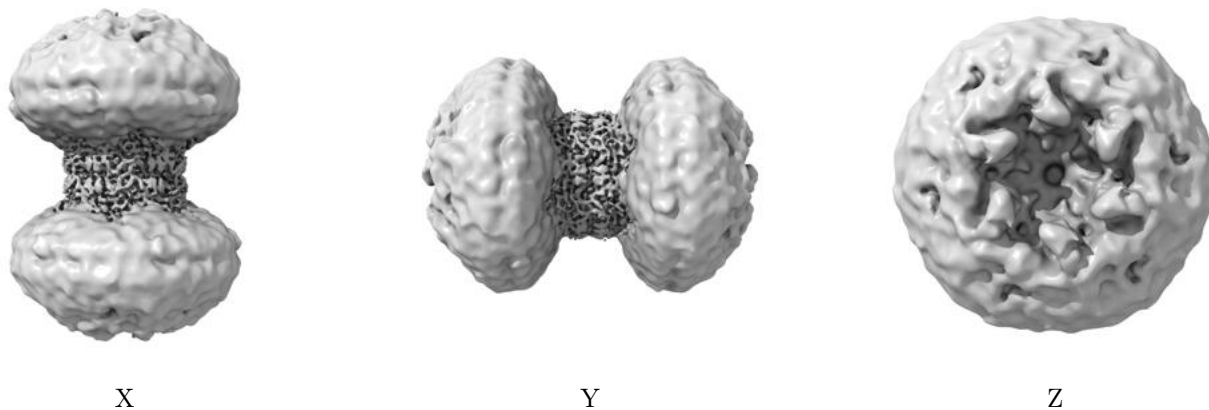


Z

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

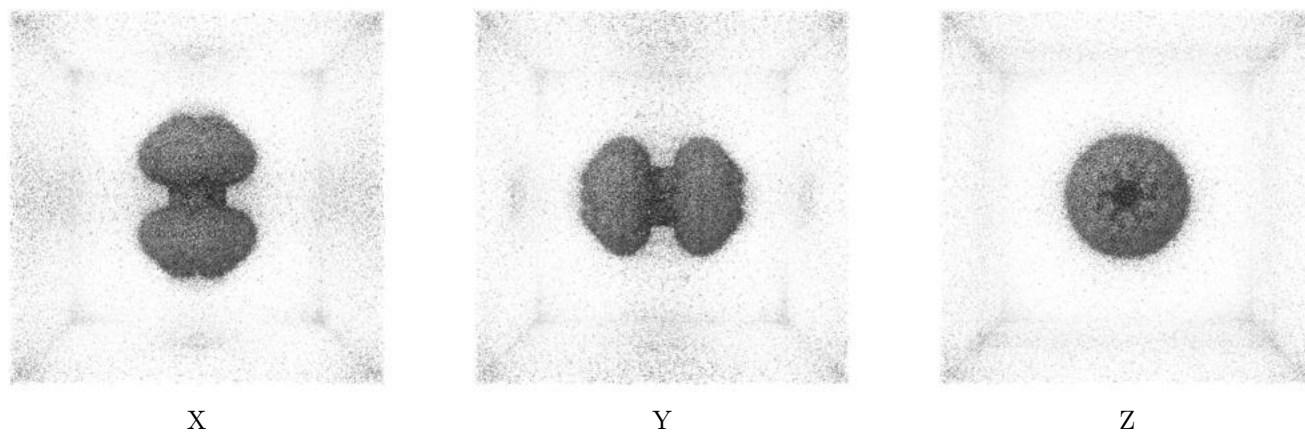
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

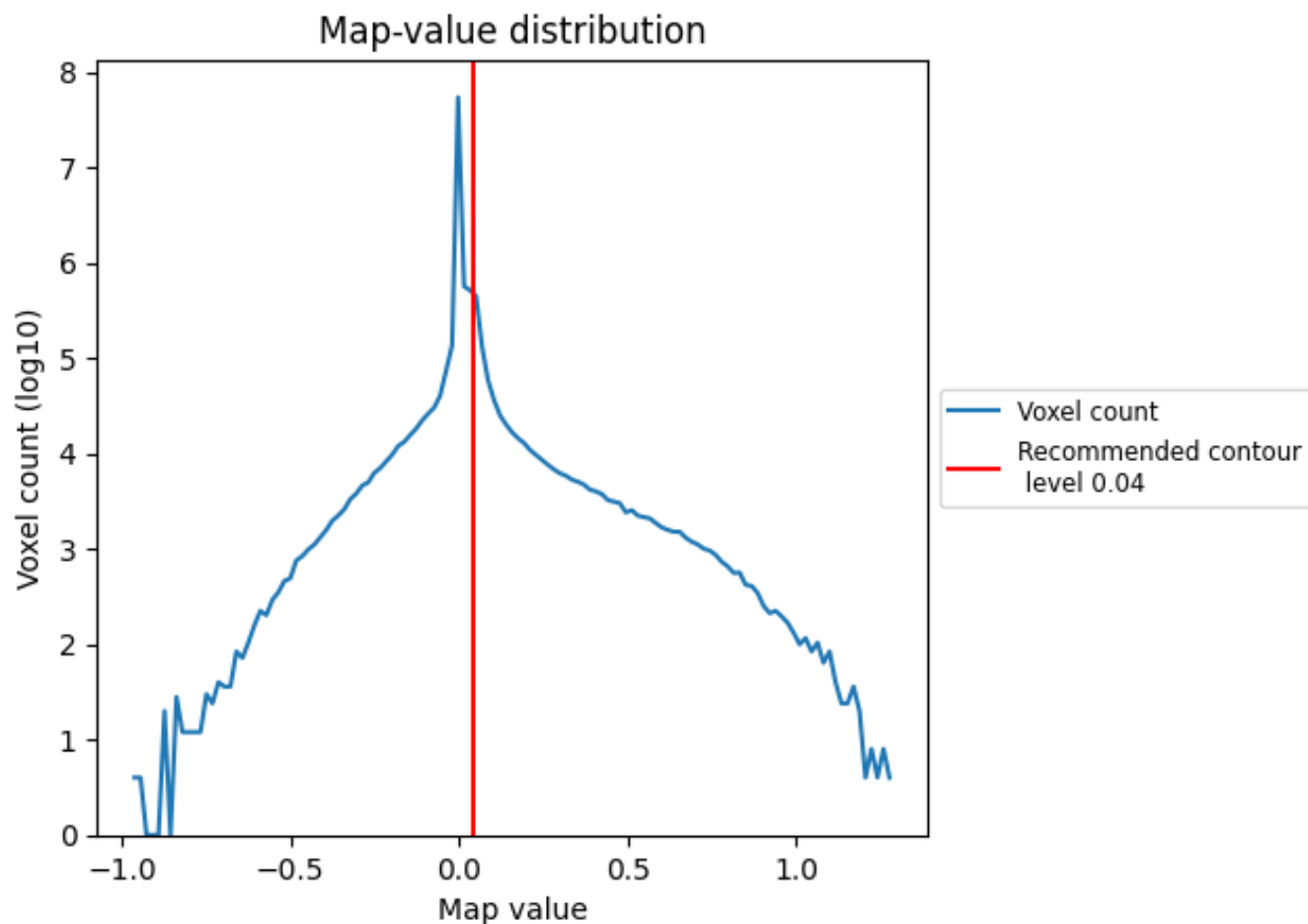
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

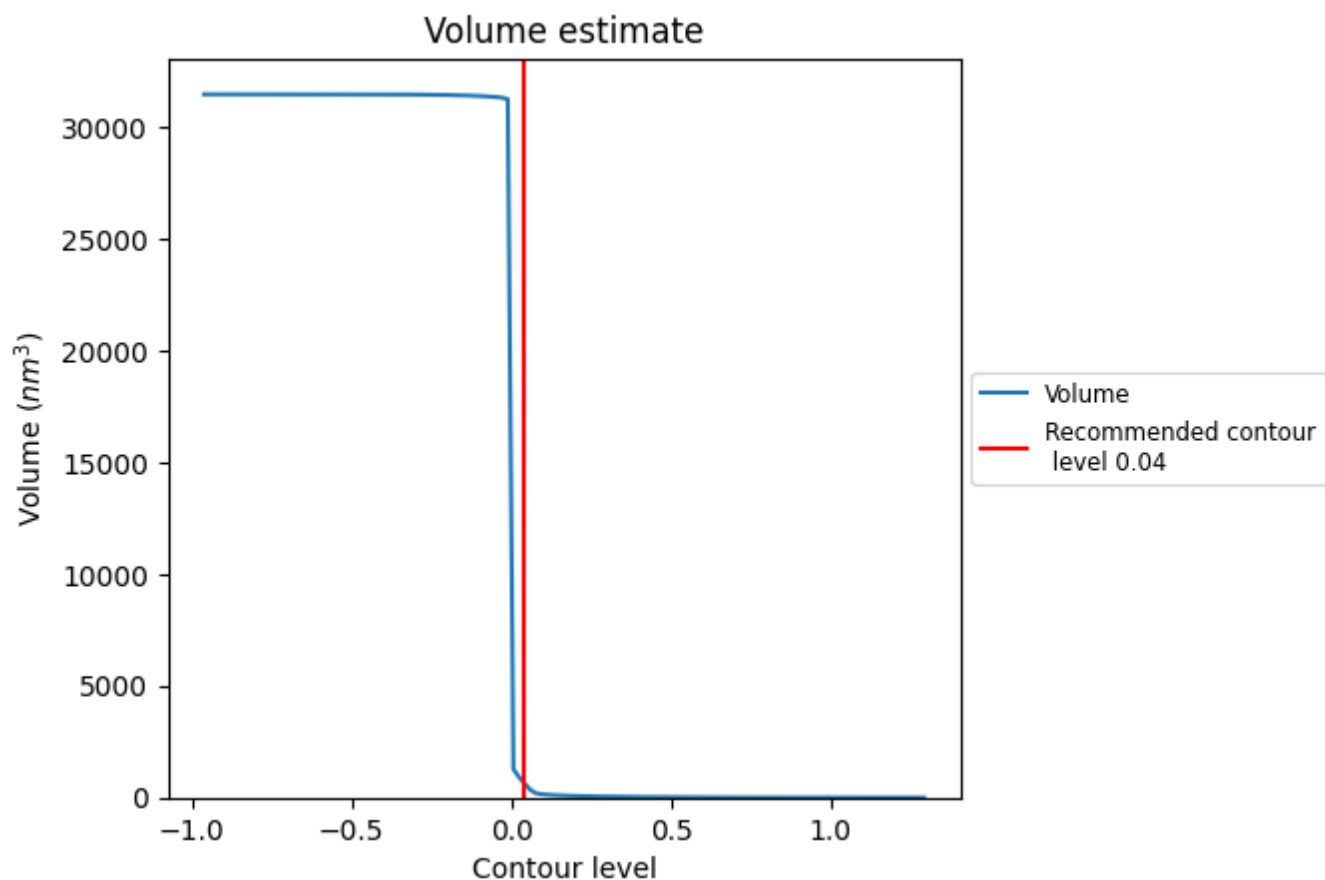
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

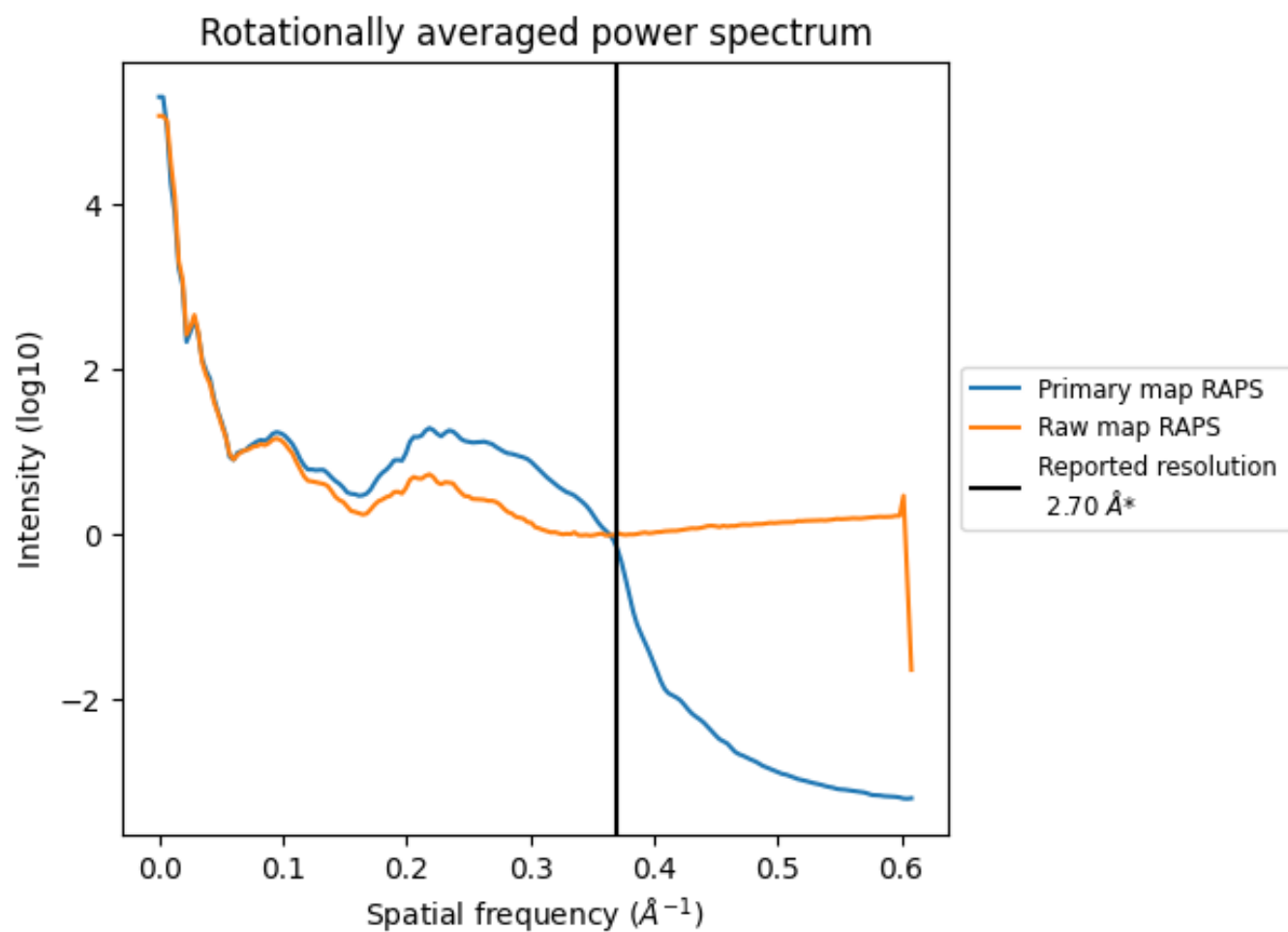
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 665 nm³; this corresponds to an approximate mass of 601 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 ⓘ

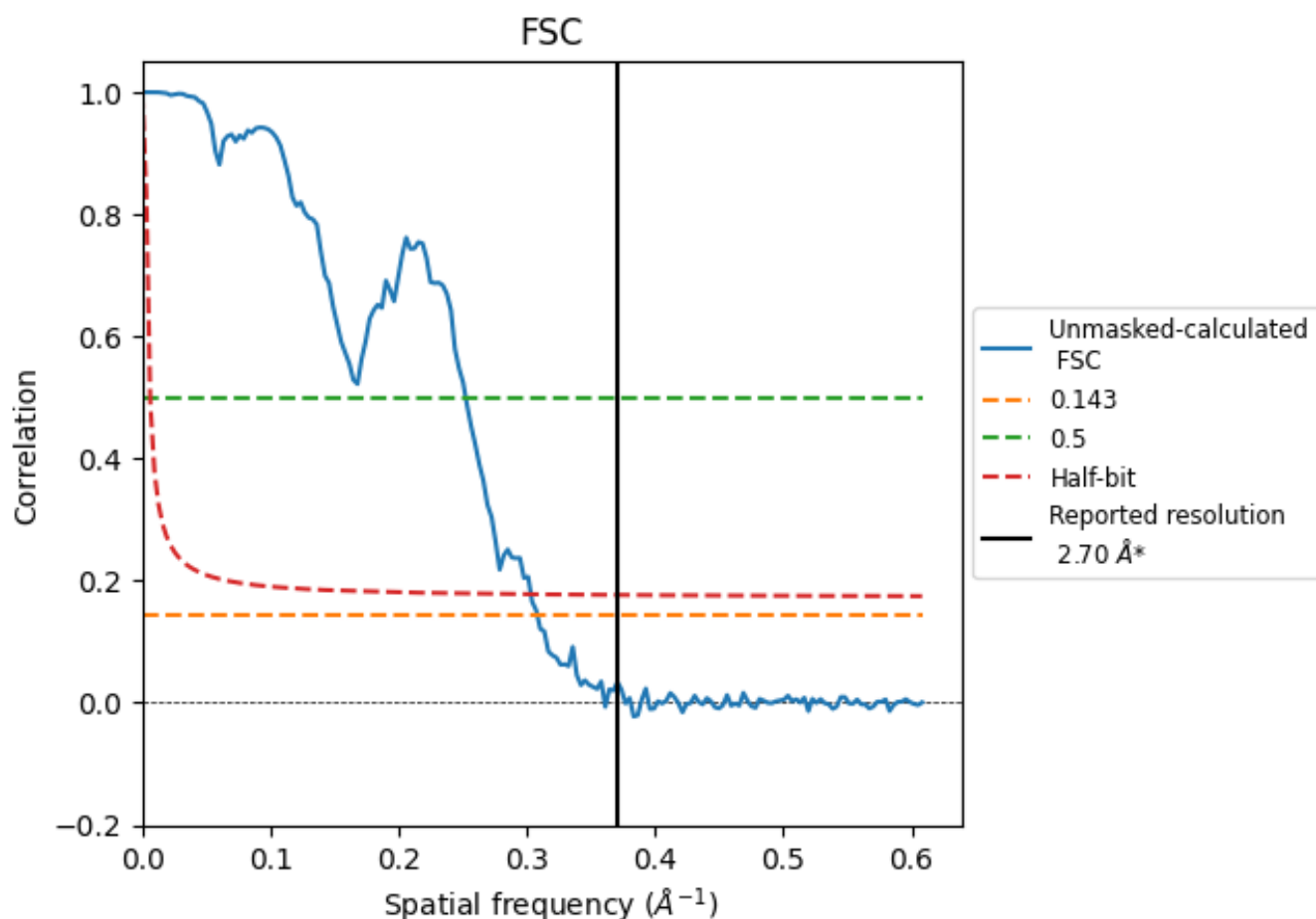


*Reported resolution corresponds to spatial frequency of $0.370 \text{ \AA}^{-1}$

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 0.370 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.24	3.96	3.30

*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 3.24 differs from the reported value 2.7 by more than 10 %

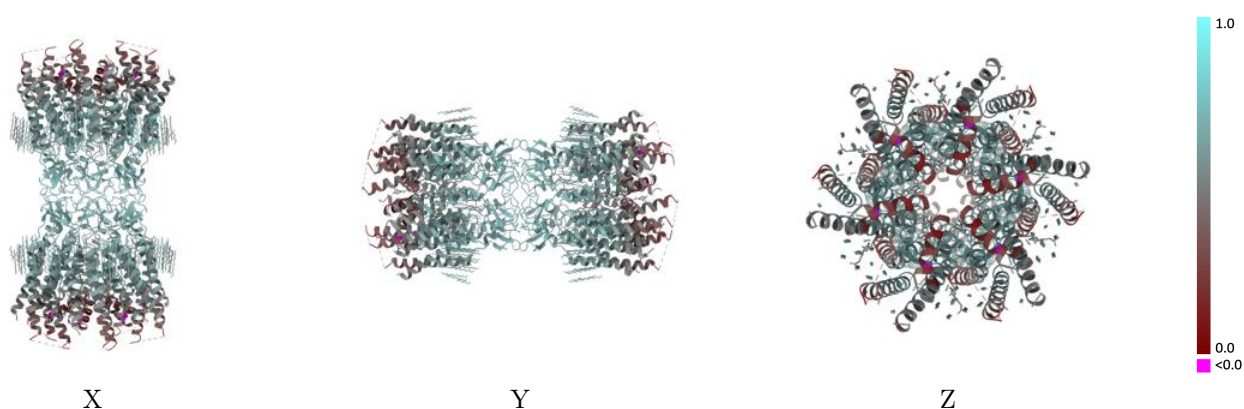
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-73900 and PDB model 9Z9B. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)

This section was not generated.

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

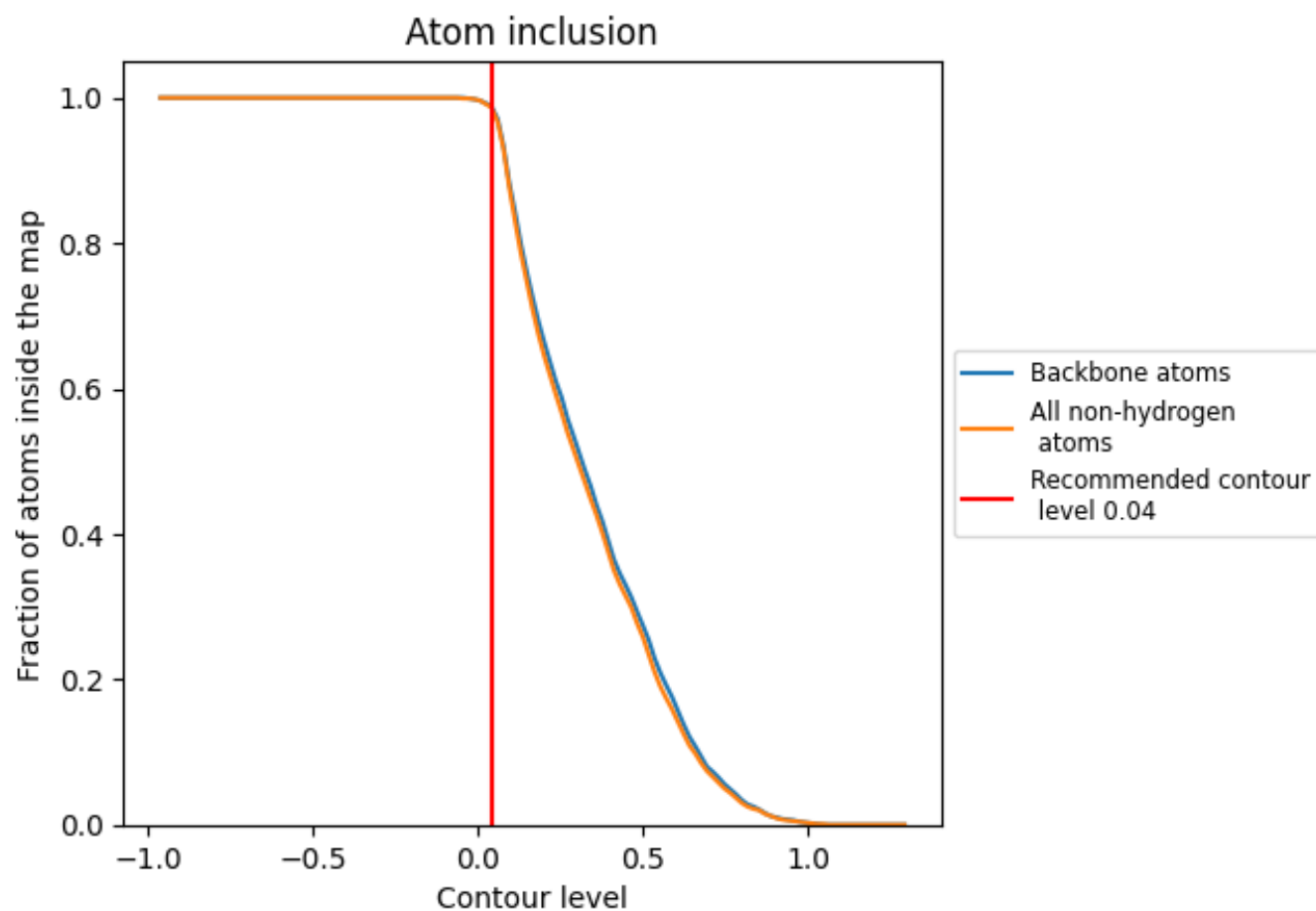


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9870	0.5540
A	0.9900	0.5560
B	0.9880	0.5530
C	0.9880	0.5540
D	0.9890	0.5560
E	0.9880	0.5540
F	0.9890	0.5550
G	0.9870	0.5530
H	0.9890	0.5560
I	0.9870	0.5540
J	0.9880	0.5530
K	0.9880	0.5510
L	0.9860	0.5520

1.0

0.0

<0.0