



Full wwPDB EM Validation Report ⓘ

Nov 4, 2024 – 06:53 AM EST

PDB ID : 8T1B
EMDB ID : EMD-40958
Title : Cryo-EM structure of full-length human TRPV4 in apo state
Authors : Nadezhdin, K.D.; Talyzina, I.A.; Neuberger, A.; Sobolevsky, A.I.
Deposited on : 2023-06-02
Resolution : 3.00 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

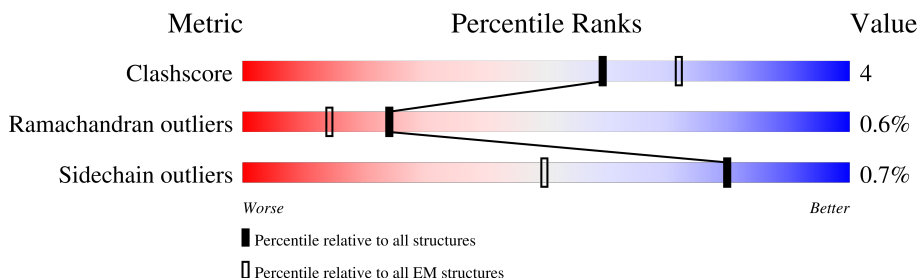
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

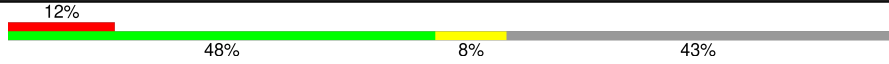
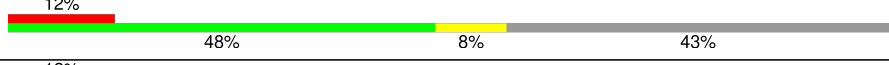
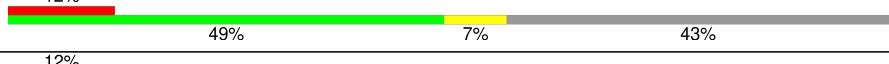
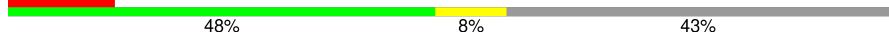
The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1132	
1	B	1132	
1	C	1132	
1	D	1132	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 23180 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Transient receptor potential cation channel subfamily V member 4/Enhanced green fluorescent protein chimera.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	644	Total	C	N	O	S	0	0
			5176	3364	859	926	27		
1	B	644	Total	C	N	O	S	0	0
			5176	3364	859	926	27		
1	C	644	Total	C	N	O	S	0	0
			5176	3364	859	926	27		
1	D	644	Total	C	N	O	S	0	0
			5176	3364	859	926	27		

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	872	LEU	-	linker	UNP Q9HBA0
A	873	VAL	-	linker	UNP Q9HBA0
A	874	PRO	-	linker	UNP Q9HBA0
A	875	ARG	-	linker	UNP Q9HBA0
A	876	GLY	-	linker	UNP Q9HBA0
A	877	SER	-	linker	UNP Q9HBA0
A	878	ALA	-	linker	UNP Q9HBA0
A	879	ALA	-	linker	UNP Q9HBA0
A	880	ALA	-	linker	UNP Q9HBA0
A	881	ALA	-	linker	UNP Q9HBA0
A	1087	LYS	ALA	engineered mutation	UNP C5MKY7
A	1120	SER	-	expression tag	UNP C5MKY7
A	1121	GLY	-	expression tag	UNP C5MKY7
A	1122	LEU	-	expression tag	UNP C5MKY7
A	1123	ARG	-	expression tag	UNP C5MKY7
A	1124	SER	-	expression tag	UNP C5MKY7
A	1125	TRP	-	expression tag	UNP C5MKY7
A	1126	SER	-	expression tag	UNP C5MKY7
A	1127	HIS	-	expression tag	UNP C5MKY7
A	1128	PRO	-	expression tag	UNP C5MKY7
A	1129	GLN	-	expression tag	UNP C5MKY7

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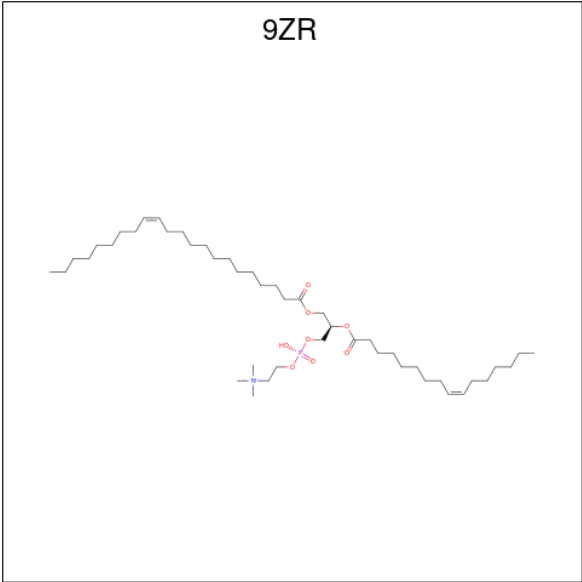
Chain	Residue	Modelled	Actual	Comment	Reference
A	1130	PHE	-	expression tag	UNP C5MKY7
A	1131	GLU	-	expression tag	UNP C5MKY7
A	1132	LYS	-	expression tag	UNP C5MKY7
B	872	LEU	-	linker	UNP Q9HBA0
B	873	VAL	-	linker	UNP Q9HBA0
B	874	PRO	-	linker	UNP Q9HBA0
B	875	ARG	-	linker	UNP Q9HBA0
B	876	GLY	-	linker	UNP Q9HBA0
B	877	SER	-	linker	UNP Q9HBA0
B	878	ALA	-	linker	UNP Q9HBA0
B	879	ALA	-	linker	UNP Q9HBA0
B	880	ALA	-	linker	UNP Q9HBA0
B	881	ALA	-	linker	UNP Q9HBA0
B	1087	LYS	ALA	engineered mutation	UNP C5MKY7
B	1120	SER	-	expression tag	UNP C5MKY7
B	1121	GLY	-	expression tag	UNP C5MKY7
B	1122	LEU	-	expression tag	UNP C5MKY7
B	1123	ARG	-	expression tag	UNP C5MKY7
B	1124	SER	-	expression tag	UNP C5MKY7
B	1125	TRP	-	expression tag	UNP C5MKY7
B	1126	SER	-	expression tag	UNP C5MKY7
B	1127	HIS	-	expression tag	UNP C5MKY7
B	1128	PRO	-	expression tag	UNP C5MKY7
B	1129	GLN	-	expression tag	UNP C5MKY7
B	1130	PHE	-	expression tag	UNP C5MKY7
B	1131	GLU	-	expression tag	UNP C5MKY7
B	1132	LYS	-	expression tag	UNP C5MKY7
C	872	LEU	-	linker	UNP Q9HBA0
C	873	VAL	-	linker	UNP Q9HBA0
C	874	PRO	-	linker	UNP Q9HBA0
C	875	ARG	-	linker	UNP Q9HBA0
C	876	GLY	-	linker	UNP Q9HBA0
C	877	SER	-	linker	UNP Q9HBA0
C	878	ALA	-	linker	UNP Q9HBA0
C	879	ALA	-	linker	UNP Q9HBA0
C	880	ALA	-	linker	UNP Q9HBA0
C	881	ALA	-	linker	UNP Q9HBA0
C	1087	LYS	ALA	engineered mutation	UNP C5MKY7
C	1120	SER	-	expression tag	UNP C5MKY7
C	1121	GLY	-	expression tag	UNP C5MKY7
C	1122	LEU	-	expression tag	UNP C5MKY7
C	1123	ARG	-	expression tag	UNP C5MKY7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1124	SER	-	expression tag	UNP C5MKY7
C	1125	TRP	-	expression tag	UNP C5MKY7
C	1126	SER	-	expression tag	UNP C5MKY7
C	1127	HIS	-	expression tag	UNP C5MKY7
C	1128	PRO	-	expression tag	UNP C5MKY7
C	1129	GLN	-	expression tag	UNP C5MKY7
C	1130	PHE	-	expression tag	UNP C5MKY7
C	1131	GLU	-	expression tag	UNP C5MKY7
C	1132	LYS	-	expression tag	UNP C5MKY7
D	872	LEU	-	linker	UNP Q9HBA0
D	873	VAL	-	linker	UNP Q9HBA0
D	874	PRO	-	linker	UNP Q9HBA0
D	875	ARG	-	linker	UNP Q9HBA0
D	876	GLY	-	linker	UNP Q9HBA0
D	877	SER	-	linker	UNP Q9HBA0
D	878	ALA	-	linker	UNP Q9HBA0
D	879	ALA	-	linker	UNP Q9HBA0
D	880	ALA	-	linker	UNP Q9HBA0
D	881	ALA	-	linker	UNP Q9HBA0
D	1087	LYS	ALA	engineered mutation	UNP C5MKY7
D	1120	SER	-	expression tag	UNP C5MKY7
D	1121	GLY	-	expression tag	UNP C5MKY7
D	1122	LEU	-	expression tag	UNP C5MKY7
D	1123	ARG	-	expression tag	UNP C5MKY7
D	1124	SER	-	expression tag	UNP C5MKY7
D	1125	TRP	-	expression tag	UNP C5MKY7
D	1126	SER	-	expression tag	UNP C5MKY7
D	1127	HIS	-	expression tag	UNP C5MKY7
D	1128	PRO	-	expression tag	UNP C5MKY7
D	1129	GLN	-	expression tag	UNP C5MKY7
D	1130	PHE	-	expression tag	UNP C5MKY7
D	1131	GLU	-	expression tag	UNP C5MKY7
D	1132	LYS	-	expression tag	UNP C5MKY7

- Molecule 2 is [(2 {R})-2-[({Z})-hexadec-9-enoyl]oxy-3-[oxidanyl-2-(trimethyl- S^4 -azanyloxy)phosphoryl]oxy-propyl] ({Z})-docos-13-enoate (three-letter code: 9ZR) (formula: $\text{C}_{46}\text{H}_{89}\text{NO}_8\text{P}$).



Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	A	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	A	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	A	1	Total	C	N	O	P	0
			44	34	1	8	1	
2	A	1	Total	C				0
			13	13				
2	A	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	A	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	A	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	A	1	Total	C	N	O	P	0
			46	36	1	8	1	
2	A	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	A	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	B	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	B	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	B	1	Total	C	N	O	P	0
			56	46	1	8	1	

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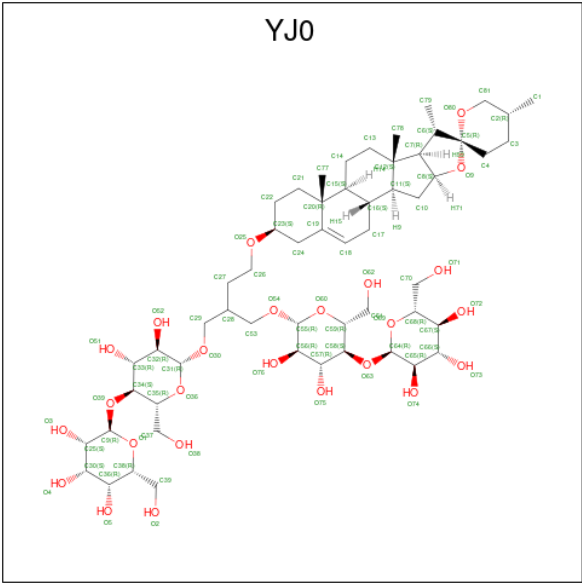
Mol	Chain	Residues	Atoms					AltConf
2	B	1	Total	C	N	O	P	0
			44	34	1	8	1	
2	B	1	Total	C				0
			13	13				
2	B	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	B	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	B	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	B	1	Total	C	N	O	P	0
			46	36	1	8	1	
2	C	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	C	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	C	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	C	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	C	1	Total	C	N	O	P	0
			44	34	1	8	1	
2	C	1	Total	C				0
			13	13				
2	C	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	C	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	C	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	C	1	Total	C	N	O	P	0
			46	36	1	8	1	
2	D	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	D	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	D	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	D	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	D	1	Total	C	N	O	P	0
			44	34	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
2	D	1	Total	C				0
			13	13				
2	D	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	D	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	D	1	Total	C	N	O	P	0
			56	46	1	8	1	
2	D	1	Total	C	N	O	P	0
			46	36	1	8	1	

- Molecule 3 is (2R)-2-{[(4-O-hexopyranosyl-beta-D-glucopyranosyl)oxy]methyl}-4-{[(25R)-5 beta,14beta,17beta-spirostan-3beta-yl]oxy}butyl 4-O-alpha-D-glucopyranosyl-beta-D-glucop yranoside (three-letter code: YJ0) (formula: C₅₆H₉₂O₂₅).



Mol	Chain	Residues	Atoms			AltConf
3	A	1	Total	C	O	0
			35	32	3	
3	A	1	Total	C	O	0
			70	50	20	
3	B	1	Total	C	O	0
			70	50	20	
3	B	1	Total	C	O	0
			35	32	3	
3	C	1	Total	C	O	0
			70	50	20	

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Mol	Chain	Residues	Atoms			AltConf
3	C	1	Total	C	O	0
			35	32	3	
3	D	1	Total	C	O	0
			70	50	20	
3	D	1	Total	C	O	0
			35	32	3	

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

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

- Molecule 5 is water.

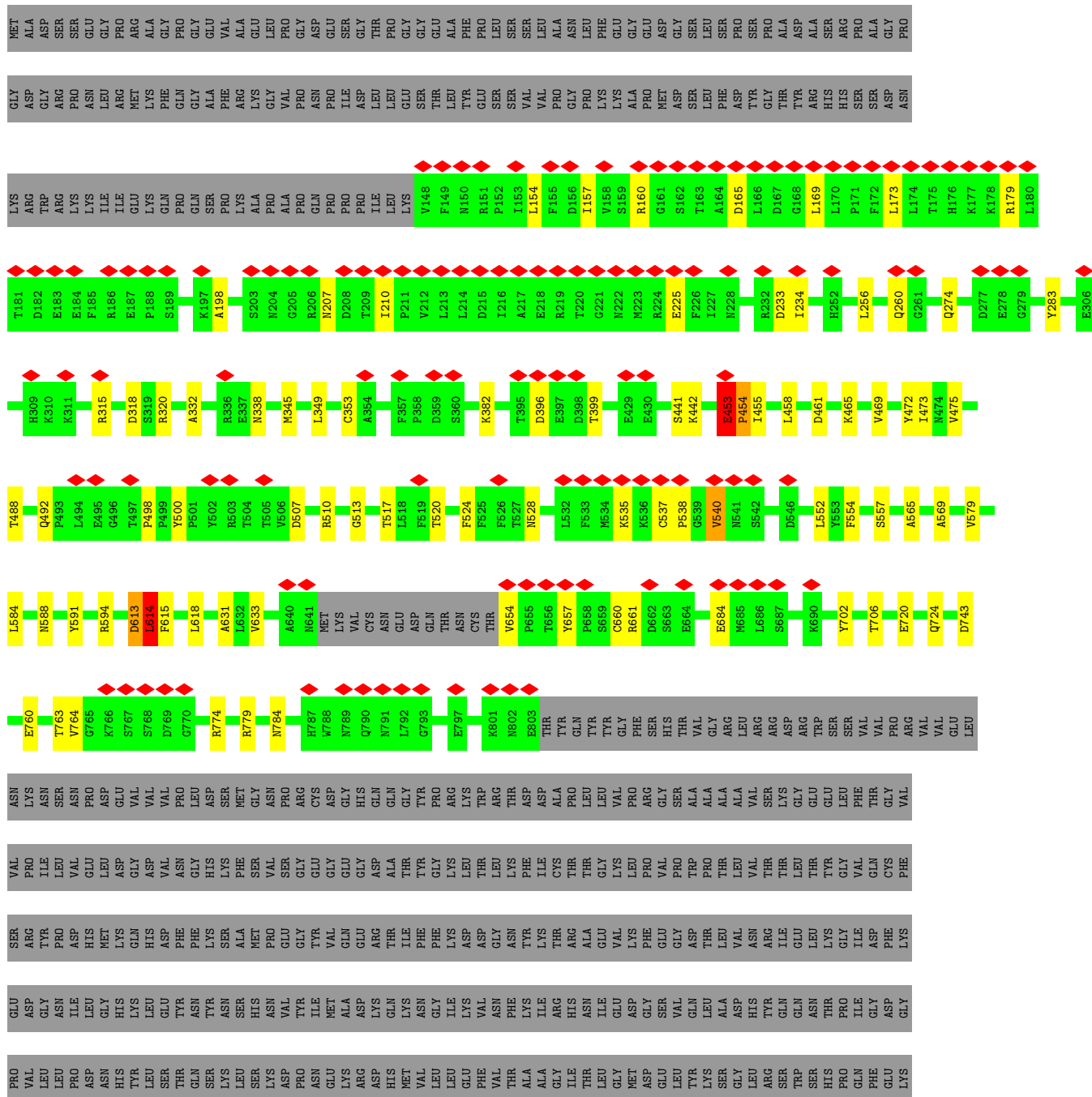
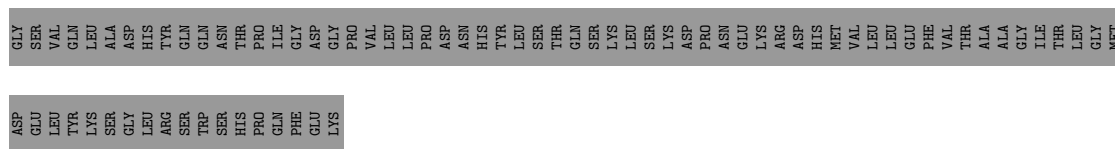
Mol	Chain	Residues	Atoms		AltConf
5	A	18	Total	O	0
			18	18	
5	B	18	Total	O	0
			18	18	
5	C	18	Total	O	0
			18	18	
5	D	18	Total	O	0
			18	18	

[illegible]

- Molecule 1: Transient receptor potential cation channel subfamily V member 4/Enhanced green fluorescent protein chimera



M685	F584	K465	H309	T181	GLY	ASN
L686	S557	V469	H310	D182	ARG	ASP
S687	A566		F311	E183	GLY	ASP
K690	A569	Y472	R315	E184	LYS	PRO
Y702	Y574	H474	D318	F185	LYS	ASN
T706	Y579	V475	S319	E187	ILE	LEU
E720		T488	R320	P188	GLY	ARG
Q724	L584	Q482	A332	S189	GLN	PHE
W725	M588	F493	R336	K197	PRO	GLN
V726		L494	E337	A198	SER	GLY
S729	Y591	E495	N338	S203	ALA	ALA
D743	R594	T497	K345	N204	LYS	VAL
E760	D613	F499	Y346	Q205	GLY	VAL
T763	L614	Y500	D347	R206	LEU	PRO
V764	F615	P501	L348	N207	ALA	GLY
G765	R616	Y502	L349	D208	PRO	ASP
K766	F617	R503	C353	T209	PRO	GLY
S767	L618	T504	A354	T210	ILE	LEU
S768	S630	Y506	F357	P211	LEU	LEU
D769	A631	D507	P358	V212	GLY	GLY
G770	L632		D359	L213	THR	GLY
R774	V633	R510	S360	L214	LYR	ALA
R779	S634	G513	K382	D215	GLU	PHE
N784	L636			T216	LEU	PRO
H787	A640	T517	H388	A217	P152	LEU
W788	M641	L518	E218	L154	VAL	SER
N789	GLY	F519	R219	F155	LEU	SER
Q790	LYS		T395	D156	VAL	ASN
N791	VAL	T520	D396	I157	GLY	ASN
L792	CYS	F524	E397	G221	LYS	PHE
G793	ASN	F525	D398	N222	LYS	GLY
E797	THR	F526	T399	M223	ALA	GLY
K801	CYS	N528	D420	R224	PRO	ASP
N802	THR	L532	S422	E225	G161	GLY
E803	V654	F533	E429	F226	S162	ASP
THR	F655	M534	E430	T227	T163	SER
TYR	T656	K536	Y439	D232	ALA	LEU
GLN	Y657	C537	N440	I234	TYR	SER
TYR	C660	P538	S441	H252	ARG	SER
GLN	R661	G539	K442	L256	ALA	ARG
TYR	D662	V540	E453	Q260	LYS	ARG
TYR	S663	N541	P454	G261	F172	PRO
GLY	F664	S542	I455	L173	F171	ALA
PHE	E684	D546	L458	L174	P170	SER
THR		L552	D461	T175	H170	HIS
VAL		Y553		K177	L170	HIS
				E278	THR	PRO
				G279	ALA	ALA
				L180	GLY	GLY
				Y283	ASN	ASN
				F206		



- Chain D: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	37266	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	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.386	Depositor
Minimum map value	-0.975	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.22	Depositor
Map size (\AA)	265.6, 265.6, 265.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.83000004, 0.83000004, 0.83000004	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: YJ0, 9ZR, NA

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	0.42	0/5297	0.67	6/7184 (0.1%)
1	B	0.42	0/5297	0.67	6/7184 (0.1%)
1	C	0.42	0/5297	0.67	6/7184 (0.1%)
1	D	0.42	0/5297	0.67	6/7184 (0.1%)
All	All	0.42	0/21188	0.67	24/28736 (0.1%)

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	3
1	B	0	3
1	C	0	3
1	D	0	3
All	All	0	12

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	764	VAL	CG1-CB-CG2	7.22	122.45	110.90
1	C	764	VAL	CG1-CB-CG2	7.22	122.45	110.90
1	D	764	VAL	CG1-CB-CG2	7.21	122.44	110.90
1	B	764	VAL	CG1-CB-CG2	7.19	122.40	110.90
1	D	540	VAL	CG1-CB-CG2	7.06	122.20	110.90
1	B	540	VAL	CG1-CB-CG2	7.03	122.14	110.90
1	C	540	VAL	CG1-CB-CG2	7.02	122.13	110.90
1	A	540	VAL	CG1-CB-CG2	7.02	122.13	110.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	633	VAL	CG1-CB-CG2	6.99	122.08	110.90
1	C	633	VAL	CG1-CB-CG2	6.97	122.06	110.90
1	B	633	VAL	CG1-CB-CG2	6.97	122.05	110.90
1	A	633	VAL	CG1-CB-CG2	6.96	122.04	110.90
1	B	654	VAL	CG1-CB-CG2	6.14	120.73	110.90
1	A	654	VAL	CG1-CB-CG2	6.12	120.69	110.90
1	D	654	VAL	CG1-CB-CG2	6.11	120.68	110.90
1	C	654	VAL	CG1-CB-CG2	6.09	120.65	110.90
1	A	614	LEU	CA-CB-CG	5.54	128.05	115.30
1	A	654	VAL	CA-CB-CG2	5.53	119.19	110.90
1	C	614	LEU	CA-CB-CG	5.53	128.01	115.30
1	D	614	LEU	CA-CB-CG	5.53	128.01	115.30
1	B	614	LEU	CA-CB-CG	5.52	128.00	115.30
1	C	654	VAL	CA-CB-CG2	5.51	119.17	110.90
1	B	654	VAL	CA-CB-CG2	5.50	119.14	110.90
1	D	654	VAL	CA-CB-CG2	5.49	119.13	110.90

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	453	GLU	Peptide
1	A	537	CYS	Peptide
1	A	614	LEU	Peptide
1	B	453	GLU	Peptide
1	B	537	CYS	Peptide
1	B	614	LEU	Peptide
1	C	453	GLU	Peptide
1	C	537	CYS	Peptide
1	C	614	LEU	Peptide
1	D	453	GLU	Peptide
1	D	537	CYS	Peptide
1	D	614	LEU	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	5176	0	5235	53	0
1	B	5176	0	5235	53	0
1	C	5176	0	5235	43	0
1	D	5176	0	5235	49	0
2	A	551	0	0	1	0
2	B	439	0	0	2	0
2	C	495	0	0	1	0
2	D	495	0	0	1	0
3	A	105	0	0	3	0
3	B	105	0	0	5	0
3	C	105	0	0	3	0
3	D	105	0	0	3	0
4	A	4	0	0	0	0
5	A	18	0	0	1	0
5	B	18	0	0	1	0
5	C	18	0	0	1	0
5	D	18	0	0	1	0
All	All	23180	0	20940	193	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 4.

All (193) 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:283:TYR:OH	1:A:318:ASP:OD2	2.02	0.77
1:D:283:TYR:OH	1:D:318:ASP:OD2	2.03	0.76
1:C:283:TYR:OH	1:C:318:ASP:OD2	2.02	0.76
1:B:283:TYR:OH	1:B:318:ASP:OD2	2.02	0.76
1:D:660:CYS:SG	1:D:661:ARG:N	2.59	0.75
1:C:660:CYS:SG	1:C:661:ARG:N	2.59	0.75
1:C:591:TYR:O	1:C:594:ARG:NH1	2.20	0.74
1:A:660:CYS:SG	1:A:661:ARG:N	2.60	0.74
1:D:591:TYR:O	1:D:594:ARG:NH1	2.20	0.74
1:A:591:TYR:O	1:A:594:ARG:NH1	2.20	0.74
1:B:591:TYR:O	1:B:594:ARG:NH1	2.20	0.74
1:A:631:ALA:HB1	1:D:579:VAL:HG13	1.71	0.72
1:B:660:CYS:SG	1:B:661:ARG:N	2.60	0.72
1:A:702:TYR:O	1:A:706:THR:OG1	2.07	0.69
1:A:720:GLU:OE2	1:A:724:GLN:NE2	2.27	0.68
1:B:720:GLU:OE2	1:B:724:GLN:NE2	2.27	0.68
1:D:720:GLU:OE2	1:D:724:GLN:NE2	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:657:TYR:O	1:B:660:CYS:N	2.28	0.67
1:C:720:GLU:OE2	1:C:724:GLN:NE2	2.27	0.67
1:B:274:GLN:OE1	1:B:320:ARG:NH2	2.28	0.67
1:C:274:GLN:OE1	1:C:320:ARG:NH2	2.28	0.67
1:D:657:TYR:O	1:D:660:CYS:N	2.28	0.67
1:C:657:TYR:O	1:C:660:CYS:N	2.28	0.66
1:A:657:TYR:O	1:A:660:CYS:N	2.28	0.66
1:D:702:TYR:O	1:D:706:THR:OG1	2.07	0.66
1:D:274:GLN:OE1	1:D:320:ARG:NH2	2.28	0.66
1:C:517:THR:O	1:C:520:THR:OG1	2.14	0.66
1:A:274:GLN:OE1	1:A:320:ARG:NH2	2.28	0.65
1:C:579:VAL:HG13	1:D:631:ALA:HB1	1.79	0.65
1:D:160:ARG:NH1	1:D:165:ASP:OD2	2.30	0.65
1:A:160:ARG:NH1	1:A:165:ASP:OD2	2.30	0.65
1:B:160:ARG:NH1	1:B:165:ASP:OD2	2.30	0.65
1:C:160:ARG:NH1	1:C:165:ASP:OD2	2.30	0.64
1:B:256:LEU:O	1:B:260:GLN:NE2	2.32	0.63
1:A:256:LEU:O	1:A:260:GLN:NE2	2.32	0.63
1:D:256:LEU:O	1:D:260:GLN:NE2	2.32	0.62
1:C:256:LEU:O	1:C:260:GLN:NE2	2.32	0.62
1:B:702:TYR:O	1:B:706:THR:OG1	2.07	0.61
1:D:524:PHE:O	1:D:528:ASN:ND2	2.34	0.61
1:D:453:GLU:O	1:D:455:ILE:N	2.34	0.61
1:C:554:PHE:O	1:C:557:SER:OG	2.17	0.61
1:B:524:PHE:O	1:B:528:ASN:ND2	2.34	0.61
1:B:618:LEU:HD23	3:C:1203:YJ0:C1	2.30	0.61
1:B:453:GLU:O	1:B:455:ILE:N	2.34	0.60
1:C:453:GLU:O	1:C:455:ILE:N	2.34	0.60
1:C:524:PHE:O	1:C:528:ASN:ND2	2.34	0.60
1:C:702:TYR:O	1:C:706:THR:OG1	2.07	0.60
1:A:524:PHE:O	1:A:528:ASN:ND2	2.34	0.60
3:A:1213:YJ0:C1	1:D:618:LEU:HD23	2.32	0.60
1:A:453:GLU:O	1:A:455:ILE:N	2.34	0.60
1:B:725:VAL:O	1:B:729:SER:OG	2.19	0.60
2:B:1201:9ZR:C7	3:B:1202:YJ0:C3	2.79	0.60
1:C:618:LEU:HD23	3:D:1203:YJ0:C1	2.32	0.60
1:A:618:LEU:HD23	3:B:1202:YJ0:C1	2.34	0.58
1:A:574:TYR:OH	5:A:1301:HOH:O	2.17	0.57
1:D:554:PHE:O	1:D:557:SER:OG	2.17	0.57
1:B:579:VAL:HG13	1:C:631:ALA:HB1	1.86	0.57
1:C:169:LEU:O	1:C:173:LEU:N	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:554:PHE:O	1:B:557:SER:OG	2.17	0.56
1:D:760:GLU:OE1	1:D:779:ARG:NH2	2.39	0.56
1:C:760:GLU:OE1	1:C:779:ARG:NH2	2.39	0.56
1:A:517:THR:O	1:A:520:THR:OG1	2.14	0.56
1:A:760:GLU:OE1	1:A:779:ARG:NH2	2.39	0.56
1:D:169:LEU:O	1:D:173:LEU:N	2.37	0.56
1:B:169:LEU:O	1:B:173:LEU:N	2.37	0.56
1:B:760:GLU:OE1	1:B:779:ARG:NH2	2.39	0.56
1:A:554:PHE:O	1:A:557:SER:OG	2.17	0.55
1:A:236:TYR:OH	1:D:799:PRO:O	2.21	0.55
1:A:332:ALA:O	1:A:382:LYS:NZ	2.33	0.55
1:B:535:LYS:NZ	1:B:743:ASP:OD1	2.40	0.54
1:D:439:TYR:OH	1:D:743:ASP:OD1	2.23	0.54
1:C:535:LYS:NZ	1:C:743:ASP:OD1	2.40	0.54
1:A:169:LEU:O	1:A:173:LEU:N	2.37	0.54
1:D:535:LYS:NZ	1:D:743:ASP:OD1	2.40	0.54
1:A:535:LYS:NZ	1:A:743:ASP:OD1	2.40	0.53
1:D:332:ALA:O	1:D:382:LYS:NZ	2.33	0.53
1:D:517:THR:O	1:D:520:THR:OG1	2.14	0.53
1:B:613:ASP:O	1:B:615:PHE:N	2.37	0.53
1:B:584:LEU:O	1:B:588:ASN:N	2.42	0.53
1:C:498:PRO:O	1:C:500:TYR:N	2.42	0.52
1:B:507:ASP:OD1	1:B:510:ARG:NH1	2.41	0.52
1:C:332:ALA:O	1:C:382:LYS:NZ	2.33	0.52
1:A:498:PRO:O	1:A:500:TYR:N	2.42	0.52
1:C:584:LEU:O	1:C:588:ASN:N	2.42	0.52
1:D:498:PRO:O	1:D:500:TYR:N	2.42	0.52
1:B:517:THR:O	1:B:520:THR:OG1	2.14	0.52
1:B:498:PRO:O	1:B:500:TYR:N	2.42	0.52
1:C:613:ASP:O	1:C:615:PHE:N	2.37	0.52
1:D:584:LEU:O	1:D:588:ASN:N	2.42	0.52
2:A:1212:9ZR:C7	3:A:1213:YJ0:C3	2.87	0.52
1:C:507:ASP:OD1	1:C:510:ARG:NH1	2.41	0.51
1:D:613:ASP:O	1:D:615:PHE:N	2.37	0.51
1:B:332:ALA:O	1:B:382:LYS:NZ	2.33	0.51
1:A:584:LEU:O	1:A:588:ASN:N	2.42	0.51
1:A:486:THR:HG23	1:B:630:SER:HB3	1.91	0.51
1:A:507:ASP:OD1	1:A:510:ARG:NH1	2.41	0.51
1:B:454:PRO:O	1:B:458:LEU:N	2.44	0.51
1:A:684:GLU:HA	3:A:1213:YJ0:O72	2.12	0.50
2:D:1202:9ZR:C7	3:D:1203:YJ0:C3	2.89	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:469:VAL:O	1:A:473:ILE:HD12	2.13	0.48
1:D:507:ASP:OD1	1:D:510:ARG:NH1	2.41	0.48
2:C:1202:9ZR:C7	3:C:1203:YJ0:C3	2.91	0.48
1:D:454:PRO:O	1:D:458:LEU:N	2.44	0.48
1:A:613:ASP:O	1:A:615:PHE:N	2.37	0.48
1:C:469:VAL:O	1:C:473:ILE:HD12	2.13	0.48
1:D:574:TYR:OH	5:D:1301:HOH:O	2.20	0.48
1:B:469:VAL:O	1:B:473:ILE:HD12	2.13	0.47
1:D:469:VAL:O	1:D:473:ILE:HD12	2.13	0.47
1:A:565:ALA:O	1:A:569:ALA:N	2.46	0.47
1:B:349:LEU:O	1:B:353:CYS:N	2.47	0.47
1:A:598:LEU:O	1:B:616:ARG:NH1	2.45	0.47
1:C:454:PRO:O	1:C:458:LEU:N	2.44	0.47
1:D:565:ALA:O	1:D:569:ALA:N	2.46	0.47
1:D:763:THR:OG1	1:D:774:ARG:NH1	2.45	0.46
1:A:454:PRO:O	1:A:458:LEU:N	2.44	0.46
1:A:763:THR:OG1	1:A:774:ARG:NH1	2.45	0.46
1:A:349:LEU:O	1:A:353:CYS:N	2.47	0.46
1:D:472:TYR:HA	1:D:475:VAL:HG12	1.97	0.46
1:C:565:ALA:O	1:C:569:ALA:N	2.46	0.46
1:C:763:THR:OG1	1:C:774:ARG:NH1	2.45	0.46
1:D:349:LEU:O	1:D:353:CYS:N	2.47	0.46
1:B:565:ALA:O	1:B:569:ALA:N	2.46	0.46
1:B:472:TYR:HA	1:B:475:VAL:HG12	1.97	0.45
1:C:472:TYR:HA	1:C:475:VAL:HG12	1.97	0.45
1:A:439:TYR:OH	1:A:743:ASP:OD1	2.23	0.45
1:A:472:TYR:HA	1:A:475:VAL:HG12	1.97	0.45
1:C:396:ASP:OD1	1:C:399:THR:OG1	2.35	0.45
1:D:396:ASP:OD1	1:D:399:THR:OG1	2.35	0.45
1:B:441:SER:OG	1:B:442:LYS:N	2.50	0.45
1:A:579:VAL:HG13	1:B:631:ALA:HB1	1.98	0.45
1:B:684:GLU:HA	3:B:1202:YJ0:O72	2.16	0.45
1:D:725:VAL:O	1:D:729:SER:OG	2.19	0.45
1:A:396:ASP:OD1	1:A:399:THR:OG1	2.35	0.45
1:C:552:LEU:HB3	1:C:588:ASN:HD21	1.81	0.45
1:D:552:LEU:HB3	1:D:588:ASN:HD21	1.81	0.45
1:C:441:SER:OG	1:C:442:LYS:N	2.50	0.44
1:C:684:GLU:HA	3:C:1203:YJ0:O72	2.17	0.44
1:D:684:GLU:HA	3:D:1203:YJ0:O72	2.16	0.44
1:A:552:LEU:HB3	1:A:588:ASN:HD21	1.81	0.44
1:B:552:LEU:HB3	1:B:588:ASN:HD21	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1201:9ZR:C7	3:B:1202:YJ0:C4	2.96	0.44
1:C:349:LEU:O	1:C:353:CYS:N	2.47	0.44
1:A:671:LEU:HD22	3:B:1202:YJ0:C18	2.47	0.44
1:B:396:ASP:OD1	1:B:399:THR:OG1	2.35	0.44
1:D:154:LEU:O	1:D:157:ILE:N	2.50	0.44
1:A:420:ASP:OD1	1:A:422:SER:OG	2.32	0.44
1:B:154:LEU:O	1:B:157:ILE:N	2.50	0.44
1:C:154:LEU:O	1:C:157:ILE:N	2.50	0.44
1:A:154:LEU:O	1:A:157:ILE:N	2.50	0.44
1:B:763:THR:OG1	1:B:774:ARG:NH1	2.45	0.43
1:B:488:THR:O	1:B:492:GLN:N	2.52	0.43
1:B:633:VAL:O	1:B:661:ARG:NH2	2.49	0.43
1:D:441:SER:OG	1:D:442:LYS:N	2.50	0.43
1:C:488:THR:O	1:C:492:GLN:N	2.52	0.43
1:A:441:SER:OG	1:A:442:LYS:N	2.50	0.43
1:A:488:THR:O	1:A:492:GLN:N	2.52	0.43
1:D:233:ASP:OD1	1:D:234:ILE:N	2.52	0.43
1:D:488:THR:O	1:D:492:GLN:N	2.52	0.43
1:B:574:TYR:OH	5:B:1301:HOH:O	2.20	0.43
1:B:439:TYR:OH	1:B:743:ASP:OD1	2.23	0.42
1:B:461:ASP:OD2	1:B:465:LYS:NZ	2.52	0.42
1:C:233:ASP:OD1	1:C:234:ILE:N	2.52	0.42
1:B:513:GLY:O	1:B:517:THR:OG1	2.30	0.42
1:A:461:ASP:OD2	1:A:465:LYS:NZ	2.52	0.42
1:D:179:ARG:NH2	1:D:225:GLU:OE1	2.50	0.42
1:C:461:ASP:OD2	1:C:465:LYS:NZ	2.52	0.42
1:D:538:PRO:O	1:D:540:VAL:N	2.53	0.42
1:C:315:ARG:NH2	5:C:1304:HOH:O	2.42	0.42
1:A:538:PRO:O	1:A:540:VAL:N	2.53	0.41
1:B:420:ASP:OD1	1:B:422:SER:OG	2.32	0.41
1:A:198:ALA:HB1	1:A:210:ILE:HD11	2.03	0.41
1:B:233:ASP:OD1	1:B:234:ILE:N	2.52	0.41
1:C:513:GLY:O	1:C:517:THR:OG1	2.30	0.41
1:A:179:ARG:NH2	1:A:225:GLU:OE1	2.50	0.41
1:B:538:PRO:O	1:B:540:VAL:N	2.53	0.41
1:C:198:ALA:HB1	1:C:210:ILE:HD11	2.03	0.41
1:B:198:ALA:HB1	1:B:210:ILE:HD11	2.03	0.41
1:C:538:PRO:O	1:C:540:VAL:N	2.53	0.41
1:D:461:ASP:OD2	1:D:465:LYS:NZ	2.52	0.41
1:A:193:THR:HG22	1:A:194:CYS:N	2.36	0.41
1:A:212:VAL:O	1:A:216:ILE:HD12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:212:VAL:O	1:B:216:ILE:HD12	2.21	0.41
1:C:179:ARG:NH2	1:C:225:GLU:OE1	2.50	0.41
1:D:193:THR:HG22	1:D:194:CYS:N	2.36	0.41
1:D:198:ALA:HB1	1:D:210:ILE:HD11	2.03	0.41
1:A:631:ALA:HB1	1:D:579:VAL:CG1	2.44	0.40
1:B:347:ASP:CG	1:B:388:HIS:HE2	2.24	0.40
1:B:179:ARG:NH2	1:B:225:GLU:OE1	2.50	0.40
1:A:575:LEU:HD21	1:B:635:LEU:HD23	2.03	0.40
1:A:694:VAL:HG23	1:D:580:PHE:CZ	2.56	0.40
1:A:347:ASP:CG	1:A:388:HIS:HE2	2.24	0.40
1:B:630:SER:O	1:B:634:SER:OG	2.33	0.40
1:D:403:SER:O	1:D:775:ARG:NH1	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	640/1132 (56%)	563 (88%)	73 (11%)	4 (1%)	22	57
1	B	640/1132 (56%)	563 (88%)	73 (11%)	4 (1%)	22	57
1	C	640/1132 (56%)	562 (88%)	74 (12%)	4 (1%)	22	57
1	D	640/1132 (56%)	563 (88%)	73 (11%)	4 (1%)	22	57
All	All	2560/4528 (56%)	2251 (88%)	293 (11%)	16 (1%)	24	57

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	614	LEU
1	B	614	LEU
1	C	614	LEU

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Mol	Chain	Res	Type
1	D	614	LEU
1	A	613	ASP
1	B	613	ASP
1	C	613	ASP
1	D	613	ASP
1	A	453	GLU
1	B	453	GLU
1	C	453	GLU
1	D	453	GLU
1	A	454	PRO
1	B	454	PRO
1	C	454	PRO
1	D	454	PRO

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	568/987 (58%)	564 (99%)	4 (1%)	81	91
1	B	568/987 (58%)	564 (99%)	4 (1%)	81	91
1	C	568/987 (58%)	564 (99%)	4 (1%)	81	91
1	D	568/987 (58%)	564 (99%)	4 (1%)	81	91
All	All	2272/3948 (58%)	2256 (99%)	16 (1%)	80	91

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	207	ASN
1	A	338	ASN
1	A	345	MET
1	A	784	ASN
1	B	207	ASN
1	B	338	ASN
1	B	345	MET
1	B	784	ASN

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Mol	Chain	Res	Type
1	C	207	ASN
1	C	338	ASN
1	C	345	MET
1	C	784	ASN
1	D	207	ASN
1	D	338	ASN
1	D	345	MET
1	D	784	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	201	ASN
1	A	207	ASN
1	A	243	HIS
1	A	492	GLN
1	A	724	GLN
1	A	784	ASN
1	B	201	ASN
1	B	207	ASN
1	B	243	HIS
1	B	260	GLN
1	B	492	GLN
1	B	724	GLN
1	B	784	ASN
1	C	201	ASN
1	C	207	ASN
1	C	243	HIS
1	C	492	GLN
1	C	724	GLN
1	C	784	ASN
1	D	201	ASN
1	D	207	ASN
1	D	243	HIS
1	D	260	GLN
1	D	492	GLN
1	D	724	GLN
1	D	784	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 52 ligands modelled in this entry, 4 are monoatomic - leaving 48 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	9ZR	A	1202	-	55,55,55	0.31	0	61,63,63	0.44	0
3	YJ0	A	1210	-	40,40,90	0.26	0	63,64,138	0.48	0
2	9ZR	D	1201	-	55,55,55	0.28	0	61,63,63	0.32	0
2	9ZR	D	1209	-	55,55,55	0.34	0	61,63,63	0.51	1 (1%)
2	9ZR	C	1208	-	55,55,55	0.29	0	61,63,63	0.34	0
2	9ZR	B	1209	-	55,55,55	0.31	0	61,63,63	0.28	0
3	YJ0	C	1212	-	40,40,90	0.27	0	63,64,138	0.47	0
2	9ZR	B	1204	-	55,55,55	0.29	0	61,63,63	0.35	0
2	9ZR	B	1203	-	55,55,55	0.32	0	61,63,63	0.44	0
2	9ZR	D	1205	-	55,55,55	0.29	0	61,63,63	0.35	0
2	9ZR	A	1201	-	55,55,55	0.28	0	61,63,63	0.34	0
2	9ZR	D	1208	-	55,55,55	0.29	0	61,63,63	0.35	0
2	9ZR	A	1206	-	55,55,55	0.29	0	61,63,63	0.35	0
2	9ZR	A	1212	-	55,55,55	0.28	0	61,63,63	0.35	0
2	9ZR	A	1208	-	55,55,55	0.31	0	61,63,63	0.28	0
2	9ZR	B	1206	-	12,12,55	0.14	0	11,11,63	0.17	0
2	9ZR	C	1209	-	55,55,55	0.34	0	61,63,63	0.51	1 (1%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	9ZR	C	1207	-	12,12,55	0.14	0	11,11,63	0.17	0
3	YJ0	B	1211	-	40,40,90	0.27	0	63,64,138	0.48	0
2	9ZR	A	1203	-	55,55,55	0.29	0	61,63,63	0.35	0
2	9ZR	C	1210	-	55,55,55	0.31	0	61,63,63	0.28	0
2	9ZR	D	1202	-	55,55,55	0.28	0	61,63,63	0.35	0
2	9ZR	C	1201	-	55,55,55	0.28	0	61,63,63	0.32	0
2	9ZR	A	1209	-	45,45,55	0.35	0	51,53,63	0.52	1 (1%)
3	YJ0	B	1202	-	78,78,90	0.24	0	116,120,138	0.47	0
2	9ZR	C	1206	-	43,43,55	0.35	0	49,51,63	0.44	0
2	9ZR	B	1208	-	55,55,55	0.34	0	61,63,63	0.51	1 (1%)
2	9ZR	D	1207	-	12,12,55	0.14	0	11,11,63	0.17	0
2	9ZR	D	1211	-	45,45,55	0.34	0	51,53,63	0.52	1 (1%)
2	9ZR	B	1205	-	43,43,55	0.35	0	49,51,63	0.44	0
3	YJ0	D	1212	-	40,40,90	0.26	0	63,64,138	0.48	0
2	9ZR	B	1207	-	55,55,55	0.29	0	61,63,63	0.34	0
2	9ZR	A	1205	-	12,12,55	0.15	0	11,11,63	0.17	0
2	9ZR	C	1205	-	55,55,55	0.29	0	61,63,63	0.35	0
2	9ZR	A	1211	-	55,55,55	0.28	0	61,63,63	0.32	0
2	9ZR	C	1211	-	45,45,55	0.35	0	51,53,63	0.52	1 (1%)
2	9ZR	D	1210	-	55,55,55	0.31	0	61,63,63	0.28	0
3	YJ0	A	1213	-	78,78,90	0.24	0	116,120,138	0.46	0
2	9ZR	B	1210	-	45,45,55	0.35	0	51,53,63	0.52	1 (1%)
3	YJ0	C	1203	-	78,78,90	0.25	0	116,120,138	0.47	0
2	9ZR	D	1206	-	43,43,55	0.35	0	49,51,63	0.44	0
2	9ZR	B	1201	-	55,55,55	0.28	0	61,63,63	0.35	0
2	9ZR	A	1204	-	43,43,55	0.34	0	49,51,63	0.44	0
2	9ZR	C	1204	-	55,55,55	0.32	0	61,63,63	0.44	0
2	9ZR	C	1202	-	55,55,55	0.28	0	61,63,63	0.35	0
2	9ZR	A	1207	-	55,55,55	0.34	0	61,63,63	0.50	1 (1%)
2	9ZR	D	1204	-	55,55,55	0.32	0	61,63,63	0.44	0
3	YJ0	D	1203	-	78,78,90	0.25	0	116,120,138	0.47	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	9ZR	A	1202	-	-	24/59/59/59	-
3	YJ0	A	1210	-	-	2/6/94/200	0/6/6/10
2	9ZR	D	1201	-	-	22/59/59/59	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	9ZR	D	1209	-	-	20/59/59/59	-
2	9ZR	C	1208	-	-	27/59/59/59	-
2	9ZR	B	1209	-	-	23/59/59/59	-
3	YJ0	C	1212	-	-	2/6/94/200	0/6/6/10
2	9ZR	B	1204	-	-	15/59/59/59	-
2	9ZR	B	1203	-	-	24/59/59/59	-
2	9ZR	D	1205	-	-	15/59/59/59	-
2	9ZR	A	1201	-	-	23/59/59/59	-
2	9ZR	D	1208	-	-	27/59/59/59	-
2	9ZR	A	1206	-	-	29/59/59/59	-
2	9ZR	A	1212	-	-	21/59/59/59	-
2	9ZR	A	1208	-	-	23/59/59/59	-
2	9ZR	B	1206	-	-	3/10/10/59	-
2	9ZR	C	1209	-	-	21/59/59/59	-
2	9ZR	C	1207	-	-	3/10/10/59	-
3	YJ0	B	1211	-	-	2/6/94/200	0/6/6/10
2	9ZR	A	1203	-	-	14/59/59/59	-
2	9ZR	C	1210	-	-	23/59/59/59	-
2	9ZR	D	1202	-	-	21/59/59/59	-
2	9ZR	C	1201	-	-	22/59/59/59	-
2	9ZR	A	1209	-	-	18/49/49/59	-
3	YJ0	B	1202	-	-	8/26/174/200	0/9/9/10
2	9ZR	C	1206	-	-	20/47/47/59	-
2	9ZR	B	1208	-	-	22/59/59/59	-
2	9ZR	D	1207	-	-	3/10/10/59	-
2	9ZR	D	1211	-	-	18/49/49/59	-
2	9ZR	B	1205	-	-	21/47/47/59	-
3	YJ0	D	1212	-	-	2/6/94/200	0/6/6/10
2	9ZR	B	1207	-	-	27/59/59/59	-
2	9ZR	A	1205	-	-	4/10/10/59	-
2	9ZR	C	1205	-	-	15/59/59/59	-
2	9ZR	A	1211	-	-	22/59/59/59	-
2	9ZR	C	1211	-	-	18/49/49/59	-
2	9ZR	D	1210	-	-	23/59/59/59	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	YJ0	A	1213	-	-	12/26/174/200	0/9/9/10
2	9ZR	B	1210	-	-	18/49/49/59	-
3	YJ0	C	1203	-	-	11/26/174/200	0/9/9/10
2	9ZR	D	1206	-	-	21/47/47/59	-
2	9ZR	B	1201	-	-	23/59/59/59	-
2	9ZR	A	1204	-	-	22/47/47/59	-
2	9ZR	C	1204	-	-	23/59/59/59	-
2	9ZR	C	1202	-	-	20/59/59/59	-
2	9ZR	A	1207	-	-	20/59/59/59	-
2	9ZR	D	1204	-	-	23/59/59/59	-
3	YJ0	D	1203	-	-	11/26/174/200	0/9/9/10

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1209	9ZR	C26-O39-C40	2.42	123.58	117.80
2	B	1210	9ZR	C26-O39-C40	2.41	123.57	117.80
2	D	1211	9ZR	C26-O39-C40	2.41	123.57	117.80
2	C	1211	9ZR	C26-O39-C40	2.40	123.53	117.80
2	B	1208	9ZR	C26-O39-C40	2.31	123.32	117.80
2	C	1209	9ZR	C26-O39-C40	2.28	123.26	117.80
2	D	1209	9ZR	C26-O39-C40	2.27	123.24	117.80
2	A	1207	9ZR	C26-O39-C40	2.24	123.16	117.80

There are no chirality outliers.

All (831) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1201	9ZR	C33-O32-P29-O30
2	A	1201	9ZR	O32-C33-C34-N35
2	A	1202	9ZR	C33-O32-P29-O31
2	A	1202	9ZR	C33-O32-P29-O28
2	A	1203	9ZR	C27-O28-P29-O31
2	A	1203	9ZR	C27-O28-P29-O32
2	A	1204	9ZR	C33-O32-P29-O31
2	A	1204	9ZR	C33-O32-P29-O28
2	A	1204	9ZR	C33-O32-P29-O30

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Mol	Chain	Res	Type	Atoms
2	A	1204	9ZR	O32-C33-C34-N35
2	A	1204	9ZR	C27-O28-P29-O30
2	A	1206	9ZR	C33-O32-P29-O31
2	A	1206	9ZR	C33-O32-P29-O28
2	A	1206	9ZR	C27-O28-P29-O31
2	A	1206	9ZR	C27-O28-P29-O32
2	A	1206	9ZR	C27-O28-P29-O30
2	A	1207	9ZR	O39-C26-C27-O28
2	A	1207	9ZR	C42-C40-O39-C26
2	A	1207	9ZR	O41-C40-O39-C26
2	A	1208	9ZR	C33-O32-P29-O31
2	A	1208	9ZR	C33-O32-P29-O28
2	A	1208	9ZR	C33-O32-P29-O30
2	A	1208	9ZR	O32-C33-C34-N35
2	A	1208	9ZR	C27-O28-P29-O32
2	A	1209	9ZR	O32-C33-C34-N35
2	A	1209	9ZR	C42-C40-O39-C26
2	A	1209	9ZR	O41-C40-O39-C26
2	A	1209	9ZR	C27-O28-P29-O31
2	A	1209	9ZR	C27-O28-P29-O32
2	A	1209	9ZR	C27-O28-P29-O30
2	A	1211	9ZR	C33-O32-P29-O30
2	A	1211	9ZR	O32-C33-C34-N35
2	A	1212	9ZR	C33-O32-P29-O31
2	A	1212	9ZR	C33-O32-P29-O28
2	A	1212	9ZR	C33-O32-P29-O30
2	A	1212	9ZR	C27-O28-P29-O32
2	B	1201	9ZR	C33-O32-P29-O28
2	B	1201	9ZR	C33-O32-P29-O30
2	B	1201	9ZR	C27-O28-P29-O32
2	B	1203	9ZR	C33-O32-P29-O31
2	B	1203	9ZR	C33-O32-P29-O28
2	B	1204	9ZR	C27-O28-P29-O31
2	B	1204	9ZR	C27-O28-P29-O32
2	B	1205	9ZR	C33-O32-P29-O31
2	B	1205	9ZR	C33-O32-P29-O28
2	B	1205	9ZR	C33-O32-P29-O30
2	B	1205	9ZR	O32-C33-C34-N35
2	B	1205	9ZR	C27-O28-P29-O30
2	B	1207	9ZR	C33-O32-P29-O31
2	B	1207	9ZR	C33-O32-P29-O28
2	B	1207	9ZR	C27-O28-P29-O31

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Mol	Chain	Res	Type	Atoms
2	B	1207	9ZR	C27-O28-P29-O32
2	B	1207	9ZR	C27-O28-P29-O30
2	B	1208	9ZR	C42-C40-O39-C26
2	B	1208	9ZR	O41-C40-O39-C26
2	B	1209	9ZR	C33-O32-P29-O31
2	B	1209	9ZR	C33-O32-P29-O28
2	B	1209	9ZR	C33-O32-P29-O30
2	B	1209	9ZR	O32-C33-C34-N35
2	B	1209	9ZR	C27-O28-P29-O32
2	B	1210	9ZR	O32-C33-C34-N35
2	B	1210	9ZR	C42-C40-O39-C26
2	B	1210	9ZR	O41-C40-O39-C26
2	B	1210	9ZR	C27-O28-P29-O31
2	B	1210	9ZR	C27-O28-P29-O32
2	B	1210	9ZR	C27-O28-P29-O30
2	C	1201	9ZR	C33-O32-P29-O30
2	C	1201	9ZR	O32-C33-C34-N35
2	C	1202	9ZR	C33-O32-P29-O28
2	C	1202	9ZR	C27-O28-P29-O32
2	C	1204	9ZR	C33-O32-P29-O31
2	C	1204	9ZR	C33-O32-P29-O28
2	C	1205	9ZR	C27-O28-P29-O31
2	C	1205	9ZR	C27-O28-P29-O32
2	C	1206	9ZR	C33-O32-P29-O31
2	C	1206	9ZR	C33-O32-P29-O28
2	C	1206	9ZR	C33-O32-P29-O30
2	C	1206	9ZR	O32-C33-C34-N35
2	C	1206	9ZR	C27-O28-P29-O30
2	C	1208	9ZR	C33-O32-P29-O31
2	C	1208	9ZR	C33-O32-P29-O28
2	C	1208	9ZR	C27-O28-P29-O31
2	C	1208	9ZR	C27-O28-P29-O32
2	C	1208	9ZR	C27-O28-P29-O30
2	C	1209	9ZR	C42-C40-O39-C26
2	C	1209	9ZR	O41-C40-O39-C26
2	C	1210	9ZR	C33-O32-P29-O31
2	C	1210	9ZR	C33-O32-P29-O28
2	C	1210	9ZR	C33-O32-P29-O30
2	C	1210	9ZR	O32-C33-C34-N35
2	C	1210	9ZR	C27-O28-P29-O32
2	C	1211	9ZR	O32-C33-C34-N35
2	C	1211	9ZR	C42-C40-O39-C26

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Mol	Chain	Res	Type	Atoms
2	C	1211	9ZR	O41-C40-O39-C26
2	C	1211	9ZR	C27-O28-P29-O31
2	C	1211	9ZR	C27-O28-P29-O32
2	C	1211	9ZR	C27-O28-P29-O30
2	D	1201	9ZR	C33-O32-P29-O30
2	D	1201	9ZR	O32-C33-C34-N35
2	D	1202	9ZR	C33-O32-P29-O31
2	D	1202	9ZR	C33-O32-P29-O28
2	D	1202	9ZR	C33-O32-P29-O30
2	D	1202	9ZR	C27-O28-P29-O32
2	D	1204	9ZR	C33-O32-P29-O31
2	D	1204	9ZR	C33-O32-P29-O28
2	D	1205	9ZR	C27-O28-P29-O31
2	D	1205	9ZR	C27-O28-P29-O32
2	D	1206	9ZR	C33-O32-P29-O31
2	D	1206	9ZR	C33-O32-P29-O28
2	D	1206	9ZR	C33-O32-P29-O30
2	D	1206	9ZR	O32-C33-C34-N35
2	D	1206	9ZR	C27-O28-P29-O30
2	D	1208	9ZR	C33-O32-P29-O31
2	D	1208	9ZR	C33-O32-P29-O28
2	D	1208	9ZR	C27-O28-P29-O31
2	D	1208	9ZR	C27-O28-P29-O32
2	D	1208	9ZR	C27-O28-P29-O30
2	D	1209	9ZR	O39-C26-C27-O28
2	D	1209	9ZR	C42-C40-O39-C26
2	D	1209	9ZR	O41-C40-O39-C26
2	D	1210	9ZR	C33-O32-P29-O31
2	D	1210	9ZR	C33-O32-P29-O28
2	D	1210	9ZR	C33-O32-P29-O30
2	D	1210	9ZR	O32-C33-C34-N35
2	D	1210	9ZR	C27-O28-P29-O32
2	D	1211	9ZR	O32-C33-C34-N35
2	D	1211	9ZR	C42-C40-O39-C26
2	D	1211	9ZR	O41-C40-O39-C26
2	D	1211	9ZR	C27-O28-P29-O31
2	D	1211	9ZR	C27-O28-P29-O32
2	D	1211	9ZR	C27-O28-P29-O30
3	A	1210	YJ0	C27-C26-O25-C23
3	A	1213	YJ0	C24-C23-O25-C26
3	A	1213	YJ0	C29-C28-C53-O54
3	B	1202	YJ0	C24-C23-O25-C26

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Mol	Chain	Res	Type	Atoms
3	B	1202	YJ0	C29-C28-C53-O54
3	B	1211	YJ0	C27-C26-O25-C23
3	C	1203	YJ0	C24-C23-O25-C26
3	C	1203	YJ0	C29-C28-C53-O54
3	C	1212	YJ0	C27-C26-O25-C23
3	D	1203	YJ0	C24-C23-O25-C26
3	D	1203	YJ0	C29-C28-C53-O54
3	D	1212	YJ0	C27-C26-O25-C23
3	D	1203	YJ0	O69-C68-C70-O71
3	B	1202	YJ0	O69-C68-C70-O71
3	C	1203	YJ0	O69-C68-C70-O71
3	A	1213	YJ0	O69-C68-C70-O71
3	C	1203	YJ0	C67-C68-C70-O71
3	D	1203	YJ0	C67-C68-C70-O71
3	B	1202	YJ0	O69-C64-O63-C58
3	D	1203	YJ0	O69-C64-O63-C58
3	A	1213	YJ0	O69-C64-O63-C58
3	C	1203	YJ0	O69-C64-O63-C58
3	B	1202	YJ0	C67-C68-C70-O71
2	A	1206	9ZR	C33-C34-N35-C38
3	A	1213	YJ0	C67-C68-C70-O71
2	A	1212	9ZR	C19-C20-C21-C22
2	B	1201	9ZR	C19-C20-C21-C22
2	C	1202	9ZR	C19-C20-C21-C22
2	D	1202	9ZR	C19-C20-C21-C22
3	A	1213	YJ0	C65-C64-O63-C58
3	B	1202	YJ0	C65-C64-O63-C58
3	C	1203	YJ0	C65-C64-O63-C58
3	D	1203	YJ0	C65-C64-O63-C58
2	A	1204	9ZR	O39-C26-C27-O28
2	B	1205	9ZR	O39-C26-C27-O28
2	B	1208	9ZR	O39-C26-C27-O28
2	C	1206	9ZR	O39-C26-C27-O28
2	C	1209	9ZR	O39-C26-C27-O28
2	D	1206	9ZR	O39-C26-C27-O28
2	A	1208	9ZR	O24-C25-C26-O39
2	B	1209	9ZR	O24-C25-C26-O39
2	C	1210	9ZR	O24-C25-C26-O39
2	D	1210	9ZR	O24-C25-C26-O39
2	A	1206	9ZR	C33-C34-N35-C36
2	D	1208	9ZR	C33-C34-N35-C38
2	B	1205	9ZR	C18-C19-C20-C21

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Mol	Chain	Res	Type	Atoms
2	C	1206	9ZR	C18-C19-C20-C21
2	D	1206	9ZR	C18-C19-C20-C21
2	A	1208	9ZR	C19-C20-C21-C22
2	B	1209	9ZR	C19-C20-C21-C22
2	C	1210	9ZR	C19-C20-C21-C22
2	D	1210	9ZR	C19-C20-C21-C22
2	A	1204	9ZR	C18-C19-C20-C21
3	A	1210	YJ0	O25-C26-C27-C28
3	B	1211	YJ0	O25-C26-C27-C28
3	C	1212	YJ0	O25-C26-C27-C28
3	D	1212	YJ0	O25-C26-C27-C28
2	B	1207	9ZR	C33-C34-N35-C38
2	C	1208	9ZR	C33-C34-N35-C38
3	A	1213	YJ0	C27-C28-C53-O54
3	B	1202	YJ0	C27-C28-C53-O54
3	C	1203	YJ0	C27-C28-C53-O54
3	D	1203	YJ0	C27-C28-C53-O54
2	D	1208	9ZR	C33-C34-N35-C36
2	B	1205	9ZR	C40-C42-C43-C44
2	C	1206	9ZR	C40-C42-C43-C44
2	D	1206	9ZR	C40-C42-C43-C44
3	C	1203	YJ0	O36-C35-C37-O38
3	D	1203	YJ0	O36-C35-C37-O38
2	A	1212	9ZR	C4-C5-C6-C7
2	A	1206	9ZR	C45-C46-C47-C48
2	C	1202	9ZR	C4-C5-C6-C7
2	D	1202	9ZR	C4-C5-C6-C7
2	D	1209	9ZR	C42-C43-C44-C45
2	B	1210	9ZR	C42-C43-C44-C45
2	A	1211	9ZR	C17-C18-C19-C20
2	B	1201	9ZR	C17-C18-C19-C20
2	B	1208	9ZR	C42-C43-C44-C45
2	C	1201	9ZR	C17-C18-C19-C20
2	C	1209	9ZR	C42-C43-C44-C45
2	C	1211	9ZR	C42-C43-C44-C45
2	D	1201	9ZR	C17-C18-C19-C20
2	D	1211	9ZR	C42-C43-C44-C45
2	A	1209	9ZR	C42-C43-C44-C45
2	A	1209	9ZR	C52-C53-C54-C55
2	B	1201	9ZR	C4-C5-C6-C7
2	A	1204	9ZR	C40-C42-C43-C44
2	C	1211	9ZR	C52-C53-C54-C55

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Mol	Chain	Res	Type	Atoms
2	D	1211	9ZR	C52-C53-C54-C55
2	C	1205	9ZR	C10-C11-C12-C13
2	A	1207	9ZR	C42-C43-C44-C45
2	B	1208	9ZR	C3-C4-C5-C6
2	A	1207	9ZR	C3-C4-C5-C6
2	C	1209	9ZR	C3-C4-C5-C6
2	D	1209	9ZR	C3-C4-C5-C6
2	B	1210	9ZR	C52-C53-C54-C55
2	D	1208	9ZR	C45-C46-C47-C48
2	A	1208	9ZR	C11-C12-C13-C14
2	B	1207	9ZR	C45-C46-C47-C48
2	C	1208	9ZR	C45-C46-C47-C48
2	C	1201	9ZR	C44-C45-C46-C47
2	C	1202	9ZR	C17-C18-C19-C20
2	D	1202	9ZR	C17-C18-C19-C20
2	A	1212	9ZR	C17-C18-C19-C20
2	A	1201	9ZR	C44-C45-C46-C47
2	A	1211	9ZR	C44-C45-C46-C47
2	D	1201	9ZR	C44-C45-C46-C47
2	B	1209	9ZR	C11-C12-C13-C14
2	C	1210	9ZR	C11-C12-C13-C14
2	D	1210	9ZR	C11-C12-C13-C14
2	C	1205	9ZR	C19-C20-C21-C22
2	D	1205	9ZR	C19-C20-C21-C22
2	A	1208	9ZR	C42-C43-C44-C45
2	B	1210	9ZR	C16-C17-C18-C19
2	A	1206	9ZR	C33-C34-N35-C37
2	C	1208	9ZR	C33-C34-N35-C36
2	D	1208	9ZR	C33-C34-N35-C37
2	C	1211	9ZR	C16-C17-C18-C19
2	A	1203	9ZR	C19-C20-C21-C22
2	B	1204	9ZR	C19-C20-C21-C22
2	D	1211	9ZR	C16-C17-C18-C19
2	A	1204	9ZR	C46-C47-C48-C49
2	D	1205	9ZR	C10-C11-C12-C13
2	A	1201	9ZR	C17-C18-C19-C20
2	A	1204	9ZR	C43-C44-C45-C46
2	A	1209	9ZR	C16-C17-C18-C19
2	B	1209	9ZR	C42-C43-C44-C45
2	D	1210	9ZR	C42-C43-C44-C45
2	C	1210	9ZR	C42-C43-C44-C45
2	A	1206	9ZR	C42-C43-C44-C45

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Mol	Chain	Res	Type	Atoms
2	B	1207	9ZR	C42-C43-C44-C45
2	C	1208	9ZR	C42-C43-C44-C45
2	D	1208	9ZR	C42-C43-C44-C45
2	B	1205	9ZR	C43-C44-C45-C46
2	C	1206	9ZR	C43-C44-C45-C46
2	D	1206	9ZR	C43-C44-C45-C46
2	C	1202	9ZR	C3-C4-C5-C6
2	D	1202	9ZR	C3-C4-C5-C6
2	A	1212	9ZR	C3-C4-C5-C6
2	B	1208	9ZR	C2-C3-C4-C5
2	B	1204	9ZR	C10-C11-C12-C13
2	B	1205	9ZR	C46-C47-C48-C49
2	C	1206	9ZR	C46-C47-C48-C49
2	D	1206	9ZR	C46-C47-C48-C49
2	A	1207	9ZR	C2-C3-C4-C5
2	A	1207	9ZR	C16-C17-C18-C19
2	B	1201	9ZR	C3-C4-C5-C6
2	C	1209	9ZR	C2-C3-C4-C5
2	C	1209	9ZR	C16-C17-C18-C19
2	D	1209	9ZR	C2-C3-C4-C5
2	D	1209	9ZR	C16-C17-C18-C19
2	B	1207	9ZR	C33-C34-N35-C36
2	C	1208	9ZR	C33-C34-N35-C37
2	B	1207	9ZR	C15-C16-C17-C18
2	B	1208	9ZR	C16-C17-C18-C19
2	C	1208	9ZR	C15-C16-C17-C18
2	D	1208	9ZR	C15-C16-C17-C18
3	A	1213	YJ0	O36-C35-C37-O38
2	A	1206	9ZR	C15-C16-C17-C18
2	A	1201	9ZR	C42-C43-C44-C45
2	A	1201	9ZR	C46-C47-C48-C49
2	A	1204	9ZR	C45-C46-C47-C48
2	A	1208	9ZR	C3-C4-C5-C6
2	B	1205	9ZR	C45-C46-C47-C48
2	C	1201	9ZR	C42-C43-C44-C45
2	D	1201	9ZR	C42-C43-C44-C45
2	A	1209	9ZR	C26-C27-O28-P29
2	B	1210	9ZR	C26-C27-O28-P29
2	C	1211	9ZR	C26-C27-O28-P29
2	D	1211	9ZR	C26-C27-O28-P29
2	A	1206	9ZR	C1-C2-C3-C4
2	A	1211	9ZR	C42-C43-C44-C45

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Mol	Chain	Res	Type	Atoms
2	C	1206	9ZR	C45-C46-C47-C48
2	D	1206	9ZR	C45-C46-C47-C48
2	B	1209	9ZR	C3-C4-C5-C6
2	C	1210	9ZR	C3-C4-C5-C6
2	D	1210	9ZR	C3-C4-C5-C6
2	B	1207	9ZR	C33-C34-N35-C37
2	A	1201	9ZR	C6-C7-C8-C9
2	A	1202	9ZR	C10-C11-C12-C13
2	A	1203	9ZR	C10-C11-C12-C13
2	A	1211	9ZR	C46-C47-C48-C49
2	A	1211	9ZR	C6-C7-C8-C9
2	B	1203	9ZR	C10-C11-C12-C13
2	C	1201	9ZR	C46-C47-C48-C49
2	C	1201	9ZR	C6-C7-C8-C9
2	C	1204	9ZR	C10-C11-C12-C13
2	D	1201	9ZR	C46-C47-C48-C49
2	D	1201	9ZR	C6-C7-C8-C9
2	D	1204	9ZR	C10-C11-C12-C13
2	A	1204	9ZR	C25-C26-C27-O28
2	A	1207	9ZR	C25-C26-C27-O28
2	B	1205	9ZR	C25-C26-C27-O28
2	B	1208	9ZR	C25-C26-C27-O28
2	C	1206	9ZR	C25-C26-C27-O28
2	D	1206	9ZR	C25-C26-C27-O28
2	A	1206	9ZR	C52-C53-C54-C55
2	D	1208	9ZR	C1-C2-C3-C4
2	A	1203	9ZR	C52-C53-C54-C55
2	B	1203	9ZR	C9-C10-C11-C12
2	C	1204	9ZR	C9-C10-C11-C12
2	D	1204	9ZR	C9-C10-C11-C12
2	D	1205	9ZR	C17-C18-C19-C20
2	B	1207	9ZR	C1-C2-C3-C4
2	A	1207	9ZR	C5-C6-C7-C8
2	C	1205	9ZR	C17-C18-C19-C20
2	A	1208	9ZR	O24-C25-C26-C27
2	A	1212	9ZR	O24-C25-C26-C27
2	B	1201	9ZR	O24-C25-C26-C27
2	B	1204	9ZR	O24-C25-C26-C27
2	B	1209	9ZR	O24-C25-C26-C27
2	C	1205	9ZR	O24-C25-C26-C27
2	C	1210	9ZR	O24-C25-C26-C27
2	D	1202	9ZR	O24-C25-C26-C27

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Mol	Chain	Res	Type	Atoms
2	D	1205	9ZR	O24-C25-C26-C27
2	D	1210	9ZR	O24-C25-C26-C27
2	D	1201	9ZR	C45-C46-C47-C48
2	B	1204	9ZR	C17-C18-C19-C20
2	A	1211	9ZR	C45-C46-C47-C48
2	C	1201	9ZR	C45-C46-C47-C48
2	C	1208	9ZR	C1-C2-C3-C4
2	D	1205	9ZR	C52-C53-C54-C55
2	B	1204	9ZR	C52-C53-C54-C55
2	A	1206	9ZR	C19-C20-C21-C22
3	B	1202	YJ0	O36-C35-C37-O38
2	A	1202	9ZR	C9-C10-C11-C12
2	C	1205	9ZR	C52-C53-C54-C55
2	C	1209	9ZR	C5-C6-C7-C8
2	D	1209	9ZR	C5-C6-C7-C8
2	A	1206	9ZR	C4-C5-C6-C7
2	B	1208	9ZR	C5-C6-C7-C8
2	D	1208	9ZR	C19-C20-C21-C22
2	D	1204	9ZR	C51-C52-C53-C54
2	B	1210	9ZR	C12-C13-C14-C15
2	C	1204	9ZR	C51-C52-C53-C54
2	C	1211	9ZR	C12-C13-C14-C15
2	D	1211	9ZR	C12-C13-C14-C15
2	B	1207	9ZR	C19-C20-C21-C22
2	A	1203	9ZR	C17-C18-C19-C20
2	A	1209	9ZR	C13-C14-C15-C16
2	A	1209	9ZR	C12-C13-C14-C15
2	B	1203	9ZR	C51-C52-C53-C54
2	C	1211	9ZR	C13-C14-C15-C16
2	D	1211	9ZR	C13-C14-C15-C16
2	A	1202	9ZR	C51-C52-C53-C54
2	B	1210	9ZR	C13-C14-C15-C16
2	C	1208	9ZR	C19-C20-C21-C22
2	B	1207	9ZR	C52-C53-C54-C55
2	B	1201	9ZR	C50-C51-C52-C53
2	D	1208	9ZR	C6-C7-C8-C9
2	D	1208	9ZR	C52-C53-C54-C55
2	C	1208	9ZR	C52-C53-C54-C55
2	B	1207	9ZR	C4-C5-C6-C7
2	A	1201	9ZR	C53-C54-C55-C56
2	B	1209	9ZR	C4-C5-C6-C7
2	C	1208	9ZR	C4-C5-C6-C7

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Mol	Chain	Res	Type	Atoms
2	C	1210	9ZR	C4-C5-C6-C7
2	D	1210	9ZR	C4-C5-C6-C7
2	A	1204	9ZR	C26-C27-O28-P29
2	B	1205	9ZR	C26-C27-O28-P29
2	C	1206	9ZR	C26-C27-O28-P29
2	D	1206	9ZR	C26-C27-O28-P29
2	A	1201	9ZR	C45-C46-C47-C48
2	A	1211	9ZR	C53-C54-C55-C56
2	C	1209	9ZR	C25-C26-C27-O28
2	C	1201	9ZR	C53-C54-C55-C56
2	D	1201	9ZR	C53-C54-C55-C56
2	A	1208	9ZR	C4-C5-C6-C7
2	A	1211	9ZR	C51-C52-C53-C54
2	D	1201	9ZR	C51-C52-C53-C54
2	C	1201	9ZR	C51-C52-C53-C54
2	A	1201	9ZR	C51-C52-C53-C54
2	D	1208	9ZR	C3-C4-C5-C6
2	D	1211	9ZR	C11-C12-C13-C14
2	C	1211	9ZR	C11-C12-C13-C14
2	A	1203	9ZR	O24-C25-C26-C27
2	A	1207	9ZR	O24-C25-C26-C27
2	C	1202	9ZR	O24-C25-C26-C27
2	D	1209	9ZR	O24-C25-C26-C27
2	B	1210	9ZR	C11-C12-C13-C14
2	A	1204	9ZR	C15-C16-C17-C18
2	A	1207	9ZR	C53-C54-C55-C56
2	B	1205	9ZR	C15-C16-C17-C18
2	C	1206	9ZR	C15-C16-C17-C18
2	A	1211	9ZR	C19-C20-C21-C22
2	C	1201	9ZR	C13-C14-C15-C16
2	D	1201	9ZR	C19-C20-C21-C22
2	B	1205	9ZR	C49-C50-C51-C52
2	A	1208	9ZR	C43-C44-C45-C46
2	A	1204	9ZR	O24-C25-C26-O39
2	A	1209	9ZR	O24-C25-C26-O39
2	A	1211	9ZR	O24-C25-C26-O39
2	A	1212	9ZR	O24-C25-C26-O39
2	B	1201	9ZR	O24-C25-C26-O39
2	B	1205	9ZR	O24-C25-C26-O39
2	B	1210	9ZR	O24-C25-C26-O39
2	C	1201	9ZR	O24-C25-C26-O39
2	C	1202	9ZR	O24-C25-C26-O39

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Mol	Chain	Res	Type	Atoms
2	C	1206	9ZR	O24-C25-C26-O39
2	C	1211	9ZR	O24-C25-C26-O39
2	D	1201	9ZR	O24-C25-C26-O39
2	D	1202	9ZR	O24-C25-C26-O39
2	D	1206	9ZR	O24-C25-C26-O39
2	D	1211	9ZR	O24-C25-C26-O39
2	A	1205	9ZR	C44-C45-C46-C47
2	D	1206	9ZR	C15-C16-C17-C18
2	D	1208	9ZR	C4-C5-C6-C7
2	A	1204	9ZR	C49-C50-C51-C52
2	C	1206	9ZR	C49-C50-C51-C52
2	D	1206	9ZR	C49-C50-C51-C52
2	A	1211	9ZR	C13-C14-C15-C16
2	A	1212	9ZR	C13-C14-C15-C16
2	B	1206	9ZR	C52-C53-C54-C55
2	D	1207	9ZR	C52-C53-C54-C55
2	D	1201	9ZR	C13-C14-C15-C16
2	B	1207	9ZR	C6-C7-C8-C9
2	C	1208	9ZR	C6-C7-C8-C9
2	A	1201	9ZR	C11-C12-C13-C14
2	C	1207	9ZR	C52-C53-C54-C55
2	B	1206	9ZR	C44-C45-C46-C47
2	C	1207	9ZR	C44-C45-C46-C47
2	D	1207	9ZR	C44-C45-C46-C47
2	D	1209	9ZR	C53-C54-C55-C56
2	C	1209	9ZR	C53-C54-C55-C56
2	B	1208	9ZR	C53-C54-C55-C56
2	D	1204	9ZR	C25-C26-C27-O28
2	D	1209	9ZR	C25-C26-C27-O28
2	A	1209	9ZR	C11-C12-C13-C14
2	D	1202	9ZR	C13-C14-C15-C16
2	C	1201	9ZR	C19-C20-C21-C22
2	A	1208	9ZR	C14-C15-C16-C17
2	C	1202	9ZR	C13-C14-C15-C16
2	A	1206	9ZR	C6-C7-C8-C9
2	C	1210	9ZR	C43-C44-C45-C46
2	D	1204	9ZR	C43-C44-C45-C46
2	A	1207	9ZR	C14-C15-C16-C17
2	D	1210	9ZR	C43-C44-C45-C46
2	D	1208	9ZR	O39-C26-C27-O28
2	B	1208	9ZR	O24-C25-C26-C27
2	B	1210	9ZR	O24-C25-C26-C27

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Mol	Chain	Res	Type	Atoms
2	C	1201	9ZR	O24-C25-C26-C27
2	C	1209	9ZR	O24-C25-C26-C27
2	D	1201	9ZR	O24-C25-C26-C27
2	B	1209	9ZR	C43-C44-C45-C46
2	C	1208	9ZR	C3-C4-C5-C6
2	D	1210	9ZR	C2-C3-C4-C5
2	B	1209	9ZR	C2-C3-C4-C5
2	C	1210	9ZR	C2-C3-C4-C5
2	A	1201	9ZR	C52-C53-C54-C55
2	A	1211	9ZR	C11-C12-C13-C14
2	A	1204	9ZR	C34-C33-O32-P29
2	A	1212	9ZR	C34-C33-O32-P29
2	B	1201	9ZR	C34-C33-O32-P29
2	B	1205	9ZR	C34-C33-O32-P29
2	C	1202	9ZR	C34-C33-O32-P29
2	C	1206	9ZR	C34-C33-O32-P29
2	D	1202	9ZR	C34-C33-O32-P29
2	D	1206	9ZR	C34-C33-O32-P29
2	B	1201	9ZR	C13-C14-C15-C16
2	A	1201	9ZR	O24-C25-C26-O39
2	B	1208	9ZR	O24-C25-C26-O39
2	B	1203	9ZR	C43-C44-C45-C46
2	A	1208	9ZR	C2-C3-C4-C5
2	A	1202	9ZR	O32-C33-C34-N35
2	A	1206	9ZR	O32-C33-C34-N35
2	B	1203	9ZR	O32-C33-C34-N35
2	B	1207	9ZR	O32-C33-C34-N35
2	C	1204	9ZR	O32-C33-C34-N35
2	C	1208	9ZR	O32-C33-C34-N35
2	D	1204	9ZR	O32-C33-C34-N35
2	D	1208	9ZR	O32-C33-C34-N35
2	C	1204	9ZR	C43-C44-C45-C46
2	B	1207	9ZR	C3-C4-C5-C6
2	D	1201	9ZR	C11-C12-C13-C14
2	A	1202	9ZR	C42-C43-C44-C45
2	B	1204	9ZR	C14-C15-C16-C17
2	D	1205	9ZR	C14-C15-C16-C17
2	D	1204	9ZR	C42-C43-C44-C45
2	A	1203	9ZR	C14-C15-C16-C17
2	C	1205	9ZR	C14-C15-C16-C17
2	A	1204	9ZR	C13-C14-C15-C16
2	A	1205	9ZR	C47-C48-C49-C50

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Mol	Chain	Res	Type	Atoms
2	B	1206	9ZR	C47-C48-C49-C50
2	C	1207	9ZR	C47-C48-C49-C50
2	D	1207	9ZR	C47-C48-C49-C50
2	D	1209	9ZR	C14-C15-C16-C17
2	A	1202	9ZR	C25-C26-C27-O28
2	A	1206	9ZR	C25-C26-C27-O28
2	B	1203	9ZR	C25-C26-C27-O28
2	B	1207	9ZR	C25-C26-C27-O28
2	C	1204	9ZR	C25-C26-C27-O28
2	C	1208	9ZR	C25-C26-C27-O28
2	D	1208	9ZR	C25-C26-C27-O28
2	D	1201	9ZR	C52-C53-C54-C55
2	C	1209	9ZR	C14-C15-C16-C17
2	A	1211	9ZR	C52-C53-C54-C55
2	C	1201	9ZR	C52-C53-C54-C55
2	A	1206	9ZR	C9-C10-C11-C12
2	B	1204	9ZR	C9-C10-C11-C12
2	A	1201	9ZR	C26-C27-O28-P29
2	D	1201	9ZR	C26-C27-O28-P29
2	A	1202	9ZR	O39-C26-C27-O28
2	A	1206	9ZR	O39-C26-C27-O28
2	B	1203	9ZR	O39-C26-C27-O28
2	B	1207	9ZR	O39-C26-C27-O28
2	C	1204	9ZR	O39-C26-C27-O28
2	C	1208	9ZR	O39-C26-C27-O28
2	D	1204	9ZR	O39-C26-C27-O28
2	C	1204	9ZR	C42-C43-C44-C45
2	A	1202	9ZR	C52-C53-C54-C55
2	A	1202	9ZR	C15-C16-C17-C18
2	C	1201	9ZR	C11-C12-C13-C14
2	C	1210	9ZR	C14-C15-C16-C17
2	A	1203	9ZR	O24-C25-C26-O39
2	A	1207	9ZR	O24-C25-C26-O39
2	B	1204	9ZR	O24-C25-C26-O39
2	C	1205	9ZR	O24-C25-C26-O39
2	C	1209	9ZR	O24-C25-C26-O39
2	D	1205	9ZR	O24-C25-C26-O39
2	D	1209	9ZR	O24-C25-C26-O39
2	B	1203	9ZR	C42-C43-C44-C45
2	A	1201	9ZR	O24-C25-C26-C27
2	A	1209	9ZR	O24-C25-C26-C27
2	A	1211	9ZR	O24-C25-C26-C27

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Mol	Chain	Res	Type	Atoms
2	C	1211	9ZR	O24-C25-C26-C27
2	D	1211	9ZR	O24-C25-C26-C27
2	A	1212	9ZR	C50-C51-C52-C53
2	D	1202	9ZR	C50-C51-C52-C53
2	C	1205	9ZR	C9-C10-C11-C12
2	D	1205	9ZR	C9-C10-C11-C12
2	B	1209	9ZR	C14-C15-C16-C17
2	D	1210	9ZR	C14-C15-C16-C17
2	B	1208	9ZR	C14-C15-C16-C17
2	A	1204	9ZR	C27-O28-P29-O32
2	A	1208	9ZR	C27-O28-P29-O30
2	A	1212	9ZR	C27-O28-P29-O30
2	B	1201	9ZR	C33-O32-P29-O31
2	B	1201	9ZR	C27-O28-P29-O30
2	B	1208	9ZR	C33-O32-P29-O30
2	B	1209	9ZR	C27-O28-P29-O30
2	C	1202	9ZR	C33-O32-P29-O30
2	C	1202	9ZR	C27-O28-P29-O30
2	C	1210	9ZR	C27-O28-P29-O30
2	D	1202	9ZR	C27-O28-P29-O30
2	D	1210	9ZR	C27-O28-P29-O30
2	C	1202	9ZR	C50-C51-C52-C53
2	A	1211	9ZR	C26-C27-O28-P29
2	C	1201	9ZR	C26-C27-O28-P29
2	D	1206	9ZR	C13-C14-C15-C16
2	A	1202	9ZR	C18-C19-C20-C21
2	B	1203	9ZR	C52-C53-C54-C55
2	A	1202	9ZR	C27-C26-O39-C40
2	A	1204	9ZR	C25-C26-O39-C40
2	B	1203	9ZR	C27-C26-O39-C40
2	B	1205	9ZR	C25-C26-O39-C40
2	C	1204	9ZR	C27-C26-O39-C40
2	C	1206	9ZR	C25-C26-O39-C40
2	D	1204	9ZR	C27-C26-O39-C40
2	D	1206	9ZR	C25-C26-O39-C40
2	B	1205	9ZR	C13-C14-C15-C16
2	C	1208	9ZR	C50-C51-C52-C53
2	A	1205	9ZR	C52-C53-C54-C55
2	A	1202	9ZR	C43-C44-C45-C46
2	C	1204	9ZR	C52-C53-C54-C55
2	A	1206	9ZR	C3-C4-C5-C6
2	A	1203	9ZR	C9-C10-C11-C12

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Mol	Chain	Res	Type	Atoms
2	B	1201	9ZR	O39-C26-C27-O28
2	D	1204	9ZR	C52-C53-C54-C55
2	C	1206	9ZR	C13-C14-C15-C16
2	D	1208	9ZR	C50-C51-C52-C53
2	B	1203	9ZR	C15-C16-C17-C18
2	A	1207	9ZR	C13-C14-C15-C16
3	C	1203	YJ0	C34-C35-C37-O38
2	B	1207	9ZR	C50-C51-C52-C53
2	B	1208	9ZR	C33-C34-N35-C37
2	D	1209	9ZR	C33-C34-N35-C37
2	C	1204	9ZR	C15-C16-C17-C18
2	A	1206	9ZR	C11-C12-C13-C14
2	D	1211	9ZR	C45-C46-C47-C48
2	C	1209	9ZR	C13-C14-C15-C16
2	A	1206	9ZR	C50-C51-C52-C53
2	C	1204	9ZR	C18-C19-C20-C21
2	C	1202	9ZR	O39-C26-C27-O28
3	A	1213	YJ0	C56-C55-O54-C53
2	C	1208	9ZR	C9-C10-C11-C12
2	B	1208	9ZR	C15-C16-C17-C18
2	C	1211	9ZR	C45-C46-C47-C48
2	D	1209	9ZR	C13-C14-C15-C16
3	D	1203	YJ0	C34-C35-C37-O38
2	C	1209	9ZR	C33-C34-N35-C37
2	D	1204	9ZR	C18-C19-C20-C21
2	B	1207	9ZR	C9-C10-C11-C12
2	B	1210	9ZR	C45-C46-C47-C48
2	B	1203	9ZR	C18-C19-C20-C21
2	D	1204	9ZR	C15-C16-C17-C18
2	C	1209	9ZR	C15-C16-C17-C18
2	B	1208	9ZR	C13-C14-C15-C16
3	A	1213	YJ0	O60-C55-O54-C53
2	A	1201	9ZR	C13-C14-C15-C16
2	A	1205	9ZR	C53-C54-C55-C56
2	D	1210	9ZR	C44-C45-C46-C47
2	A	1202	9ZR	C44-C45-C46-C47
2	B	1209	9ZR	C44-C45-C46-C47
2	D	1208	9ZR	C9-C10-C11-C12
2	A	1208	9ZR	C44-C45-C46-C47
2	C	1210	9ZR	C44-C45-C46-C47
2	D	1209	9ZR	C15-C16-C17-C18
2	A	1207	9ZR	C43-C44-C45-C46

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Mol	Chain	Res	Type	Atoms
2	D	1202	9ZR	O39-C26-C27-O28
2	A	1209	9ZR	C45-C46-C47-C48
2	D	1209	9ZR	C43-C44-C45-C46
2	B	1209	9ZR	C10-C11-C12-C13
2	C	1210	9ZR	C10-C11-C12-C13
2	D	1210	9ZR	C10-C11-C12-C13
2	D	1201	9ZR	C3-C4-C5-C6
2	A	1207	9ZR	C15-C16-C17-C18
2	A	1201	9ZR	C3-C4-C5-C6
2	A	1206	9ZR	C14-C15-C16-C17
2	C	1209	9ZR	C43-C44-C45-C46
2	A	1211	9ZR	C3-C4-C5-C6
2	B	1205	9ZR	O24-C25-C26-C27
2	C	1206	9ZR	O24-C25-C26-C27
2	D	1206	9ZR	O24-C25-C26-C27
2	A	1209	9ZR	C14-C15-C16-C17
3	A	1213	YJ0	C26-C27-C28-C53
3	C	1203	YJ0	C26-C27-C28-C53
3	D	1203	YJ0	C26-C27-C28-C53
2	C	1201	9ZR	C3-C4-C5-C6
2	B	1210	9ZR	C14-C15-C16-C17
2	A	1211	9ZR	C9-C10-C11-C12
2	C	1201	9ZR	C9-C10-C11-C12
2	D	1201	9ZR	C9-C10-C11-C12
2	A	1208	9ZR	C10-C11-C12-C13
2	B	1201	9ZR	C33-C34-N35-C36
2	C	1208	9ZR	C11-C12-C13-C14
2	C	1211	9ZR	C14-C15-C16-C17
2	D	1208	9ZR	C16-C17-C18-C19
2	D	1211	9ZR	C14-C15-C16-C17
2	C	1208	9ZR	C14-C15-C16-C17
2	B	1208	9ZR	C43-C44-C45-C46
2	A	1208	9ZR	C7-C8-C9-C10
2	D	1210	9ZR	C7-C8-C9-C10
2	B	1201	9ZR	C1-C2-C3-C4
2	B	1207	9ZR	C14-C15-C16-C17
2	D	1204	9ZR	C4-C5-C6-C7
2	B	1207	9ZR	C11-C12-C13-C14
2	D	1202	9ZR	C1-C2-C3-C4
2	A	1207	9ZR	C33-C34-N35-C37
2	C	1204	9ZR	C4-C5-C6-C7
2	B	1204	9ZR	C47-C48-C49-C50

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Mol	Chain	Res	Type	Atoms
2	B	1204	9ZR	C49-C50-C51-C52
2	B	1209	9ZR	C49-C50-C51-C52
2	B	1209	9ZR	C7-C8-C9-C10
2	B	1210	9ZR	C49-C50-C51-C52
2	C	1210	9ZR	C49-C50-C51-C52
2	D	1205	9ZR	C47-C48-C49-C50
2	D	1205	9ZR	C49-C50-C51-C52
2	B	1203	9ZR	C4-C5-C6-C7
2	A	1202	9ZR	C50-C51-C52-C53
2	B	1203	9ZR	C50-C51-C52-C53
2	A	1212	9ZR	C1-C2-C3-C4
2	C	1202	9ZR	C1-C2-C3-C4
2	C	1205	9ZR	C47-C48-C49-C50
2	C	1205	9ZR	C49-C50-C51-C52
2	C	1210	9ZR	C7-C8-C9-C10
2	D	1210	9ZR	C49-C50-C51-C52
2	A	1208	9ZR	C26-C27-O28-P29
2	B	1209	9ZR	C26-C27-O28-P29
2	A	1212	9ZR	O39-C26-C27-O28
2	B	1203	9ZR	C33-C34-N35-C36
2	B	1208	9ZR	C33-C34-N35-C38
2	D	1209	9ZR	C33-C34-N35-C38
2	A	1202	9ZR	C11-C12-C13-C14
2	A	1201	9ZR	C9-C10-C11-C12
2	A	1208	9ZR	C49-C50-C51-C52
2	D	1211	9ZR	C49-C50-C51-C52
2	A	1206	9ZR	C16-C17-C18-C19
2	A	1202	9ZR	O39-C40-C42-C43
2	C	1204	9ZR	C11-C12-C13-C14
2	C	1204	9ZR	C50-C51-C52-C53
2	A	1201	9ZR	C14-C15-C16-C17
2	A	1203	9ZR	C49-C50-C51-C52
2	C	1211	9ZR	C49-C50-C51-C52
2	D	1202	9ZR	O39-C40-C42-C43
2	D	1204	9ZR	C11-C12-C13-C14
2	B	1208	9ZR	C33-C34-N35-C36
2	C	1204	9ZR	C33-C34-N35-C36
2	C	1209	9ZR	C33-C34-N35-C38
2	D	1204	9ZR	C33-C34-N35-C36
2	D	1209	9ZR	C33-C34-N35-C36
3	A	1213	YJ0	C34-C35-C37-O38
2	C	1202	9ZR	O39-C40-C42-C43

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Mol	Chain	Res	Type	Atoms
2	C	1204	9ZR	O39-C40-C42-C43
2	A	1203	9ZR	C47-C48-C49-C50
2	A	1209	9ZR	C49-C50-C51-C52
2	B	1201	9ZR	C9-C10-C11-C12
2	D	1208	9ZR	C14-C15-C16-C17
2	C	1210	9ZR	C12-C13-C14-C15
2	B	1201	9ZR	C26-C27-O28-P29
2	C	1210	9ZR	C26-C27-O28-P29
2	D	1210	9ZR	C26-C27-O28-P29
2	B	1209	9ZR	C12-C13-C14-C15
2	B	1201	9ZR	O39-C40-C42-C43
2	B	1203	9ZR	C11-C12-C13-C14
2	A	1212	9ZR	O39-C40-C42-C43
2	B	1203	9ZR	O39-C40-C42-C43
2	D	1210	9ZR	C12-C13-C14-C15
2	A	1211	9ZR	O39-C40-C42-C43
2	C	1208	9ZR	C16-C17-C18-C19
2	A	1212	9ZR	C33-C34-N35-C36
2	C	1209	9ZR	C33-C34-N35-C36
2	B	1207	9ZR	C16-C17-C18-C19
2	A	1203	9ZR	O39-C40-C42-C43
2	C	1201	9ZR	O39-C40-C42-C43
2	D	1201	9ZR	O39-C40-C42-C43
2	D	1204	9ZR	O39-C40-C42-C43
2	D	1208	9ZR	C11-C12-C13-C14
2	C	1202	9ZR	C26-C27-O28-P29
2	A	1202	9ZR	C20-C21-C22-O24
2	A	1206	9ZR	C20-C21-C22-O24
2	D	1202	9ZR	C33-C34-N35-C36
3	C	1203	YJ0	O60-C55-O54-C53
3	D	1203	YJ0	O60-C55-O54-C53
2	A	1201	9ZR	O39-C40-C42-C43
2	B	1203	9ZR	C20-C21-C22-O24
2	B	1204	9ZR	O39-C40-C42-C43
2	C	1204	9ZR	C20-C21-C22-O24
2	C	1208	9ZR	C20-C21-C22-O24
2	D	1204	9ZR	C20-C21-C22-O24
2	D	1202	9ZR	C9-C10-C11-C12
2	D	1209	9ZR	C49-C50-C51-C52
2	D	1205	9ZR	O39-C40-C42-C43
2	D	1208	9ZR	C20-C21-C22-O24
2	A	1208	9ZR	C5-C6-C7-C8

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Mol	Chain	Res	Type	Atoms
2	B	1207	9ZR	C20-C21-C22-O24
2	C	1205	9ZR	O39-C40-C42-C43
2	A	1202	9ZR	C4-C5-C6-C7
2	A	1212	9ZR	C9-C10-C11-C12
2	A	1207	9ZR	C33-C34-N35-C36
2	A	1207	9ZR	C33-C34-N35-C38
2	C	1202	9ZR	C33-C34-N35-C36
2	B	1208	9ZR	C18-C19-C20-C21
2	C	1210	9ZR	C5-C6-C7-C8
2	D	1210	9ZR	C5-C6-C7-C8
2	B	1209	9ZR	C5-C6-C7-C8
2	C	1204	9ZR	O41-C40-C42-C43
2	B	1208	9ZR	C49-C50-C51-C52
2	C	1202	9ZR	C9-C10-C11-C12
2	A	1206	9ZR	C43-C44-C45-C46
2	A	1212	9ZR	C26-C27-O28-P29
2	D	1202	9ZR	C26-C27-O28-P29
2	B	1204	9ZR	C43-C44-C45-C46
2	A	1208	9ZR	C12-C13-C14-C15
2	A	1201	9ZR	O41-C40-C42-C43
2	B	1201	9ZR	O41-C40-C42-C43
2	C	1209	9ZR	C49-C50-C51-C52
2	A	1211	9ZR	O41-C40-C42-C43
2	B	1203	9ZR	O41-C40-C42-C43
2	D	1204	9ZR	O41-C40-C42-C43
2	A	1202	9ZR	C33-C34-N35-C36
2	B	1201	9ZR	C33-C34-N35-C37
2	B	1203	9ZR	C33-C34-N35-C37
2	C	1204	9ZR	C33-C34-N35-C37
2	D	1204	9ZR	C33-C34-N35-C37
2	B	1204	9ZR	O41-C40-C42-C43
2	D	1201	9ZR	O41-C40-C42-C43
2	A	1203	9ZR	O41-C40-C42-C43
2	C	1201	9ZR	O41-C40-C42-C43
2	A	1211	9ZR	C49-C50-C51-C52
2	A	1202	9ZR	O41-C40-C42-C43
2	A	1206	9ZR	C20-C21-C22-O23
2	C	1202	9ZR	O41-C40-C42-C43
2	C	1208	9ZR	C20-C21-C22-O23
2	D	1204	9ZR	C20-C21-C22-O23
2	A	1201	9ZR	C50-C51-C52-C53
2	D	1204	9ZR	C50-C51-C52-C53

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	C	1209	9ZR	C18-C19-C20-C21
2	A	1212	9ZR	O41-C40-C42-C43
2	D	1202	9ZR	O41-C40-C42-C43
2	B	1203	9ZR	C20-C21-C22-O23
2	B	1207	9ZR	C20-C21-C22-O23
2	D	1208	9ZR	C20-C21-C22-O23
2	A	1204	9ZR	O24-C25-C26-C27
2	C	1204	9ZR	C20-C21-C22-O23
2	D	1205	9ZR	C43-C44-C45-C46
2	B	1201	9ZR	C33-C34-N35-C38
2	B	1203	9ZR	C33-C34-N35-C38
2	D	1205	9ZR	O41-C40-C42-C43
2	A	1204	9ZR	O39-C40-C42-C43
2	C	1205	9ZR	O41-C40-C42-C43
2	D	1201	9ZR	C49-C50-C51-C52
2	A	1206	9ZR	O39-C40-C42-C43
2	C	1205	9ZR	C43-C44-C45-C46
2	A	1207	9ZR	C18-C19-C20-C21
2	A	1202	9ZR	C3-C4-C5-C6
2	B	1205	9ZR	O39-C40-C42-C43
2	D	1206	9ZR	O39-C40-C42-C43
2	A	1201	9ZR	C49-C50-C51-C52
2	C	1201	9ZR	C49-C50-C51-C52
2	A	1202	9ZR	C20-C21-C22-O23

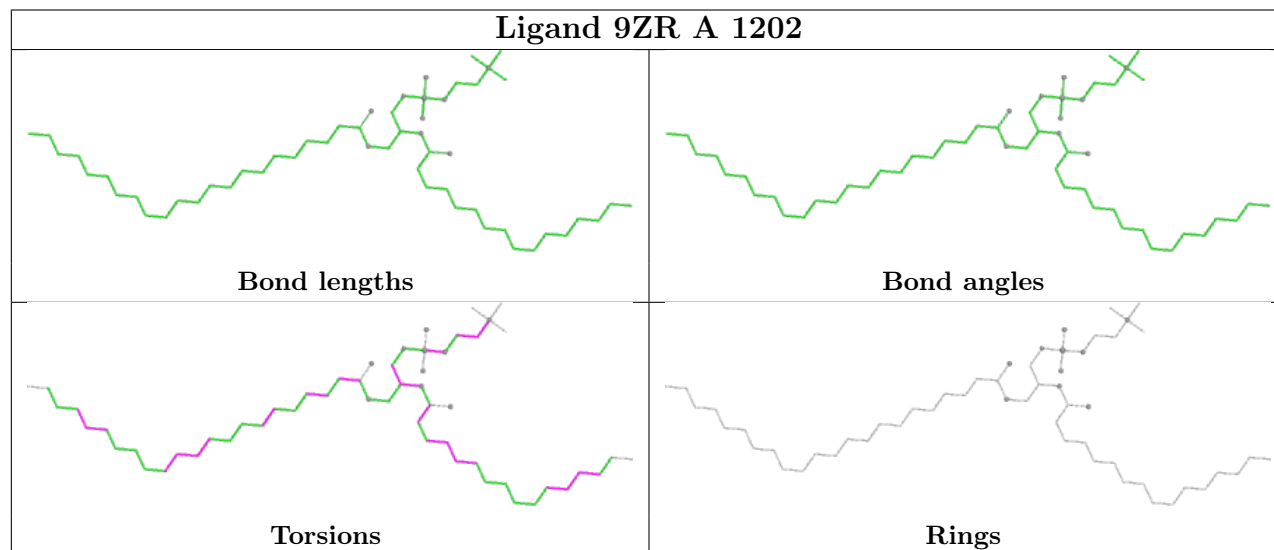
There are no ring outliers.

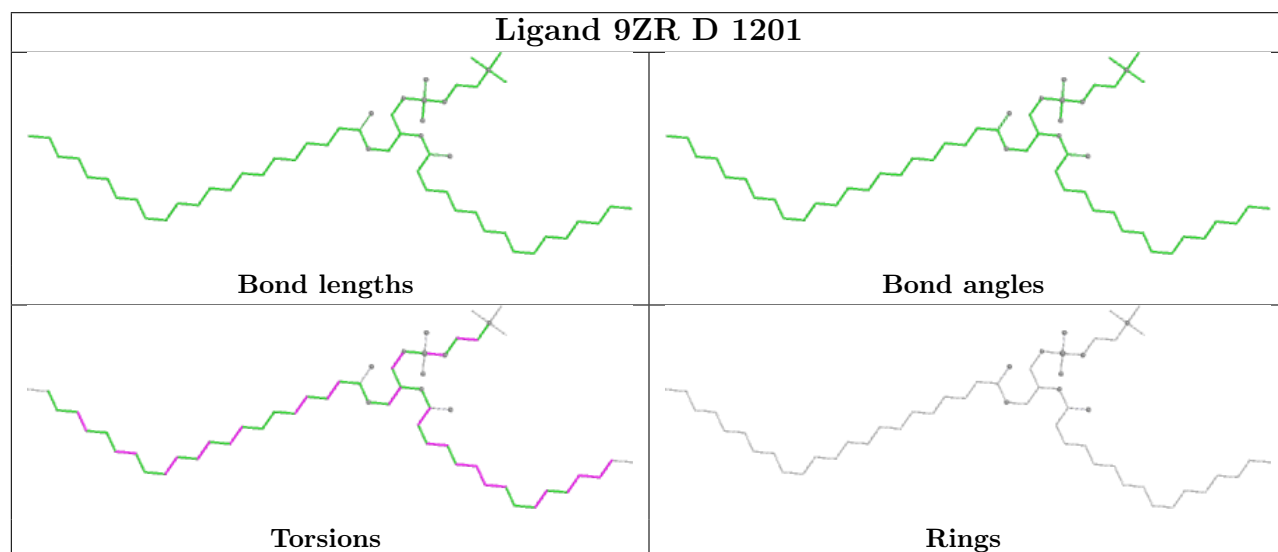
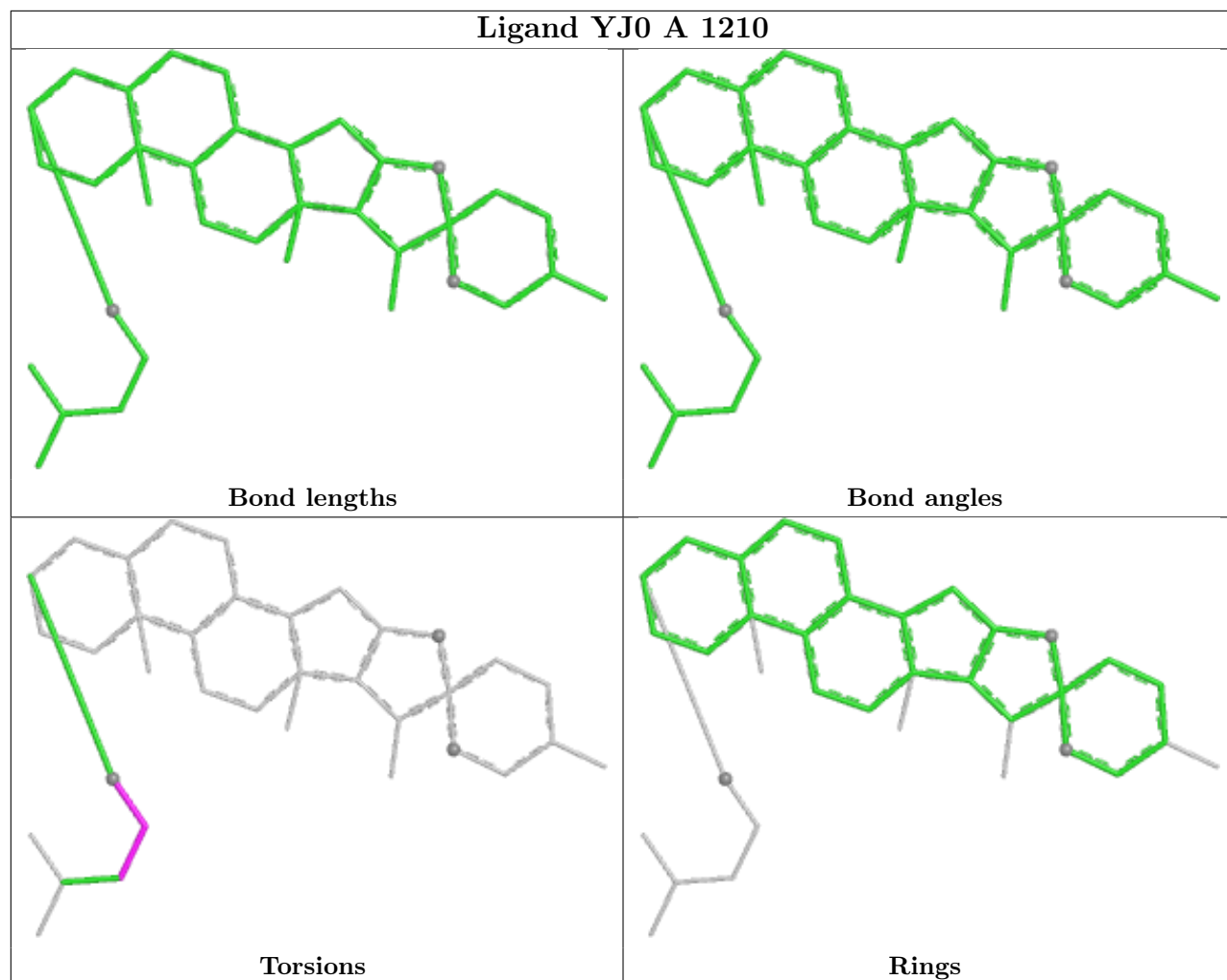
8 monomers are involved in 14 short contacts:

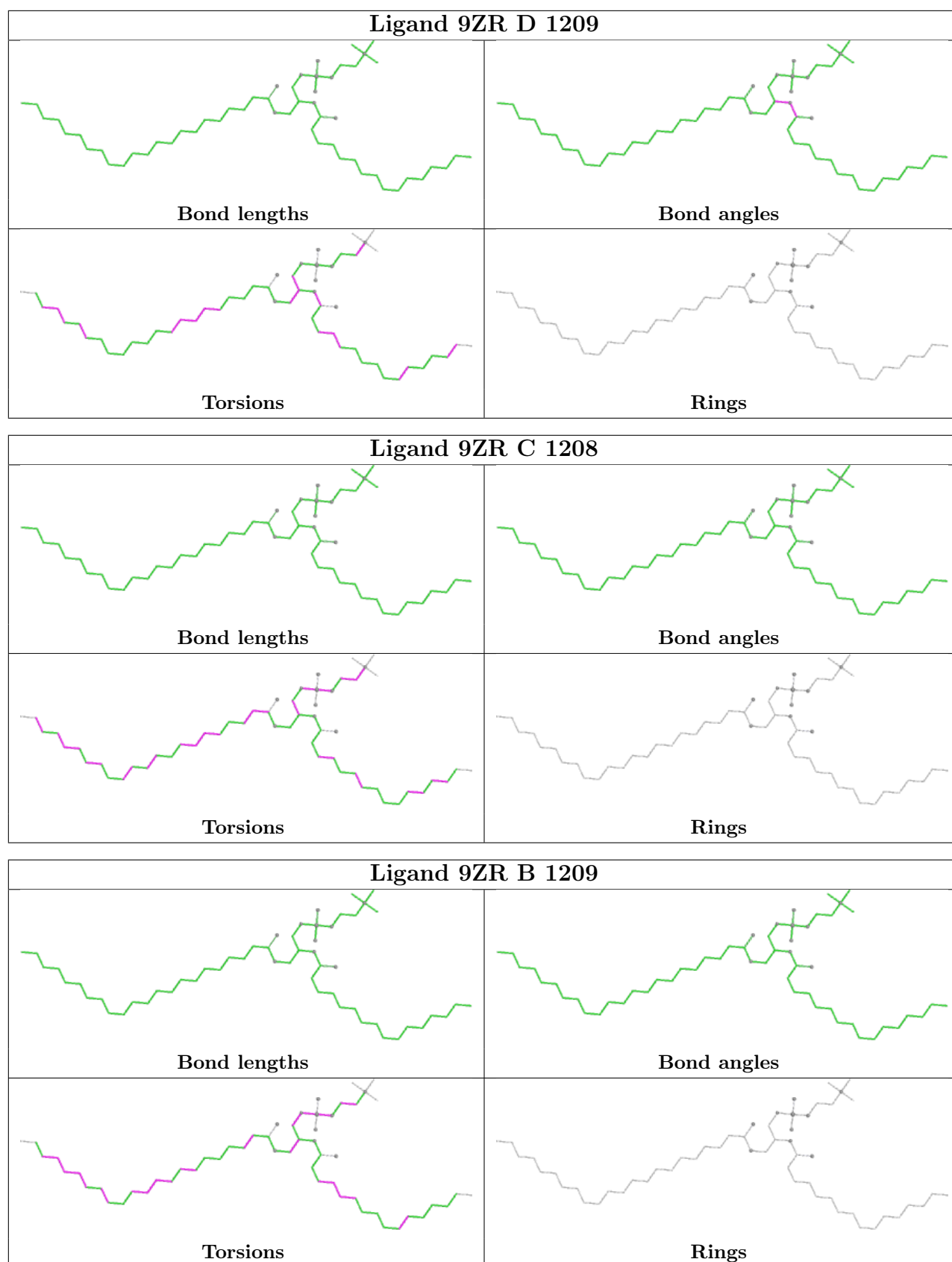
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1212	9ZR	1	0
2	D	1202	9ZR	1	0
3	B	1202	YJ0	5	0
3	A	1213	YJ0	3	0
3	C	1203	YJ0	3	0
2	B	1201	9ZR	2	0
2	C	1202	9ZR	1	0
3	D	1203	YJ0	3	0

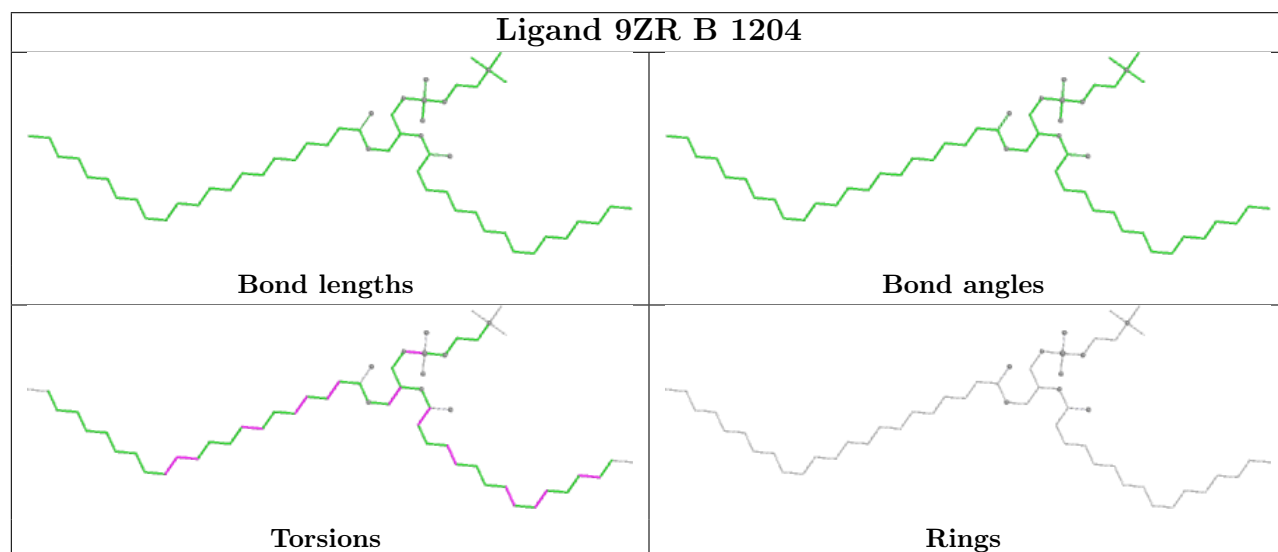
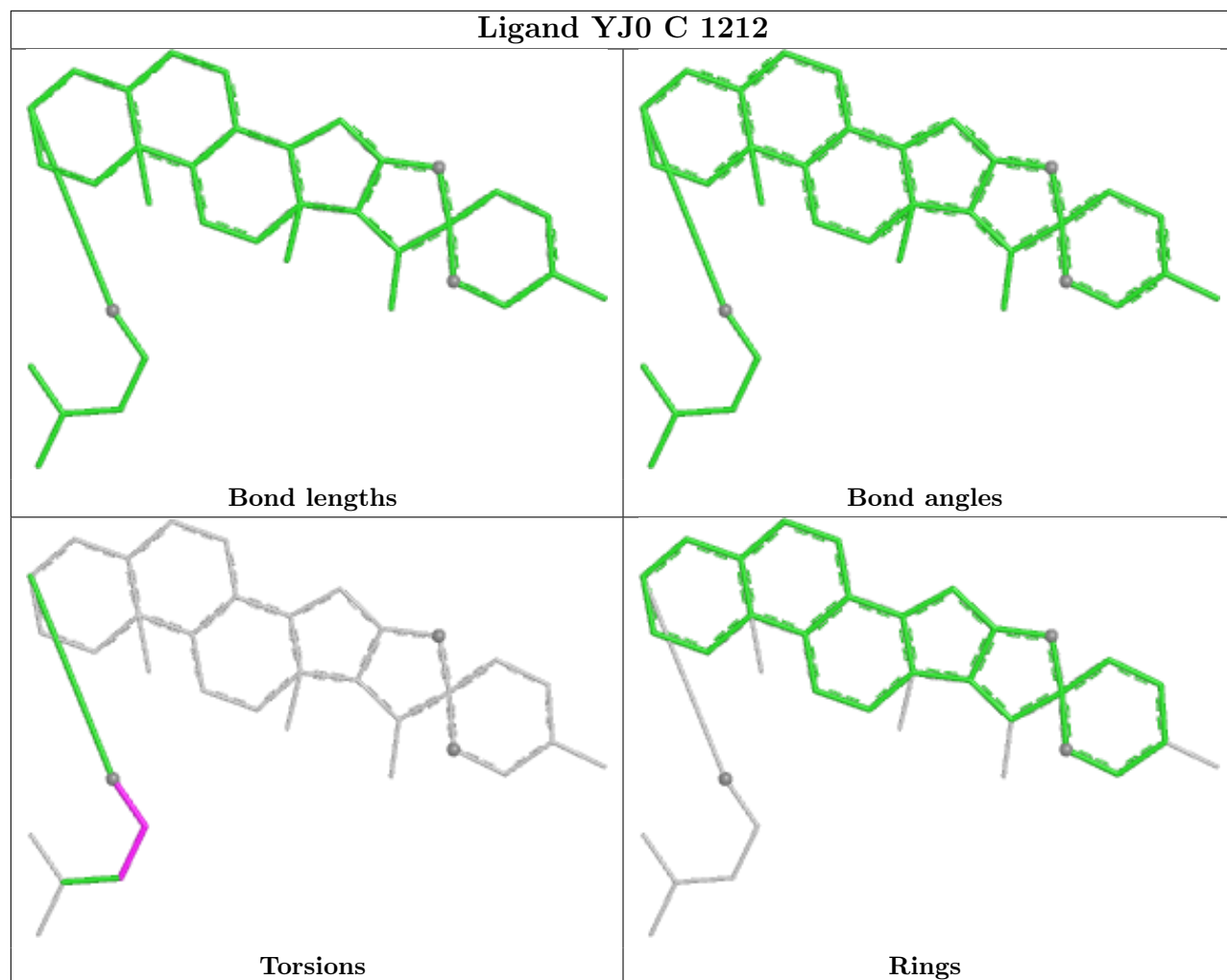
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

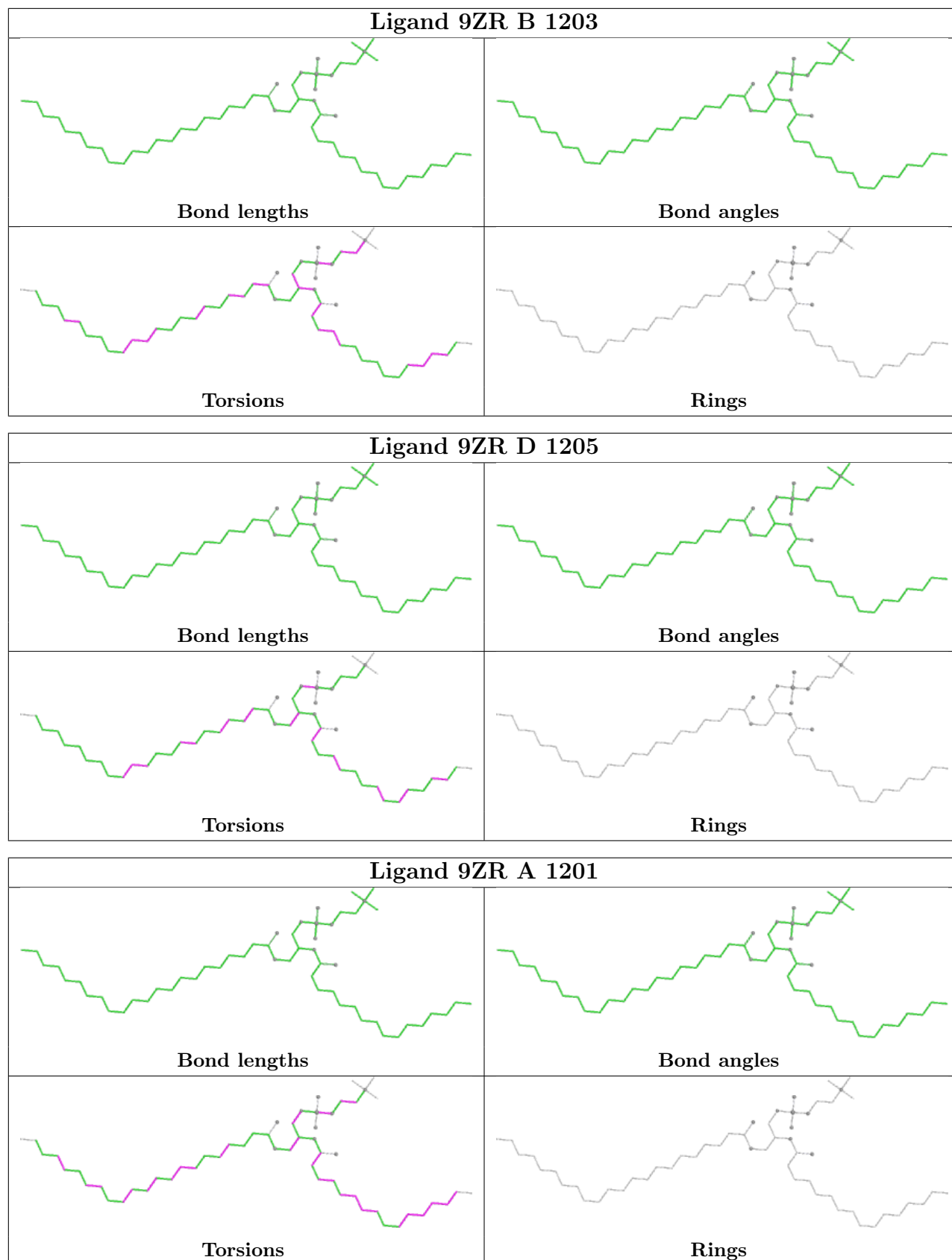
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question 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.

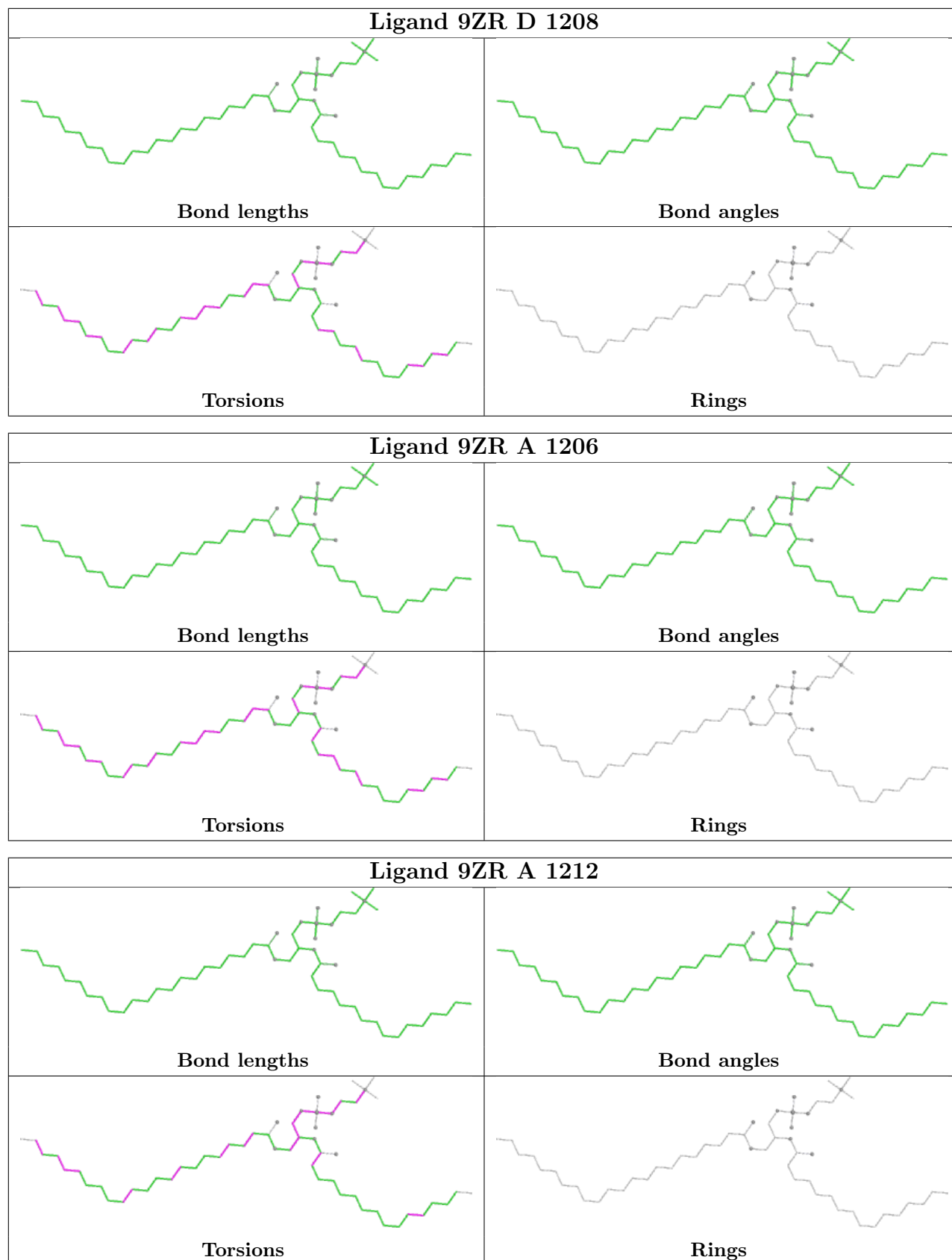


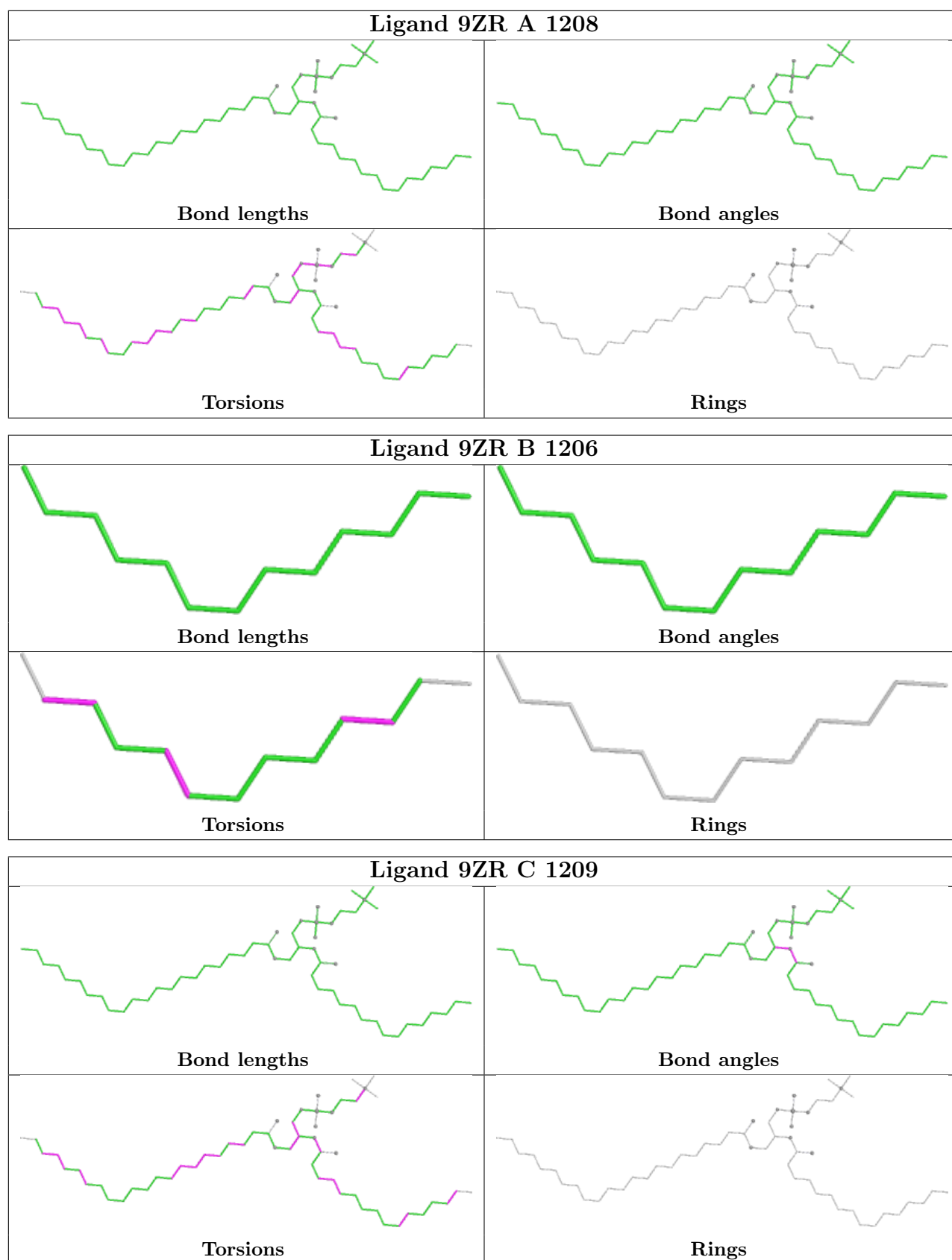


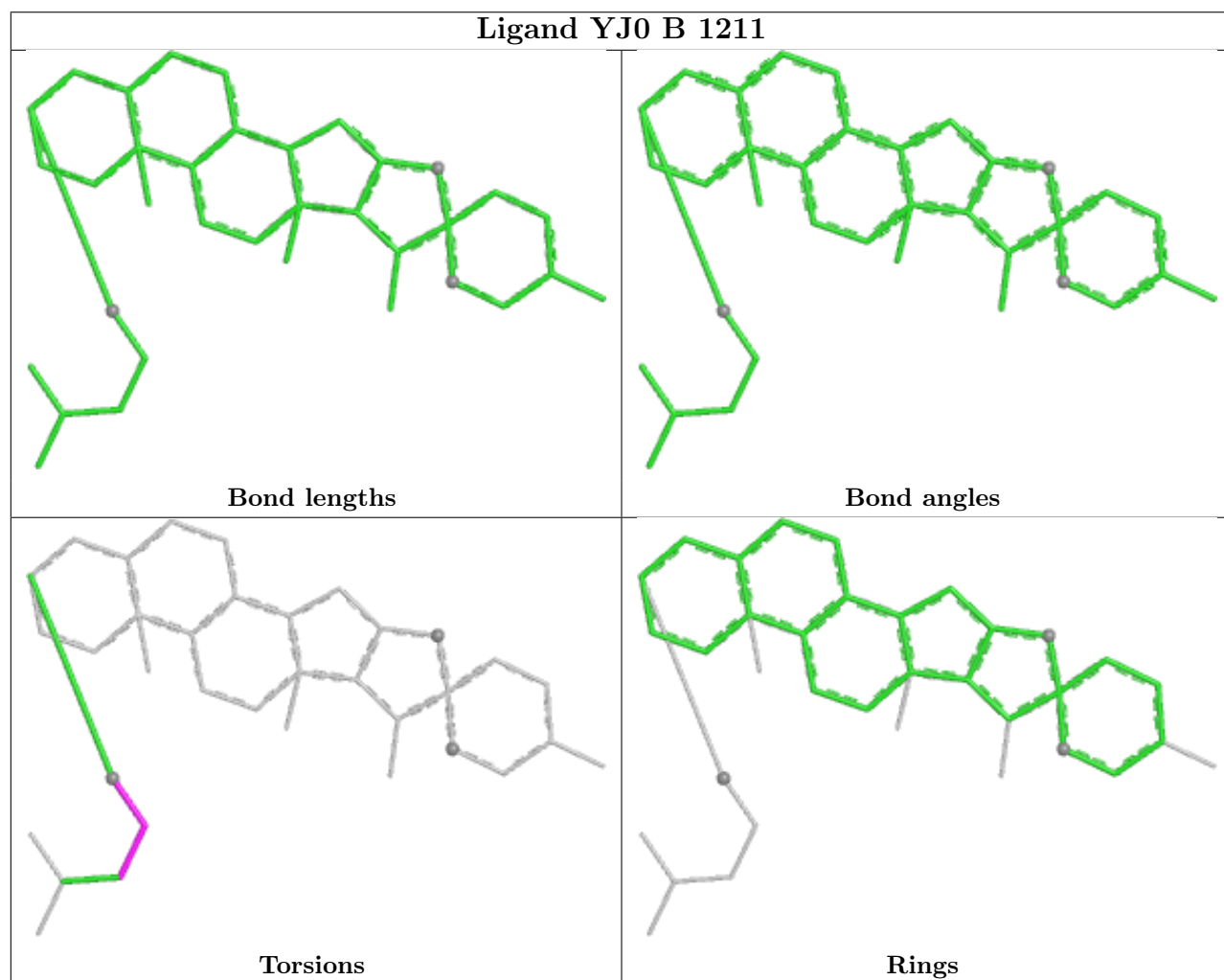
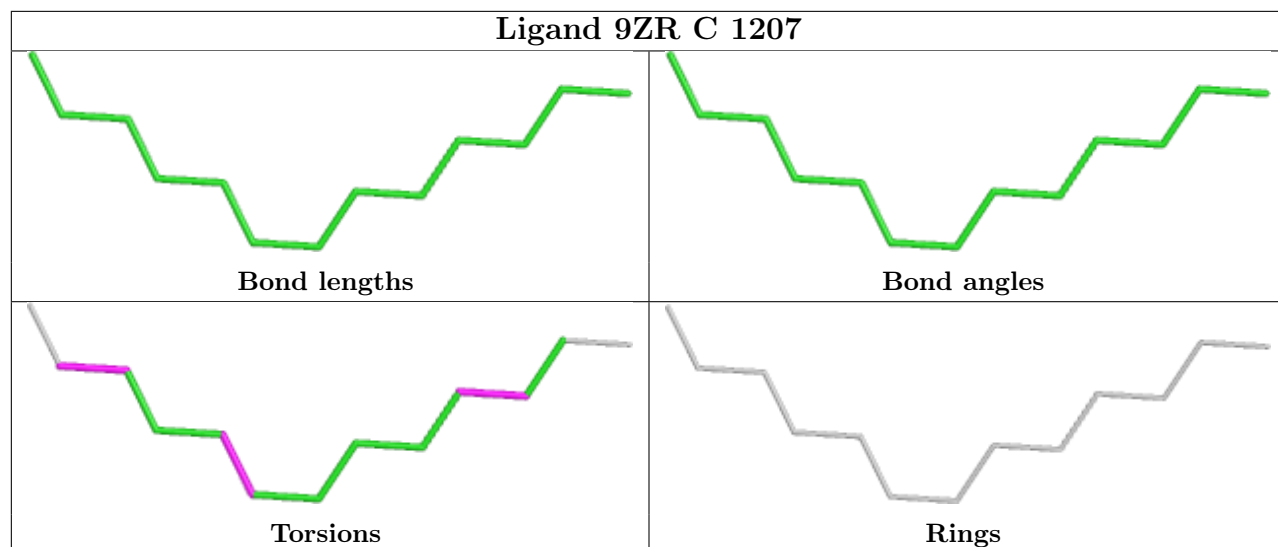


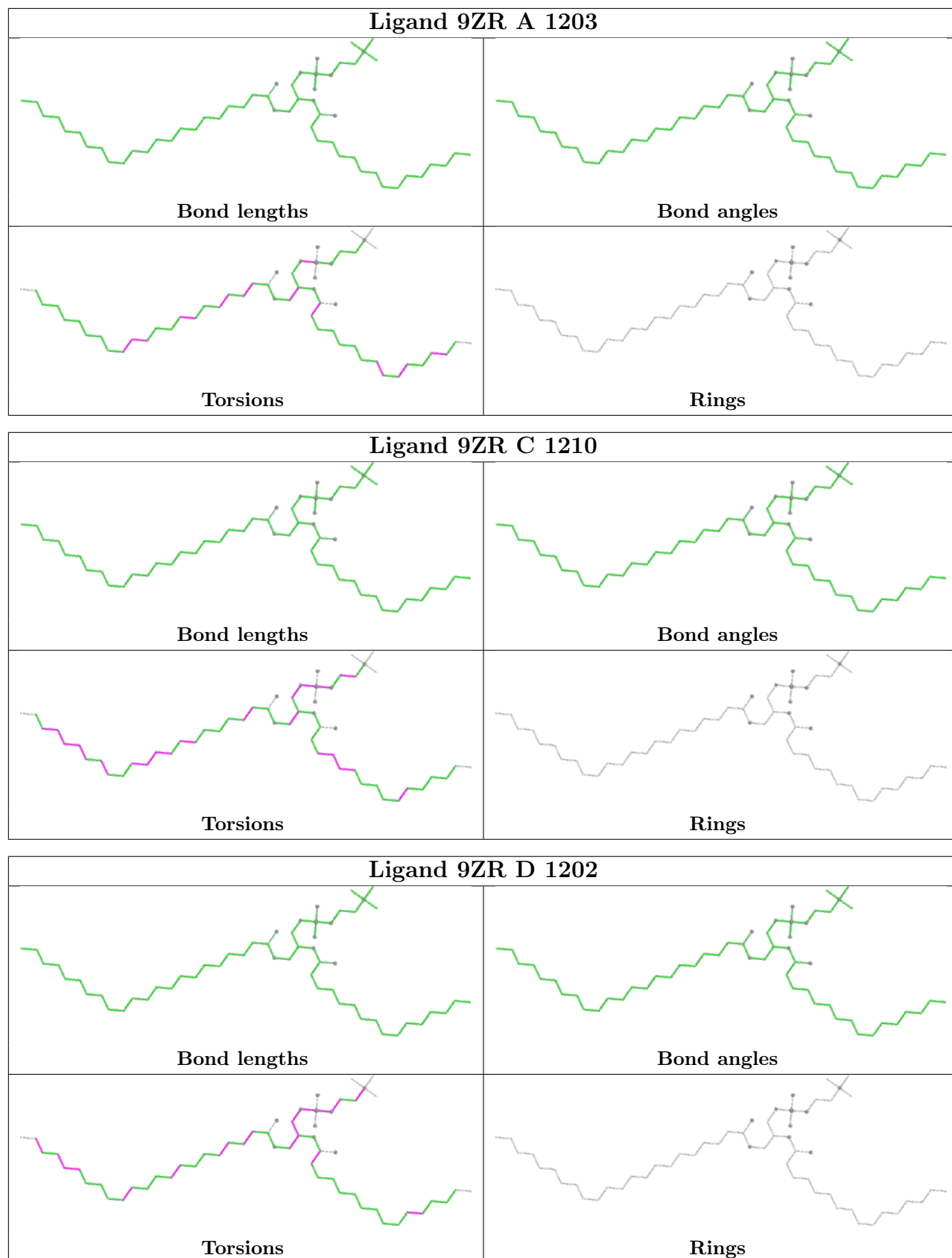


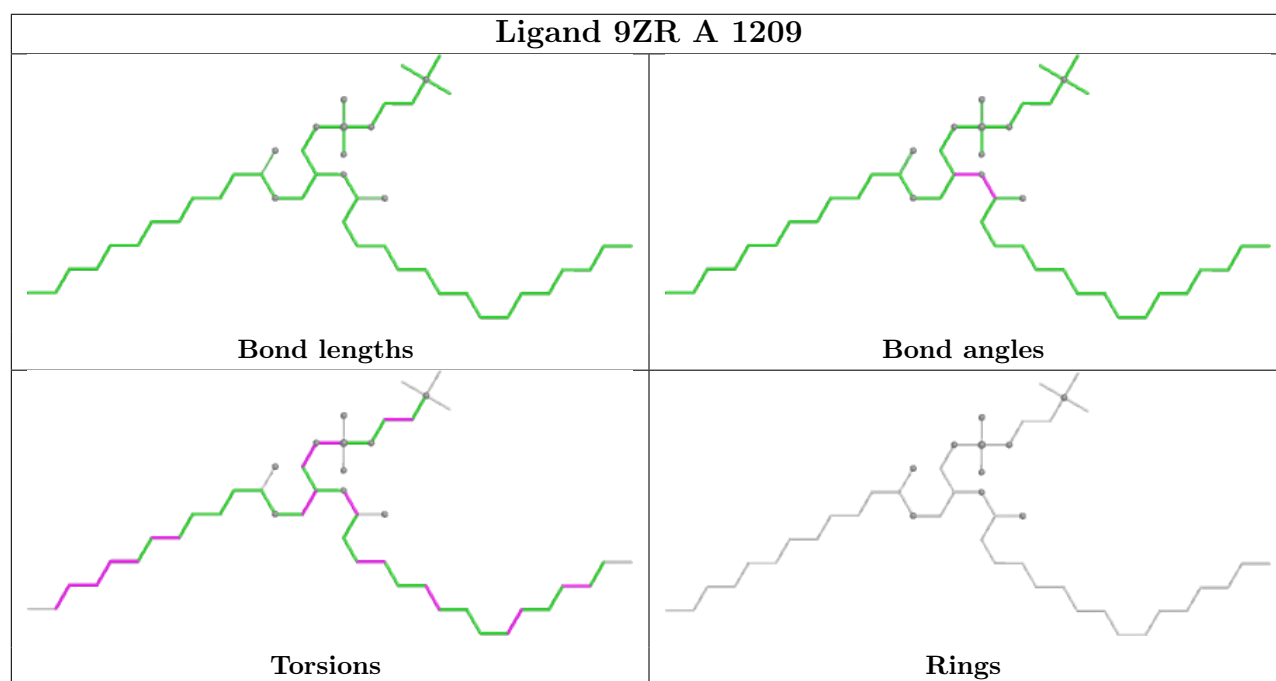
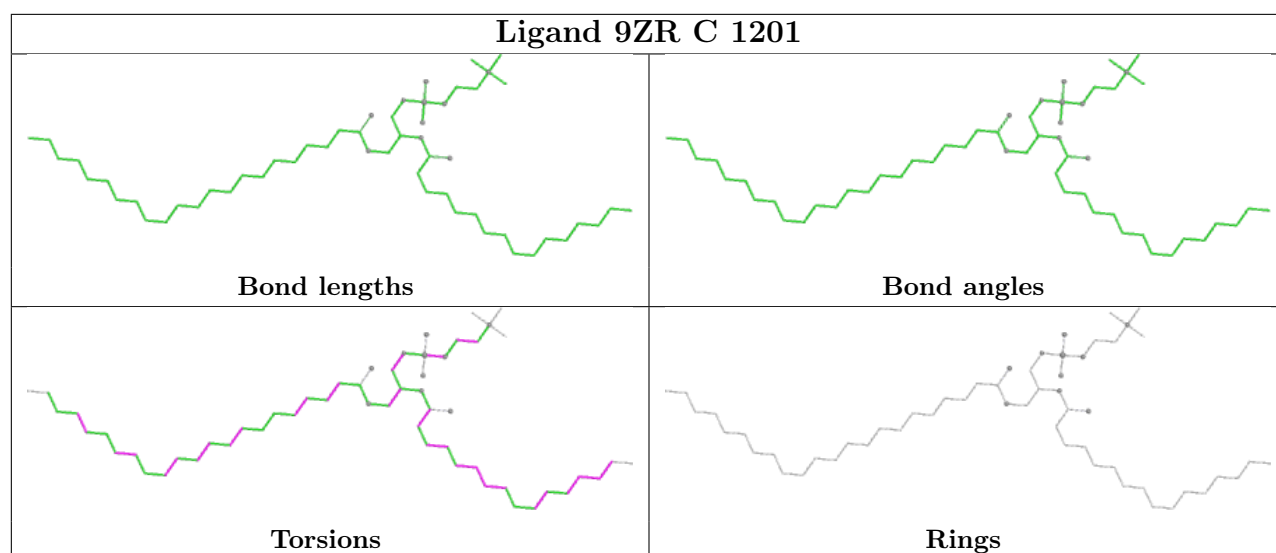


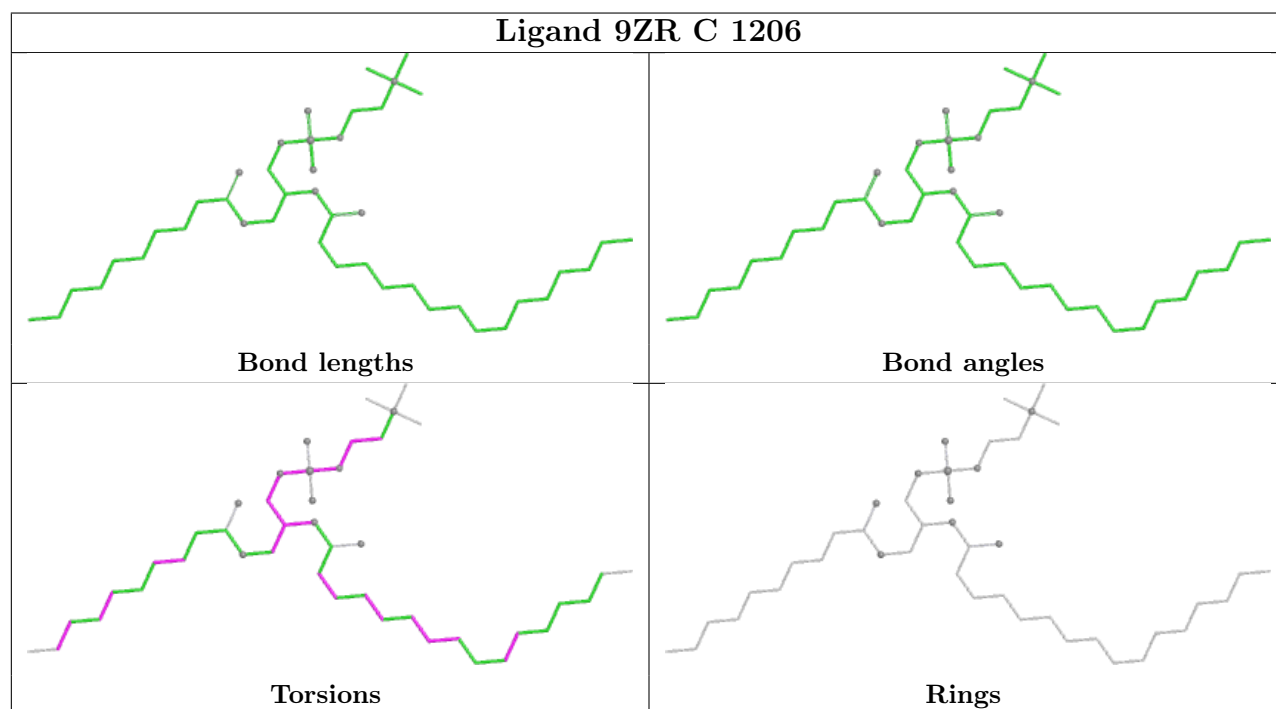
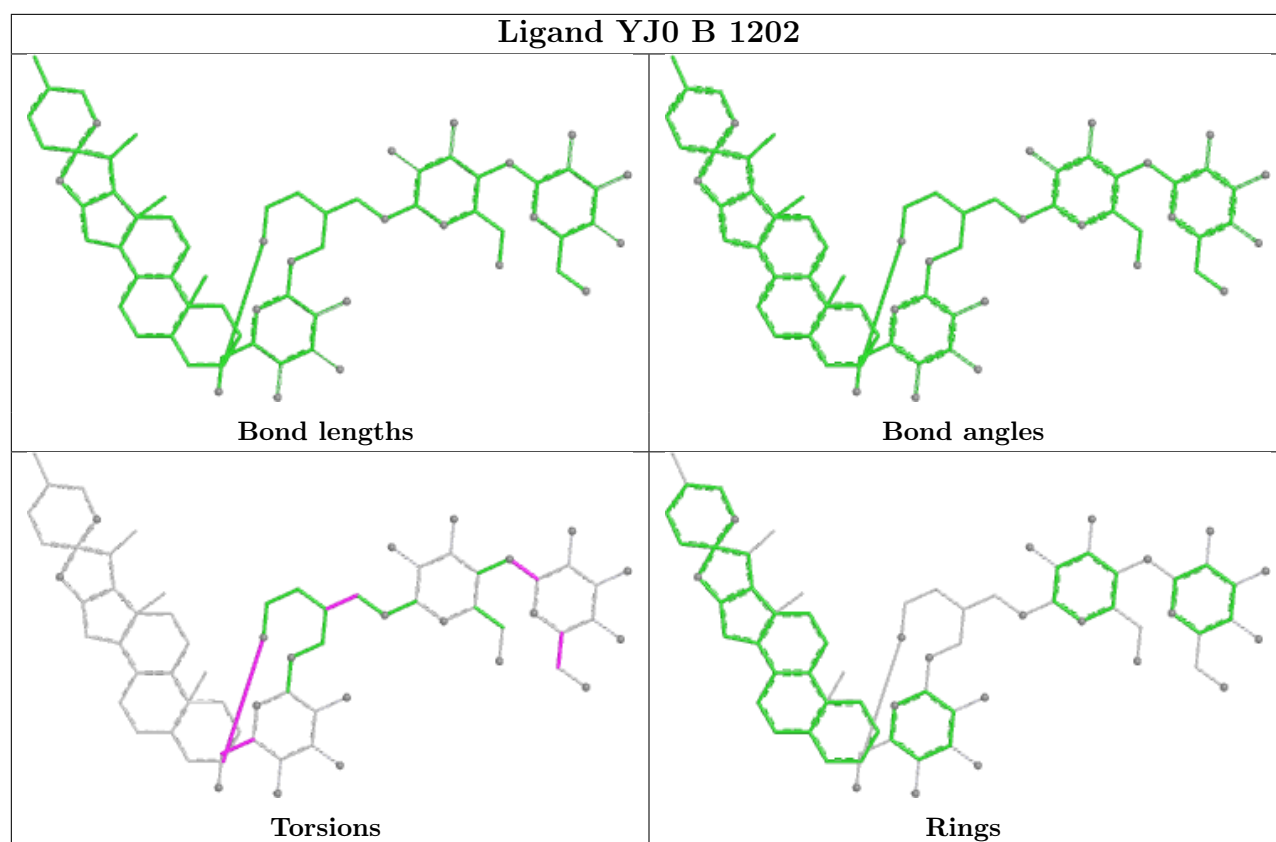


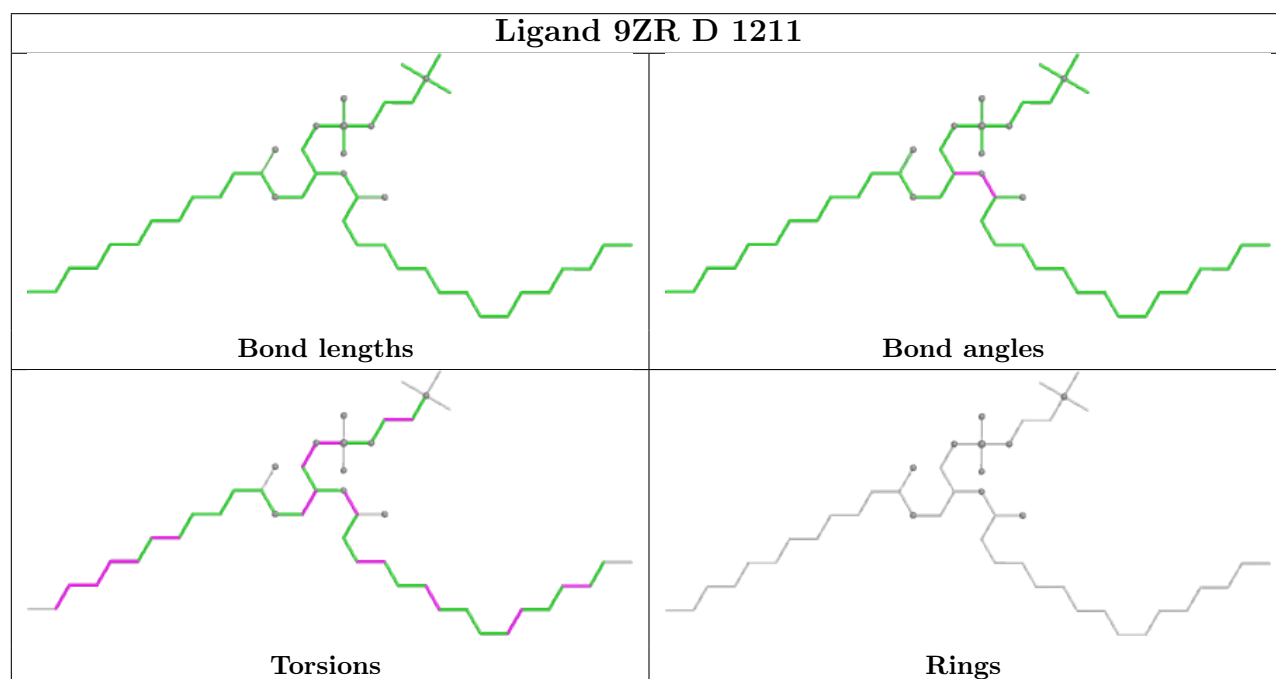
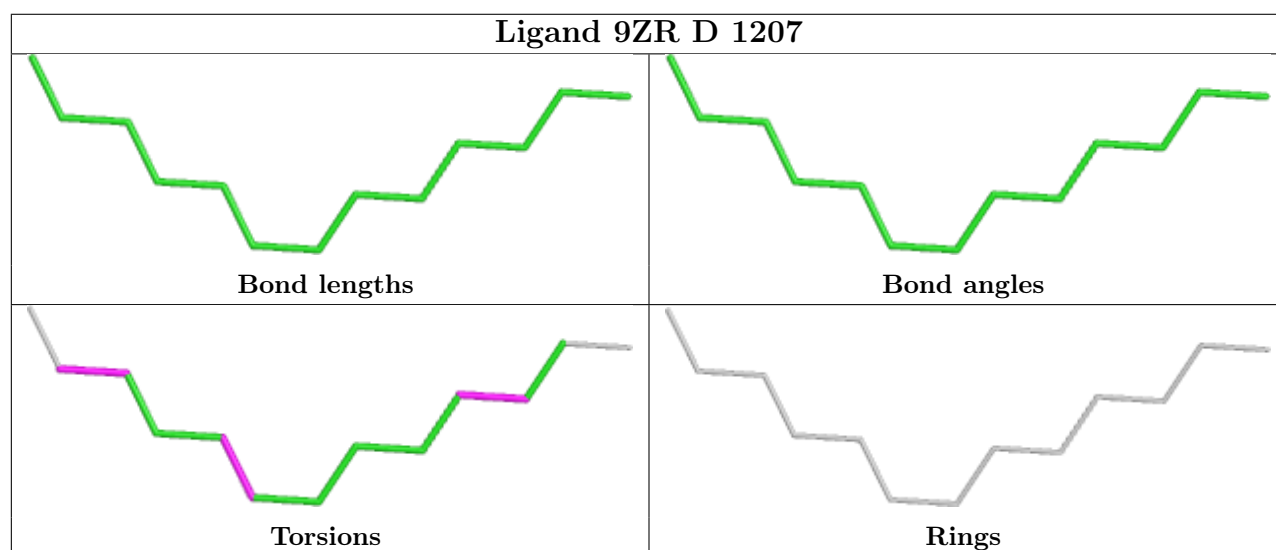
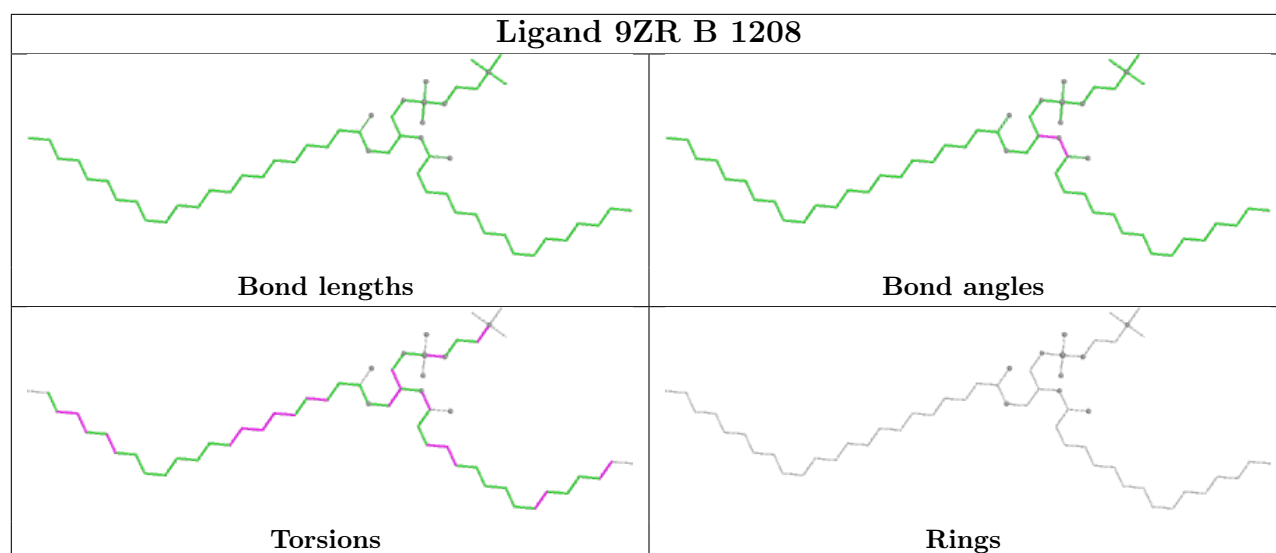


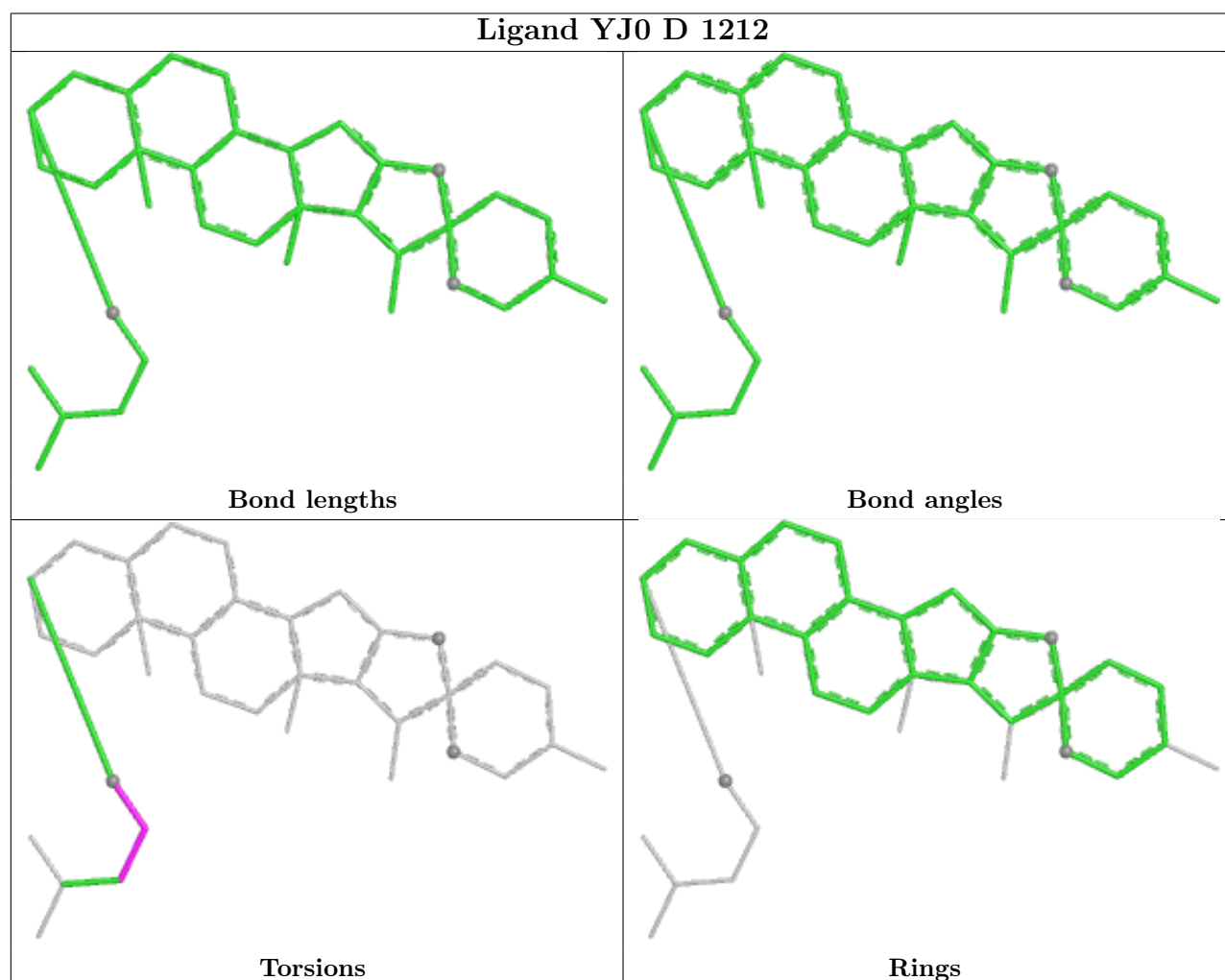
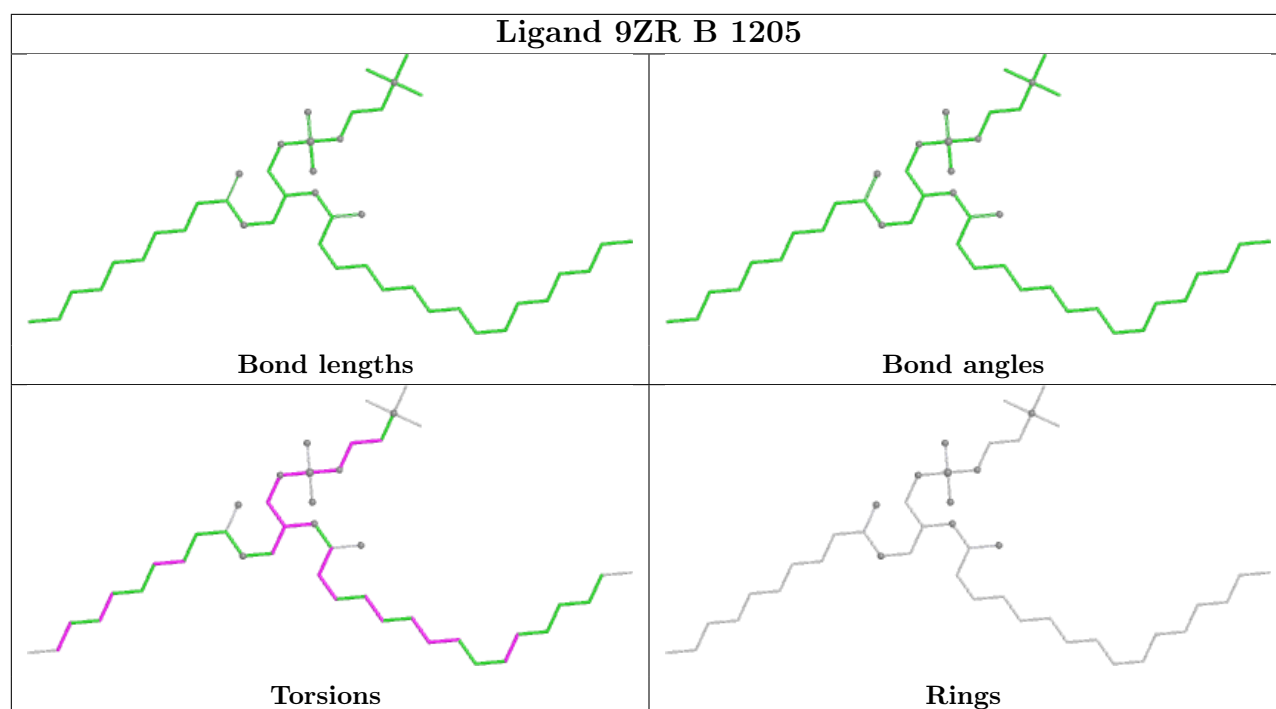


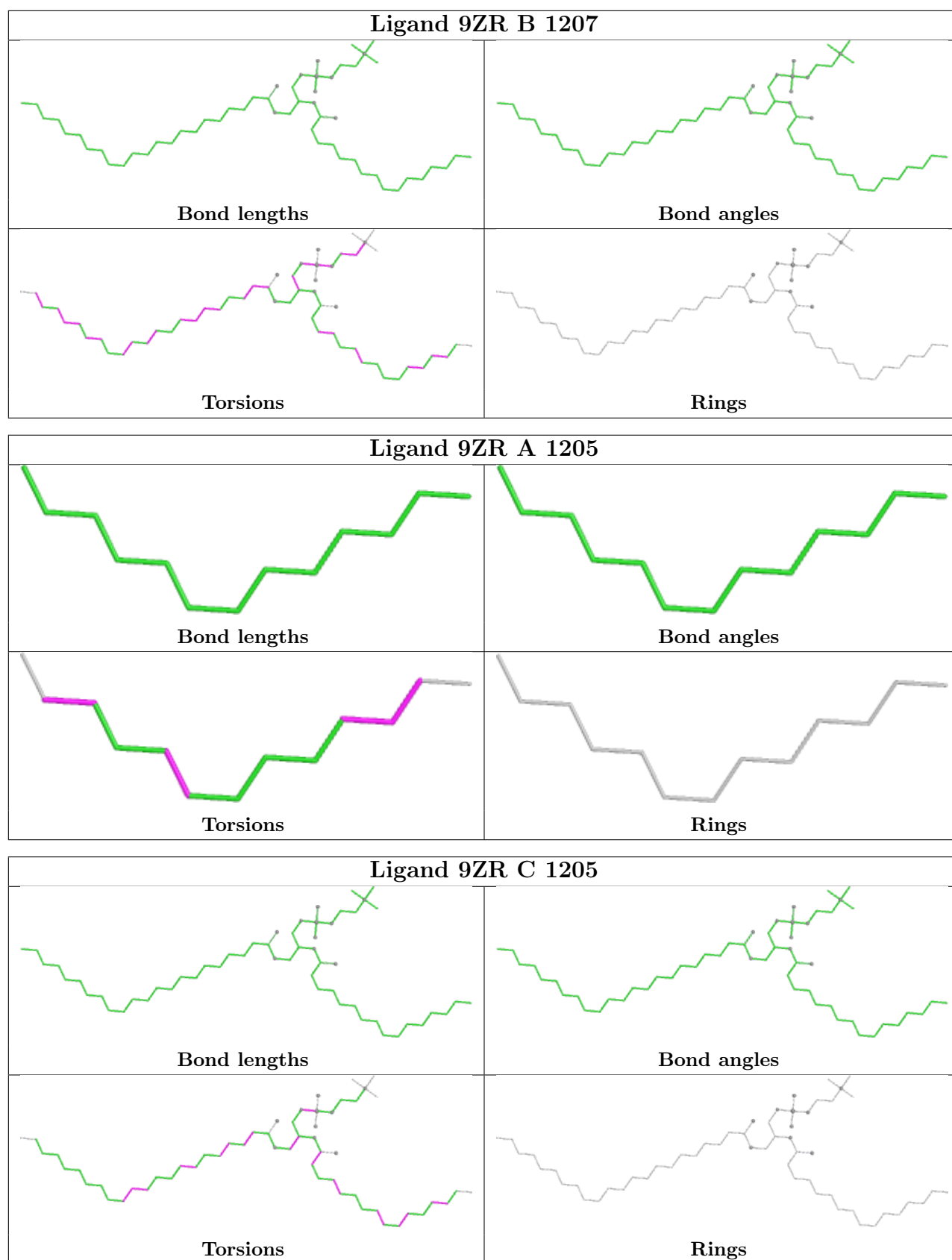


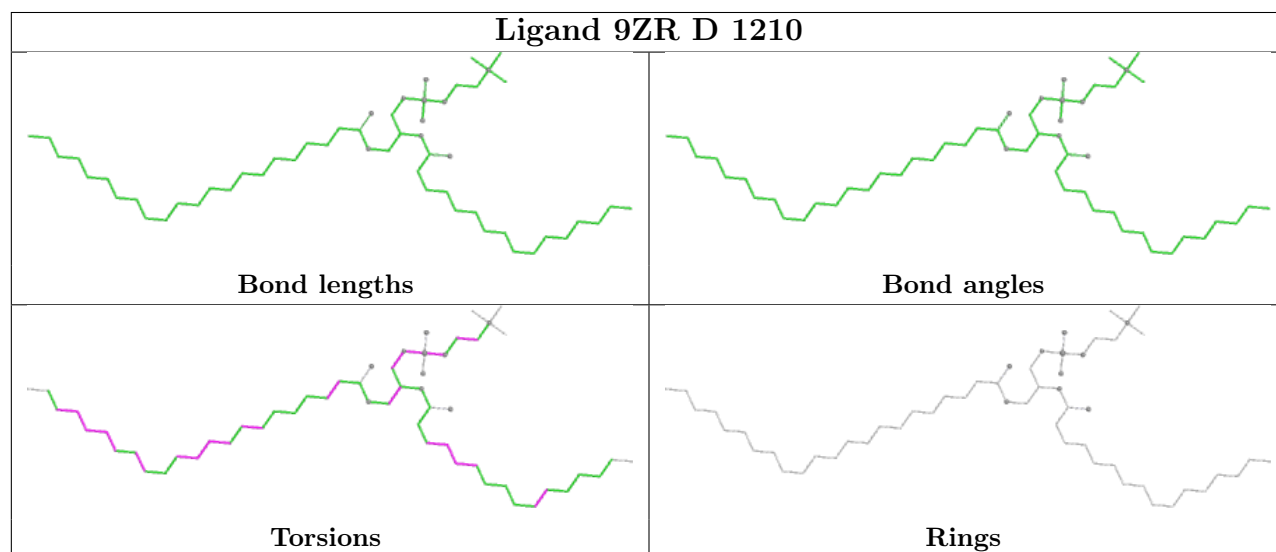
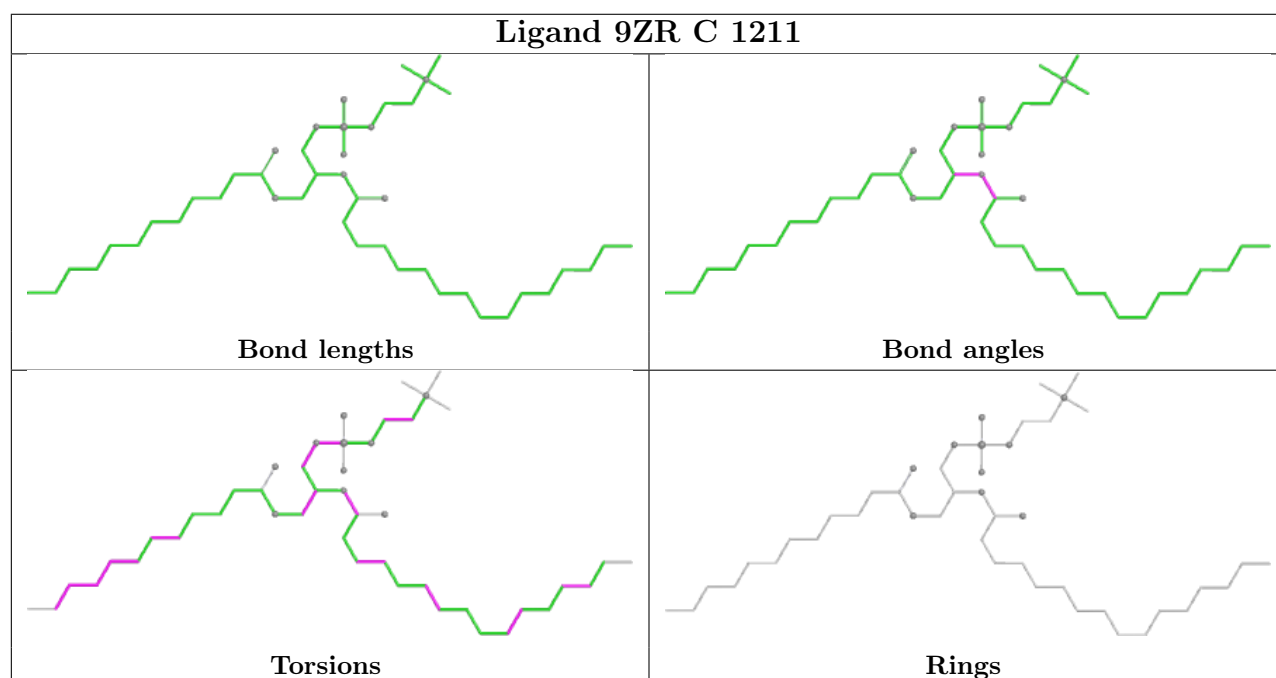
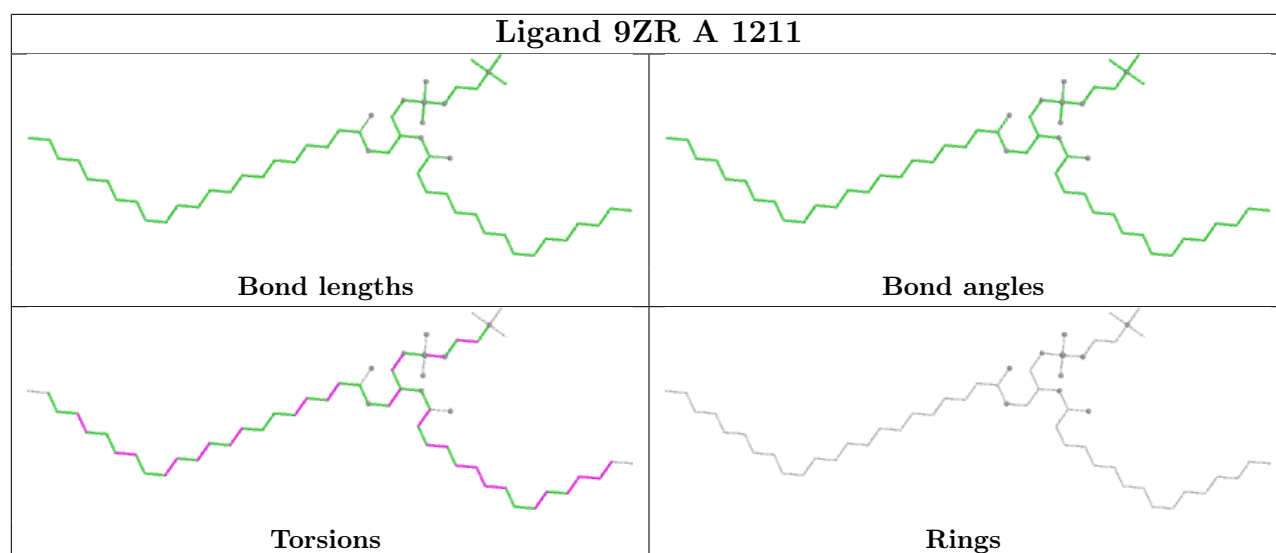


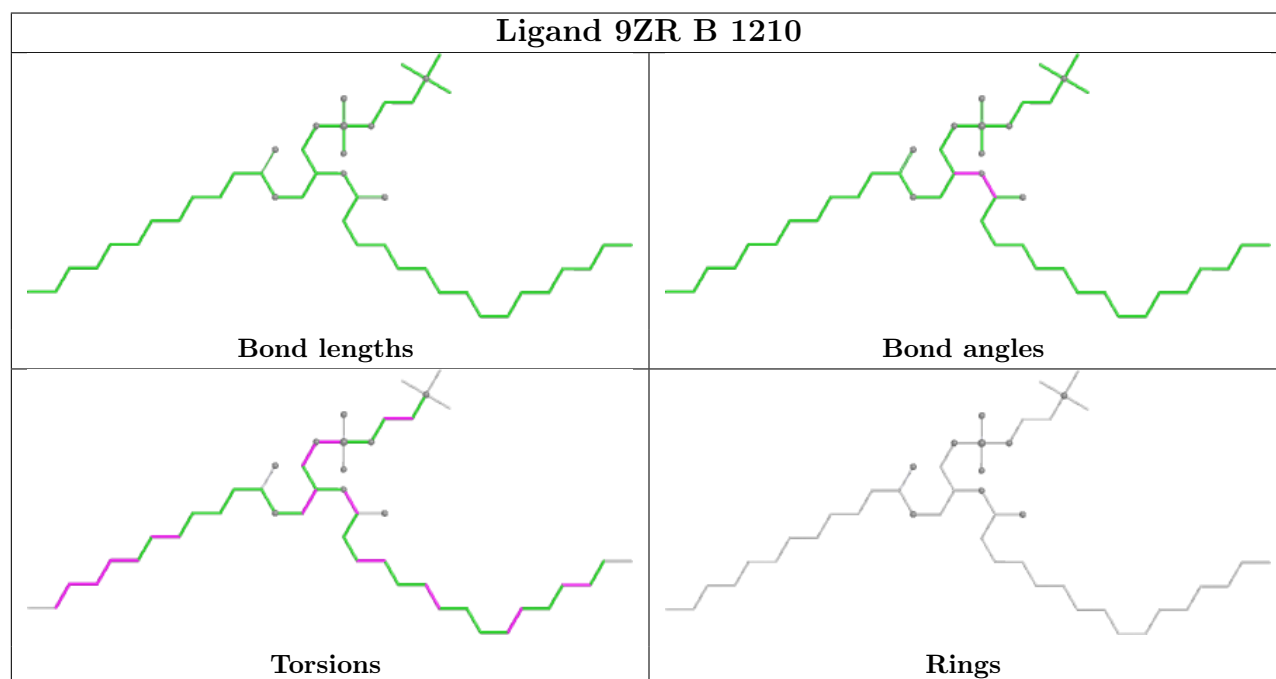
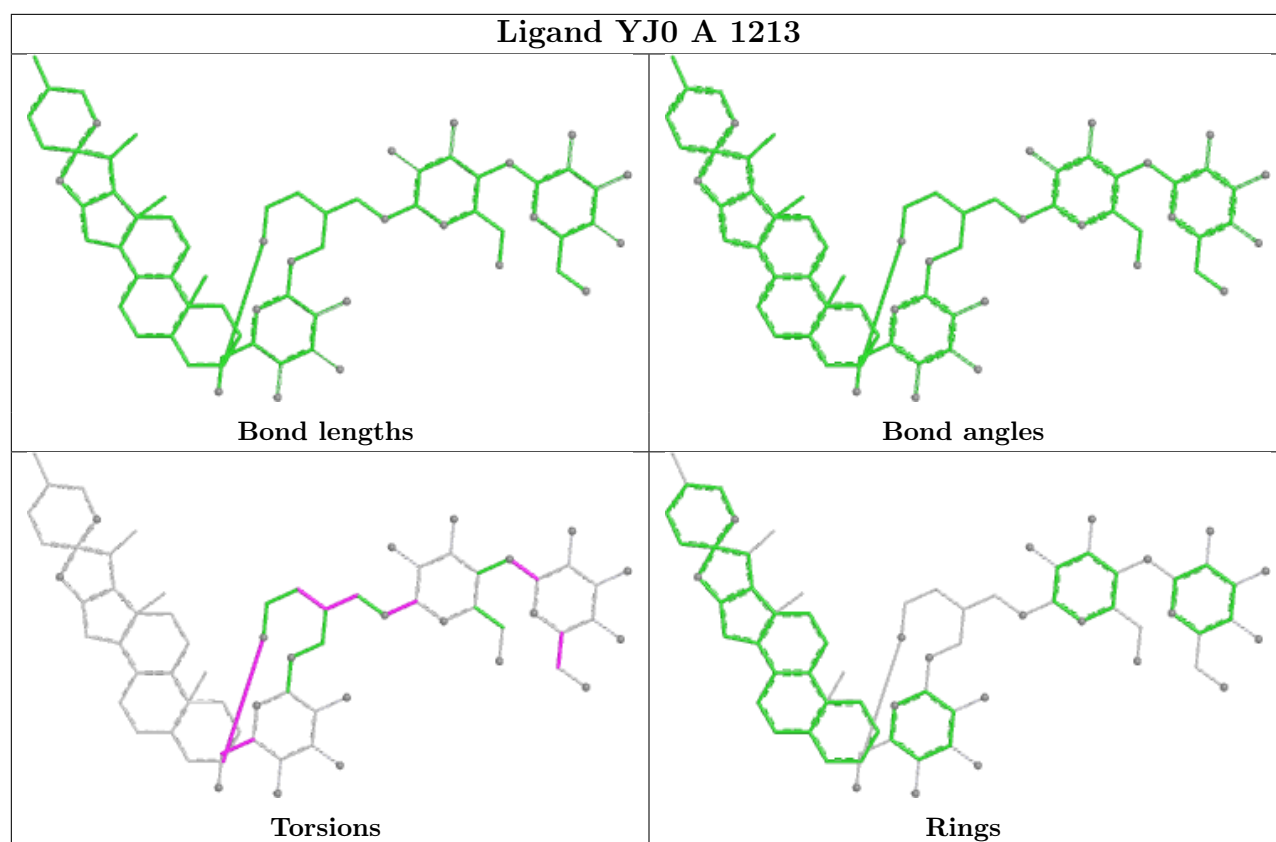


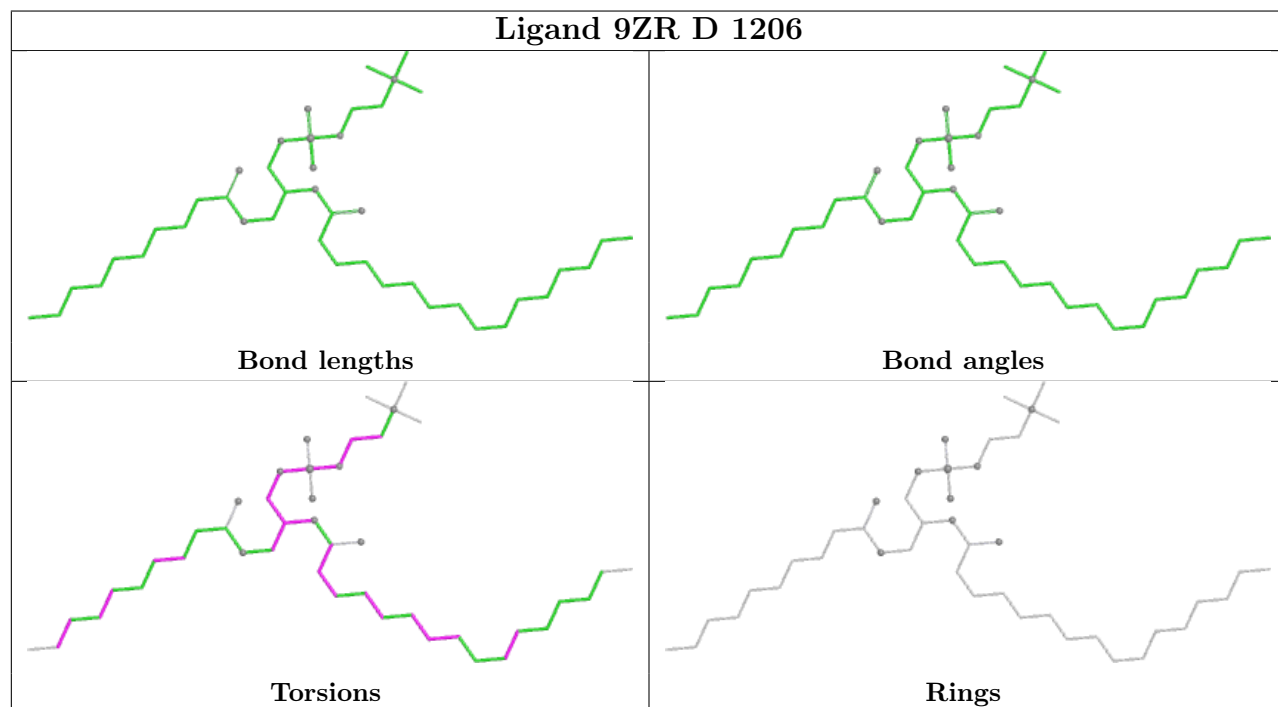
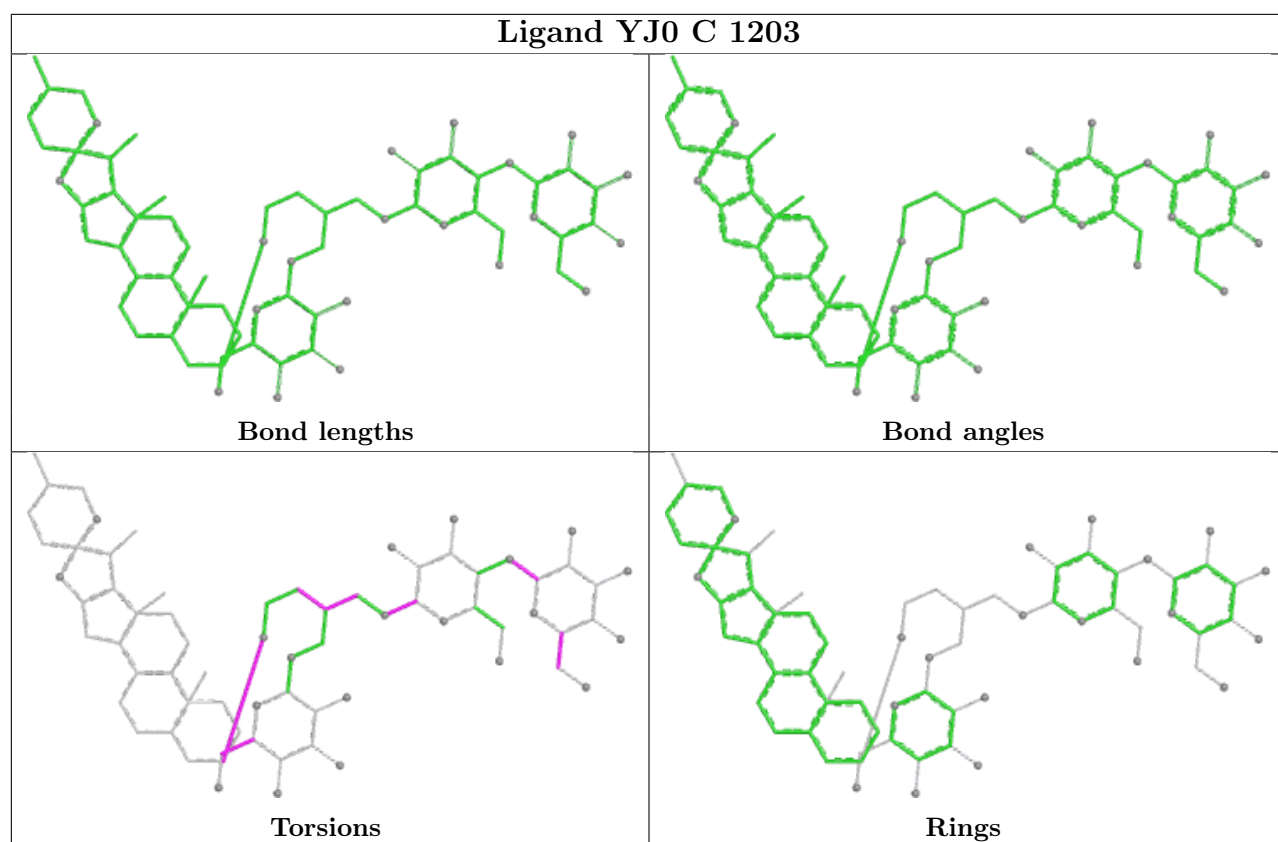


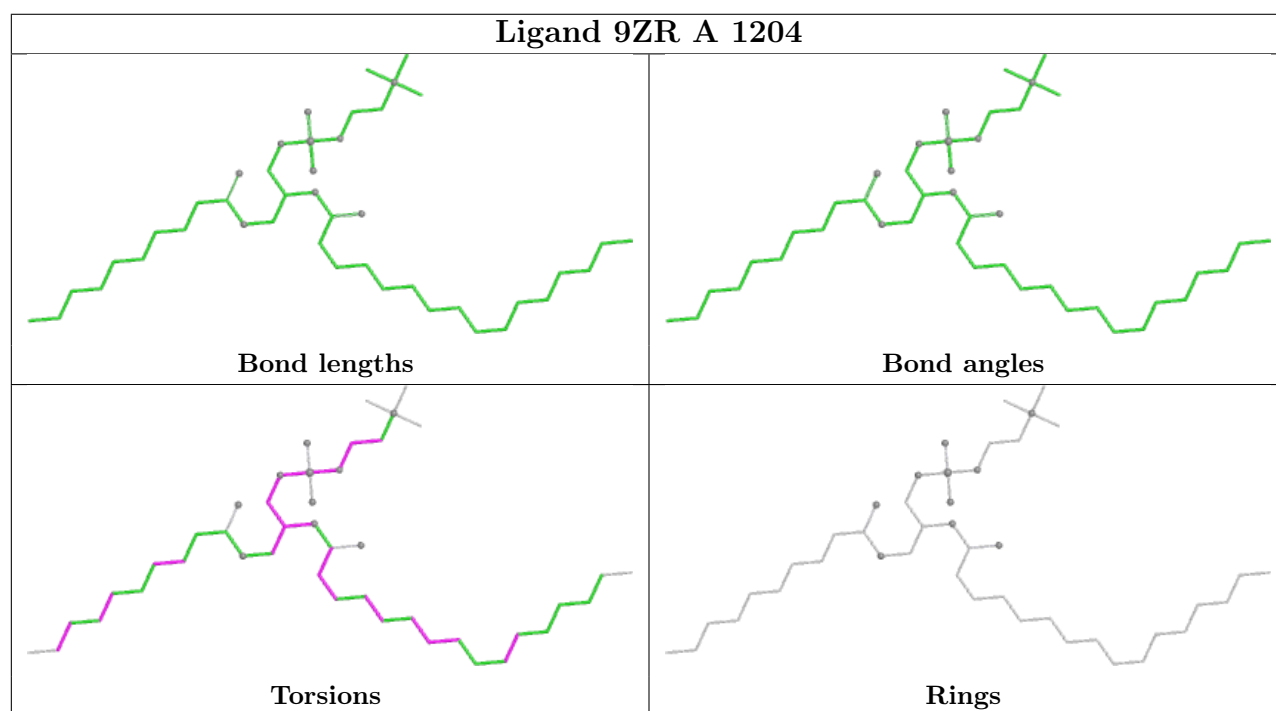
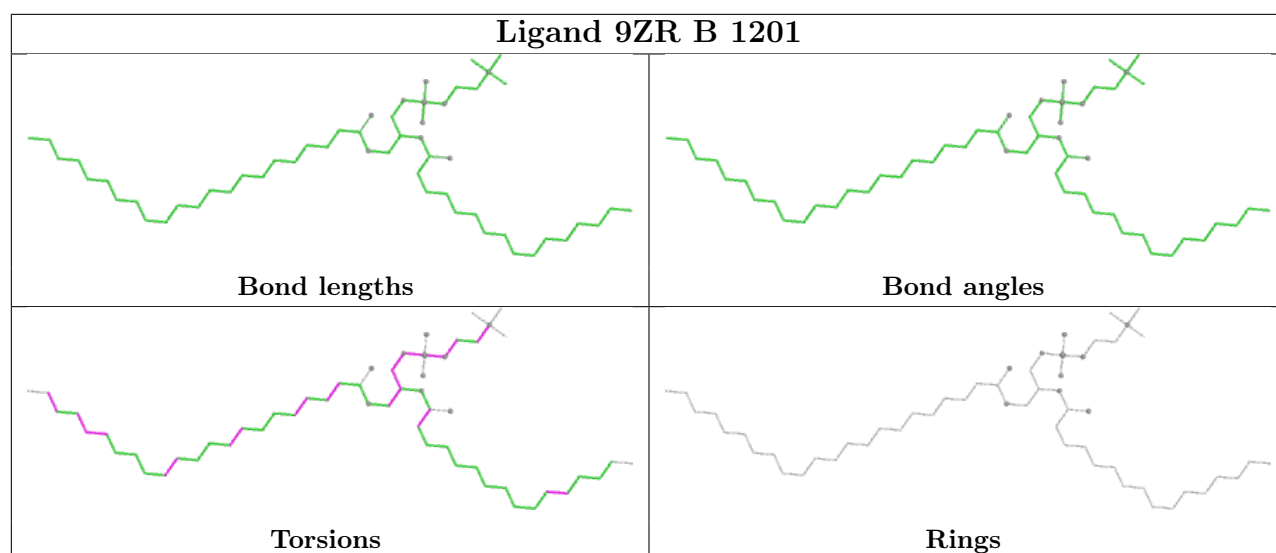


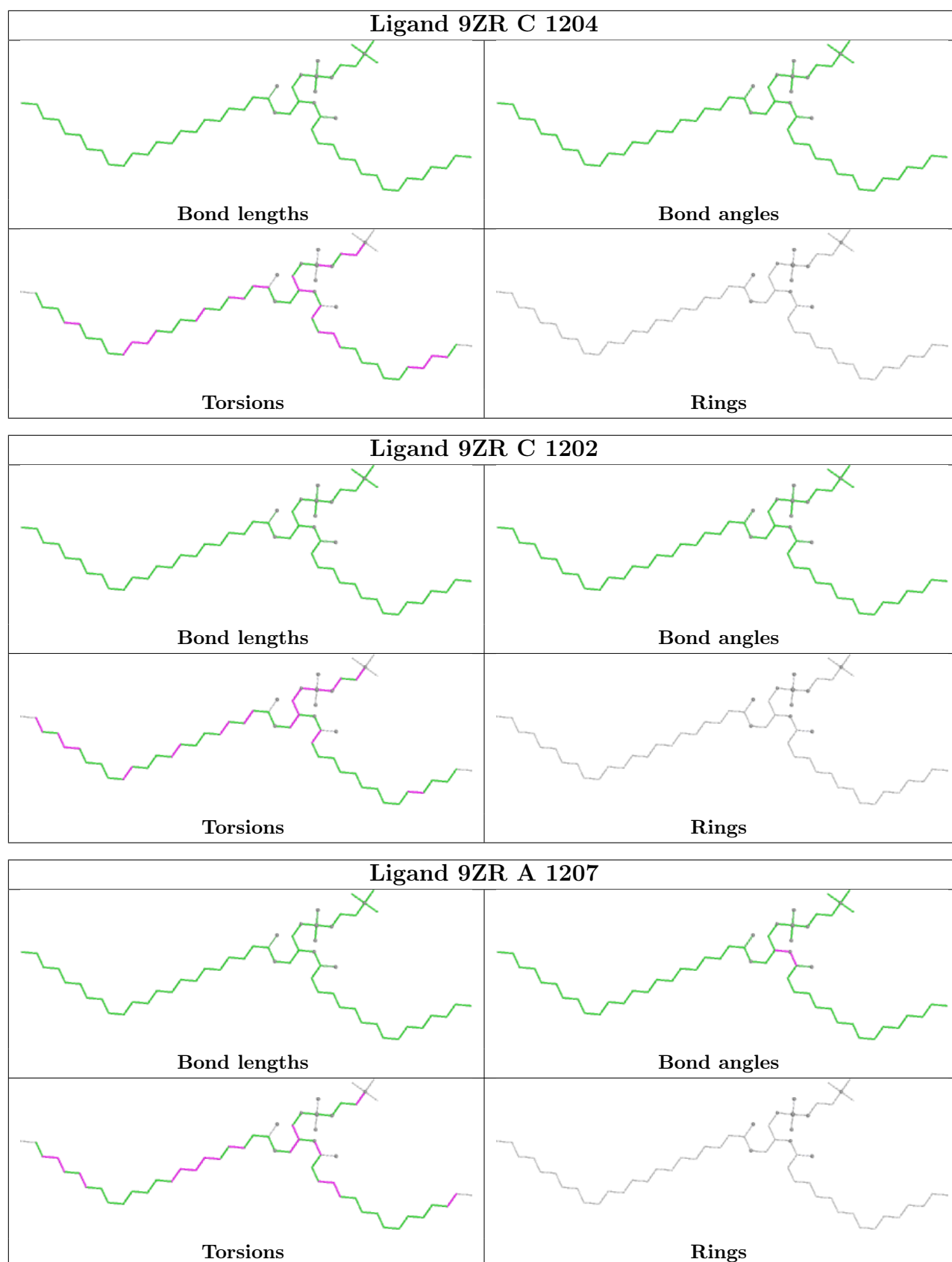


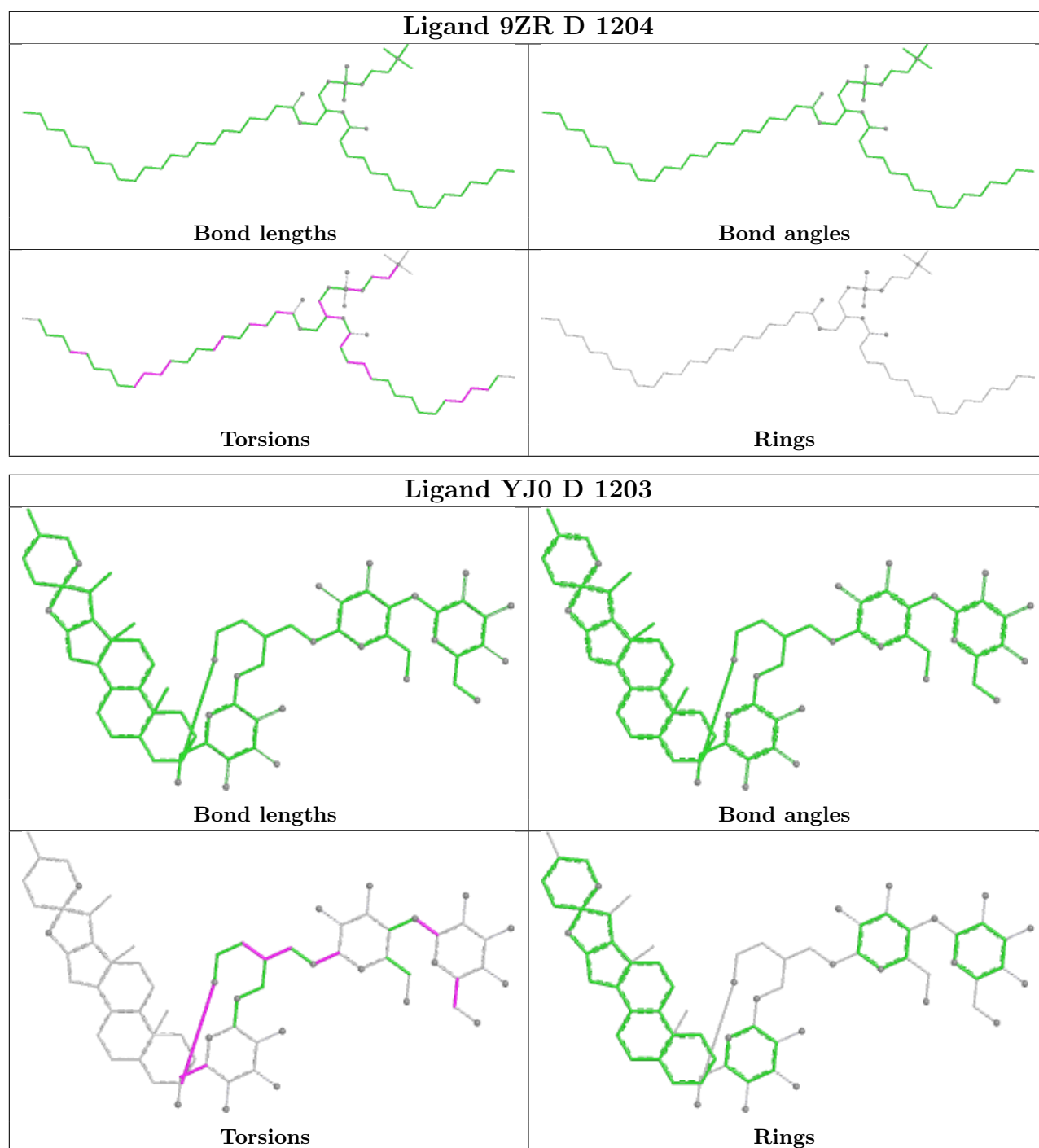












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

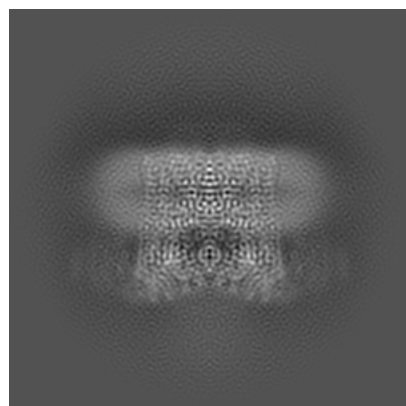
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40958. These allow visual inspection of the internal detail of the map and identification of artifacts.

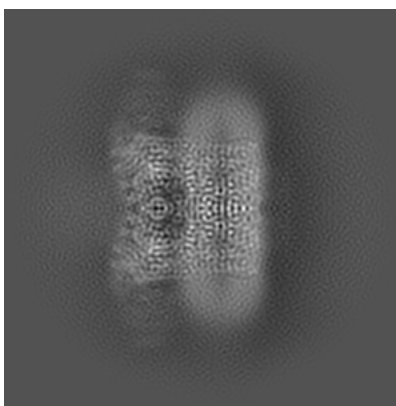
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

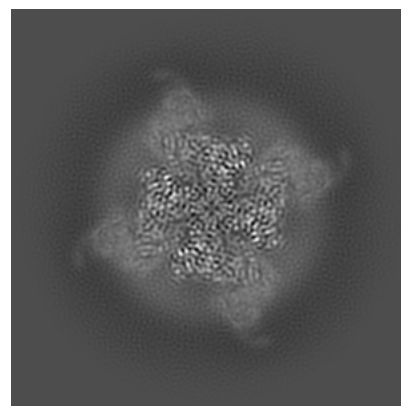
6.1.1 Primary map



X

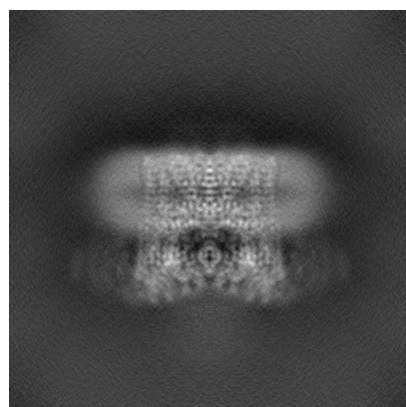


Y

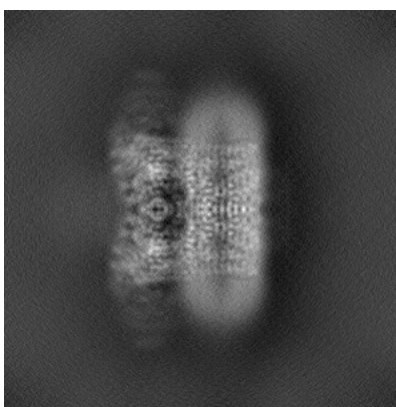


Z

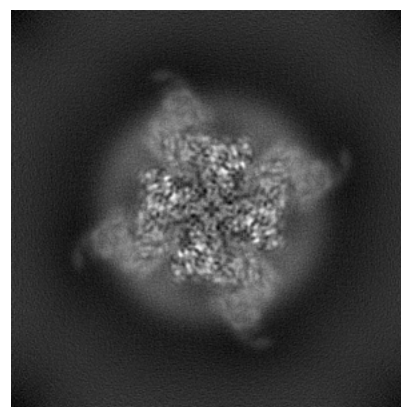
6.1.2 Raw map



X



Y

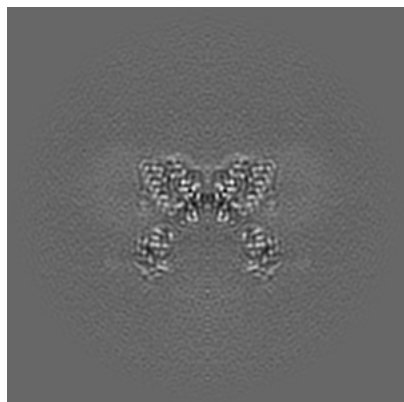


Z

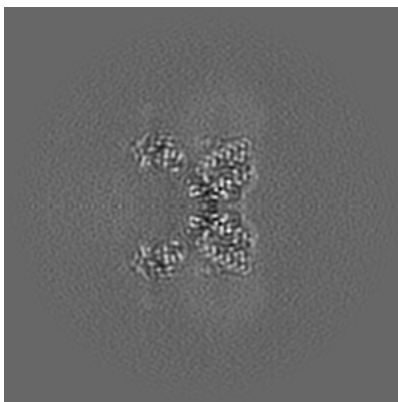
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

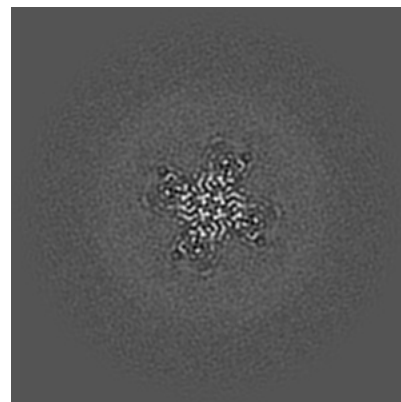
6.2.1 Primary map



X Index: 160

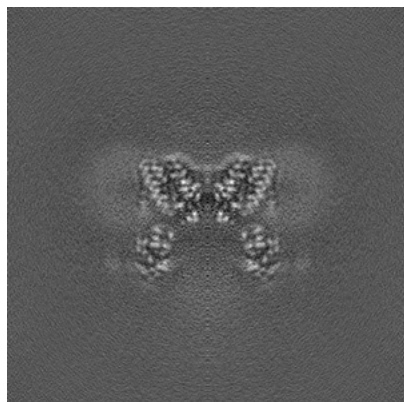


Y Index: 160

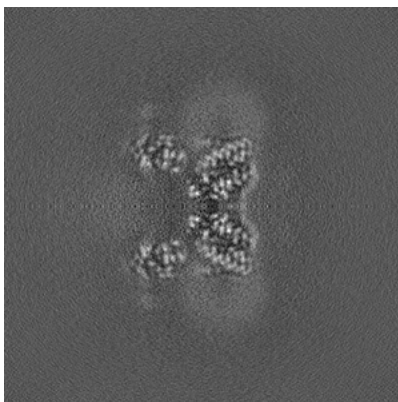


Z Index: 160

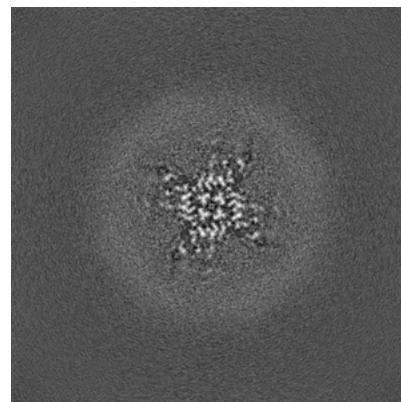
6.2.2 Raw map



X Index: 160



Y Index: 160

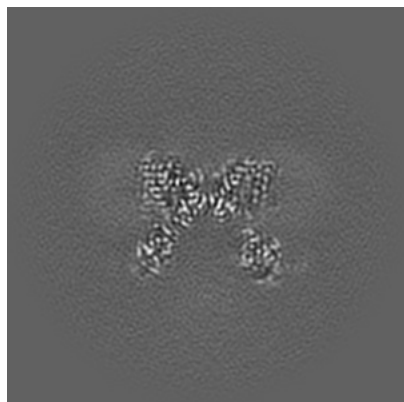


Z Index: 160

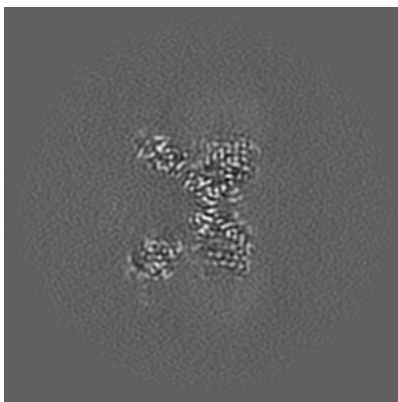
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

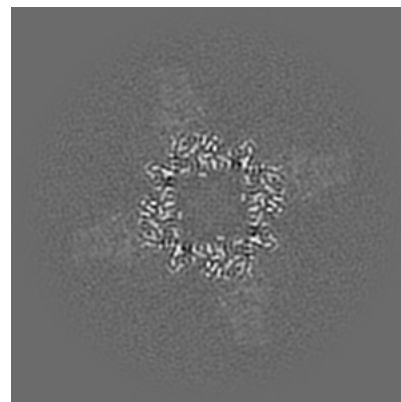
6.3.1 Primary map



X Index: 157

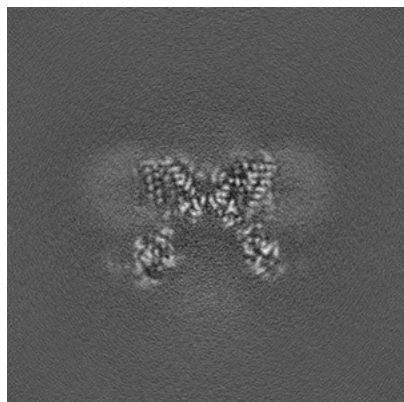


Y Index: 157

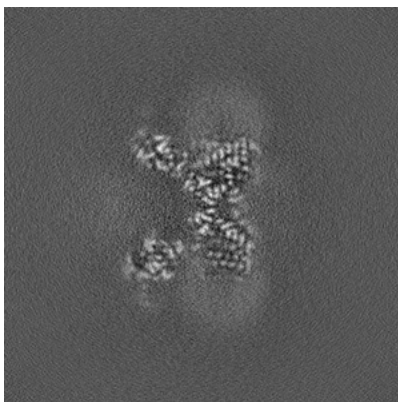


Z Index: 123

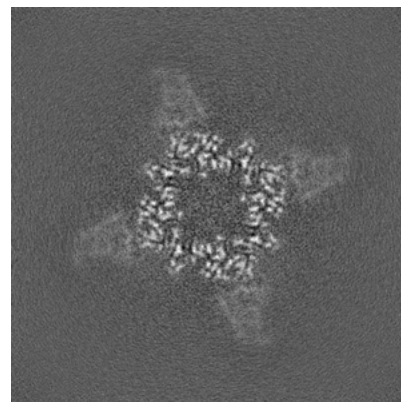
6.3.2 Raw map



X Index: 163



Y Index: 157

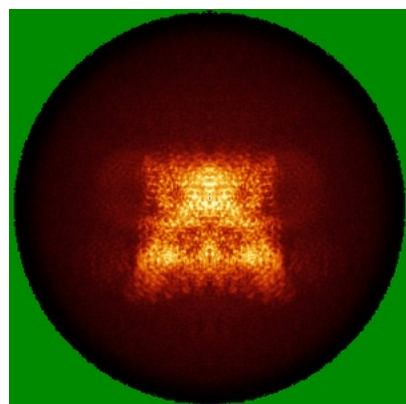


Z Index: 123

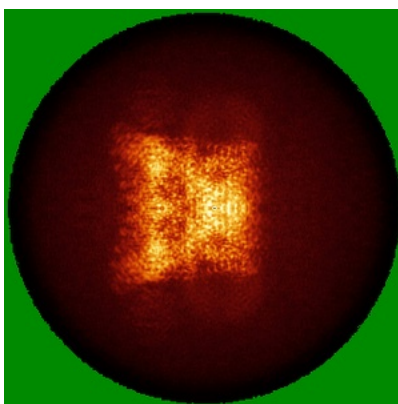
The images above show the largest variance slices of the map in three orthogonal directions.

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

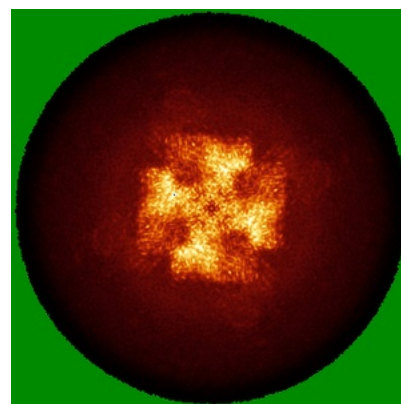
6.4.1 Primary map



X

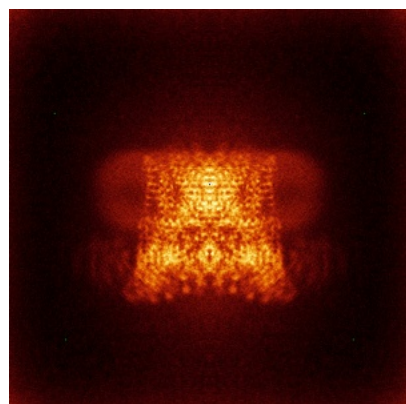


Y

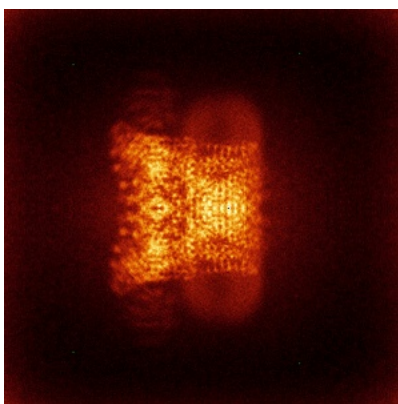


Z

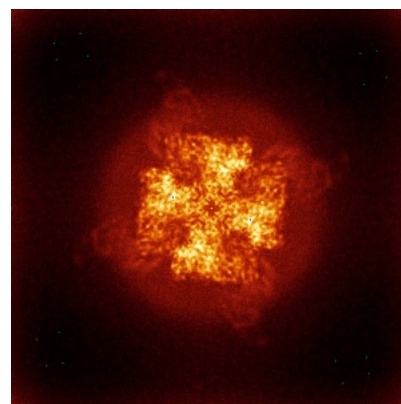
6.4.2 Raw map



X



Y

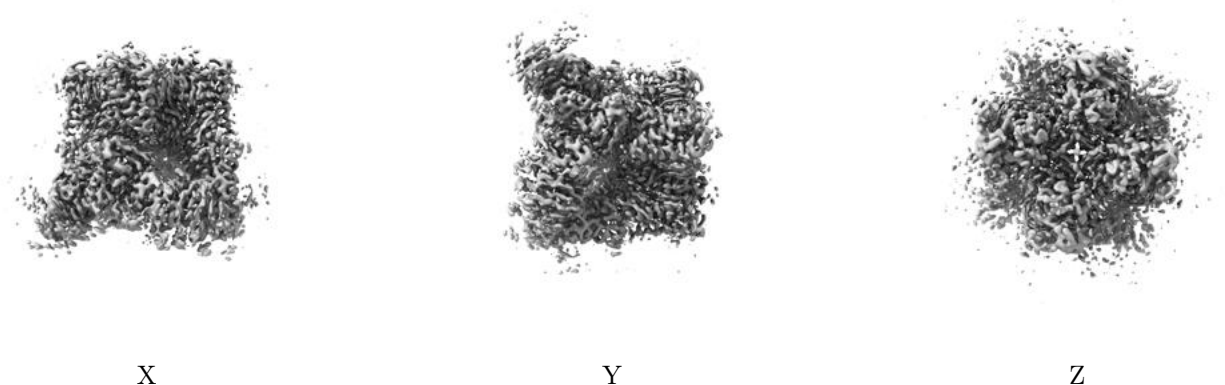


Z

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 0.22. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

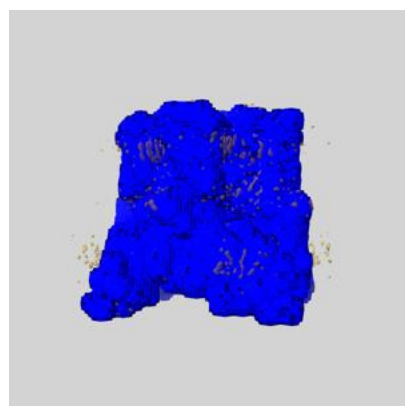
6.6 Mask visualisation [i](#)

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

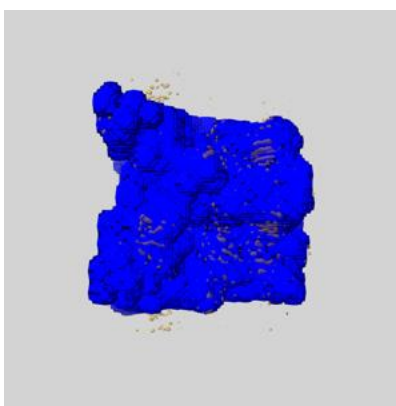
A mask typically either:

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

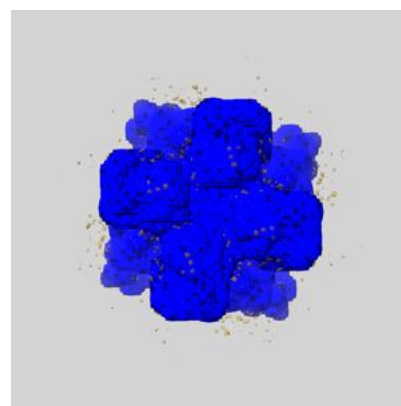
6.6.1 emd_40958_msk_1.map [i](#)



X



Y

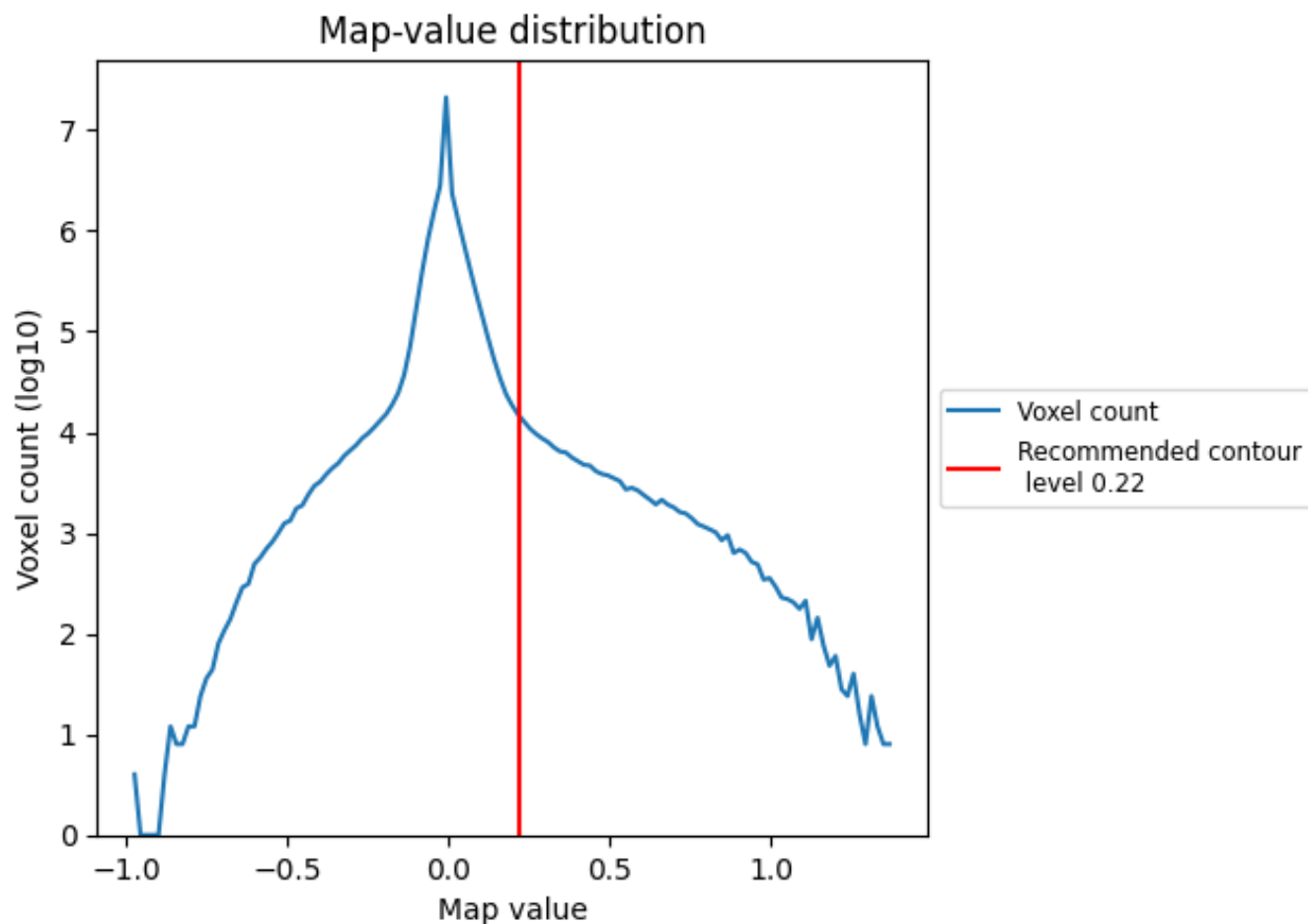


Z

7 Map analysis [i](#)

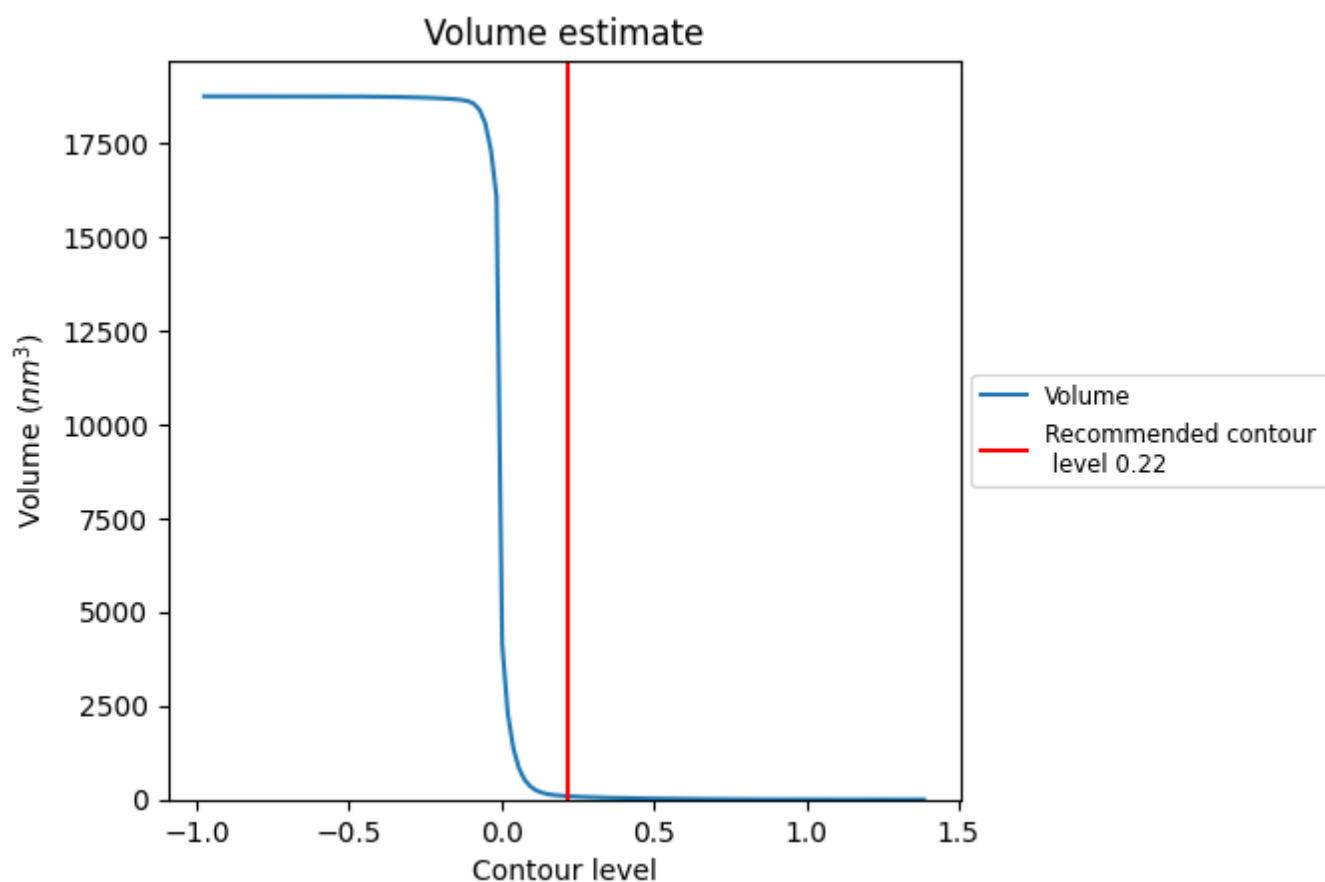
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

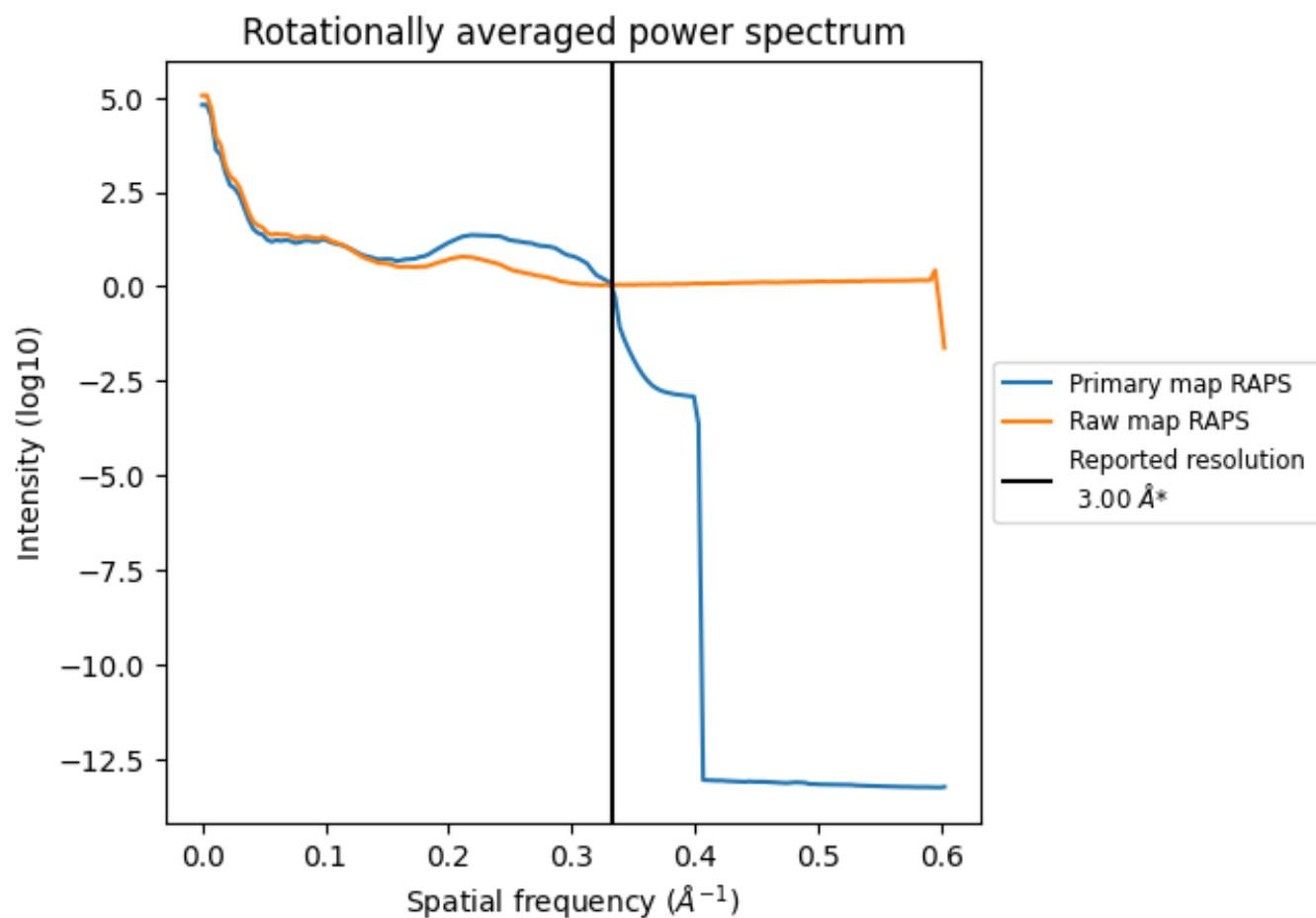
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 89 nm³; this corresponds to an approximate mass of 81 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 ⓘ

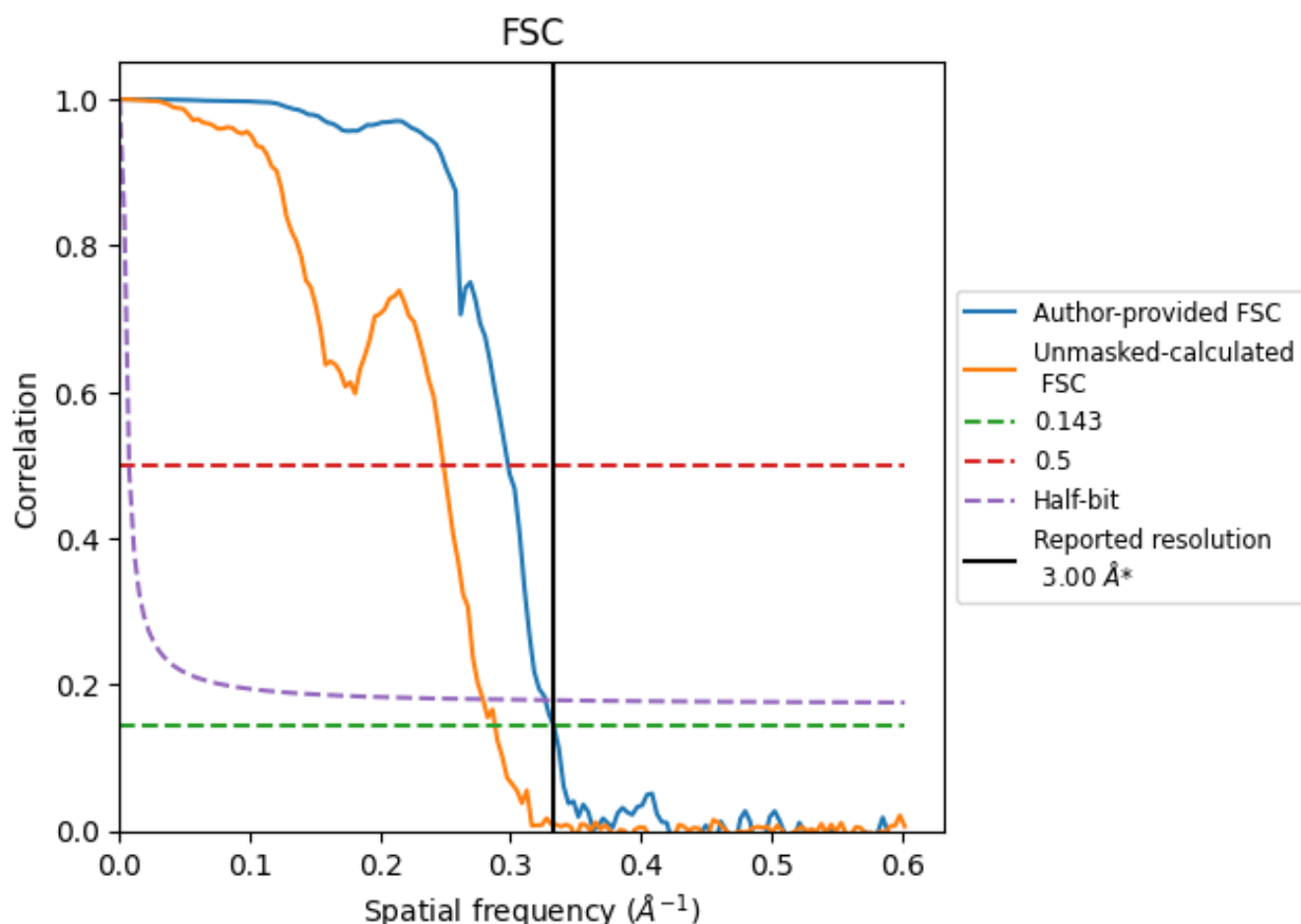


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 \AA^{-1}

8.2 Resolution estimates [i](#)

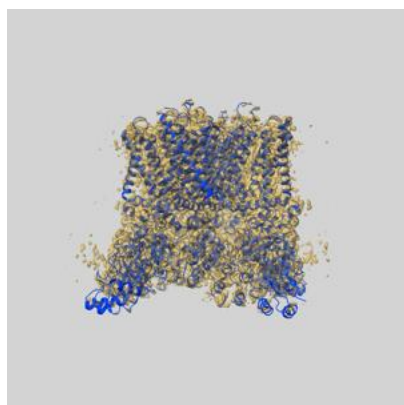
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.00	3.35	3.06
Unmasked-calculated*	3.47	4.02	3.59

*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 3.47 differs from the reported value 3.0 by more than 10 %

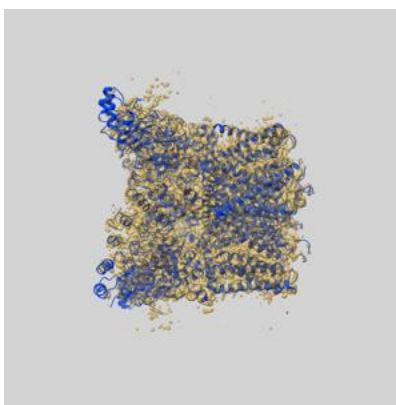
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-40958 and PDB model 8T1B. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

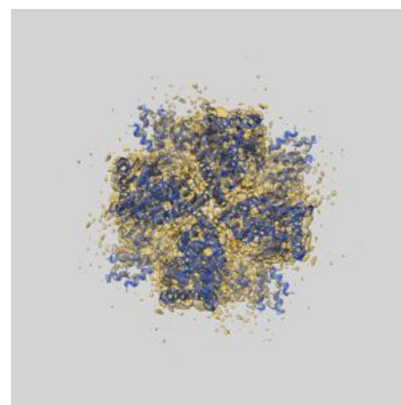
9.1 Map-model overlay [i](#)



X



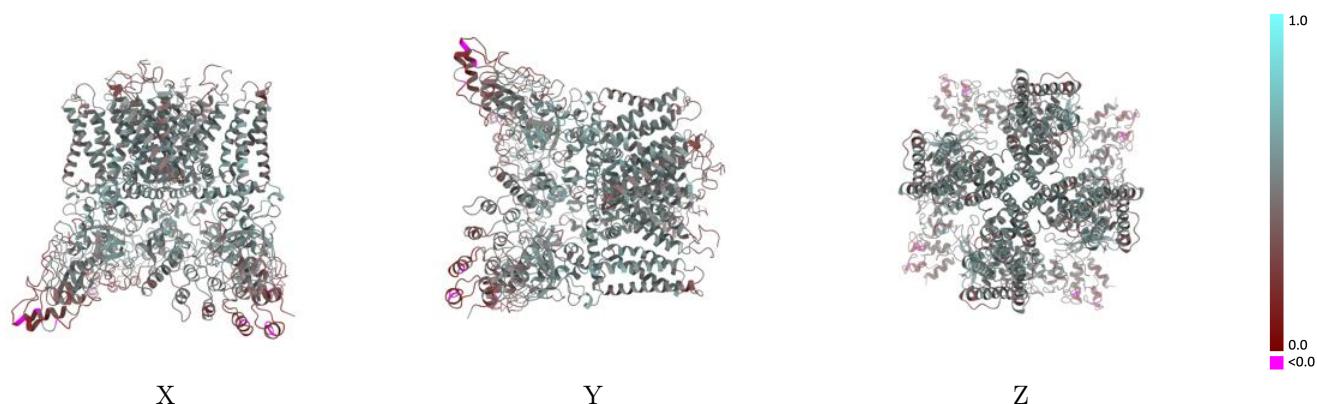
Y



Z

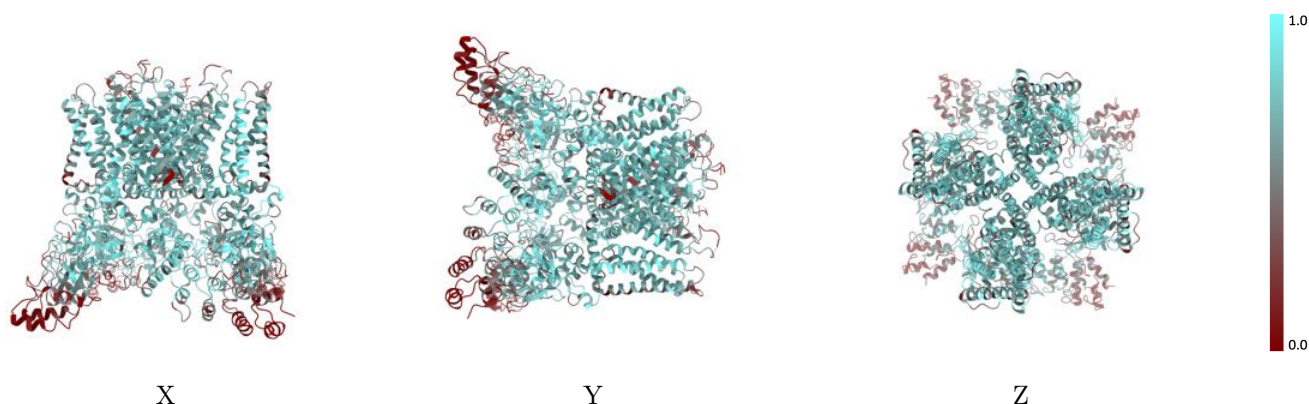
The images above show the 3D surface view of the map at the recommended contour level 0.22 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



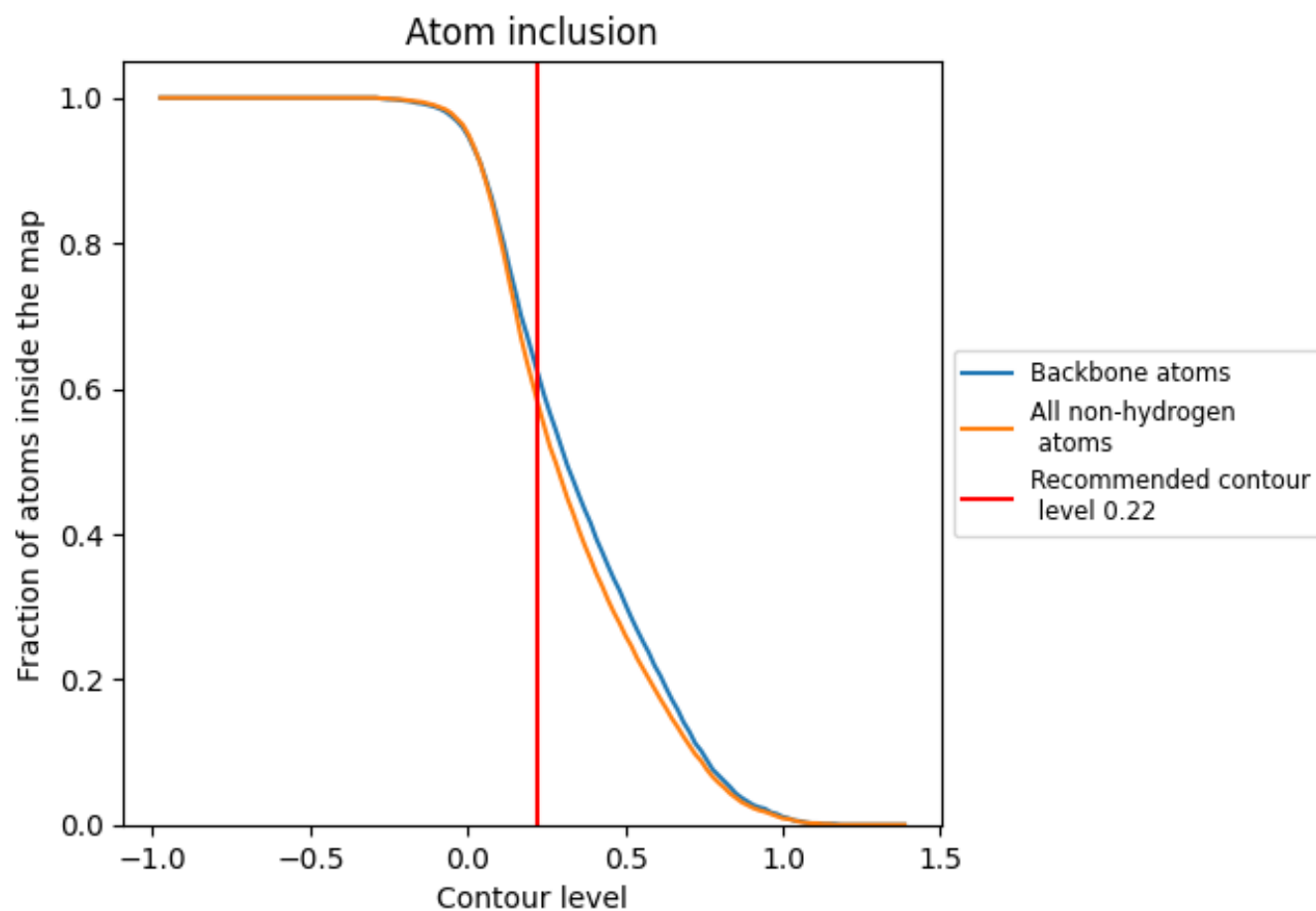
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.22).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 58% 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 (0.22) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5830	<div></div> 0.4670
A	<div></div> 0.5870	<div></div> 0.4680
B	<div></div> 0.5900	<div></div> 0.4660
C	<div></div> 0.5900	<div></div> 0.4670
D	<div></div> 0.5890	<div></div> 0.4690

