



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 11:02 AM UTC

PDB ID : 7Y6I / pdb_00007y6i
EMDB ID : EMD-33641
Title : Cryo-EM structure of human sodium-chloride cotransporter
Authors : Nan, J.; Yang, X.; Shan, Z.; Yuan, Y.; Zhang, Y.Q.
Deposited on : 2022-06-20
Resolution : 2.85 Å(reported)

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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

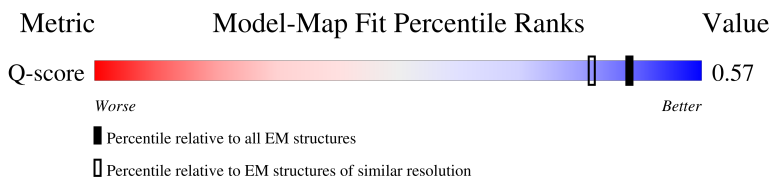
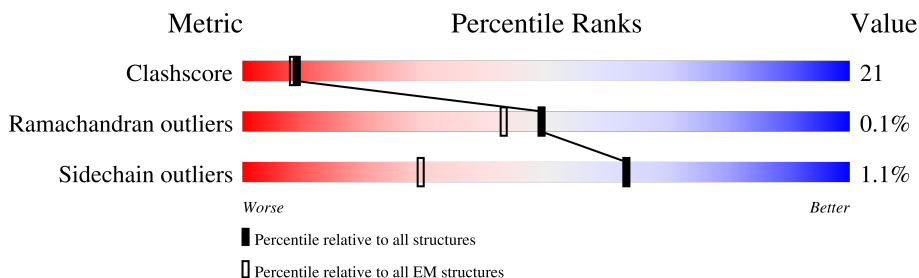
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.85 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	11965 (2.35 - 3.35)

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	1053	 32% 12% 55%
1	B	1053	 32% 12% 55%
2	C	2	 50% 50%
2	D	2	 50% 50%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	Y01	B	1109	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 8176 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 Solute carrier family 12 member 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	469	Total	C	N	O	S	0	0
			3564	2362	557	624	21		
1	B	469	Total	C	N	O	S	0	0
			3564	2362	557	624	21		

There are 70 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLN	deletion	UNP P55017
A	264	GLY	ALA	engineered mutation	UNP P55017
A	1022	LEU	-	expression tag	UNP P55017
A	1023	GLU	-	expression tag	UNP P55017
A	1024	GLY	-	expression tag	UNP P55017
A	1025	SER	-	expression tag	UNP P55017
A	1026	ASP	-	expression tag	UNP P55017
A	1027	GLU	-	expression tag	UNP P55017
A	1028	VAL	-	expression tag	UNP P55017
A	1029	ASP	-	expression tag	UNP P55017
A	1030	ALA	-	expression tag	UNP P55017
A	1031	GLY	-	expression tag	UNP P55017
A	1032	SER	-	expression tag	UNP P55017
A	1033	HIS	-	expression tag	UNP P55017
A	1034	HIS	-	expression tag	UNP P55017
A	1035	HIS	-	expression tag	UNP P55017
A	1036	HIS	-	expression tag	UNP P55017
A	1037	HIS	-	expression tag	UNP P55017
A	1038	HIS	-	expression tag	UNP P55017
A	1039	HIS	-	expression tag	UNP P55017
A	1040	HIS	-	expression tag	UNP P55017
A	1041	HIS	-	expression tag	UNP P55017
A	1042	HIS	-	expression tag	UNP P55017
A	1043	GLY	-	expression tag	UNP P55017
A	1044	SER	-	expression tag	UNP P55017
A	1045	VAL	-	expression tag	UNP P55017

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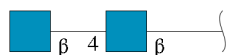
Chain	Residue	Modelled	Actual	Comment	Reference
A	1046	GLU	-	expression tag	UNP P55017
A	1047	ASP	-	expression tag	UNP P55017
A	1048	TYR	-	expression tag	UNP P55017
A	1049	LYS	-	expression tag	UNP P55017
A	1050	ASP	-	expression tag	UNP P55017
A	1051	ASP	-	expression tag	UNP P55017
A	1052	ASP	-	expression tag	UNP P55017
A	1053	ASP	-	expression tag	UNP P55017
A	1054	LYS	-	expression tag	UNP P55017
B	?	-	GLN	deletion	UNP P55017
B	264	GLY	ALA	engineered mutation	UNP P55017
B	1022	LEU	-	expression tag	UNP P55017
B	1023	GLU	-	expression tag	UNP P55017
B	1024	GLY	-	expression tag	UNP P55017
B	1025	SER	-	expression tag	UNP P55017
B	1026	ASP	-	expression tag	UNP P55017
B	1027	GLU	-	expression tag	UNP P55017
B	1028	VAL	-	expression tag	UNP P55017
B	1029	ASP	-	expression tag	UNP P55017
B	1030	ALA	-	expression tag	UNP P55017
B	1031	GLY	-	expression tag	UNP P55017
B	1032	SER	-	expression tag	UNP P55017
B	1033	HIS	-	expression tag	UNP P55017
B	1034	HIS	-	expression tag	UNP P55017
B	1035	HIS	-	expression tag	UNP P55017
B	1036	HIS	-	expression tag	UNP P55017
B	1037	HIS	-	expression tag	UNP P55017
B	1038	HIS	-	expression tag	UNP P55017
B	1039	HIS	-	expression tag	UNP P55017
B	1040	HIS	-	expression tag	UNP P55017
B	1041	HIS	-	expression tag	UNP P55017
B	1042	HIS	-	expression tag	UNP P55017
B	1043	GLY	-	expression tag	UNP P55017
B	1044	SER	-	expression tag	UNP P55017
B	1045	VAL	-	expression tag	UNP P55017
B	1046	GLU	-	expression tag	UNP P55017
B	1047	ASP	-	expression tag	UNP P55017
B	1048	TYR	-	expression tag	UNP P55017
B	1049	LYS	-	expression tag	UNP P55017
B	1050	ASP	-	expression tag	UNP P55017
B	1051	ASP	-	expression tag	UNP P55017
B	1052	ASP	-	expression tag	UNP P55017

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1053	ASP	-	expression tag	UNP P55017
B	1054	LYS	-	expression tag	UNP P55017

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



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

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

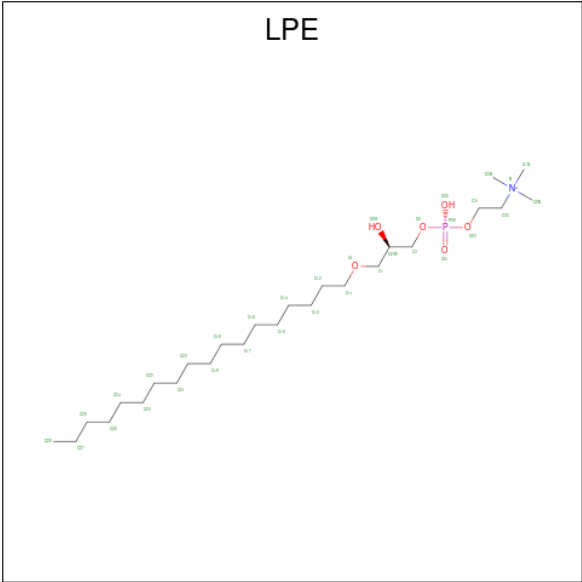
Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	Cl	0
			2	2	
3	B	2	Total	Cl	0
			2	2	

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	A	2	Total	Na	0
			2	2	
4	B	2	Total	Na	0
			2	2	

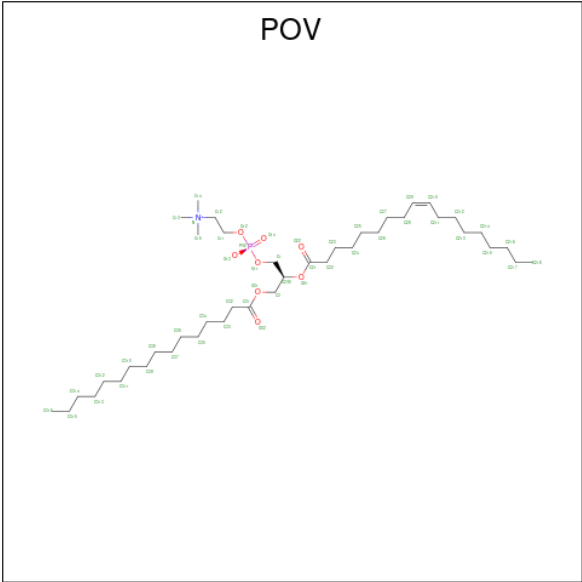
- Molecule 5 is CHOLESTEROL HEMISUCCINATE (CCD ID: Y01) (formula: C₃₁H₅₀O₄).





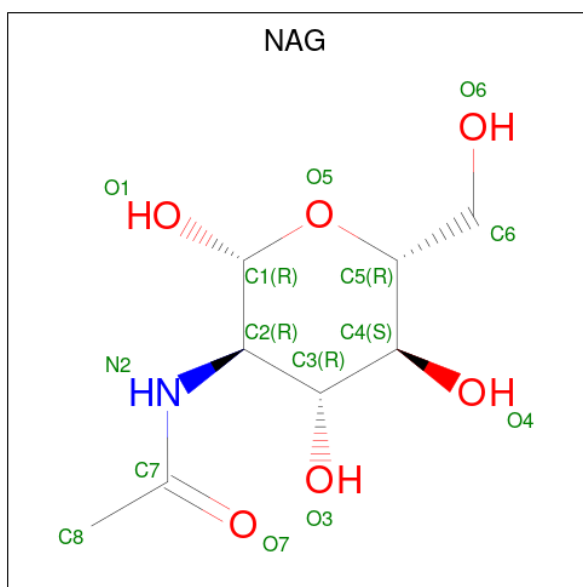
Mol	Chain	Residues	Atoms					AltConf
6	A	1	Total	C	N	O	P	0
			34	26	1	6	1	
6	A	1	Total	C	N	O	P	0
			34	26	1	6	1	
6	A	1	Total	C	N	O	P	0
			34	26	1	6	1	
6	A	1	Total	C	N	O	P	0
			34	26	1	6	1	
6	B	1	Total	C	N	O	P	0
			34	26	1	6	1	
6	B	1	Total	C	N	O	P	0
			34	26	1	6	1	
6	B	1	Total	C	N	O	P	0
			34	26	1	6	1	
6	B	1	Total	C	N	O	P	0
			34	26	1	6	1	

- Molecule 7 is (2S)-3-(hexadecanoyloxy)-2-[(9Z)-octadec-9-enoyloxy]propyl 2-(trimethylamm onio)ethyl phosphate (CCD ID: POV) (formula: C₄₂H₈₂NO₈P).



Mol	Chain	Residues	Atoms					AltConf
7	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
7	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
7	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
7	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
7	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
7	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
7	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
7	B	1	Total	C	N	O	P	0
			52	42	1	8	1	

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



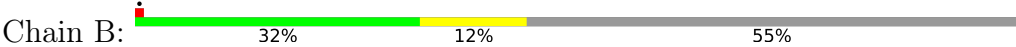
Mol	Chain	Residues	Atoms				AltConf
8	A	1	Total	C	N	O	0
			14	8	1	5	
8	B	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		AltConf
9	A	3	Total	O	0
			3	3	
9	B	3	Total	O	0
			3	3	

ILE	VAL	ILE	THR	LEU	PRO	THR	ILE	GLY	ARG	LYS	VAL	PRO	ASP	GLY	ASP	ASP	LYS
HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	GLY	VAL	GLU	ASP	TYR	SER	LYS	THR

- Molecule 1: Solute carrier family 12 member 3



MET	ALA	GLU	LEU	PRO	THR	THR	GLU	THR	PRO	TYR	THR	GLY	ASP	VAL	THR	THR	THR
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ILE	ASP	VAL	THR	THR	TYR	GLU	HIS	TYR	PRO	GLY	ALA	ASN	PRO	THR	THR	GLN	GLY
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ALA	GLY	THR	SER	SER	GLU	LYS	ASN	PRO	PRO	VAL	ARG	ARG	GLY	G137	G141	V142	M143
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R209	S210	L211	L219	F225	A226	A228	V229	V231	A232	M233	H234	T235	R243	E248	G250	D255	N258
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F341	S342	M343	F344	S345	F347	S350	A351	A356	C357	A358	I359	I360	R365	D366	I369	A370	I371
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L456	I457	I461	S468	A469	L470	A476	V479	F480	Q481	E485	V489	P490	L491	I492	G493	F494	P505
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L593	G594	L597	Y602	Y605	LYS	PRO	GLU	VAL	ASN	TRP	GLY	SER	SER	VAL	ALA	GLY	SER
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ALA	LEU	VAL	ASP	PHE	VAL	GLY	THR	PHE	THR	THR	ARG	ASN	LEU	SER	LEU	GLY	CYS
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LEU	ARG	ARG	GLY	ASN	VAL	GLN	ILE	LEU	GLN	ALA	ARG	LEU	GLY	VAL	GLY	PHE	HIS
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ARG	GLU	GLY	ASN	VAL	VAL	SER	LYS	MET	GLN	ALA	ARG	ALA	GLY	VAL	GLY	ALA	LYS
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PHE	ASP	GLY	GLY	LEU	THR	LEU	LEU	LEU	ILE	THR	THR	GLY	GLY	ILE	ARG	ASP	PRO
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PRO	ASP	ILE	ASN	GLN	ASN	PRO	ARG	ALA	HIS	THR	THR	LYS	ARG	PHE	GLY	ALA	ARG
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VAL	ARG	LEU	ASN	GLU	ILE	VAL	VAL	LEU	ASP	THR	THR	GLY	VAL	ILE	THR	THR	THR
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THR	PHE	TYR	CYS	GLN	LEU	GLY	VAL	ASP	VAL	ASP	ALA	ALA	GLY	SER	HIS	HIS	HIS
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- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:  50% 50%


MAG1
MAG2

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  50% 50%


MAG1
MAG2

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	382235	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52.8	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	5.307	Depositor
Minimum map value	-3.732	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.102	Depositor
Recommended contour level	0.282	Depositor
Map size ($\text{\AA}$)	267.776, 267.776, 267.776	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.046, 1.046, 1.046	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: NAG, CL, Y01, LPE, NA, POV

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	0.27	2/3659 (0.1%)	0.42	0/4996
1	B	0.33	4/3659 (0.1%)	0.47	1/4996 (0.0%)
All	All	0.30	6/7318 (0.1%)	0.45	1/9992 (0.0%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	422	SER	N-CA	-6.00	1.38	1.46
1	A	563	GLN	CD-OE1	5.14	1.33	1.23
1	B	165	GLN	CD-OE1	5.11	1.33	1.23
1	B	359	ASN	CG-OD1	5.05	1.33	1.23
1	A	426	ASN	C-N	-5.03	1.27	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	198	VAL	N-CA-C	-5.71	101.35	108.89

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	3564	0	3605	106	0
1	B	3564	0	3605	104	0
2	C	28	0	25	4	0
2	D	28	0	25	3	0
3	A	2	0	0	1	0
3	B	2	0	0	1	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	105	0	147	41	0
5	B	105	0	147	55	0
6	A	136	0	224	24	0
6	B	136	0	223	32	0
7	A	260	0	410	52	0
7	B	208	0	328	38	0
8	A	14	0	13	0	0
8	B	14	0	13	0	0
9	A	3	0	0	0	0
9	B	3	0	0	0	0
All	All	8176	0	8765	352	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 21.

The worst 5 of 352 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)
5:A:1105:Y01:HAI	5:A:1107:Y01:HAK2	1.22	1.09
5:B:1109:Y01:HAJ1	6:B:1112:LPE:H281	1.38	1.04
5:B:1107:Y01:HAS1	5:B:1109:Y01:HAK1	1.40	1.02
5:B:1107:Y01:HAT2	5:B:1109:Y01:HAI	1.47	0.93
5:B:1109:Y01:HAA3	6:B:1112:LPE:H232	1.53	0.91

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	467/1053 (44%)	455 (97%)	12 (3%)	0	100	100
1	B	467/1053 (44%)	448 (96%)	18 (4%)	1 (0%)	43	62
All	All	934/2106 (44%)	903 (97%)	30 (3%)	1 (0%)	49	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	407	ASP

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	376/890 (42%)	372 (99%)	4 (1%)	65	81
1	B	376/890 (42%)	372 (99%)	4 (1%)	65	81
All	All	752/1780 (42%)	744 (99%)	8 (1%)	63	81

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	457	ILE
1	B	292	VAL
1	B	243	ARG
1	A	522	ILE
1	B	248	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	286	GLN
1	A	359	ASN

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Mol	Chain	Res	Type
1	A	481	GLN
1	B	327	GLN

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 ⓘ

4 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	C	1	2,1	14,14,15	0.23	0	17,19,21	0.48	0
2	NAG	C	2	2	14,14,15	0.50	0	17,19,21	0.76	0
2	NAG	D	1	2,1	14,14,15	0.46	0	17,19,21	0.63	0
2	NAG	D	2	2	14,14,15	0.30	0	17,19,21	0.84	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	NAG	C	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	3/6/23/26	0/1/1/1
2	NAG	D	1	2,1	-	3/6/23/26	0/1/1/1
2	NAG	D	2	2	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

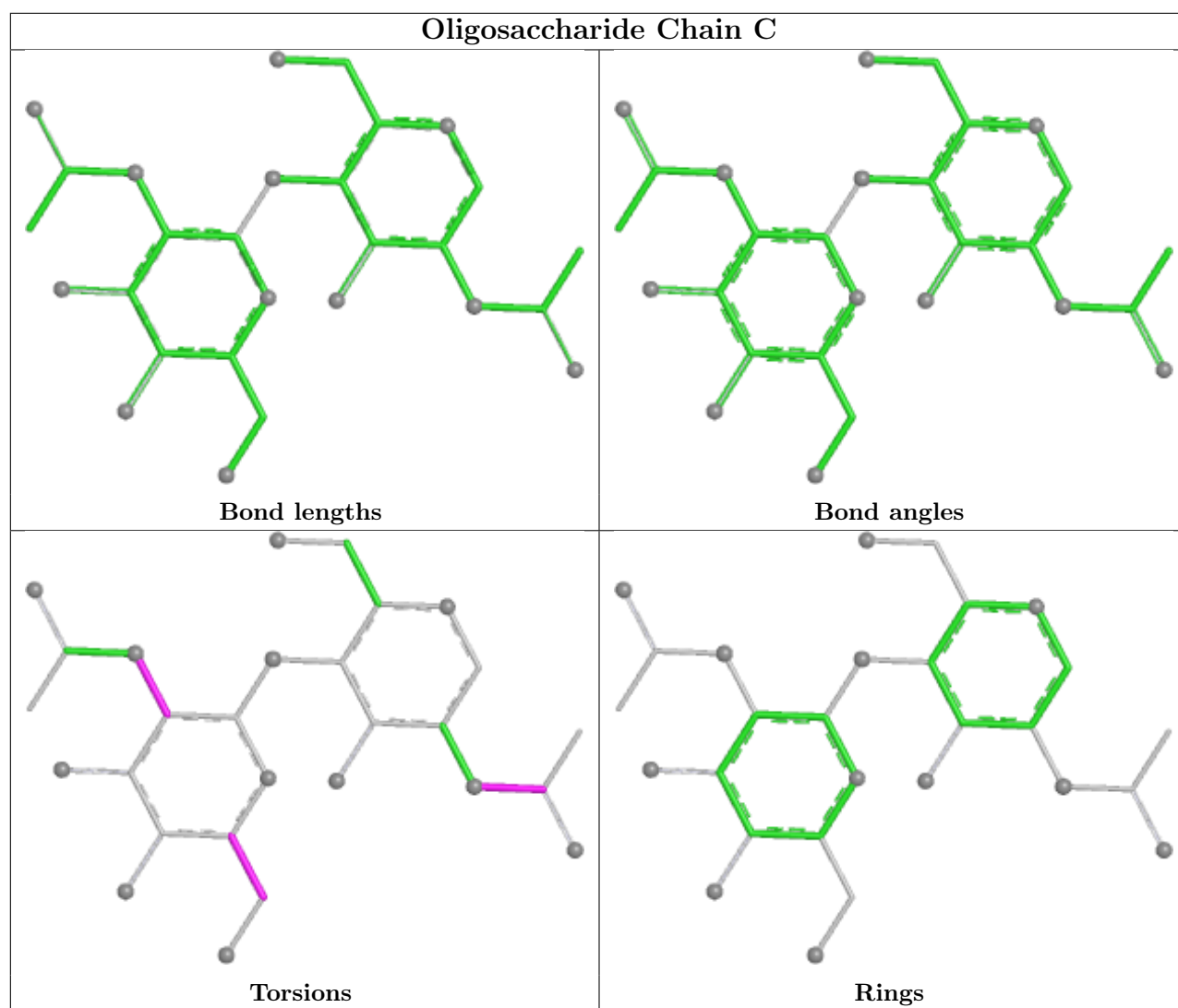
Mol	Chain	Res	Type	Atoms
2	D	1	NAG	C8-C7-N2-C2
2	D	1	NAG	O7-C7-N2-C2
2	C	1	NAG	C8-C7-N2-C2
2	C	1	NAG	O7-C7-N2-C2
2	D	1	NAG	O5-C5-C6-O6

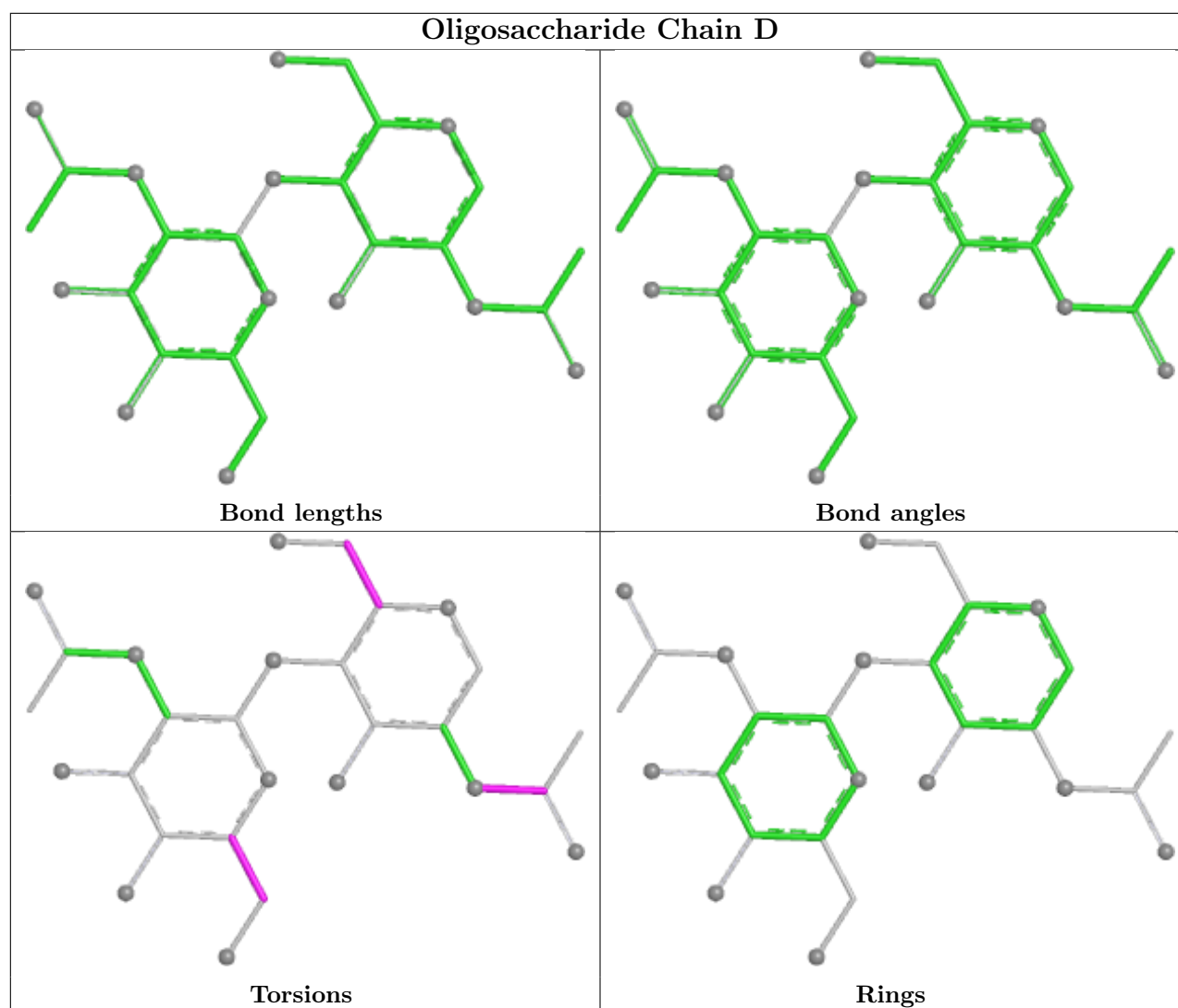
There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1	NAG	3	0
2	C	1	NAG	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





5.6 Ligand geometry [i](#)

Of 33 ligands modelled in this entry, 8 are monoatomic - leaving 25 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	$\# Z > 2$
6	LPE	B	1110	-	33,33,33	1.51	5 (15%)	37,39,39	2.35	16 (43%)
5	Y01	B	1108	-	38,38,38	0.22	0	57,57,57	0.45	0
7	POV	A	1113	-	51,51,51	0.95	2 (3%)	57,59,59	1.05	5 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	POV	B	1101	-	51,51,51	1.32	6 (11%)	57,59,59	2.12	23 (40%)
6	LPE	B	1113	-	33,33,33	1.07	0	37,39,39	1.66	7 (18%)
6	LPE	A	1109	-	33,33,33	1.03	1 (3%)	37,39,39	2.01	14 (37%)
7	POV	B	1115	-	51,51,51	1.24	2 (3%)	57,59,59	1.95	12 (21%)
7	POV	A	1114	-	51,51,51	0.97	2 (3%)	57,59,59	1.05	3 (5%)
5	Y01	A	1105	-	38,38,38	0.17	0	57,57,57	0.47	0
7	POV	B	1114	-	51,51,51	0.94	2 (3%)	57,59,59	1.10	4 (7%)
5	Y01	B	1109	-	38,38,38	0.24	0	57,57,57	0.39	0
6	LPE	B	1111	-	33,33,33	1.22	1 (3%)	37,39,39	1.48	5 (13%)
5	Y01	A	1107	-	38,38,38	0.21	0	57,57,57	0.58	0
7	POV	A	1112	-	51,51,51	0.94	2 (3%)	57,59,59	1.11	4 (7%)
7	POV	B	1102	-	51,51,51	1.09	4 (7%)	57,59,59	1.83	12 (21%)
7	POV	A	1116	-	51,51,51	1.21	5 (9%)	57,59,59	1.89	16 (28%)
8	NAG	A	1117	1	14,14,15	0.29	0	17,19,21	0.60	0
5	Y01	B	1107	-	38,38,38	0.25	0	57,57,57	0.69	1 (1%)
7	POV	A	1115	-	51,51,51	1.14	4 (7%)	57,59,59	1.85	10 (17%)
5	Y01	A	1106	-	38,38,38	0.22	0	57,57,57	0.51	1 (1%)
6	LPE	A	1108	-	33,33,33	1.02	3 (9%)	37,39,39	1.15	3 (8%)
8	NAG	B	1116	1	14,14,15	0.33	0	17,19,21	0.57	0
6	LPE	A	1111	-	33,33,33	1.13	0	37,39,39	1.89	8 (21%)
6	LPE	A	1110	-	33,33,33	1.00	1 (3%)	37,39,39	1.43	6 (16%)
6	LPE	B	1112	-	33,33,33	0.46	0	37,39,39	0.80	1 (2%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	LPE	B	1110	-	-	16/34/34/34	-
5	Y01	B	1108	-	-	7/19/77/77	0/4/4/4
7	POV	A	1113	-	-	9/55/55/55	-
7	POV	B	1101	-	-	33/55/55/55	-
6	LPE	B	1113	-	-	19/34/34/34	-
6	LPE	A	1109	-	-	15/34/34/34	-
7	POV	B	1115	-	-	25/55/55/55	-
7	POV	A	1114	-	-	17/55/55/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	Y01	A	1105	-	-	7/19/77/77	0/4/4/4
7	POV	B	1114	-	-	21/55/55/55	-
5	Y01	B	1109	-	-	10/19/77/77	0/4/4/4
6	LPE	B	1111	-	-	16/34/34/34	-
5	Y01	A	1107	-	-	5/19/77/77	0/4/4/4
7	POV	A	1112	-	-	15/55/55/55	-
7	POV	B	1102	-	-	24/55/55/55	-
7	POV	A	1116	-	-	30/55/55/55	-
8	NAG	A	1117	1	-	2/6/23/26	0/1/1/1
5	Y01	B	1107	-	-	10/19/77/77	0/4/4/4
7	POV	A	1115	-	-	29/55/55/55	-
5	Y01	A	1106	-	-	8/19/77/77	0/4/4/4
6	LPE	A	1108	-	-	13/34/34/34	-
8	NAG	B	1116	1	-	2/6/23/26	0/1/1/1
6	LPE	A	1111	-	-	16/34/34/34	-
6	LPE	A	1110	-	-	22/34/34/34	-
6	LPE	B	1112	-	-	15/34/34/34	-

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	1115	POV	O31-C31	4.86	1.47	1.33
7	B	1101	POV	O31-C31	4.75	1.47	1.33
7	A	1116	POV	O21-C21	4.46	1.46	1.34
7	B	1102	POV	O21-C21	4.45	1.46	1.34
7	A	1115	POV	O21-C21	4.45	1.46	1.34

The worst 5 of 151 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	1115	POV	O31-C31-O32	-7.01	106.10	123.63
7	B	1115	POV	O31-C3-C2	6.09	125.96	108.40
7	B	1102	POV	C3-C2-C1	-5.71	98.48	111.78
7	A	1115	POV	O21-C21-C22	5.70	123.81	111.48
7	B	1115	POV	C3-C2-C1	-5.65	98.61	111.78

There are no chirality outliers.

5 of 386 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1106	Y01	OAG-CAY-OAW-CBC
5	A	1106	Y01	CAM-CAY-OAW-CBC
5	B	1107	Y01	OAG-CAY-OAW-CBC
5	B	1107	Y01	CAM-CAY-OAW-CBC
5	B	1108	Y01	CAM-CAY-OAW-CBC

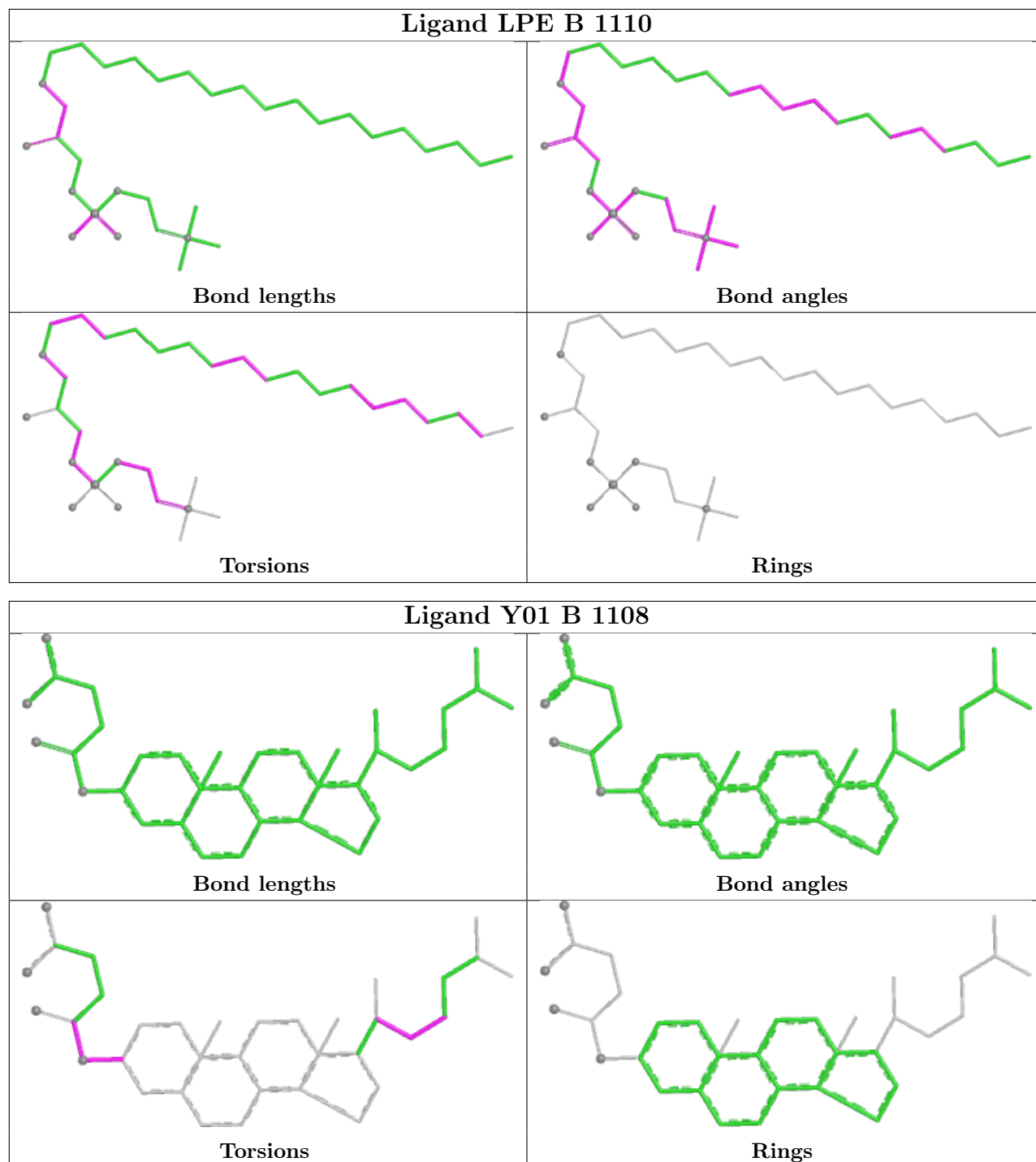
There are no ring outliers.

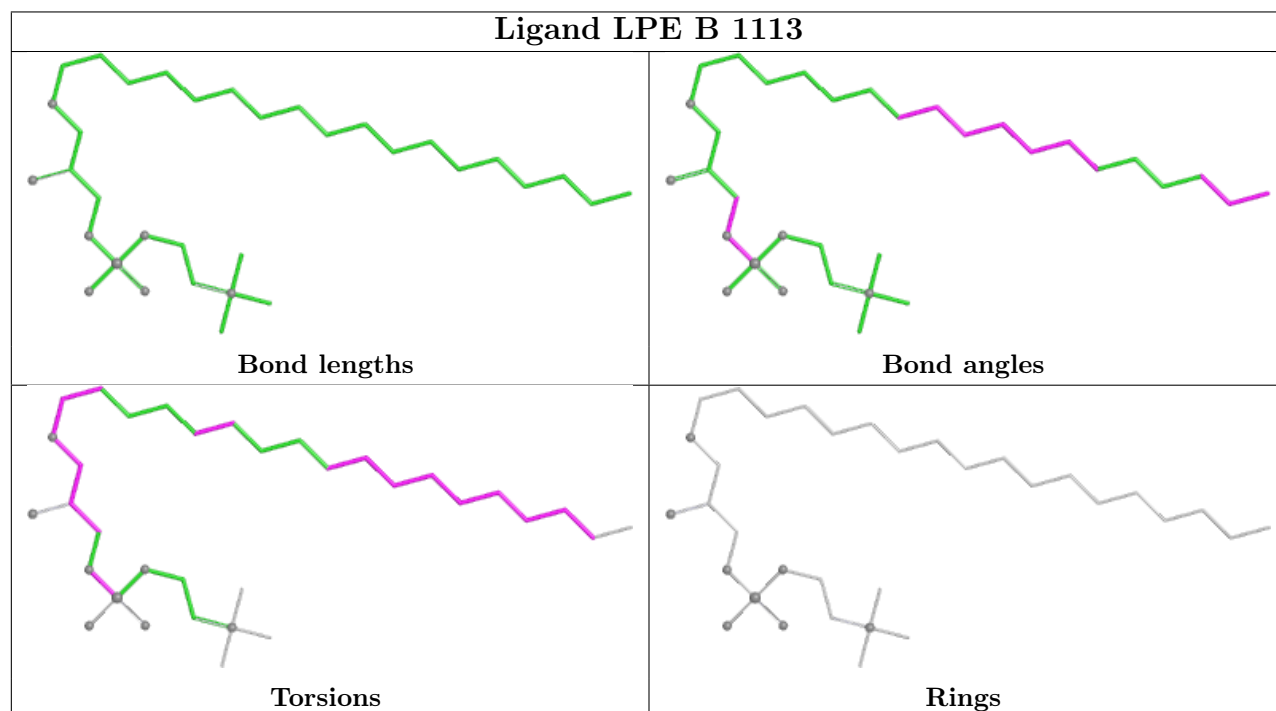
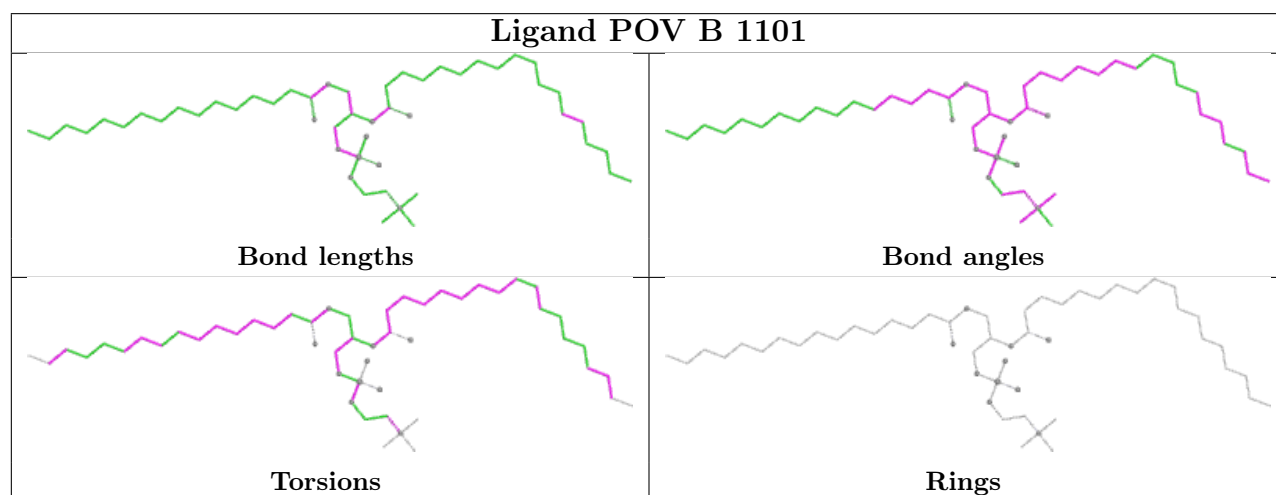
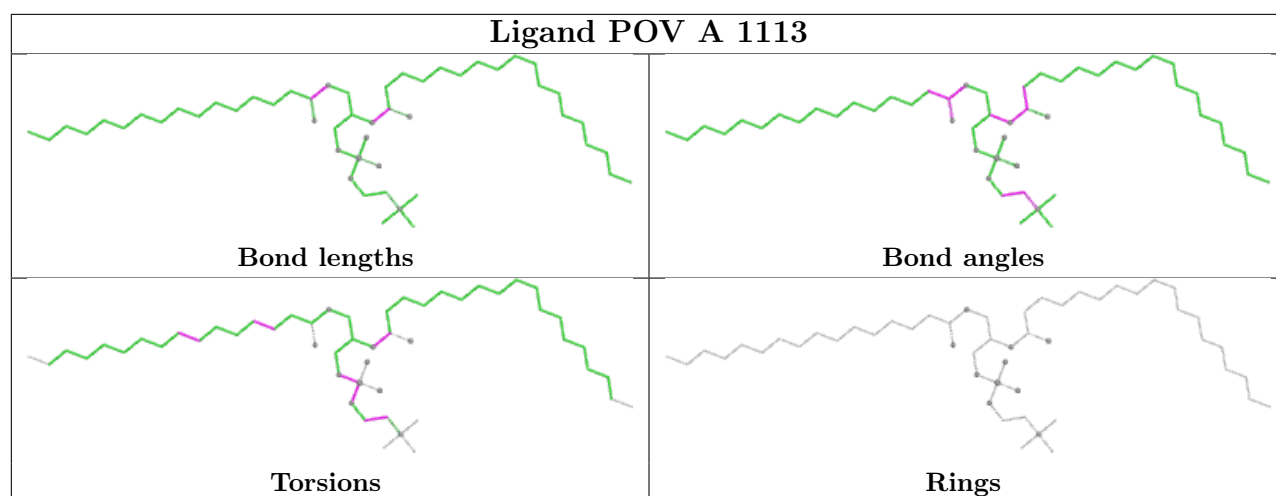
23 monomers are involved in 208 short contacts:

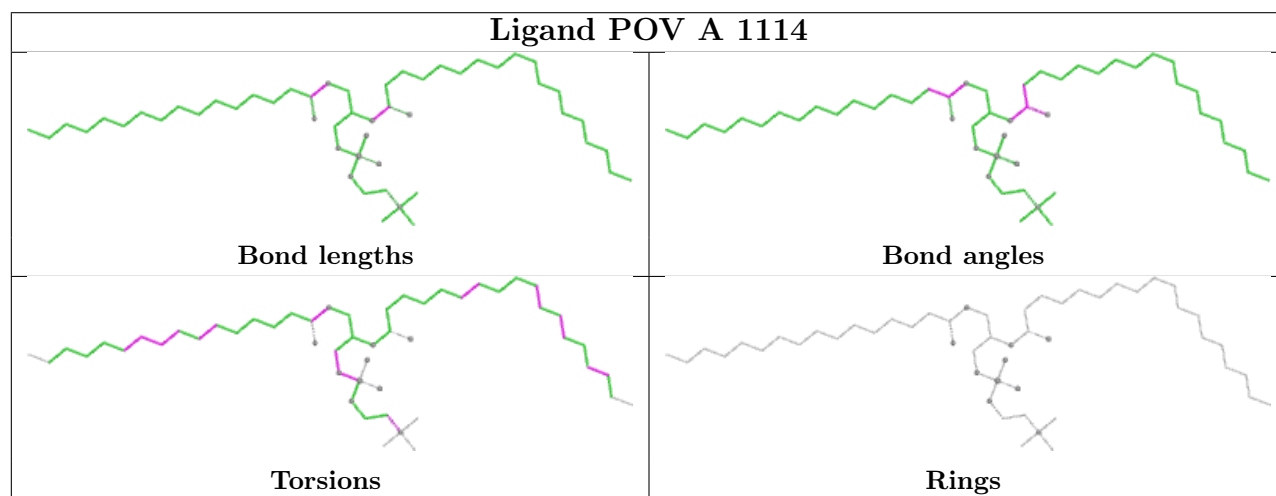
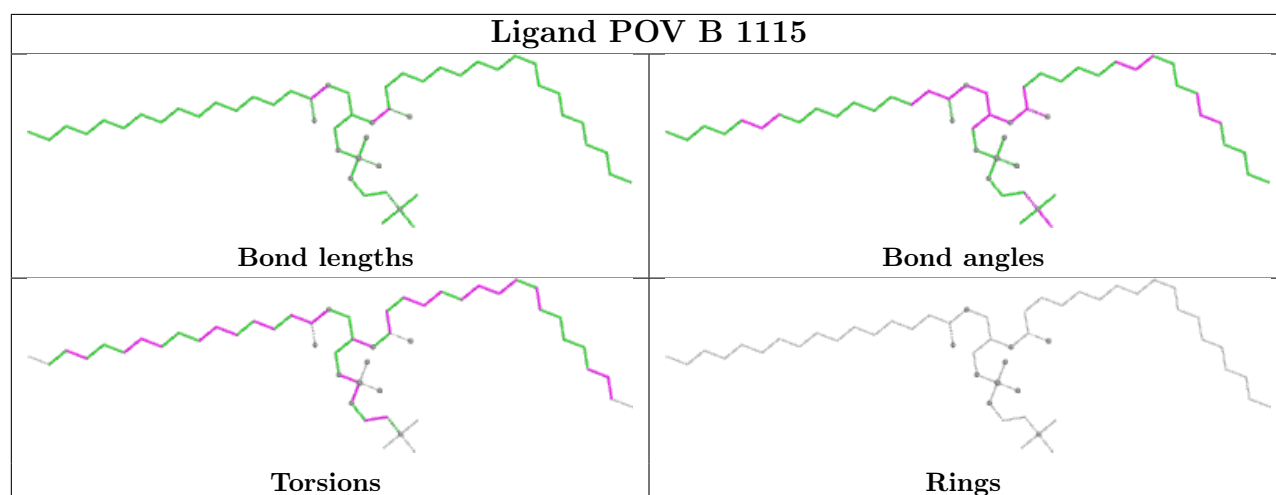
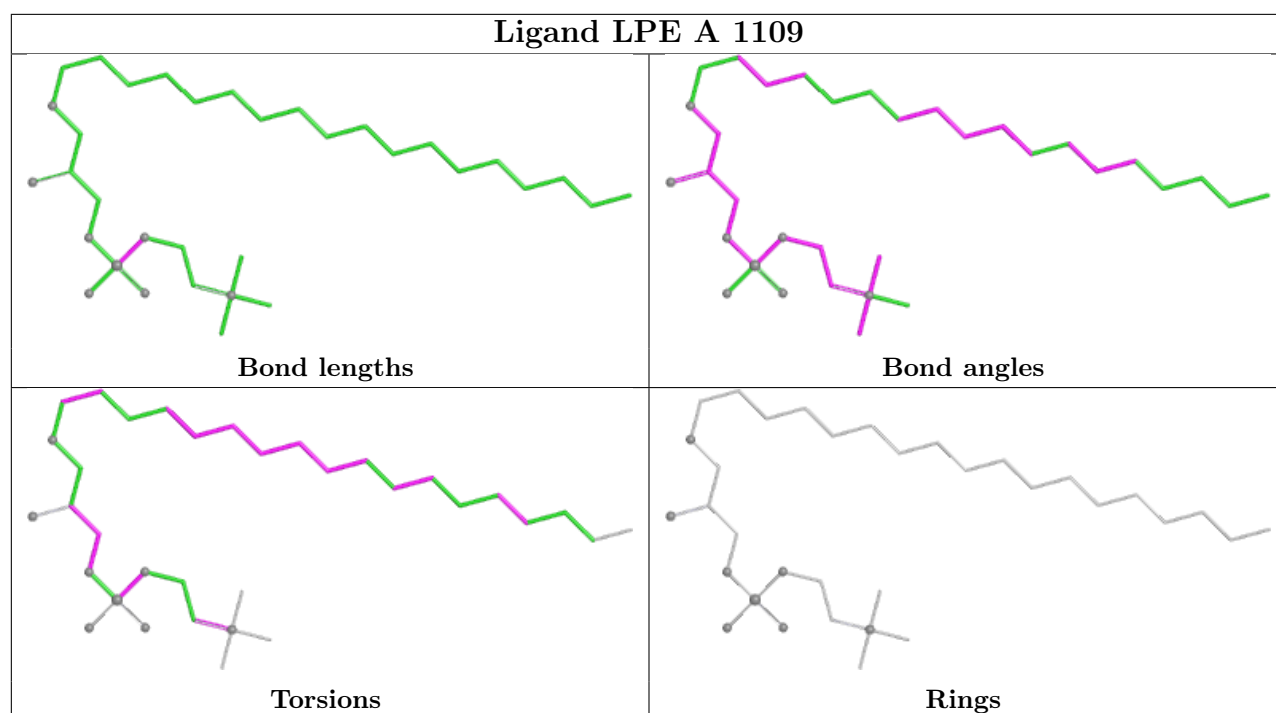
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	1110	LPE	5	0
5	B	1108	Y01	7	0
7	A	1113	POV	6	0
7	B	1101	POV	6	0
6	B	1113	LPE	6	0
6	A	1109	LPE	8	0
7	B	1115	POV	10	0
7	A	1114	POV	7	0
5	A	1105	Y01	19	0
7	B	1114	POV	18	0
5	B	1109	Y01	42	0
6	B	1111	LPE	5	0
5	A	1107	Y01	17	0
7	A	1112	POV	16	0
7	B	1102	POV	4	0
7	A	1116	POV	13	0
5	B	1107	Y01	17	0
7	A	1115	POV	10	0
5	A	1106	Y01	10	0
6	A	1108	LPE	6	0
6	A	1111	LPE	6	0
6	A	1110	LPE	4	0
6	B	1112	LPE	16	0

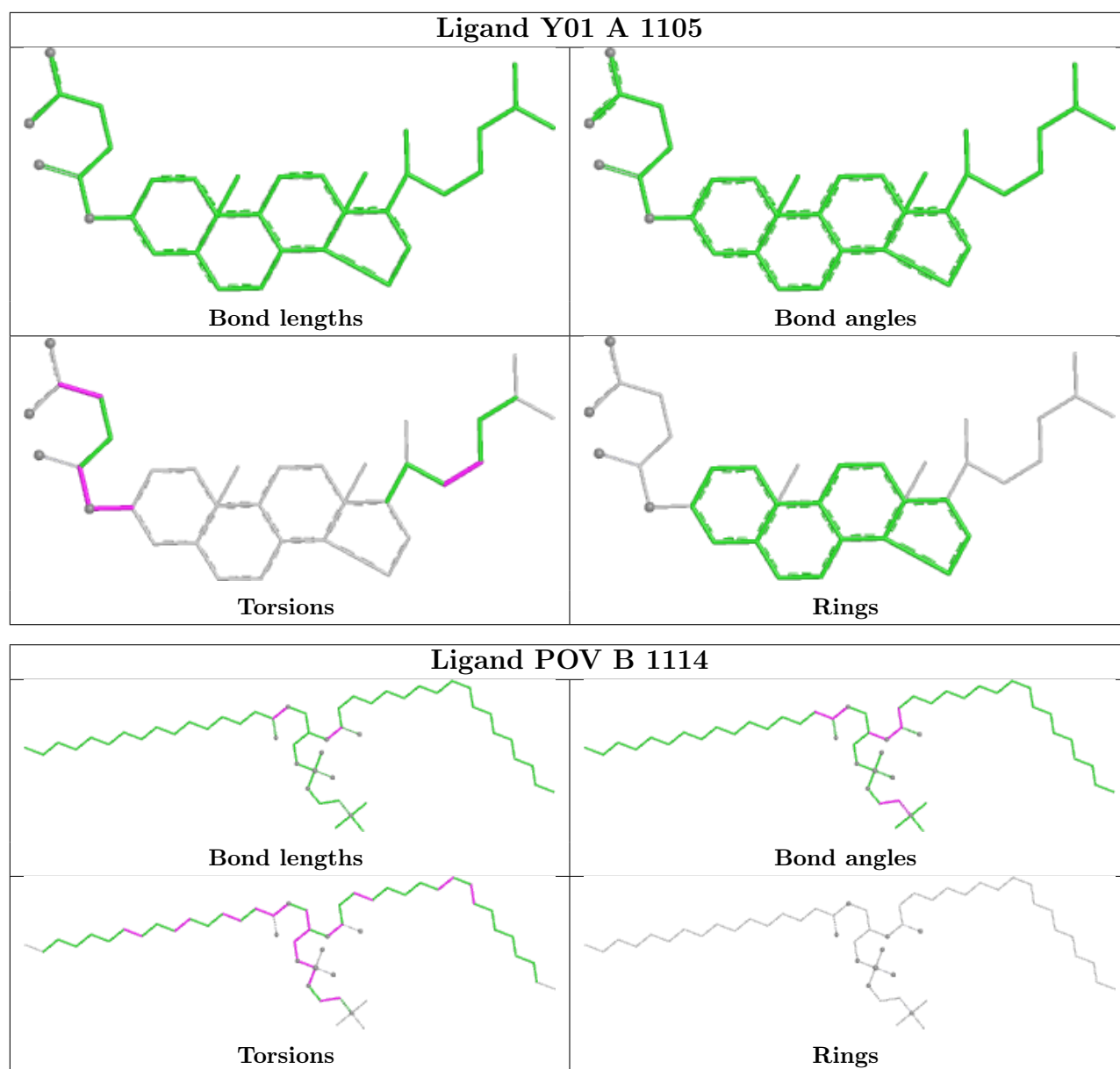
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

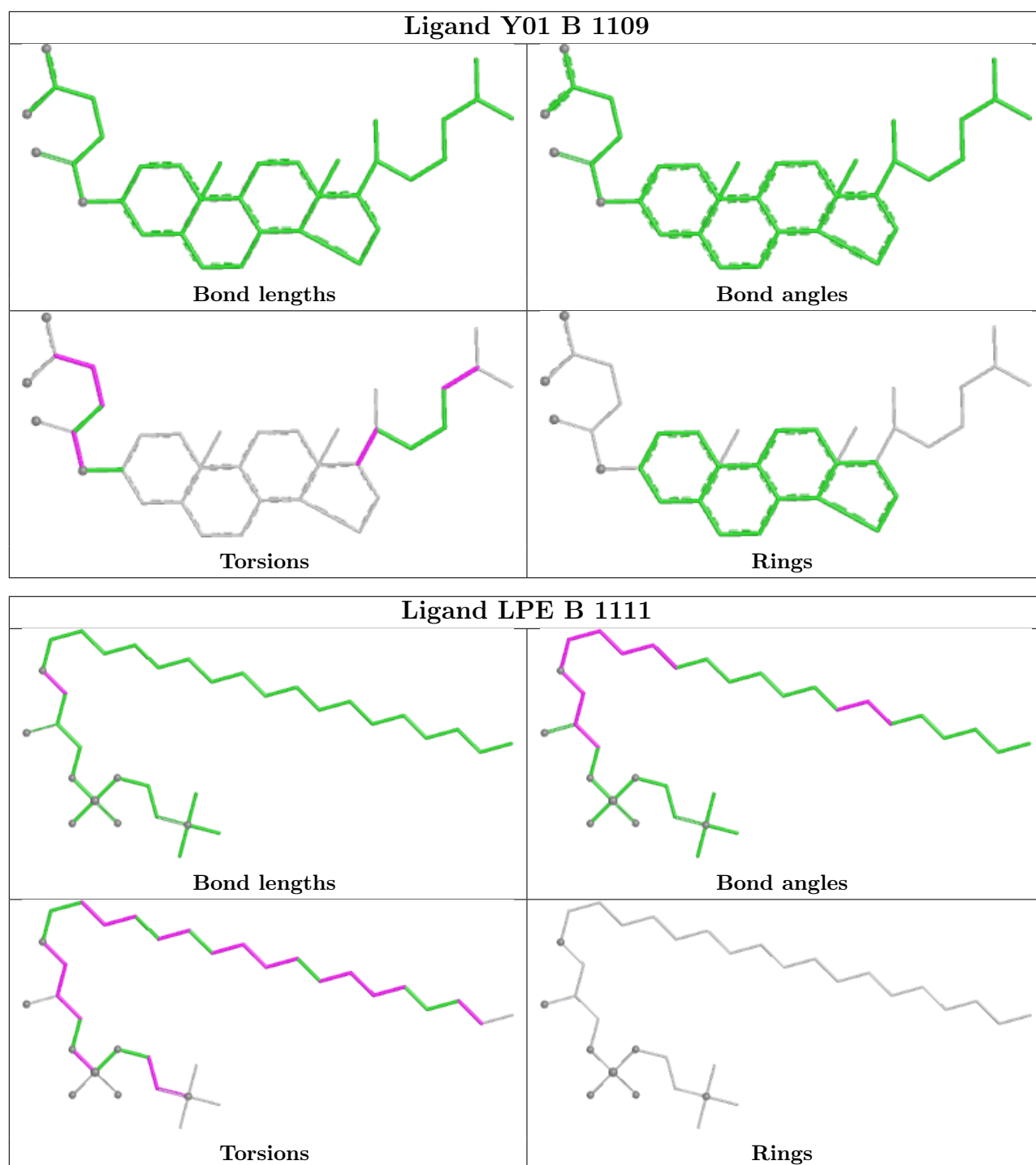
any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

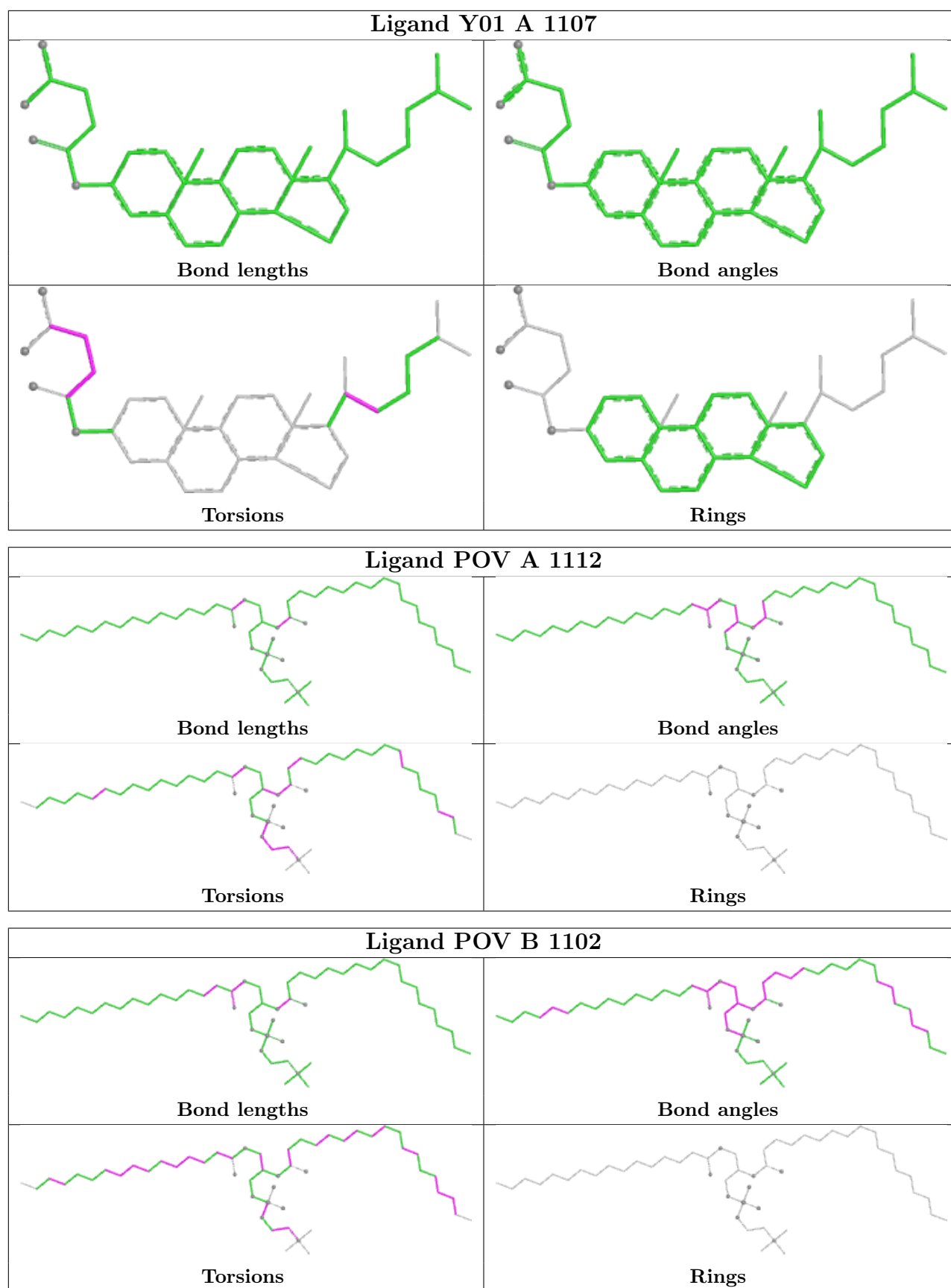


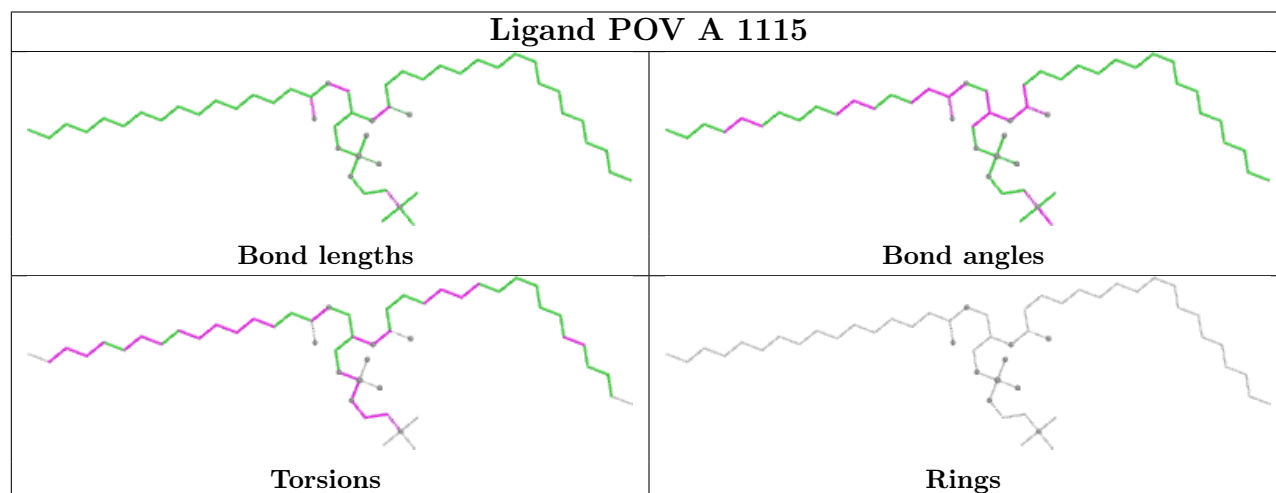
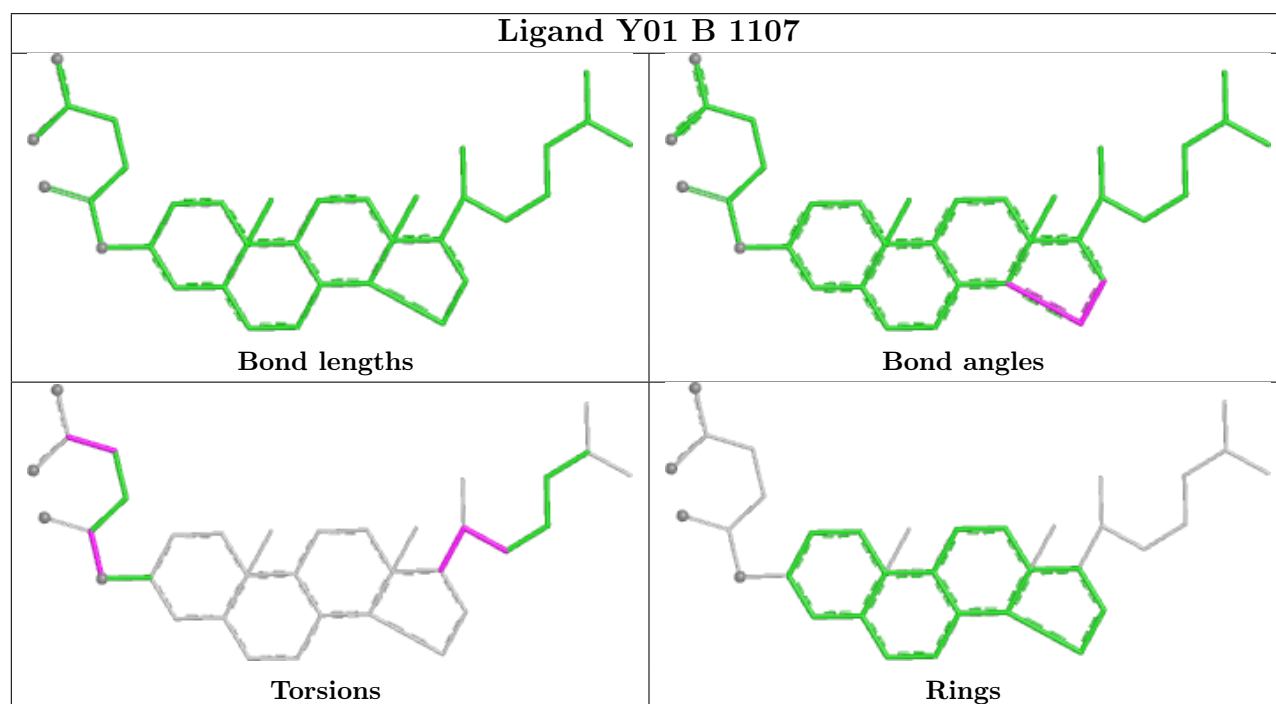
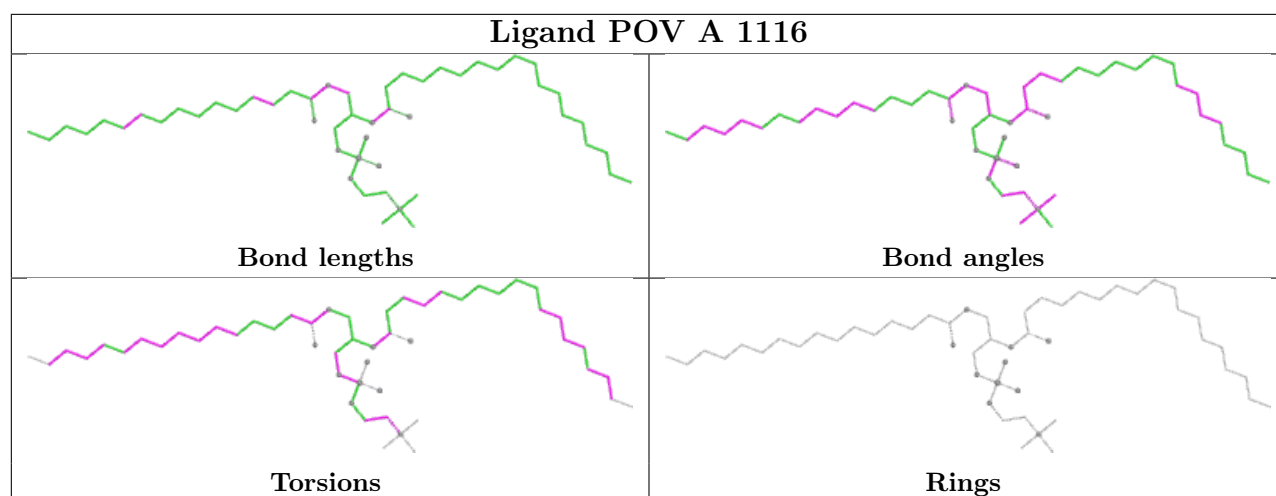


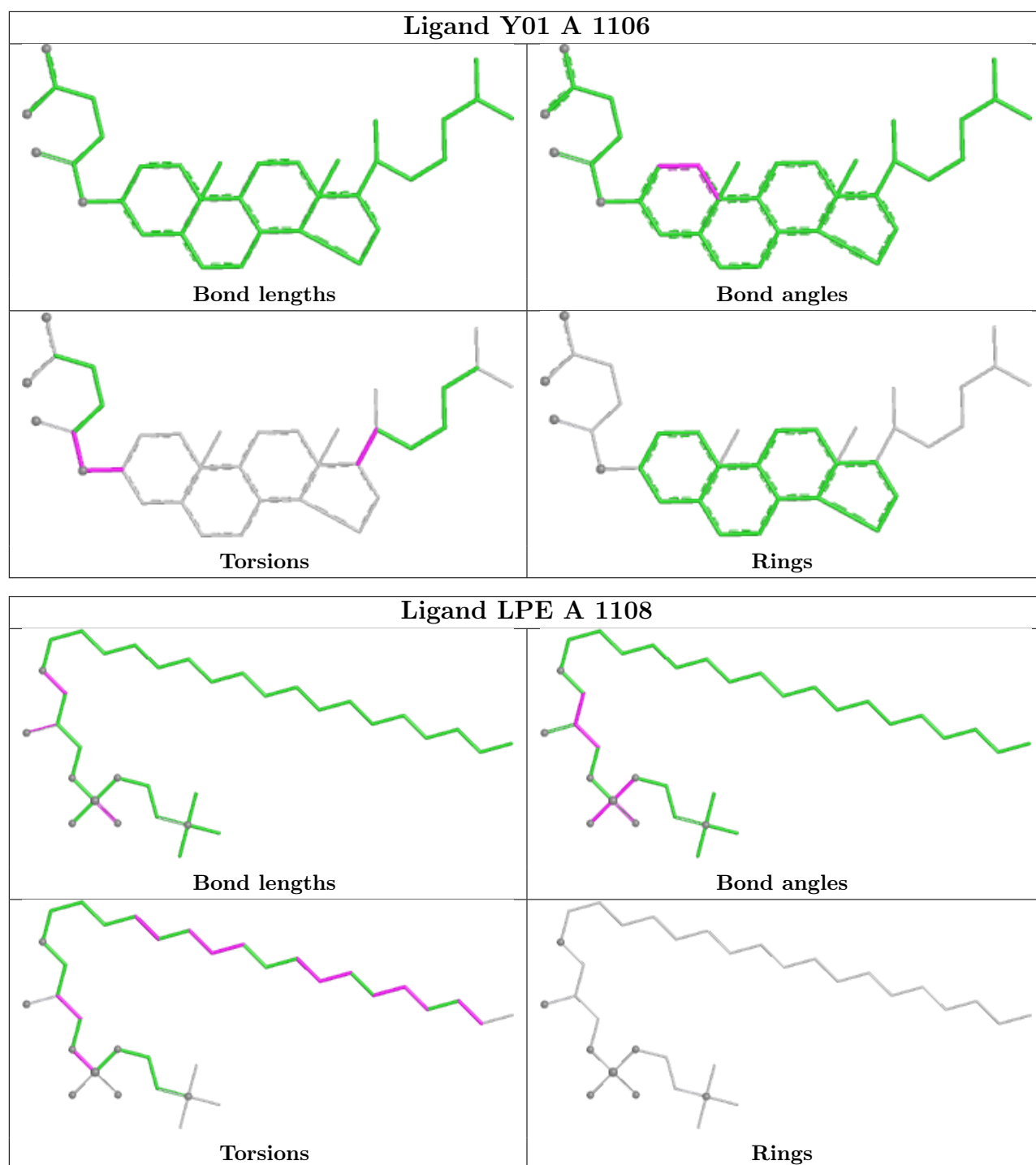


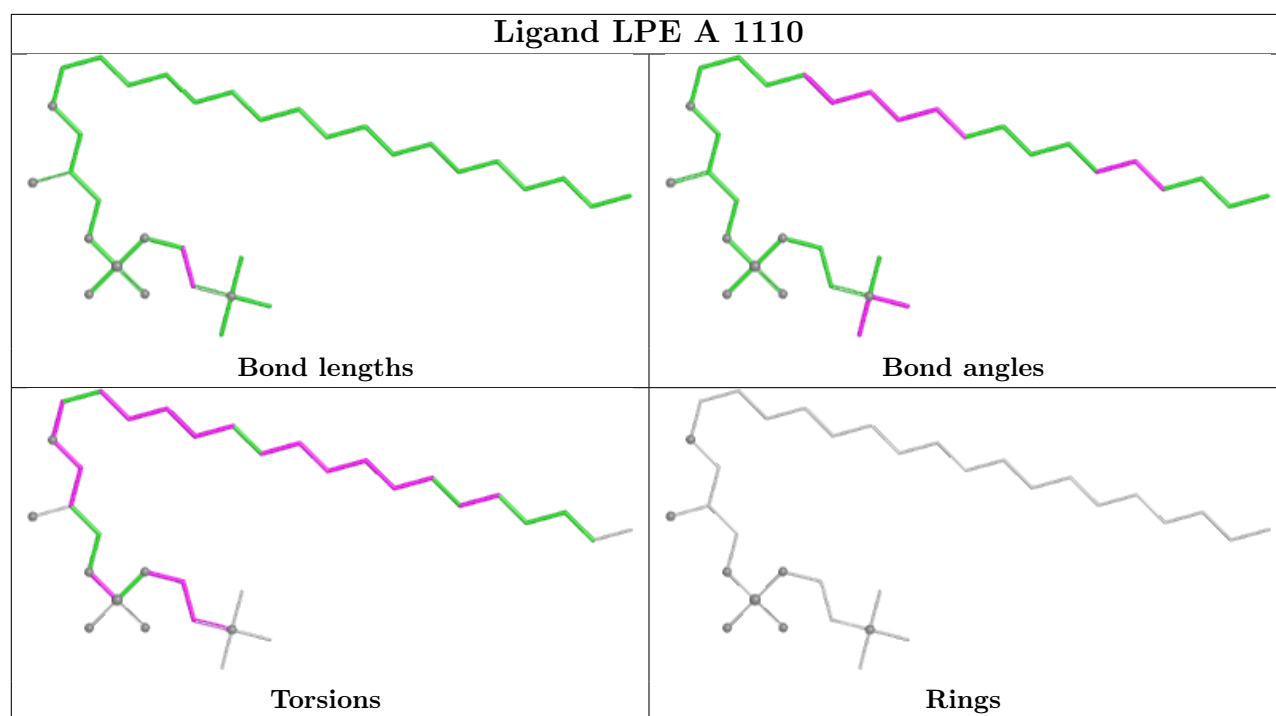
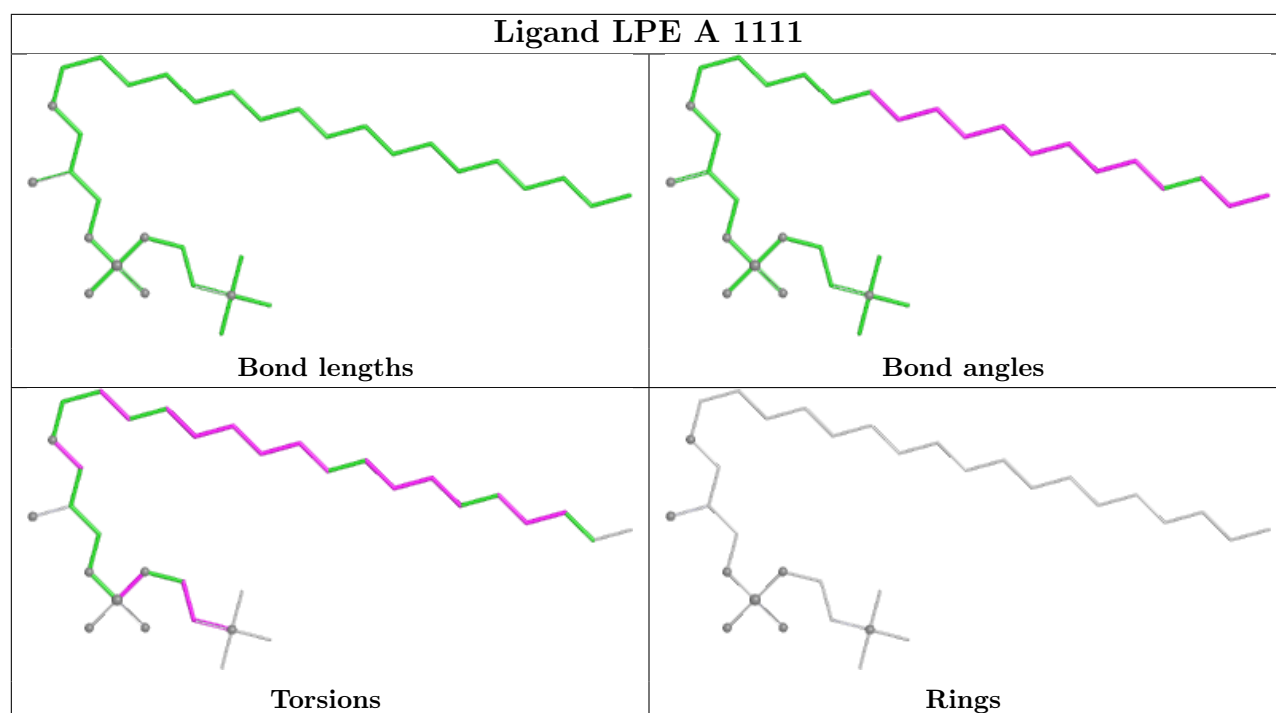


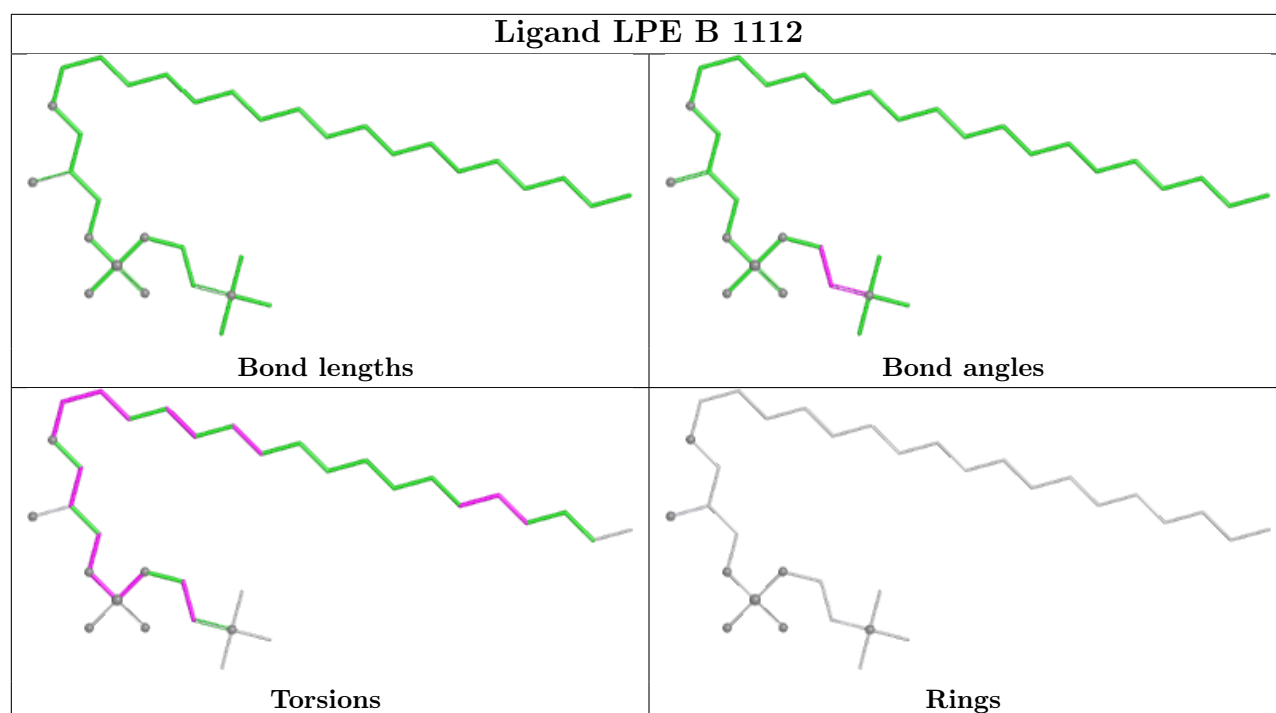












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

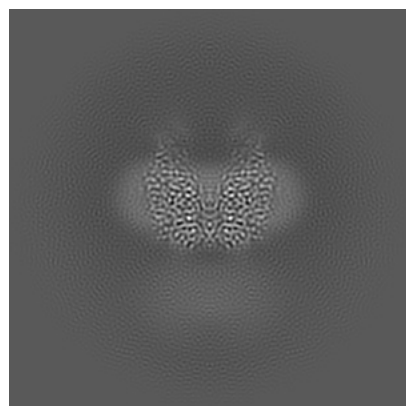
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33641. These allow visual inspection of the internal detail of the map and identification of artifacts.

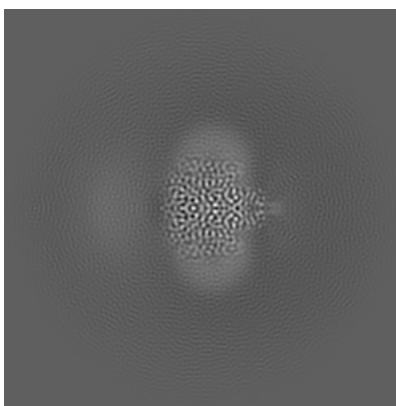
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

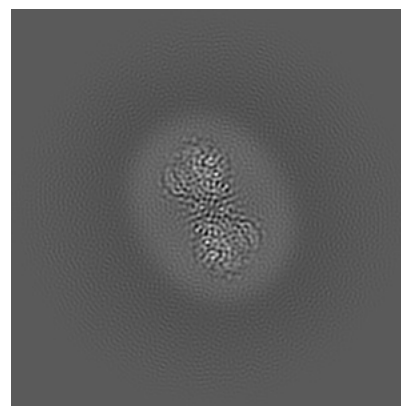
6.1.1 Primary map



X

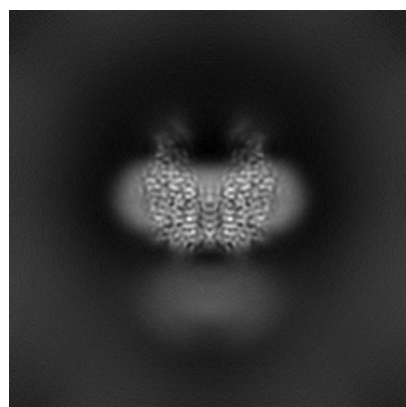


Y

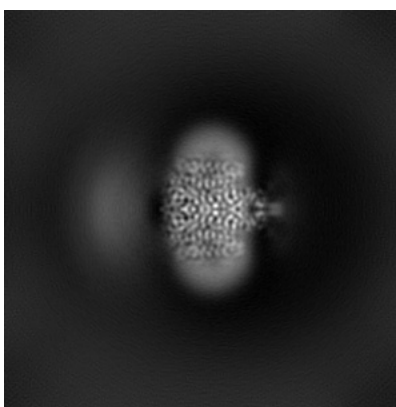


Z

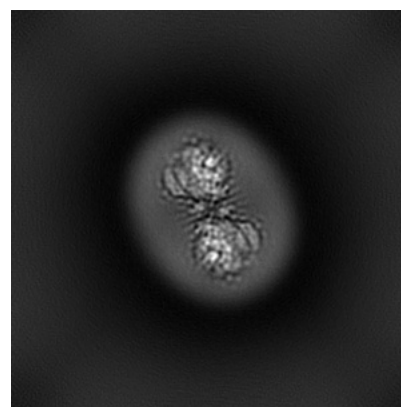
6.1.2 Raw map



X



Y

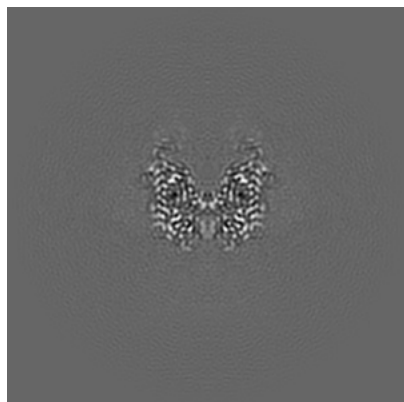


Z

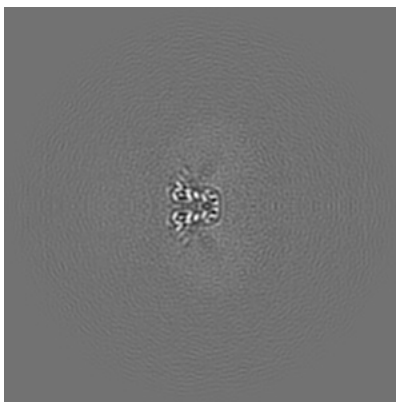
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

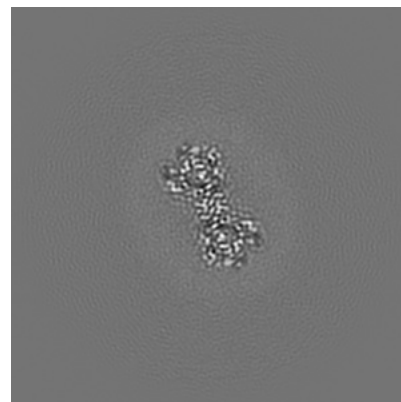
6.2.1 Primary map



X Index: 128

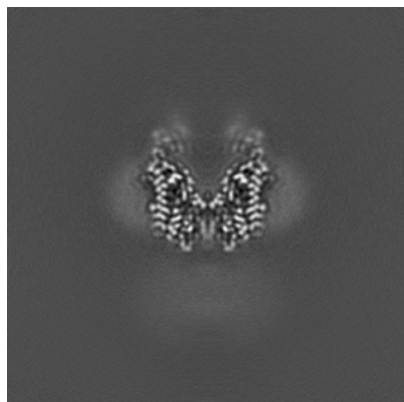


Y Index: 128

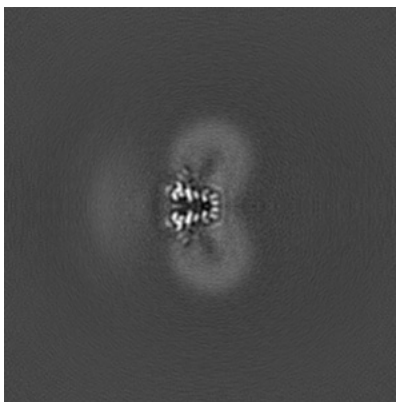


Z Index: 128

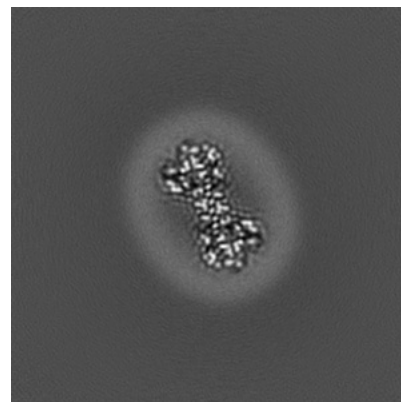
6.2.2 Raw map



X Index: 128



Y Index: 128

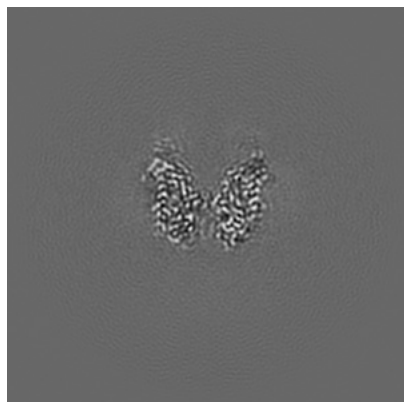


Z Index: 128

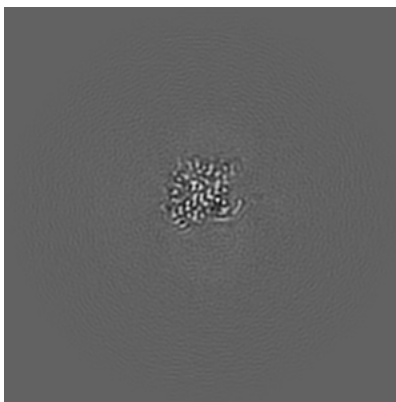
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

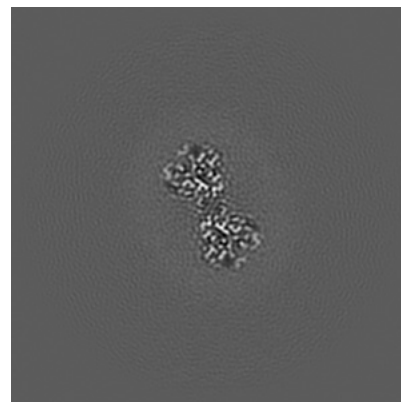
6.3.1 Primary map



X Index: 129

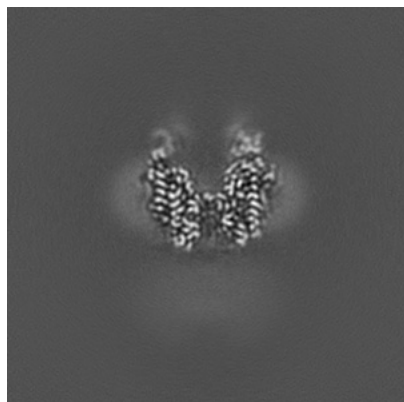


Y Index: 115

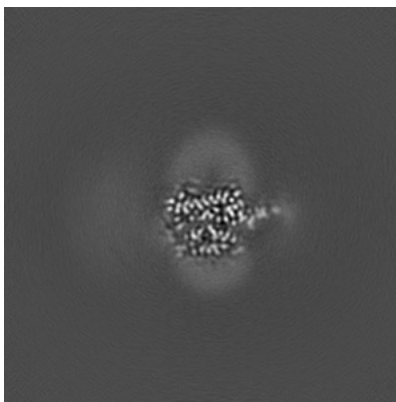


Z Index: 126

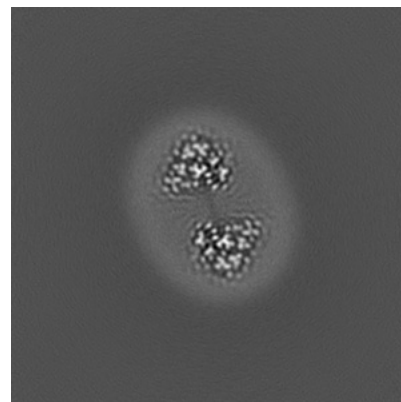
6.3.2 Raw map



X Index: 126



Y Index: 149

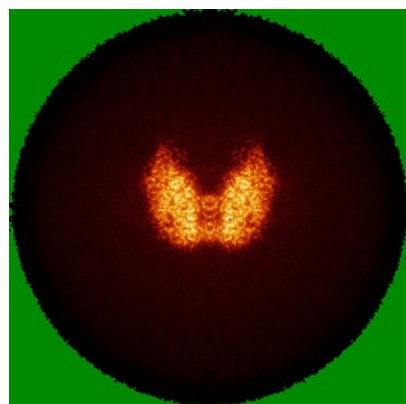


Z Index: 142

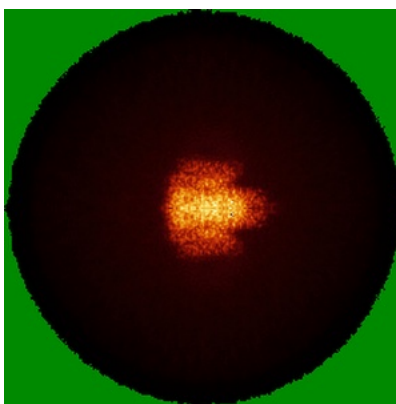
The images above show the largest variance slices of the map in three orthogonal directions.

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

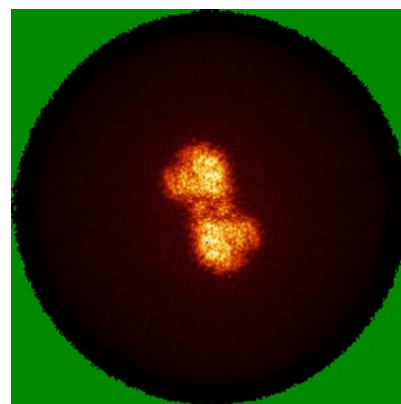
6.4.1 Primary map



X

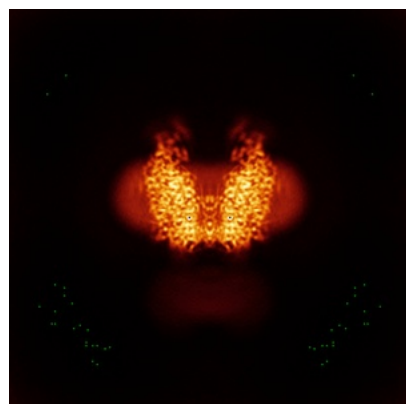


Y

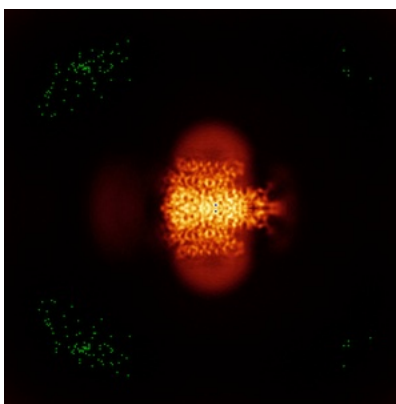


Z

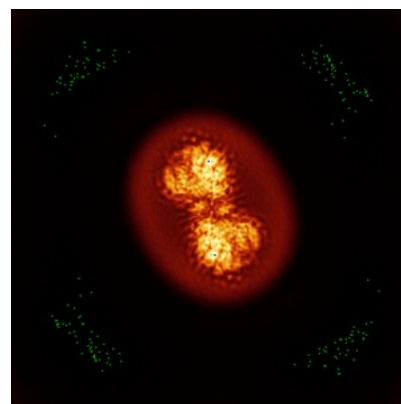
6.4.2 Raw map



X



Y

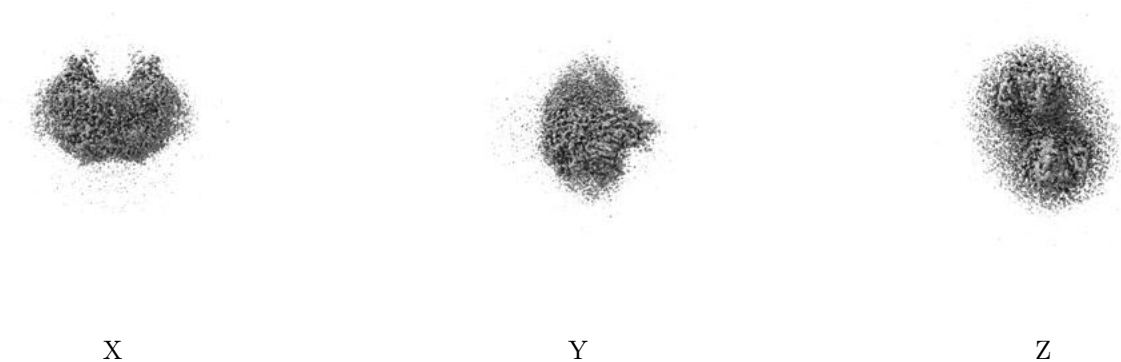


Z

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.

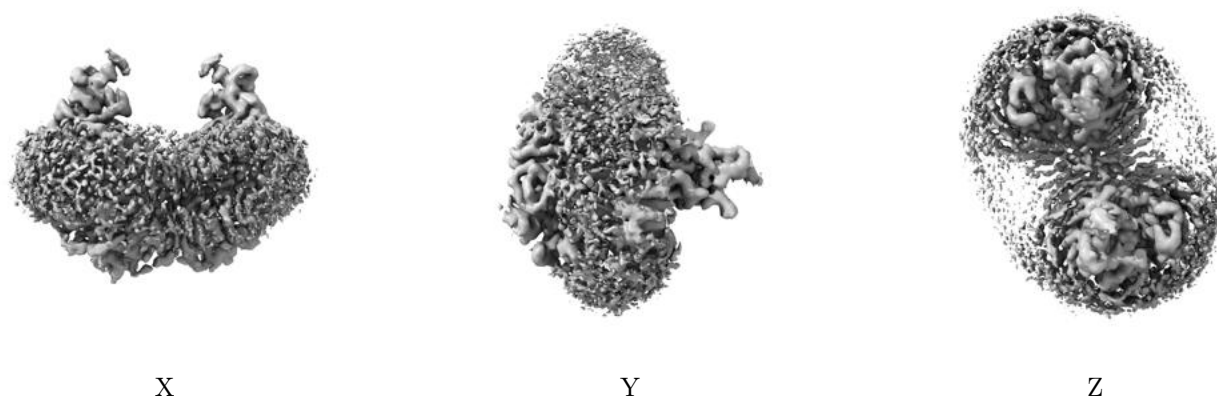
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.282. 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.

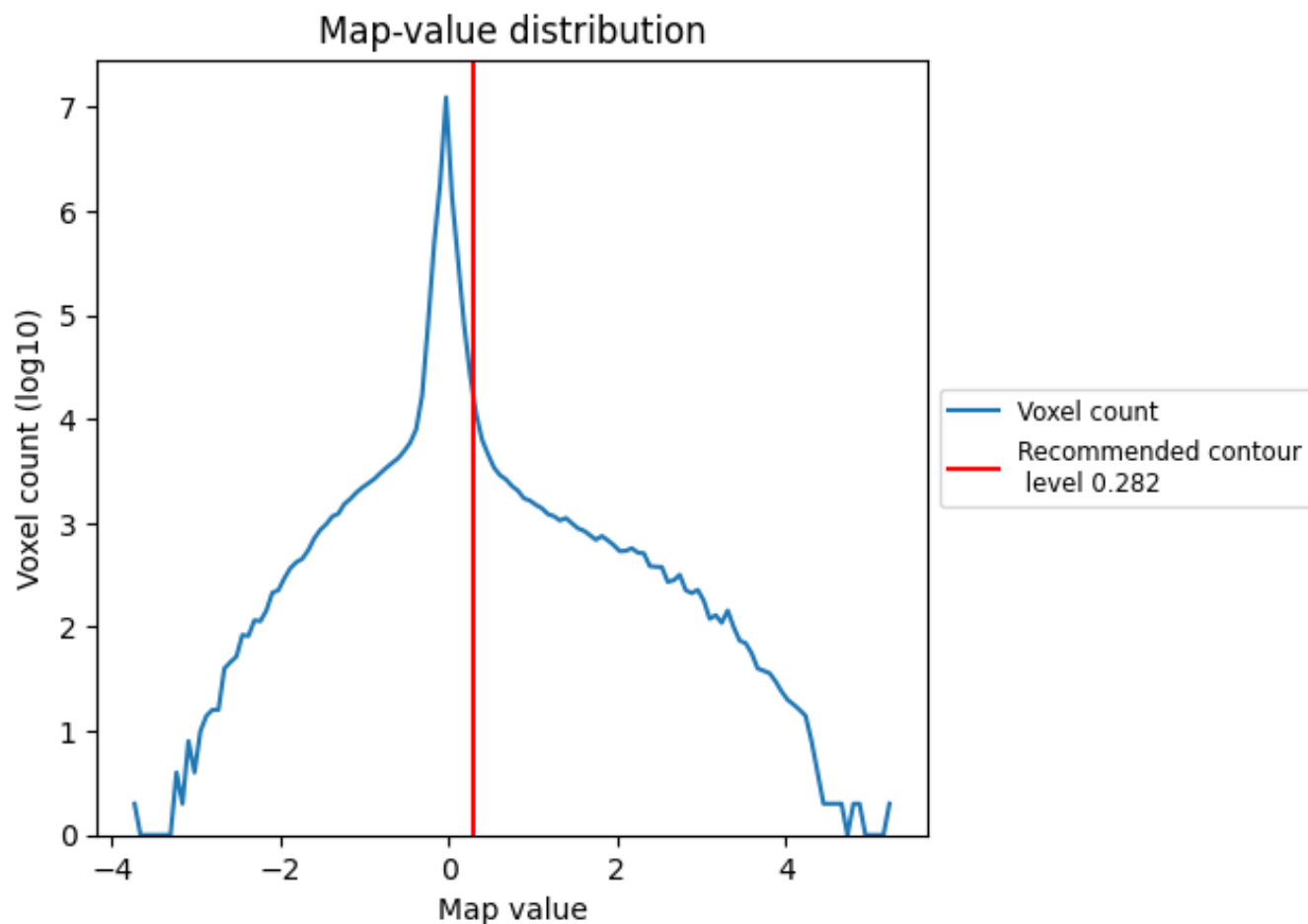
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

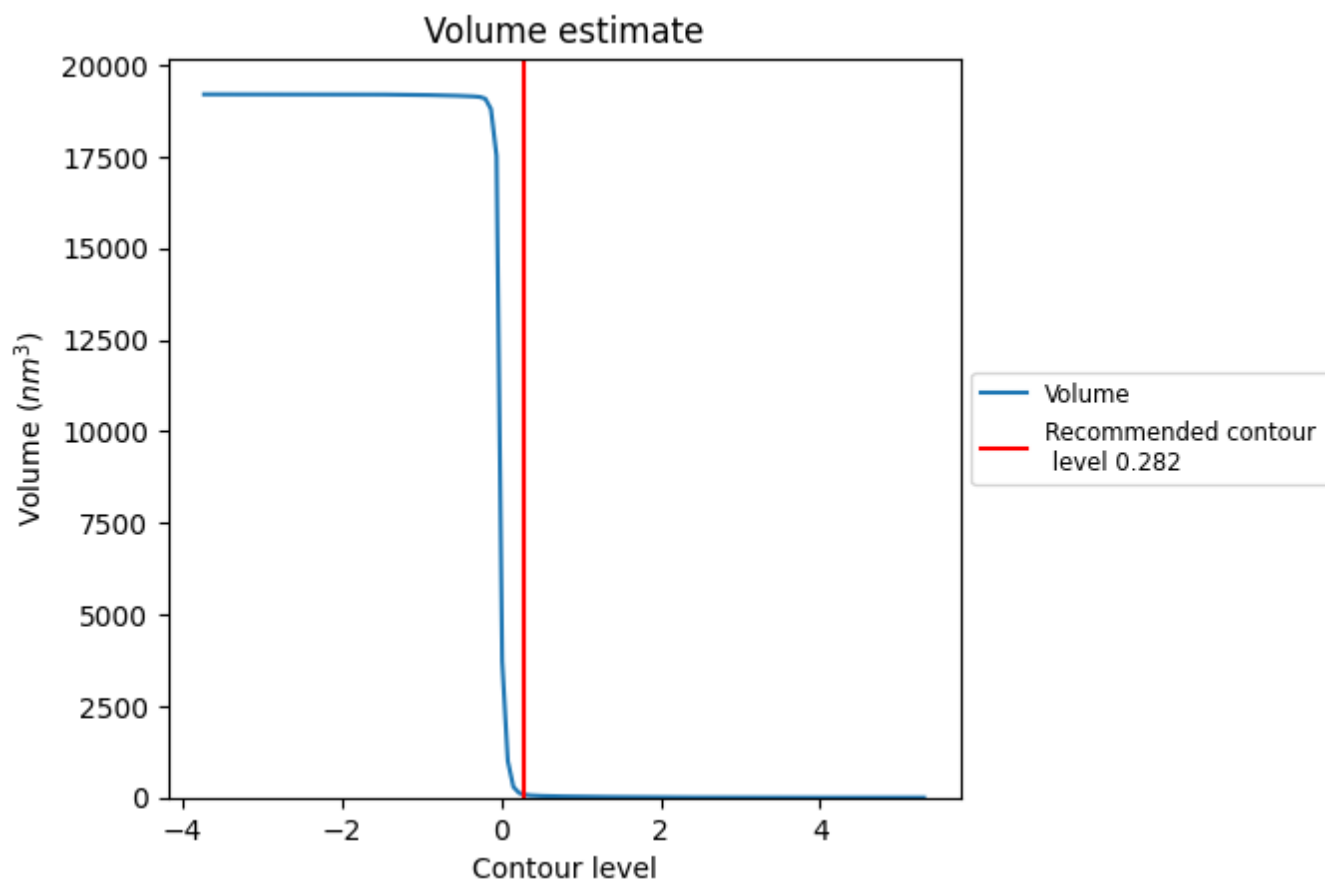
This section contains the results of statistical analysis of the map.

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.

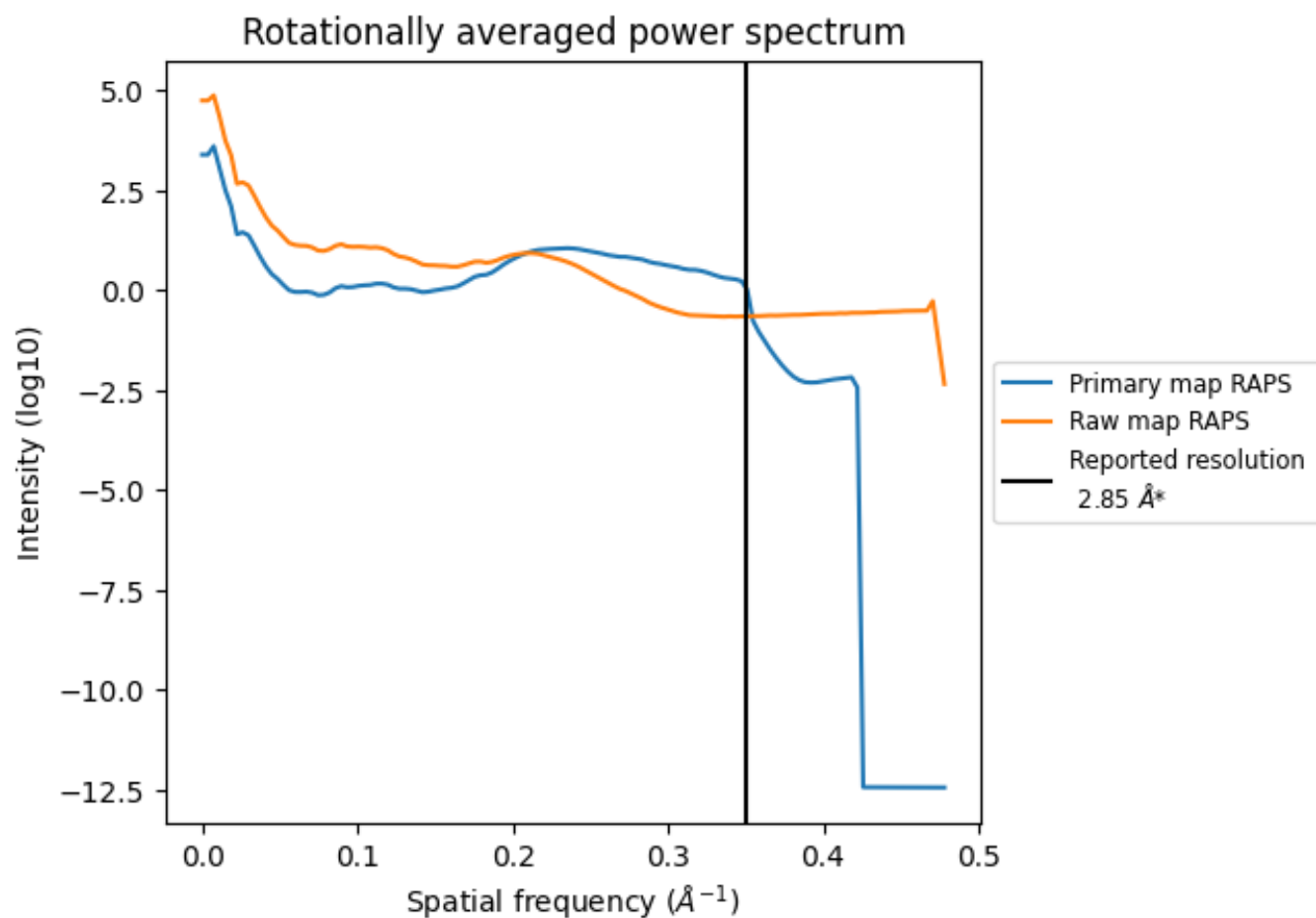
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 86 nm³; this corresponds to an approximate mass of 77 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 ⓘ

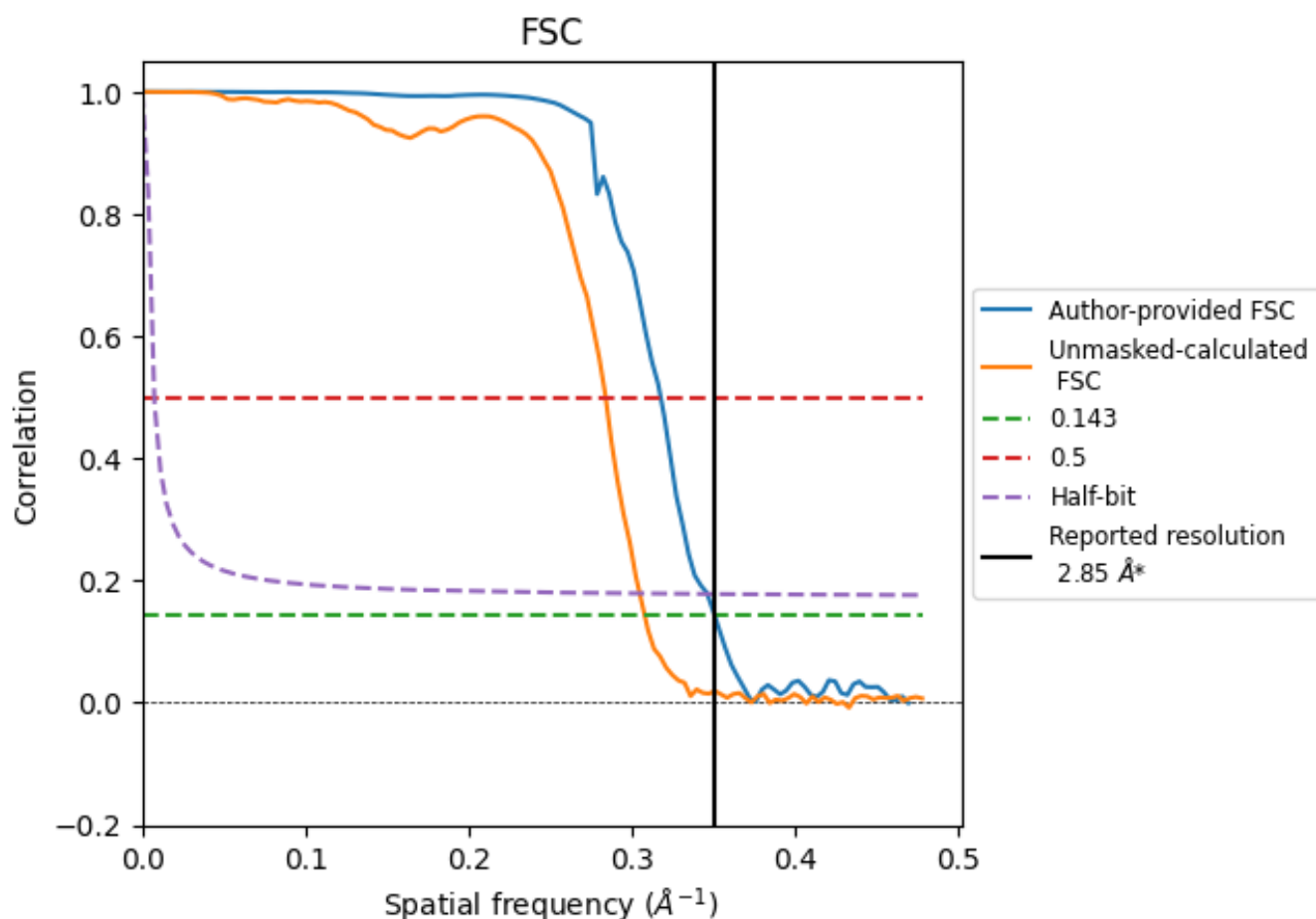


*Reported resolution corresponds to spatial frequency of 0.351 Å⁻¹

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 0.351 Å⁻¹

8.2 Resolution estimates [i](#)

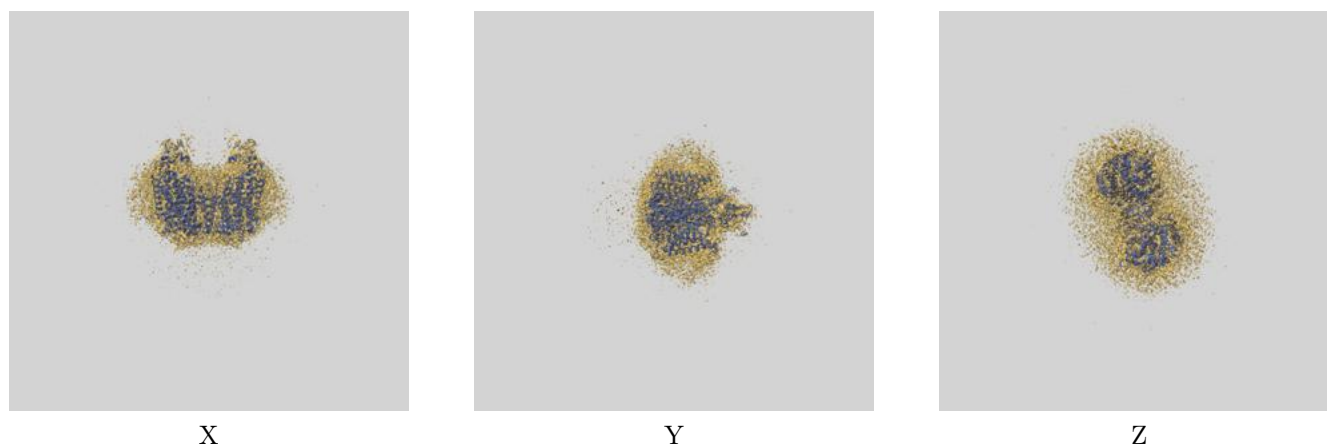
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.85	-	-
Author-provided FSC curve	2.85	3.15	2.89
Unmasked-calculated*	3.25	3.52	3.28

*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 3.25 differs from the reported value 2.85 by more than 10 %

9 Map-model fit [i](#)

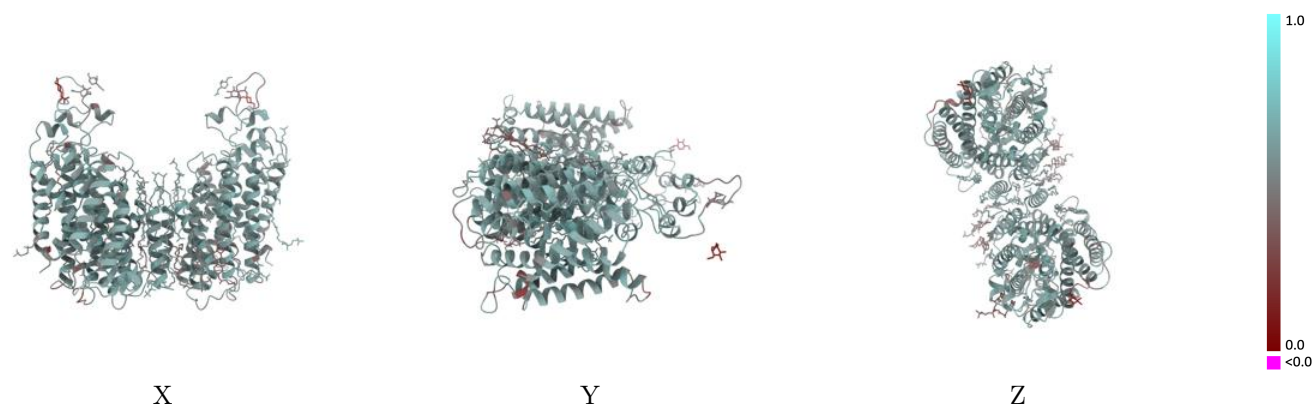
This section contains information regarding the fit between EMDB map EMD-33641 and PDB model 7Y6I. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



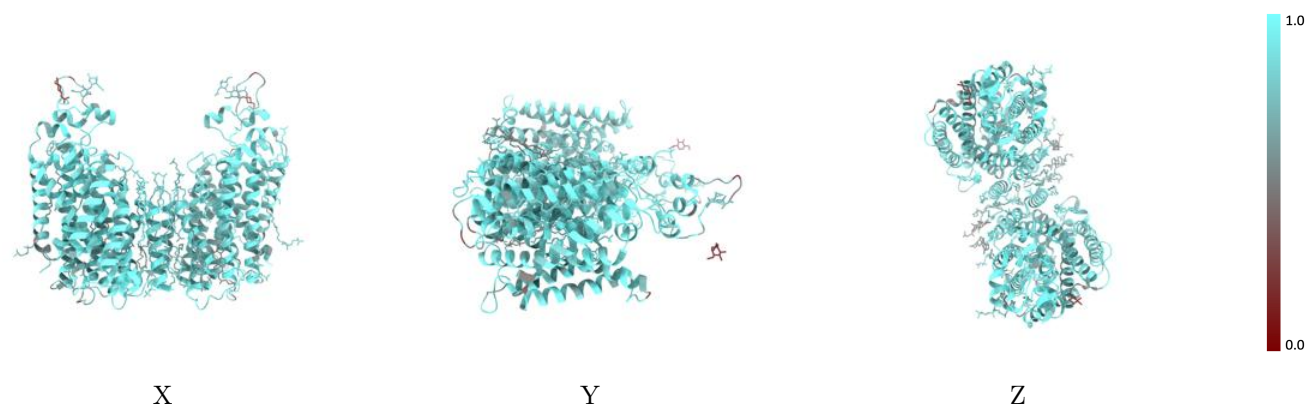
The images above show the 3D surface view of the map at the recommended contour level 0.282 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



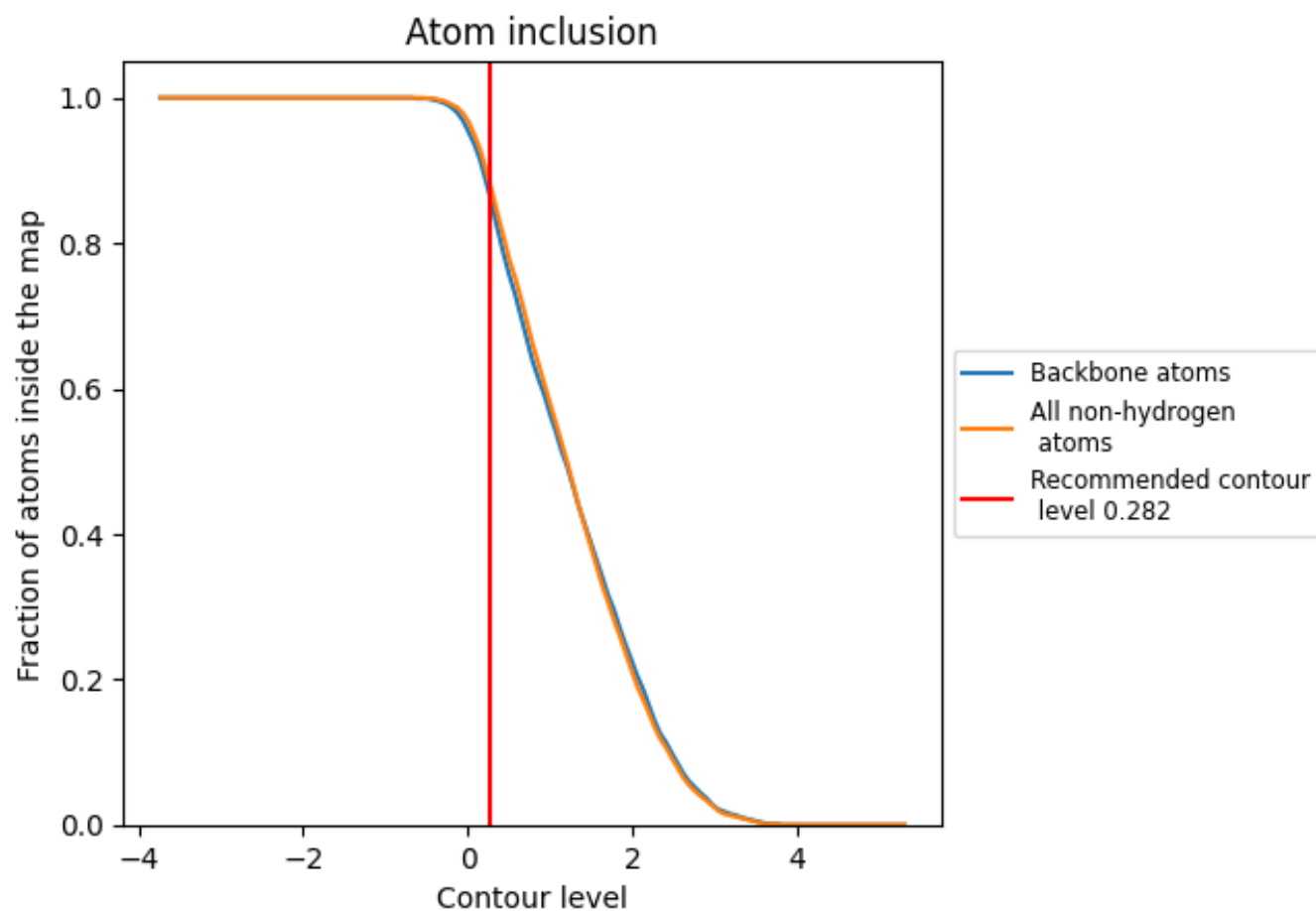
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.282).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 88% 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 (0.282) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8770	0.5700
A	0.8790	0.5690
B	0.8790	0.5730
C	0.7500	0.4720
D	0.7140	0.4570

