



## wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 01:28 PM UTC

PDB ID : 8IMX / pdb\_00008imx  
EMDB ID : EMD-35575  
Title : Cryo-EM structure of GPI-T with a chimeric GPI-anchored protein  
Authors : Xu, Y.; Li, T.; Qu, Q.; Li, D.  
Deposited on : 2023-03-07  
Resolution : 2.85 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

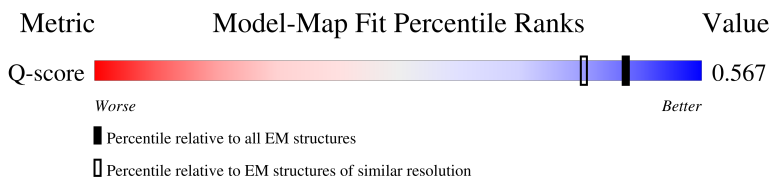
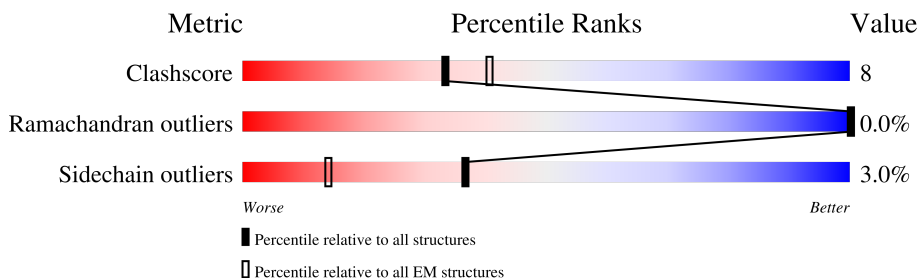
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (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 i

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.




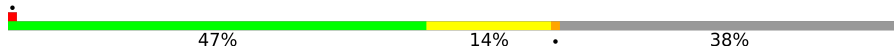

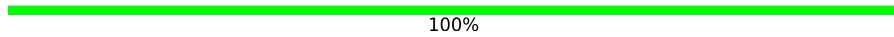
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11965 ( 2.35 - 3.35 )

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

Mol	Chain	Length	Quality of chain
1	D	327	<p>5% 92%</p>
2	G	886	<p>53% 12% 35%</p>
3	K	647	<p>39% 11% 49%</p>
4	S	816	<p>10% 53% 9% 37%</p>

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Mol	Chain	Length	Quality of chain
5	T	831	
6	U	678	
7	P	3	
8	R	2	

## 2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 19779 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 UL16-binding protein 2,GFP-like fluorescent chromoprotein cFP484.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	D	27	200	133	31	33	3	0	0

There are 93 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-80	MET	-	initiating methionine	UNP Q9BZM5
D	-55	GLY	-	linker	UNP Q9BZM5
D	-54	GLY	-	linker	UNP Q9BZM5
D	-53	SER	-	linker	UNP Q9BZM5
D	-52	GLY	-	linker	UNP Q9BZM5
D	-51	GLY	-	linker	UNP Q9BZM5
D	-50	SER	-	linker	UNP Q9BZM5
D	-49	ALA	-	linker	UNP Q9BZM5
D	-48	SER	-	linker	UNP Q9BZM5
D	-43	GLU	ASP	conflict	UNP Q9U6Y3
D	-37	ARG	LYS	conflict	UNP Q9U6Y3
D	-33	ALA	ASN	conflict	UNP Q9U6Y3
D	-28	LYS	ALA	conflict	UNP Q9U6Y3
D	-20	ILE	GLU	conflict	UNP Q9U6Y3
D	-15	GLU	ASP	conflict	UNP Q9U6Y3
D	-12	GLN	HIS	conflict	UNP Q9U6Y3
D	-9	ASP	ASN	conflict	UNP Q9U6Y3
D	-7	THR	GLU	conflict	UNP Q9U6Y3
D	-5	GLU	LYS	conflict	UNP Q9U6Y3
D	8	THR	SER	conflict	UNP Q9U6Y3
D	9	PRO	ASN	conflict	UNP Q9U6Y3
D	18	PHE	LEU	conflict	UNP Q9U6Y3
D	23	GLU	ASP	conflict	UNP Q9U6Y3
D	26	PRO	ALA	conflict	UNP Q9U6Y3
D	32	ALA	SER	conflict	UNP Q9U6Y3
D	42	SER	THR	conflict	UNP Q9U6Y3
D	45	TYR	PHE	conflict	UNP Q9U6Y3

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Chain	Residue	Modelled	Actual	Comment	Reference
D	48	GLN	LYS	conflict	UNP Q9U6Y3
D	51	CYS	VAL	conflict	UNP Q9U6Y3
D	52	ILE	LYS	conflict	UNP Q9U6Y3
D	53	ALA	VAL	conflict	UNP Q9U6Y3
D	54	THR	LYS	conflict	UNP Q9U6Y3
D	58	THR	SER	conflict	UNP Q9U6Y3
D	61	GLY	GLU	conflict	UNP Q9U6Y3
D	63	CYS	SER	conflict	UNP Q9U6Y3
D	65	PHE	ILE	conflict	UNP Q9U6Y3
D	73	THR	MET	conflict	UNP Q9U6Y3
D	95	LYS	ILE	conflict	UNP Q9U6Y3
D	99	GLU	ARG	conflict	UNP Q9U6Y3
D	104	LYS	VAL	conflict	UNP Q9U6Y3
D	107	VAL	ILE	conflict	UNP Q9U6Y3
D	108	GLU	SER	conflict	UNP Q9U6Y3
D	109	MET	HIS	conflict	UNP Q9U6Y3
D	110	ALA	SER	conflict	UNP Q9U6Y3
D	125	THR	SER	conflict	UNP Q9U6Y3
D	126	THR	ILE	conflict	UNP Q9U6Y3
D	132	ASP	VAL	conflict	UNP Q9U6Y3
D	134	ARG	LYS	conflict	UNP Q9U6Y3
D	138	ALA	TYR	conflict	UNP Q9U6Y3
D	140	GLU	PHE	conflict	UNP Q9U6Y3
D	149	SER	ASN	conflict	UNP Q9U6Y3
D	158	ARG	THR	conflict	UNP Q9U6Y3
D	162	HIS	ASN	conflict	UNP Q9U6Y3
D	164	GLU	VAL	conflict	UNP Q9U6Y3
D	169	GLY	-	linker	UNP Q9U6Y3
D	170	GLY	-	linker	UNP Q9U6Y3
D	171	GLY	-	linker	UNP Q9U6Y3
D	172	SER	-	linker	UNP Q9U6Y3
D	173	GLY	-	linker	UNP Q9U6Y3
D	174	GLY	-	linker	UNP Q9U6Y3
D	175	GLY	-	linker	UNP Q9U6Y3
D	176	SER	-	linker	UNP Q9U6Y3
D	177	ALA	-	linker	UNP Q9U6Y3
D	178	TRP	-	linker	UNP Q9U6Y3
D	179	SER	-	linker	UNP Q9U6Y3
D	180	HIS	-	linker	UNP Q9U6Y3
D	181	PRO	-	linker	UNP Q9U6Y3
D	182	GLN	-	linker	UNP Q9U6Y3
D	183	PHE	-	linker	UNP Q9U6Y3

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Chain	Residue	Modelled	Actual	Comment	Reference
D	184	GLU	-	linker	UNP Q9U6Y3
D	185	LYS	-	linker	UNP Q9U6Y3
D	186	GLY	-	linker	UNP Q9U6Y3
D	187	GLY	-	linker	UNP Q9U6Y3
D	188	GLY	-	linker	UNP Q9U6Y3
D	189	SER	-	linker	UNP Q9U6Y3
D	190	GLY	-	linker	UNP Q9U6Y3
D	191	GLY	-	linker	UNP Q9U6Y3
D	192	GLY	-	linker	UNP Q9U6Y3
D	193	SER	-	linker	UNP Q9U6Y3
D	194	GLY	-	linker	UNP Q9U6Y3
D	195	GLY	-	linker	UNP Q9U6Y3
D	196	SER	-	linker	UNP Q9U6Y3
D	197	ALA	-	linker	UNP Q9U6Y3
D	198	TRP	-	linker	UNP Q9U6Y3
D	199	SER	-	linker	UNP Q9U6Y3
D	200	HIS	-	linker	UNP Q9U6Y3
D	201	PRO	-	linker	UNP Q9U6Y3
D	202	GLN	-	linker	UNP Q9U6Y3
D	203	PHE	-	linker	UNP Q9U6Y3
D	204	GLU	-	linker	UNP Q9U6Y3
D	205	LYS	-	linker	UNP Q9U6Y3
D	206	GLY	-	linker	UNP Q9U6Y3
D	207	SER	-	linker	UNP Q9U6Y3

- Molecule 2 is a protein called Glycosylphosphatidylinositol anchor attachment 1 protein, GFP-like fluorescent chromoprotein cFP484.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	G	579	4398	2881	744	754	19	0	0

There are 95 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-1	MET	-	initiating methionine	UNP O43292
G	0	GLY	-	expression tag	UNP O43292
G	1	SER	-	expression tag	UNP O43292
G	622	GLY	-	linker	UNP O43292
G	623	THR	-	linker	UNP O43292
G	624	LEU	-	linker	UNP O43292
G	625	GLU	-	linker	UNP O43292

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Chain	Residue	Modelled	Actual	Comment	Reference
G	626	VAL	-	linker	UNP O43292
G	627	LEU	-	linker	UNP O43292
G	628	PHE	-	linker	UNP O43292
G	629	GLN	-	linker	UNP O43292
G	630	GLY	-	linker	UNP O43292
G	631	PRO	-	linker	UNP O43292
G	632	GLY	-	linker	UNP O43292
G	633	GLY	-	linker	UNP O43292
G	634	SER	-	linker	UNP O43292
G	635	GLY	-	linker	UNP O43292
G	636	GLY	-	linker	UNP O43292
G	637	SER	-	linker	UNP O43292
G	638	ALA	-	linker	UNP O43292
G	639	SER	-	linker	UNP O43292
G	644	GLU	ASP	conflict	UNP Q9U6Y3
G	650	ARG	LYS	conflict	UNP Q9U6Y3
G	654	ALA	ASN	conflict	UNP Q9U6Y3
G	659	LYS	ALA	conflict	UNP Q9U6Y3
G	667	ILE	GLU	conflict	UNP Q9U6Y3
G	672	GLU	ASP	conflict	UNP Q9U6Y3
G	675	GLN	HIS	conflict	UNP Q9U6Y3
G	678	ASP	ASN	conflict	UNP Q9U6Y3
G	680	THR	GLU	conflict	UNP Q9U6Y3
G	682	GLU	LYS	conflict	UNP Q9U6Y3
G	695	THR	SER	conflict	UNP Q9U6Y3
G	696	PRO	ASN	conflict	UNP Q9U6Y3
G	705	PHE	LEU	conflict	UNP Q9U6Y3
G	710	GLU	ASP	conflict	UNP Q9U6Y3
G	713	PRO	ALA	conflict	UNP Q9U6Y3
G	719	ALA	SER	conflict	UNP Q9U6Y3
G	729	SER	THR	conflict	UNP Q9U6Y3
G	732	TYR	PHE	conflict	UNP Q9U6Y3
G	735	GLN	LYS	conflict	UNP Q9U6Y3
G	738	CYS	VAL	conflict	UNP Q9U6Y3
G	739	ILE	LYS	conflict	UNP Q9U6Y3
G	740	ALA	VAL	conflict	UNP Q9U6Y3
G	741	THR	LYS	conflict	UNP Q9U6Y3
G	745	THR	SER	conflict	UNP Q9U6Y3
G	748	GLY	GLU	conflict	UNP Q9U6Y3
G	750	CYS	SER	conflict	UNP Q9U6Y3
G	752	PHE	ILE	conflict	UNP Q9U6Y3
G	760	THR	MET	conflict	UNP Q9U6Y3

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Chain	Residue	Modelled	Actual	Comment	Reference
G	782	LYS	ILE	conflict	UNP Q9U6Y3
G	786	GLU	ARG	conflict	UNP Q9U6Y3
G	791	LYS	VAL	conflict	UNP Q9U6Y3
G	794	VAL	ILE	conflict	UNP Q9U6Y3
G	795	GLU	SER	conflict	UNP Q9U6Y3
G	796	MET	HIS	conflict	UNP Q9U6Y3
G	797	ALA	SER	conflict	UNP Q9U6Y3
G	812	THR	SER	conflict	UNP Q9U6Y3
G	813	THR	ILE	conflict	UNP Q9U6Y3
G	819	ASP	VAL	conflict	UNP Q9U6Y3
G	821	ARG	LYS	conflict	UNP Q9U6Y3
G	825	ALA	TYR	conflict	UNP Q9U6Y3
G	827	GLU	PHE	conflict	UNP Q9U6Y3
G	836	SER	ASN	conflict	UNP Q9U6Y3
G	845	ARG	THR	conflict	UNP Q9U6Y3
G	849	HIS	ASN	conflict	UNP Q9U6Y3
G	851	GLU	VAL	conflict	UNP Q9U6Y3
G	856	GLY	-	expression tag	UNP Q9U6Y3
G	857	GLY	-	expression tag	UNP Q9U6Y3
G	858	GLY	-	expression tag	UNP Q9U6Y3
G	859	SER	-	expression tag	UNP Q9U6Y3
G	860	GLY	-	expression tag	UNP Q9U6Y3
G	861	GLY	-	expression tag	UNP Q9U6Y3
G	862	GLY	-	expression tag	UNP Q9U6Y3
G	863	GLY	-	expression tag	UNP Q9U6Y3
G	864	SER	-	expression tag	UNP Q9U6Y3
G	865	GLY	-	expression tag	UNP Q9U6Y3
G	866	GLY	-	expression tag	UNP Q9U6Y3
G	867	GLY	-	expression tag	UNP Q9U6Y3
G	868	GLY	-	expression tag	UNP Q9U6Y3
G	869	ASP	-	expression tag	UNP Q9U6Y3
G	870	TYR	-	expression tag	UNP Q9U6Y3
G	871	LYS	-	expression tag	UNP Q9U6Y3
G	872	ASP	-	expression tag	UNP Q9U6Y3
G	873	ASP	-	expression tag	UNP Q9U6Y3
G	874	ASP	-	expression tag	UNP Q9U6Y3
G	875	ASP	-	expression tag	UNP Q9U6Y3
G	876	ALA	-	expression tag	UNP Q9U6Y3
G	877	ASP	-	expression tag	UNP Q9U6Y3
G	878	TYR	-	expression tag	UNP Q9U6Y3
G	879	LYS	-	expression tag	UNP Q9U6Y3
G	880	ASP	-	expression tag	UNP Q9U6Y3

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Chain	Residue	Modelled	Actual	Comment	Reference
G	881	ASP	-	expression tag	UNP Q9U6Y3
G	882	ASP	-	expression tag	UNP Q9U6Y3
G	883	ASP	-	expression tag	UNP Q9U6Y3
G	884	ALA	-	expression tag	UNP Q9U6Y3

- Molecule 3 is a protein called GPI-anchor transamidase, GFP-like fluorescent chromoprotein cFP484.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	K	330	2634	1685	451	483	15	0	0

There are 82 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	-1	MET	-	initiating methionine	UNP Q92643
K	0	GLY	-	expression tag	UNP Q92643
K	1	SER	-	expression tag	UNP Q92643
K	396	GLY	-	linker	UNP Q92643
K	397	THR	-	linker	UNP Q92643
K	398	LEU	-	linker	UNP Q92643
K	399	GLU	-	linker	UNP Q92643
K	400	VAL	-	linker	UNP Q92643
K	401	LEU	-	linker	UNP Q92643
K	402	PHE	-	linker	UNP Q92643
K	403	GLN	-	linker	UNP Q92643
K	404	GLY	-	linker	UNP Q92643
K	405	PRO	-	linker	UNP Q92643
K	406	GLY	-	linker	UNP Q92643
K	407	GLY	-	linker	UNP Q92643
K	408	SER	-	linker	UNP Q92643
K	409	GLY	-	linker	UNP Q92643
K	410	GLY	-	linker	UNP Q92643
K	411	SER	-	linker	UNP Q92643
K	412	ALA	-	linker	UNP Q92643
K	413	SER	-	linker	UNP Q92643
K	418	GLU	ASP	conflict	UNP Q9U6Y3
K	424	ARG	LYS	conflict	UNP Q9U6Y3
K	428	ALA	ASN	conflict	UNP Q9U6Y3
K	433	LYS	ALA	conflict	UNP Q9U6Y3
K	441	ILE	GLU	conflict	UNP Q9U6Y3
K	446	GLU	ASP	conflict	UNP Q9U6Y3

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Chain	Residue	Modelled	Actual	Comment	Reference
K	449	GLN	HIS	conflict	UNP Q9U6Y3
K	452	ASP	ASN	conflict	UNP Q9U6Y3
K	454	THR	GLU	conflict	UNP Q9U6Y3
K	456	GLU	LYS	conflict	UNP Q9U6Y3
K	469	THR	SER	conflict	UNP Q9U6Y3
K	470	PRO	ASN	conflict	UNP Q9U6Y3
K	479	PHE	LEU	conflict	UNP Q9U6Y3
K	484	GLU	ASP	conflict	UNP Q9U6Y3
K	487	PRO	ALA	conflict	UNP Q9U6Y3
K	493	ALA	SER	conflict	UNP Q9U6Y3
K	503	SER	THR	conflict	UNP Q9U6Y3
K	506	TYR	PHE	conflict	UNP Q9U6Y3
K	509	GLN	LYS	conflict	UNP Q9U6Y3
K	512	CYS	VAL	conflict	UNP Q9U6Y3
K	513	ILE	LYS	conflict	UNP Q9U6Y3
K	514	ALA	VAL	conflict	UNP Q9U6Y3
K	515	THR	LYS	conflict	UNP Q9U6Y3
K	519	THR	SER	conflict	UNP Q9U6Y3
K	522	GLY	GLU	conflict	UNP Q9U6Y3
K	524	CYS	SER	conflict	UNP Q9U6Y3
K	526	PHE	ILE	conflict	UNP Q9U6Y3
K	534	THR	MET	conflict	UNP Q9U6Y3
K	556	LYS	ILE	conflict	UNP Q9U6Y3
K	560	GLU	ARG	conflict	UNP Q9U6Y3
K	565	LYS	VAL	conflict	UNP Q9U6Y3
K	568	VAL	ILE	conflict	UNP Q9U6Y3
K	569	GLU	SER	conflict	UNP Q9U6Y3
K	570	MET	HIS	conflict	UNP Q9U6Y3
K	571	ALA	SER	conflict	UNP Q9U6Y3
K	586	THR	SER	conflict	UNP Q9U6Y3
K	587	THR	ILE	conflict	UNP Q9U6Y3
K	593	ASP	VAL	conflict	UNP Q9U6Y3
K	595	ARG	LYS	conflict	UNP Q9U6Y3
K	599	ALA	TYR	conflict	UNP Q9U6Y3
K	601	GLU	PHE	conflict	UNP Q9U6Y3
K	610	SER	ASN	conflict	UNP Q9U6Y3
K	619	ARG	THR	conflict	UNP Q9U6Y3
K	623	HIS	ASN	conflict	UNP Q9U6Y3
K	625	GLU	VAL	conflict	UNP Q9U6Y3
K	630	GLY	-	expression tag	UNP Q9U6Y3
K	631	GLY	-	expression tag	UNP Q9U6Y3
K	632	GLY	-	expression tag	UNP Q9U6Y3

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Chain	Residue	Modelled	Actual	Comment	Reference
K	633	SER	-	expression tag	UNP Q9U6Y3
K	634	GLY	-	expression tag	UNP Q9U6Y3
K	635	GLY	-	expression tag	UNP Q9U6Y3
K	636	GLY	-	expression tag	UNP Q9U6Y3
K	637	TYR	-	expression tag	UNP Q9U6Y3
K	638	PRO	-	expression tag	UNP Q9U6Y3
K	639	TYR	-	expression tag	UNP Q9U6Y3
K	640	ASP	-	expression tag	UNP Q9U6Y3
K	641	VAL	-	expression tag	UNP Q9U6Y3
K	642	PRO	-	expression tag	UNP Q9U6Y3
K	643	ASP	-	expression tag	UNP Q9U6Y3
K	644	TYR	-	expression tag	UNP Q9U6Y3
K	645	ALA	-	expression tag	UNP Q9U6Y3

- Molecule 4 is a protein called GPI transamidase component PIG-S, GFP-like fluorescent chromoprotein cFP484.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	S	513	3820	2482	639	686	13	0	0

There are 91 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	-1	MET	-	initiating methionine	UNP Q96S52
S	0	GLY	-	expression tag	UNP Q96S52
S	1	SER	-	expression tag	UNP Q96S52
S	556	GLY	-	linker	UNP Q96S52
S	557	THR	-	linker	UNP Q96S52
S	558	LEU	-	linker	UNP Q96S52
S	559	GLU	-	linker	UNP Q96S52
S	560	VAL	-	linker	UNP Q96S52
S	561	LEU	-	linker	UNP Q96S52
S	562	PHE	-	linker	UNP Q96S52
S	563	GLN	-	linker	UNP Q96S52
S	564	GLY	-	linker	UNP Q96S52
S	565	PRO	-	linker	UNP Q96S52
S	566	GLY	-	linker	UNP Q96S52
S	567	GLY	-	linker	UNP Q96S52
S	568	SER	-	linker	UNP Q96S52
S	569	GLY	-	linker	UNP Q96S52
S	570	GLY	-	linker	UNP Q96S52

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Chain	Residue	Modelled	Actual	Comment	Reference
S	571	SER	-	linker	UNP Q96S52
S	572	ALA	-	linker	UNP Q96S52
S	573	SER	-	linker	UNP Q96S52
S	578	GLU	ASP	conflict	UNP Q9U6Y3
S	584	ARG	LYS	conflict	UNP Q9U6Y3
S	588	ALA	ASN	conflict	UNP Q9U6Y3
S	593	LYS	ALA	conflict	UNP Q9U6Y3
S	601	ILE	GLU	conflict	UNP Q9U6Y3
S	606	GLU	ASP	conflict	UNP Q9U6Y3
S	609	GLN	HIS	conflict	UNP Q9U6Y3
S	612	ASP	ASN	conflict	UNP Q9U6Y3
S	614	THR	GLU	conflict	UNP Q9U6Y3
S	616	GLU	LYS	conflict	UNP Q9U6Y3
S	629	THR	SER	conflict	UNP Q9U6Y3
S	630	PRO	ASN	conflict	UNP Q9U6Y3
S	639	PHE	LEU	conflict	UNP Q9U6Y3
S	644	GLU	ASP	conflict	UNP Q9U6Y3
S	647	PRO	ALA	conflict	UNP Q9U6Y3
S	653	ALA	SER	conflict	UNP Q9U6Y3
S	663	SER	THR	conflict	UNP Q9U6Y3
S	666	TYR	PHE	conflict	UNP Q9U6Y3
S	669	GLN	LYS	conflict	UNP Q9U6Y3
S	672	CYS	VAL	conflict	UNP Q9U6Y3
S	673	ILE	LYS	conflict	UNP Q9U6Y3
S	674	ALA	VAL	conflict	UNP Q9U6Y3
S	675	THR	LYS	conflict	UNP Q9U6Y3
S	679	THR	SER	conflict	UNP Q9U6Y3
S	682	GLY	GLU	conflict	UNP Q9U6Y3
S	684	CYS	SER	conflict	UNP Q9U6Y3
S	686	PHE	ILE	conflict	UNP Q9U6Y3
S	694	THR	MET	conflict	UNP Q9U6Y3
S	716	LYS	ILE	conflict	UNP Q9U6Y3
S	720	GLU	ARG	conflict	UNP Q9U6Y3
S	725	LYS	VAL	conflict	UNP Q9U6Y3
S	728	VAL	ILE	conflict	UNP Q9U6Y3
S	729	GLU	SER	conflict	UNP Q9U6Y3
S	730	MET	HIS	conflict	UNP Q9U6Y3
S	731	ALA	SER	conflict	UNP Q9U6Y3
S	746	THR	SER	conflict	UNP Q9U6Y3
S	747	THR	ILE	conflict	UNP Q9U6Y3
S	753	ASP	VAL	conflict	UNP Q9U6Y3
S	755	ARG	LYS	conflict	UNP Q9U6Y3

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Chain	Residue	Modelled	Actual	Comment	Reference
S	759	ALA	TYR	conflict	UNP Q9U6Y3
S	761	GLU	PHE	conflict	UNP Q9U6Y3
S	770	SER	ASN	conflict	UNP Q9U6Y3
S	779	ARG	THR	conflict	UNP Q9U6Y3
S	783	HIS	ASN	conflict	UNP Q9U6Y3
S	785	GLU	VAL	conflict	UNP Q9U6Y3
S	790	GLY	-	expression tag	UNP Q9U6Y3
S	791	GLY	-	expression tag	UNP Q9U6Y3
S	792	GLY	-	expression tag	UNP Q9U6Y3
S	793	SER	-	expression tag	UNP Q9U6Y3
S	794	GLY	-	expression tag	UNP Q9U6Y3
S	795	GLY	-	expression tag	UNP Q9U6Y3
S	796	GLY	-	expression tag	UNP Q9U6Y3
S	797	GLY	-	expression tag	UNP Q9U6Y3
S	798	GLY	-	expression tag	UNP Q9U6Y3
S	799	GLY	-	expression tag	UNP Q9U6Y3
S	800	GLY	-	expression tag	UNP Q9U6Y3
S	801	GLY	-	expression tag	UNP Q9U6Y3
S	802	GLY	-	expression tag	UNP Q9U6Y3
S	803	GLY	-	expression tag	UNP Q9U6Y3
S	804	GLY	-	expression tag	UNP Q9U6Y3
S	805	GLU	-	expression tag	UNP Q9U6Y3
S	806	GLN	-	expression tag	UNP Q9U6Y3
S	807	LYS	-	expression tag	UNP Q9U6Y3
S	808	LEU	-	expression tag	UNP Q9U6Y3
S	809	ILE	-	expression tag	UNP Q9U6Y3
S	810	SER	-	expression tag	UNP Q9U6Y3
S	811	GLU	-	expression tag	UNP Q9U6Y3
S	812	GLU	-	expression tag	UNP Q9U6Y3
S	813	ASP	-	expression tag	UNP Q9U6Y3
S	814	LEU	-	expression tag	UNP Q9U6Y3

- Molecule 5 is a protein called GPI transamidase component PIG-T,GFP-like fluorescent chromoprotein cFP484.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	T	530	4223	2747	708	754	14	0	0

There are 83 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	-1	MET	-	initiating methionine	UNP Q969N2
T	0	GLY	-	expression tag	UNP Q969N2
T	1	SER	-	expression tag	UNP Q969N2
T	579	GLY	-	linker	UNP Q969N2
T	580	THR	-	linker	UNP Q969N2
T	581	LEU	-	linker	UNP Q969N2
T	582	GLU	-	linker	UNP Q969N2
T	583	VAL	-	linker	UNP Q969N2
T	584	LEU	-	linker	UNP Q969N2
T	585	PHE	-	linker	UNP Q969N2
T	586	GLN	-	linker	UNP Q969N2
T	587	GLY	-	linker	UNP Q969N2
T	588	PRO	-	linker	UNP Q969N2
T	589	GLY	-	linker	UNP Q969N2
T	590	GLY	-	linker	UNP Q969N2
T	591	SER	-	linker	UNP Q969N2
T	592	GLY	-	linker	UNP Q969N2
T	593	GLY	-	linker	UNP Q969N2
T	594	SER	-	linker	UNP Q969N2
T	595	ALA	-	linker	UNP Q969N2
T	596	SER	-	linker	UNP Q969N2
T	601	GLU	ASP	conflict	UNP Q9U6Y3
T	607	ARG	LYS	conflict	UNP Q9U6Y3
T	611	ALA	ASN	conflict	UNP Q9U6Y3
T	616	LYS	ALA	conflict	UNP Q9U6Y3
T	624	ILE	GLU	conflict	UNP Q9U6Y3
T	629	GLU	ASP	conflict	UNP Q9U6Y3
T	632	GLN	HIS	conflict	UNP Q9U6Y3
T	635	ASP	ASN	conflict	UNP Q9U6Y3
T	637	THR	GLU	conflict	UNP Q9U6Y3
T	639	GLU	LYS	conflict	UNP Q9U6Y3
T	652	THR	SER	conflict	UNP Q9U6Y3
T	653	PRO	ASN	conflict	UNP Q9U6Y3
T	662	PHE	LEU	conflict	UNP Q9U6Y3
T	667	GLU	ASP	conflict	UNP Q9U6Y3
T	670	PRO	ALA	conflict	UNP Q9U6Y3
T	676	ALA	SER	conflict	UNP Q9U6Y3
T	686	SER	THR	conflict	UNP Q9U6Y3
T	689	TYR	PHE	conflict	UNP Q9U6Y3
T	692	GLN	LYS	conflict	UNP Q9U6Y3
T	695	CYS	VAL	conflict	UNP Q9U6Y3
T	696	ILE	LYS	conflict	UNP Q9U6Y3
T	697	ALA	VAL	conflict	UNP Q9U6Y3

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Chain	Residue	Modelled	Actual	Comment	Reference
T	698	THR	LYS	conflict	UNP Q9U6Y3
T	702	THR	SER	conflict	UNP Q9U6Y3
T	705	GLY	GLU	conflict	UNP Q9U6Y3
T	707	CYS	SER	conflict	UNP Q9U6Y3
T	709	PHE	ILE	conflict	UNP Q9U6Y3
T	717	THR	MET	conflict	UNP Q9U6Y3
T	739	LYS	ILE	conflict	UNP Q9U6Y3
T	743	GLU	ARG	conflict	UNP Q9U6Y3
T	748	LYS	VAL	conflict	UNP Q9U6Y3
T	751	VAL	ILE	conflict	UNP Q9U6Y3
T	752	GLU	SER	conflict	UNP Q9U6Y3
T	753	MET	HIS	conflict	UNP Q9U6Y3
T	754	ALA	SER	conflict	UNP Q9U6Y3
T	769	THR	SER	conflict	UNP Q9U6Y3
T	770	THR	ILE	conflict	UNP Q9U6Y3
T	776	ASP	VAL	conflict	UNP Q9U6Y3
T	778	ARG	LYS	conflict	UNP Q9U6Y3
T	782	ALA	TYR	conflict	UNP Q9U6Y3
T	784	GLU	PHE	conflict	UNP Q9U6Y3
T	793	SER	ASN	conflict	UNP Q9U6Y3
T	802	ARG	THR	conflict	UNP Q9U6Y3
T	806	HIS	ASN	conflict	UNP Q9U6Y3
T	808	GLU	VAL	conflict	UNP Q9U6Y3
T	813	GLY	-	expression tag	UNP Q9U6Y3
T	814	GLY	-	expression tag	UNP Q9U6Y3
T	815	GLY	-	expression tag	UNP Q9U6Y3
T	816	SER	-	expression tag	UNP Q9U6Y3
T	817	GLY	-	expression tag	UNP Q9U6Y3
T	818	GLY	-	expression tag	UNP Q9U6Y3
T	819	GLY	-	expression tag	UNP Q9U6Y3
T	820	HIS	-	expression tag	UNP Q9U6Y3
T	821	HIS	-	expression tag	UNP Q9U6Y3
T	822	HIS	-	expression tag	UNP Q9U6Y3
T	823	HIS	-	expression tag	UNP Q9U6Y3
T	824	HIS	-	expression tag	UNP Q9U6Y3
T	825	HIS	-	expression tag	UNP Q9U6Y3
T	826	HIS	-	expression tag	UNP Q9U6Y3
T	827	HIS	-	expression tag	UNP Q9U6Y3
T	828	HIS	-	expression tag	UNP Q9U6Y3
T	829	HIS	-	expression tag	UNP Q9U6Y3

- Molecule 6 is a protein called Phosphatidylinositol glycan anchor biosynthesis class U protein, GFP-like fluorescent chromoprotein cFP484.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	U	420	3422	2345	508	555	14	0	0

There are 73 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	-1	MET	-	initiating methionine	UNP Q9H490
U	0	GLY	-	expression tag	UNP Q9H490
U	1	SER	-	expression tag	UNP Q9H490
U	436	GLY	-	linker	UNP Q9H490
U	437	THR	-	linker	UNP Q9H490
U	438	LEU	-	linker	UNP Q9H490
U	439	GLU	-	linker	UNP Q9H490
U	440	VAL	-	linker	UNP Q9H490
U	441	LEU	-	linker	UNP Q9H490
U	442	PHE	-	linker	UNP Q9H490
U	443	GLN	-	linker	UNP Q9H490
U	444	GLY	-	linker	UNP Q9H490
U	445	PRO	-	linker	UNP Q9H490
U	446	GLY	-	linker	UNP Q9H490
U	447	GLY	-	linker	UNP Q9H490
U	448	SER	-	linker	UNP Q9H490
U	449	GLY	-	linker	UNP Q9H490
U	450	GLY	-	linker	UNP Q9H490
U	451	SER	-	linker	UNP Q9H490
U	452	ALA	-	linker	UNP Q9H490
U	453	SER	-	linker	UNP Q9H490
U	458	GLU	ASP	conflict	UNP Q9U6Y3
U	464	ARG	LYS	conflict	UNP Q9U6Y3
U	468	ALA	ASN	conflict	UNP Q9U6Y3
U	473	LYS	ALA	conflict	UNP Q9U6Y3
U	481	ILE	GLU	conflict	UNP Q9U6Y3
U	486	GLU	ASP	conflict	UNP Q9U6Y3
U	489	GLN	HIS	conflict	UNP Q9U6Y3
U	492	ASP	ASN	conflict	UNP Q9U6Y3
U	494	THR	GLU	conflict	UNP Q9U6Y3
U	496	GLU	LYS	conflict	UNP Q9U6Y3
U	509	THR	SER	conflict	UNP Q9U6Y3
U	510	PRO	ASN	conflict	UNP Q9U6Y3
U	519	PHE	LEU	conflict	UNP Q9U6Y3
U	524	GLU	ASP	conflict	UNP Q9U6Y3
U	527	PRO	ALA	conflict	UNP Q9U6Y3
U	533	ALA	SER	conflict	UNP Q9U6Y3

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Chain	Residue	Modelled	Actual	Comment	Reference
U	543	SER	THR	conflict	UNP Q9U6Y3
U	546	TYR	PHE	conflict	UNP Q9U6Y3
U	549	GLN	LYS	conflict	UNP Q9U6Y3
U	552	CYS	VAL	conflict	UNP Q9U6Y3
U	553	ILE	LYS	conflict	UNP Q9U6Y3
U	554	ALA	VAL	conflict	UNP Q9U6Y3
U	555	THR	LYS	conflict	UNP Q9U6Y3
U	559	THR	SER	conflict	UNP Q9U6Y3
U	562	GLY	GLU	conflict	UNP Q9U6Y3
U	564	CYS	SER	conflict	UNP Q9U6Y3
U	566	PHE	ILE	conflict	UNP Q9U6Y3
U	574	THR	MET	conflict	UNP Q9U6Y3
U	596	LYS	ILE	conflict	UNP Q9U6Y3
U	600	GLU	ARG	conflict	UNP Q9U6Y3
U	605	LYS	VAL	conflict	UNP Q9U6Y3
U	608	VAL	ILE	conflict	UNP Q9U6Y3
U	609	GLU	SER	conflict	UNP Q9U6Y3
U	610	MET	HIS	conflict	UNP Q9U6Y3
U	611	ALA	SER	conflict	UNP Q9U6Y3
U	626	THR	SER	conflict	UNP Q9U6Y3
U	627	THR	ILE	conflict	UNP Q9U6Y3
U	633	ASP	VAL	conflict	UNP Q9U6Y3
U	635	ARG	LYS	conflict	UNP Q9U6Y3
U	639	ALA	TYR	conflict	UNP Q9U6Y3
U	641	GLU	PHE	conflict	UNP Q9U6Y3
U	650	SER	ASN	conflict	UNP Q9U6Y3
U	659	ARG	THR	conflict	UNP Q9U6Y3
U	663	HIS	ASN	conflict	UNP Q9U6Y3
U	665	GLU	VAL	conflict	UNP Q9U6Y3
U	670	GLY	-	expression tag	UNP Q9U6Y3
U	671	GLY	-	expression tag	UNP Q9U6Y3
U	672	GLY	-	expression tag	UNP Q9U6Y3
U	673	SER	-	expression tag	UNP Q9U6Y3
U	674	GLY	-	expression tag	UNP Q9U6Y3
U	675	GLY	-	expression tag	UNP Q9U6Y3
U	676	GLY	-	expression tag	UNP Q9U6Y3

- Molecule 7 is a protein called Met-Ser-Ser peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	P	3	20	11	3	5	1	0	0



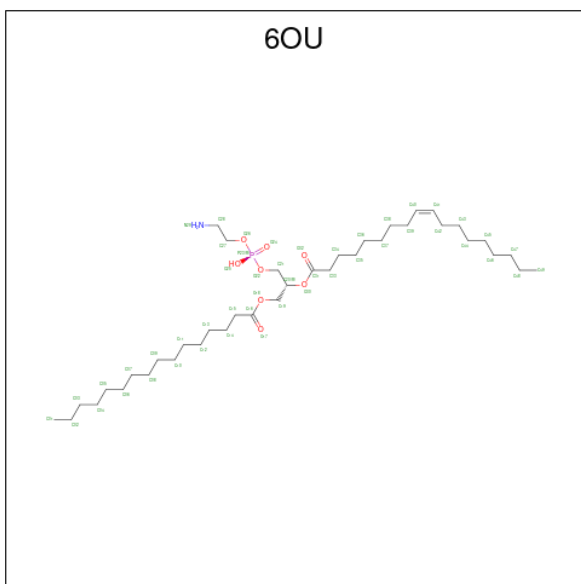
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Mol	Chain	Residues	Atoms			AltConf
9	G	1	Total	C	O	0
			35	31	4	
9	U	1	Total	C	O	0
			35	31	4	
9	U	1	Total	C	O	0
			35	31	4	
9	U	1	Total	C	O	0
			35	31	4	
9	U	1	Total	C	O	0
			35	31	4	

- Molecule 10 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
10	G	1	Total	Mg	0
			1	1	

- Molecule 11 is [(2 {R})-1-[2-azanylethoxy(oxidanyl)phosphoryl]oxy-3-hexadecanoyloxy-propan-2-yl] ( {Z})-octadec-9-enoate (CCD ID: 6OU) (formula: C<sub>39</sub>H<sub>76</sub>NO<sub>8</sub>P).



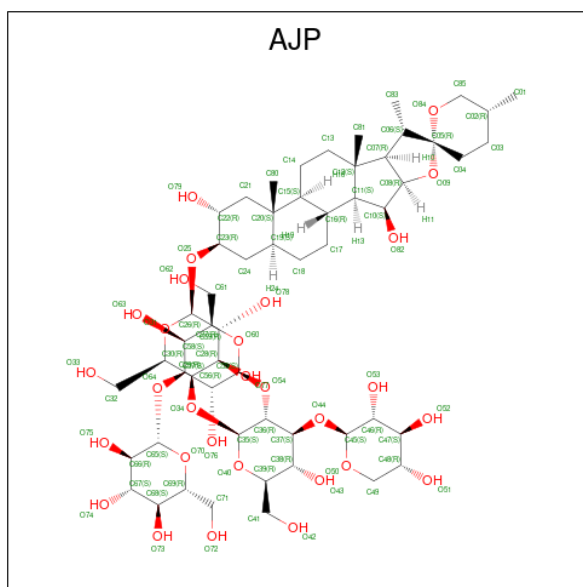
Mol	Chain	Residues	Atoms					AltConf
11	G	1	Total	C	N	O	P	0
			45	35	1	8	1	
11	G	1	Total	C	N	O	P	0
			49	39	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
11	G	1	Total	C	N	O	P	0
			39	29	1	8	1	
11	U	1	Total	C	N	O	P	0
			49	39	1	8	1	

- Molecule 12 is Digitonin (CCD ID: AJP) (formula:  $C_{56}H_{92}O_{29}$ ).

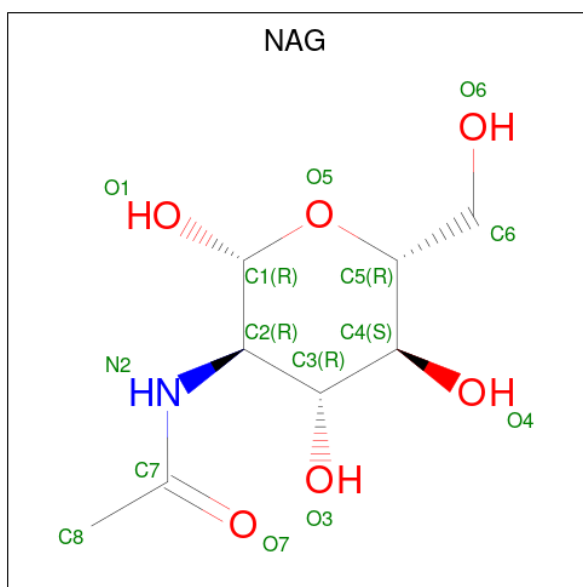


Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
12	G	1	Total	C	O	0
			85	56	29	

- Molecule 13 is CALCIUM ION (CCD ID: CA) (formula: Ca).

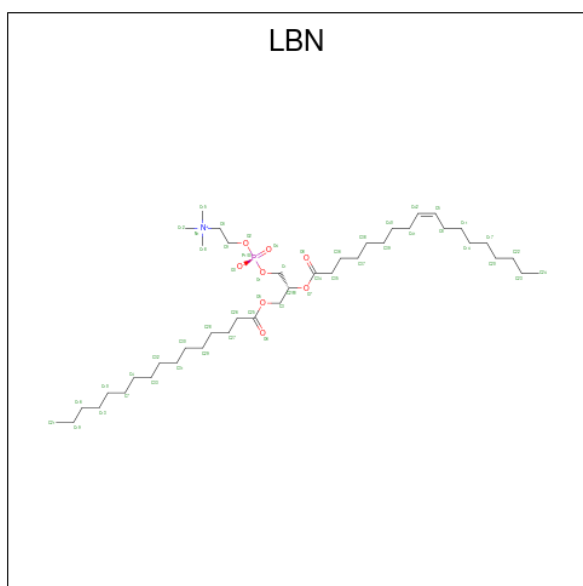
Mol	Chain	Residues	Atoms		AltConf
			Total	Ca	
13	K	1	Total	Ca	0
			1	1	

- Molecule 14 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula:  $C_8H_{15}NO_6$ ).



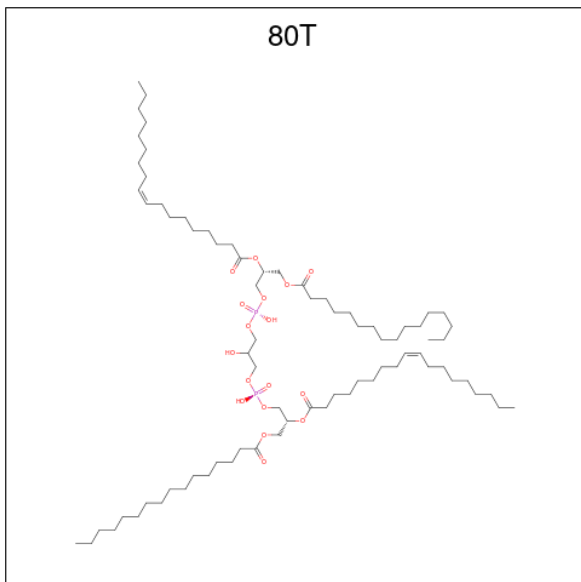
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
14	S	1	14	8	1	5	0
14	T	1	14	8	1	5	0

- Molecule 15 is 1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine (CCD ID: LBN) (formula:  $C_{42}H_{82}NO_8P$ ).



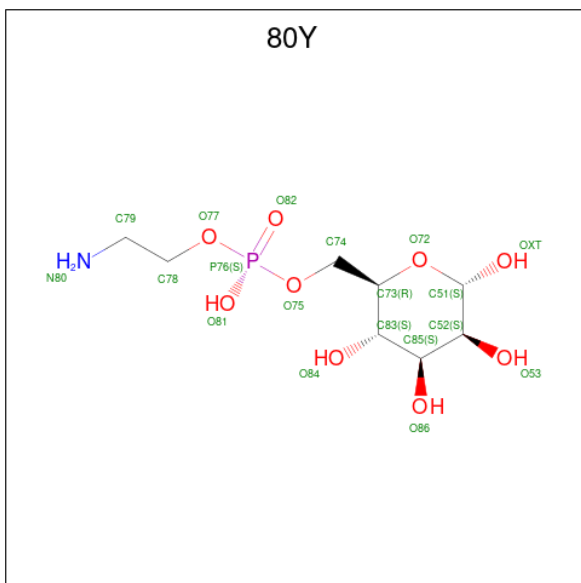
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
15	S	1	52	42	1	8	1	0

- Molecule 16 is [(2R)-1-hexadecanoyloxy-3-[[3-[(2R)-3-hexadecanoyloxy-2-[(Z)-octadec-9-enoyl]oxy-propoxy]-oxidanyl-phosphoryl]oxy-2-oxidanyl-propoxy]-oxidanyl-phosphoryl]oxy-propan-2-yl] (Z)-octadec-9-enoate (CCD ID: 80T) (formula:  $C_{77}H_{146}O_{17}P_2$ ).



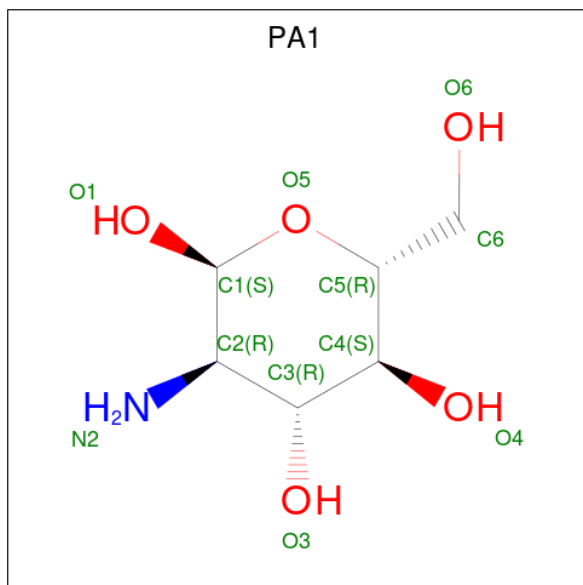
Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
16	U	1	88	69	17	2	0

- Molecule 17 is 2-azanylethyl [(2R,3S,4S,5S,6S)-3,4,5,6-tetrakis(oxidanyl)oxan-2-yl]methyl hydrogen phosphate (CCD ID: 80Y) (formula:  $C_8H_{18}NO_9P$ ) (labeled as "Ligand of Interest" by depositor).



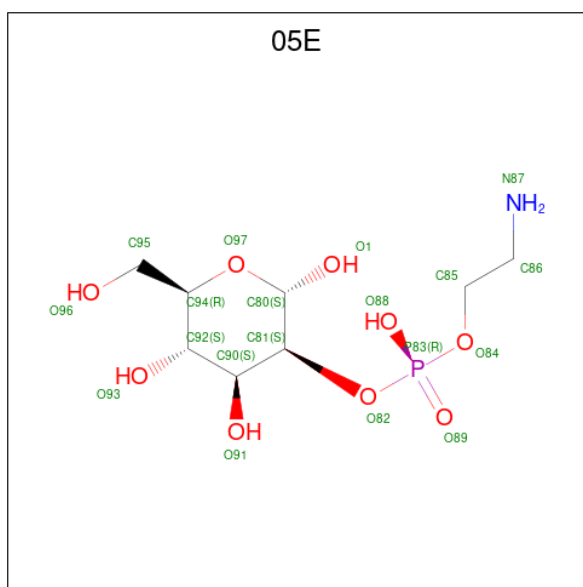
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
17	P	1	18	8	1	8	1	0
17	P	1	18	8	1	8	1	0

- Molecule 18 is 2-amino-2-deoxy-alpha-D-glucopyranose (CCD ID: PA1) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>5</sub>) (labeled as "Ligand of Interest" by depositor).



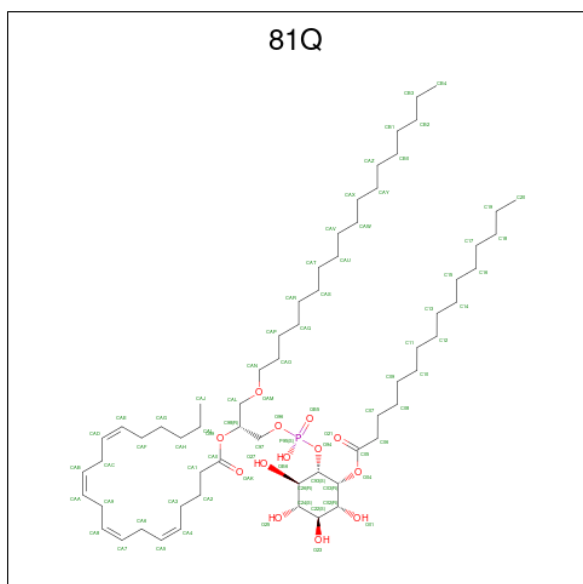
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
18	P	1	11	6	1	4	0

- Molecule 19 is 2-azanylethyl [(2 {S},3 {S},4 {S},5 {S},6 {R})-6-(hydroxymethyl)-2,4,5-tris(oxidanyl)oxan-3-yl] hydrogen phosphate (CCD ID: 05E) (formula: C<sub>8</sub>H<sub>18</sub>NO<sub>9</sub>P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf	
			Total	C	N	O		P
19	P	1	18	8	1	8	1	0

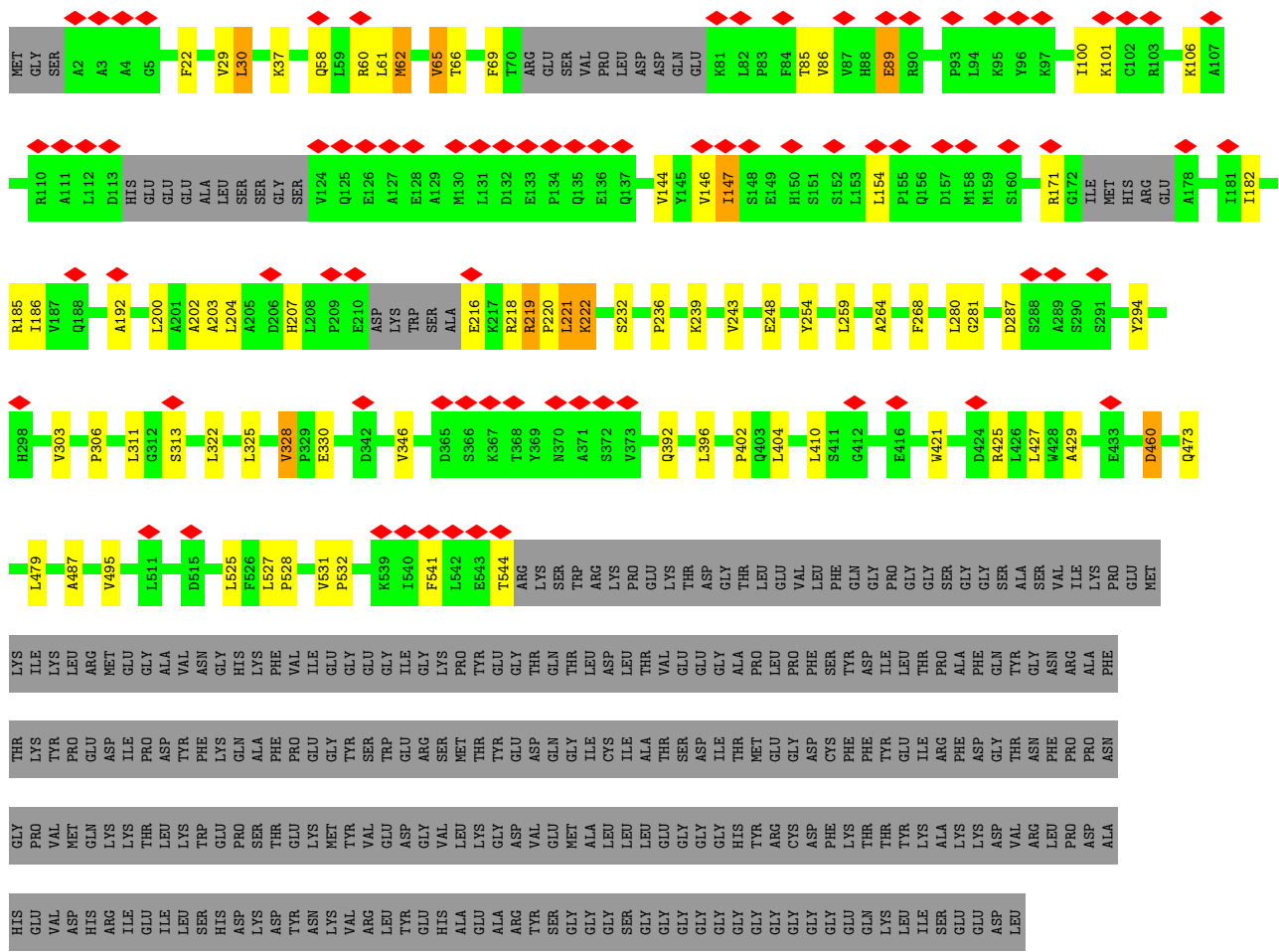
- Molecule 20 is [(2R)-1-[[[(1S,2R,3R,4S,5S,6R)-2-hexadecanoyloxy-3,4,5,6-tetrakis(oxidanyl)cyclohexyl]oxy-oxidanyl-phosphoryl]oxy-3-octadecoxy-propan-2-yl] (5Z,8Z,11Z,14Z)-icosa-5,8,11,14-tetraenoate (CCD ID: 81Q) (formula: C<sub>63</sub>H<sub>115</sub>O<sub>13</sub>P) (labeled as "Ligand of Interest" by depositor).



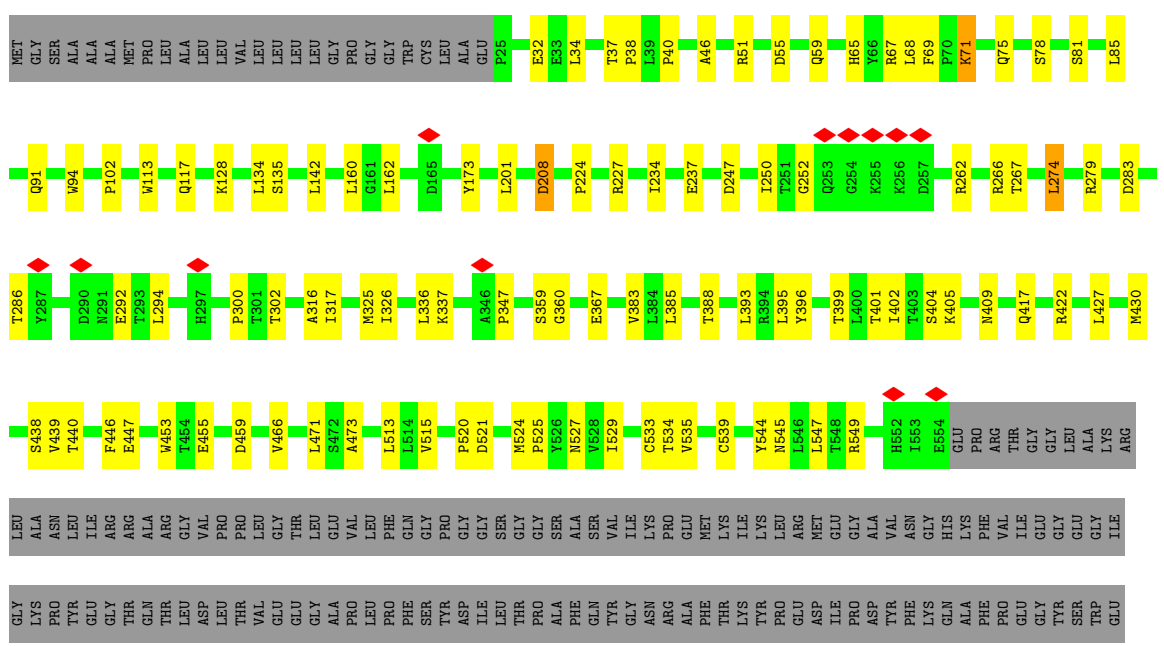
Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
20	P	1	77	63	13	1	0







● Molecule 5: GPI transamidase component PIG-T, GFP-like fluorescent chromoprotein cFP484





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	34261	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	3.088	Depositor
Minimum map value	-1.888	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.113	Depositor
Recommended contour level	0.48	Depositor
Map size (Å)	260.96, 260.96, 260.96	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.932, 0.932, 0.932	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: 6OU, CA, NAG, 05E, AJP, LBN, PA1, Y01, 81Q, MG, 80Y, 80T

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	D	0.37	0/202	0.76	0/277
2	G	0.18	0/4503	0.36	0/6141
3	K	0.14	0/2702	0.33	0/3674
4	S	0.17	0/3909	0.33	0/5350
5	T	0.16	0/4356	0.31	0/5969
6	U	0.23	0/3535	0.40	0/4831
7	P	0.50	0/19	1.13	0/23
All	All	0.18	0/19226	0.36	0/26265

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	200	0	227	12	0
2	G	4398	0	4469	68	0
3	K	2634	0	2549	58	0
4	S	3820	0	3754	51	0
5	T	4223	0	4146	65	0
6	U	3422	0	3487	82	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	P	20	0	21	6	0
8	R	28	0	25	0	0
9	D	35	0	49	5	0
9	G	245	0	343	10	0
9	U	175	0	245	20	0
10	G	1	0	0	0	0
11	G	133	0	0	0	0
11	U	49	0	0	0	0
12	G	85	0	0	0	0
13	K	1	0	0	0	0
14	S	14	0	13	0	0
14	T	14	0	13	0	0
15	S	52	0	0	0	0
16	U	88	0	0	0	0
17	P	36	0	0	1	0
18	P	11	0	10	1	0
19	P	18	0	0	0	0
20	P	77	0	0	6	0
All	All	19779	0	19351	326	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 8.

The worst 5 of 326 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)
9:U:704:Y01:HAR1	9:U:704:Y01:HAL1	1.54	0.89
5:T:32:GLU:HG3	5:T:201:LEU:HD12	1.66	0.78
6:U:372:LEU:HD13	6:U:386:PHE:HB3	1.66	0.77
3:K:87:ALA:HB1	3:K:173:GLN:HE21	1.51	0.76
1:D:228:THR:HG21	9:D:301:Y01:HAL1	1.71	0.73

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	D	25/327 (8%)	23 (92%)	2 (8%)	0	100	100
2	G	573/886 (65%)	558 (97%)	15 (3%)	0	100	100
3	K	326/647 (50%)	315 (97%)	11 (3%)	0	100	100
4	S	503/816 (62%)	495 (98%)	8 (2%)	0	100	100
5	T	528/831 (64%)	520 (98%)	8 (2%)	0	100	100
6	U	418/678 (62%)	410 (98%)	8 (2%)	0	100	100
7	P	1/3 (33%)	0	0	1 (100%)	0	0
All	All	2374/4188 (57%)	2321 (98%)	52 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	P	2	SER

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	24/261 (9%)	24 (100%)	0	100	100
2	G	445/714 (62%)	435 (98%)	10 (2%)	45	69
3	K	288/563 (51%)	280 (97%)	8 (3%)	38	62
4	S	385/681 (56%)	366 (95%)	19 (5%)	22	45
5	T	465/728 (64%)	455 (98%)	10 (2%)	45	69
6	U	367/585 (63%)	355 (97%)	12 (3%)	33	58
7	P	3/3 (100%)	2 (67%)	1 (33%)	0	0
All	All	1977/3535 (56%)	1917 (97%)	60 (3%)	37	61

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	S	219	ARG
6	U	307	LYS
4	S	473	GLN
6	U	276	TYR
7	P	1	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
4	S	188	GLN
5	T	149	ASN
6	U	383	ASN
5	T	415	HIS
2	G	593	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

2 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	$\# Z  > 2$
8	NAG	R	1	2,8	14,14,15	0.23	0	17,19,21	0.42	0
8	NAG	R	2	8	14,14,15	0.21	0	17,19,21	0.50	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
8	NAG	R	1	2,8	-	2/6/23/26	0/1/1/1
8	NAG	R	2	8	-	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.

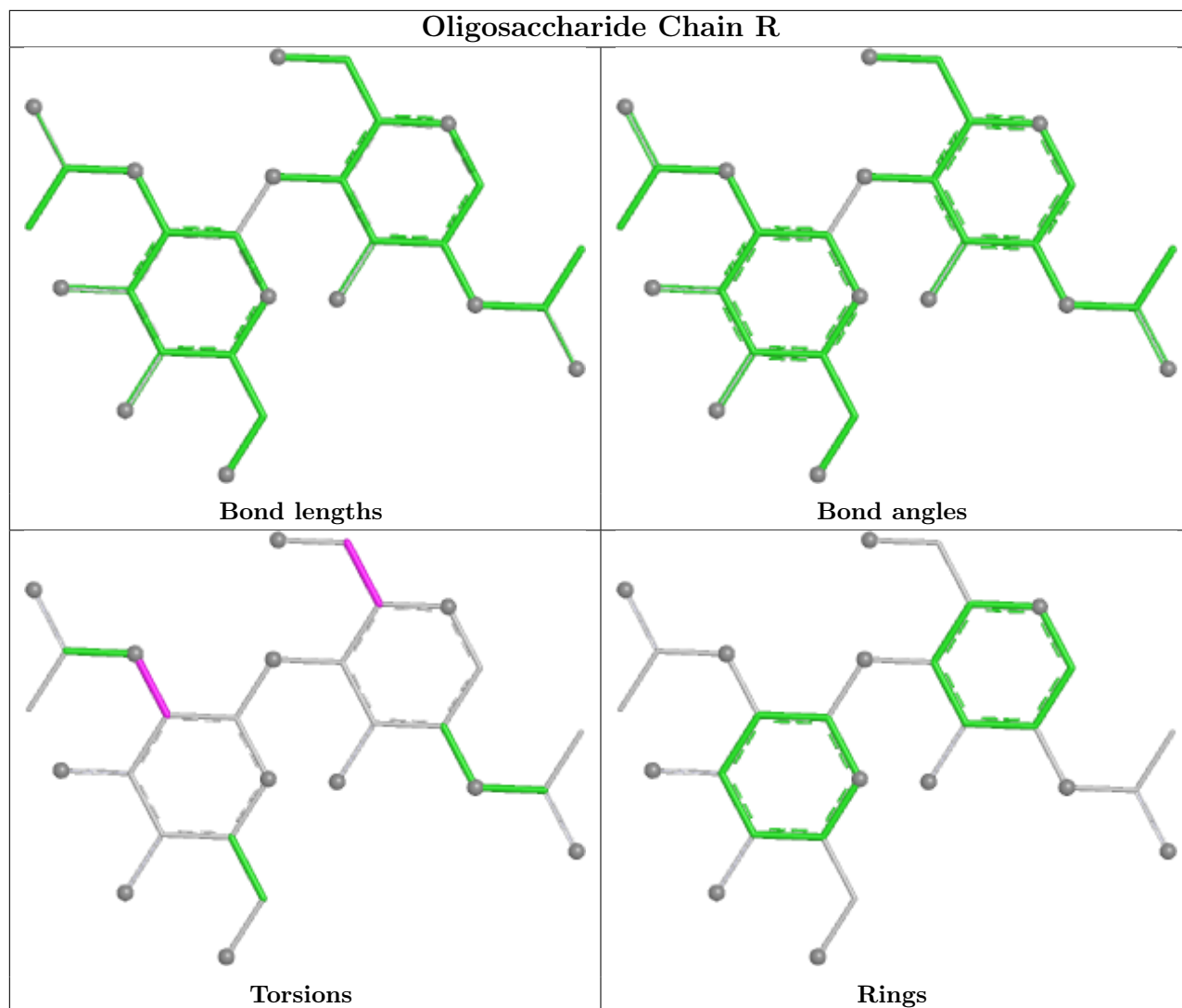
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	R	1	NAG	O5-C5-C6-O6
8	R	1	NAG	C4-C5-C6-O6
8	R	2	NAG	C1-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

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 29 ligands modelled in this entry, 2 are monoatomic - leaving 27 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$
9	Y01	U	705	-	38,38,38	0.65	2 (5%)	57,57,57	0.61	2 (3%)
12	AJP	G	912	-	95,95,95	0.13	0	144,149,149	0.44	0
19	05E	P	104	17,18,10	18,18,19	0.64	0	21,25,27	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
9	Y01	U	703	-	38,38,38	0.65	2 (5%)	57,57,57	0.62	2 (3%)
9	Y01	D	301	-	38,38,38	0.66	2 (5%)	57,57,57	0.61	2 (3%)
9	Y01	U	704	-	38,38,38	0.65	2 (5%)	57,57,57	0.62	2 (3%)
20	81Q	P	105	18	77,77,77	0.35	0	86,89,89	0.80	2 (2%)
9	Y01	G	908	-	38,38,38	0.65	2 (5%)	57,57,57	0.59	2 (3%)
14	NAG	T	901	5	14,14,15	0.27	0	17,19,21	0.42	0
11	6OU	G	905	-	38,38,48	1.00	4 (10%)	41,43,53	0.99	2 (4%)
17	80Y	P	103	17,19	18,18,19	0.56	0	24,25,27	0.69	0
9	Y01	G	907	-	38,38,38	0.65	2 (5%)	57,57,57	0.62	2 (3%)
9	Y01	G	911	-	38,38,38	0.65	2 (5%)	57,57,57	0.61	2 (3%)
14	NAG	S	901	4	14,14,15	0.25	0	17,19,21	0.48	0
9	Y01	G	910	-	38,38,38	0.65	2 (5%)	57,57,57	0.61	2 (3%)
11	6OU	G	904	-	48,48,48	0.90	3 (6%)	51,53,53	0.91	2 (3%)
16	80T	U	702	-	87,87,95	1.52	14 (16%)	93,99,107	0.97	4 (4%)
9	Y01	G	906	-	38,38,38	0.65	2 (5%)	57,57,57	0.60	2 (3%)
11	6OU	U	701	-	48,48,48	0.90	4 (8%)	51,53,53	0.90	2 (3%)
9	Y01	U	706	-	38,38,38	0.65	2 (5%)	57,57,57	0.61	2 (3%)
18	PA1	P	102	20,19	11,11,12	1.11	1 (9%)	13,15,17	1.38	2 (15%)
15	LBN	S	902	-	51,51,51	1.06	4 (7%)	57,59,59	0.88	2 (3%)
9	Y01	U	707	-	38,38,38	0.66	2 (5%)	57,57,57	0.63	2 (3%)
9	Y01	G	909	-	38,38,38	0.65	2 (5%)	57,57,57	0.63	2 (3%)
17	80Y	P	101	17,7	18,18,19	0.50	0	24,25,27	0.65	0
9	Y01	G	902	-	38,38,38	0.67	2 (5%)	57,57,57	0.69	2 (3%)
11	6OU	G	903	-	44,44,48	0.94	4 (9%)	47,49,53	0.87	2 (4%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	Y01	U	705	-	-	13/19/77/77	0/4/4/4
12	AJP	G	912	-	-	7/28/220/220	0/11/11/11
19	05E	P	104	17,18,10	-	6/12/29/32	0/1/1/1
9	Y01	U	703	-	-	3/19/77/77	0/4/4/4
9	Y01	D	301	-	-	7/19/77/77	0/4/4/4
9	Y01	U	704	-	-	12/19/77/77	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
20	81Q	P	105	18	-	43/73/97/97	0/1/1/1
9	Y01	G	908	-	-	8/19/77/77	0/4/4/4
14	NAG	T	901	5	-	1/6/23/26	0/1/1/1
11	6OU	G	905	-	-	22/42/42/52	-
17	80Y	P	103	17,19	-	3/11/28/31	0/1/1/1
9	Y01	G	907	-	-	4/19/77/77	0/4/4/4
9	Y01	G	911	-	-	10/19/77/77	0/4/4/4
14	NAG	S	901	4	-	2/6/23/26	0/1/1/1
9	Y01	G	910	-	-	9/19/77/77	0/4/4/4
11	6OU	G	904	-	-	22/52/52/52	-
16	80T	U	702	-	-	48/98/98/106	-
9	Y01	G	906	-	-	10/19/77/77	0/4/4/4
11	6OU	U	701	-	-	33/52/52/52	-
9	Y01	U	706	-	-	14/19/77/77	0/4/4/4
18	PA1	P	102	20,19	-	1/2/19/22	0/1/1/1
15	LBN	S	902	-	-	31/55/55/55	-
9	Y01	U	707	-	-	11/19/77/77	0/4/4/4
9	Y01	G	909	-	-	8/19/77/77	0/4/4/4
17	80Y	P	101	17,7	-	10/11/28/31	1/1/1/1
9	Y01	G	902	-	-	6/19/77/77	0/4/4/4
11	6OU	G	903	-	-	20/48/48/52	-

The worst 5 of 60 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	U	702	80T	O23-C24	4.69	1.47	1.33
16	U	702	80T	O54-C55	3.83	1.44	1.33
16	U	702	80T	O72-C52	-3.81	1.37	1.46
16	U	702	80T	O20-C02	3.74	1.44	1.34
18	P	102	PA1	C1-C2	-3.25	1.48	1.52

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	U	702	80T	O20-C02-C03	4.27	120.71	111.48
11	G	904	6OU	O30-C31-C33	4.12	120.40	111.48
11	G	905	6OU	O30-C31-C33	4.09	120.34	111.48
16	U	702	80T	O72-C73-C74	4.07	120.28	111.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	U	701	6OU	O30-C31-C33	3.98	120.08	111.48

There are no chirality outliers.

5 of 364 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	D	301	Y01	CAM-CAY-OAW-CBC
9	G	902	Y01	CAM-CAY-OAW-CBC
9	G	907	Y01	CAM-CAY-OAW-CBC
9	G	909	Y01	OAG-CAY-OAW-CBC
9	G	909	Y01	CAM-CAY-OAW-CBC

All (1) ring outliers are listed below:

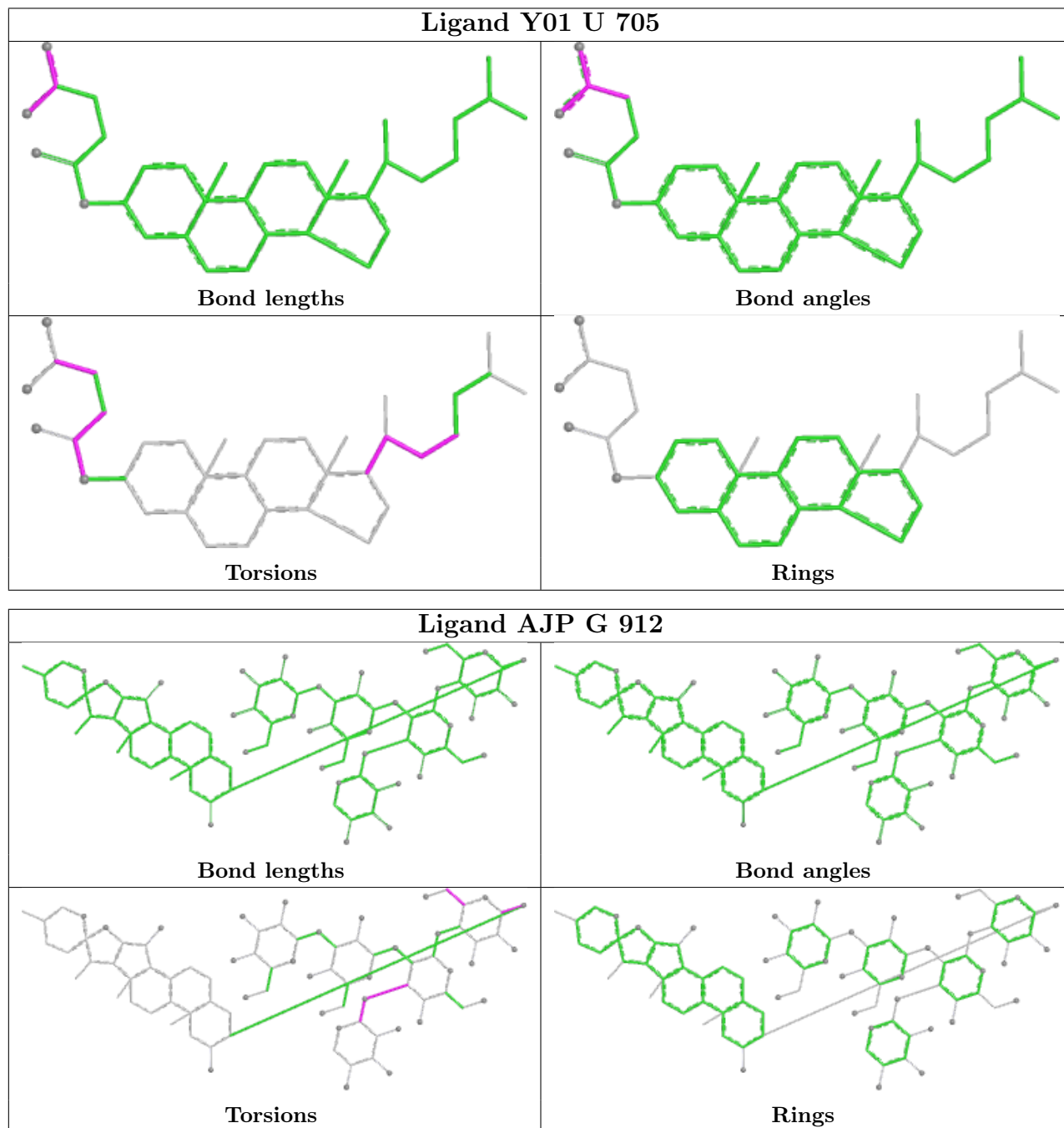
Mol	Chain	Res	Type	Atoms
17	P	101	80Y	C51-C52-C73-C83-C85-O72

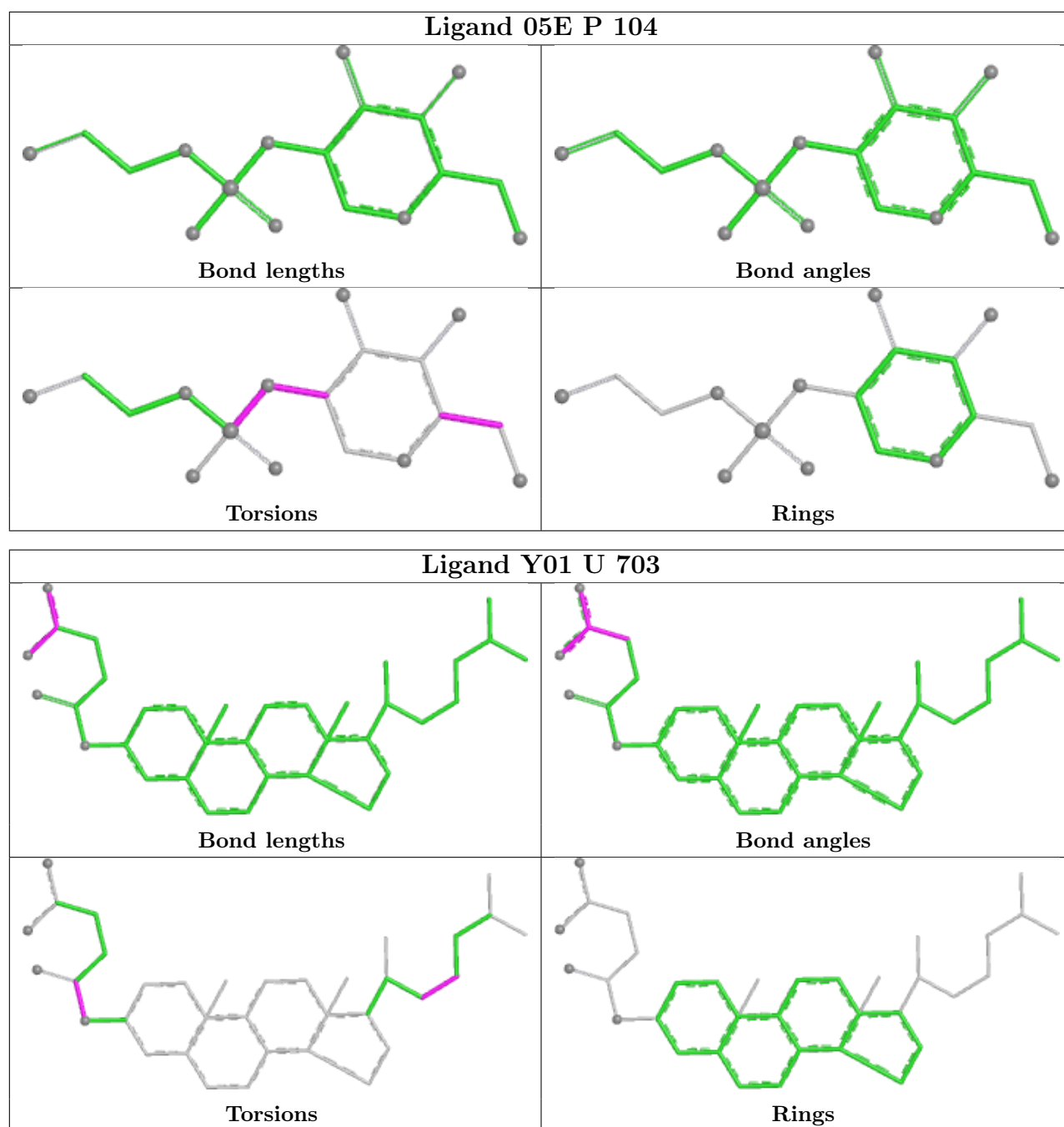
15 monomers are involved in 39 short contacts:

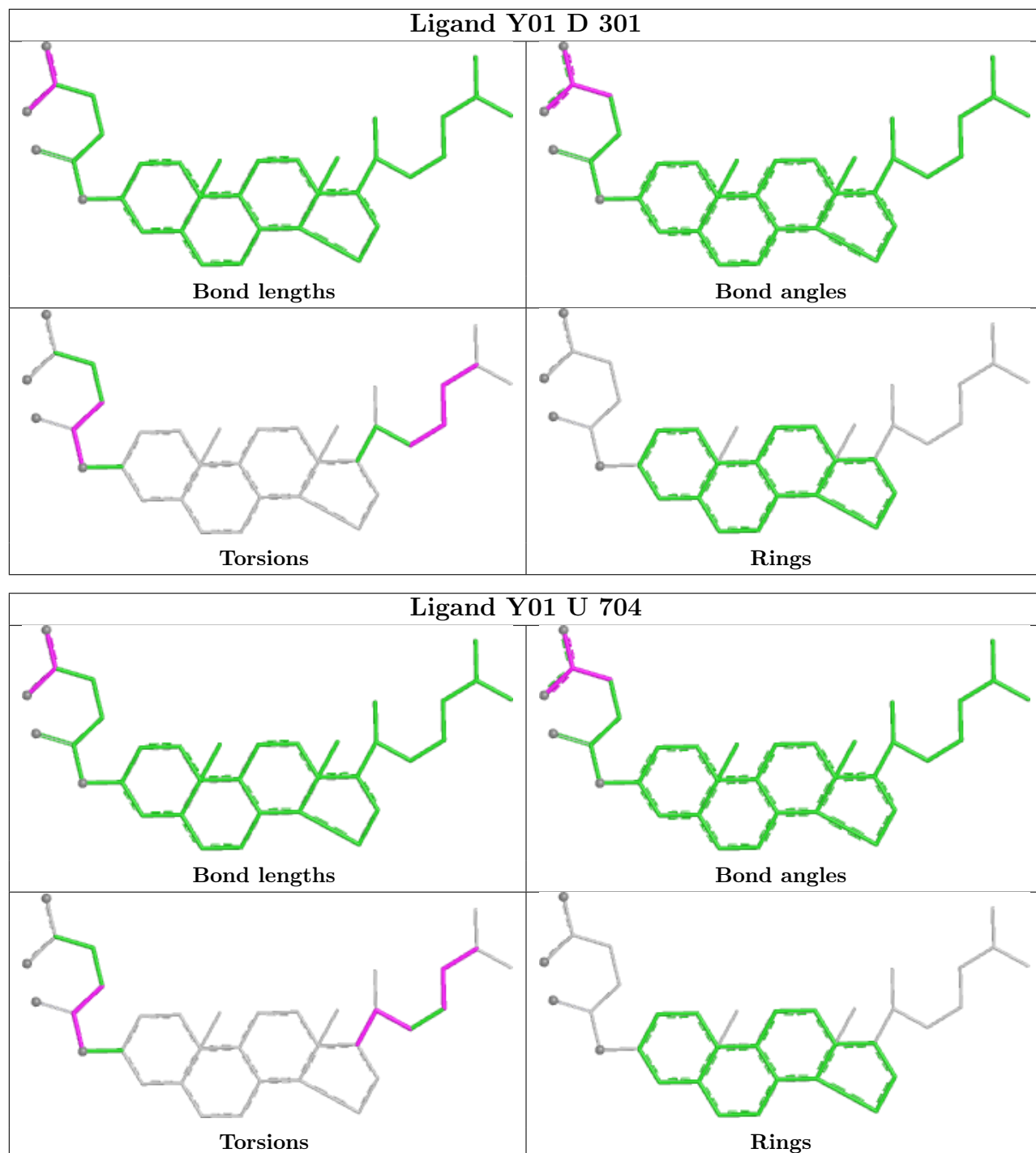
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	U	705	Y01	1	0
9	U	703	Y01	3	0
9	D	301	Y01	5	0
9	U	704	Y01	15	0
20	P	105	81Q	6	0
9	G	907	Y01	3	0
9	G	911	Y01	1	0
9	G	910	Y01	2	0
9	G	906	Y01	2	0
9	U	706	Y01	1	0
18	P	102	PA1	1	0
9	U	707	Y01	3	0
9	G	909	Y01	3	0
17	P	101	80Y	1	0
9	G	902	Y01	1	0

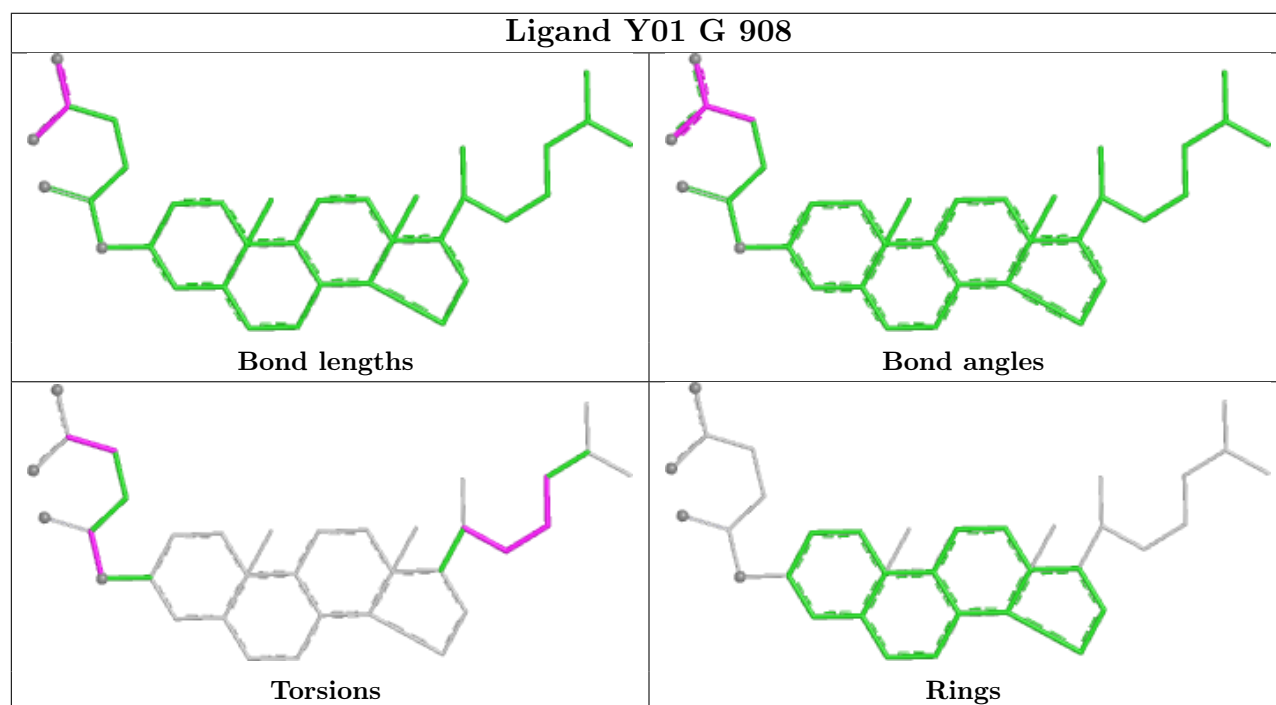
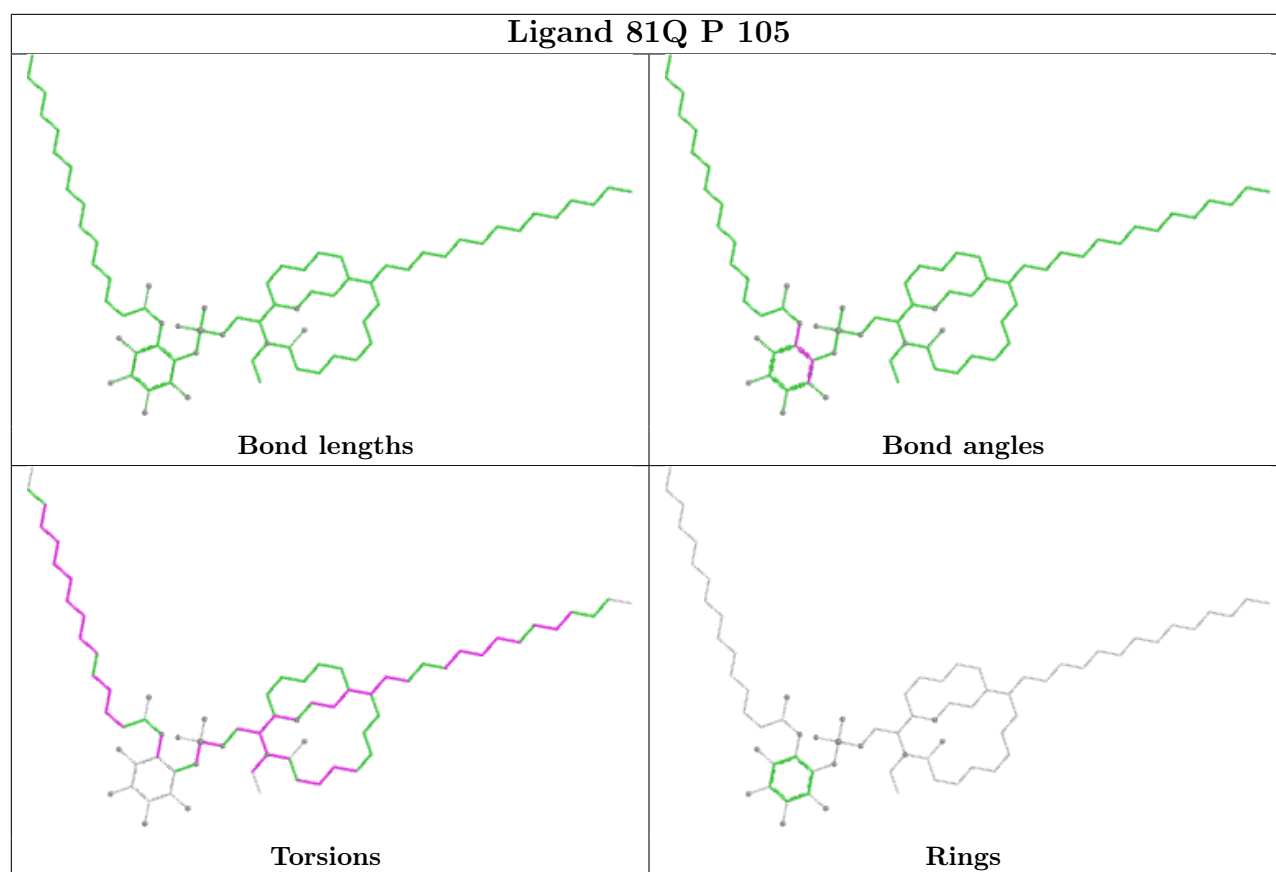
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

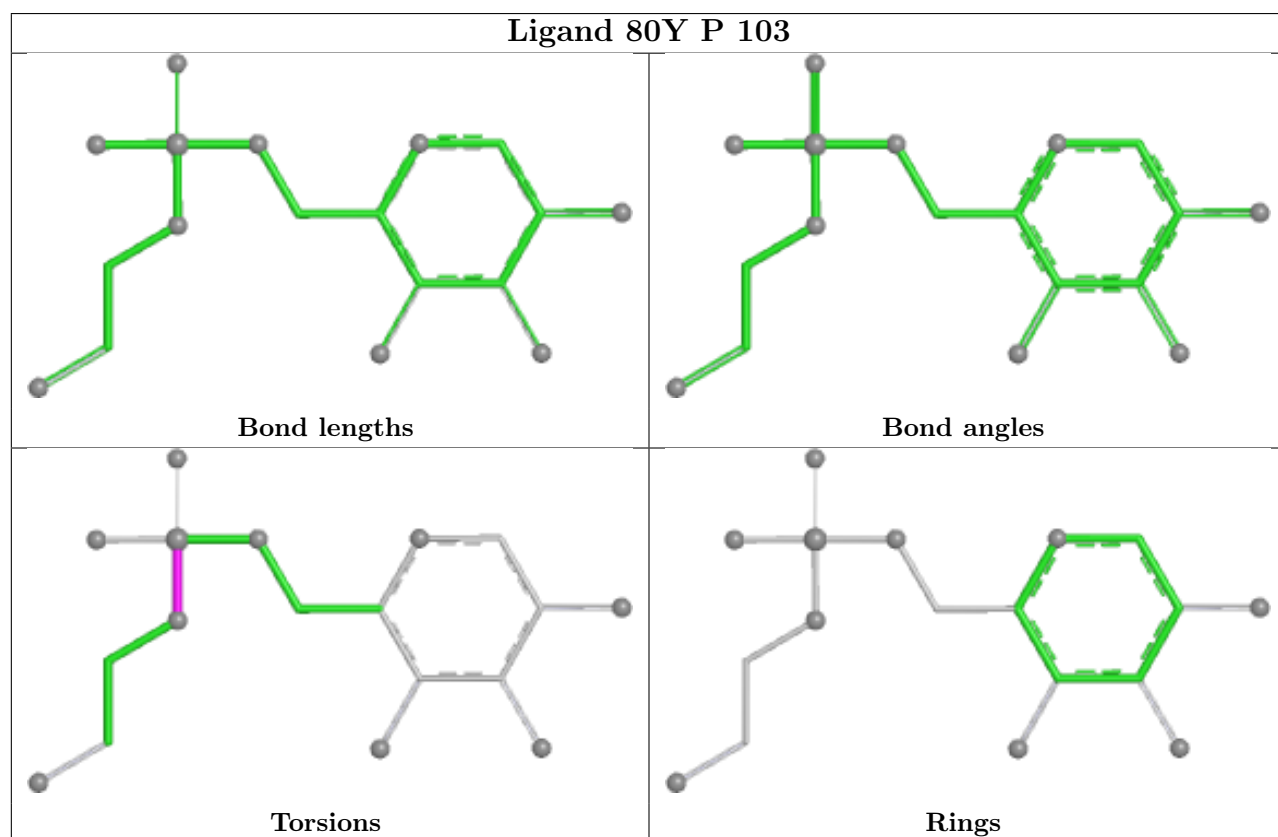
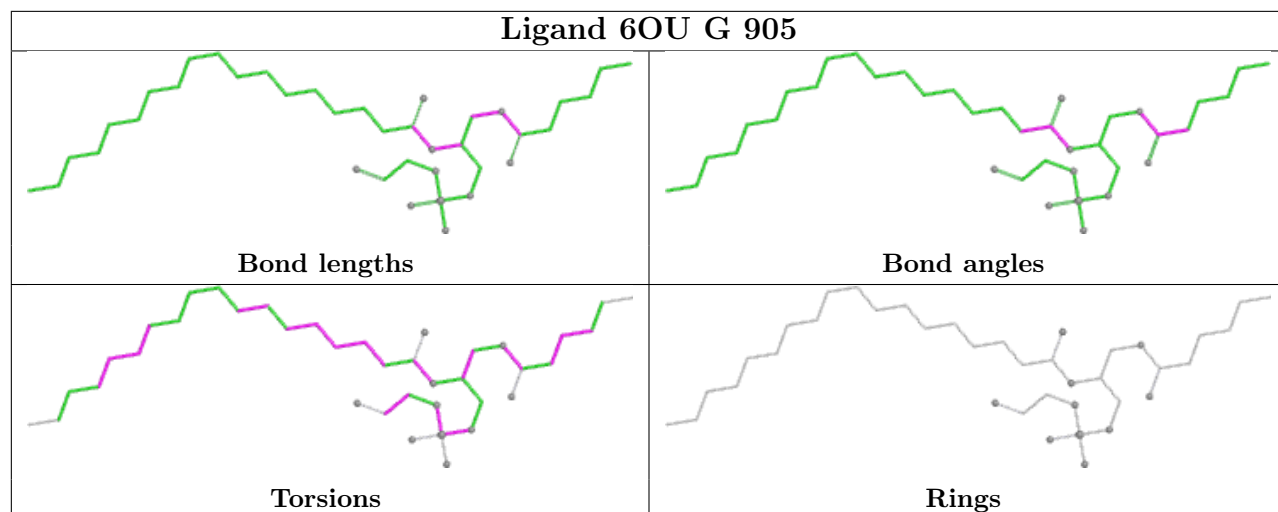
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

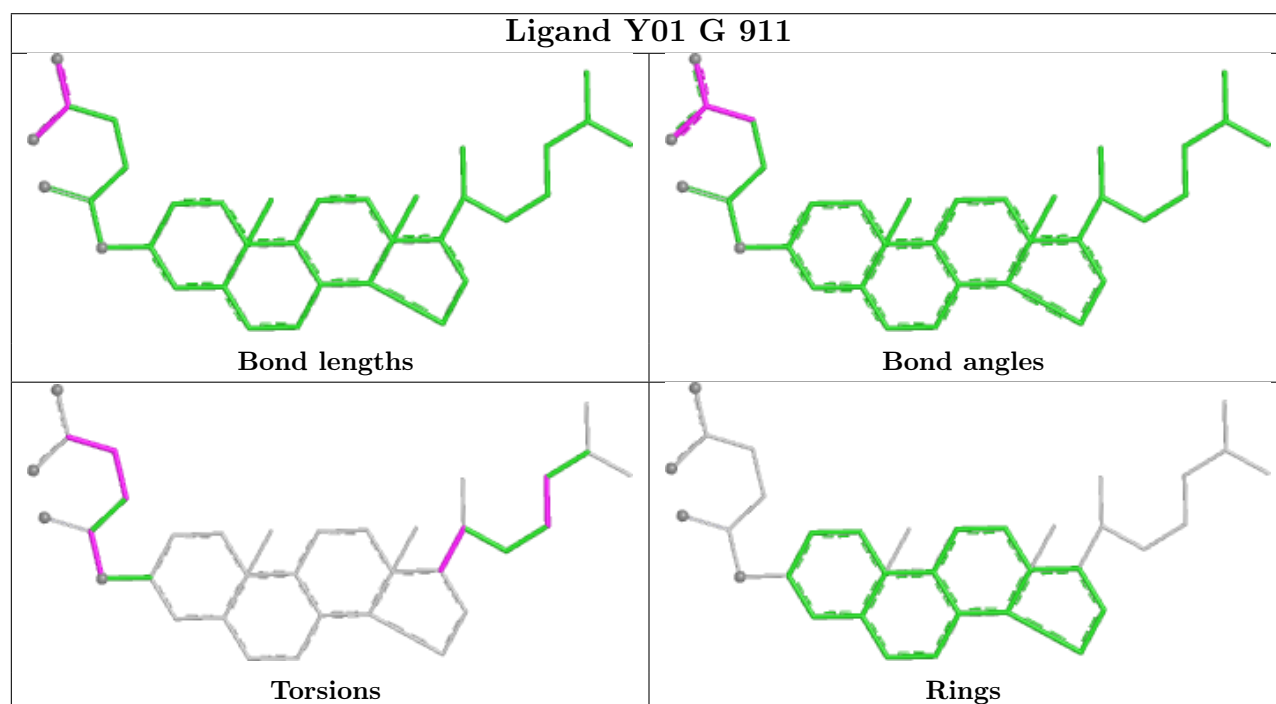
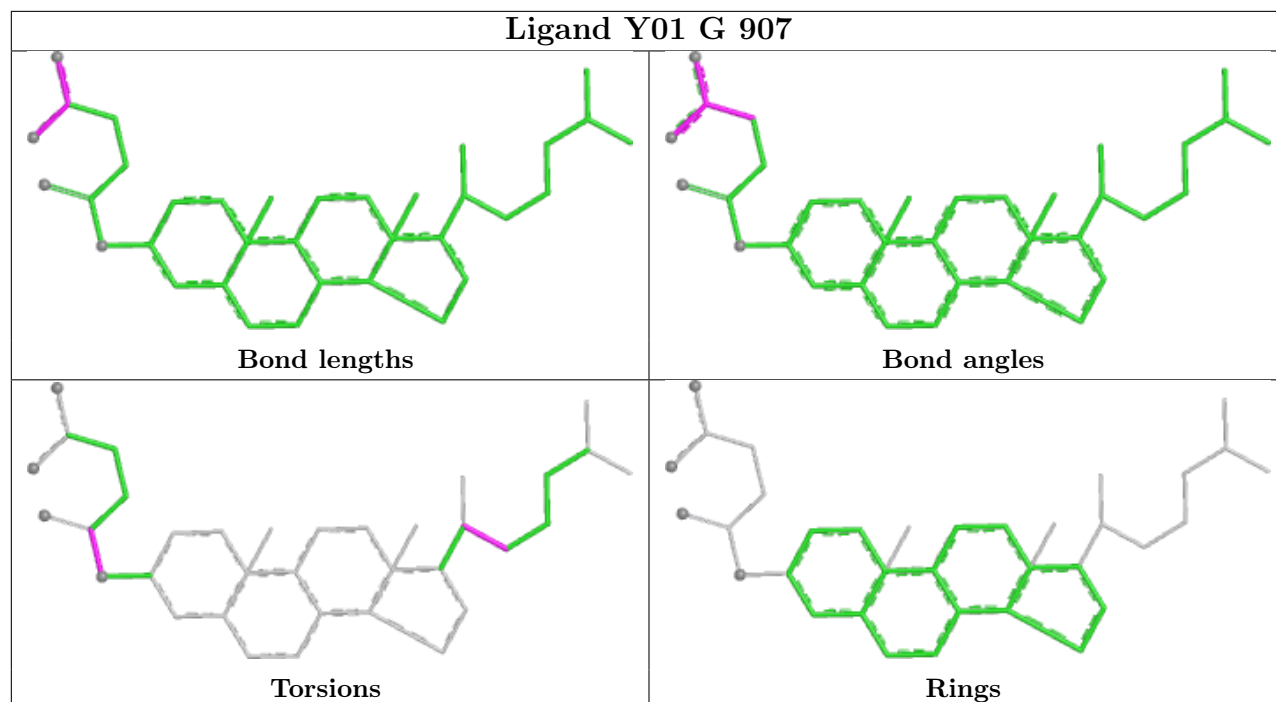


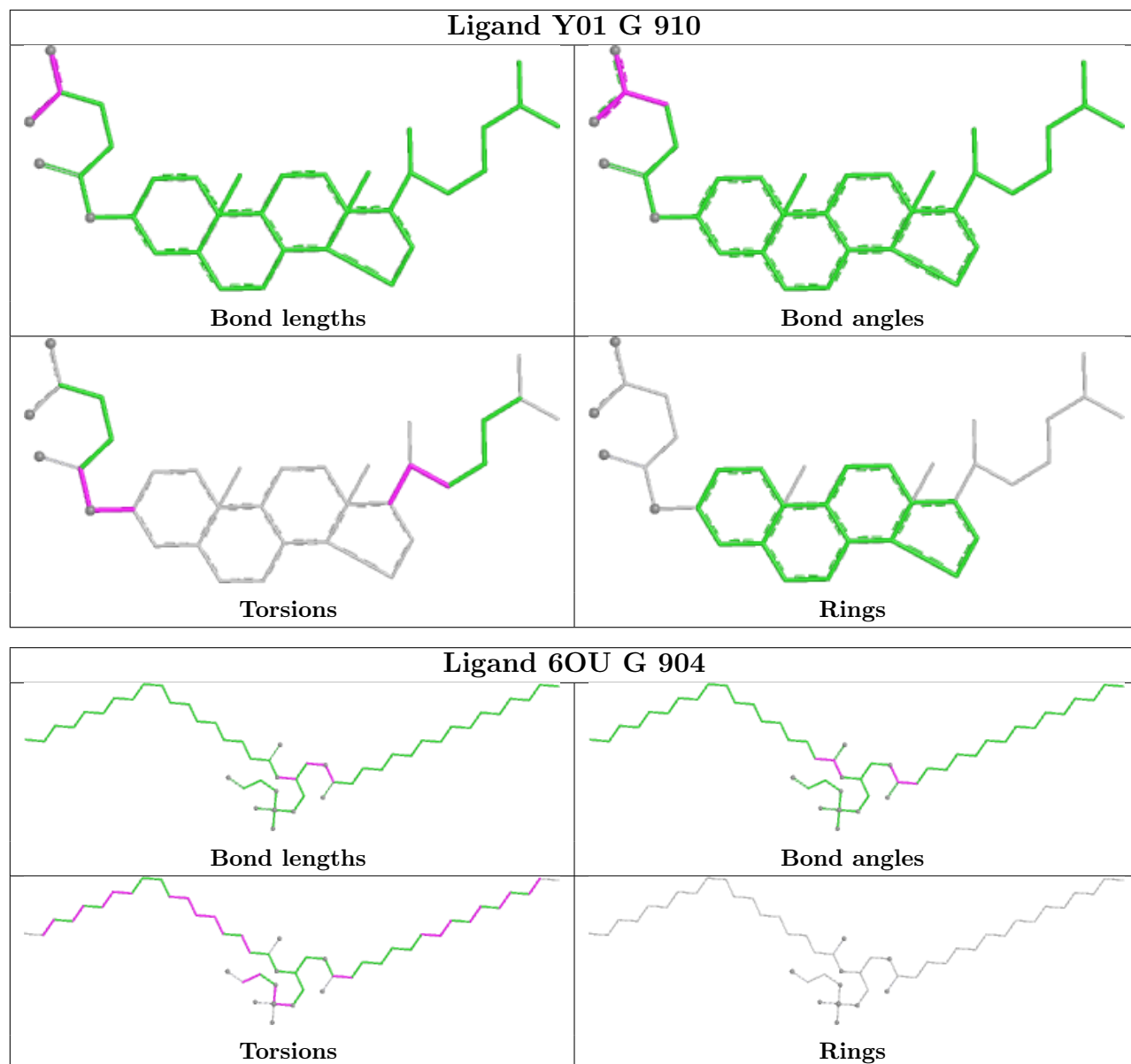


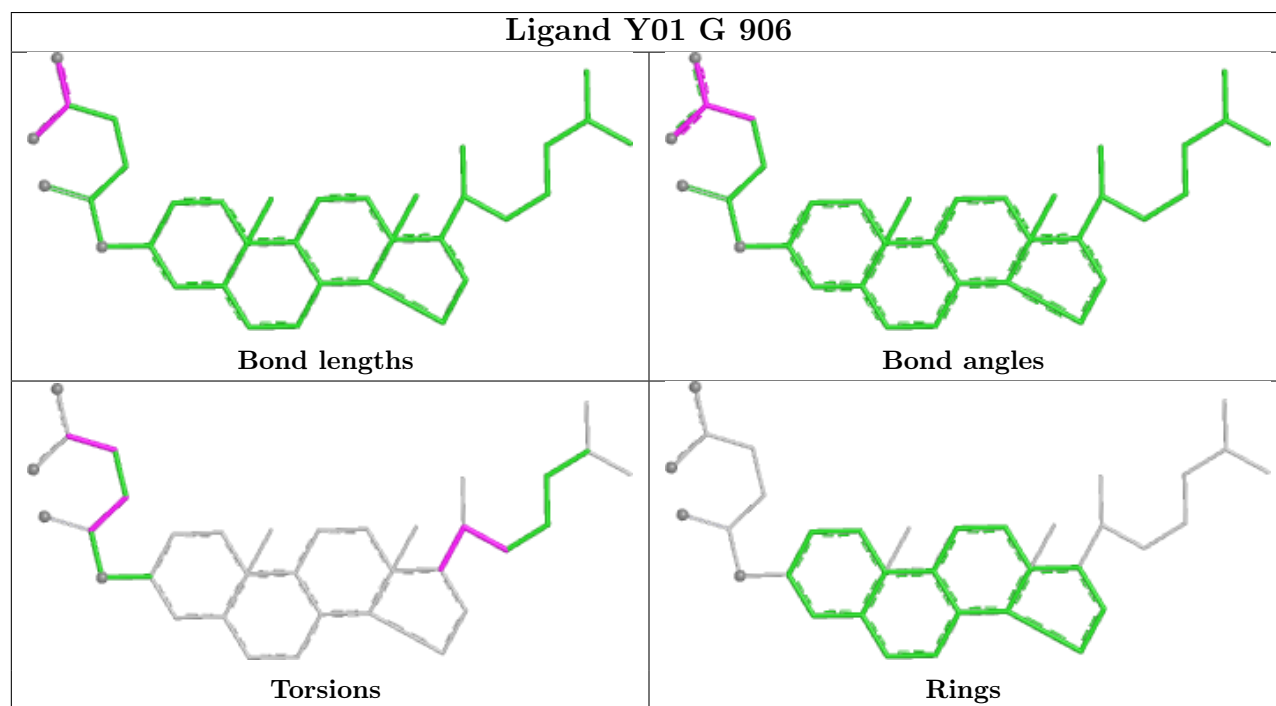
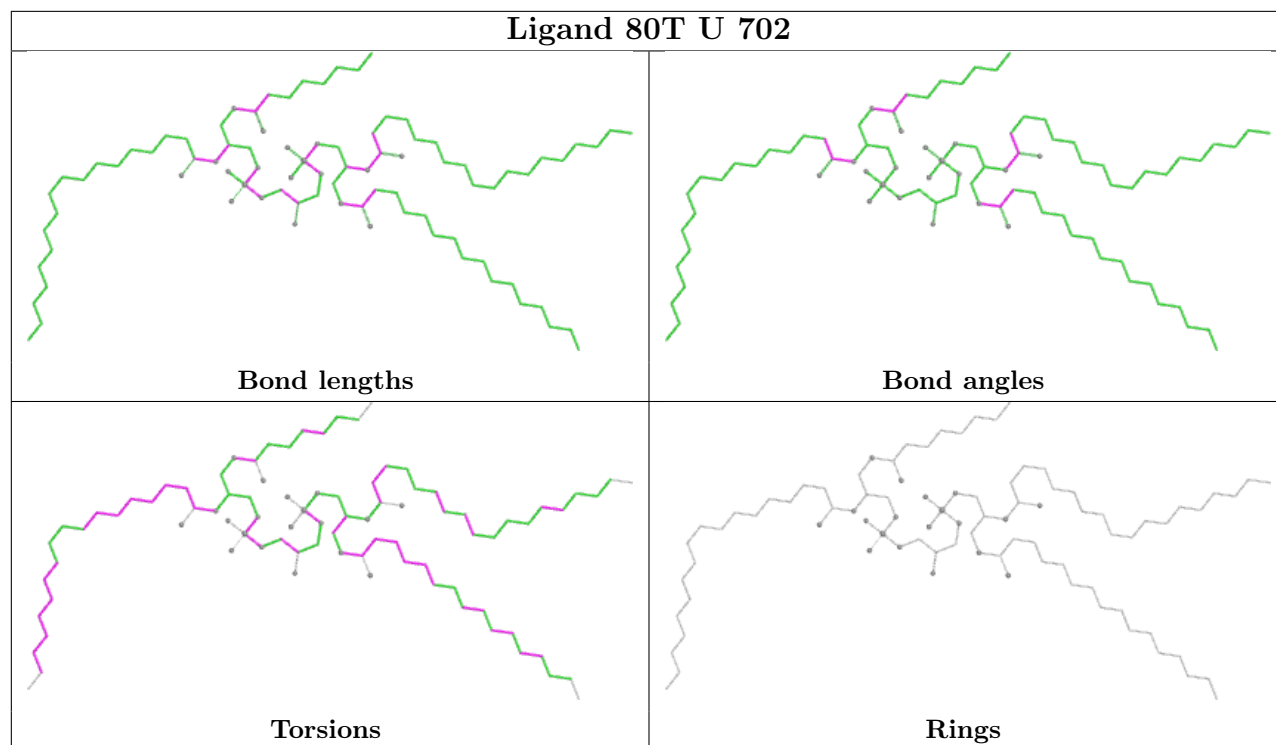


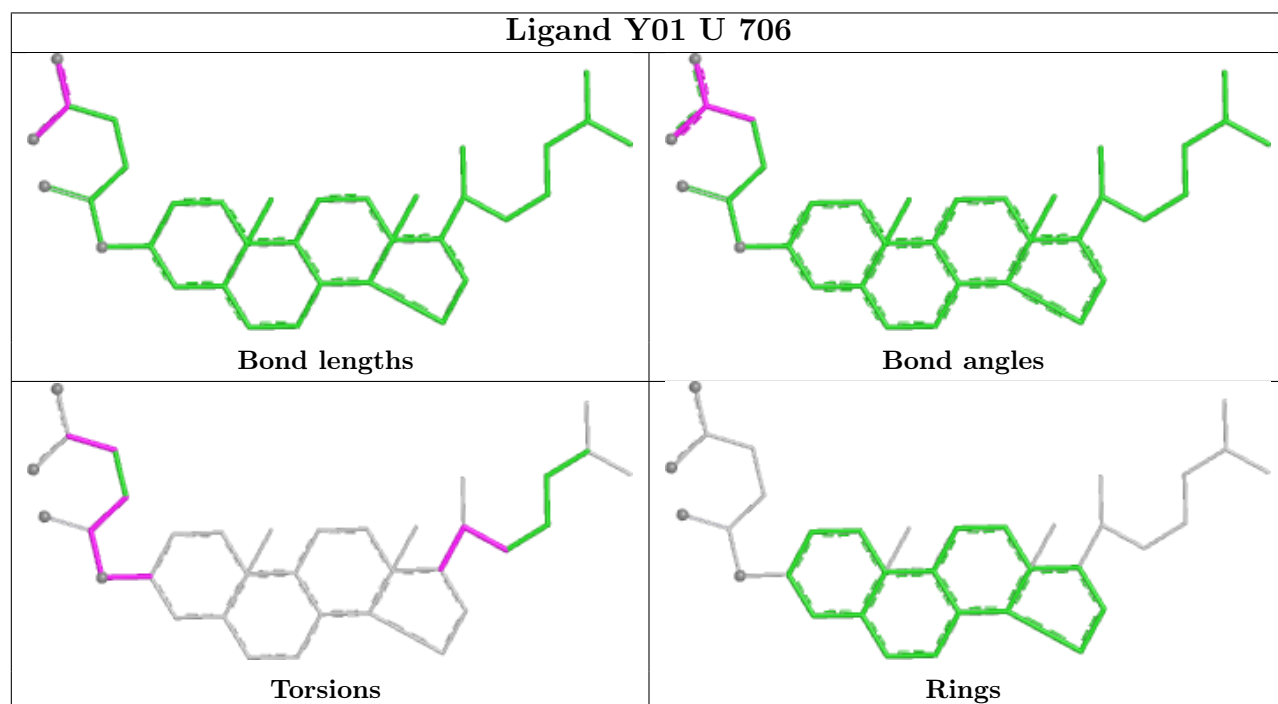
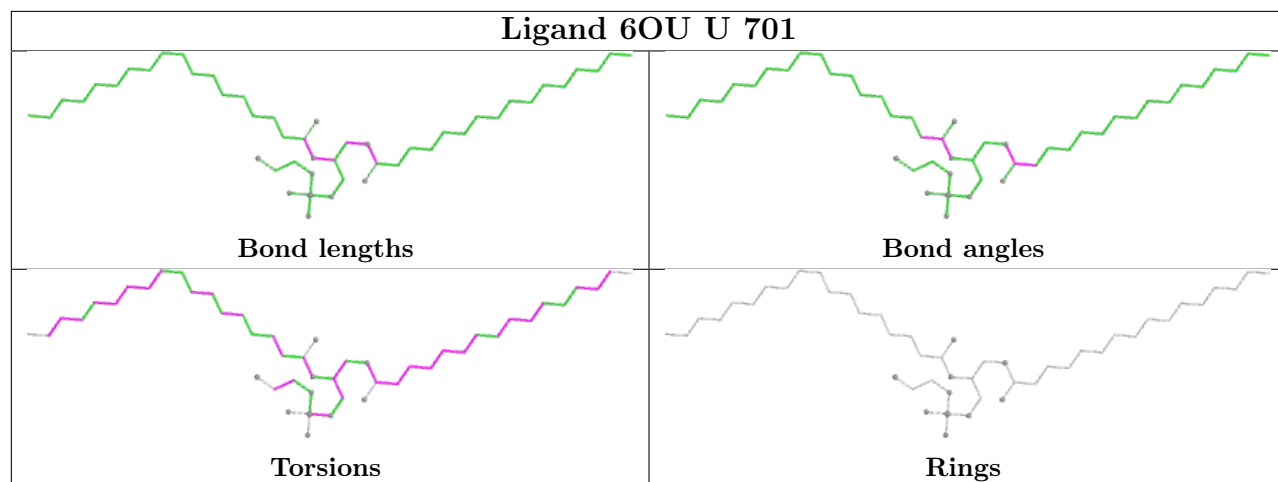


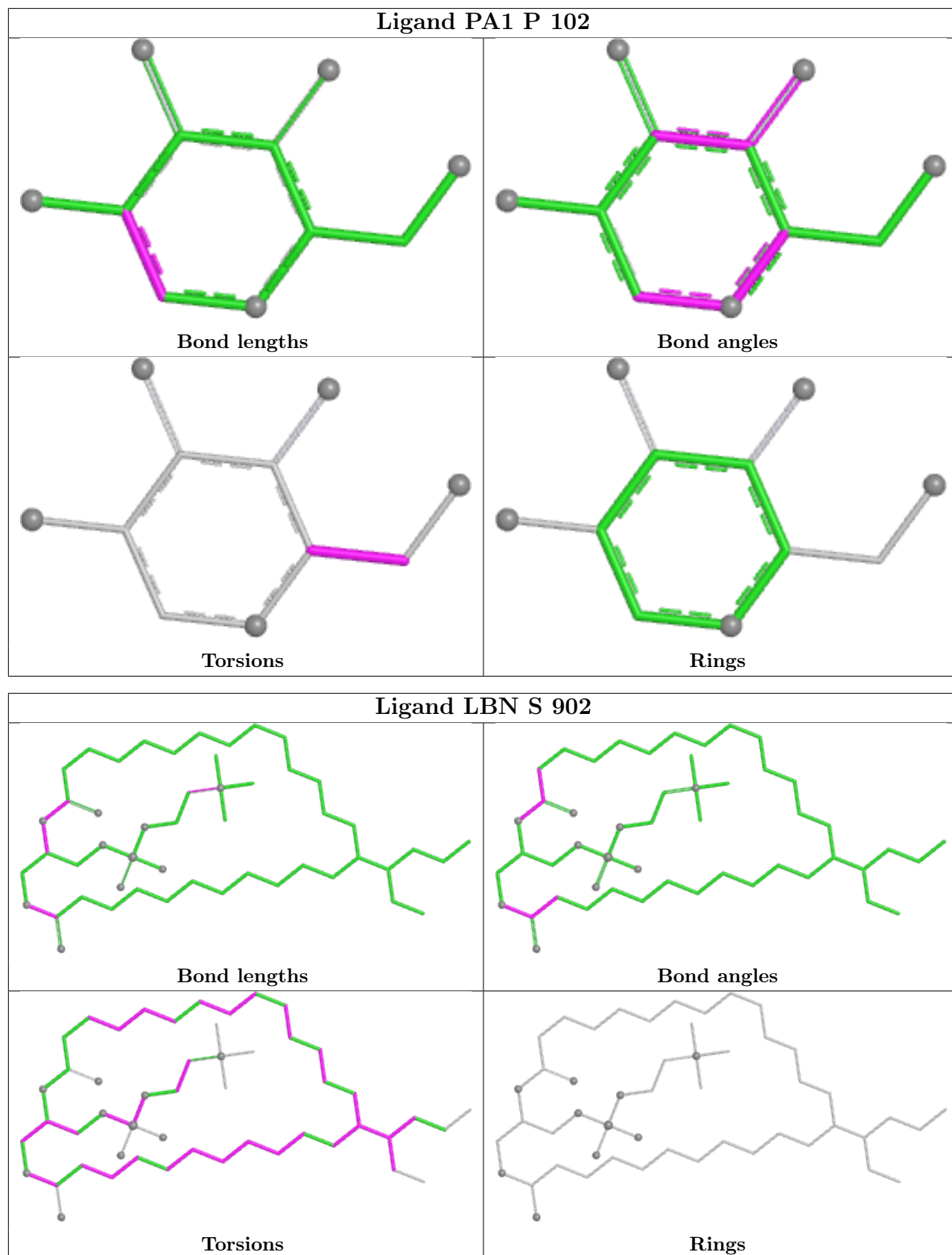


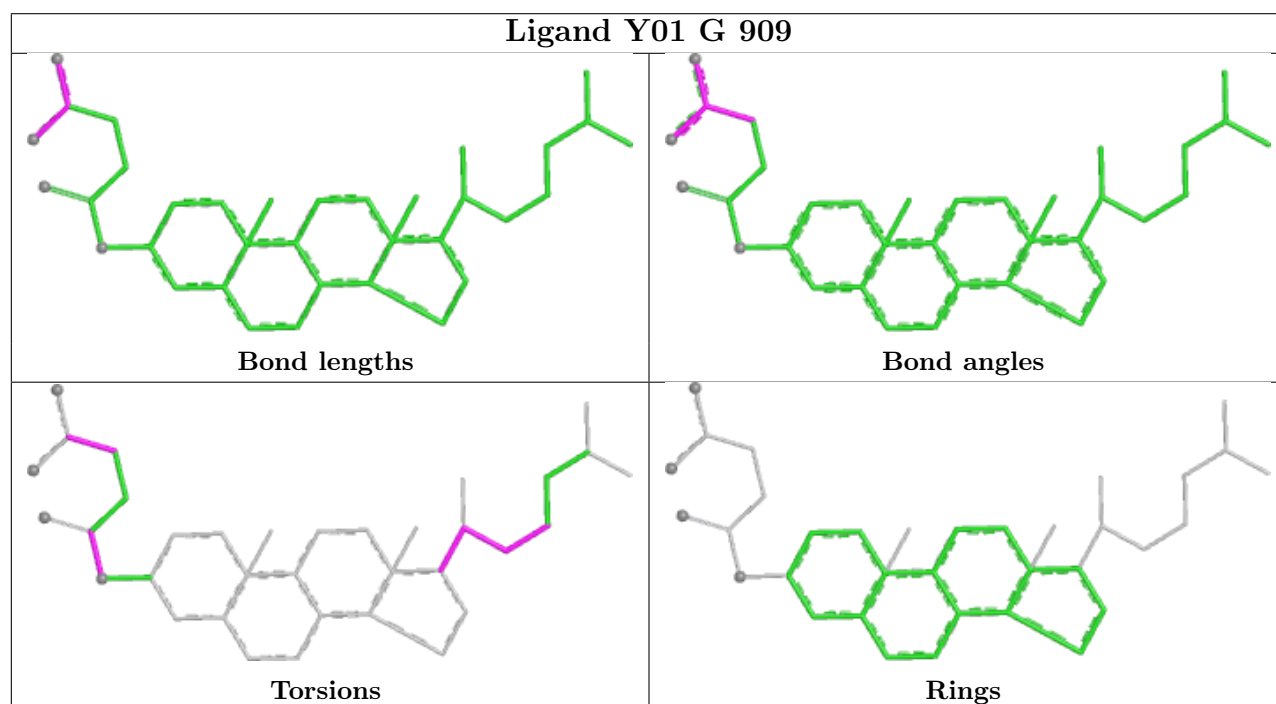
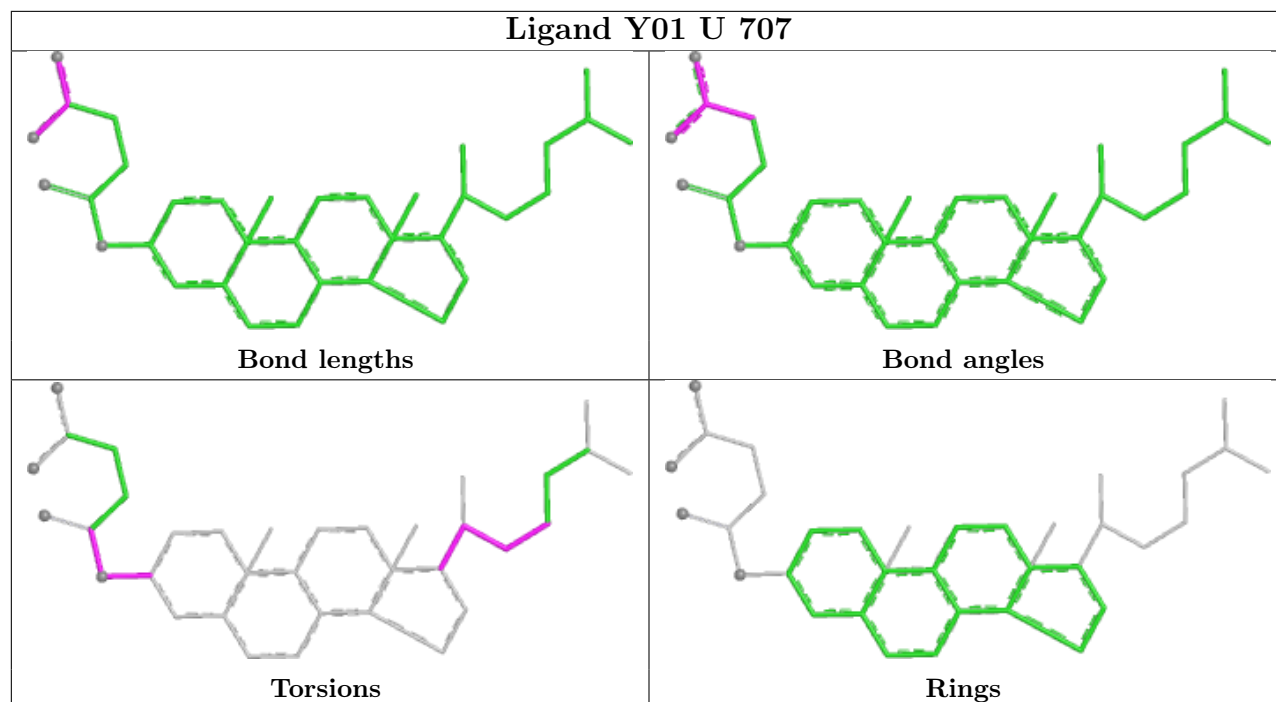


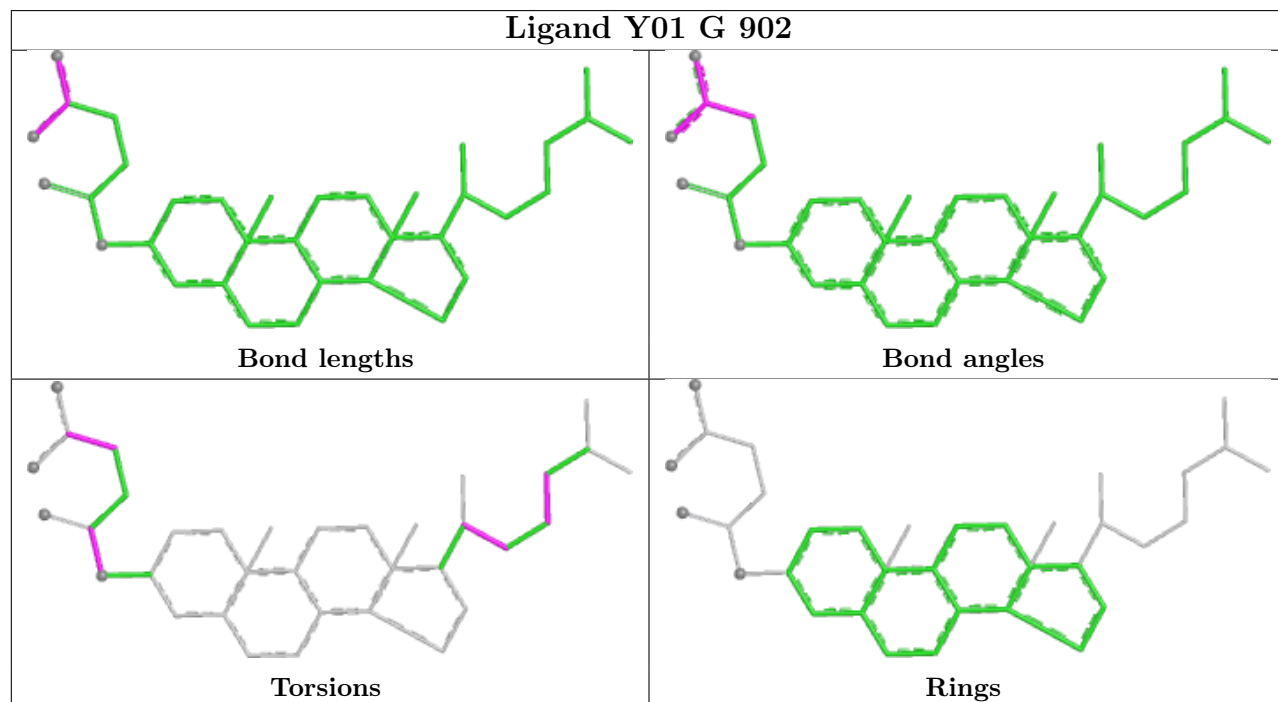
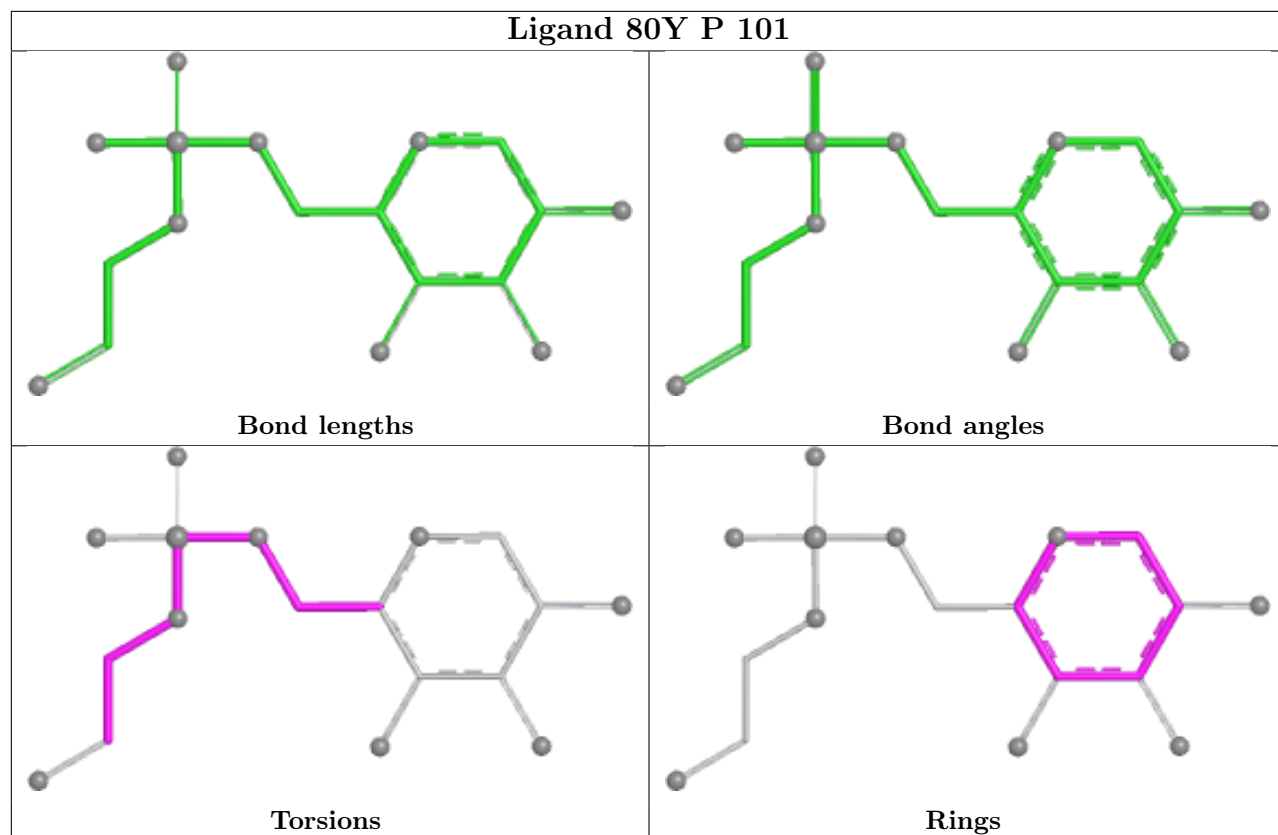


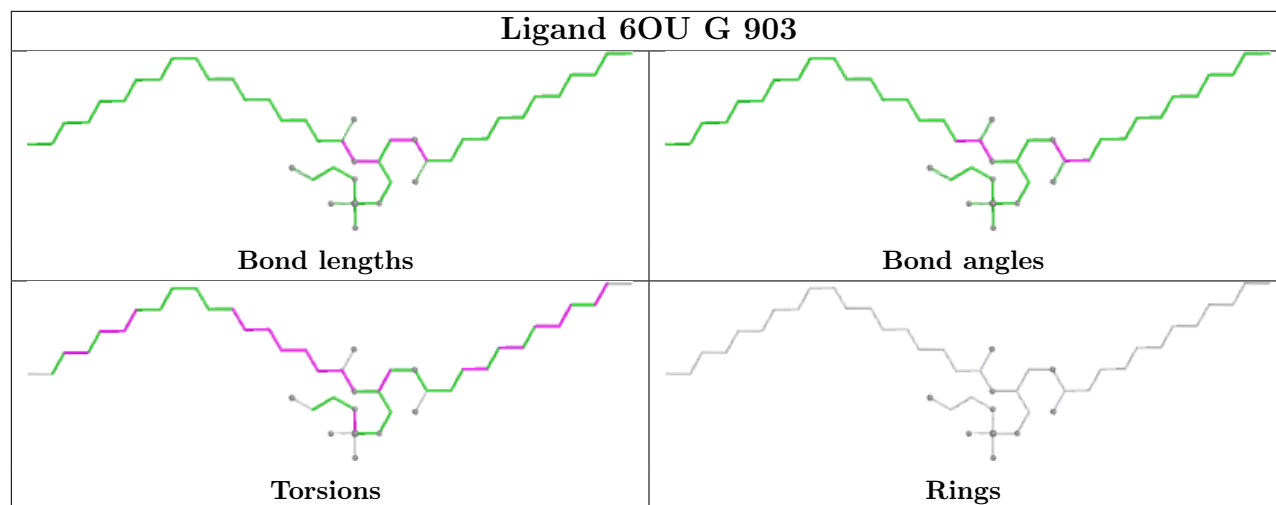












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

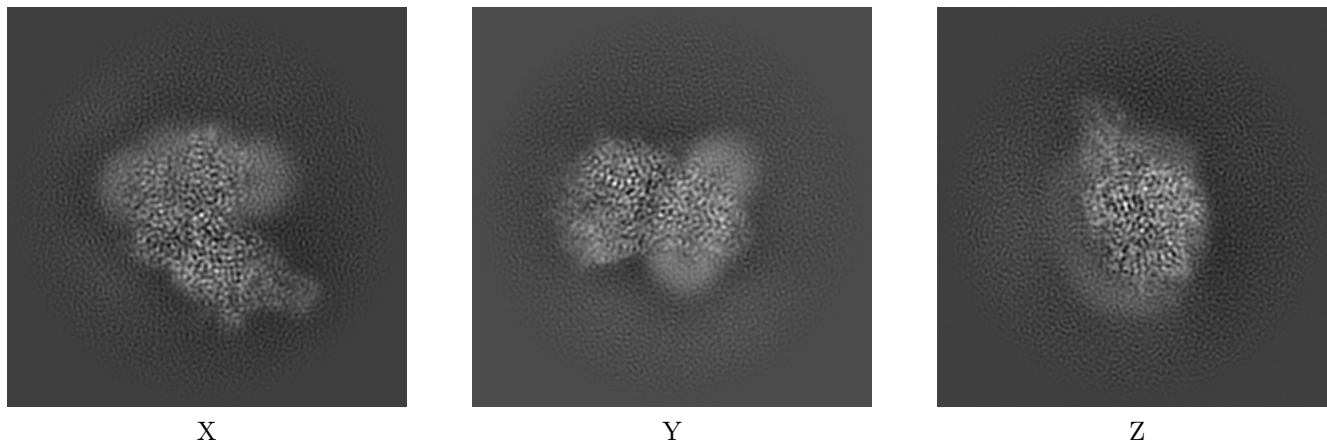
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35575. These allow visual inspection of the internal detail of the map and identification of artifacts.

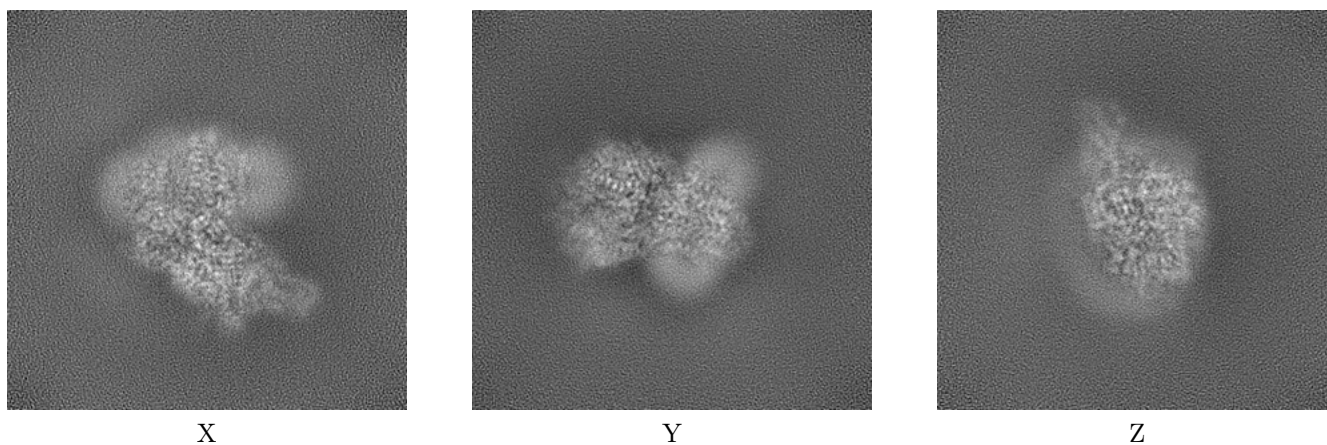
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

#### 6.1.1 Primary map



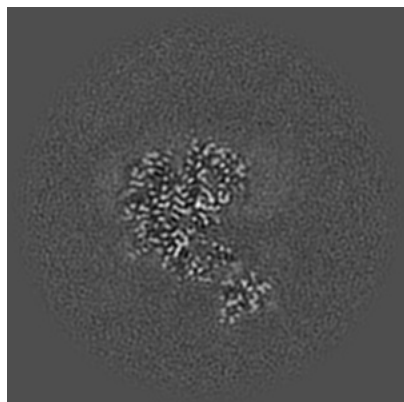
#### 6.1.2 Raw map



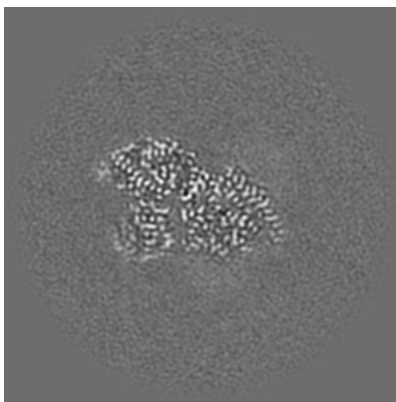
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

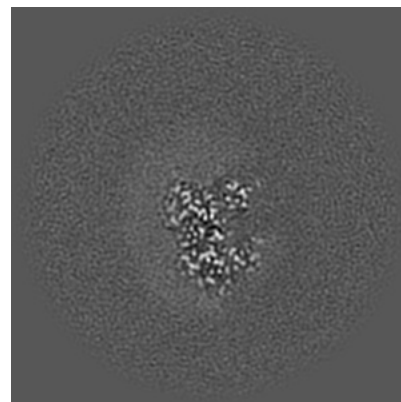
### 6.2.1 Primary map



X Index: 140

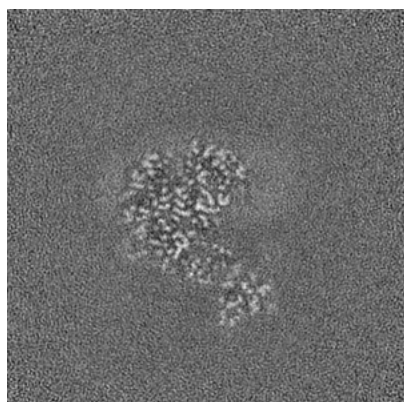


Y Index: 140

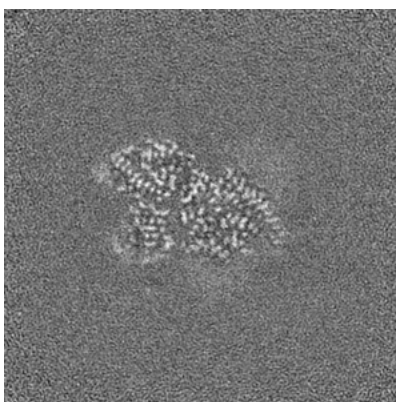


Z Index: 140

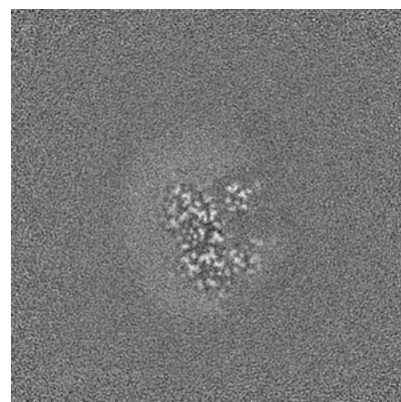
### 6.2.2 Raw map



X Index: 140



Y Index: 140

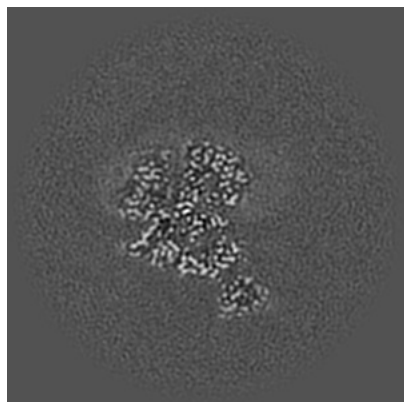


Z Index: 140

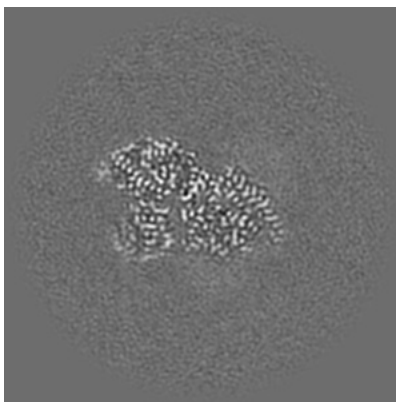
The images above show central slices of the map in three orthogonal directions.

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

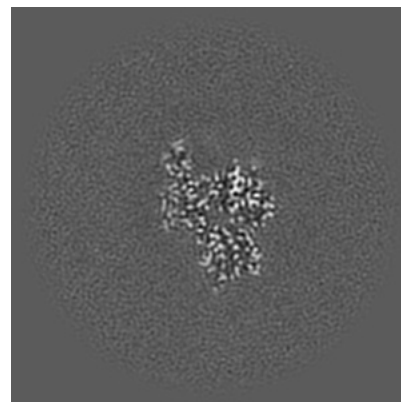
### 6.3.1 Primary map



X Index: 144

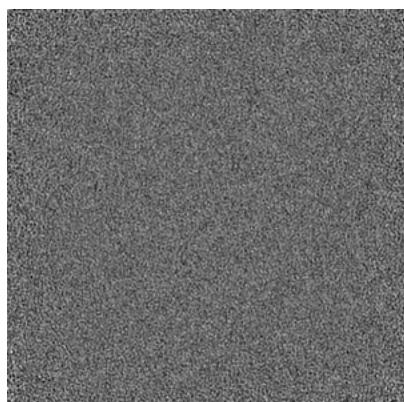


Y Index: 140

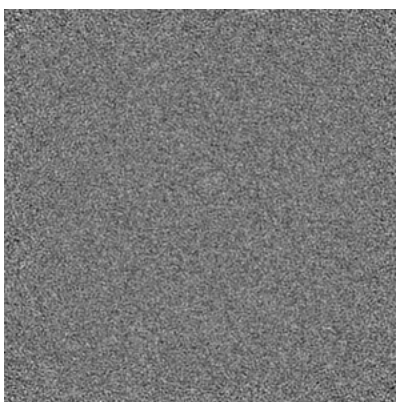


Z Index: 110

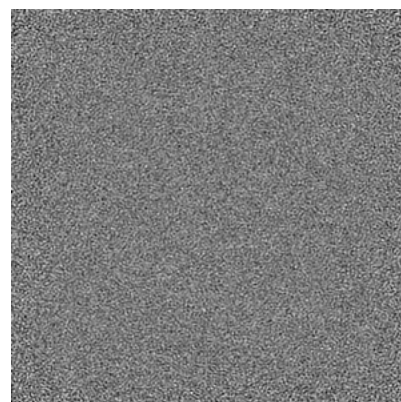
### 6.3.2 Raw map



X Index: 0



Y Index: 0

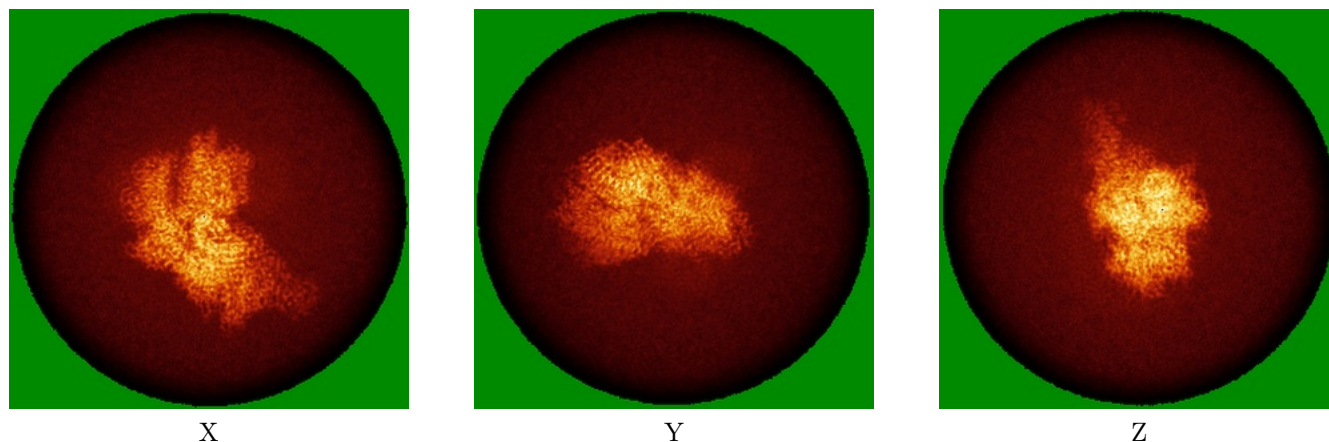


Z Index: 279

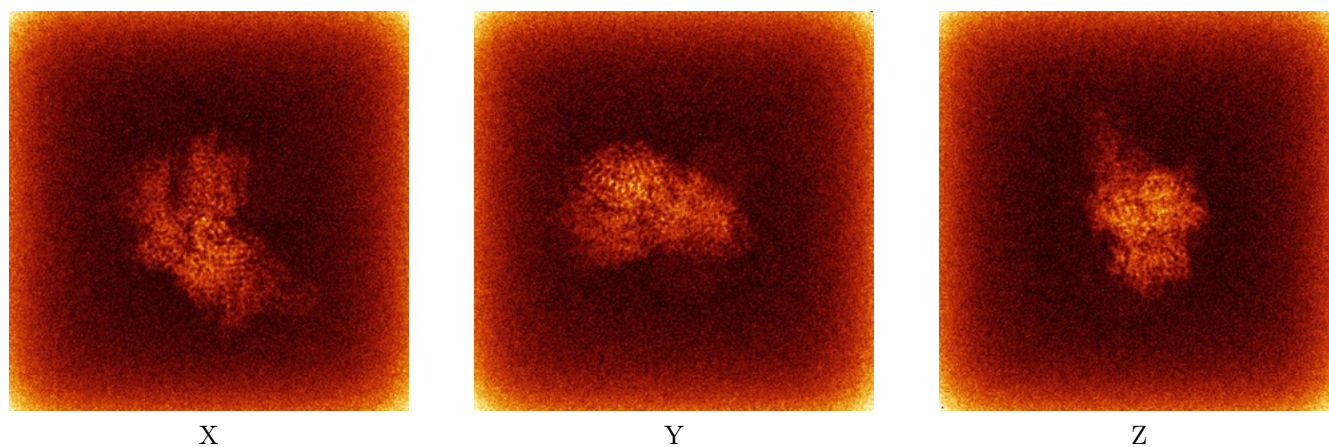
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



### 6.4.2 Raw map



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

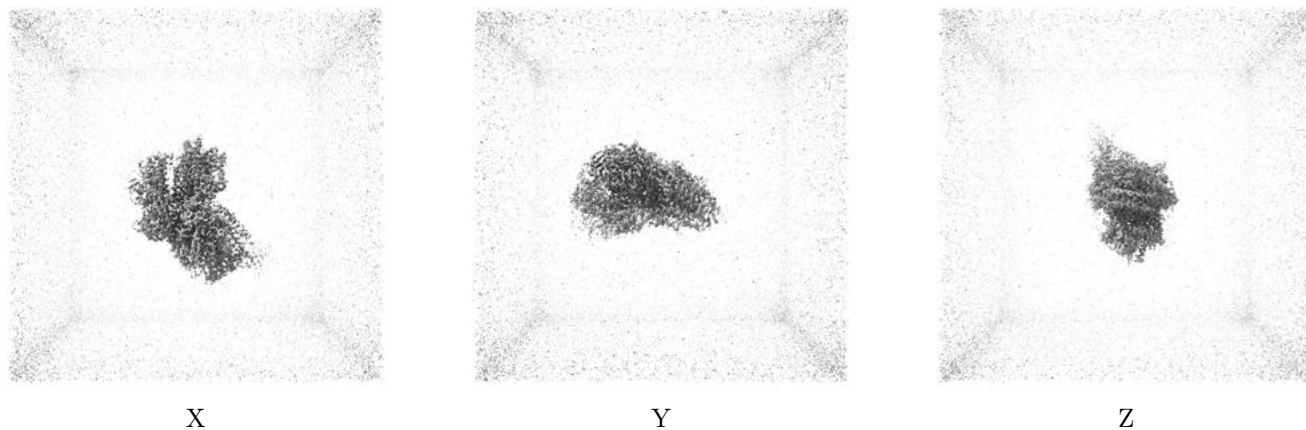
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.48. 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.

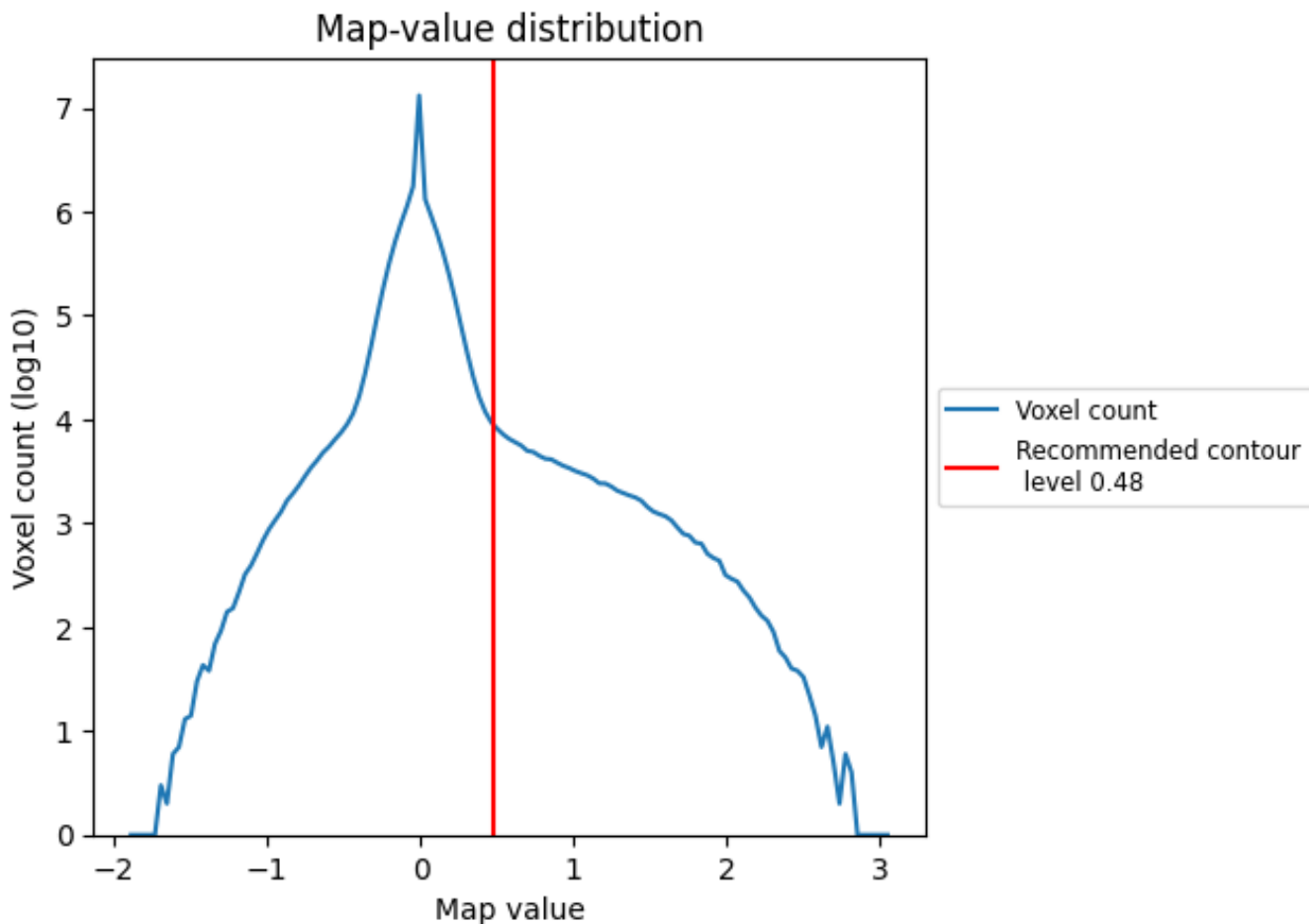
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

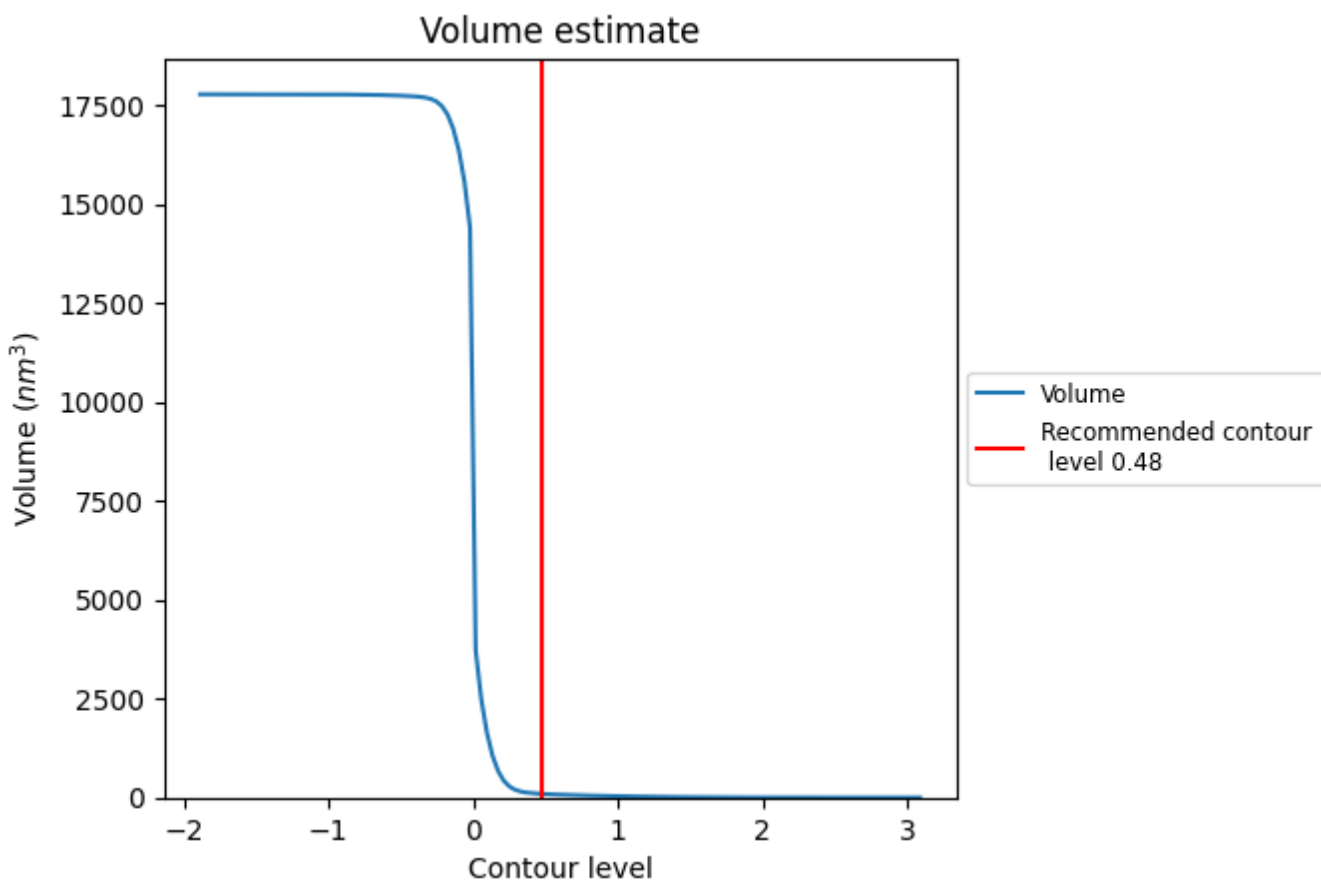
This section contains the results of statistical analysis of the map.

### 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.

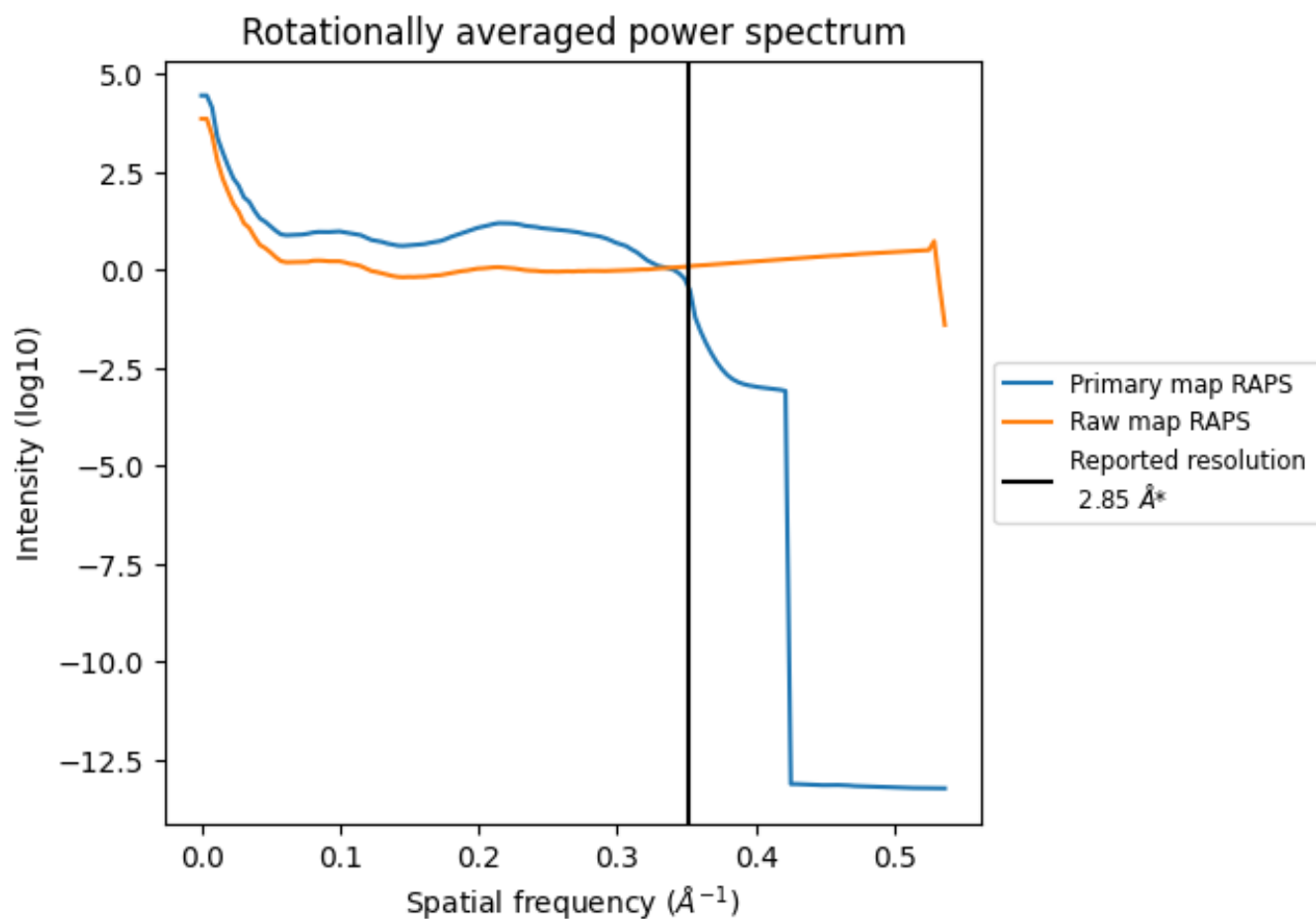
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 92 nm<sup>3</sup>; this corresponds to an approximate mass of 83 kDa.

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

### 7.3 Rotationally averaged power spectrum [i](#)

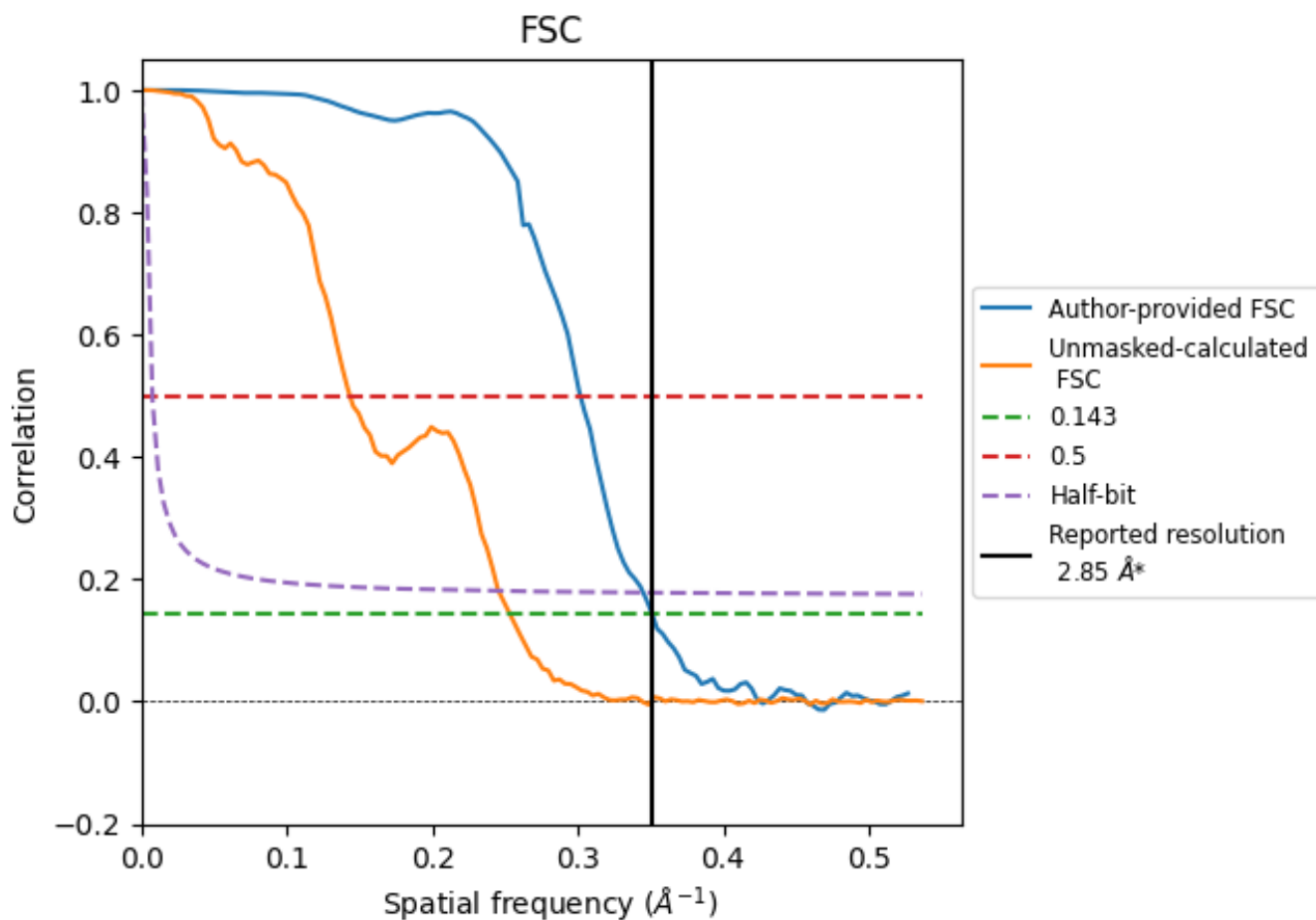


\*Reported resolution corresponds to spatial frequency of 0.351 Å<sup>-1</sup>

## 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  $0.351 \text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

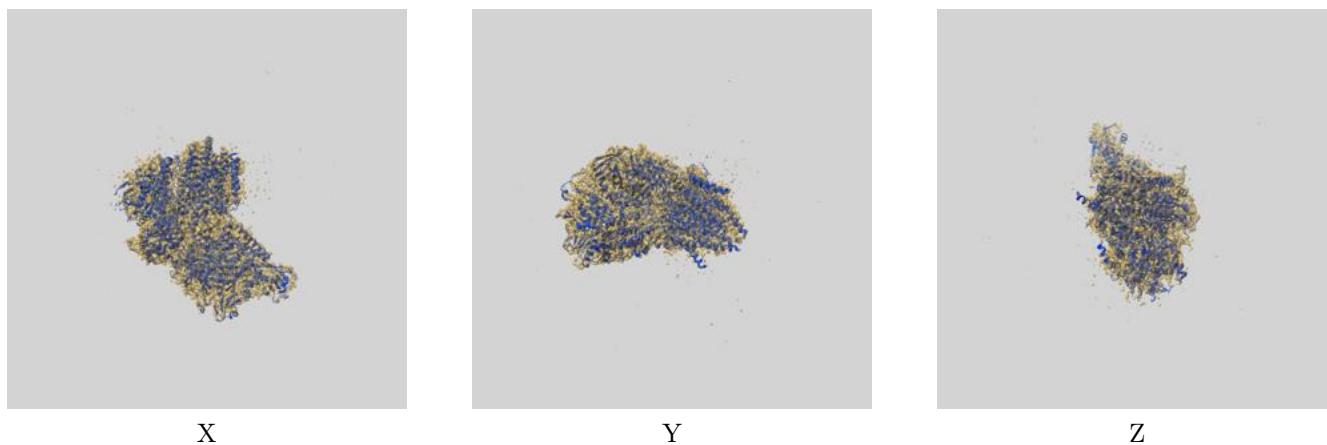
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.85	-	-
Author-provided FSC curve	2.85	3.31	2.90
Unmasked-calculated*	3.94	6.97	4.07

\*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 3.94 differs from the reported value 2.85 by more than 10 %

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

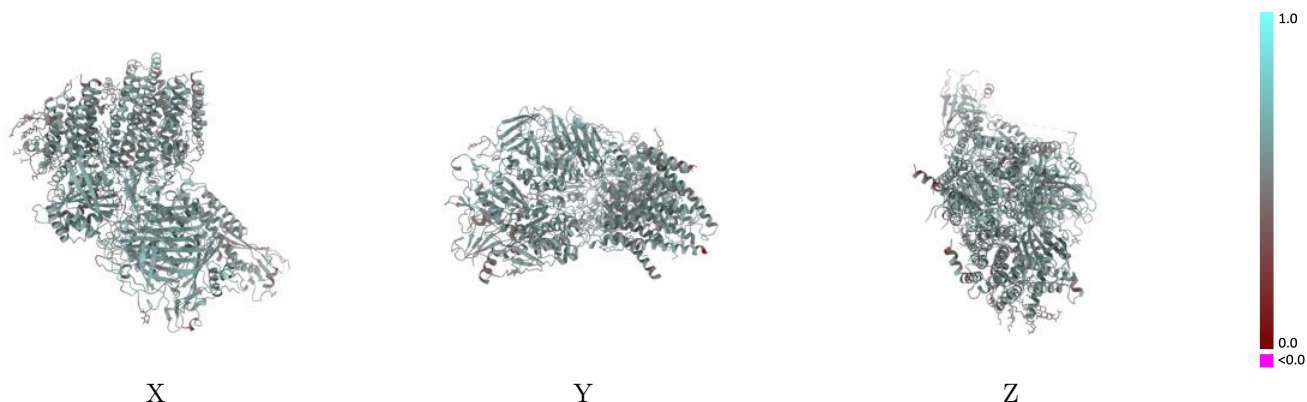
This section contains information regarding the fit between EMDB map EMD-35575 and PDB model 8IMX. Per-residue inclusion information can be found in section 3 on page 25.

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



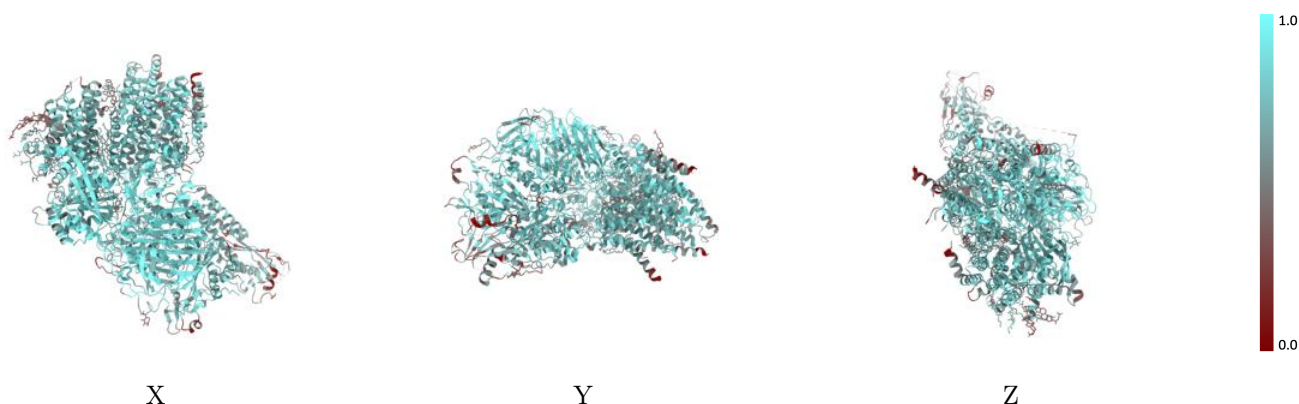
The images above show the 3D surface view of the map at the recommended contour level 0.48 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



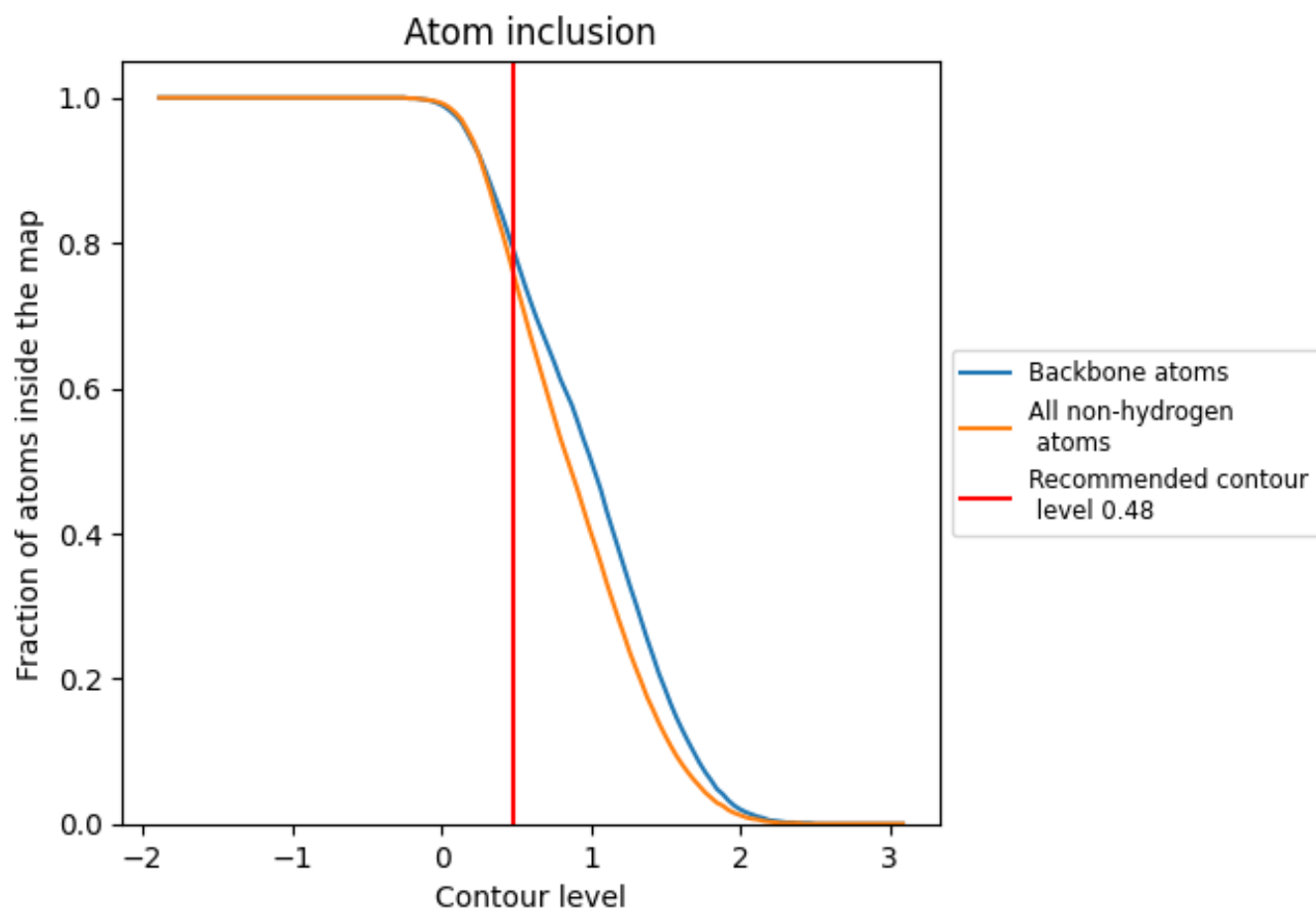
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.48).



















## 9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 76% 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 (0.48) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7590	 0.5670
D	 0.5370	 0.5000
G	 0.7670	 0.5670
K	 0.7560	 0.5620
P	 0.6150	 0.5520
R	 0.6790	 0.5620
S	 0.6560	 0.5410
T	 0.8430	 0.5940
U	 0.7850	 0.5700

