wwPDB EM Validation Summary Report

Mar 5, 2026 – 09:24 PM UTC

PDB ID	:	6Z16 / pdb_00006z16
EMDB ID	:	EMD-11027
Title	:	Structure of the Mrp antiporter complex
Authors	:	Steiner, J.; Sazanov, L.A.
Deposited on	:	2020-05-12
Resolution	:	2.98 Å(reported)
Based on initial models	:	4HEA, 6CFW

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

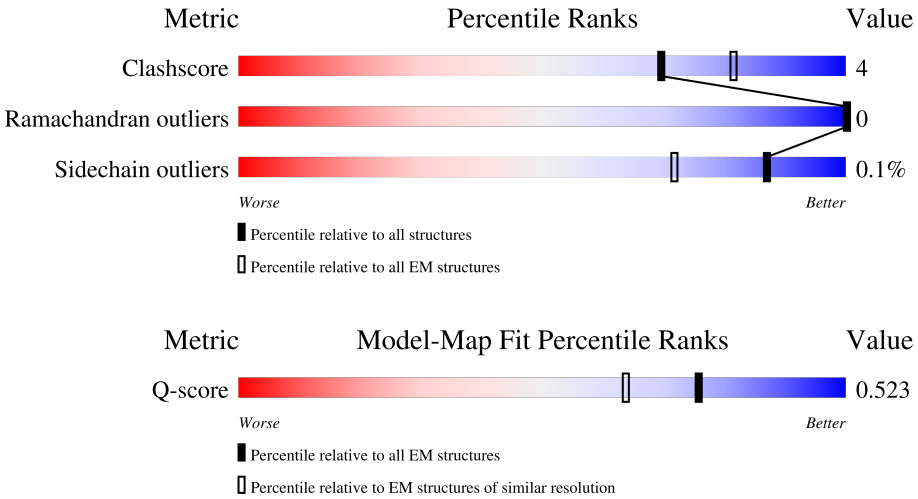
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.98 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.



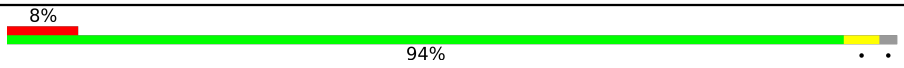
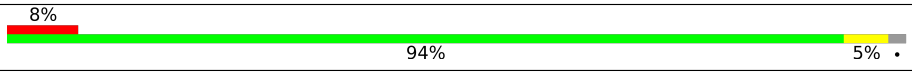
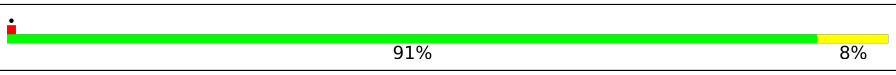
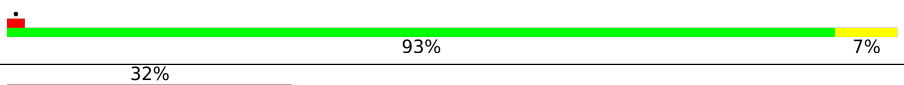
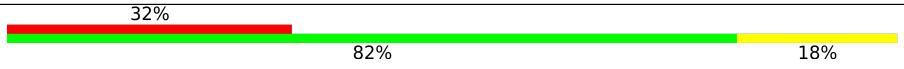
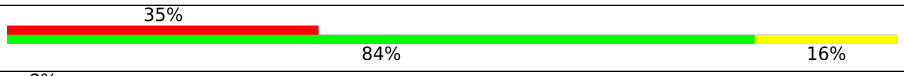
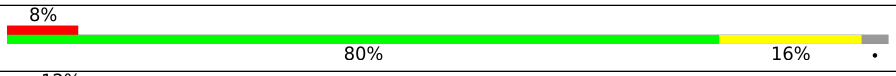
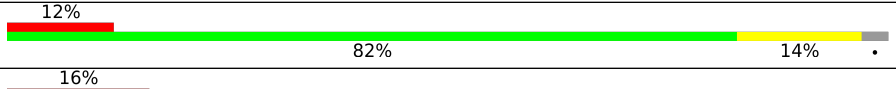
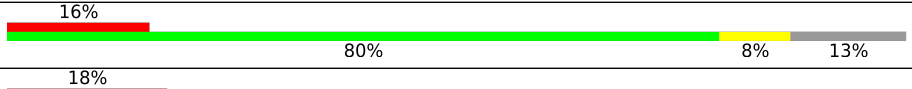
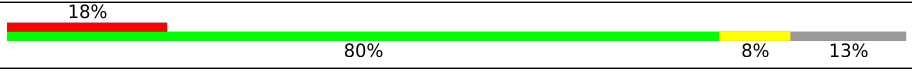
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13236 (2.48 - 3.48)

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 <=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	821	17% 86% 10% ·
1	a	821	20% 87% 9% ·
2	B	140	11% 84% 14% ·
2	b	140	16% 88% 11% ·

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Mol	Chain	Length	Quality of chain
3	C	109	
3	c	109	
4	D	490	
4	d	490	
5	E	158	
5	e	158	
6	F	91	
6	f	91	
7	G	119	
7	g	119	

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 30250 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 Multisubunit Na+/H+ antiporter, A subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	788	Total	C	N	O	S	0	0
			6221	4180	979	1029	33		
1	a	788	Total	C	N	O	S	0	0
			6221	4180	979	1029	33		

- Molecule 2 is a protein called Multisubunit Na+/H+ antiporter, B subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	138	Total	C	N	O	S	0	0
			1070	716	167	182	5		
2	b	138	Total	C	N	O	S	0	0
			1070	716	167	182	5		

- Molecule 3 is a protein called Multisubunit Na+/H+ antiporter, C subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	107	Total	C	N	O	S	0	0
			802	531	128	137	6		
3	c	107	Total	C	N	O	S	0	0
			802	531	128	137	6		

- Molecule 4 is a protein called Multisubunit Na+/H+ antiporter, D subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	489	Total	C	N	O	S	0	0
			3796	2570	577	635	14		
4	d	489	Total	C	N	O	S	0	0
			3796	2570	577	635	14		

- Molecule 5 is a protein called Multisubunit Na+/H+ antiporter, E subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	158	Total	C	N	O	S	0	0
			1274	860	193	215	6		
5	e	158	Total	C	N	O	S	0	0
			1274	860	193	215	6		

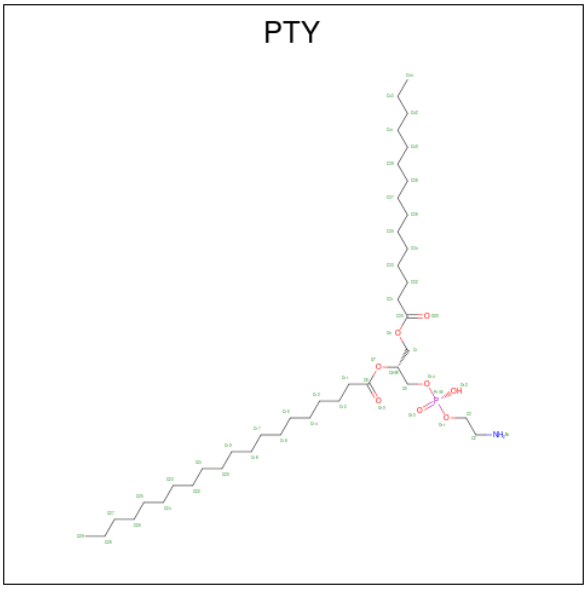
- Molecule 6 is a protein called Multisubunit Na+/H+ antiporter, F subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	88	Total	C	N	O	S	0	0
			648	431	103	110	4		
6	f	88	Total	C	N	O	S	0	0
			648	431	103	110	4		

- Molecule 7 is a protein called Multisubunit Na+/H+ antiporter, G subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	104	Total	C	N	O	S	0	0
			804	527	137	137	3		
7	g	104	Total	C	N	O	S	0	0
			804	527	137	137	3		

- Molecule 8 is PHOSPHATIDYLETHANOLAMINE (CCD ID: PTY) (formula: $C_{40}H_{80}NO_8P$).



Mol	Chain	Residues	Atoms					AltConf
8	A	1	Total	C	N	O	P	0
			30	20	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
8	A	1	Total	C	N	O	P	0
			34	24	1	8	1	
8	A	1	Total	C	N	O	P	0
			43	33	1	8	1	
8	A	1	Total	C	N	O	P	0
			40	30	1	8	1	
8	A	1	Total	C	N	O	P	0
			47	37	1	8	1	
8	A	1	Total	C	N	O	P	0
			34	24	1	8	1	
8	A	1	Total	C	N	O	P	0
			47	37	1	8	1	
8	B	1	Total	C	N	O	P	0
			34	24	1	8	1	
8	D	1	Total	C	N	O	P	0
			34	24	1	8	1	
8	D	1	Total	C	N	O	P	0
			39	29	1	8	1	
8	D	1	Total	C	N	O	P	0
			43	33	1	8	1	
8	E	1	Total	C	N	O	P	0
			34	24	1	8	1	
8	F	1	Total	C	N	O	P	0
			50	40	1	8	1	
8	F	1	Total	C	N	O	P	0
			33	23	1	8	1	
8	a	1	Total	C	N	O	P	0
			30	20	1	8	1	
8	a	1	Total	C	N	O	P	0
			34	24	1	8	1	
8	a	1	Total	C	N	O	P	0
			43	33	1	8	1	
8	a	1	Total	C	N	O	P	0
			40	30	1	8	1	
8	a	1	Total	C	N	O	P	0
			47	37	1	8	1	
8	a	1	Total	C	N	O	P	0
			34	24	1	8	1	
8	a	1	Total	C	N	O	P	0
			47	37	1	8	1	
8	d	1	Total	C	N	O	P	0
			34	24	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
8	d	1	Total	C	N	O	P	0
			39	29	1	8	1	
8	d	1	Total	C	N	O	P	0
			43	33	1	8	1	
8	f	1	Total	C	N	O	P	0
			50	40	1	8	1	
8	f	1	Total	C	N	O	P	0
			33	23	1	8	1	

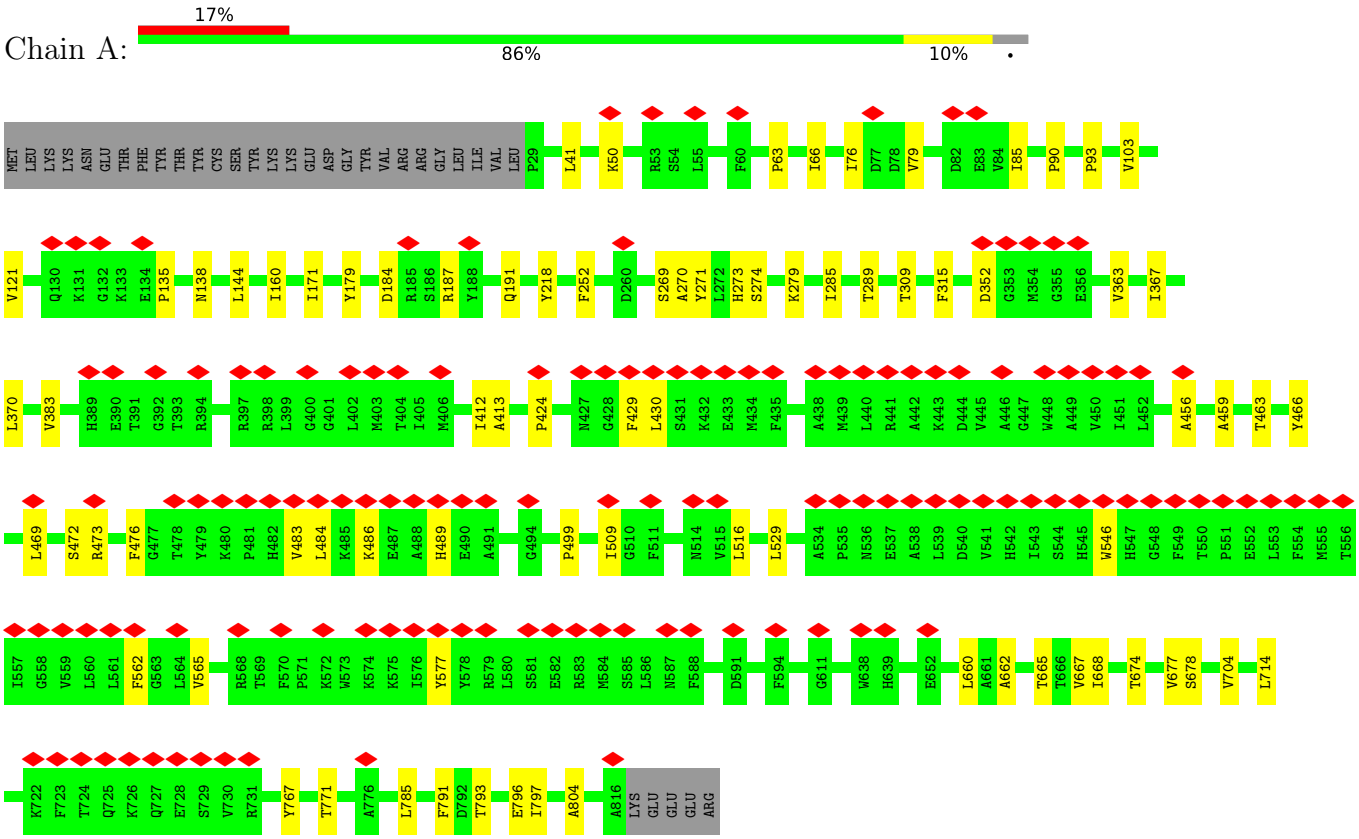
- Molecule 9 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
9	A	1	Total	K	0
			1	1	
9	C	1	Total	K	0
			1	1	
9	a	1	Total	K	0
			1	1	
9	c	1	Total	K	0
			1	1	

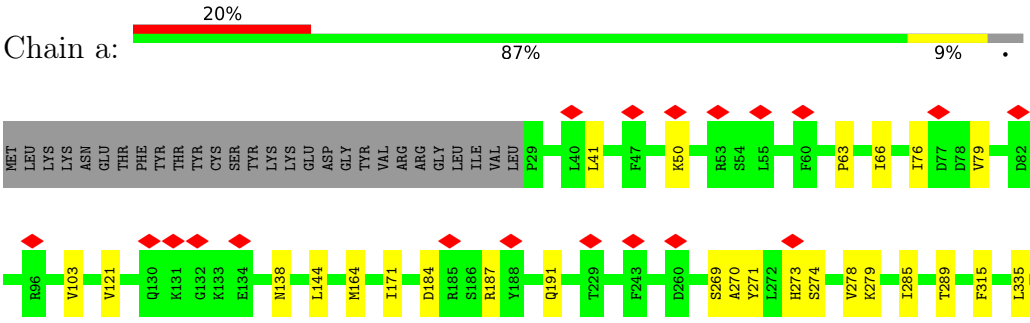
3 Residue-property plots (i)

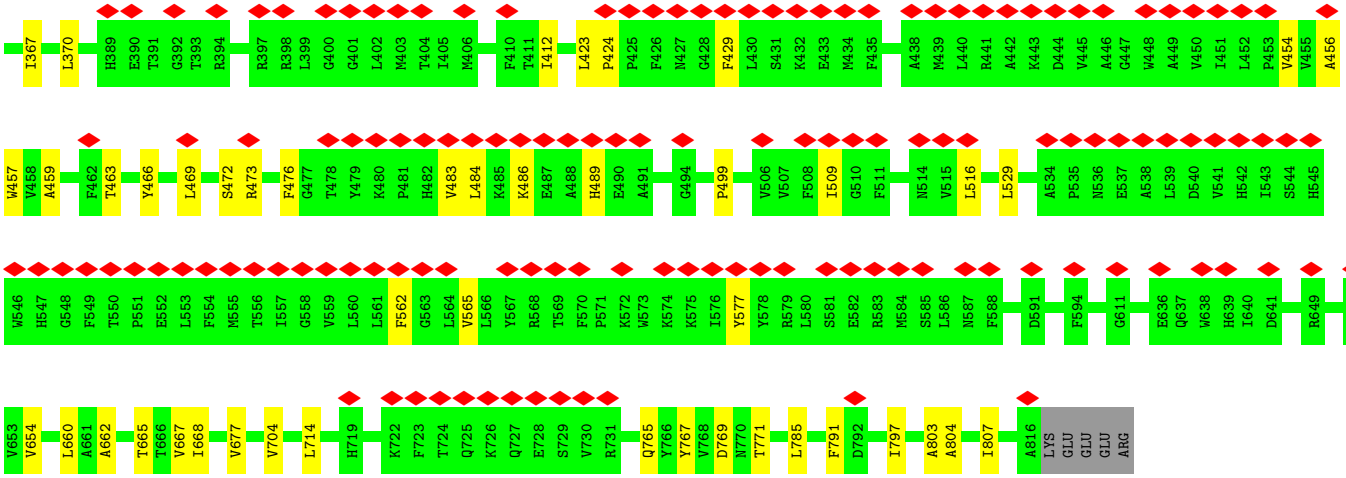
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Multisubunit Na+/H+ antiporter, A subunit

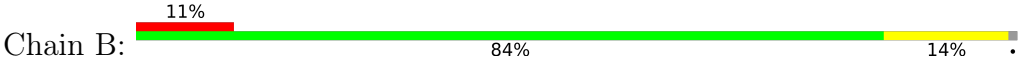


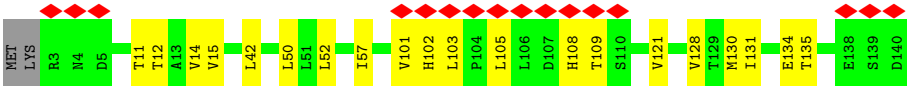
• Molecule 1: Multisubunit Na+/H+ antiporter, A subunit



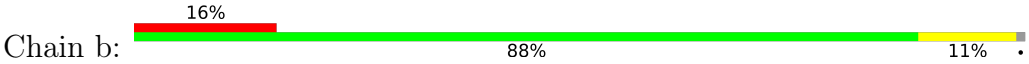


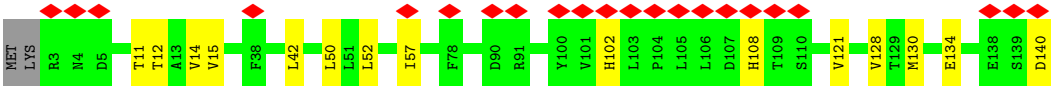
• Molecule 2: Multisubunit Na+/H+ antiporter, B subunit



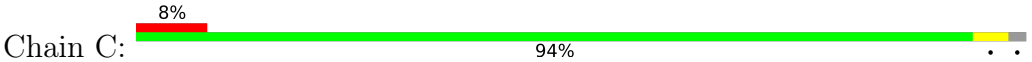


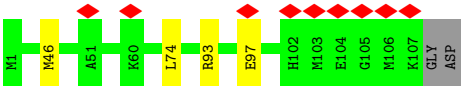
• Molecule 2: Multisubunit Na+/H+ antiporter, B subunit





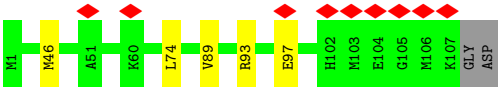
• Molecule 3: Multisubunit Na+/H+ antiporter, C subunit



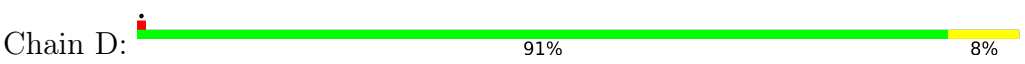


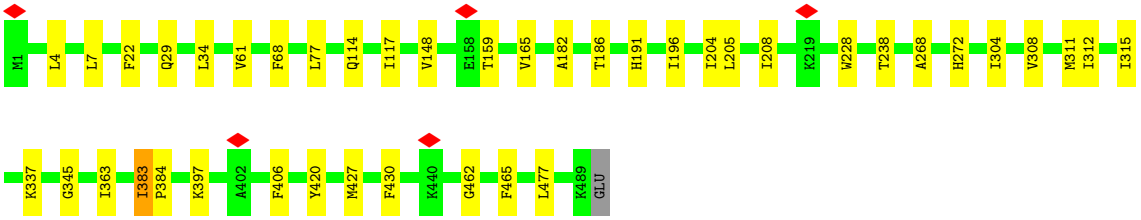
• Molecule 3: Multisubunit Na+/H+ antiporter, C subunit



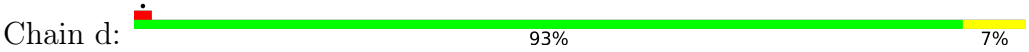


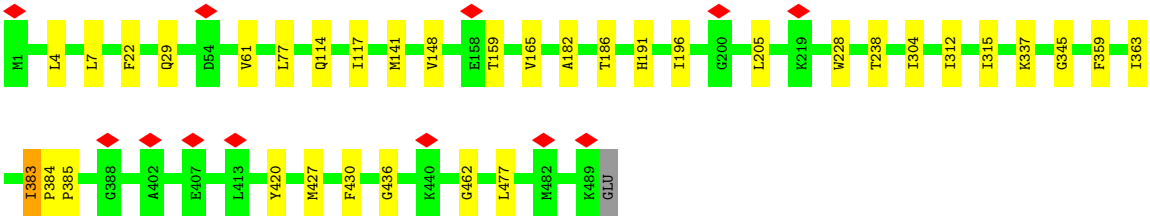
• Molecule 4: Multisubunit Na+/H+ antiporter, D subunit



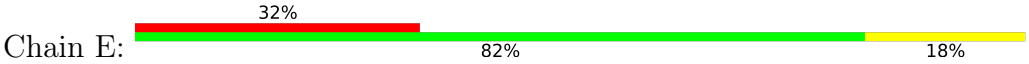


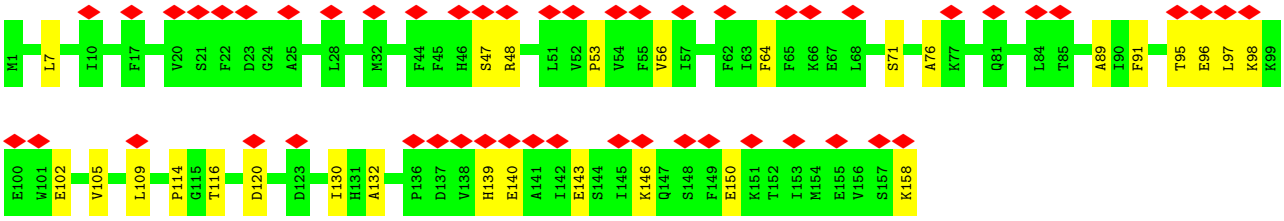
• Molecule 4: Multisubunit Na+/H+ antiporter, D subunit



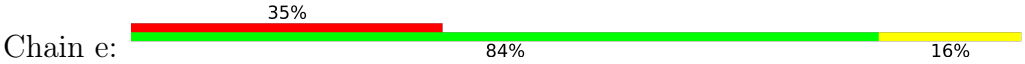


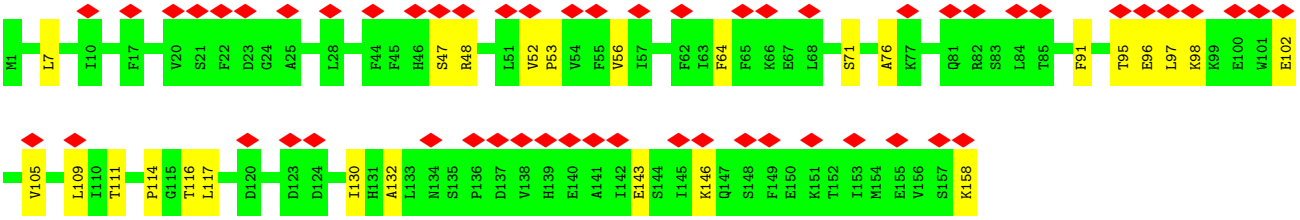
• Molecule 5: Multisubunit Na+/H+ antiporter, E subunit



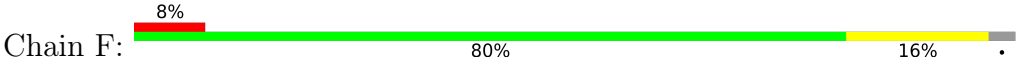


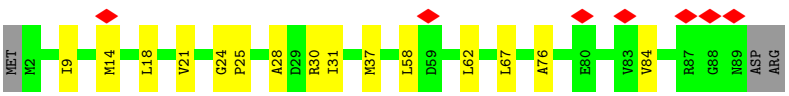
• Molecule 5: Multisubunit Na+/H+ antiporter, E subunit





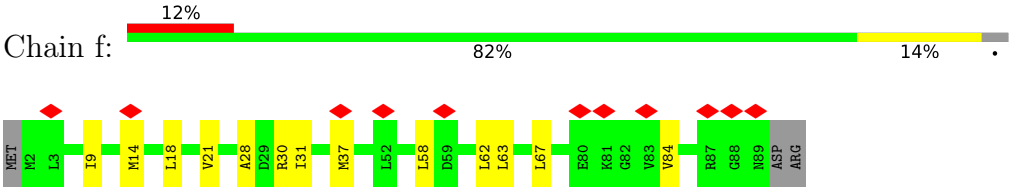
• Molecule 6: Multisubunit Na+/H+ antiporter, F subunit





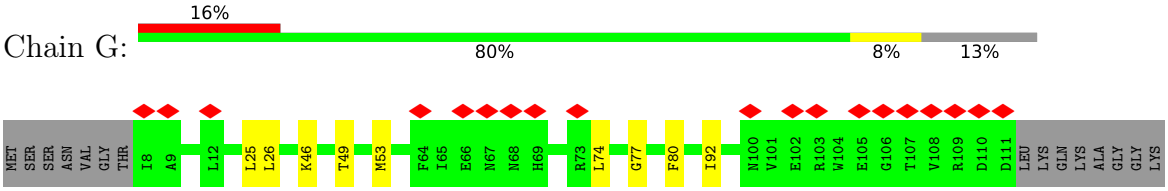
• Molecule 6: Multisubunit Na+/H+ antiporter, F subunit

Chain f:



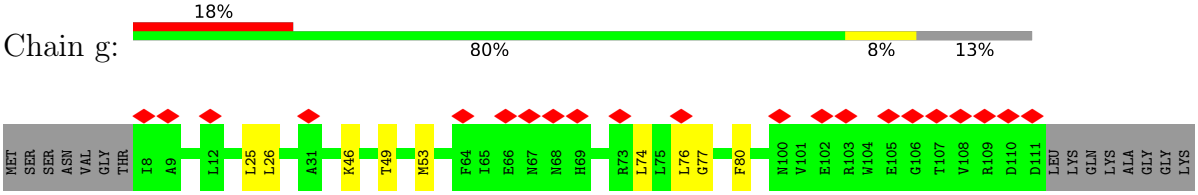
• Molecule 7: Multisubunit Na+/H+ antiporter, G subunit

Chain G:



• Molecule 7: Multisubunit Na+/H+ antiporter, G subunit

Chain g:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	285688	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 ($e^-/Å^2$)	88	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.097	Depositor
Minimum map value	-0.050	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.018	Depositor
Map size (Å)	213.36, 222.59999, 91.56	wwPDB
Map dimensions	109, 265, 254	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84, 0.84, 0.84	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: K, PTY

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	0.31	0/6402	0.61	0/8721
1	a	0.30	0/6402	0.60	0/8721
2	B	0.31	0/1097	0.69	0/1497
2	b	0.30	0/1097	0.69	0/1497
3	C	0.30	0/816	0.54	0/1105
3	c	0.29	0/816	0.52	0/1105
4	D	0.33	0/3893	0.61	1/5315 (0.0%)
4	d	0.31	0/3893	0.60	1/5315 (0.0%)
5	E	0.26	0/1304	0.55	0/1768
5	e	0.26	0/1304	0.54	0/1768
6	F	0.30	0/654	0.55	0/886
6	f	0.30	0/654	0.54	0/886
7	G	0.30	0/820	0.72	0/1117
7	g	0.29	0/820	0.70	0/1117
All	All	0.30	0/29972	0.61	2/40818 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
5	E	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	D	384	PRO	N-CA-C	5.73	117.69	110.70
4	d	384	PRO	N-CA-C	5.44	117.34	110.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	E	120	ASP	Peptide

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	6221	0	6407	53	0
1	a	6221	0	6407	52	0
2	B	1070	0	1108	13	0
2	b	1070	0	1108	11	0
3	C	802	0	866	3	0
3	c	802	0	866	4	0
4	D	3796	0	3987	26	0
4	d	3796	0	3987	21	0
5	E	1274	0	1346	17	0
5	e	1274	0	1346	16	0
6	F	648	0	717	12	0
6	f	648	0	717	12	0
7	G	804	0	837	8	0
7	g	804	0	837	8	0
8	A	275	0	373	8	0
8	B	34	0	41	2	0
8	D	116	0	154	4	0
8	E	34	0	41	2	0
8	F	83	0	118	5	0
8	a	275	0	373	9	0
8	d	116	0	154	1	0
8	f	83	0	118	5	0
9	A	1	0	0	0	0
9	C	1	0	0	0	0
9	a	1	0	0	0	0
9	c	1	0	0	0	0
All	All	30250	0	31908	224	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 224 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:270:ALA:O	1:a:274:SER:HB2	1.96	0.66
1:A:270:ALA:O	1:A:274:SER:HB2	2.00	0.61
5:E:95:THR:HG22	5:E:97:LEU:H	1.65	0.61
5:e:95:THR:HG22	5:e:97:LEU:H	1.66	0.60
2:B:102:HIS:HB3	2:B:108:HIS:H	1.66	0.60

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	786/821 (96%)	752 (96%)	34 (4%)	0	100	100
1	a	786/821 (96%)	746 (95%)	40 (5%)	0	100	100
2	B	136/140 (97%)	128 (94%)	8 (6%)	0	100	100
2	b	136/140 (97%)	130 (96%)	6 (4%)	0	100	100
3	C	105/109 (96%)	102 (97%)	3 (3%)	0	100	100
3	c	105/109 (96%)	102 (97%)	3 (3%)	0	100	100
4	D	487/490 (99%)	469 (96%)	18 (4%)	0	100	100
4	d	487/490 (99%)	470 (96%)	17 (4%)	0	100	100
5	E	156/158 (99%)	148 (95%)	8 (5%)	0	100	100
5	e	156/158 (99%)	148 (95%)	8 (5%)	0	100	100
6	F	86/91 (94%)	82 (95%)	4 (5%)	0	100	100
6	f	86/91 (94%)	83 (96%)	3 (4%)	0	100	100
7	G	102/119 (86%)	95 (93%)	7 (7%)	0	100	100
7	g	102/119 (86%)	95 (93%)	7 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	3716/3856 (96%)	3550 (96%)	166 (4%)	0	100 100

There are no Ramachandran outliers to report.

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	A	659/690 (96%)	658 (100%)	1 (0%)	87 92
1	a	659/690 (96%)	659 (100%)	0	100 100
2	B	116/118 (98%)	116 (100%)	0	100 100
2	b	116/118 (98%)	116 (100%)	0	100 100
3	C	85/86 (99%)	85 (100%)	0	100 100
3	c	85/86 (99%)	85 (100%)	0	100 100
4	D	409/411 (100%)	408 (100%)	1 (0%)	87 92
4	d	409/411 (100%)	408 (100%)	1 (0%)	87 92
5	E	143/143 (100%)	143 (100%)	0	100 100
5	e	143/143 (100%)	143 (100%)	0	100 100
6	F	69/72 (96%)	69 (100%)	0	100 100
6	f	69/72 (96%)	69 (100%)	0	100 100
7	G	86/97 (89%)	86 (100%)	0	100 100
7	g	86/97 (89%)	86 (100%)	0	100 100
All	All	3134/3234 (97%)	3131 (100%)	3 (0%)	87 94

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	160	ILE
4	D	383	ILE
4	d	383	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
4	d	266	HIS
4	d	428	ASN
4	D	155	GLN
4	D	57	GLN
5	e	87	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 30 ligands modelled in this entry, 4 are monoatomic - leaving 26 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	$\#\|Z\| > 2$
8	PTY	d	503	-	42,42,49	0.36	0	45,47,54	0.53	1 (2%)
8	PTY	D	501	-	33,33,49	0.33	0	36,38,54	0.36	0
8	PTY	F	1801	-	49,49,49	0.30	0	52,54,54	0.48	1 (1%)
8	PTY	a	906	-	33,33,49	1.10	3 (9%)	36,38,54	0.60	1 (2%)
8	PTY	f	1801	-	49,49,49	0.29	0	52,54,54	0.45	0
8	PTY	a	907	-	46,46,49	0.32	0	49,51,54	0.52	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
8	PTY	A	903	-	42,42,49	0.33	0	45,47,54	0.28	0
8	PTY	a	902	-	33,33,49	1.06	3 (9%)	36,38,54	0.31	0
8	PTY	a	904	-	39,39,49	0.35	0	42,44,54	0.38	0
8	PTY	A	902	-	33,33,49	1.06	3 (9%)	36,38,54	0.32	0
8	PTY	B	201	-	33,33,49	1.10	3 (9%)	36,38,54	0.57	0
8	PTY	D	503	-	42,42,49	0.35	0	45,47,54	0.53	1 (2%)
8	PTY	f	1802	-	32,32,49	0.36	0	35,37,54	0.32	0
8	PTY	a	903	-	42,42,49	0.33	0	45,47,54	0.29	0
8	PTY	F	1802	-	32,32,49	0.36	0	35,37,54	0.32	0
8	PTY	d	501	-	33,33,49	0.33	0	36,38,54	0.35	0
8	PTY	a	905	-	46,46,49	0.30	0	49,51,54	0.26	0
8	PTY	A	907	-	46,46,49	0.32	0	49,51,54	0.52	1 (2%)
8	PTY	E	201	-	33,33,49	1.09	3 (9%)	36,38,54	0.58	0
8	PTY	A	901	-	29,29,49	0.36	0	32,34,54	0.31	0
8	PTY	A	904	-	39,39,49	0.34	0	42,44,54	0.40	0
8	PTY	A	906	-	33,33,49	1.09	3 (9%)	36,38,54	0.61	1 (2%)
8	PTY	A	905	-	46,46,49	0.30	0	49,51,54	0.26	0
8	PTY	D	502	-	38,38,49	0.31	0	41,43,54	0.32	0
8	PTY	a	901	-	29,29,49	0.37	0	32,34,54	0.30	0
8	PTY	d	502	-	38,38,49	0.32	0	41,43,54	0.31	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	PTY	d	503	-	-	12/46/46/53	-
8	PTY	D	501	-	-	9/37/37/53	-
8	PTY	F	1801	-	-	13/53/53/53	-
8	PTY	a	906	-	-	10/37/37/53	-
8	PTY	f	1801	-	-	14/53/53/53	-
8	PTY	a	907	-	-	9/50/50/53	-
8	PTY	A	903	-	-	8/46/46/53	-
8	PTY	a	902	-	-	5/37/37/53	-
8	PTY	a	904	-	-	11/43/43/53	-
8	PTY	A	902	-	-	8/37/37/53	-
8	PTY	B	201	-	-	13/37/37/53	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	PTY	D	503	-	-	11/46/46/53	-
8	PTY	f	1802	-	-	5/36/36/53	-
8	PTY	a	903	-	-	8/46/46/53	-
8	PTY	F	1802	-	-	3/36/36/53	-
8	PTY	d	501	-	-	4/37/37/53	-
8	PTY	a	905	-	-	9/50/50/53	-
8	PTY	A	907	-	-	10/50/50/53	-
8	PTY	E	201	-	-	14/37/37/53	-
8	PTY	A	901	-	-	4/33/33/53	-
8	PTY	A	904	-	-	10/43/43/53	-
8	PTY	A	906	-	-	10/37/37/53	-
8	PTY	A	905	-	-	11/50/50/53	-
8	PTY	D	502	-	-	10/42/42/53	-
8	PTY	a	901	-	-	3/33/33/53	-
8	PTY	d	502	-	-	8/42/42/53	-

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	B	201	PTY	P1-O12	-4.14	1.36	1.55
8	A	906	PTY	P1-O12	-4.12	1.36	1.55
8	E	201	PTY	P1-O12	-4.09	1.36	1.55
8	a	906	PTY	P1-O12	-4.09	1.36	1.55
8	A	902	PTY	P1-O12	-4.03	1.36	1.55

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	F	1801	PTY	O4-C1-C6	2.24	114.86	108.40
8	d	503	PTY	C6-O7-C8	2.15	122.94	117.80
8	A	907	PTY	C6-O7-C8	2.15	122.94	117.80
8	a	907	PTY	C6-O7-C8	2.14	122.93	117.80
8	A	906	PTY	C6-O7-C8	2.14	122.92	117.80

There are no chirality outliers.

5 of 232 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	901	PTY	N1-C2-C3-O11
8	A	902	PTY	N1-C2-C3-O11
8	A	902	PTY	C5-O14-P1-O11
8	A	902	PTY	C5-O14-P1-O13
8	A	903	PTY	C5-O14-P1-O11

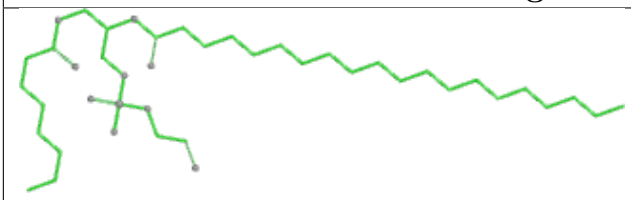
There are no ring outliers.

16 monomers are involved in 34 short contacts:

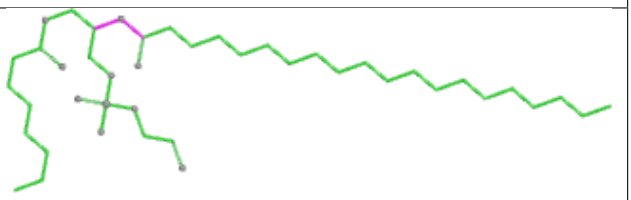
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	d	503	PTY	1	0
8	F	1801	PTY	5	0
8	f	1801	PTY	5	0
8	a	907	PTY	3	0
8	A	903	PTY	2	0
8	a	904	PTY	2	0
8	B	201	PTY	2	0
8	D	503	PTY	3	0
8	a	903	PTY	3	0
8	a	905	PTY	2	0
8	A	907	PTY	2	0
8	E	201	PTY	2	0
8	A	904	PTY	2	0
8	A	906	PTY	1	0
8	A	905	PTY	2	0
8	D	502	PTY	1	0

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 then 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.

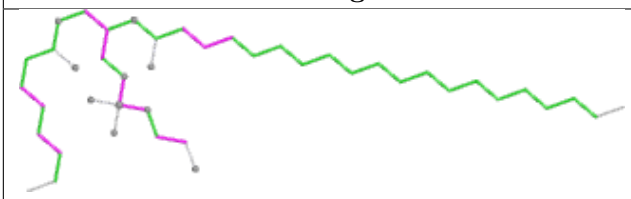
Ligand PTY d 503



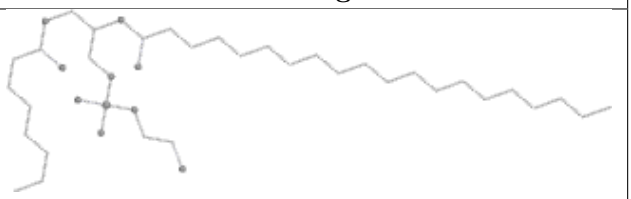
Bond lengths



Bond angles

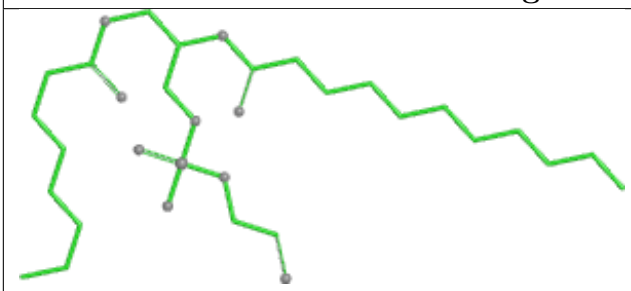


Torsions

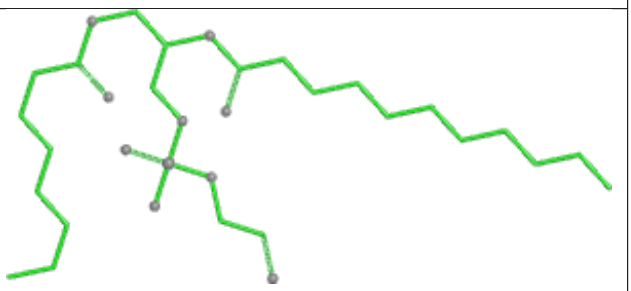


Rings

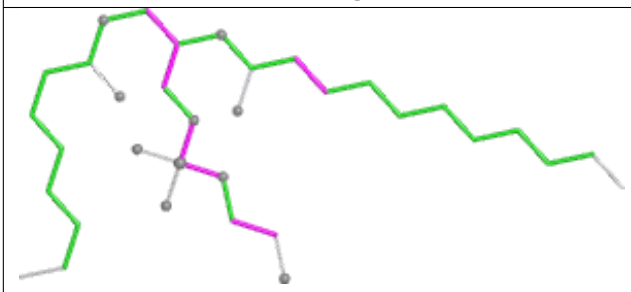
Ligand PTY D 501



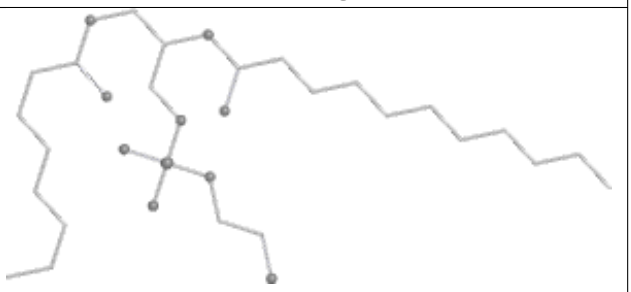
Bond lengths



Bond angles

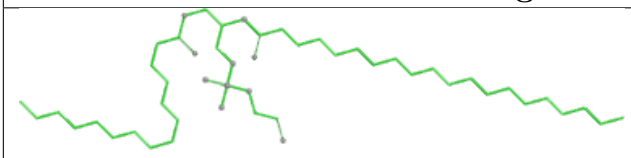


Torsions

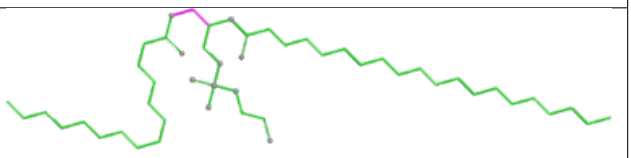


Rings

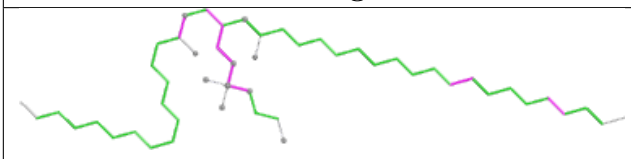
Ligand PTY F 1801



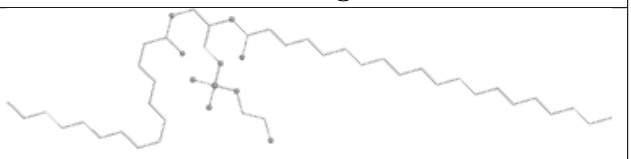
Bond lengths



Bond angles

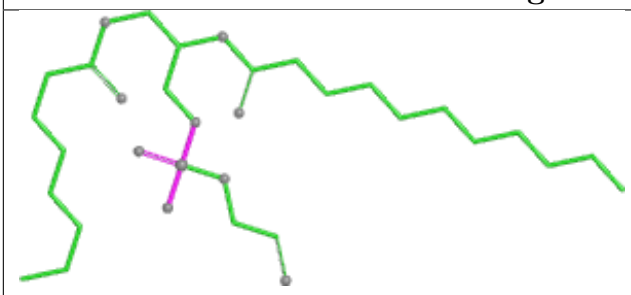


Torsions

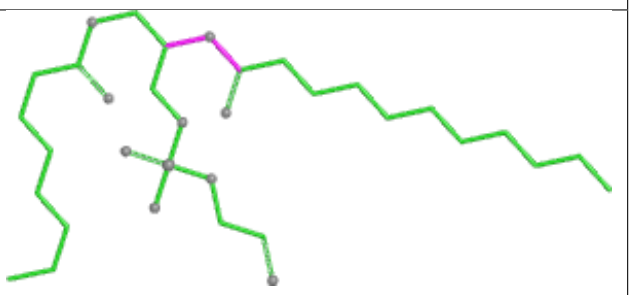


Rings

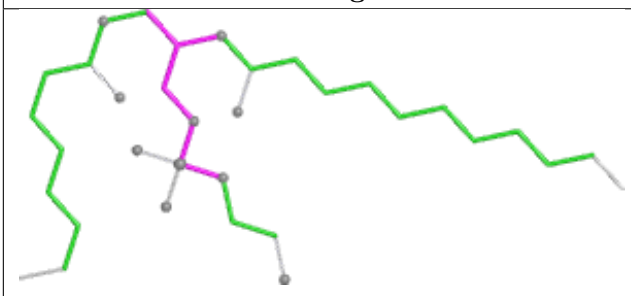
Ligand PTY a 906



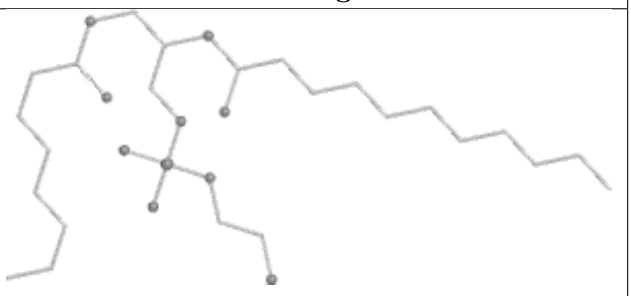
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Bond angles

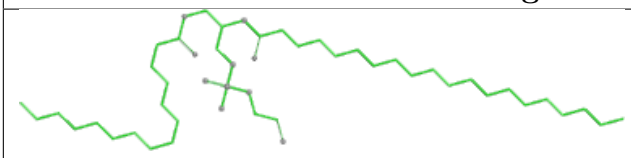


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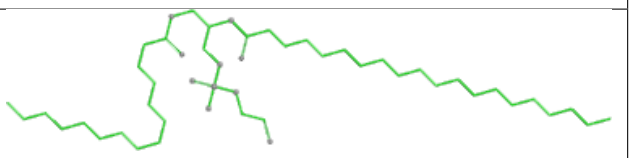


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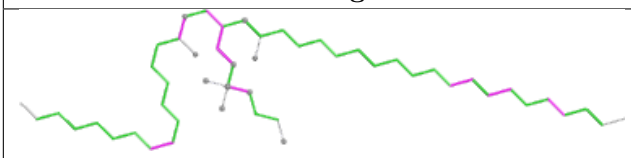
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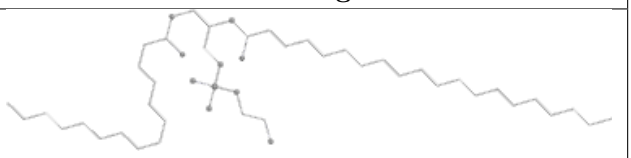
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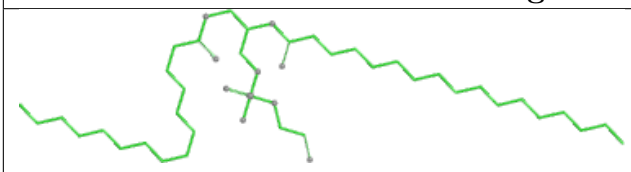


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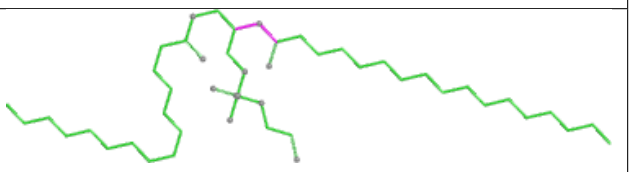


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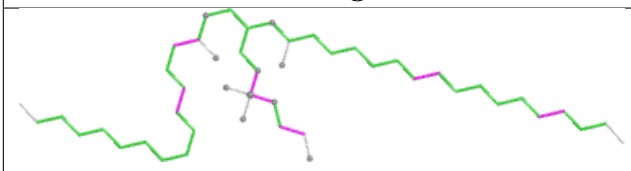
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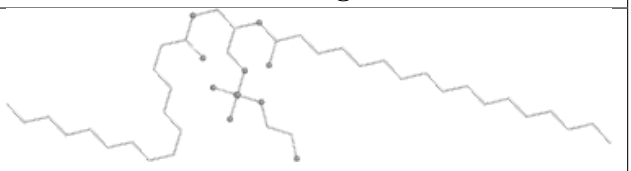
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Bond angles

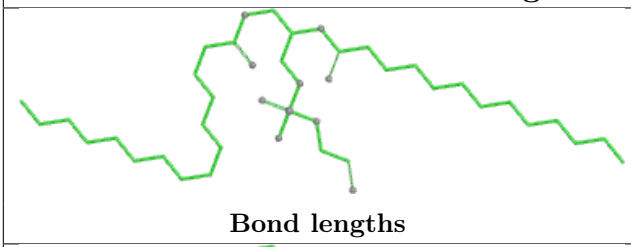


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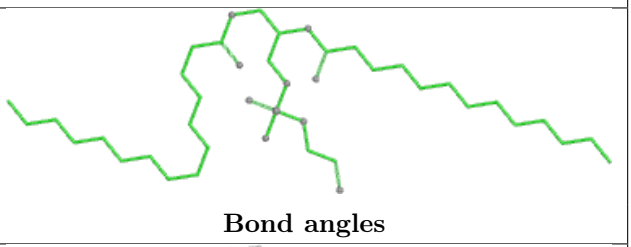


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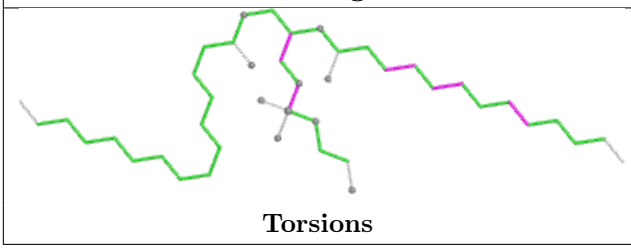
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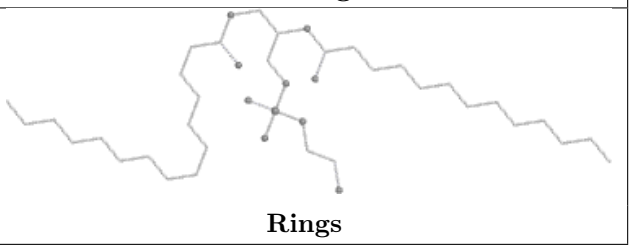
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Bond angles

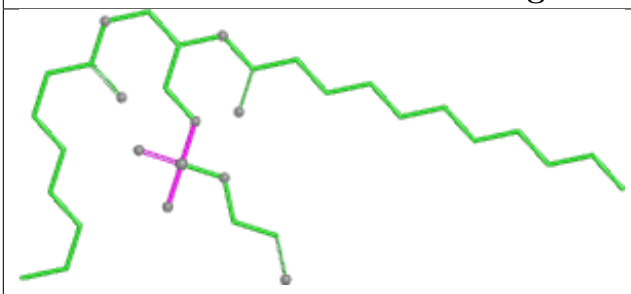


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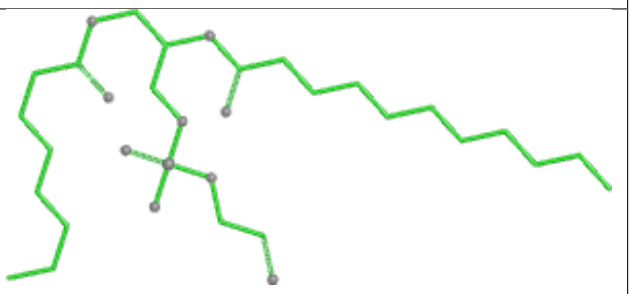


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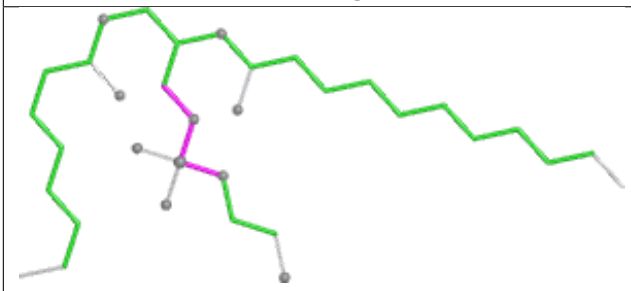
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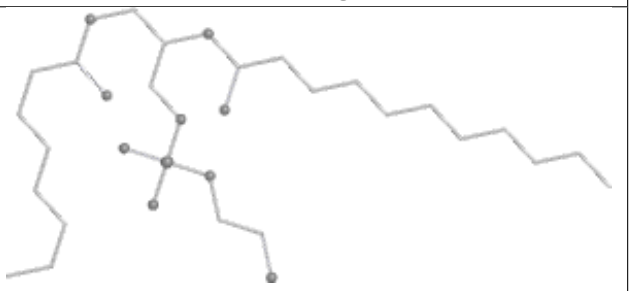
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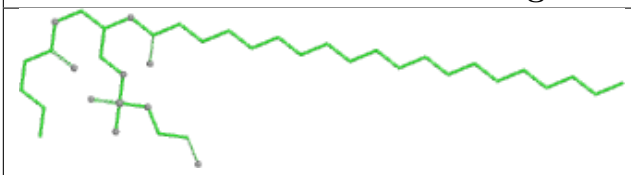


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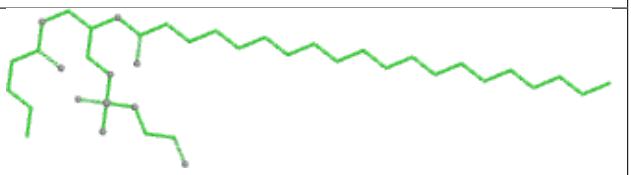


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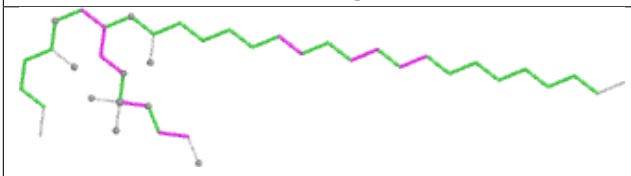
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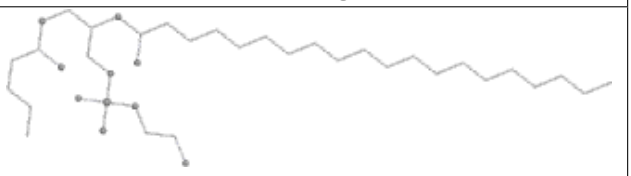
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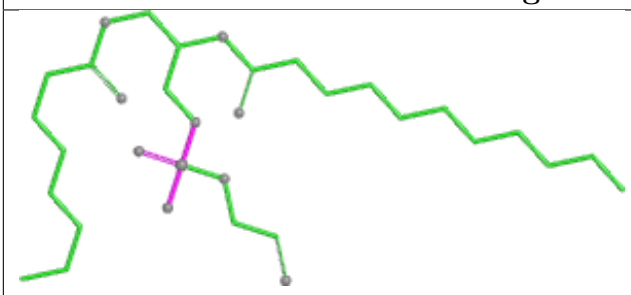


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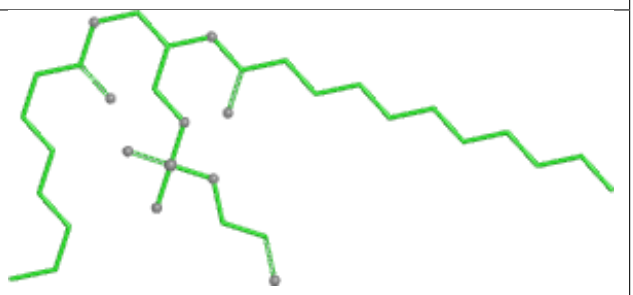


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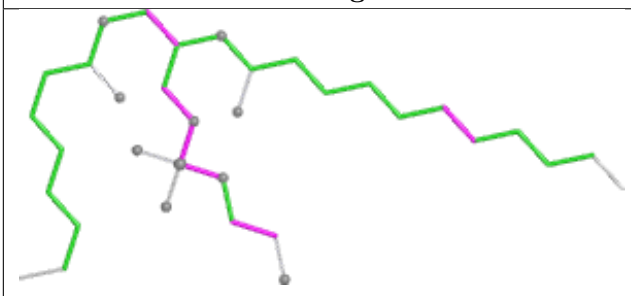
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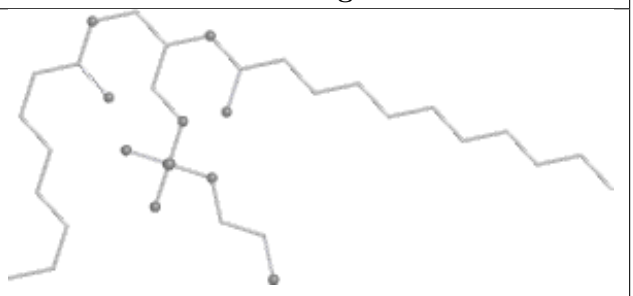
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Bond angles

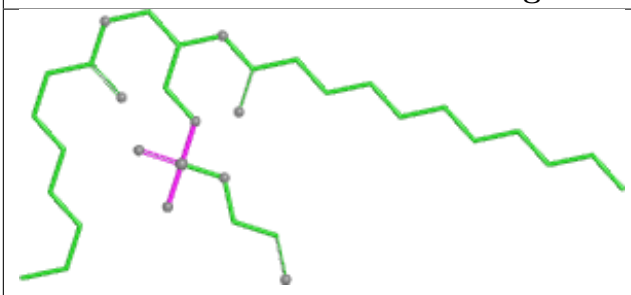


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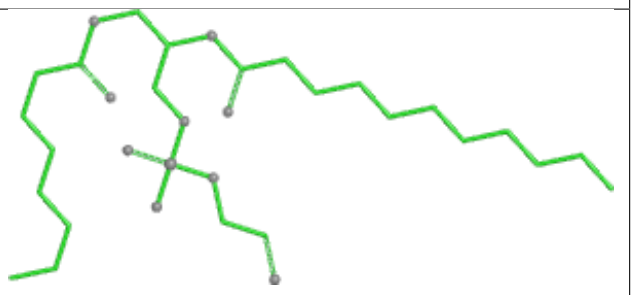


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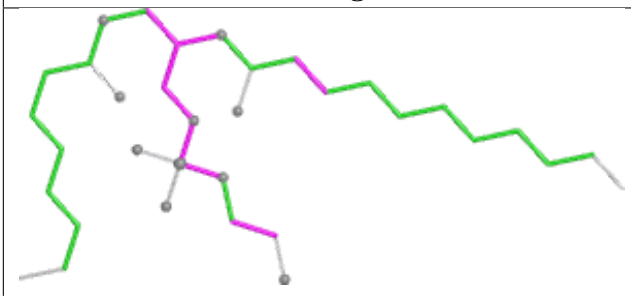
Ligand PTY B 201



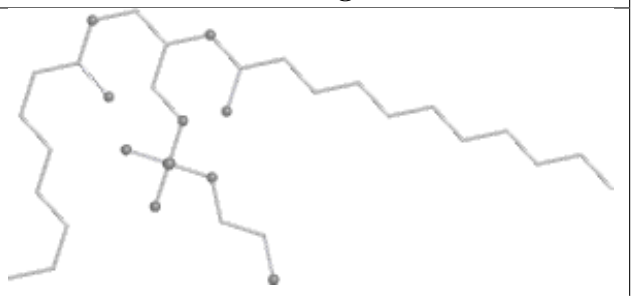
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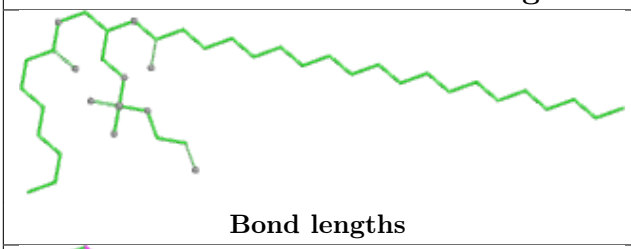


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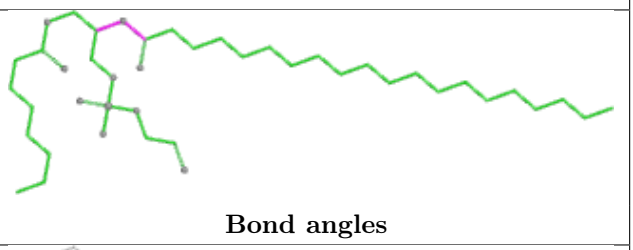


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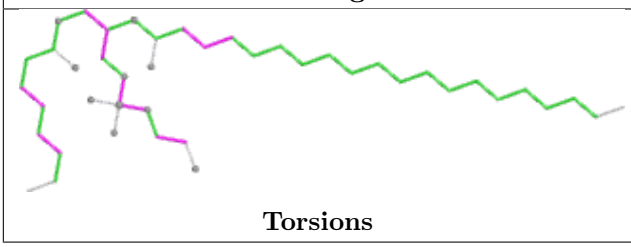
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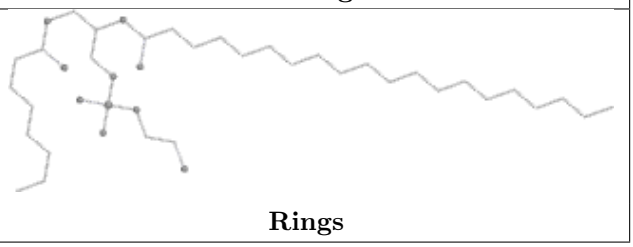
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Bond angles

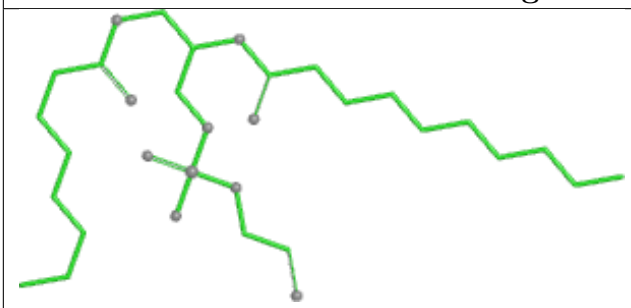


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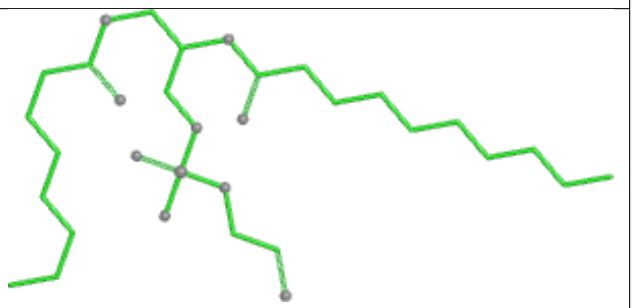


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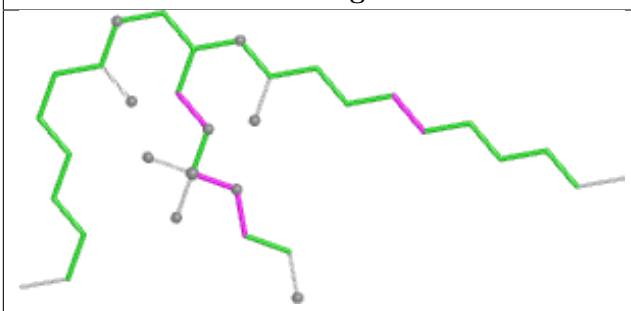
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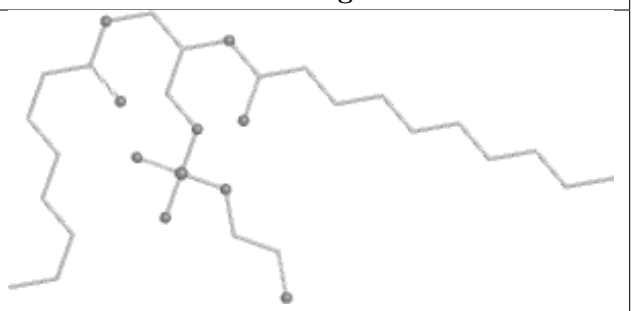
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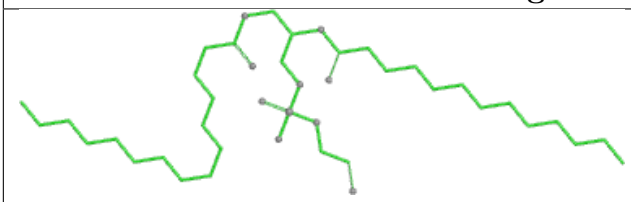


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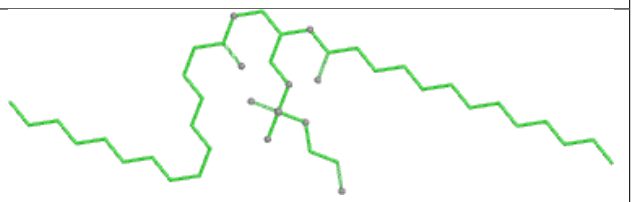


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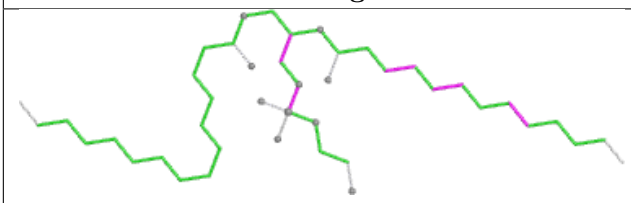
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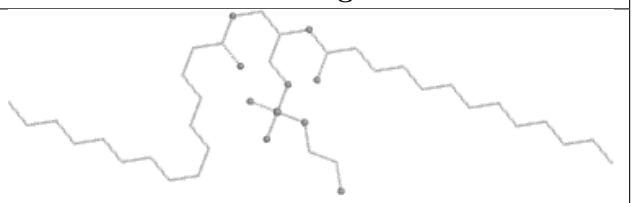
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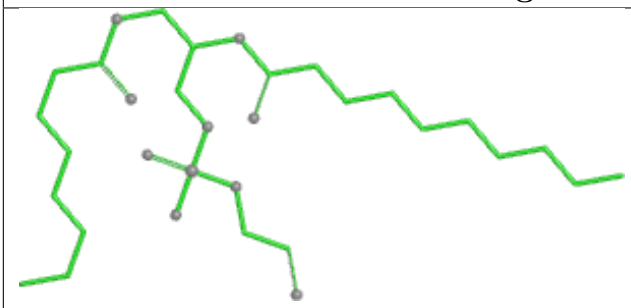


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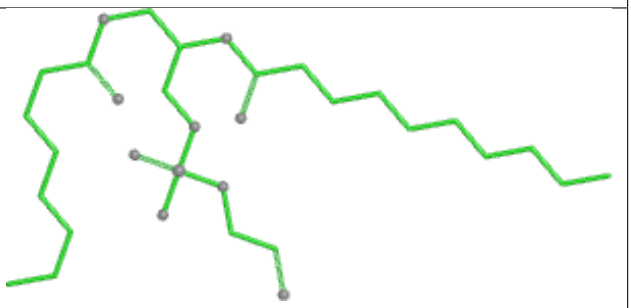


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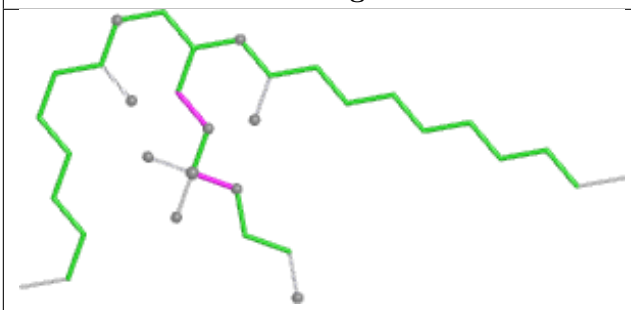
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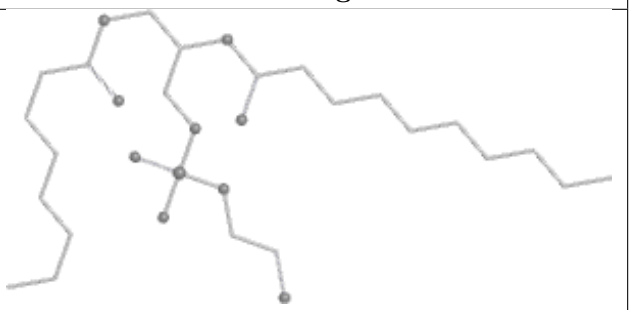
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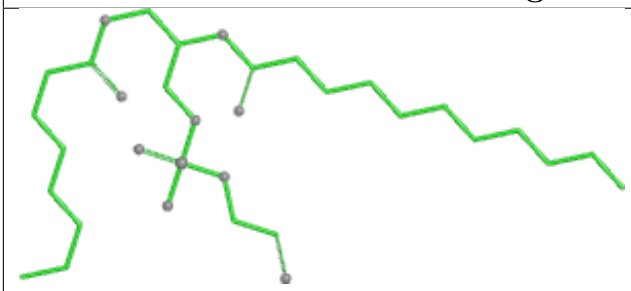


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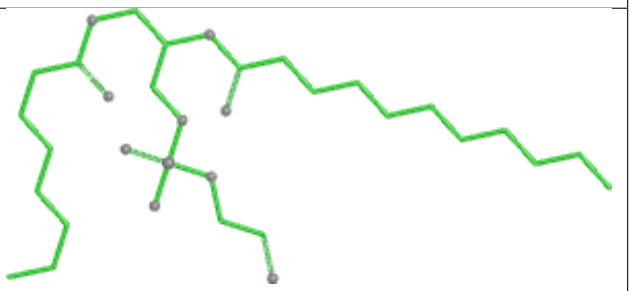


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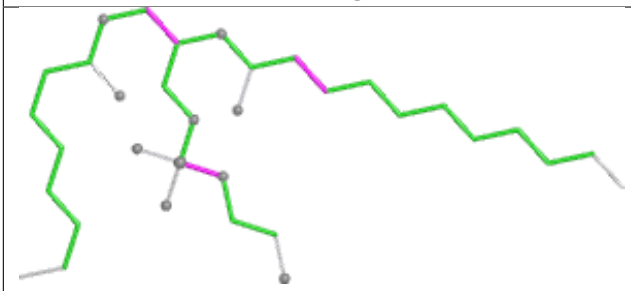
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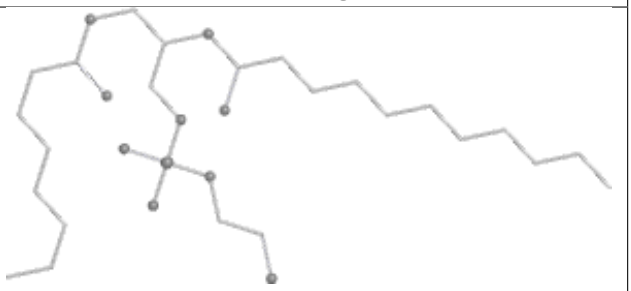
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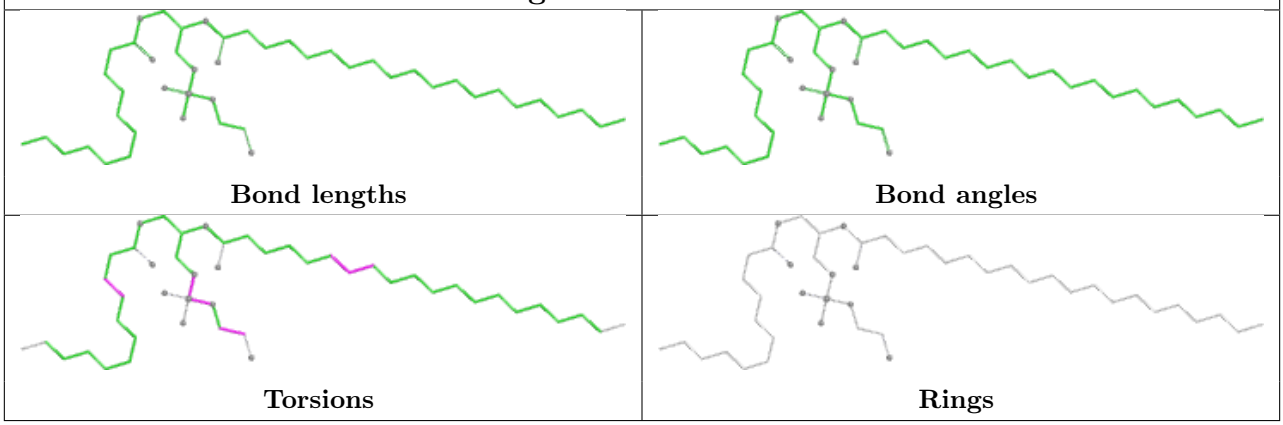


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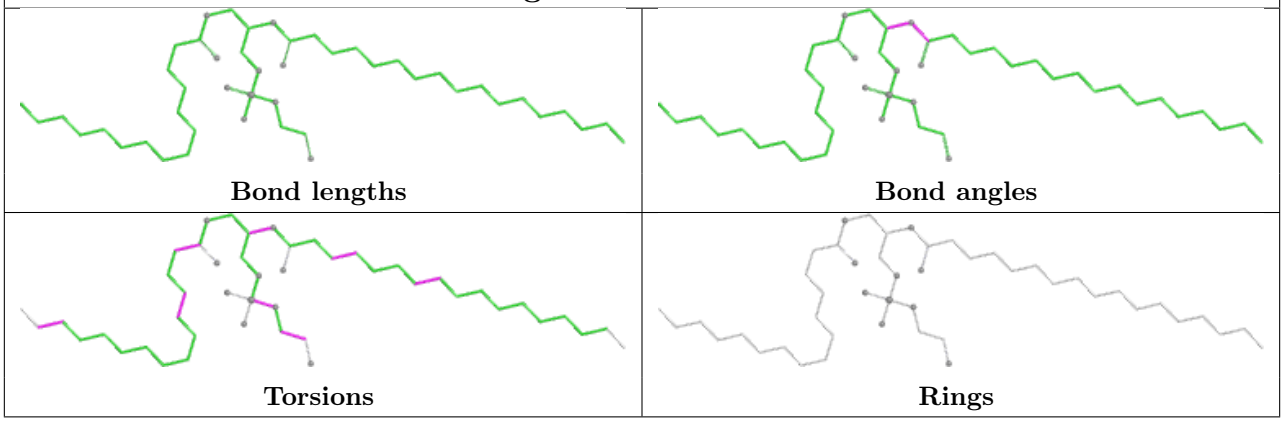


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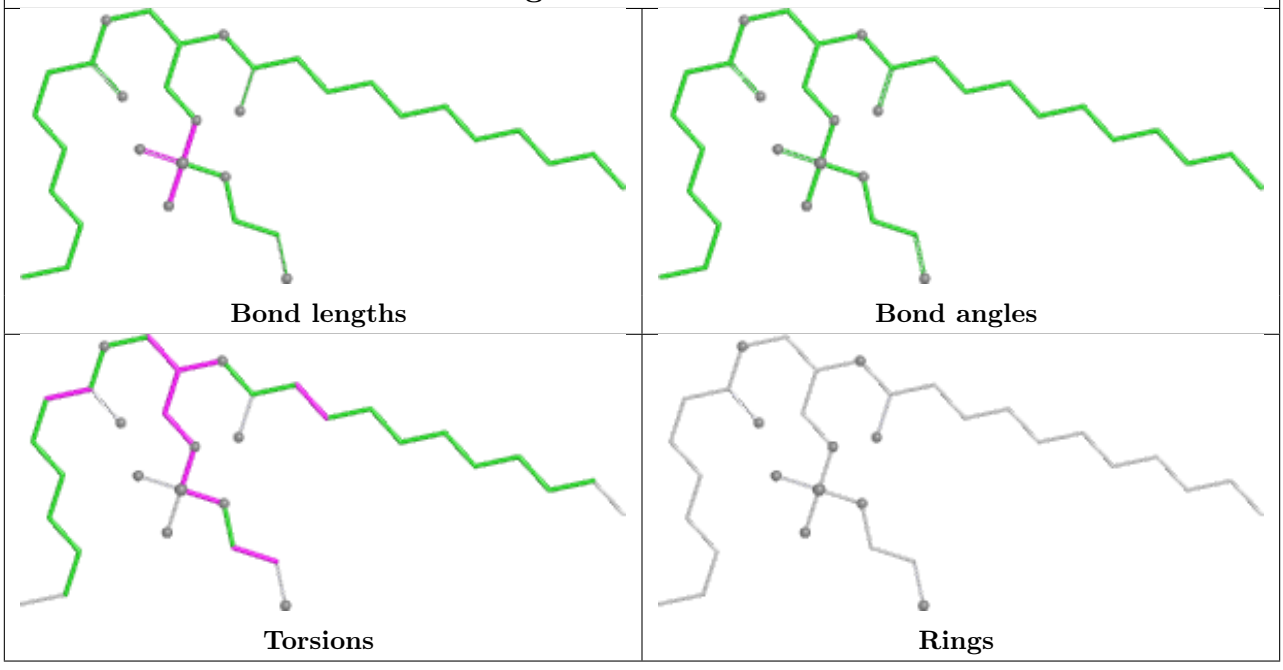
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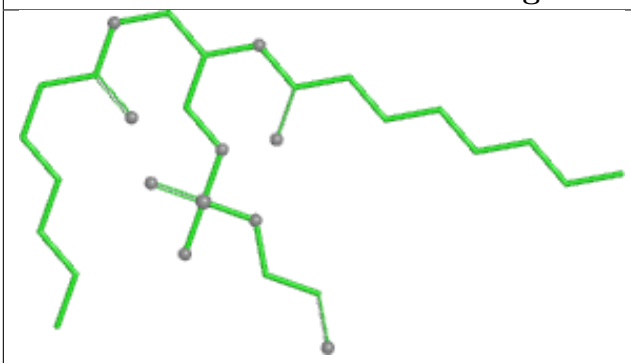
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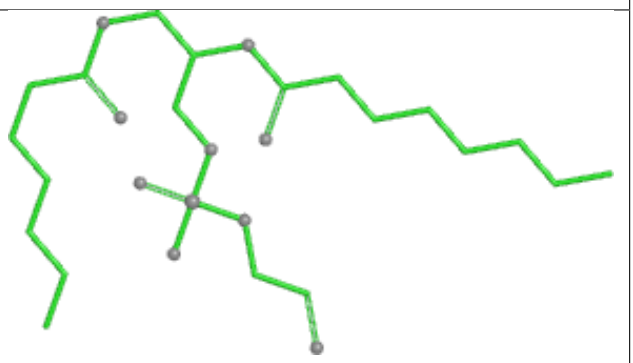
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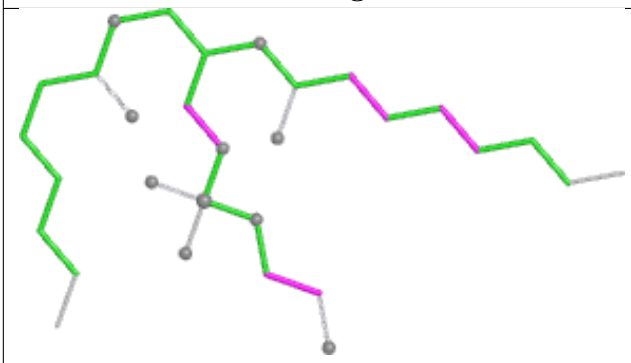
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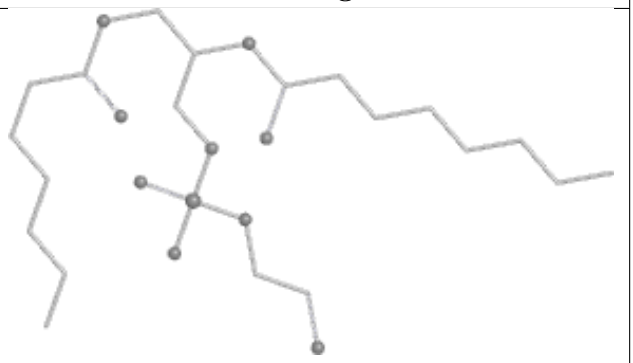
Bond lengths



Bond angles

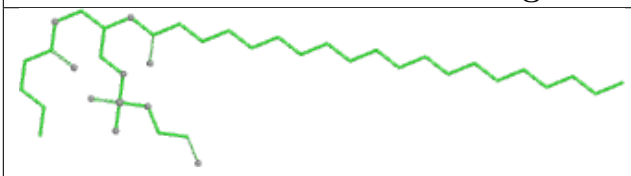


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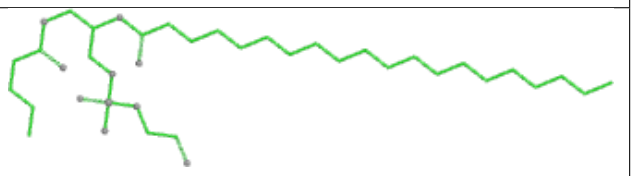


Rings

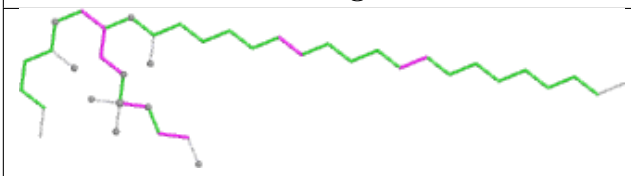
Ligand PTY A 904



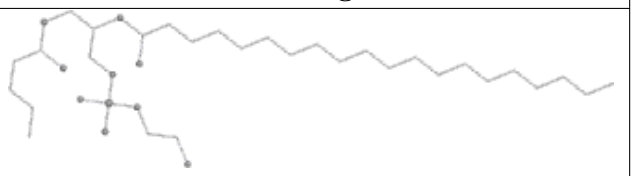
Bond lengths



Bond angles

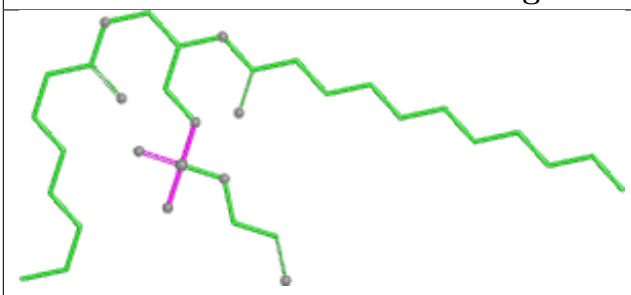


Torsions

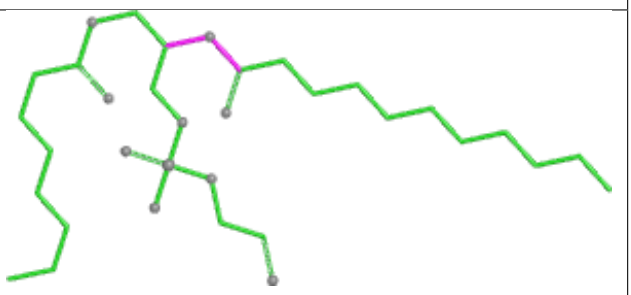


Rings

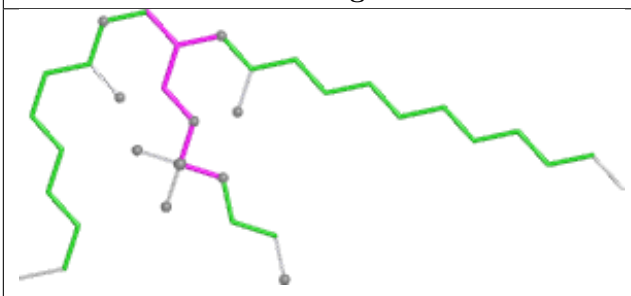
Ligand PTY A 906



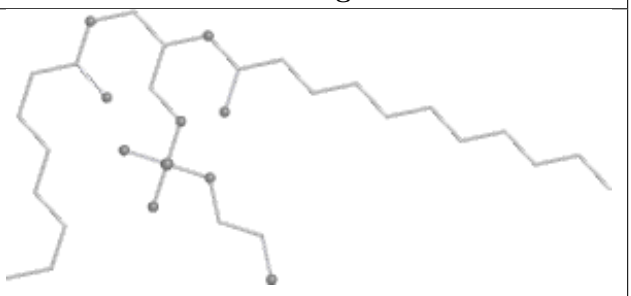
Bond lengths



Bond angles

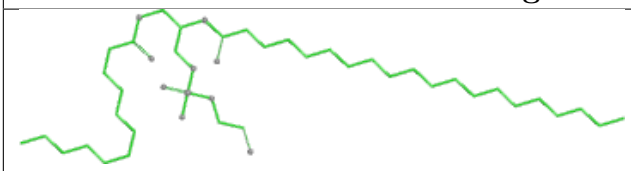


Torsions

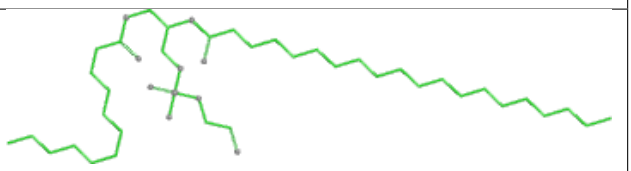


Rings

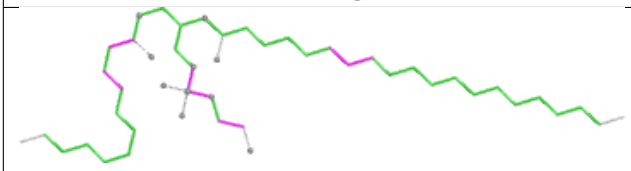
Ligand PTY A 905



Bond lengths



Bond angles

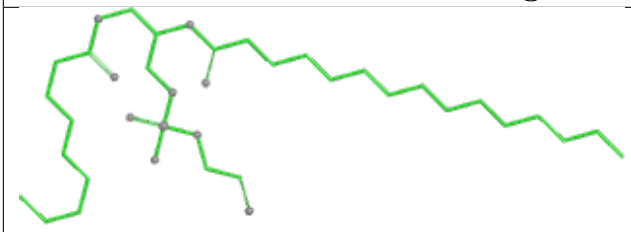


Torsions

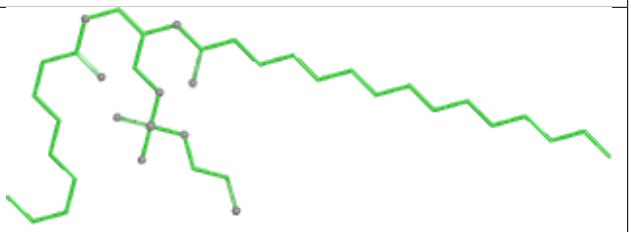


Rings

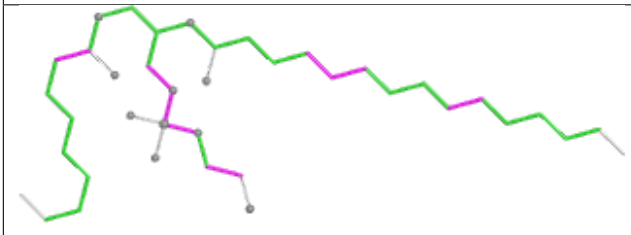
Ligand PTY D 502



Bond lengths



Bond angles

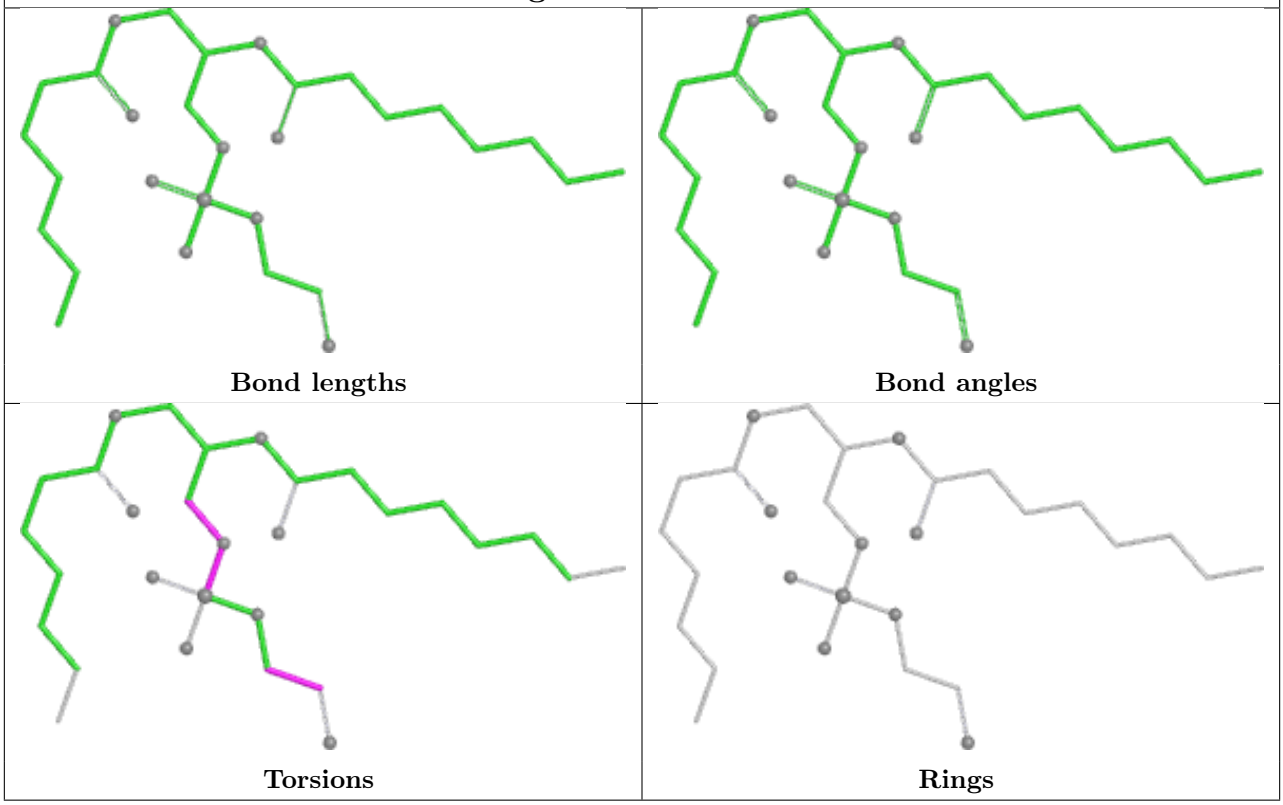


Torsions

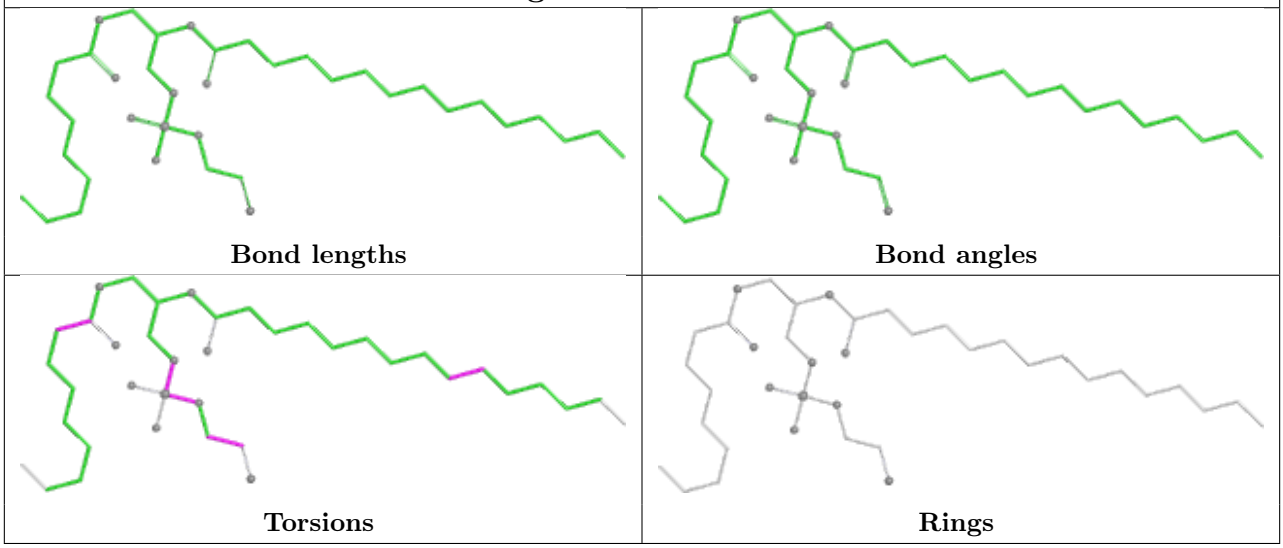


Rings

Ligand PTY a 901



Ligand PTY d 502



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.

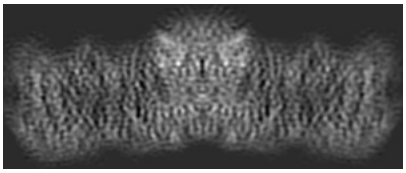
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-11027. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections

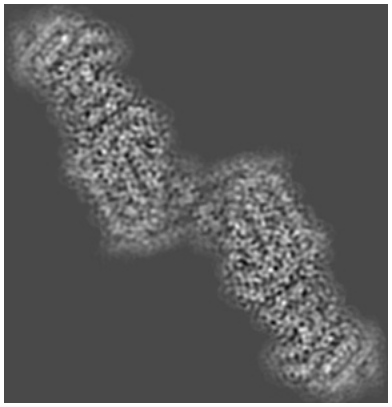
6.1.1 Primary map



X



Y



Z

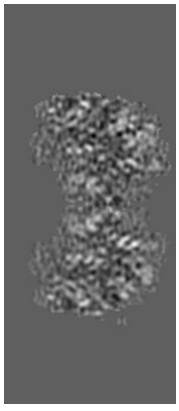
The images above show the map projected in three orthogonal directions.

6.2 Central slices

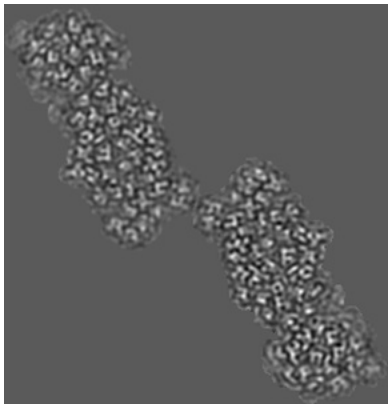
6.2.1 Primary map



X Index: 127



Y Index: 132

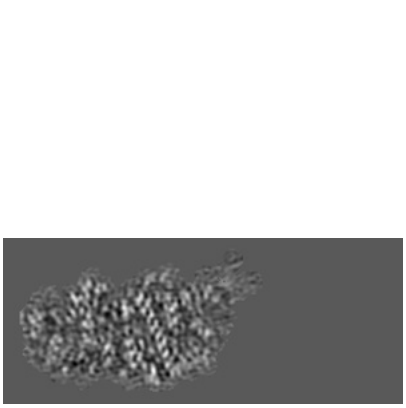


Z Index: 54

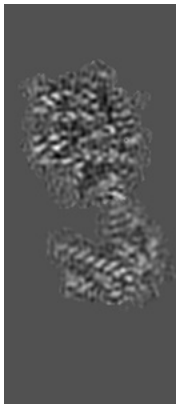
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

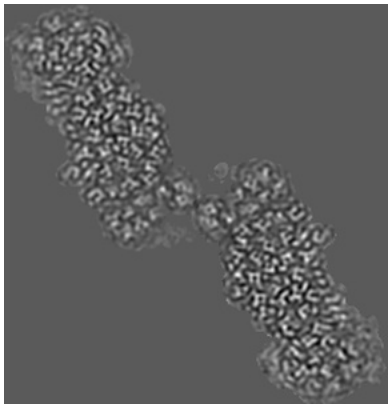
6.3.1 Primary map



X Index: 187



Y Index: 116

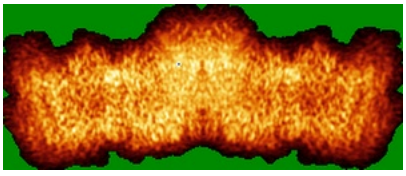


Z Index: 58

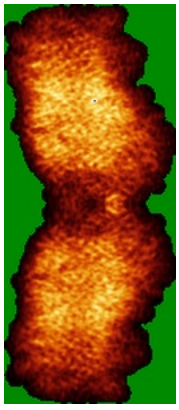
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

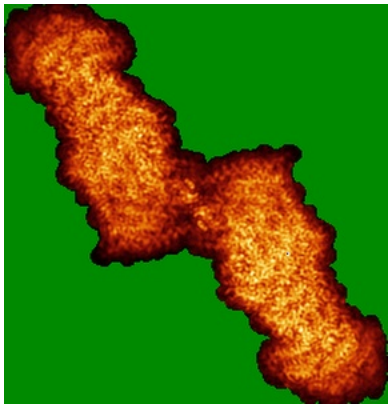
6.4.1 Primary map



X



Y



Z

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)

This section was not generated.

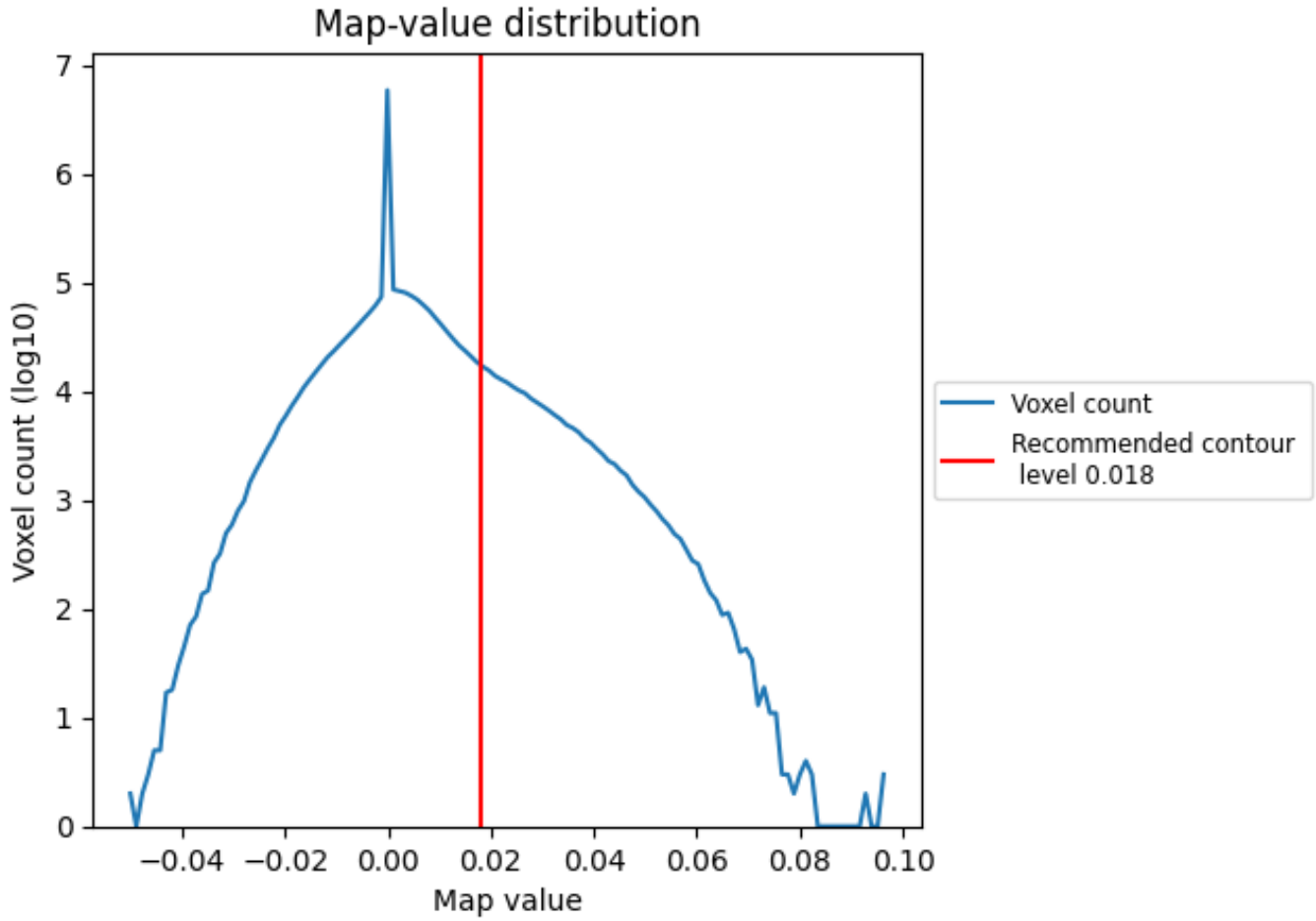
6.6 Mask visualisation (i)

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

7 Map analysis

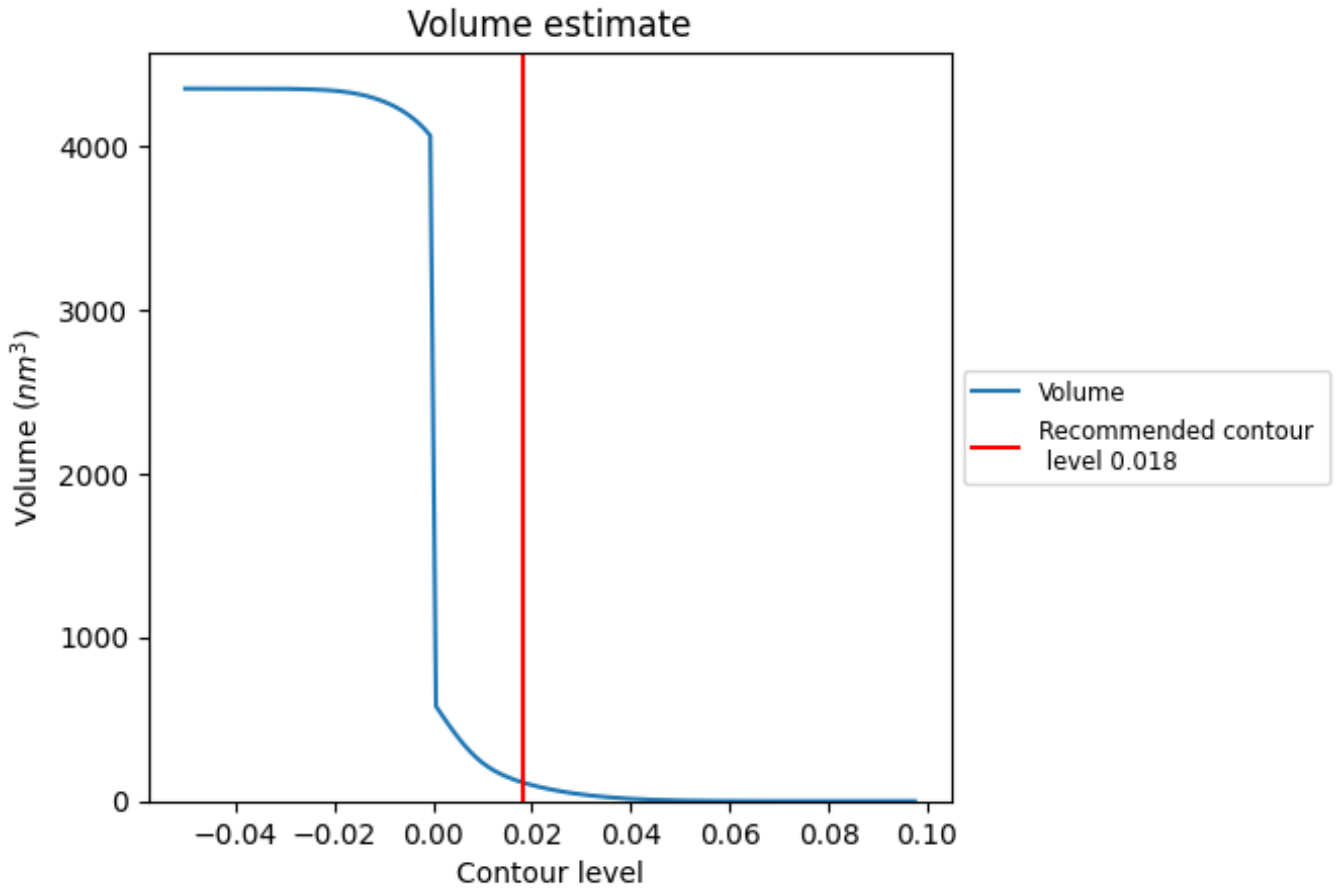
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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 115 nm^3; this corresponds to an approximate mass of 104 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.

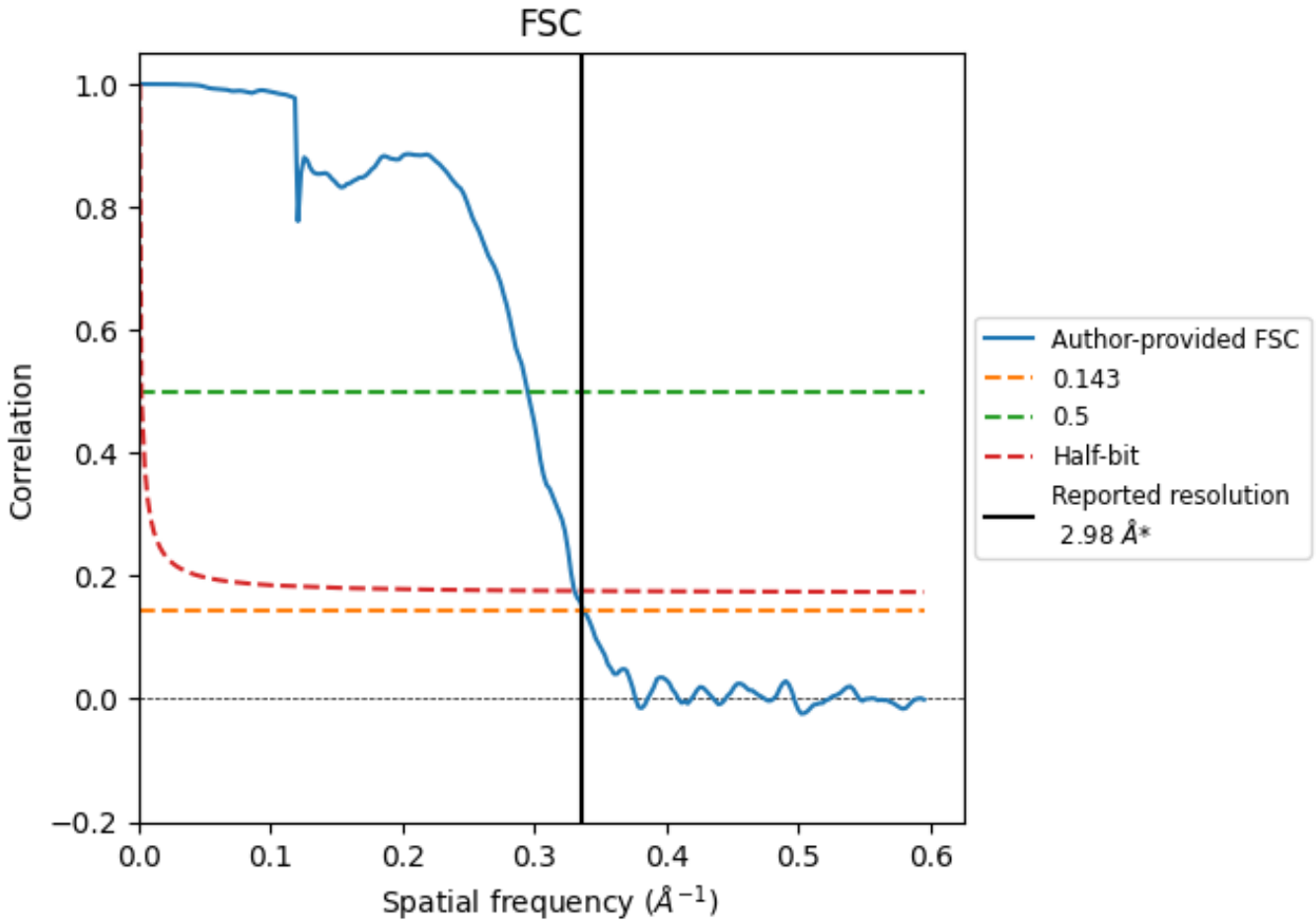
7.3 Rotationally averaged power spectrum (i)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.336 $Å^{-1}$

8.2 Resolution estimates (i)

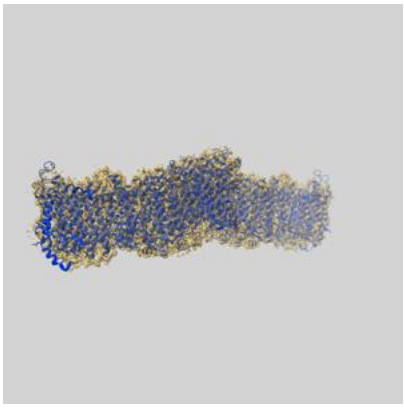
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.98	-	-
Author-provided FSC curve	2.97	3.39	3.03
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

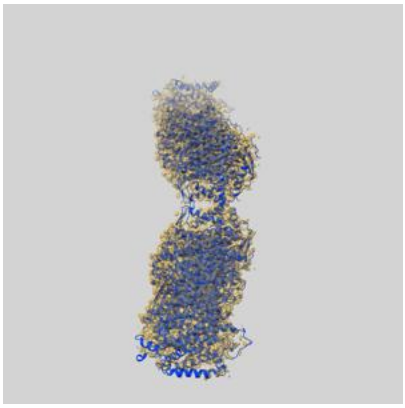
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-11027 and PDB model 6Z16. Per-residue inclusion information can be found in section 3 on page 8.

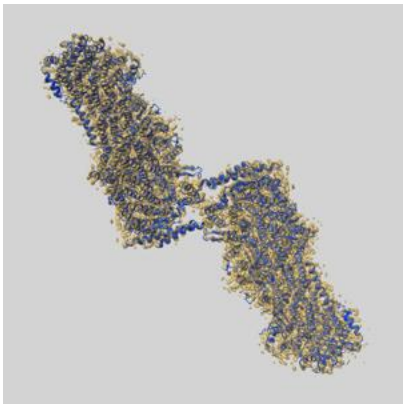
9.1 Map-model overlay



X



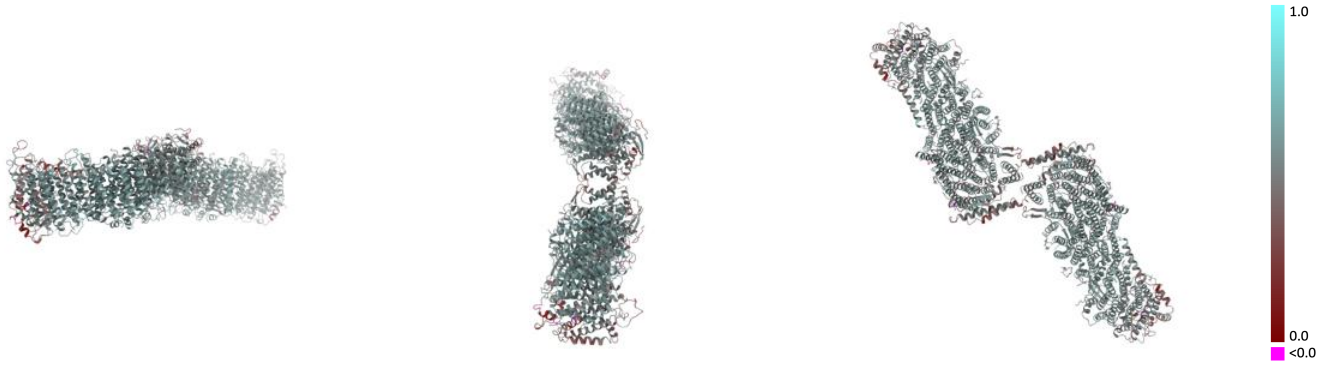
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.018 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.

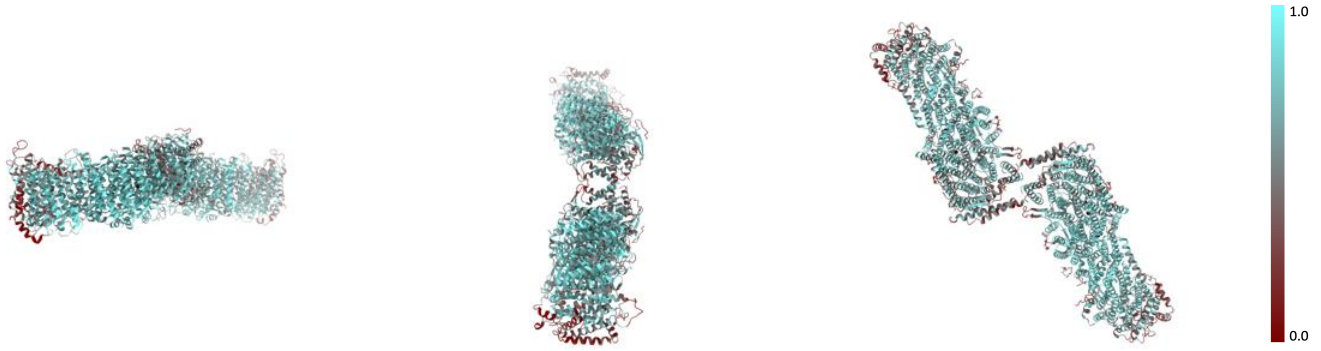
9.2 Q-score mapped to coordinate model



X Y Z

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.

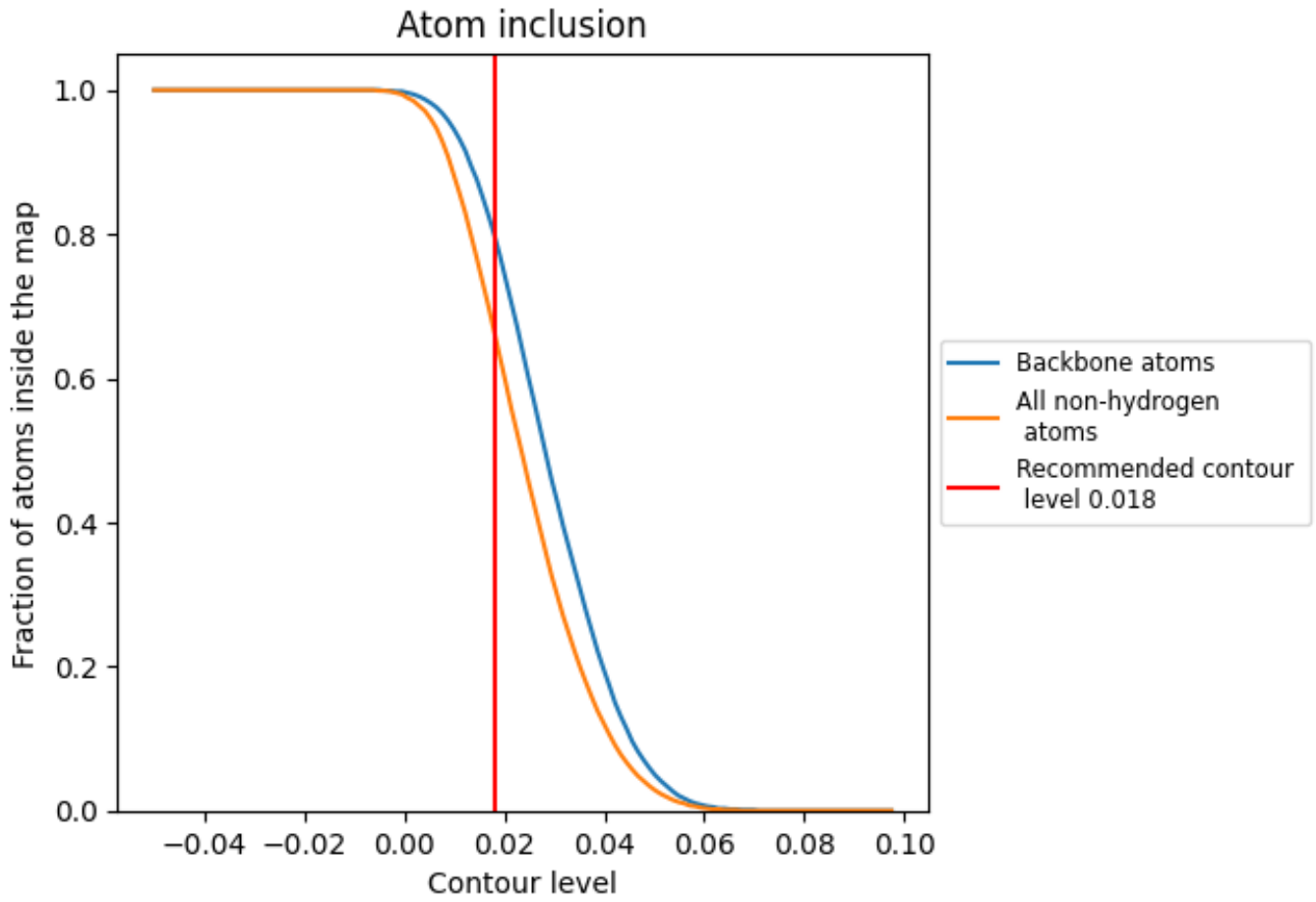
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.018).

9.4 Atom inclusion (i)



At the recommended contour level, 80% of all backbone atoms, 66% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6630	0.5230
A	0.6500	0.5090
B	0.6570	0.5220
C	0.7550	0.5610
D	0.8210	0.5740
E	0.5030	0.4670
F	0.6310	0.5290
G	0.6100	0.5010
a	0.5940	0.5020
b	0.6280	0.5160
c	0.7160	0.5540
d	0.7780	0.5690
e	0.4970	0.4610
f	0.5860	0.5200
g	0.5740	0.4920

