

Building your system

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Martinize
Insane
Backward
DAFT

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Martinize

Insane

Backward

DAFT

Vermouth/Martinize2

Polyply

TS2CG

Coby

...

Building your system

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Every simulation has a purpose

Every simulation has a start

starting structure

What to build?

- Resolution
- Organization
- Composition
- Components

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Atomistic dynamics?
Atomistic structure?

What to build?

- Resolution
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- Components

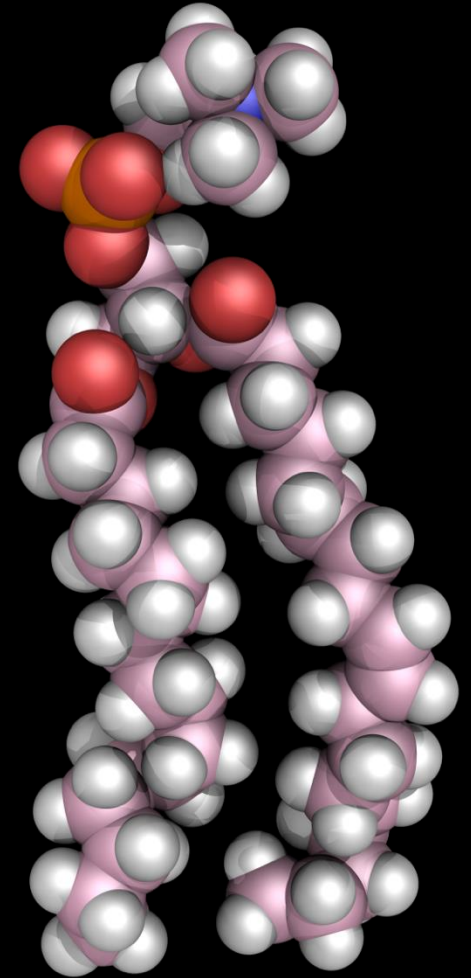
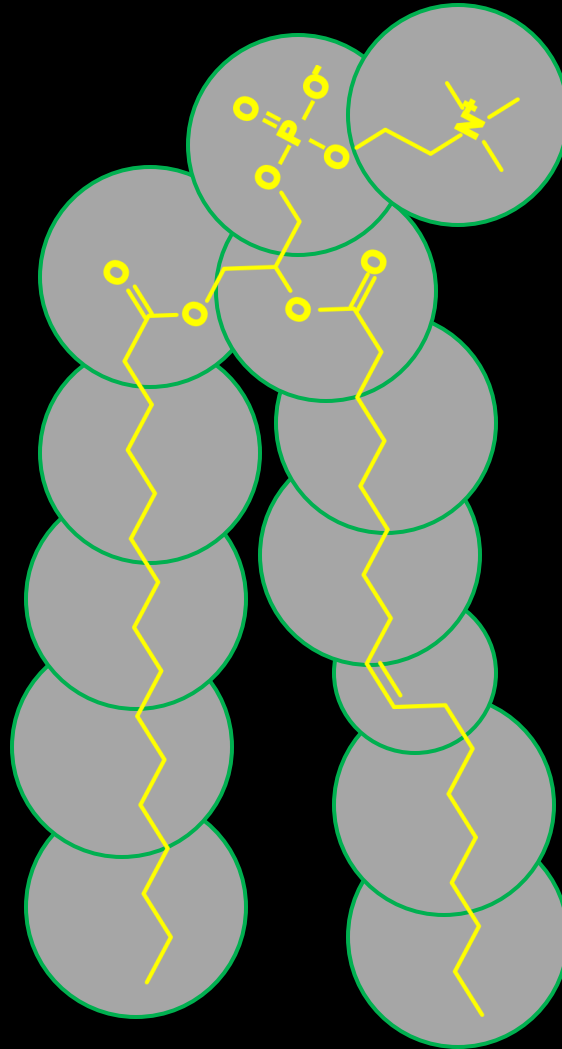
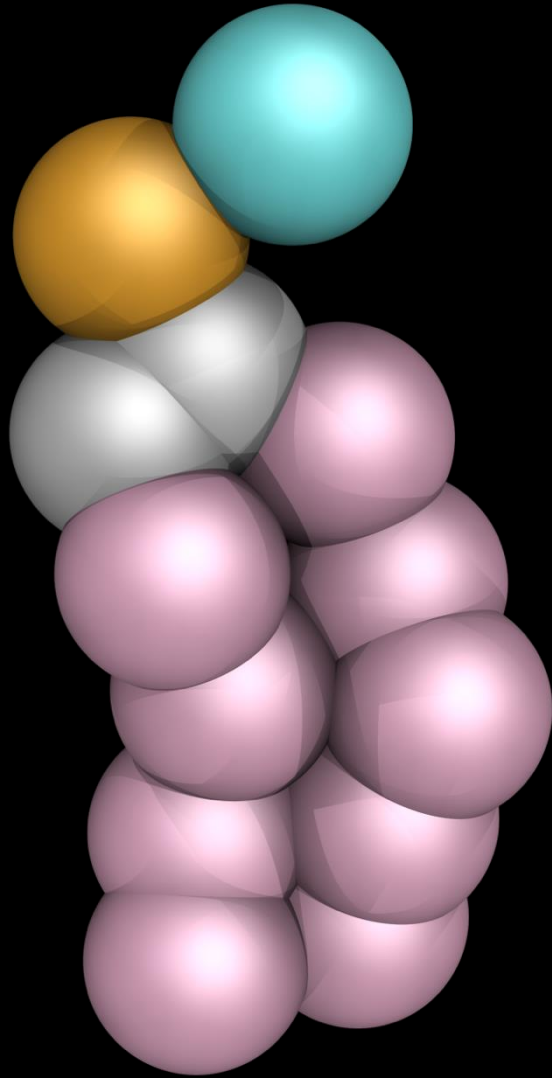
Atomistic dynamics?

Atomistic structure?

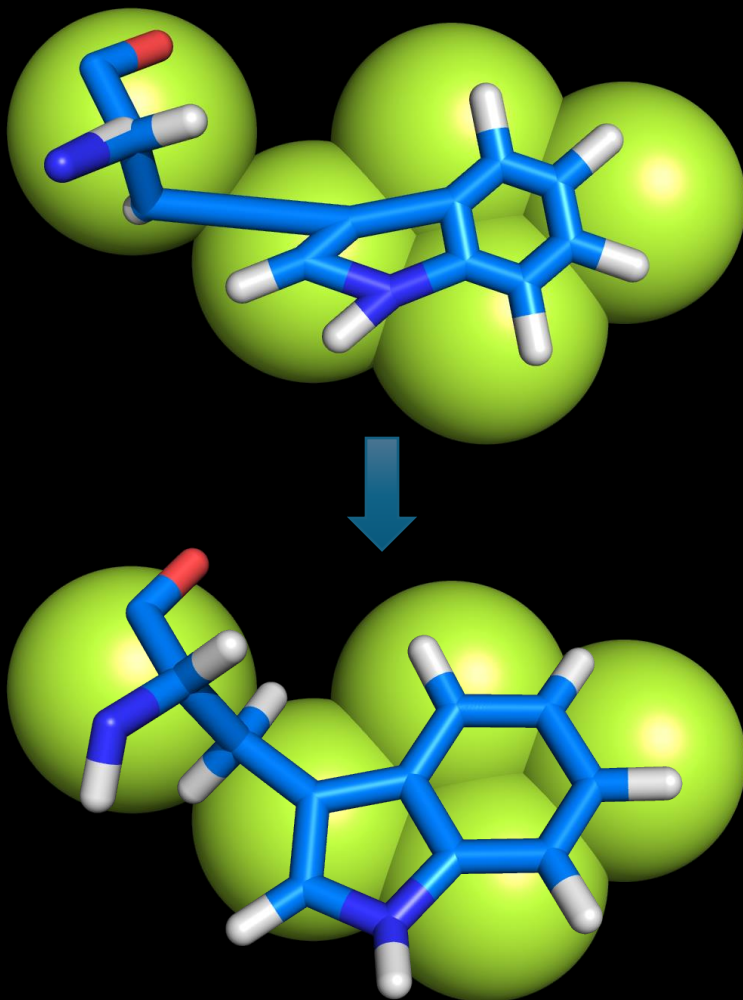
Coarse grain simulation

Backmapping

Backmapping



Backmapping Tryptophan



```
[ molecule ]
```

```
TRP
```

```
[ martini ]
```

```
BB SC1 SC2 SC3 SC4
```

```
[ mapping ]
```

```
charmm36
```

```
[ atoms ]
```

1	N	BB
2	HN	BB
3	CA	BB
4	HA	BB
5	CB	SC1 BB
6	HB1	SC1 BB
7	HB2	SC1 BB
8	CG	SC1 SC1 SC1 SC1 SC3 SC3
9	CD1	SC1
10	HD1	SC1
11	NE1	SC2 SC1
12	HE1	SC2
13	CE2	SC2 SC2 SC3
14	CD2	SC3 SC3 SC2
15	CE3	SC3 SC3 SC4
16	HE3	SC3
17	CZ3	SC4 SC4 SC3
18	HZ3	SC4
19	CZ2	SC2 SC2 SC4
20	HZ2	SC2
21	CH2	SC4 SC4 SC2
22	HH2	SC4
23	C	BB
24	O	BB

```
[ trans ]
```

CB	CG	CD2	CE2
HD1	CD1	NE1	CE2
HE1	NE1	CD1	CG
HE3	CE3	CD2	CE2
HZ2	CZ2	CE2	CD2
HZ3	CZ3	CE3	CD2
HH2	CH2	CZ3	CE3

```
[ chiral ]
```

CB	CA	N	C
HB1	CA	N	C
HB2	CA	N	C

```
[ chiral ]
```

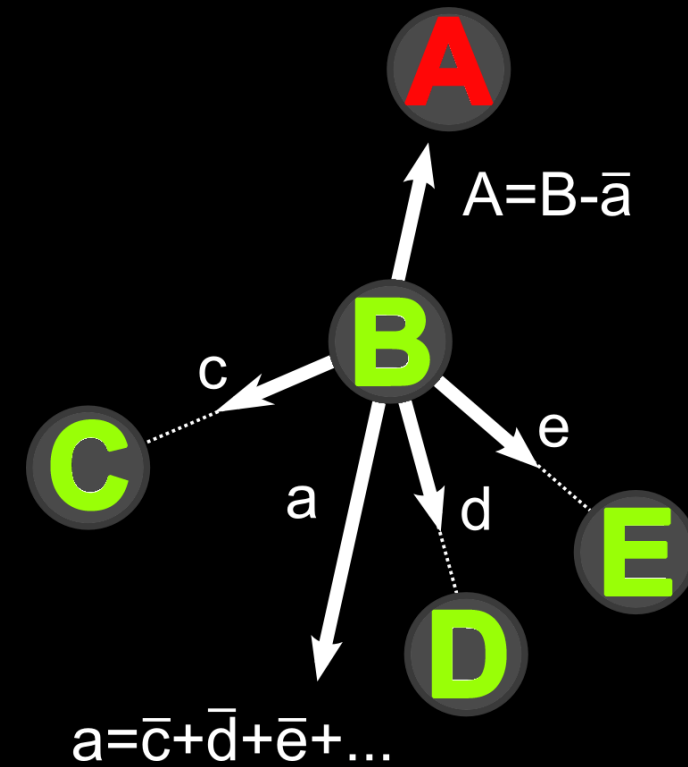
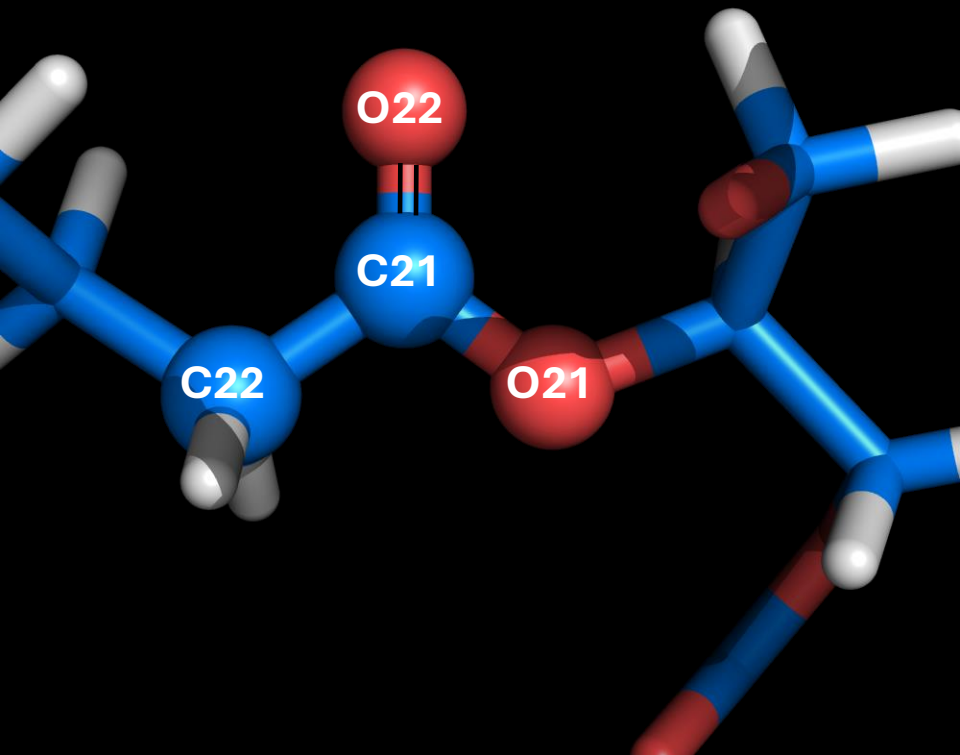
HA	CA	N	CB	C
----	----	---	----	---

Backmapping

; ester group

[out]

O22 C21 O21 C22



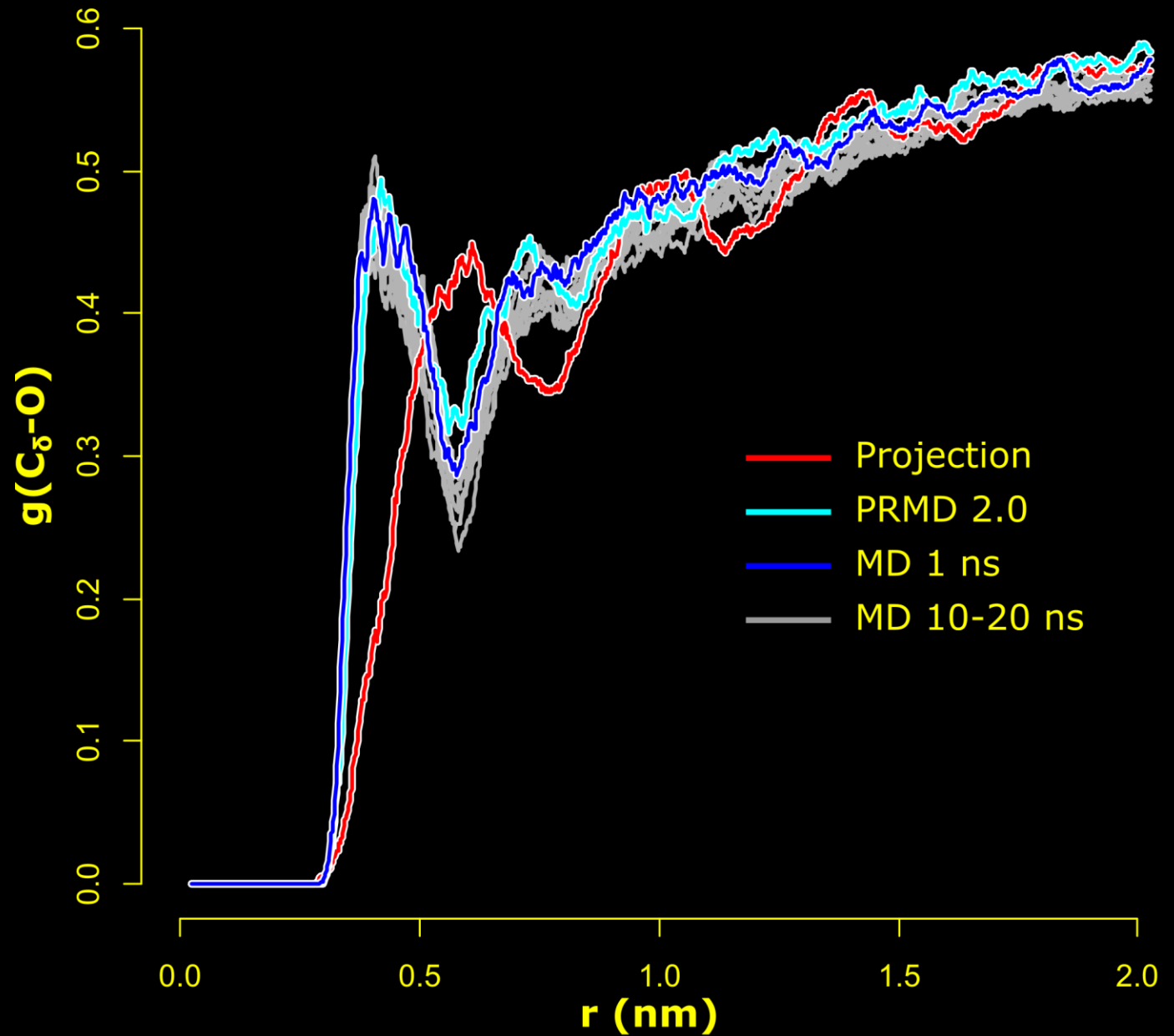
A, B, C, D, E atoms

a, b, c, d, e vectors

\bar{a} normalized vector

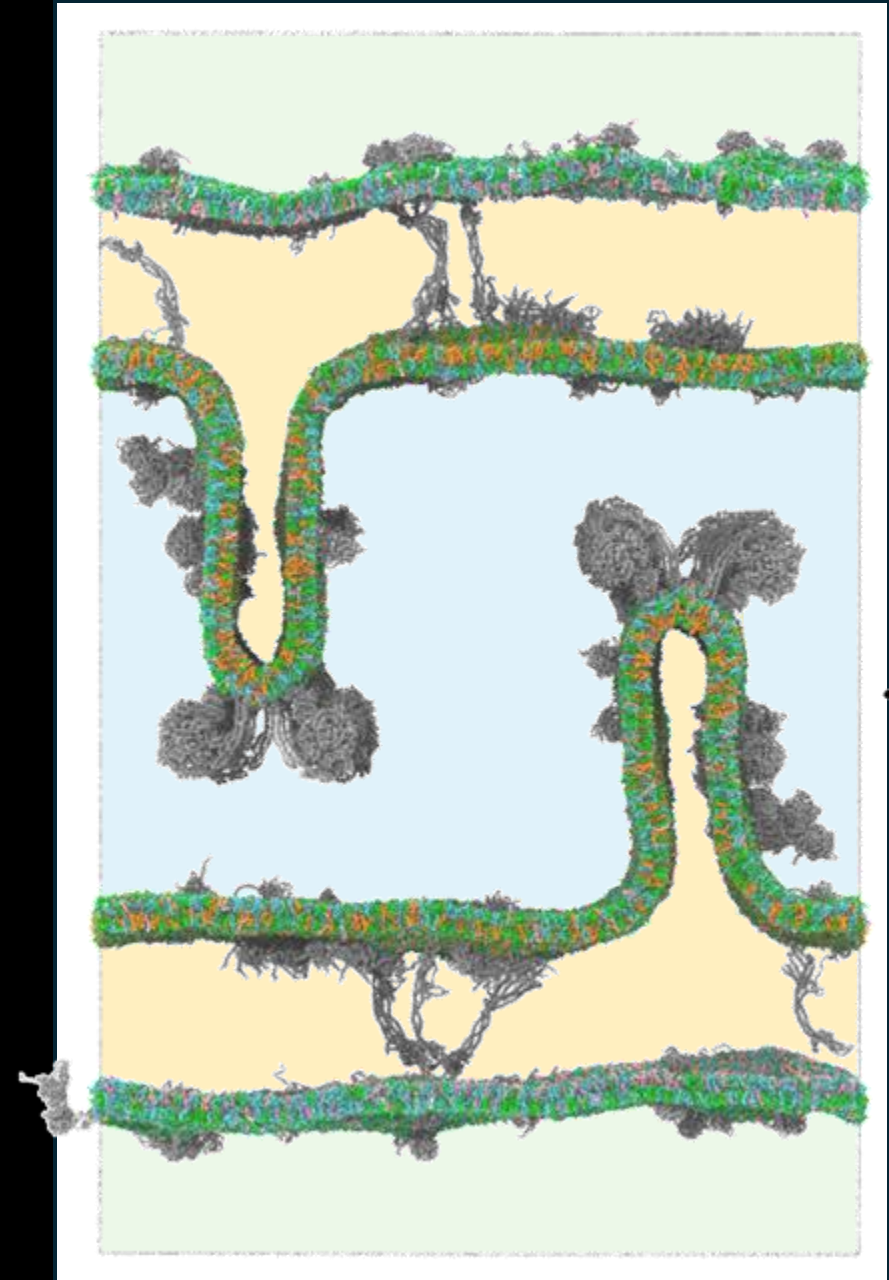
Backmapping

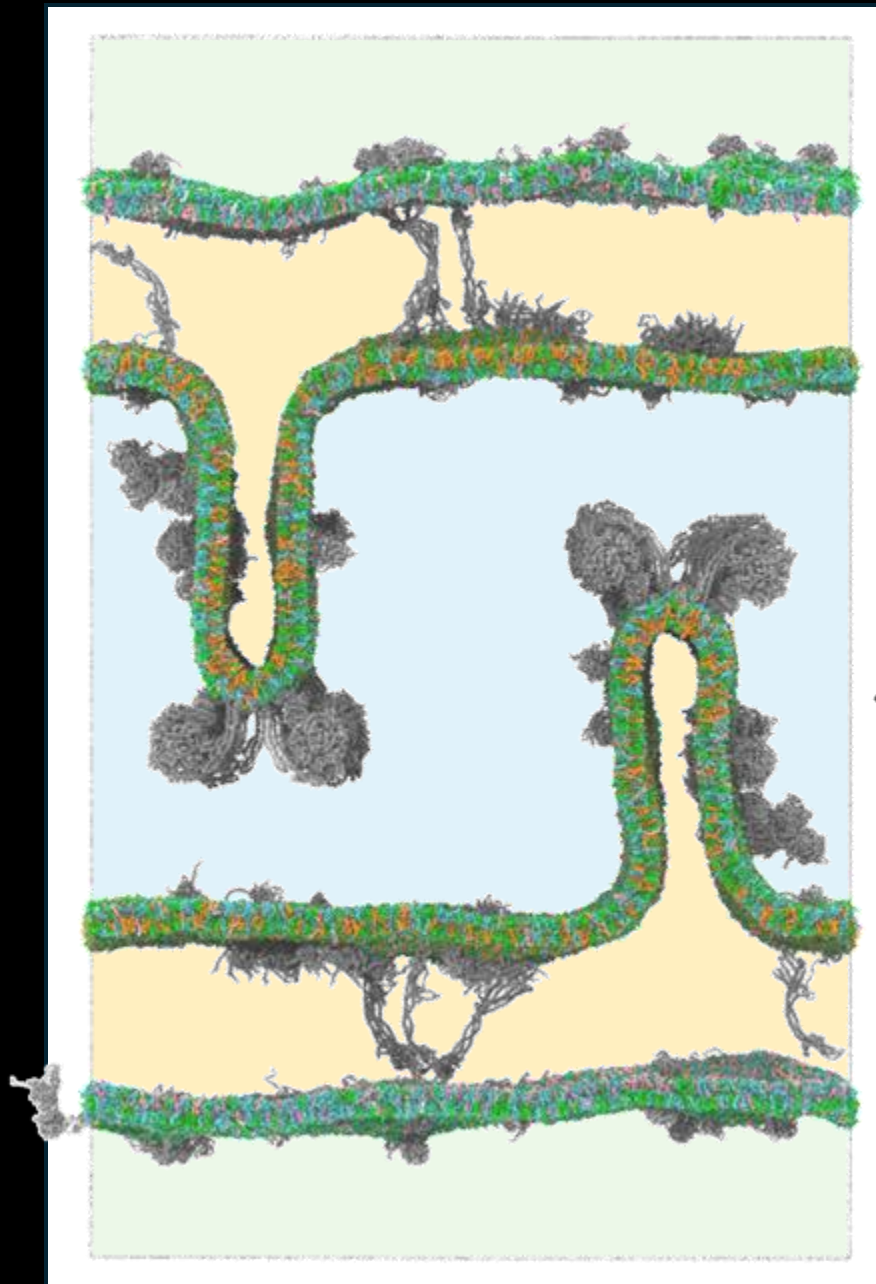
Solvent



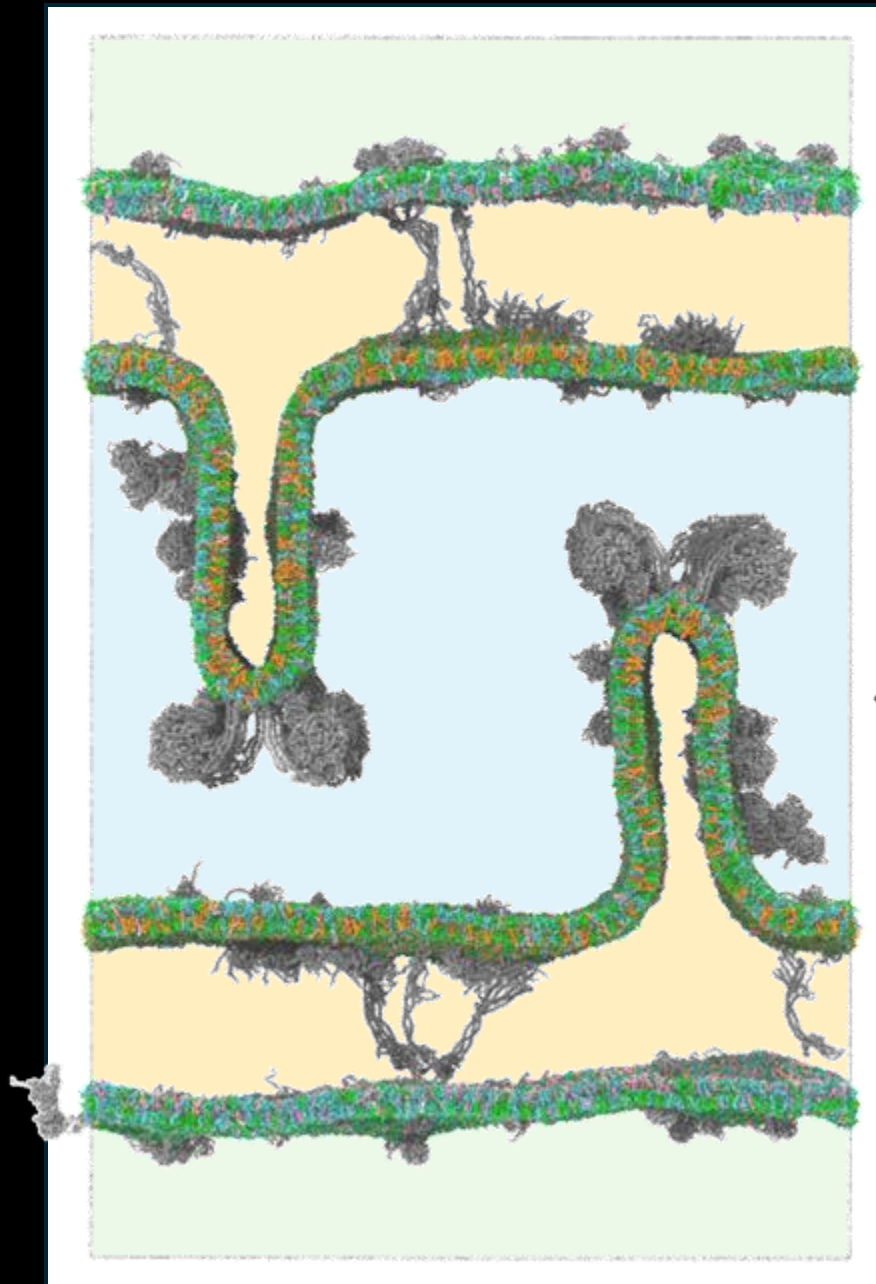
What to build?

- Resolution
- Organization
- Composition
- Components



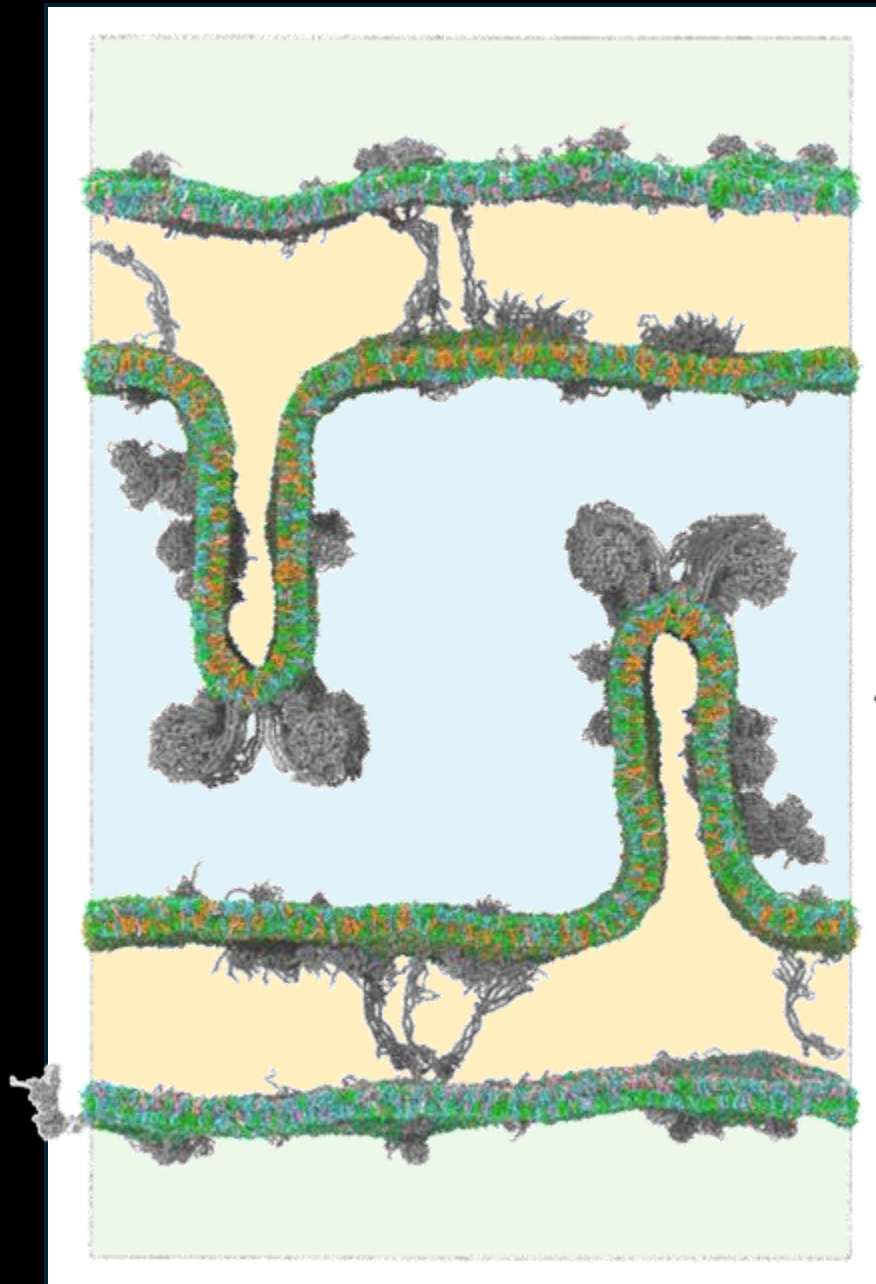


Relaxation time...



Relaxation time...

Given infinite time,
any system will
converge to its
proper ensemble

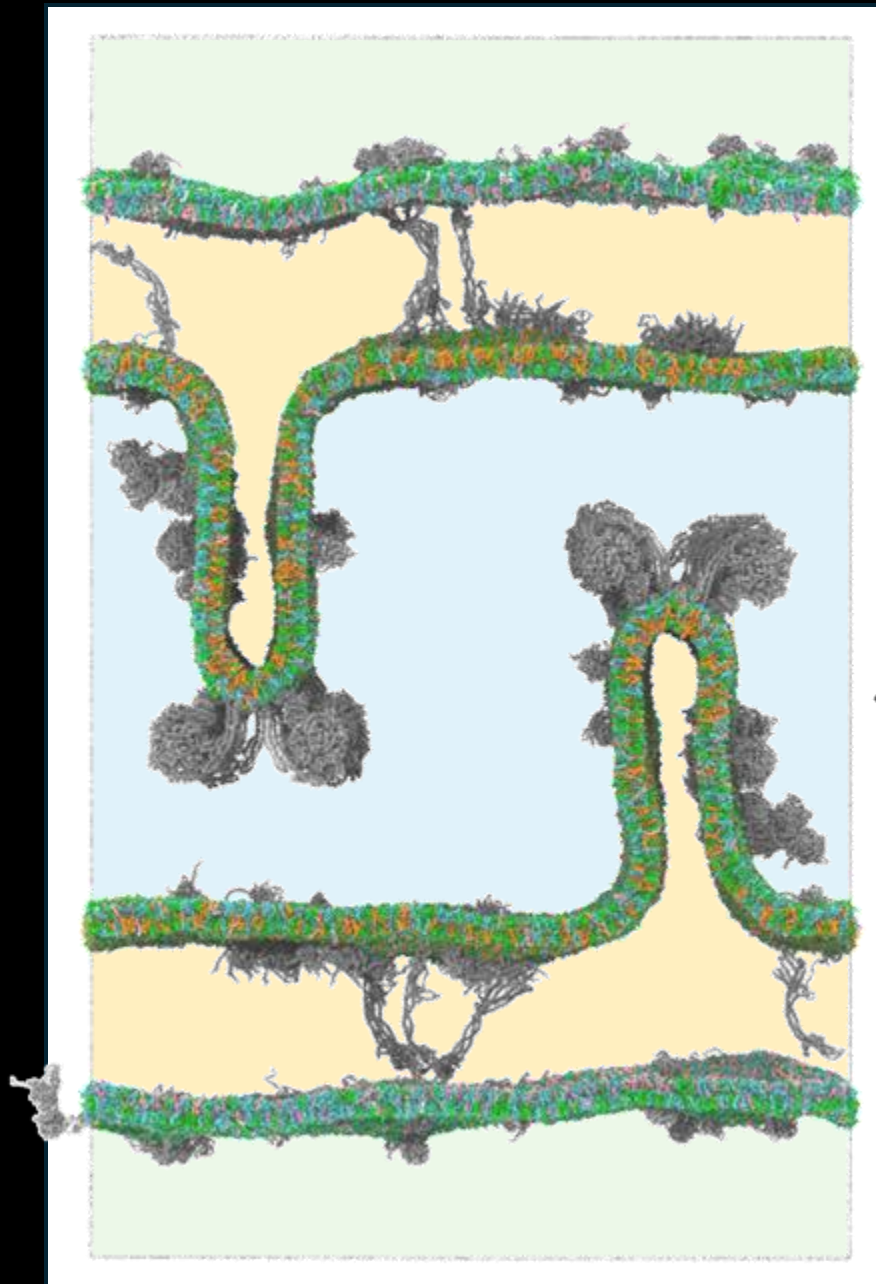


Relaxation time...



finite time

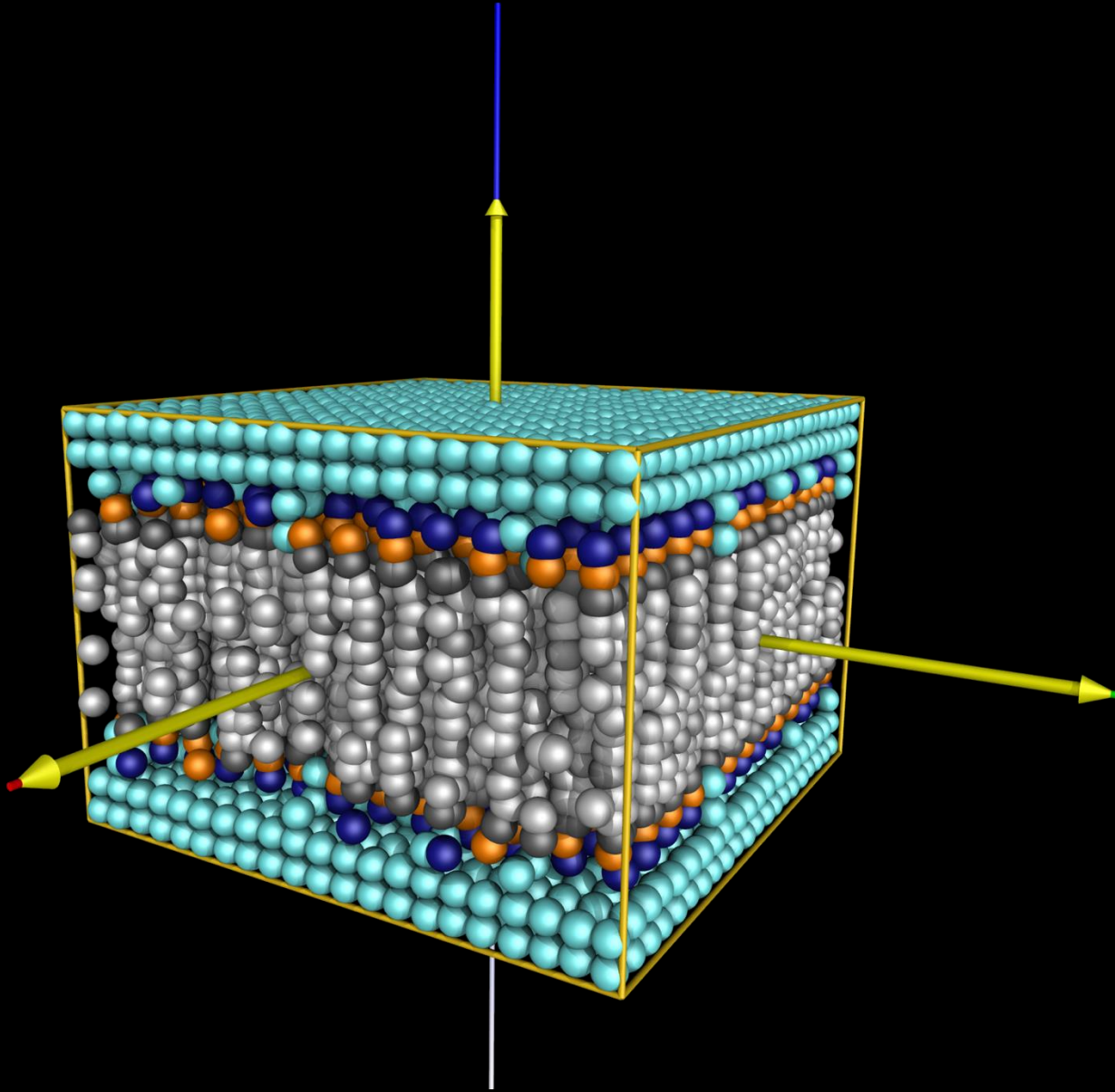
proper ensemble



If there were a perfect solution, it wouldn't be moving in simulation

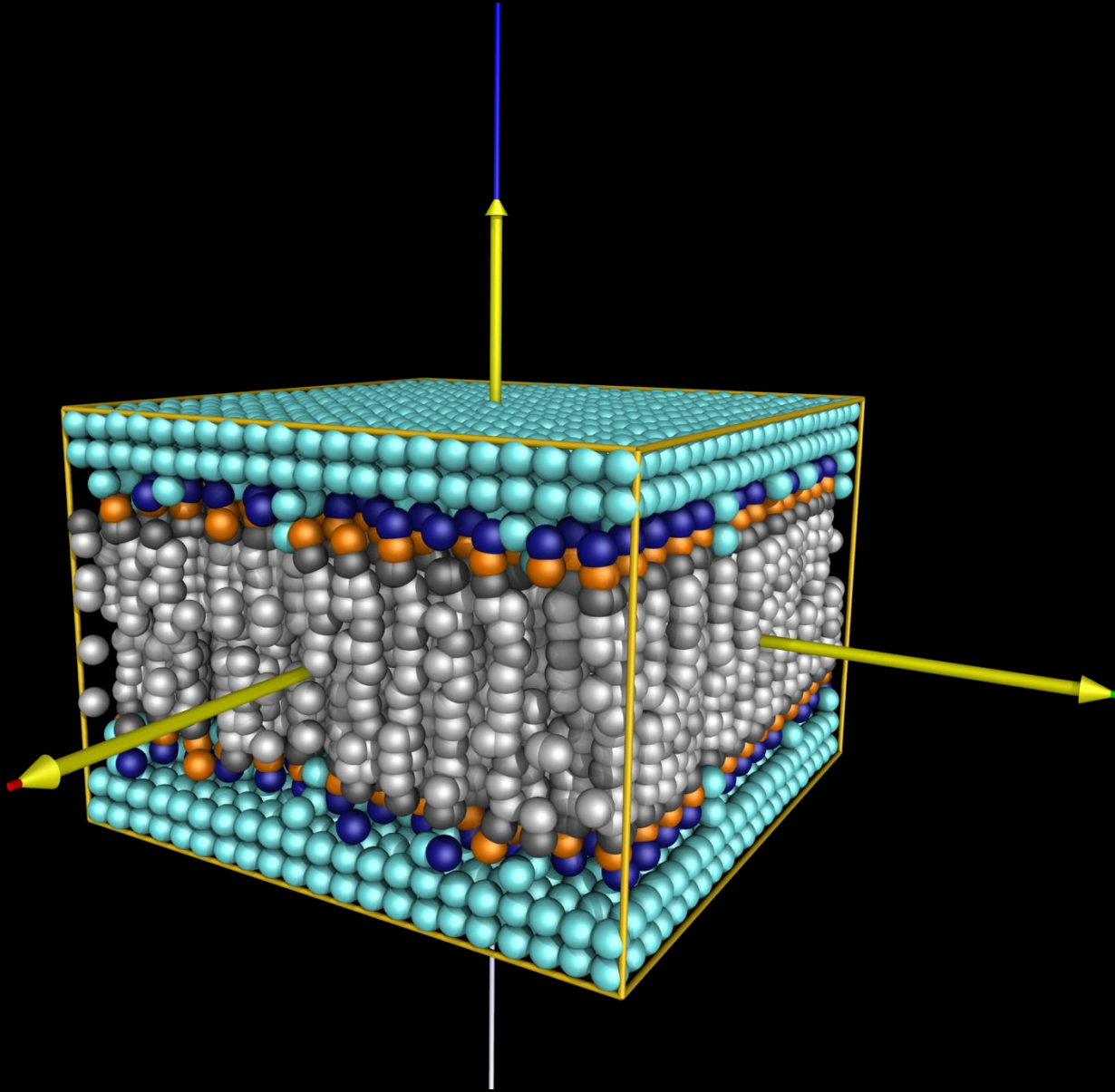
The **insane** philosophy:

If it's good enough,
then it's good enough



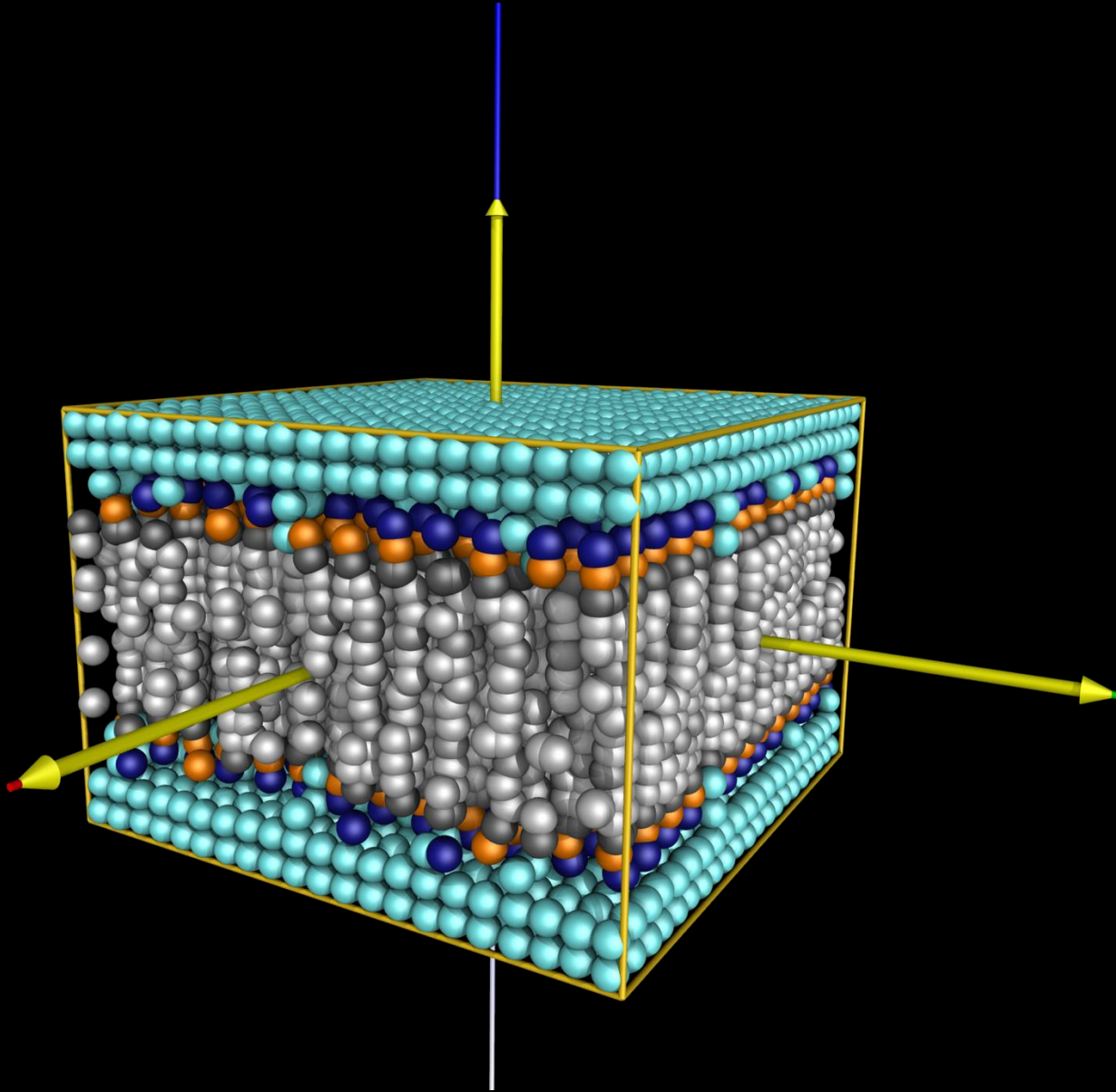
The **insane** philosophy:

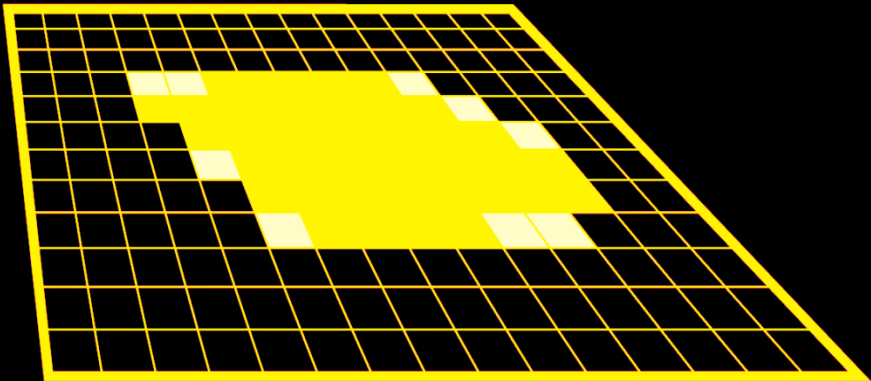
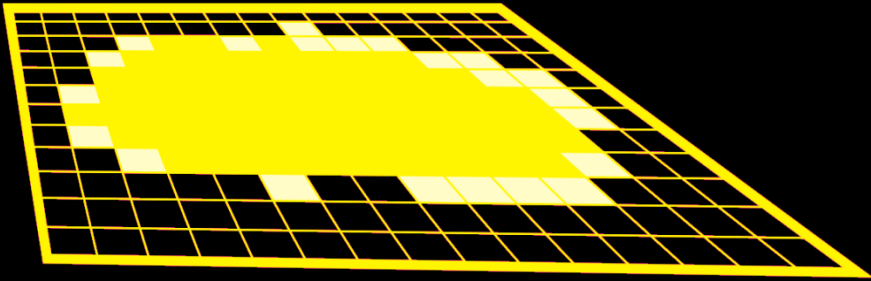
As simple as possible
but not any simpler



The **insane** philosophy:

Whatever I can
get away with

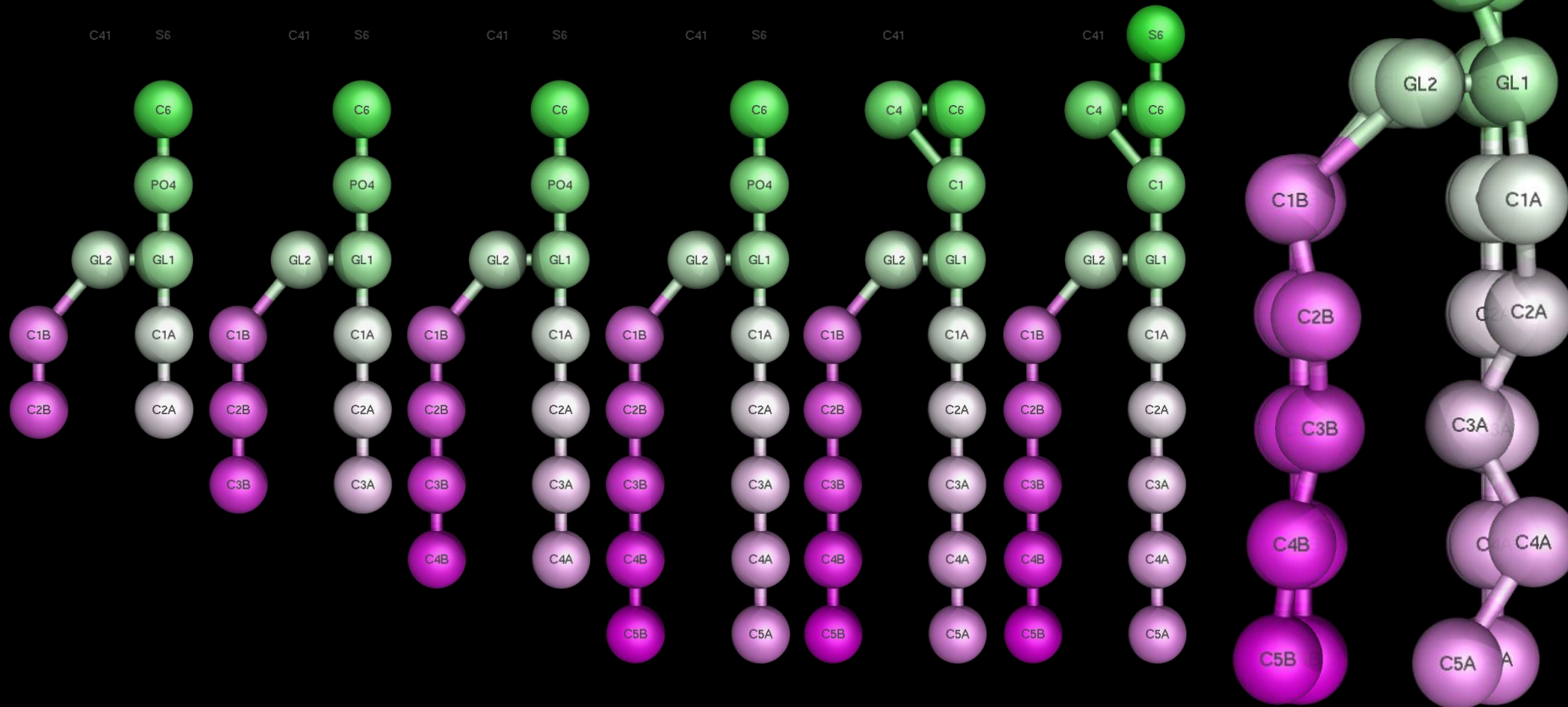


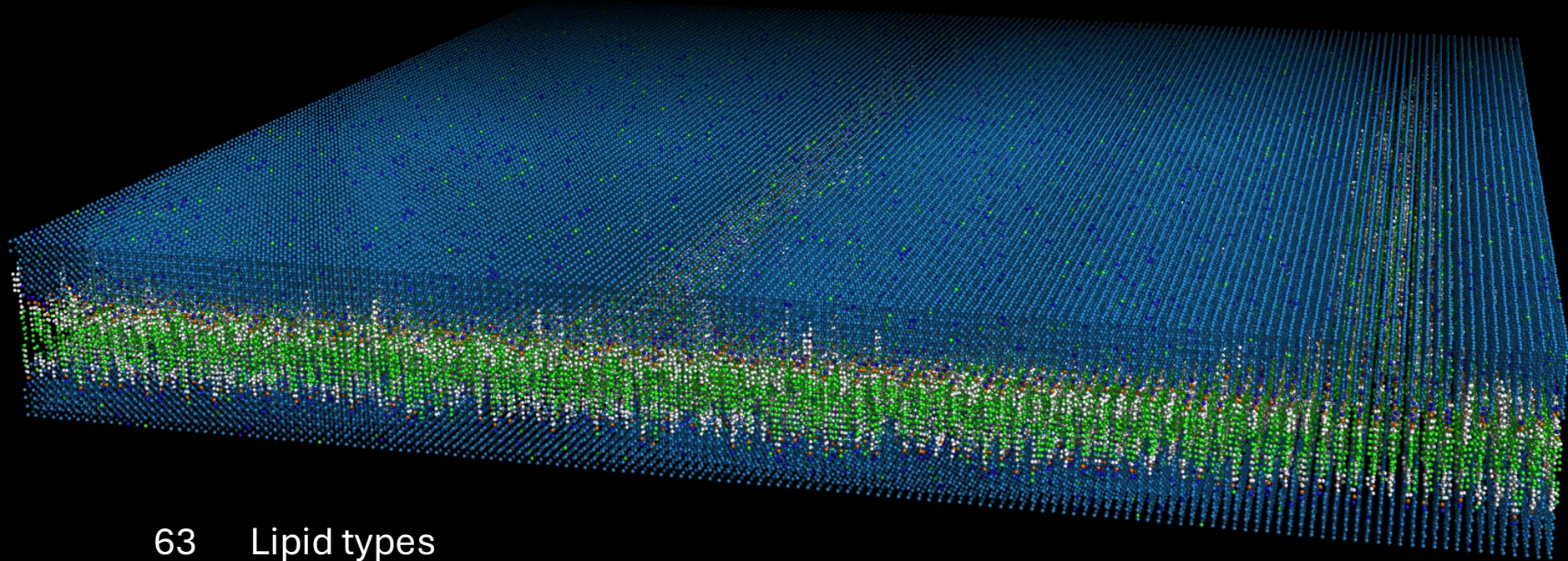


The **insane** philosophy:

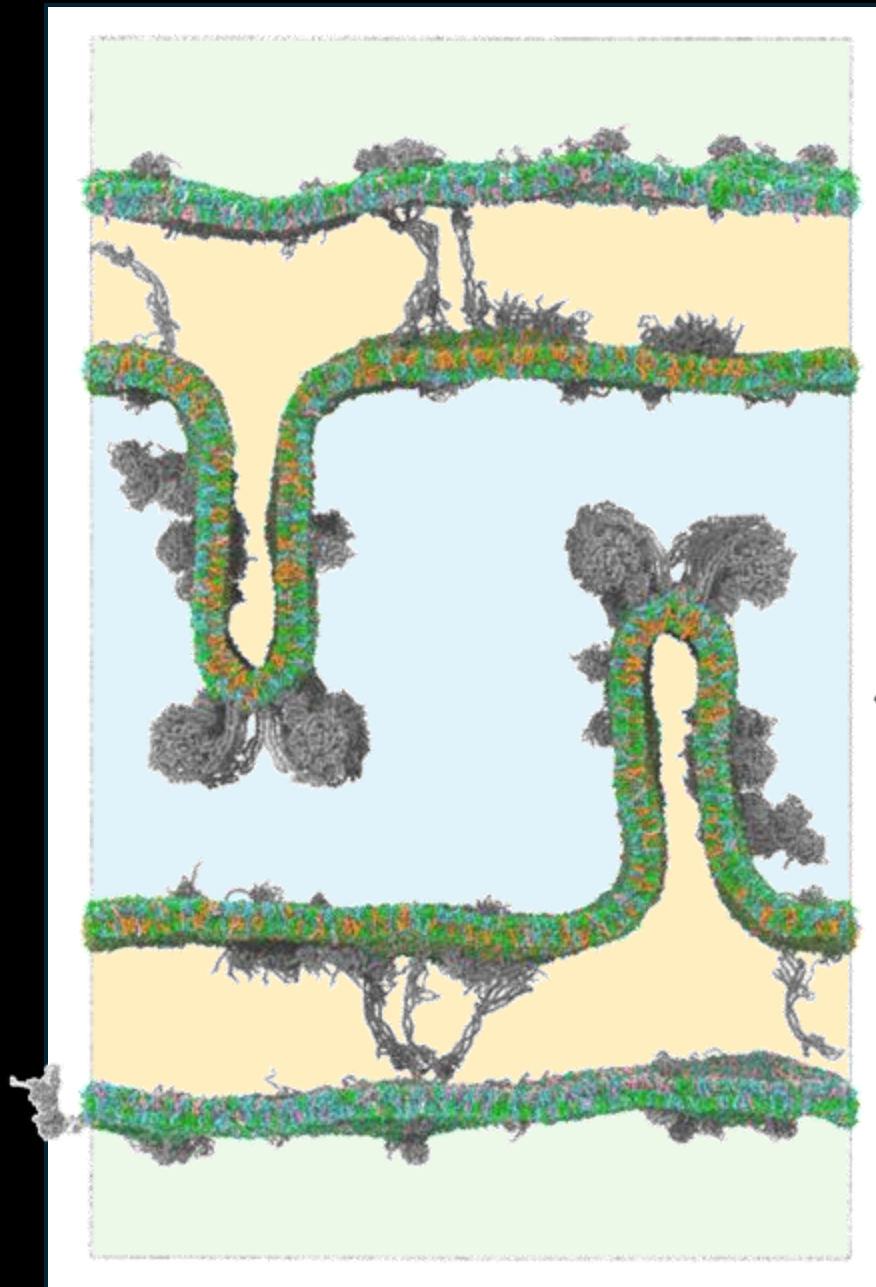
Whatever I can
get away with

Lipid structures built from templates
Simple lipids can be defined from cmdline



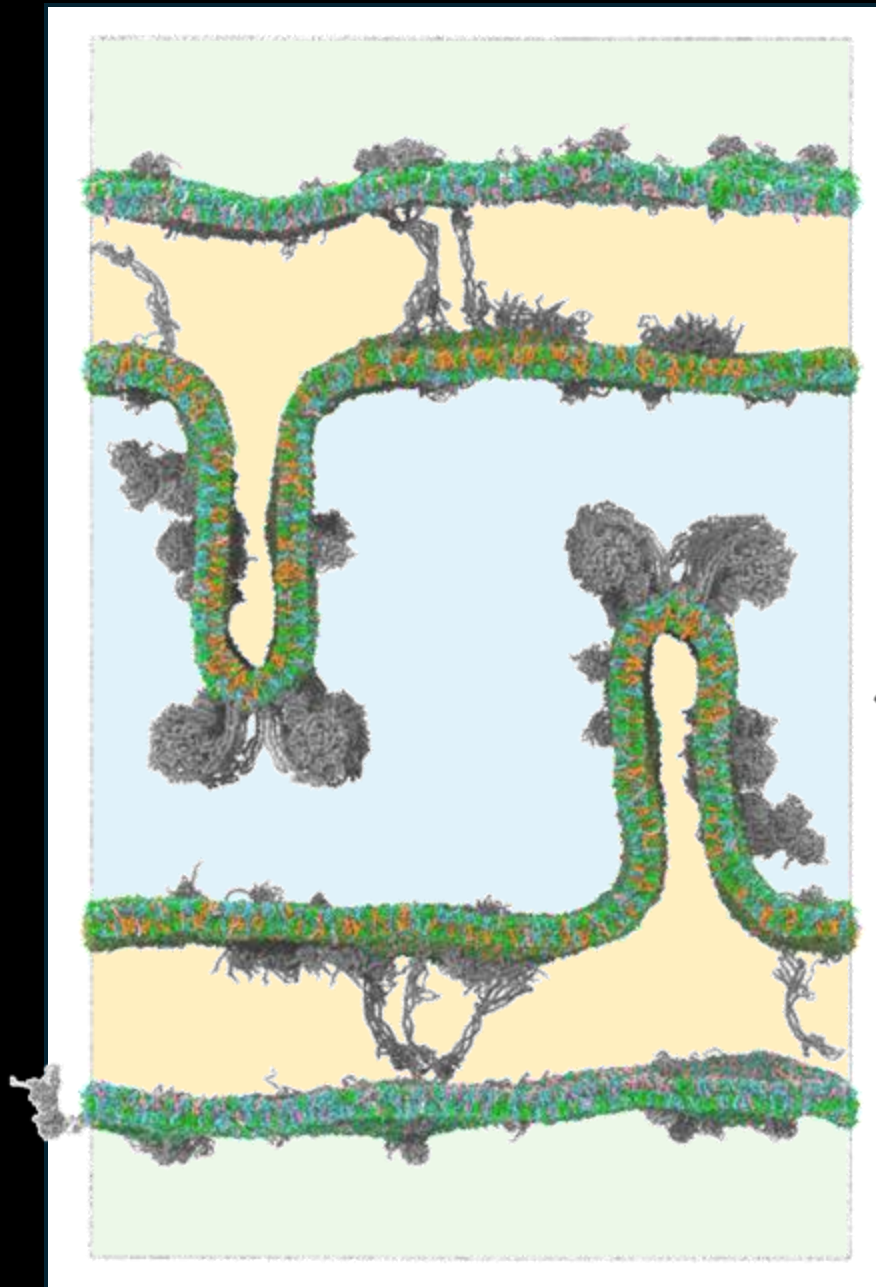


63	Lipid types
19280	Lipids
292221	Water molecules
9294	Ions
523616	Particles
16	Seconds



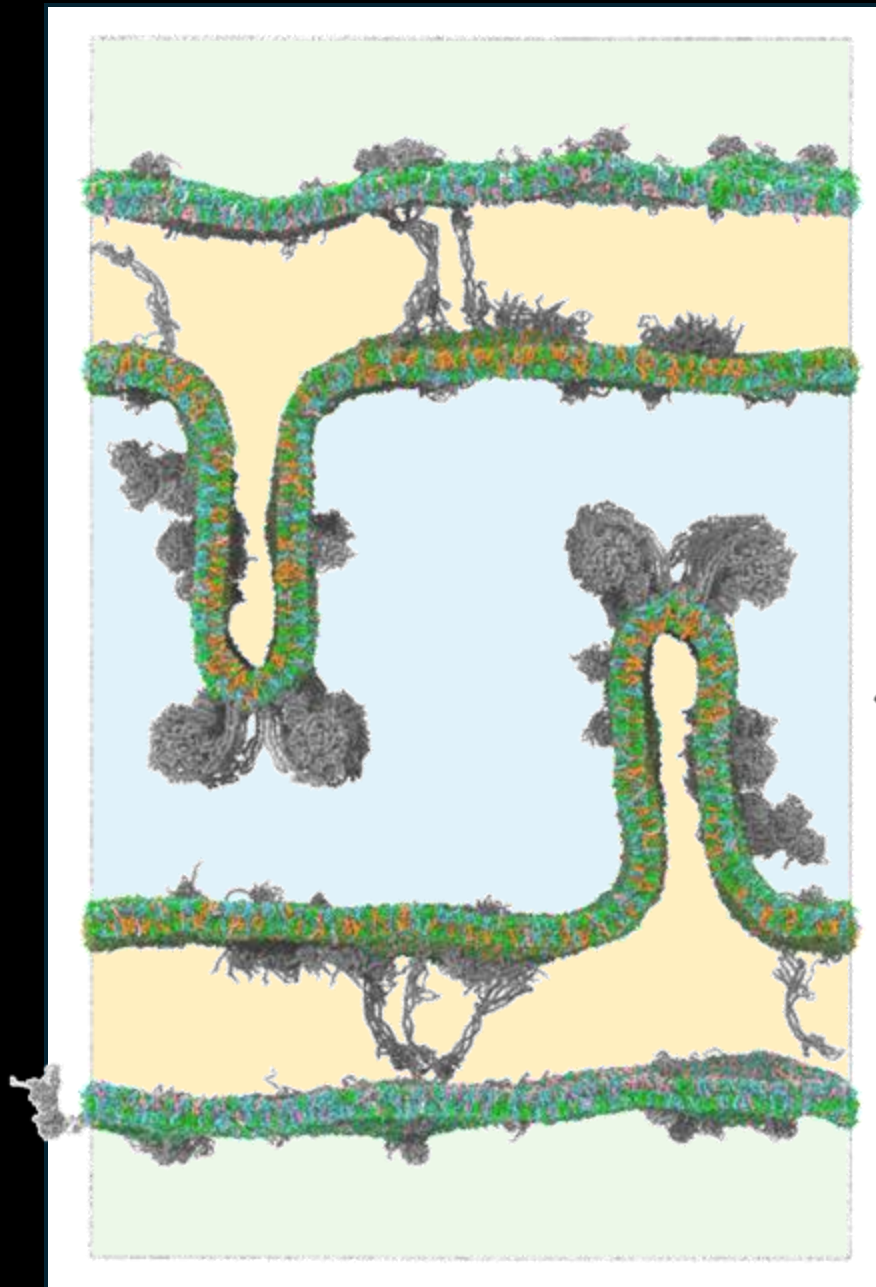
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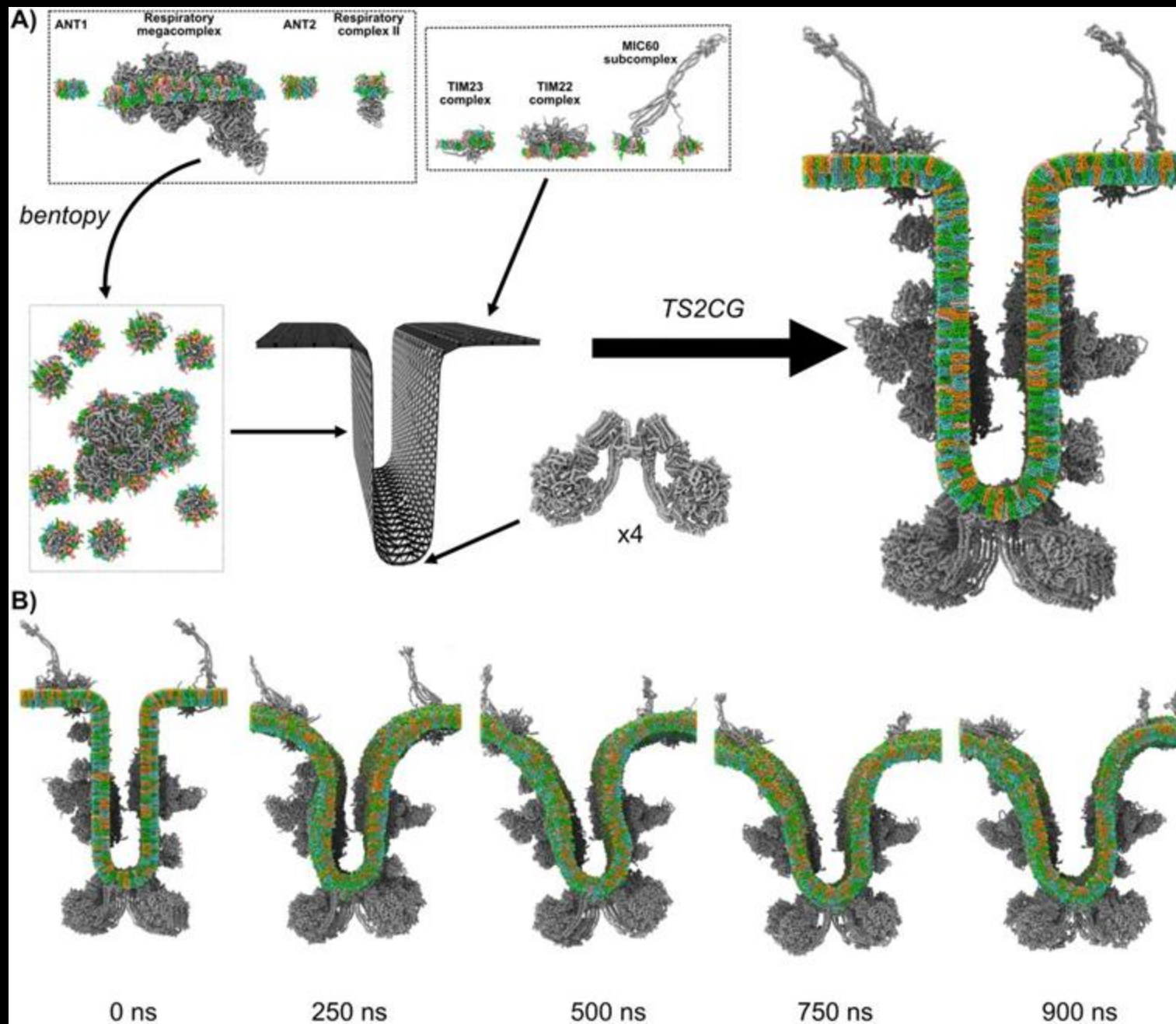
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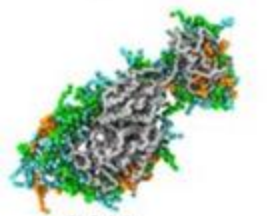


The **insane** philosophy:

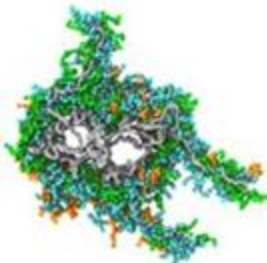
Whatever I can
get away with



SAM
complex



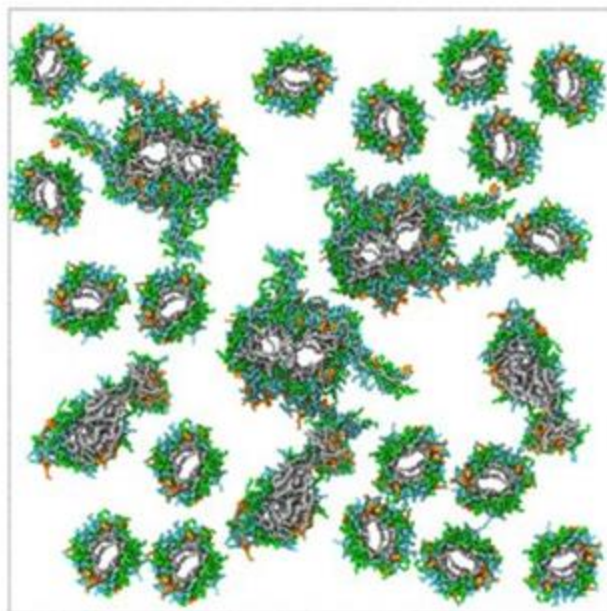
TOM
complex



VDAC1



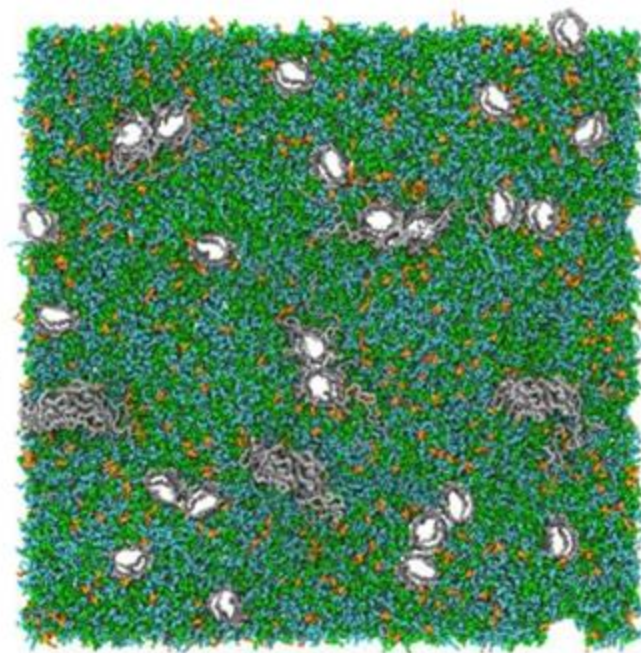
bentopy



insane



$1 \mu s$ MD



What to build?

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What to build?

- Resolution
- Organization
- **Composition**
- Components

Martini 3
5 μ s

POPC

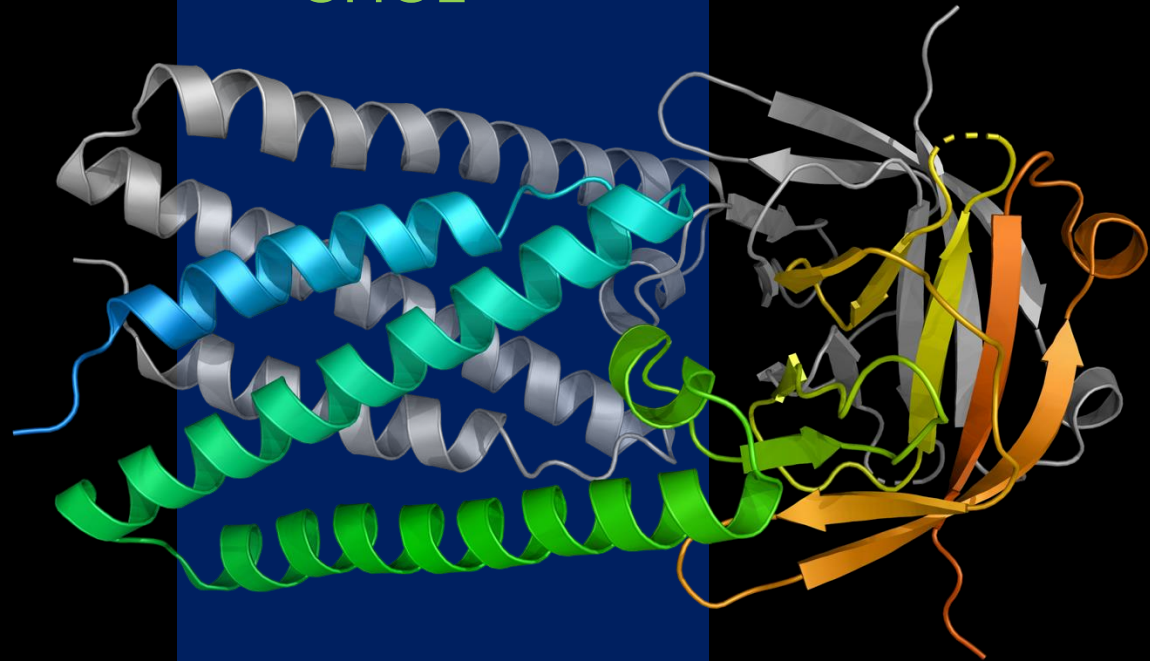
POPE

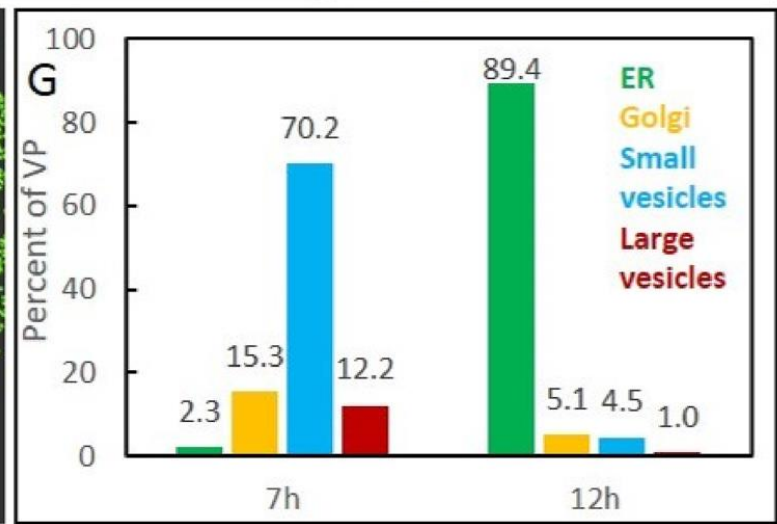
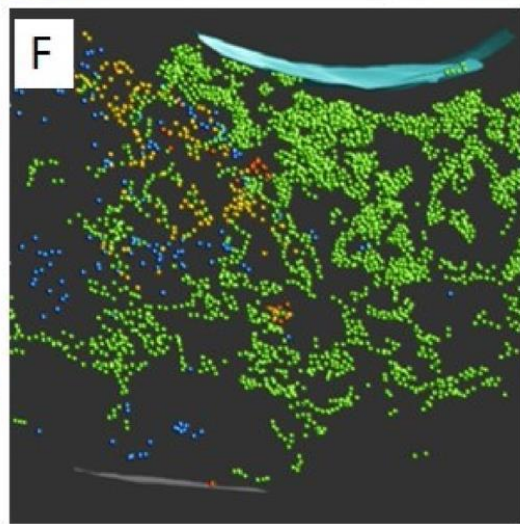
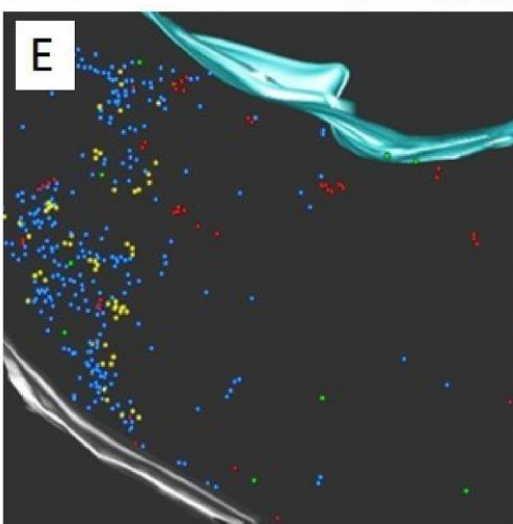
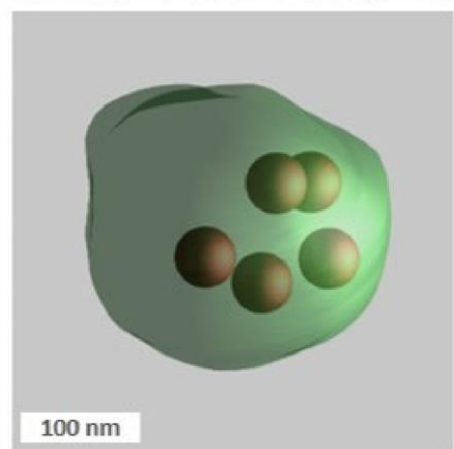
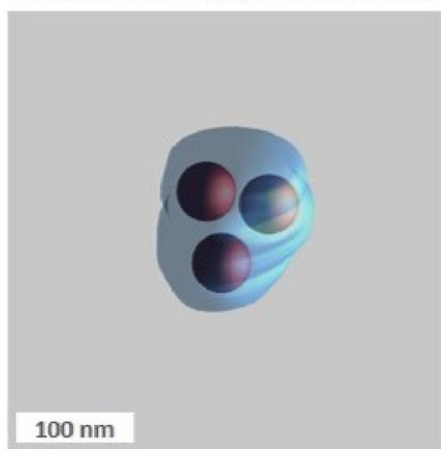
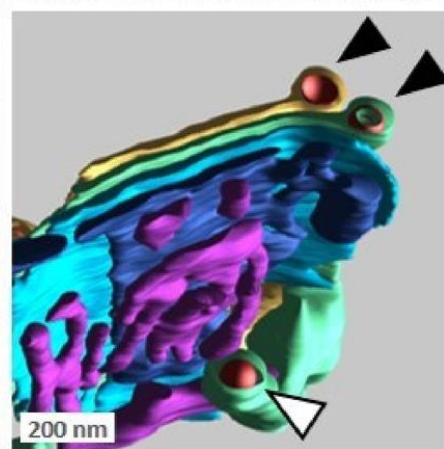
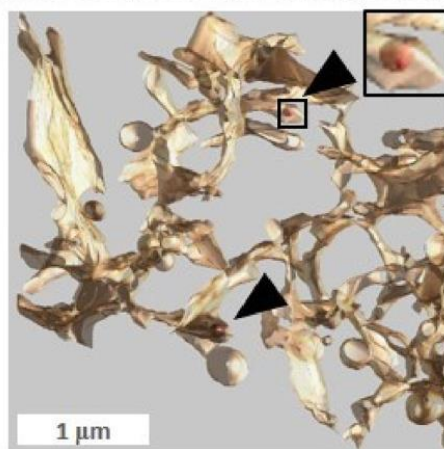
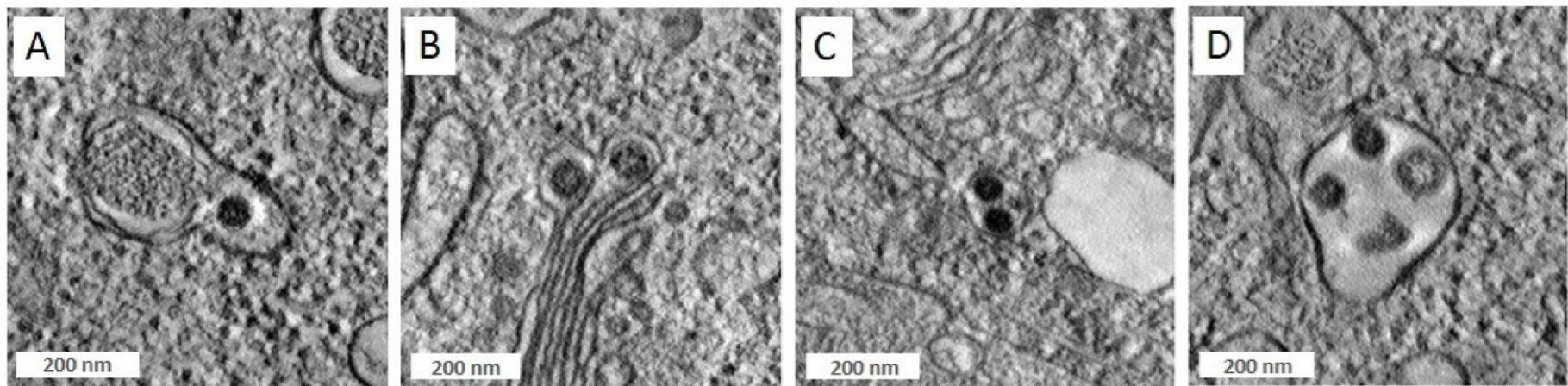
POPS

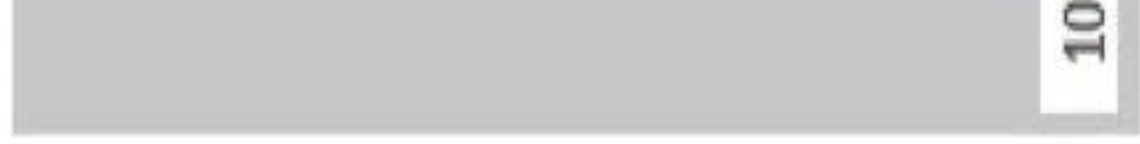
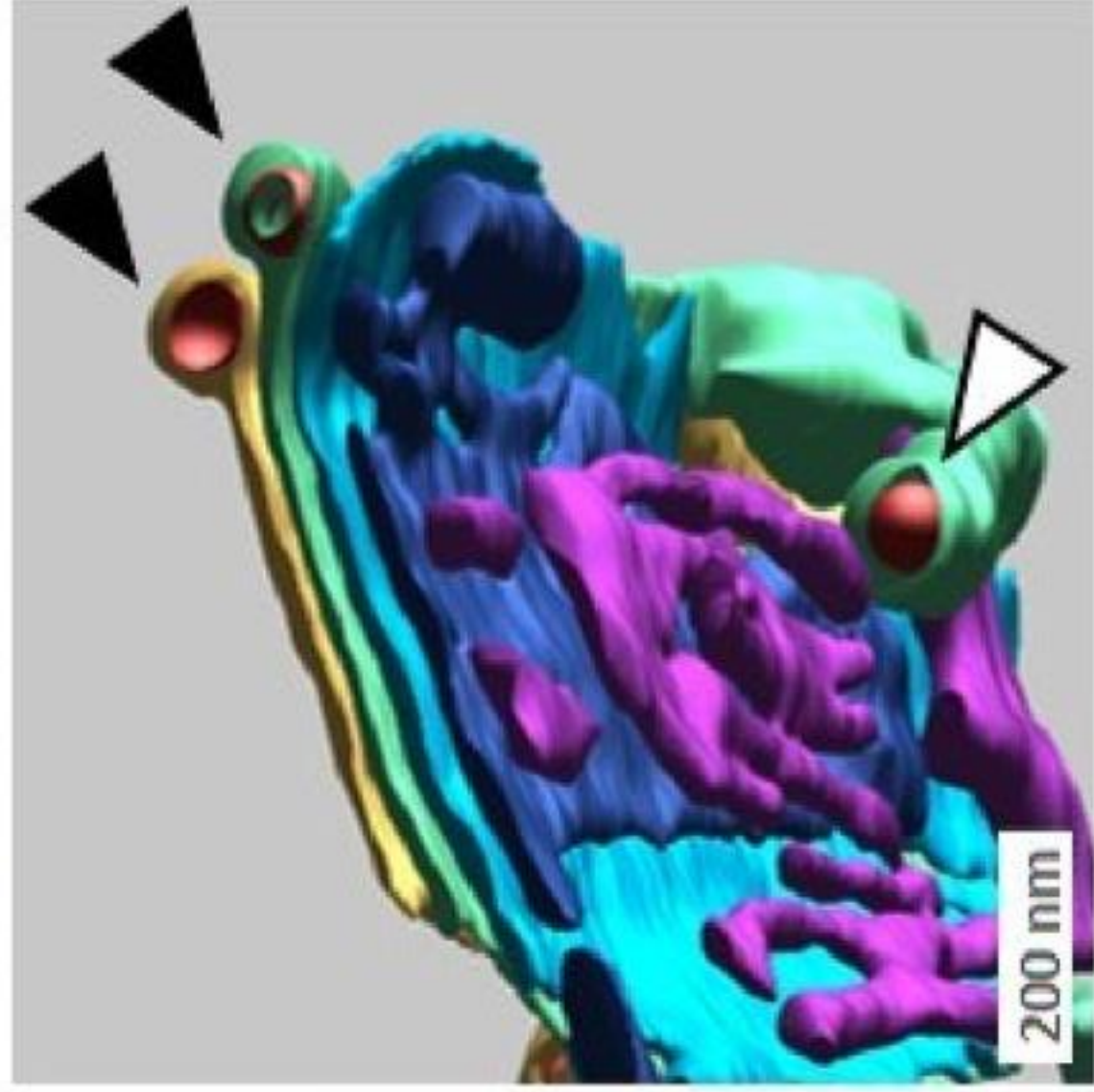
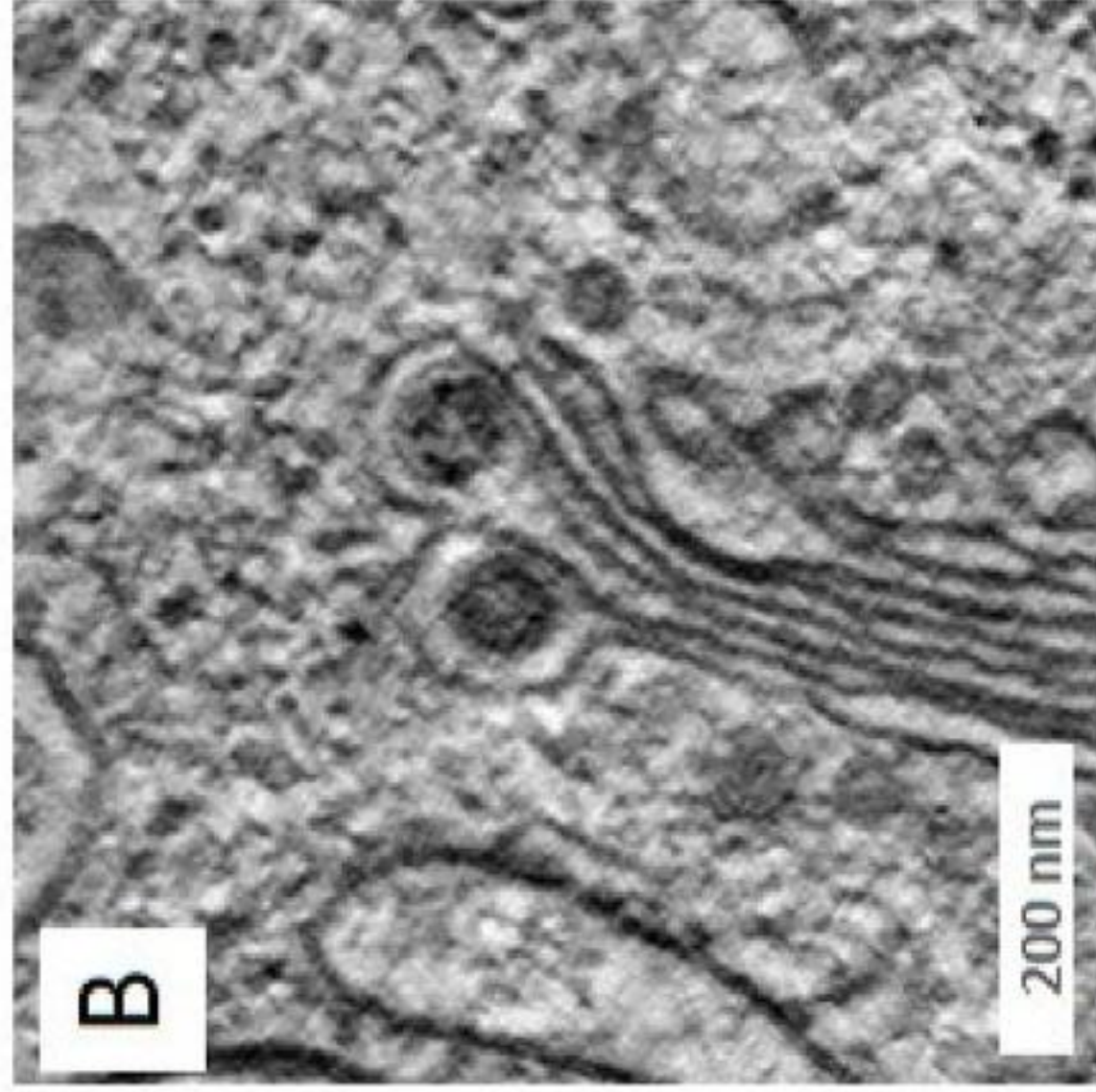
POPI

CDL2

CHOL







What to build?

- Resolution
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Martini 3
5 μ s

POPC

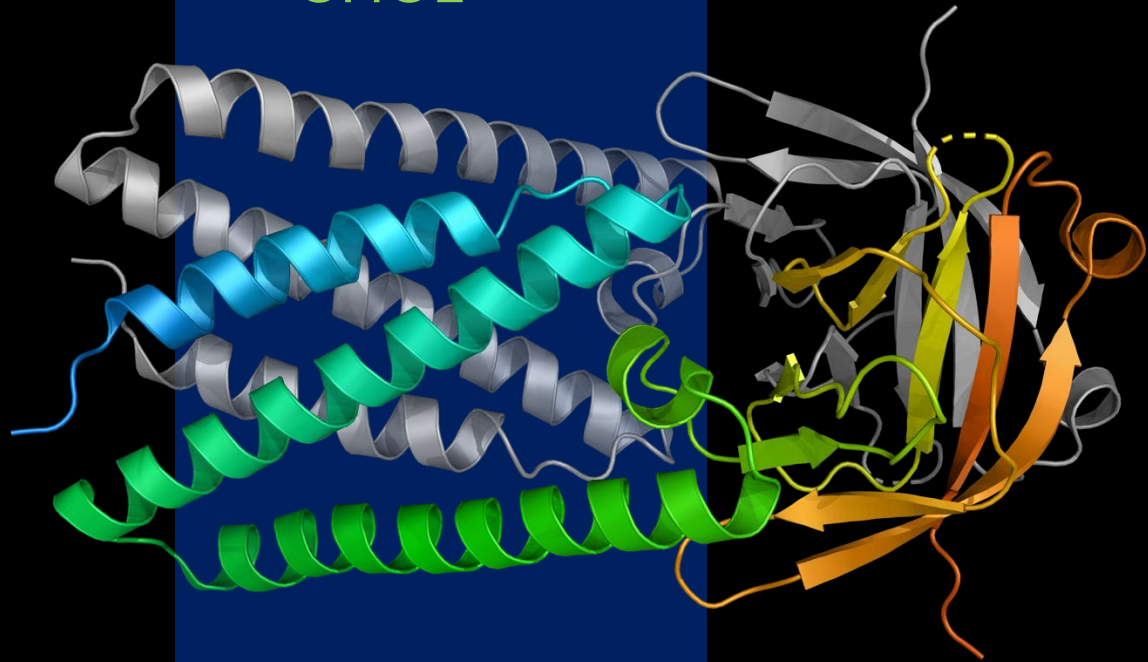
POPE

POPS

POPI

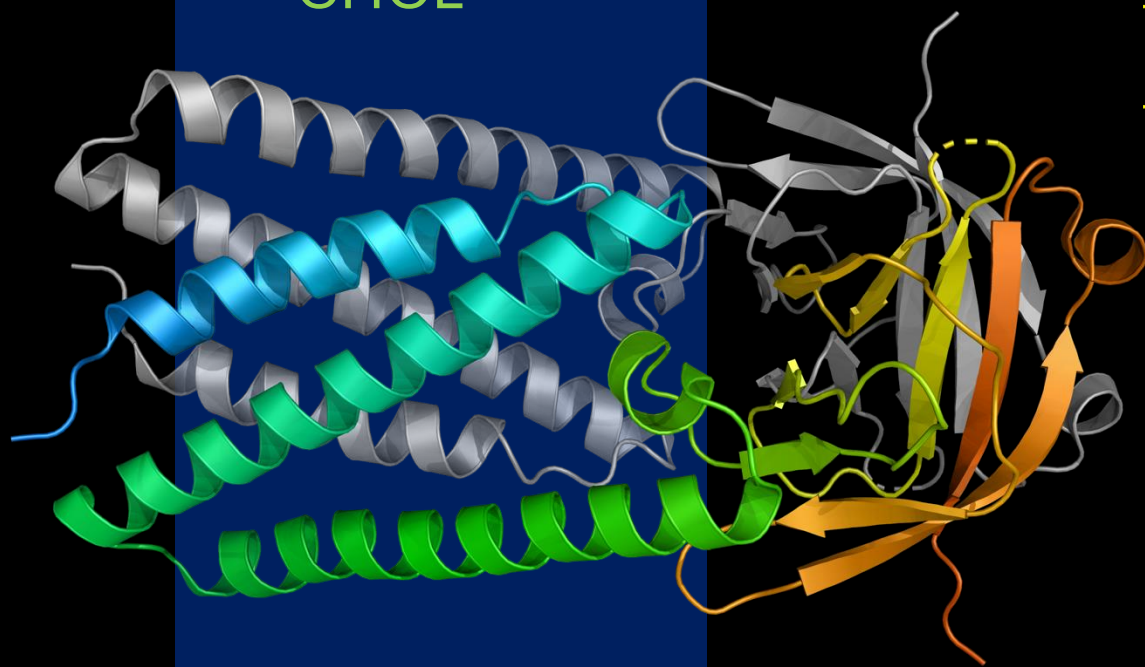
CDL2

CHOL

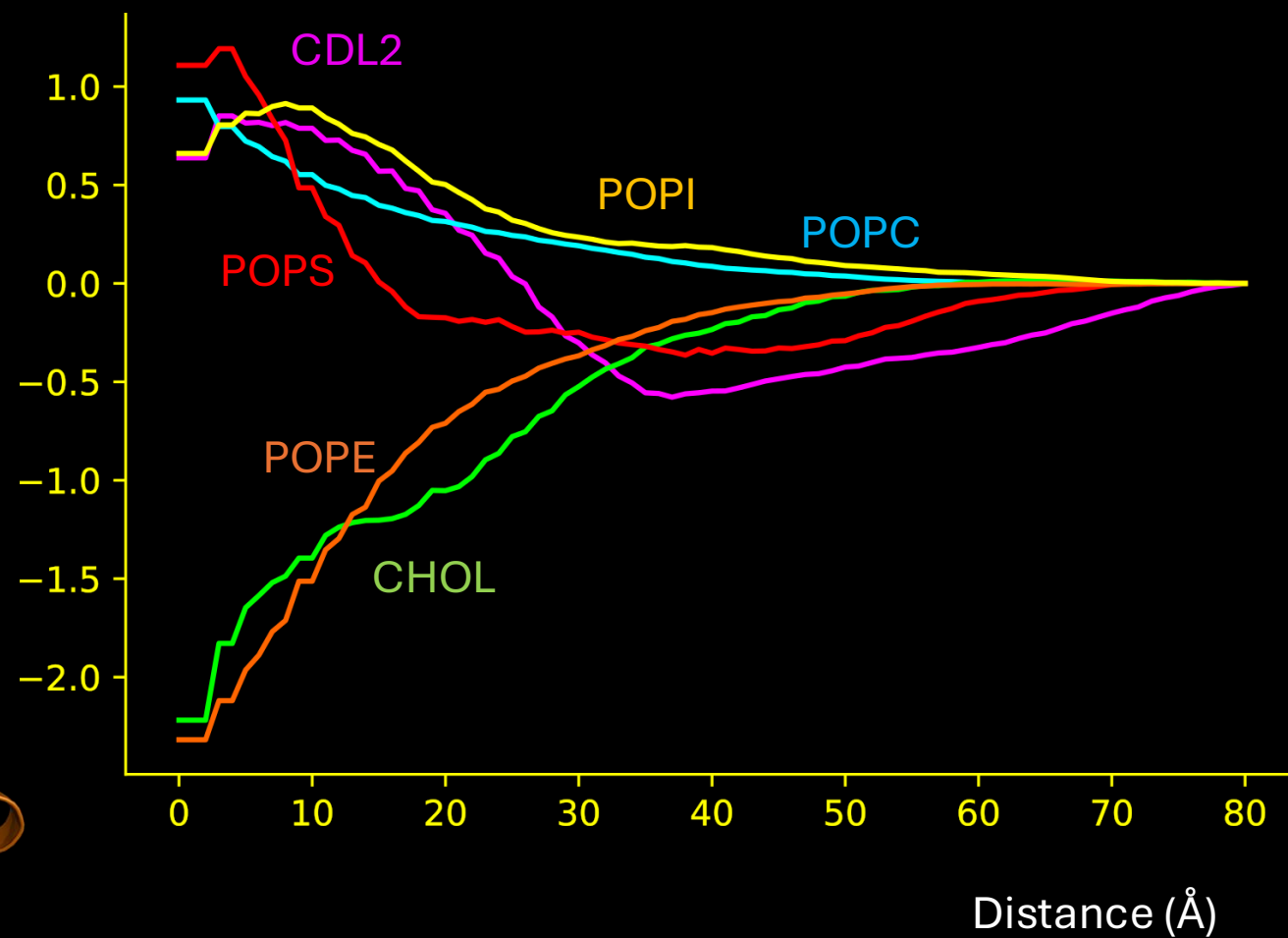


Martini 3
5 μ s

POPC
POPE
POPS
POPI
CDL2
CHOL



Log_{1.1} enrichment



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build!

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