

Introduction to Martini

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“Martini Basics”

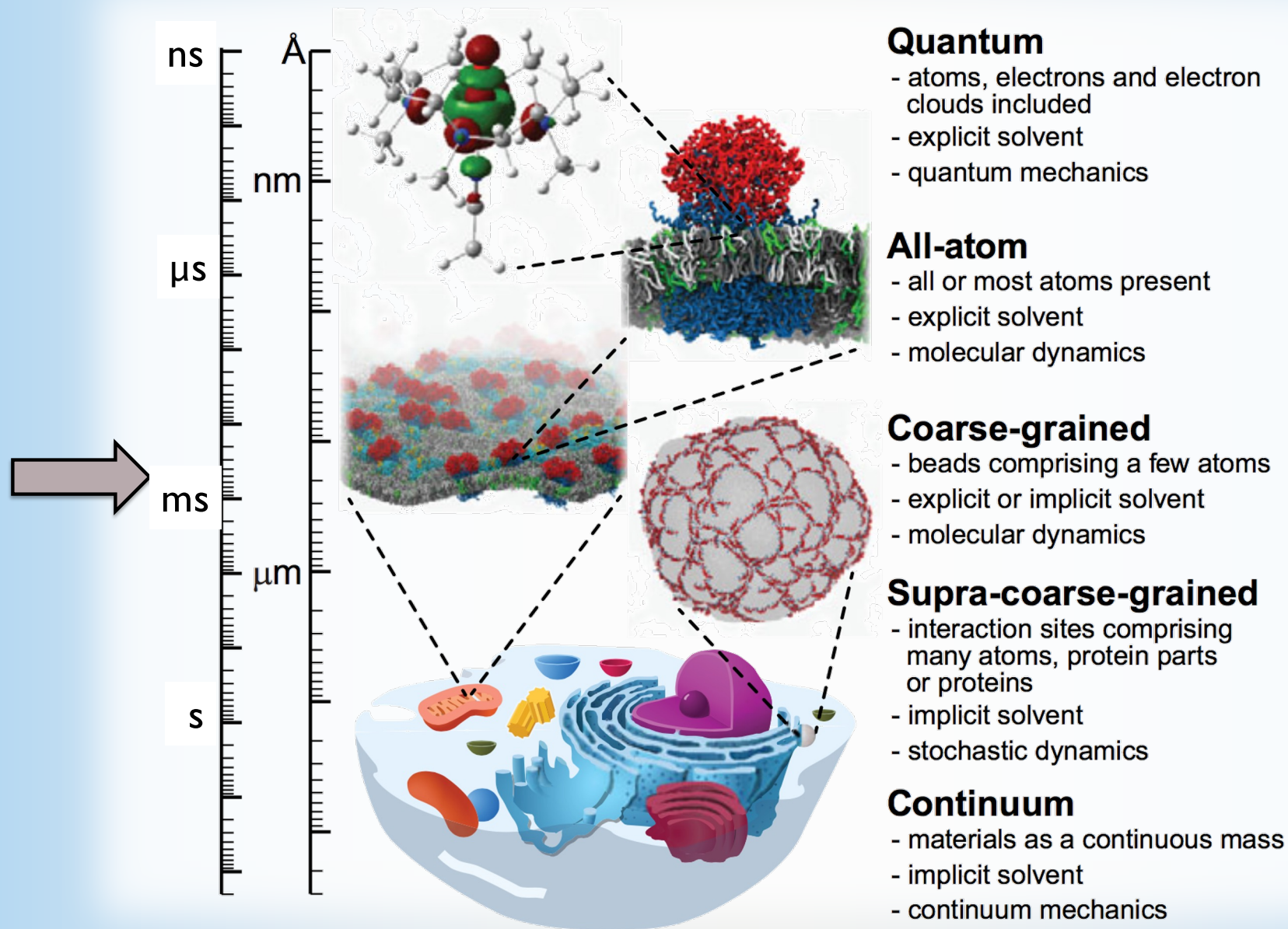
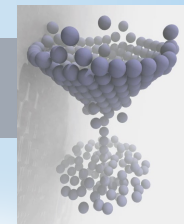
Hands on: how to prepare a Martini

“gin and vermouth are combined at a ratio of 2:1,
stirred in a mixing glass with ice cubes,
then strained into a chilled cocktail glass and garnished with an olive”

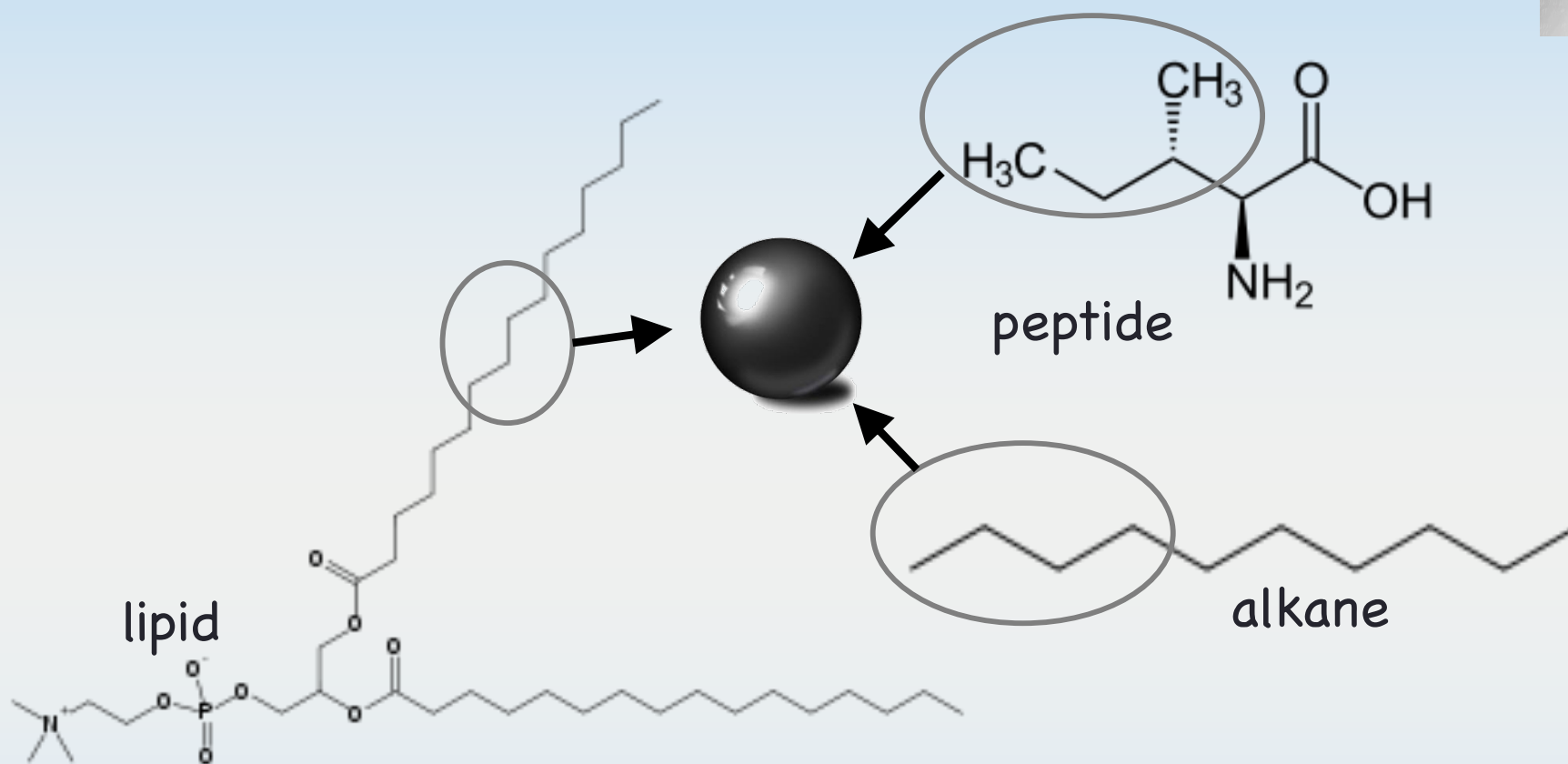
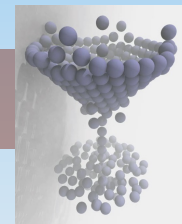
- A **Dry Martini** is made with dry gin and white vermouth
 - **Martini Rosso** uses red vermouth (caramel flavor)
 - **Vodka Martini** uses vodka instead of gin
- A **Perfect Martini** uses equal amounts of sweet and dry vermouth
- **Zen Martini**: Martini with no gin at all, and no vermouth either

“Martini should be made by filling a glass with gin, then waving it in the
general direction of Italy”

Bridging the all-atom to the continuum scale



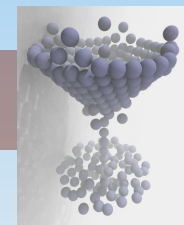
Mapping of atoms to building blocks



The Martini model reduces complexity of real molecules by considering groups of atoms as building blocks – the “Lego” principle

On average 4 heavy atoms (and associated hydrogens) are considered as building block and mapped to a coarse-grain bead

The building block principle



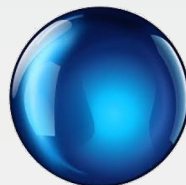
Building block types

C1
C2
C3
C4
C5



Apolar

N0
Nd/a
Nda



Intermediate

P1
P2
P3
P4
P5

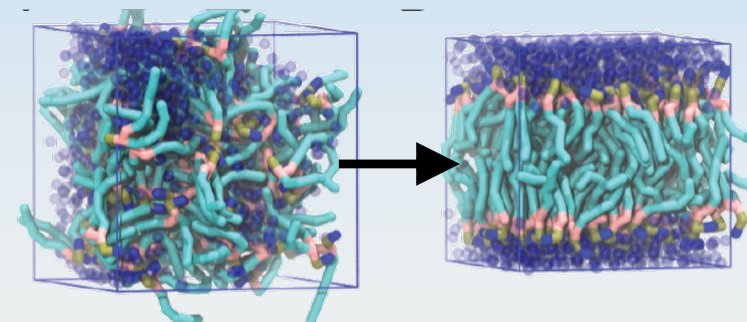
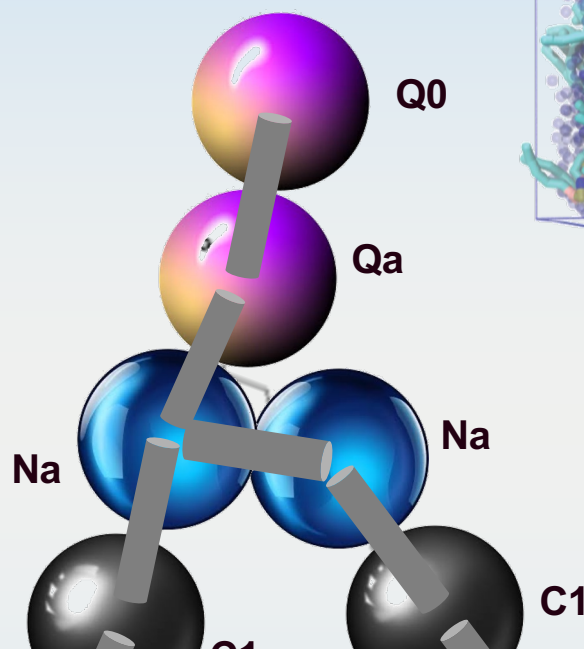


Polar

Q0
Qd/a
Qda



Charged

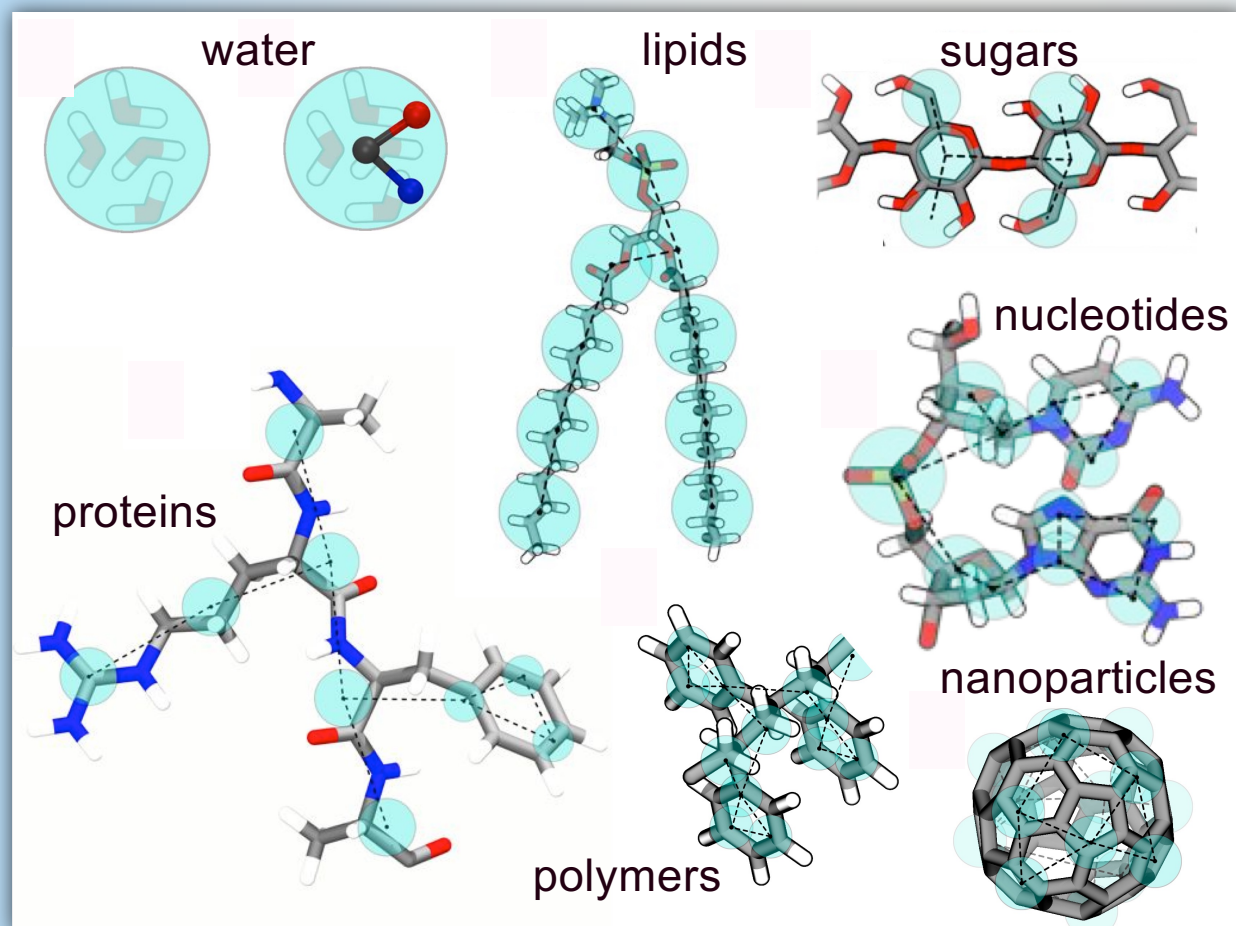
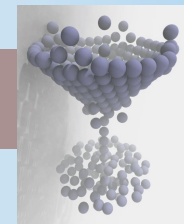


Lipids self-assemble
into a bilayer,
reproducing
known membrane
properties

Non-bonded interactions of building blocks
parameterized based on reproducing
experimental thermodynamic data

Bonded interactions parameterized to
match conformations of all-atom simulations
(or structural databases)

Welcome to the Martinidome



Key features:

- Chemical specificity
- Fast (10^3 speed-up)
- Compatibility
- Versatility

Parameterization:

TOP DOWN

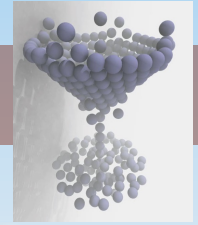
Thermodynamic data

BOTTOM UP

Atomistic simulations

"TOP UP"

What's in a name?



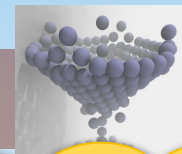
The Martini force field is developed in Groningen
and named after **Saint Martin**, patron saint of Groningen

(any association with cocktails is entirely coincidental)



Martini tower

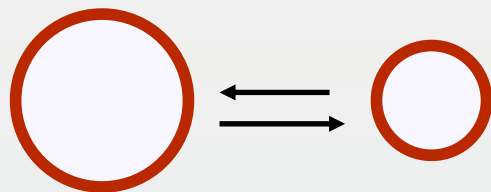
Non-bonded interactions: LJ & Coulomb



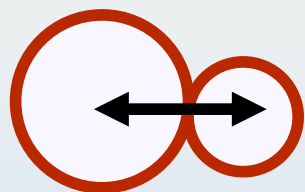
- **Non-bonded interactions** described by standard LJ and Coulombic energy functions



electrostatic



dispersion



overlap

Coulomb
(screened, $\epsilon_R=15$)

} *Lennard-Jones*

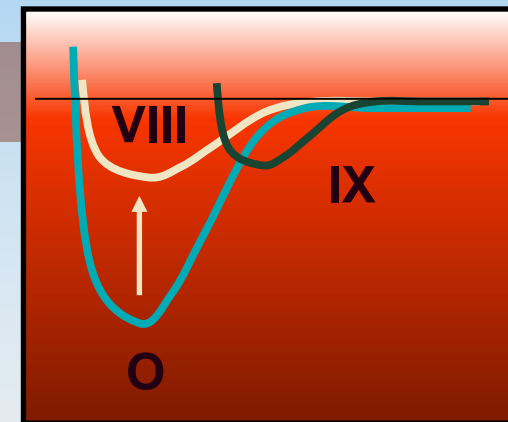
effectively
distant-dependent
screening,
 $\epsilon_R=\infty$ at cut-off

Limitation:
change in
environment not
felt by charges

- Potentials are **short-ranged** by use of *cut-off* (1.1 nm, 2-3 neighbors)
- Cut-off artefacts prevented by using potential/force modifiers (so potentials/forces vanish at cut-off)

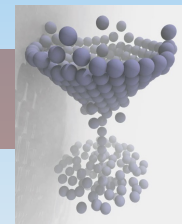
LJ interaction matrix for Martini beads

- LJ interactions depend on type of CG bead
- Beads have fixed size (Regular, Small, Tiny)
- LJ cross interactions explicitly parameterized (*no combination rule!*)



		charged (Q)				polar (P)					intermediate (N)					apolar (C)				
		da	d	a	0	5	4	3	2	1	da	d	a	0	5	4	3	2	1	
Q	da	O	O	O	II	O	O	O	I	I	I	I	I	IV	V	VI	VII	IX	IX	
	d	O	I	O	II	O	O	O	I	I	I	III	I	IV	V	VI	VII	IX	IX	
	a	O	O	I	II	O	O	O	I	I	I	I	III	IV	V	VI	VII	IX	IX	
	0	II	II	II	IV	I	O	I	II	III	III	III	III	IV	V	VI	VII	IX	IX	
P	5	O	O	O	I	O	O	O	O	O	I	I	I	IV	V	VI	VI	VII	VIII	
	4	O	O	O	O	O	I	I	II	II	III	III	III	IV	V	VI	VI	VII	VIII	
	3	O	O	O	I	O	I	I	II	II	II	II	II	IV	IV	V	V	VI	VII	
	2	I	I	I	II	O	II	II	II	II	II	II	II	III	IV	IV	V	VI	VII	
N	1	I	I	I	III	O	II	II	II	II	II	II	II	III	IV	IV	IV	V	VI	
	da	I	I	I	III	I	III	II	II	II	II	II	II	IV	IV	V	VI	VI	VI	
	d	I	III	I	III	I	III	II	II	II	II	III	II	IV	IV	V	VI	VI	VI	
	a	I	I	III	III	I	III	II	II	II	II	II	III	IV	IV	V	VI	VI	VI	
C	0	IV	IV	IV	IV	IV	IV	IV	III	III	IV	IV	IV	IV	IV	IV	IV	V	VI	
	5	V	V	V	V	V	V	IV	IV	IV	IV	IV	IV	IV	IV	IV	IV	V	V	
	4	VI	VI	VI	VI	VI	VI	V	IV	IV	V	V	V	IV	IV	IV	IV	V	V	
	3	VII	VII	VII	VII	VI	VI	V	V	IV	VI	VI	VI	IV	IV	IV	IV	IV	IV	
	2	IX	IX	IX	IX	VII	VII	VI	VI	V	VI	VI	VI	V	V	V	IV	IV	IV	
	1	IX	IX	IX	IX	VIII	VIII	VII	VII	VI	VI	VI	VI	VI	V	V	IV	IV	IV	

Top-down: reproducing experimental partitioning data

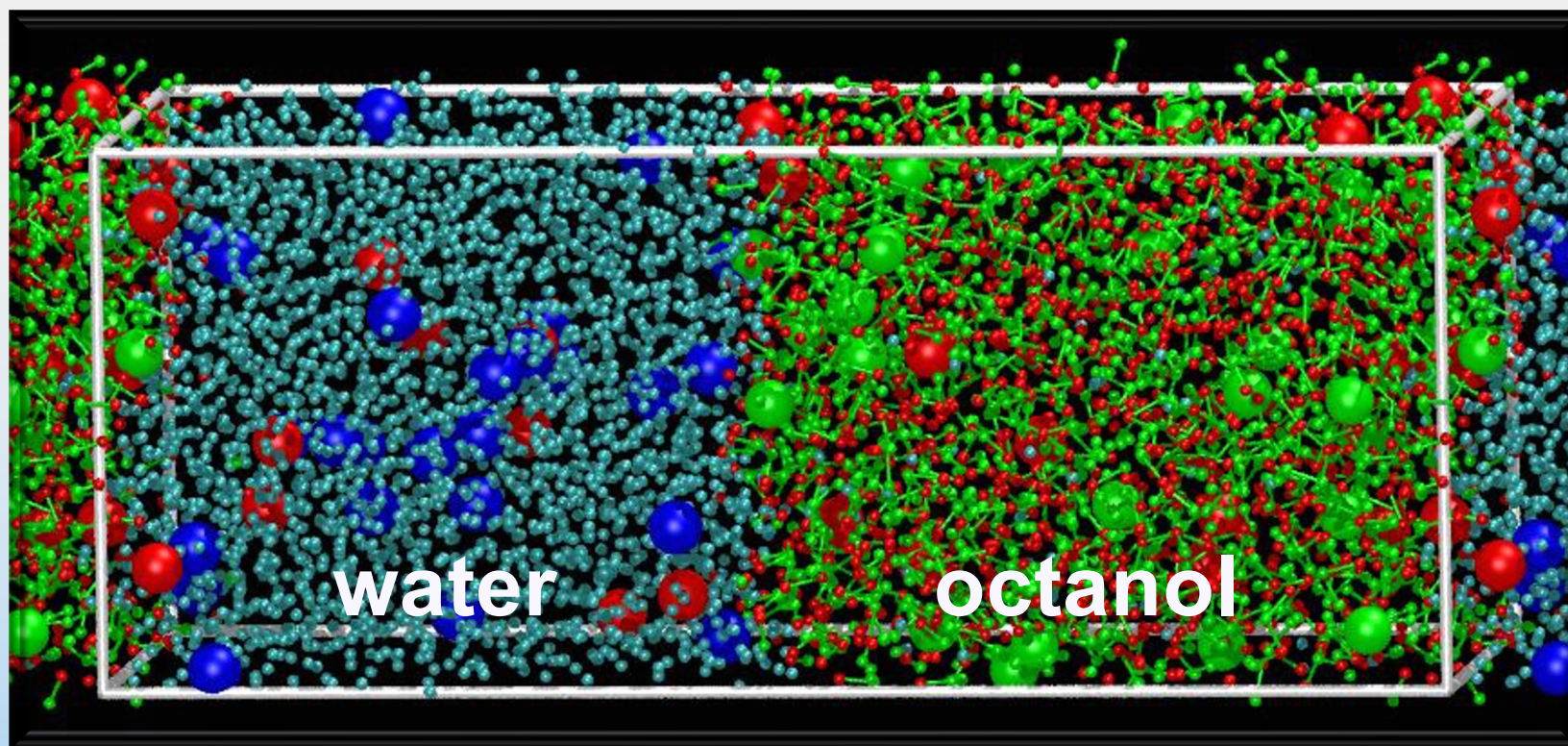


- LJ interactions are mainly parameterized based on reproducing experimental partitioning free energies
- Free energies obtained from “direct counting”:
$$\Delta G_{wat/oct} = \frac{1}{kT} \ln \frac{\rho_{wat}}{\rho_{oct}}$$

● Polar (P)

● Intermediate (N)

● Apolar (C)

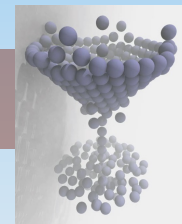


The Martini bible: mapping CG bead types to chemical build

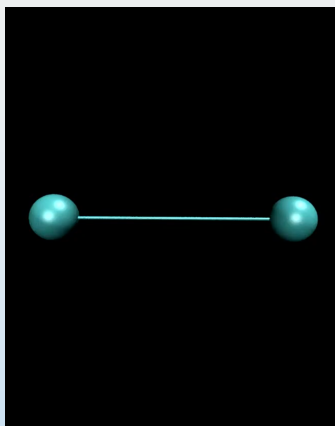
type	building block	examples	$\Delta G_{\text{HW}}^{\text{part}}$		$\Delta G_{\text{CW}}^{\text{part}}$		$\Delta G_{\text{EW}}^{\text{part}}$		$\Delta G_{\text{OW}}^{\text{part}}$	
			exp	CG	exp	CG	exp	CG	exp	CG
Q _{da}	H ₃ N ⁺ -C ₂ -OH	ethanolamine (protonated)		< -30		-18		-13		-18
Q _d	H ₃ N ⁺ -C ₃	1-propylamine (protonated)		< -30		-18		-13		-18
	NA ⁺ OH	sodium (hydrated)		< -30		-18		-13		-18
Q _a	PO ₄ ⁻	phosphate		< -30		-18		-13		-18
	CL ⁻ HO	chloride (hydrated)		< -30		-18		-13		-18
Q ₀	C ₃ N ⁺	choline		< -30		-18		-13		-18
P ₅	H ₂ N-C ₂ =O	acetamide	-27	-28	(-20)	-18	-15	-13	-8	-10
P ₄	HOH (× 4)	water	-25	-23		-14	-10	-7	-8	-9
	HO-C ₂ -OH	ethanediol	-21	-23		-14		-7	-8	-9
P ₃	HO-C ₂ =O	acetic acid	-19	-21	-9	-10	-2	-6	-1	-7
	C-NH-C=O	methylformamide		-21		-10		-6	-5	-7
P ₂	C ₂ -OH	ethanol	-13	-17	-5	-2	-3	1	-2	-2
P ₁	C ₃ -OH	1-propanol	-9	-11	-2	-2	0	1	1	-1
		2-propanol	-10	-11	-2	-2	-1	1	0	-1
N _{da}	C ₄ -OH	1-butanol	-5	-7	2	0	4	2	4	3
N _d	H ₂ N-C ₃	1-propylamine	(-6)	-7	(1)	0	(-3)	2	(3)	3
N _a	C ₃ =O	2-propanone	-6	-7	1	0	-1	2	-1	3
	C-NO ₂	nitromethane	-6	-7		0		2	-2	3
	C ₃ =N	propionitrile	-5	-7		0		2	1	3
	C-O-C=O	methylformate	(-6)	-7	(4)	0	(-1)	2	(0)	3
	C ₂ HC=O	propanal	-4	-7		0	2	2	3	3
N ₀	C-O-C ₂	methoxyethane	(1)	-2		6	(3)	6	(3)	5
C ₅	C ₃ -SH	1-propanethiol		5		10		10		6
	C-S-C ₂	methyl ethyl sulfide	(7)	5		10		10	(9)	6
C ₄	C ₂ =C ₂	2-butyne		9		13		13	9	9
	C=C-C=C	1,3-butadiene	11	9		13		13	11	9
	C-X ₄	chloroform	(7)	9	14	13		13	11	9
C ₃	C ₂ =C ₂	2-butene		13		13		13	13	14
	C ₃ -X	1-chloropropane	12	13		13		13	12	14
		2-bromopropane		13		13		13	12	14
C ₂	C ₃	propane		16		15		14	14	16
C ₁	C ₄	butane	18	18		18		14	16	17
		isopropane		18		18		14	16	17

	EXP	CG
P ₅	-27	-28
P ₄	-25	-23
	-21	-23
P ₃	-19	-21
		-21
P ₂	-13	-17
P ₁	-9	-11
	-10	-11
<hr/>		
N _{da}	-5	-7
N _d	(-6)	-7
N _a	-6	-7
	-6	-7
	-5	-7
	(-6)	-7
	-4	-7
N ₀	(1)	-2
<hr/>		
C ₅		5
	(7)	5
C ₄		9
	11	9
	(7)	9
C ₃		13
	12	13
		13
C ₂		16
C ₁	18	18
		18

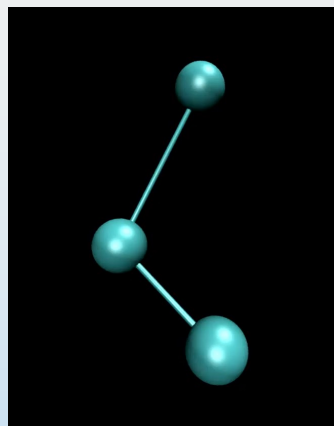
Simple harmonic forms for bonded interactions



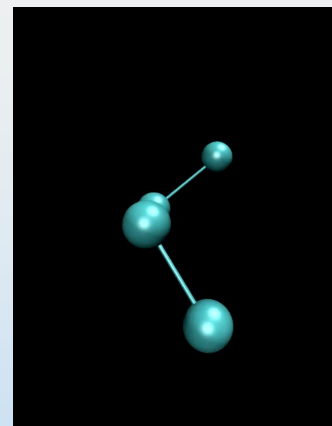
Bonds



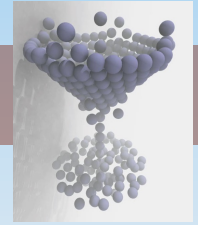
Angles



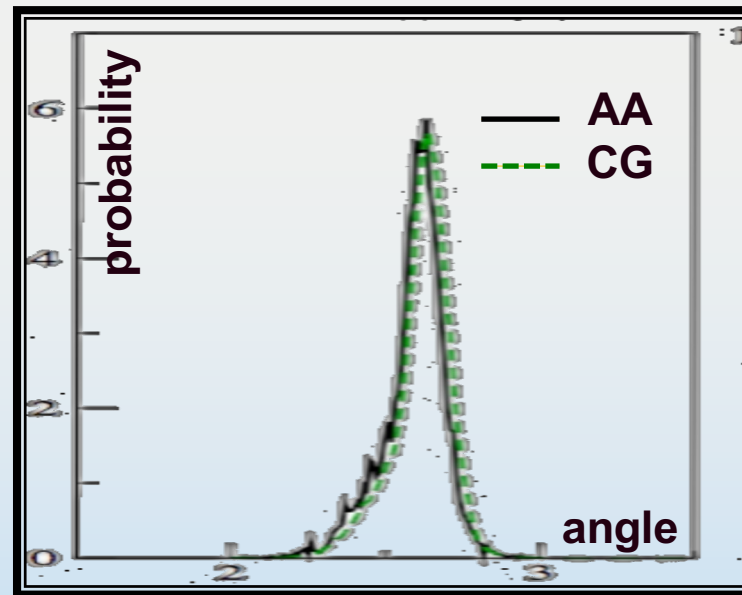
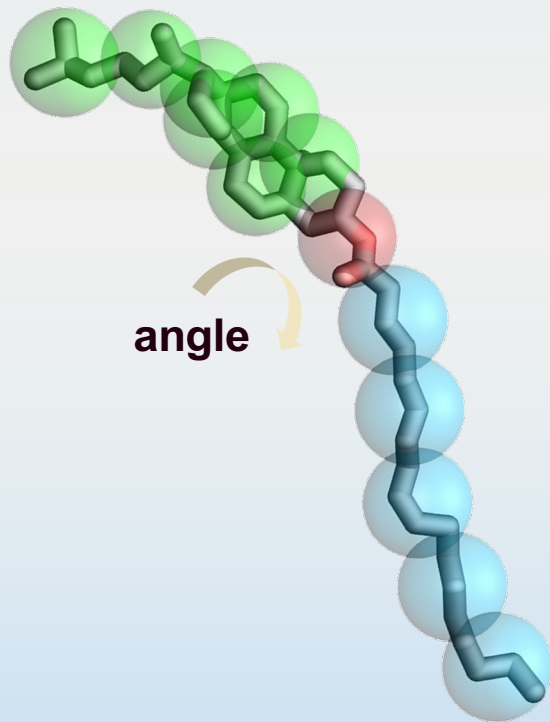
Dihedrals



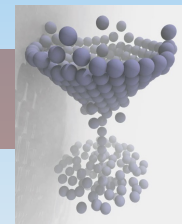
Bottom-up approach for bonded interactions



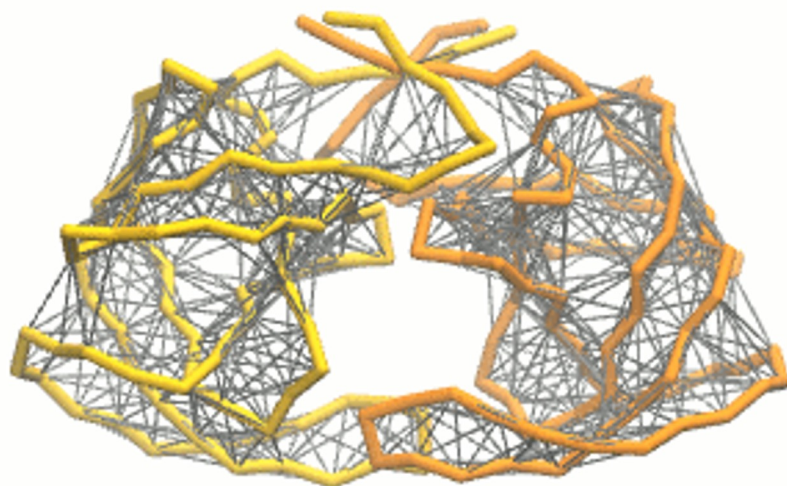
- **Bonded interactions** are parameterized by mapping to all-atom simulations



Proteins require elastic network



- **Elastic network approach (EINeDyn)** required to maintain 2ndary structure of proteins (directional H-bonds are missing in Martini !)

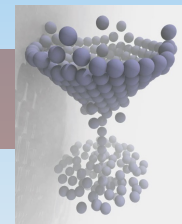


EINeDyn: harmonic potentials between all $C\alpha$ beads within a cut-off

Limitation:
Folding/unfolding
not possible with
Martini

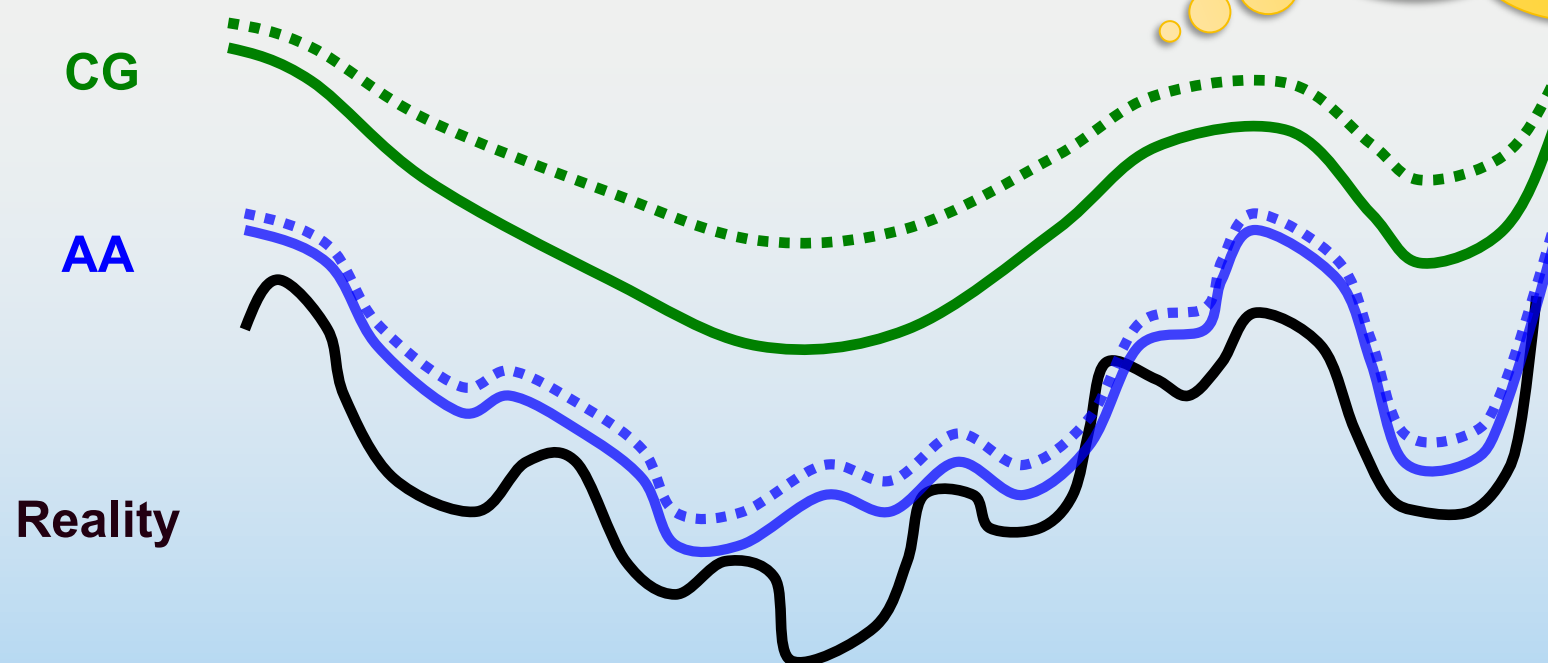
However:
GoMartini offers
some flexibility

Why is Martini so fast (1000 x speedup)

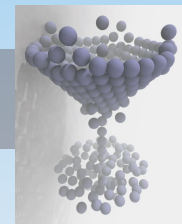


- Less particles, so less interactions to compute
- Short range potentials only
- Less friction, so faster sampling
- Time steps of 20-30 fs can be used
(*accurate sampling is less critical*)

Limitation:
Timescale should
be interpreted
with care



Martini 3



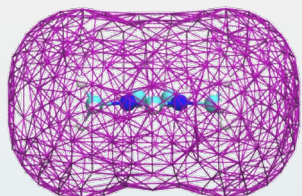
Martini 1: for lipids
Marrink et al. JPCB, 2004



Martini 2: for biomolecules
Marrink et al. JPCB, 2007



Martini 3: for general purpose
Souza et al. Nature Methods, 2021



1) Improved interactions and packing

Reparametrized all bead-bead interactions and bonds using center-of-geometry

2) Better coverage of chemical space

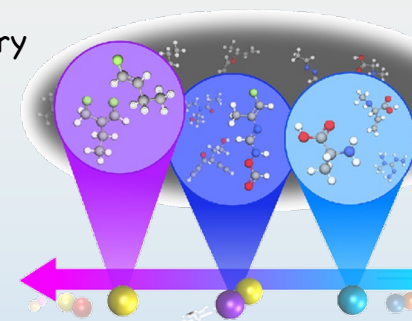
New beads and ways to modify them

3) Reformulation of charged beads

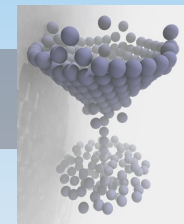
Including bare ions and double charged ions, Hoffmeister series

4) Embracing Gō models for proteins

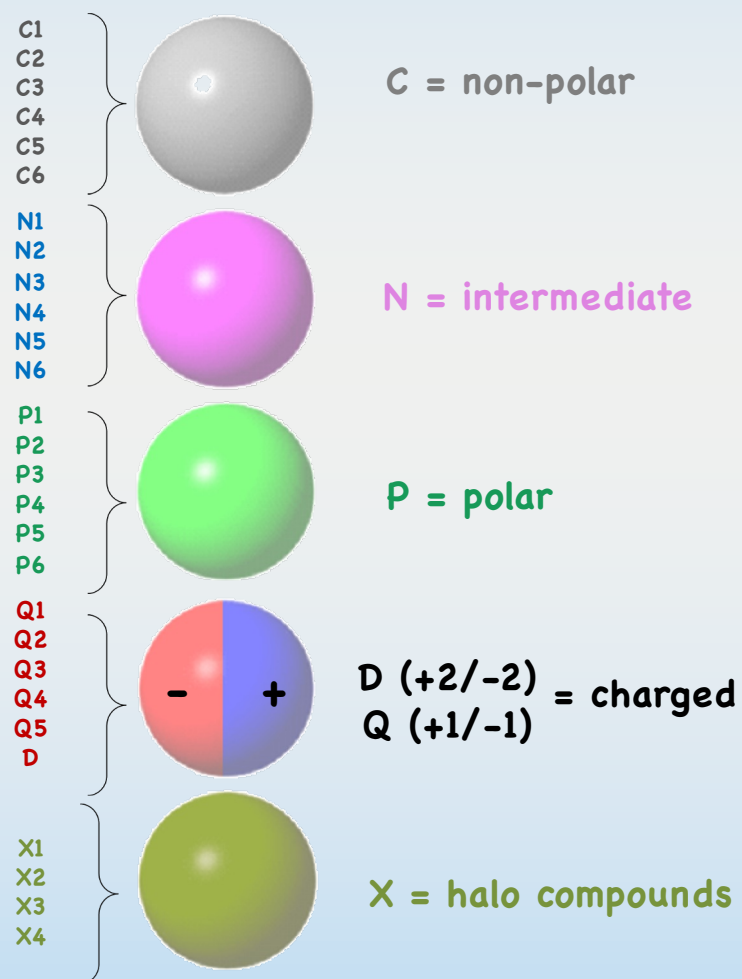
Allowing allostery and folding/unfolding transitions



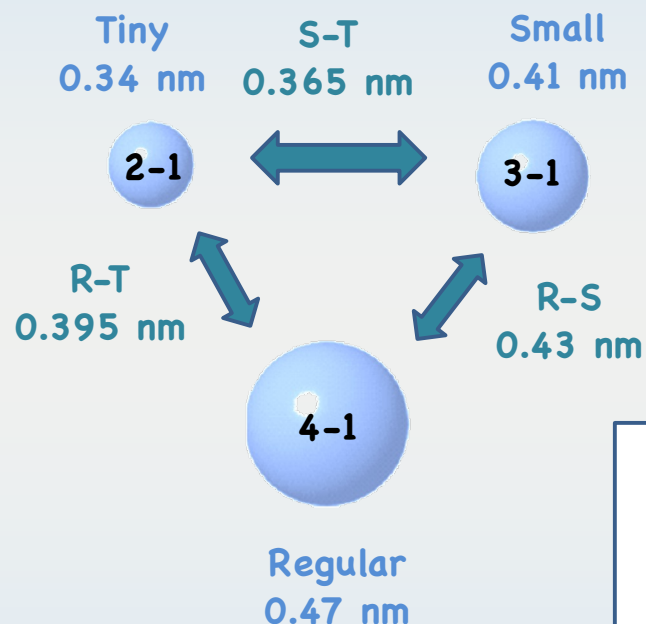
Martini 3: Just bead it ...



28 Bead Chemical Types



3 Bead Sizes



Specific bead for water



W = water

From M2 to M3:

54 → 843 beads
1,485 → 355,746 pairs
60 → 1,301 parameters

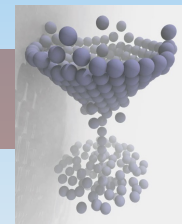
9 Bead Labels



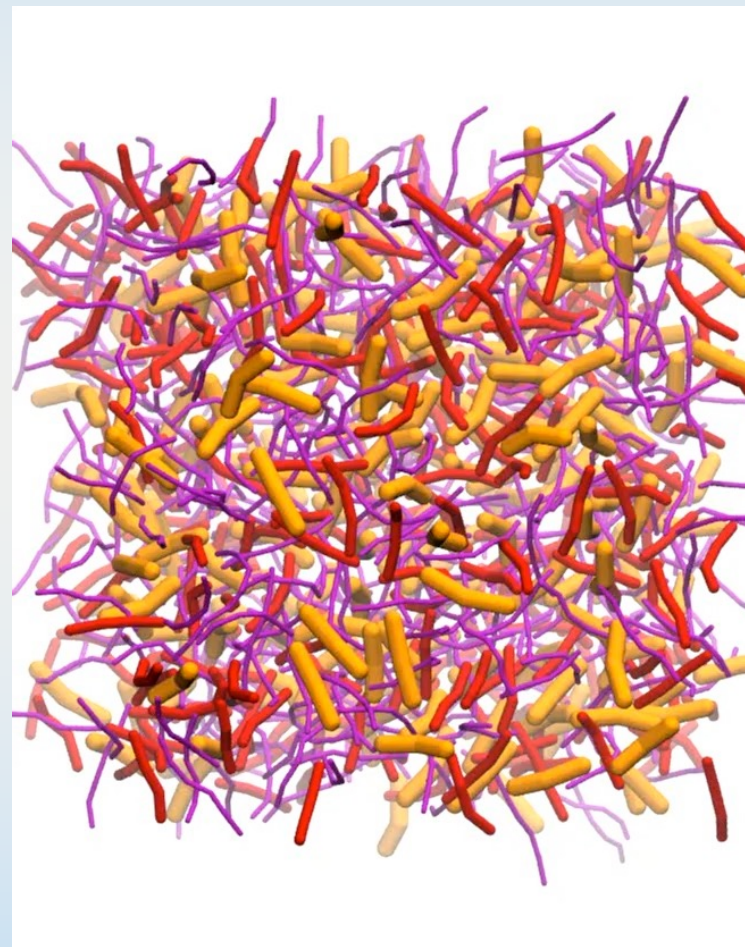
Examples:

H-donor (d) / H-acceptor (a)
Electron rich (e) / Electron poor (v)

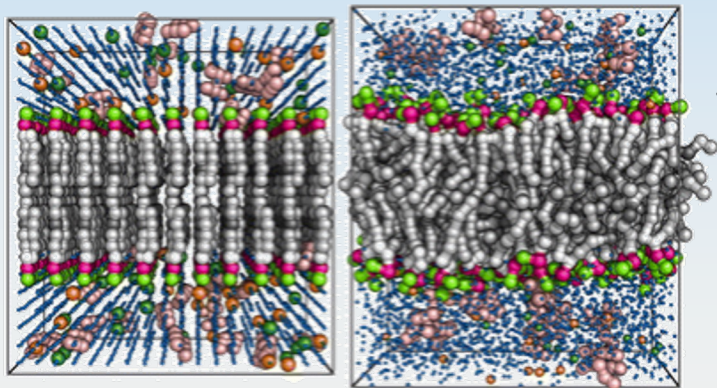
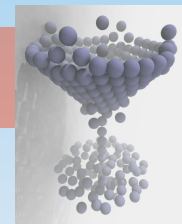
Martini 3.0 bead sizes well balanced



Mixing different resolutions
of liquid dodecane with:
3 *N* beads (orange),
4 *S* beads (red), and
6 *T* beads (magenta)



High-throughput tools

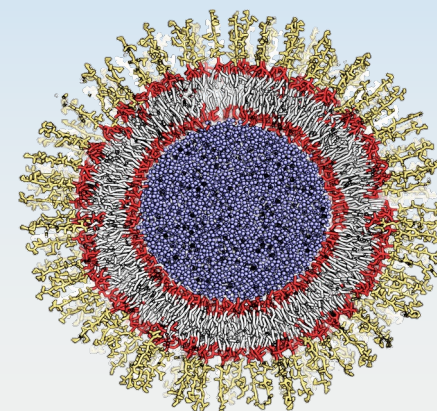
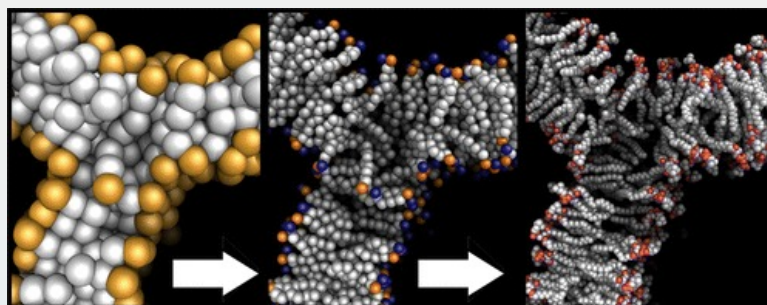


Insane

Wassenaar et al., *JCTC* (2015)

Backward

Wassenaar et al., *JCTC* (2014)

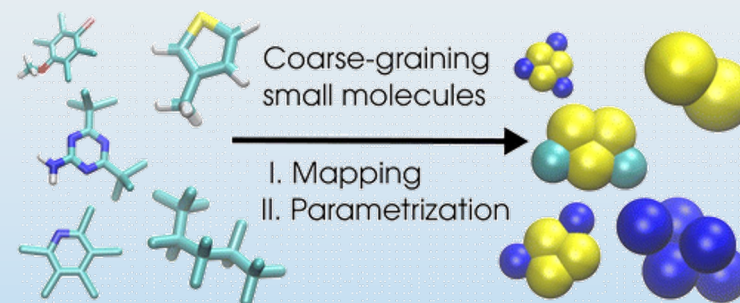
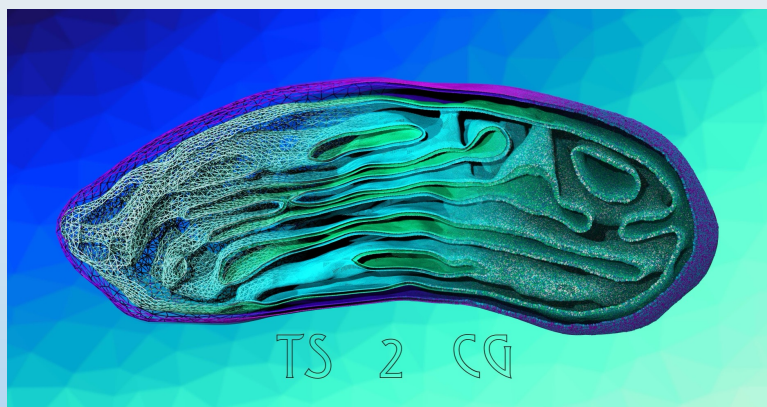


Martini-Maker (Charmm-GUI)

Qi et al., *JCTC* (2015)

TS2CG

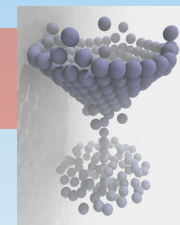
Pezeshkian et al., *Nature Comm* (2020)



ATB

Bereau & Kremer, *JCTC* (2015)

More high-throughput tools



Martinize2

Kroon et al., *eLife* (2023)

Polyply

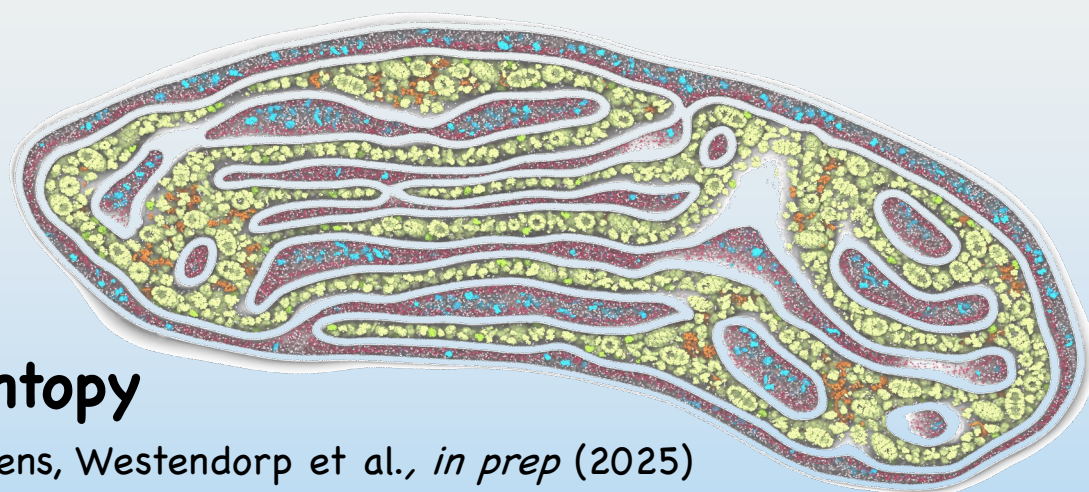
Grünewald et al., *Nat. Comm.* (2022)

Total inputs 87084

Martinize step	#	Fraction of total
Success	64134	73.6
Missing side chain beads	21730	25.0
Unrecognized residues	331	0.4
Missing backbone atoms	889	1.0

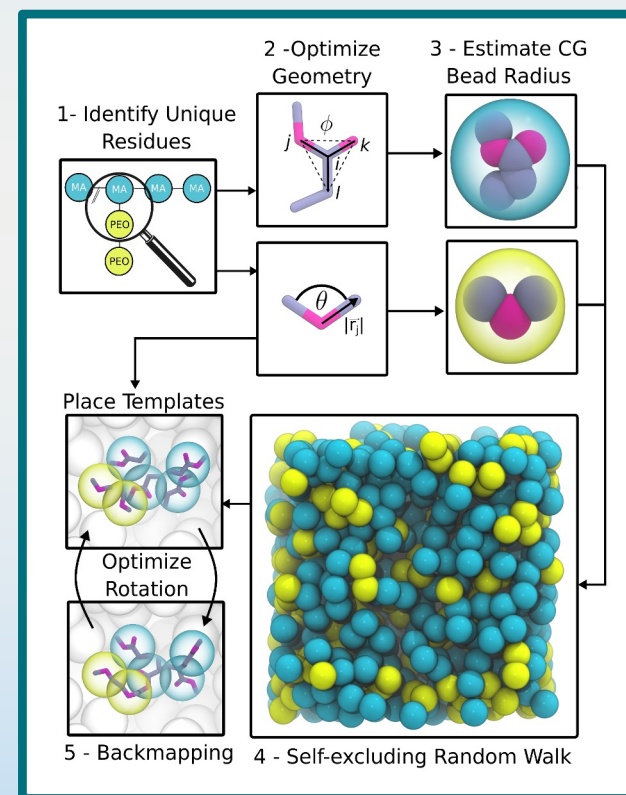
Grompp step	#	Fraction of total	Fraction of previous step
Success	64134	73.6	100.0
Errors	0	0.0	0.0

Mdrun step	#	Fraction of total	Fraction of previous step
Success	63784	73.2	99.5
Errors	350	0.4	0.5

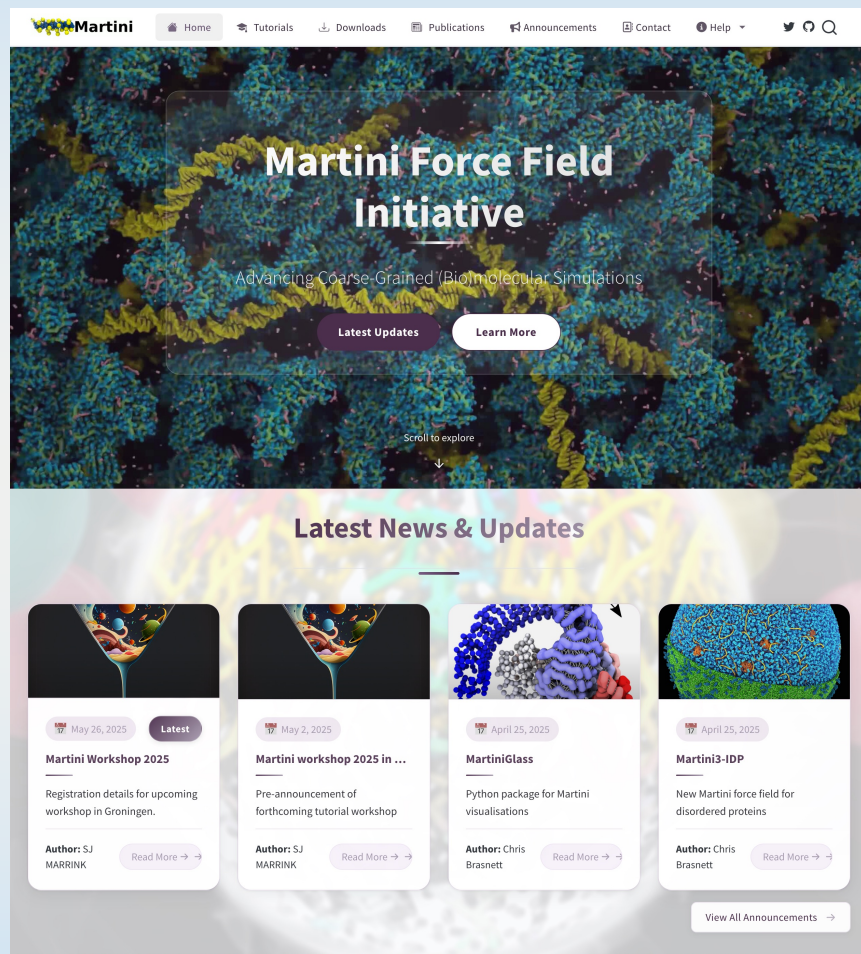


Bentopy

Stevens, Westendorp et al., *in prep* (2025)

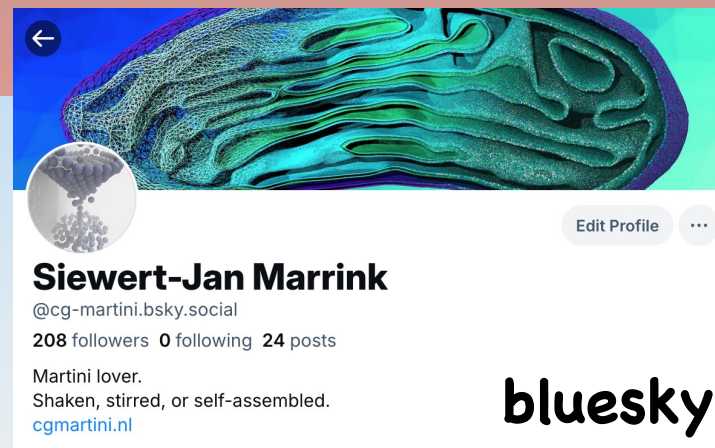


Open science

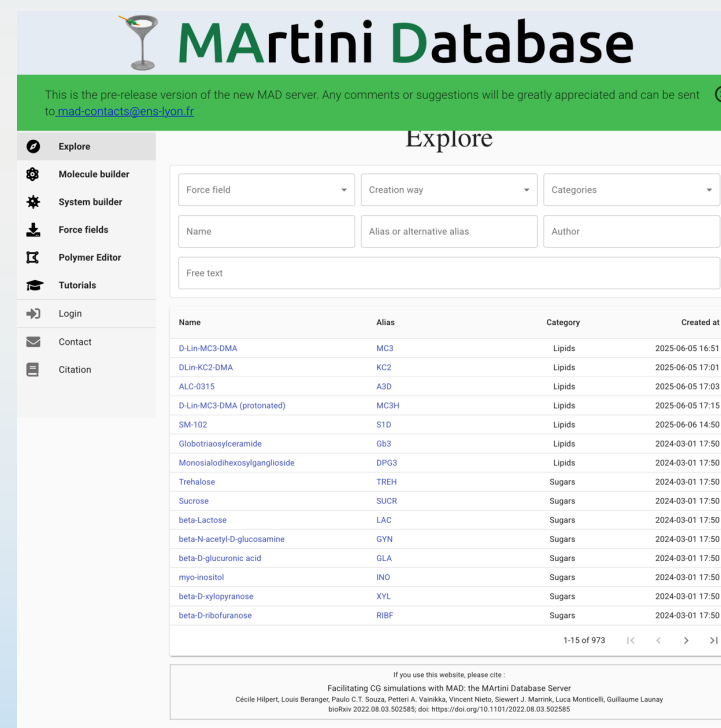


The screenshot shows the Martini website homepage. At the top is a navigation bar with links: Home, Tutorials, Downloads, Publications, Announcements, Contact, Help, and social media icons. The main banner features a molecular simulation background with the text "Martini Force Field Initiative" and "Advancing Coarse-Grained (Bio)molecular Simulations". Below this are buttons for "Latest Updates" and "Learn More", and a "Scroll to explore" arrow. The "Latest News & Updates" section contains four cards: "Martini Workshop 2025" (May 26, 2025), "Martini workshop 2025 in ..." (May 2, 2025), "MartiniGlass" (April 25, 2025), and "Martini3-IDP" (April 25, 2025). Each card includes a brief description and an author (SJ MARRINK or Chris Brasnett) with a "Read More" link. A "View All Announcements" link is at the bottom right.

cgmartini.nl



The screenshot shows the Bluesky profile of Siewert-Jan Marrink. The profile picture is a circular image of a molecular simulation. The header image is a large, colorful molecular simulation. The profile information includes the name "Siewert-Jan Marrink", the handle "@cg-martini.bsky.social", 208 followers, 0 following, and 24 posts. The bio reads "Martini lover. Shaken, stirred, or self-assembled." and includes the link "cgmartini.nl". The Bluesky logo is visible on the right.



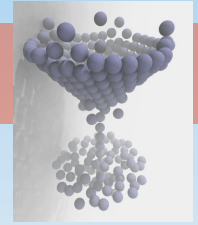
The screenshot shows the Martini Database website. The header features the "MARTINI Database" logo and a green banner stating: "This is the pre-release version of the new MAD server. Any comments or suggestions will be greatly appreciated and can be sent to mad-contact@ens-lyon.fr". The "Explore" section has a sidebar with navigation links: Explore, Molecule builder, System builder, Force fields, Polymer Editor, Tutorials, Login, Contact, and Citation. The main content area has search filters for "Force field", "Creation way", and "Categories", along with input fields for "Name", "Alias or alternative alias", and "Author". Below the filters is a table of entries:

Name	Alias	Category	Created at
D-Lin-MC3-DMA	MC3	Lipids	2025-06-05 16:51
D-Lin-KC2-DMA	KC2	Lipids	2025-06-05 17:01
ALC-0315	A3D	Lipids	2025-06-05 17:03
D-Lin-MC3-DMA (protonated)	MC3H	Lipids	2025-06-05 17:15
SM-102	STD	Lipids	2025-06-06 14:50
Globotriaosylceramide	GB3	Lipids	2024-03-01 17:50
Monosialodihexosylganglioside	DPG3	Lipids	2024-03-01 17:50
Trehalose	TREH	Sugars	2024-03-01 17:50
Sucrose	SUCR	Sugars	2024-03-01 17:50
beta-Lactose	LAC	Sugars	2024-03-01 17:50
beta-N-acetyl-D-glucosamine	GYN	Sugars	2024-03-01 17:50
beta-D-glucuronic acid	GLA	Sugars	2024-03-01 17:50
myo-inositol	INO	Sugars	2024-03-01 17:50
beta-D-xylopyranose	XYL	Sugars	2024-03-01 17:50
beta-D-ribofuranose	RIBF	Sugars	2024-03-01 17:50

At the bottom, there is a footer with the text: "If you use this website, please cite: Facilitating CG simulations with MAD: the MARTINI Database Server Cécile Hilbert, Louis Beranger, Paulo C.T. Sousa, Petteri A. Vainikka, Vincent Nieto, Siewert J. Marrink, Luca Monticelli, Guillaume Launay bioRxiv 2022.08.03.502585; doi: <https://doi.org/10.1101/2022.08.03.502585>

mad.ens-lyon.fr

The schedule



Day 1: Lipids

Morning lectures
Afernoon tutorial

Day 2: Proteins

Morning lectures
Afernoon tutorial
Evening poster session

Day 3: Parameterization

Morning lectures
Afernoon tutorial

Day 4: Complex Systems

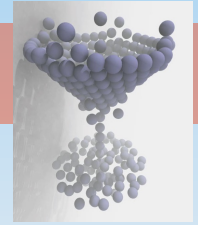
Morning lectures
Afernoon tutorial
Evening conference dinner

Day 5: Your Own

Morning tutorial

Note: tutorials available at both
beginner and advanced levels

The workshop team



Lecturers

Tsjerk Wassenaar
Helgi Ingolfsson
Manel Melo
Sebastian Thallmair
Adolfo Poma
Riccardo Alessandri
Fabian Grünewald
Linus Grünewald
Weria Pezeshkian
Chris Brasnett
Luis Borges
Daniel Ramirez
Jan Stevens
Chelsea Brown

TAs

Abby Dommer
Bart Bruininks
Rubi Zarmiento
Pietro Sillano
Wietske Nauta
Marieke Westendorp
...

Support

Alex de Vries
Jannet Nijhuis



Enjoy Sampling Martinis !!

"A man must defend his home, his wife, his children, and his martini." - Jackie Gleason

