Working with ODYSSEY Molecular Explorer

in the Chemistry Classroom

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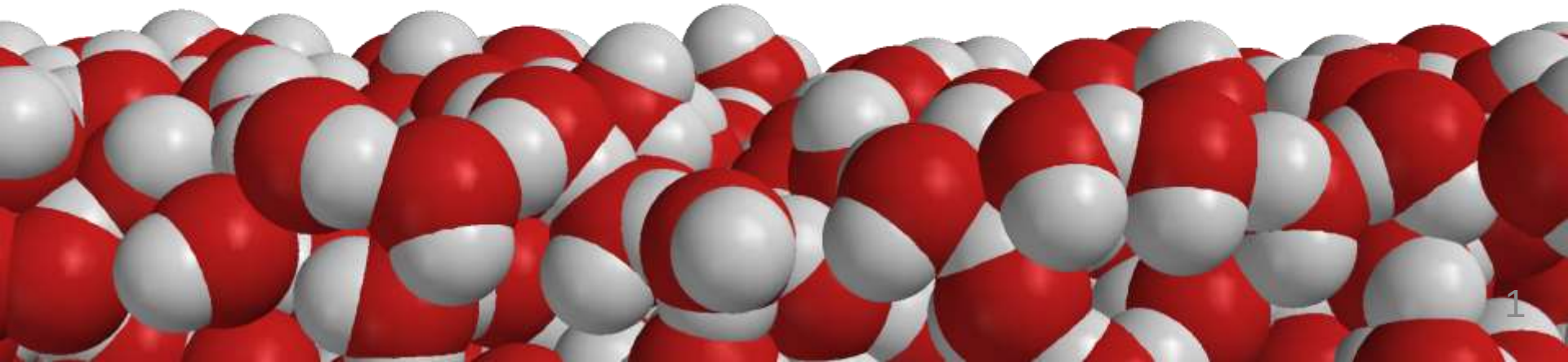


In This Document…

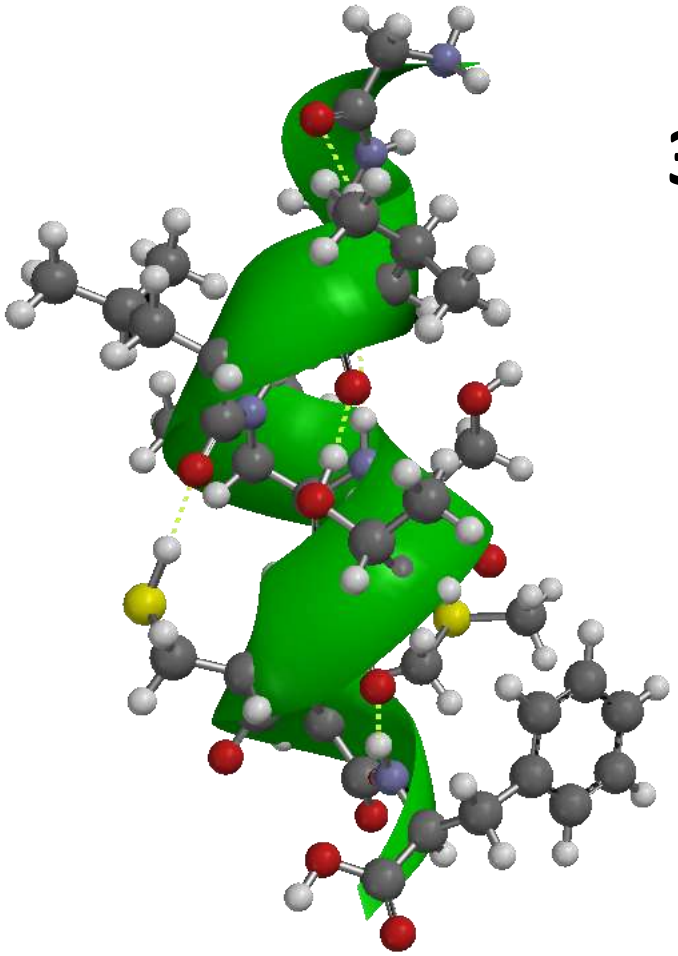
ODYSSEY Molecular Explorer

Molecular Modeling

Using Science to Teach Science

What Is ODYSSEY Molecular Explorer ?

How Is It Unique ?



3D Visualization & Simulation

a) **At the Molecular Level**…Always

b) ***Very* Science-Based**…Always
(Closely Related to "Real"
Molecular Modeling Programs)

c) **Explorable**…Always

ODYSSEY Molecular Explorer and the NGSS*

Content **AND** Practices **AND** Crosscutting Concepts

Traditional

~~**Content**~~
(“Memorization”)

~~**Practices**~~
(”Activities”)

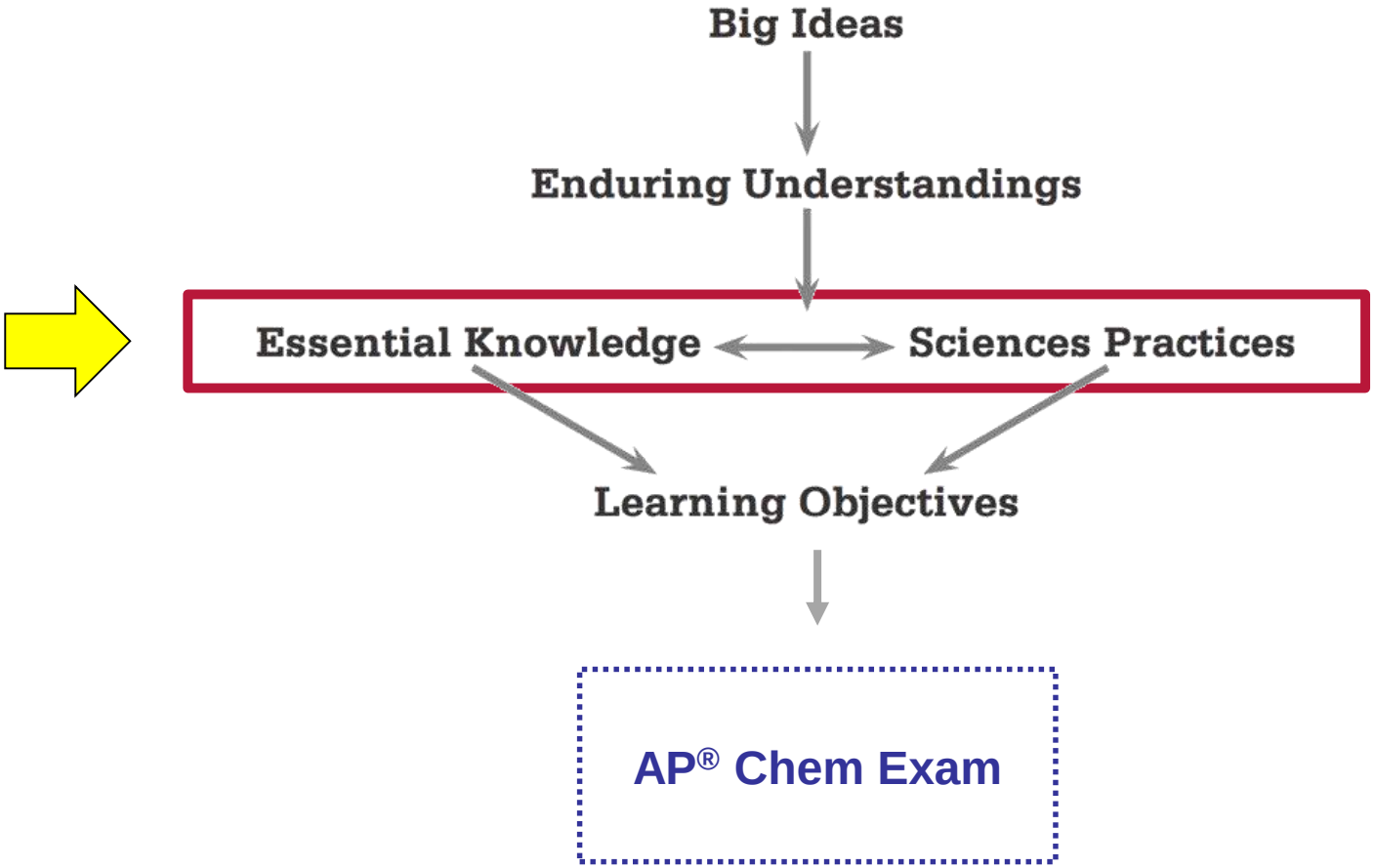
NGSS

Couple Content with Practices

*NGSS is a registered trademark of Achieve. Neither Achieve nor the lead states and partners that developed the Next Generation Science Standards was involved in the production of, and does not endorse, this product.

ODYSSEY Molecular Explorer and AP® Chemistry*

Knowledge + Skill = Exam Question



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How Can ODYSSEY Molecular Explorer Be Used?

- **Direct Demonstrations**
  ("The Molecular Perspective")
- **Inquiry/Exploration**
  (Ask Leading Questions!)
- **Computer Lab Experiments**
  (Complement Wet Lab)
- **Take-Home Labs**
- **Enrichment**
- **Self-Study**

Teacher Computer

Classroom Computers

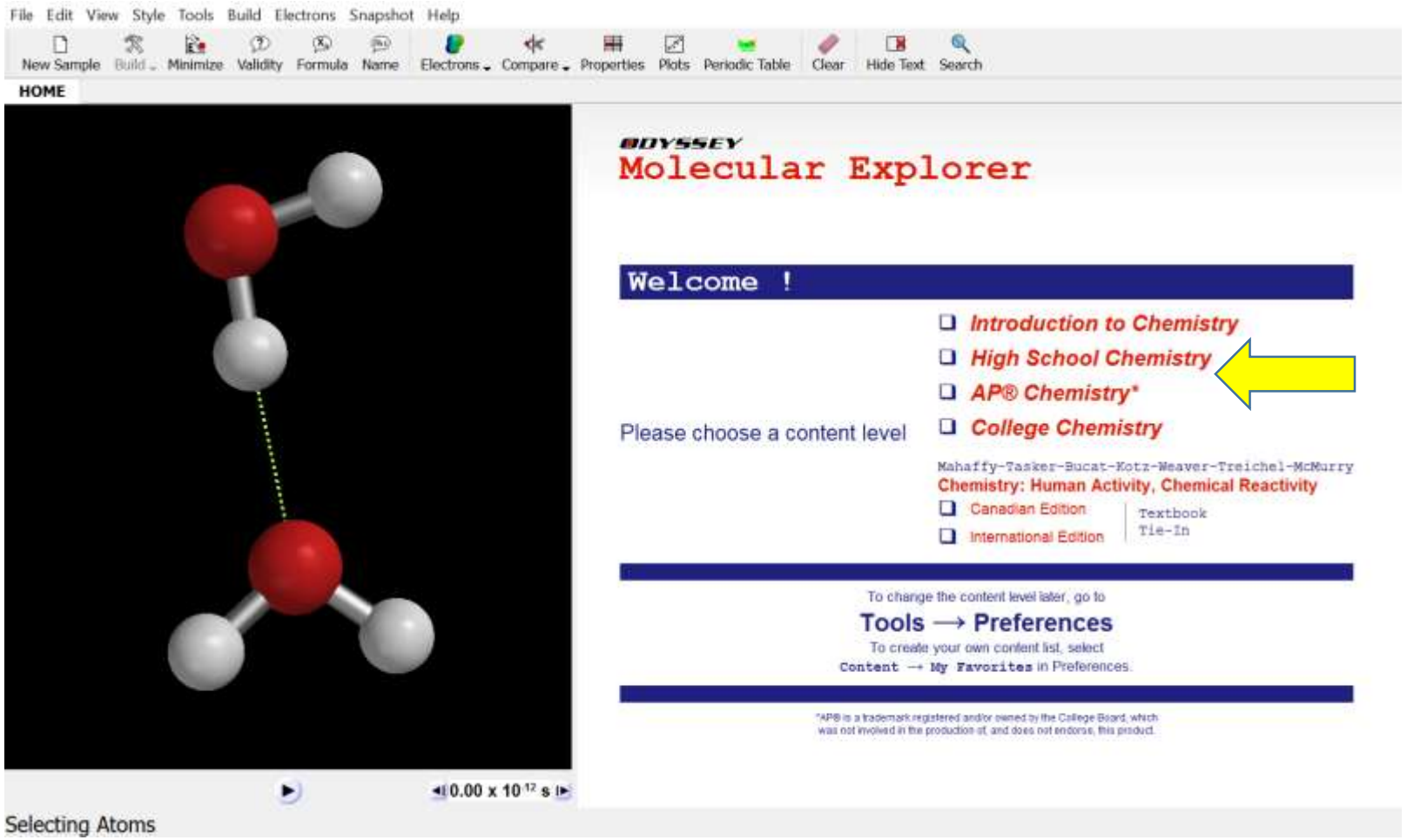
Student Computers

Scientific Content

ODYSSEY Models + Teaching Units

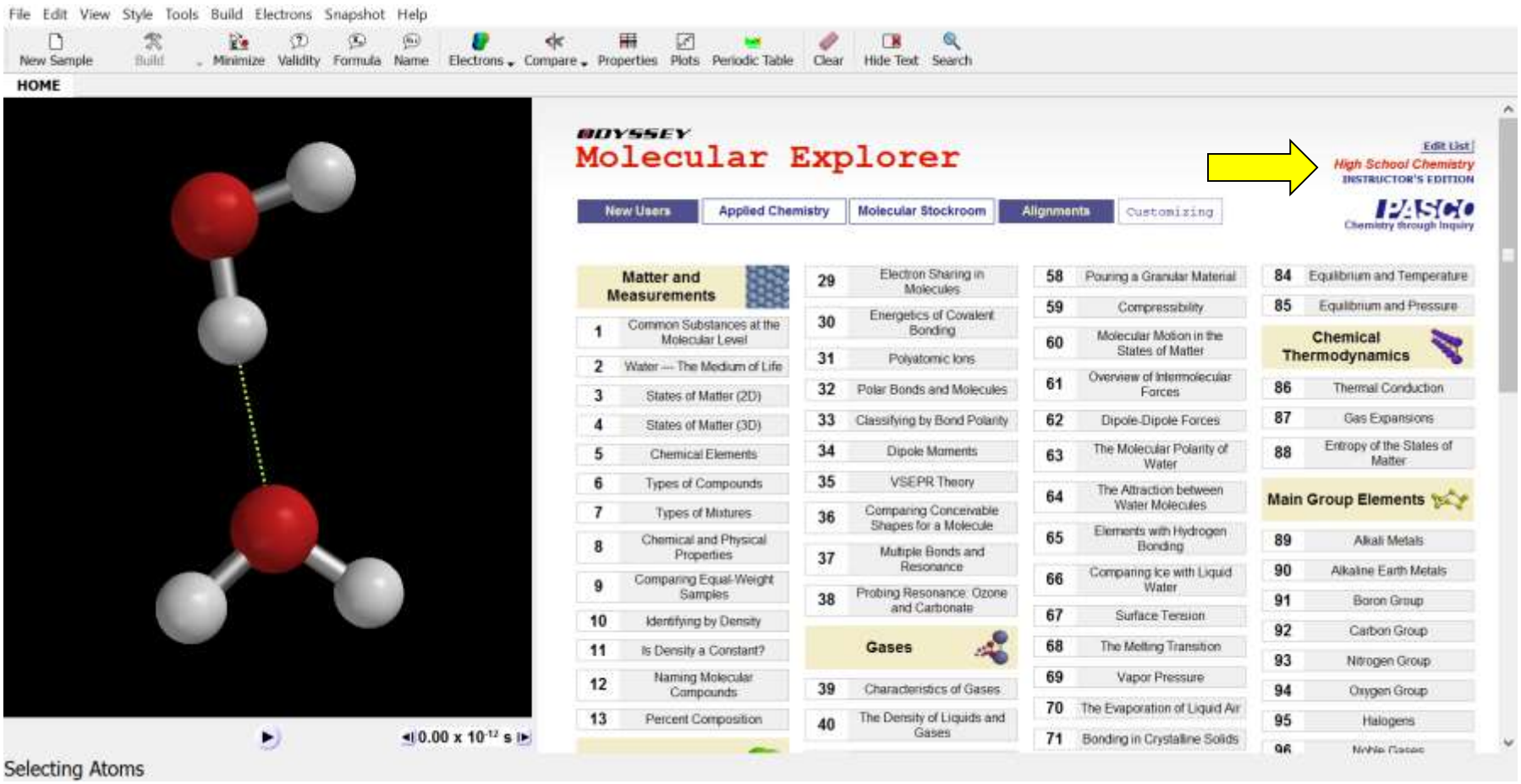
Molecular Labs (I)

Select a Content Level



ODYSSEY Molecular Explorer — Molecular Labs (II)

High School: ~110 Units | AP® Chemistry: ~148 Units*



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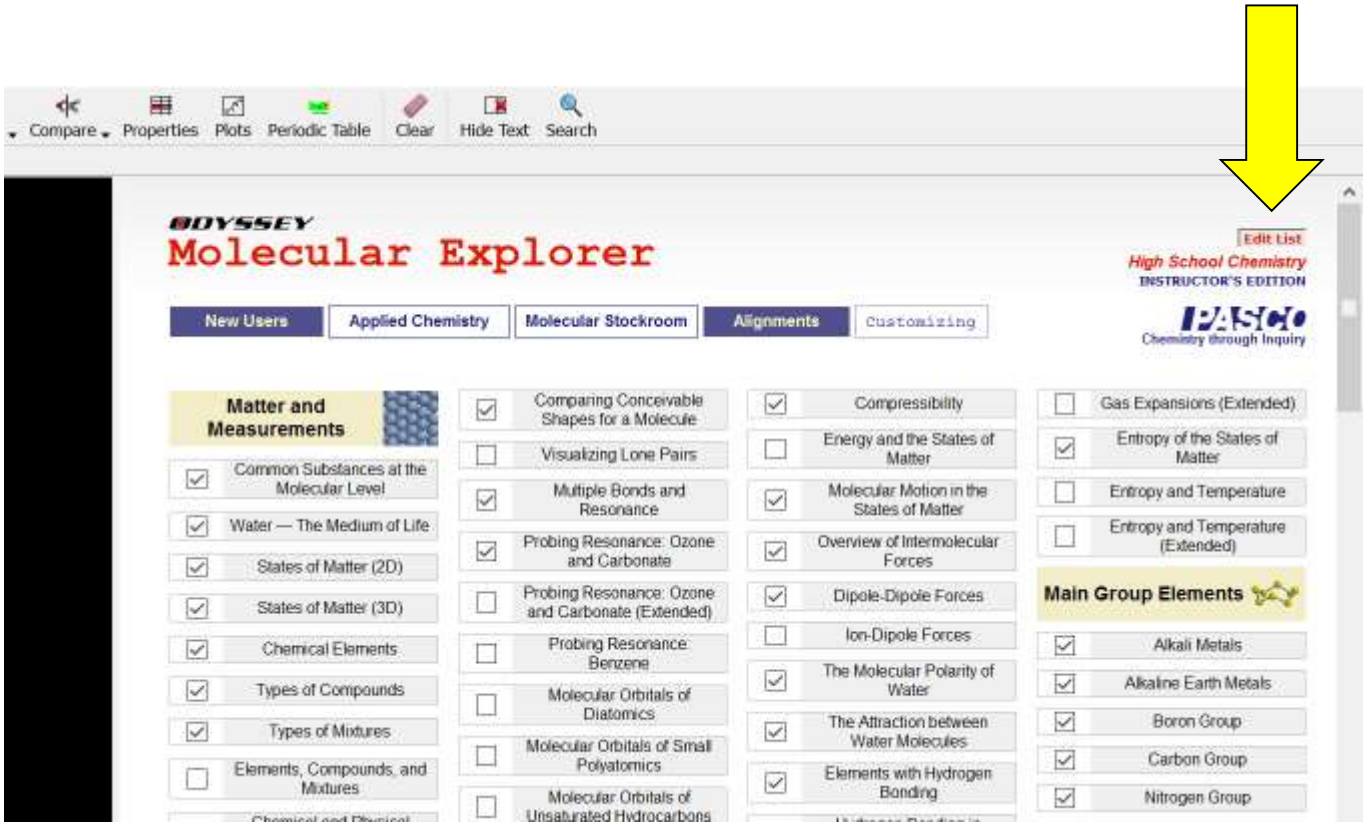
Molecular Labs (III)

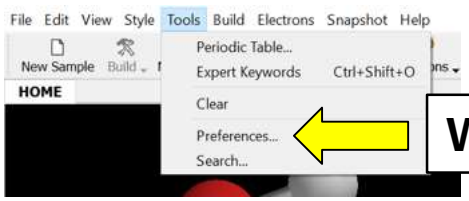
How Do I Customize the Table of Contents?



Set/Unset Checkmarks

Molecular Labs (IV)

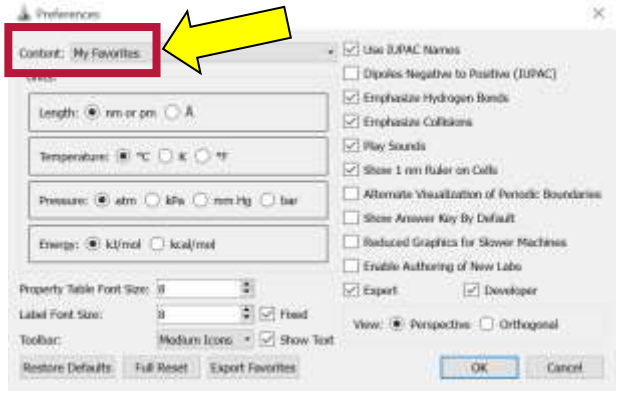
How Do I Create My Own Table of Contents?

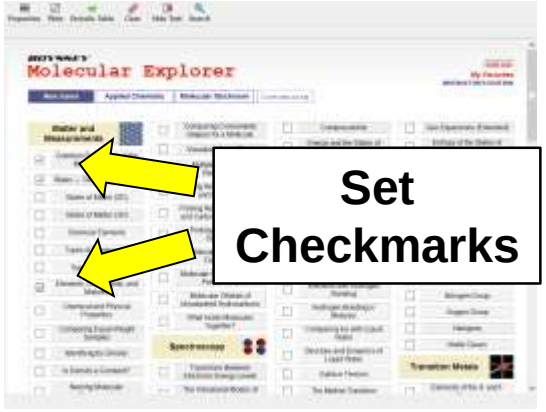


Win

Mac

Custom Table !



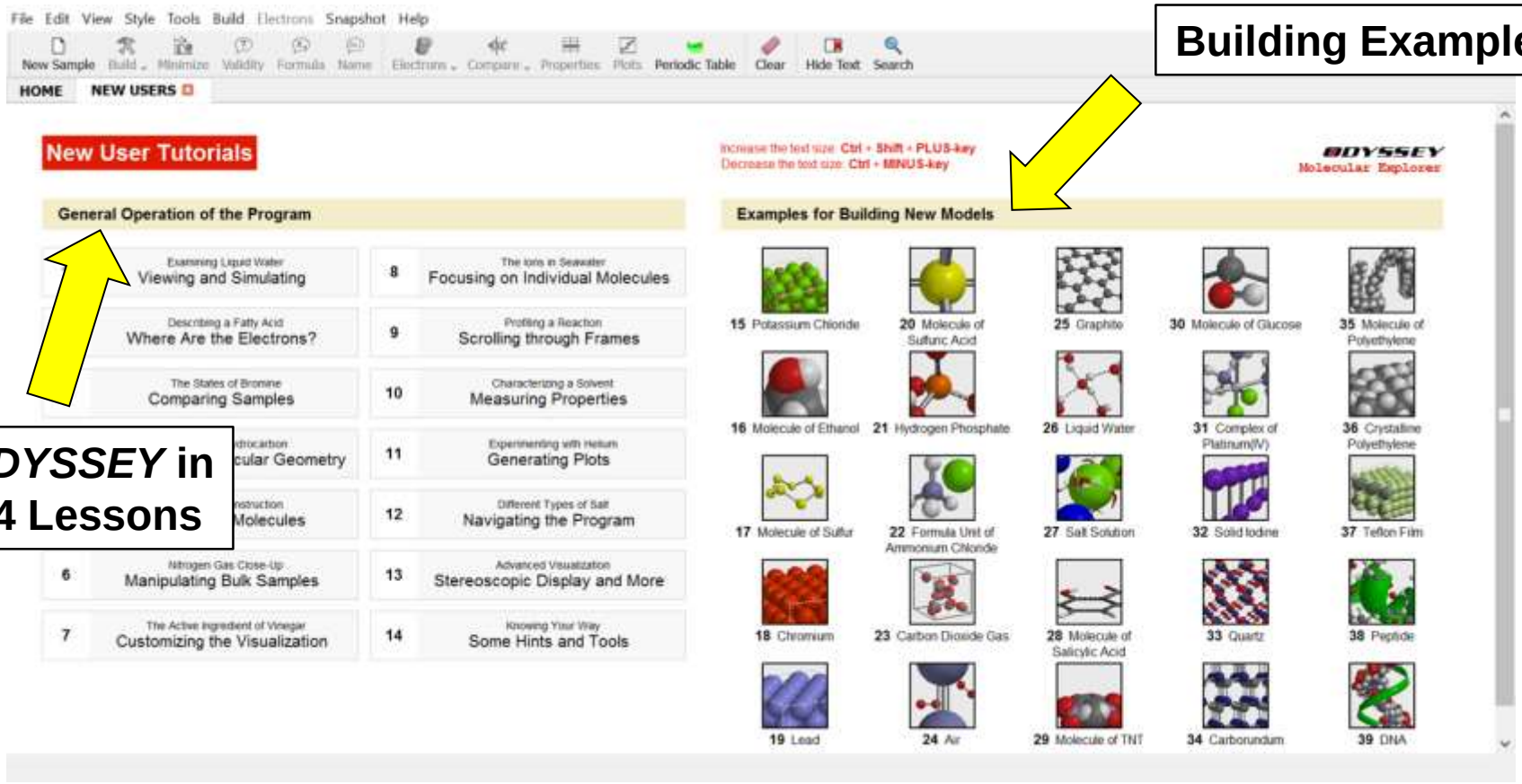


Set Checkmarks

Unset Edit button

ODYSSEY Molecular Explorer Tutorials

Learning About the Program / Refreshing Your Memory

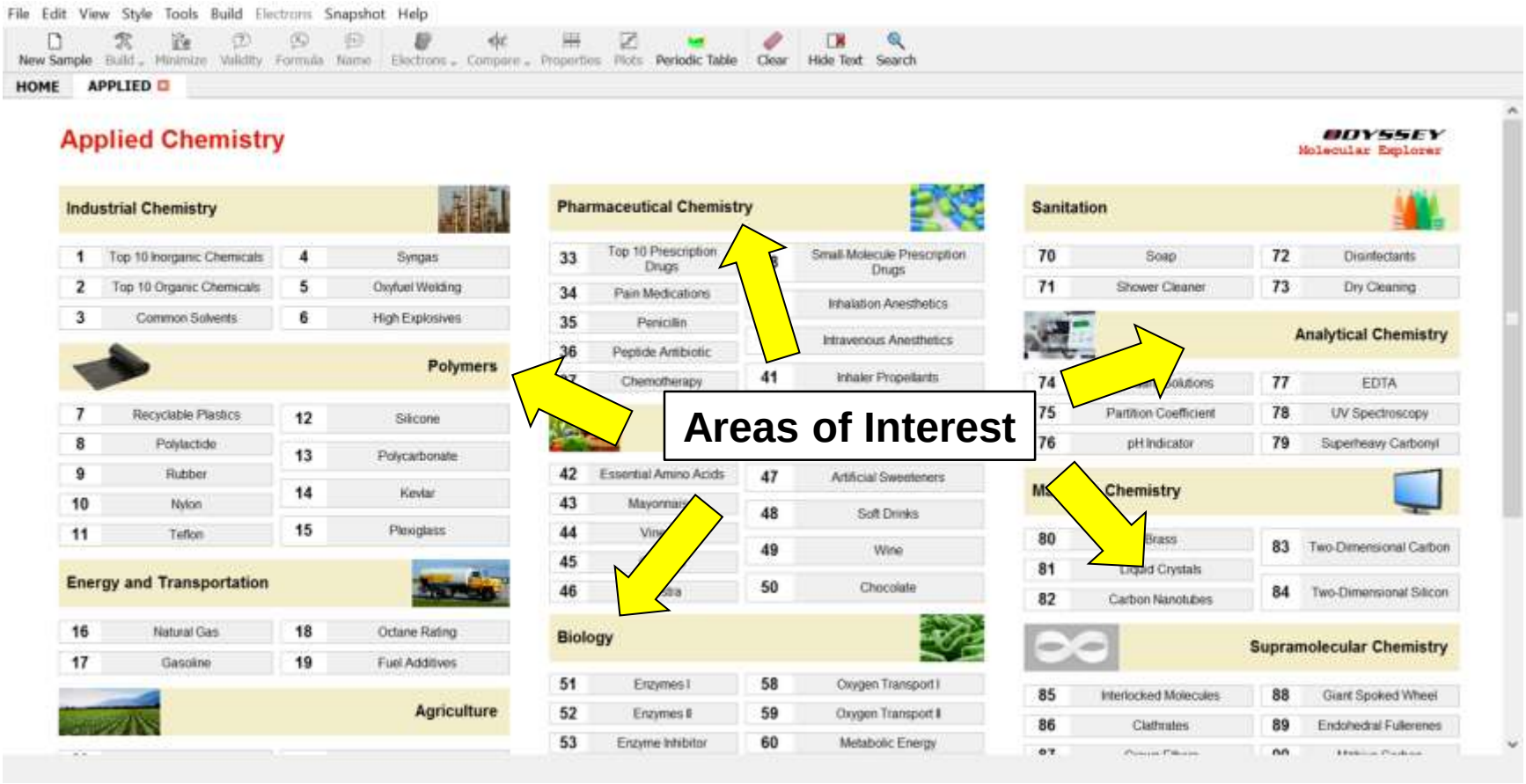


Building Examples

***ODYSSEY* in 14 Lessons**

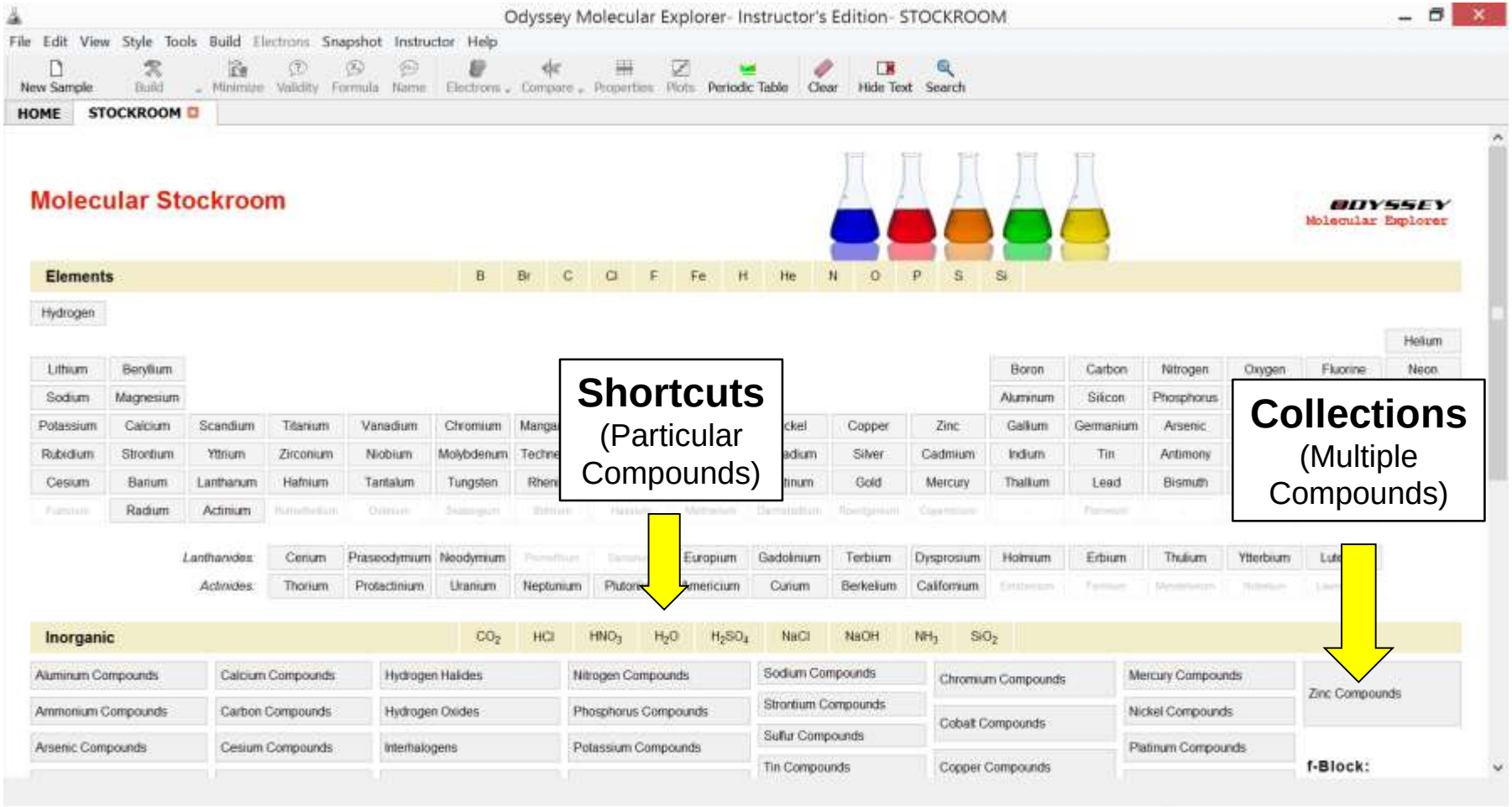
Applied Chemistry

Science Matters!



Molecular Stockroom

~100 Elements | ~700 Inorganic and Organic Compounds



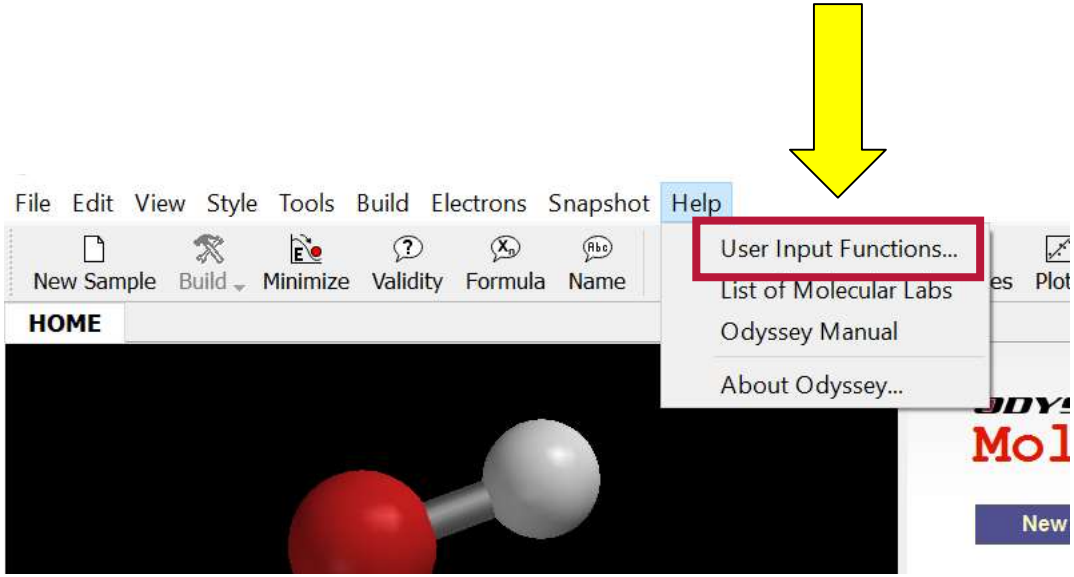
ODYSSEY Molecular Explorer

User Input Functions

Touchscreen, Trackpad, Mouse

How Do I Manipulate the Models?

In-Program Reference:
***Help* Menu**
(Tailored for Windows/Macintosh)



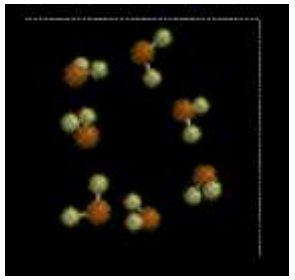
Main 3D Functions

- **Rotate**
  - Drag (Touchscreen)
  - **Left** Button + Drag (Trackpad / Mouse)
- **Translate**
  - **Long** Press + Drag (Touchscreen)
  - **Right** Button + Drag (Win Touchpad / Mouse)
  - ⌘ + **Button** + Drag (Mac Trackpad)
- **Zoom**
  - **Pinch** (Touchscreen / Trackpad)
  - **Scroll Wheel** (Mouse)

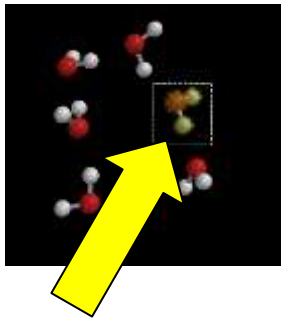
Further options are available, especially for older computers
→ Consult ***User Input Functions…*** in the **Help** menu

Models with Multiple Molecules

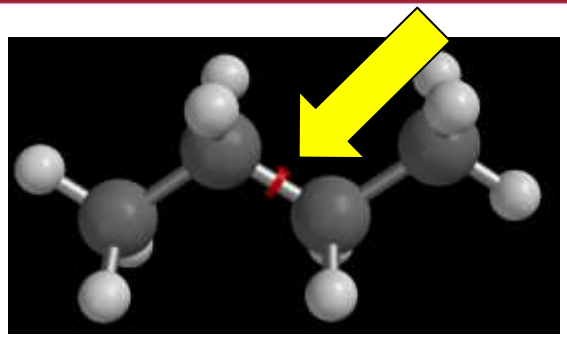
- CTRL key not held down → Rotate / Translate **Entire** Model (= All Molecules)



- **CTRL key held down** → Rotate / Translate **Selected** Molecule Only



Manipulating a Selected Bond



- **Double**-tap / **double**-click on bond to select it (Red wrap-around arrow confirms selection)

- ALT key not held down →

  Rotate Model — Translate Model

- **ALT key held down** →

  Rotate Around Bond — Change Bond **Length**

Drag (Touchscreen)
Left Button + Drag

Long Press + Drag (Touchscreen)
Right Button + Drag
⌘ + **Button** + Drag (Mac Trackpad)

ODYSSEY Molecular Explorer

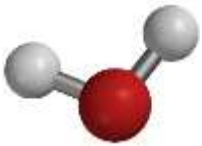
Visualization

Model Styles and Other Display Options

What Style Should I Choose?

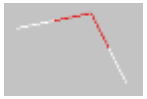
- Start with **Space Filling** — it shows what things "really look like"
  - Molecular shape
  - Packing in solids and liquids
  - Emptiness of gases

- To see details, switch to **Ball and Spoke** (or **Ball and Wire**)
  - Covalent bonds
  - Distance / Angle measurements !



- **Tube** — very useful in conjunction with hydrogen bonds

- **Wire** — useful for the solvent of solutions

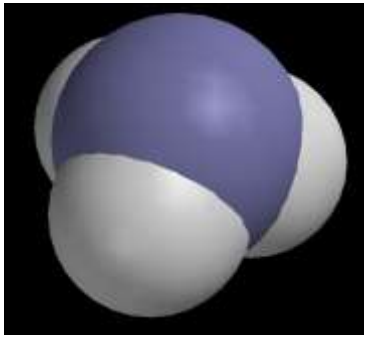


→ **Ball and Spoke** is the default style for the build panels

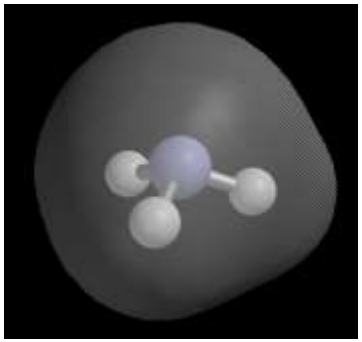
→ Use **Space Filling** for gases…or you will hardly see anything !

Custom Visualization (I)

Molecular Shape / Polarity

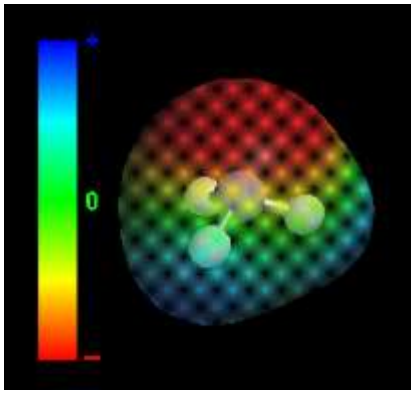


- **Space Filling** style — Approximate Shape



- **Outer Surface** — True Shape

  (Electron Cloud, ~98% of the total density)

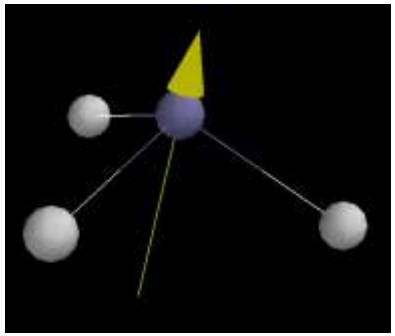


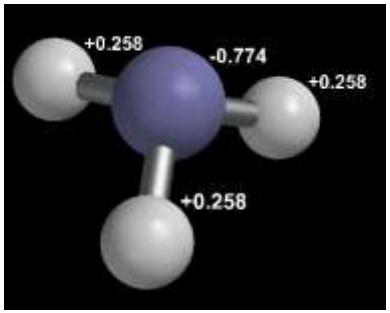
- **Polarity Map** — True Shape + Polarity

Custom Visualization (II)

Molecular Shape / Polarity

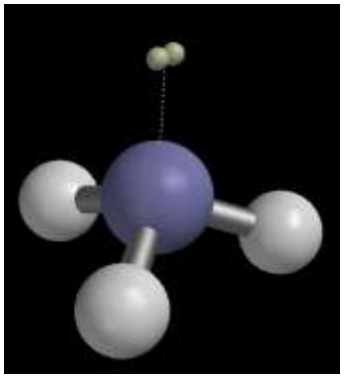
- **Dipole Arrow(s)** —
  Combine with **Ball and Wire** (or **Wire**) style





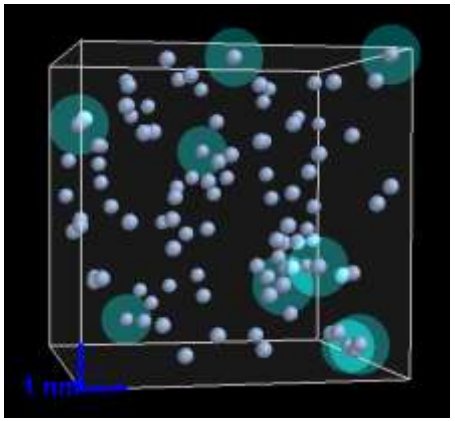
- **Charge Labels** — Atomic Partial Charges

- **Lone Pairs** — Cartoon Representation

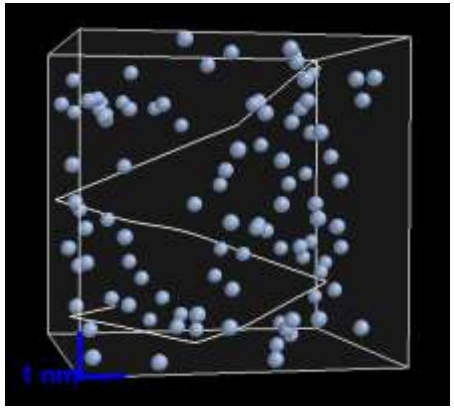


Custom Visualization (IV)

Gas Laws / Kinetic Theory



- **Collisions —**
  select **Molecule-Wall**
  → Concept of “Pressure”

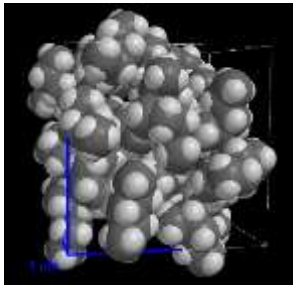


- **Trails** — *Right-click* on an atom and select **Set Trail**

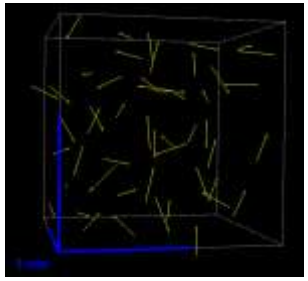
Custom Visualization (III)

Intermolecular Forces

- **Space Filling** style
  → *Dispersion forces*



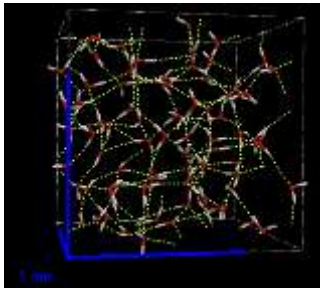
C_5H_{12} (*l*)



CH_2Cl_2 (*l*)

- **Dipole Arrows**
  (Combine with the **Hide** style)
  → *Dipole-dipole forces*

- **Hydrogen Bonds**
  (Combine with the **Tube** style)
  → *Hydrogen bonding forces*

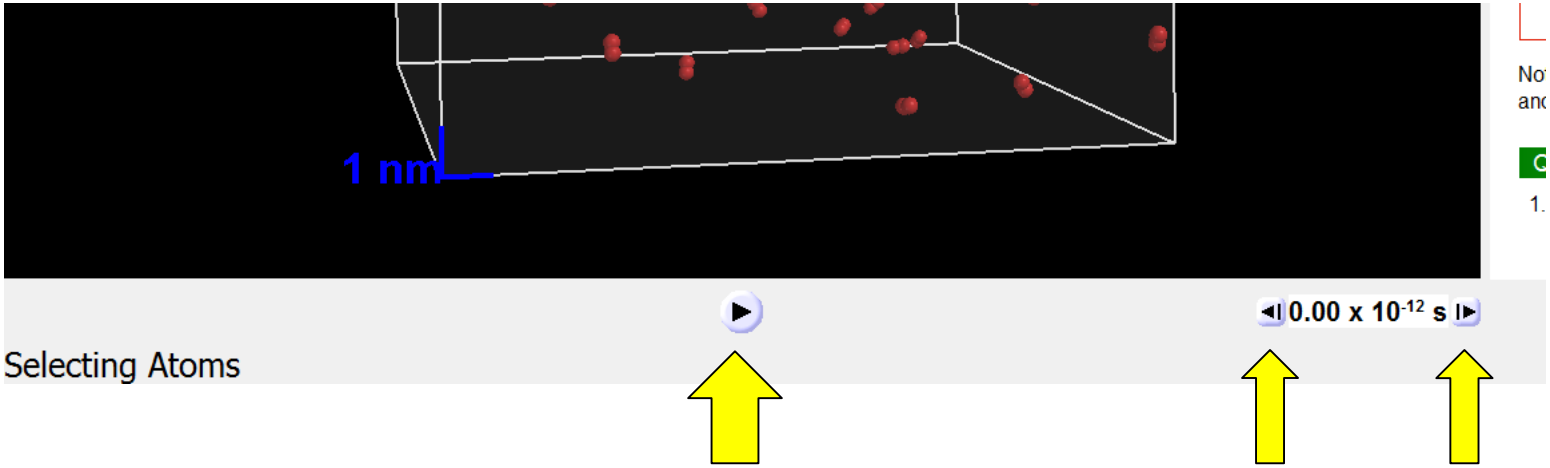


H_2O (*l*)

Dynamics

Starting and Controlling Simulations

Molecular Dynamics (I)



Go/Stop Toggle
(Continuous Simulation)

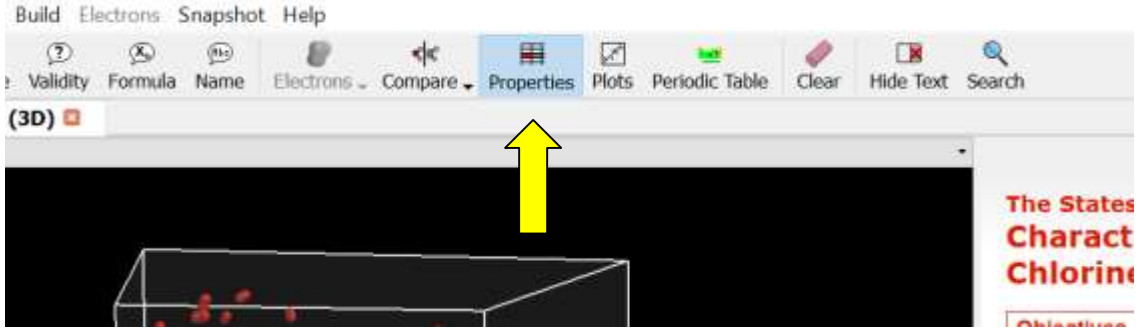
Go Back / Go Forward
(Step-by-Step)

Time Scales

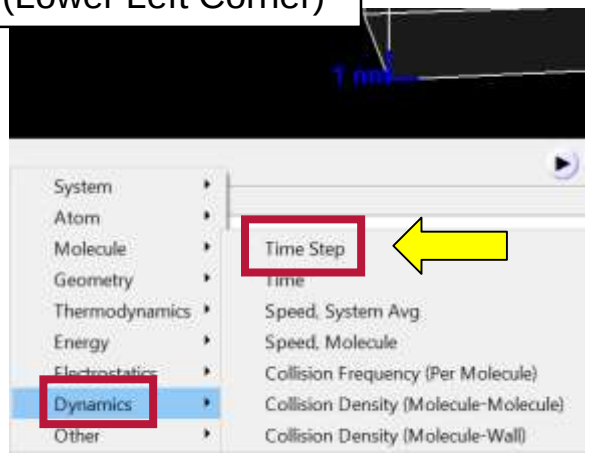
- ~10^{-15} s (femtoseconds) ← Actual Molecular Time Step (as assigned by the program)
- ~10^{-12} s (picoseconds) ← Typical "Step-by-Step" Interval
- ~10^{-9} s (nanoseconds) ← Maximum Length of Simulations (long simulations of hours duration)

Molecular Dynamics (II)

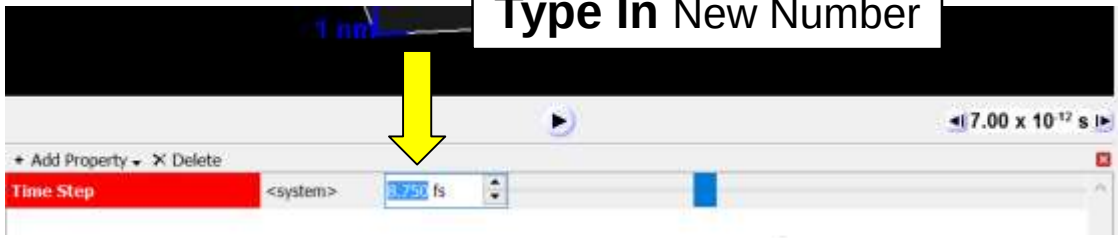
Slowing Down (and Speeding Up)



Add Property…
(Lower Left Corner)



Select Field and
Type In New Number



Molecular Dynamics (III)

Slowing Down (and Speeding Up)

Smaller Time Step

Larger Time Step

Number of Computational Steps
Per Minute of Wall-Clock Time (!) Stays the Same

Simulation Effectively
Slows Down

Simulation Effectively
Speeds Up

Can always **reduce** the time step size…

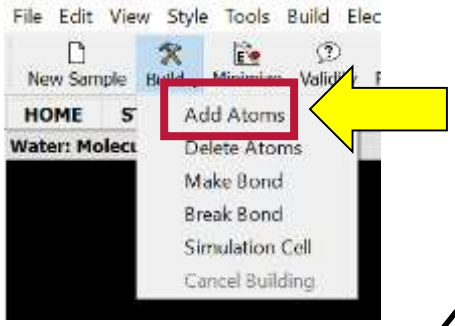
...but should **not** significantly increase step size or may provoke a numerical instability (and possibly program crash)
(→ automatically assigned time step is already "large")

Building

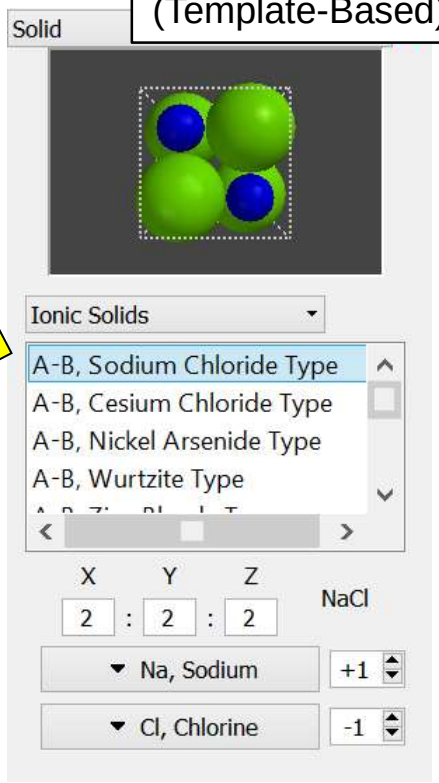
From Molecules to Simulation Cells

Simple Building

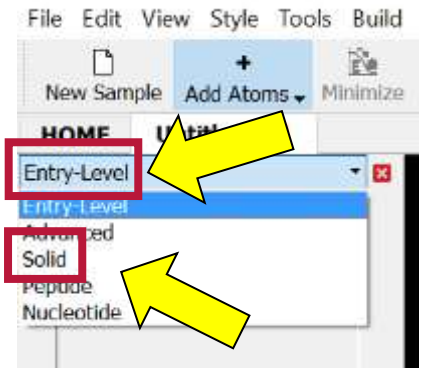
Molecules, Solids



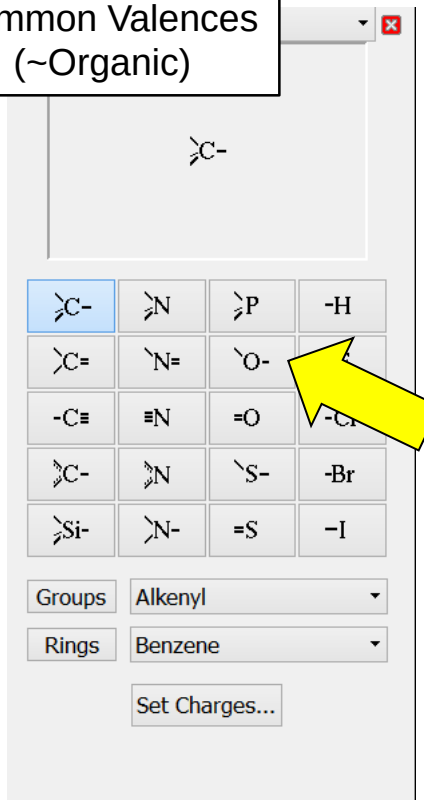
Solid
(Template-Based)



NaCl



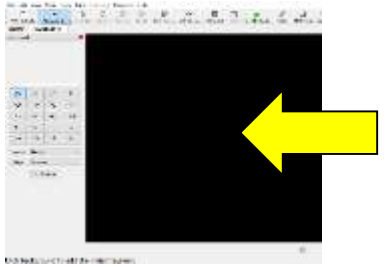
Entry-Level
Common Valences
(~Organic)

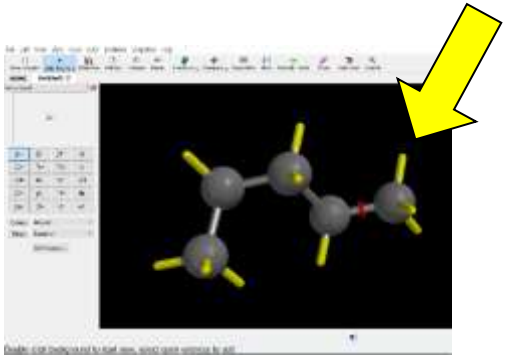


H_2O

Molecule Building (I)

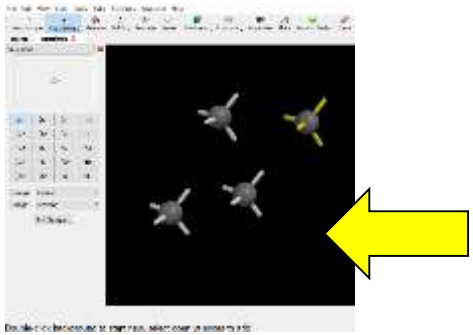
- Initial single click on background
  → Start molecule (first building block)

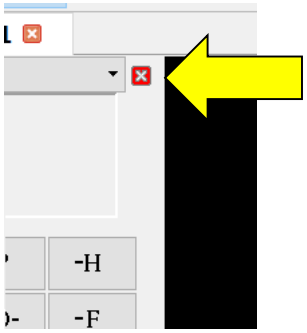




- **Single** click on yellow spoke (free valence)
  → Continue with the *same* molecule

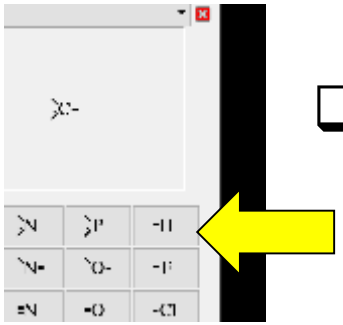
- **Double**-click on background
  → Start *new* (additional) molecule



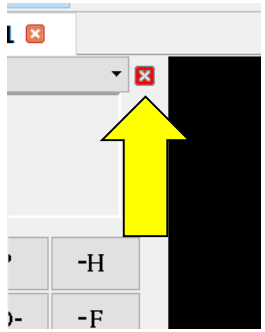


- Close the build panel with its **Close** button
  (Starting a simulation will also close the build panel)

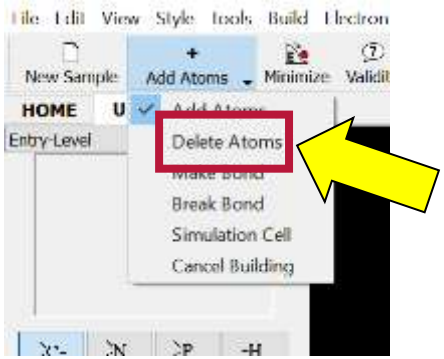
Molecule Building (II)



- **Hydrogens** can be added manually…



…or are filled in automatically as soon as the build panel is closed !



- **Deleting** is modal
  → Will keep deleting until returning to “Add Atoms”

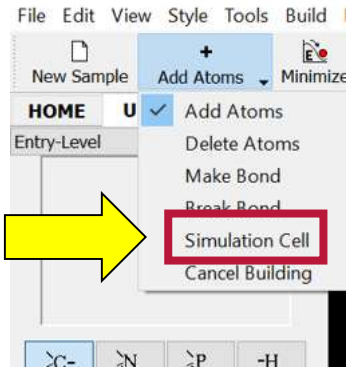
- Always **Minimize** (or run a simulation ▶) when done building!

Building of Gases and Liquids (I)

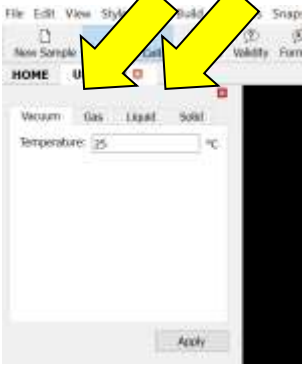
- Must build molecule first

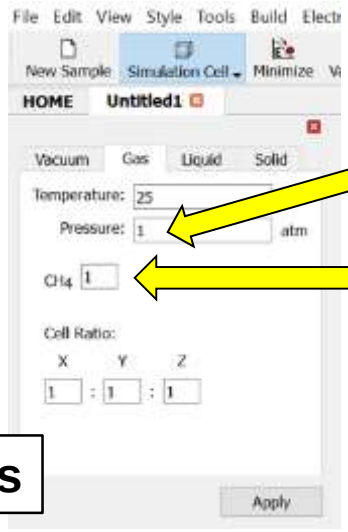
  (Mixture: need one molecule for each of the components)

- Then use *Simulation Cell* panel



Gas or Liquid

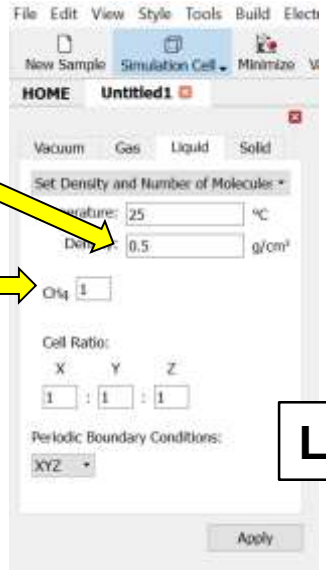




Pressure

Density

# of Molecules



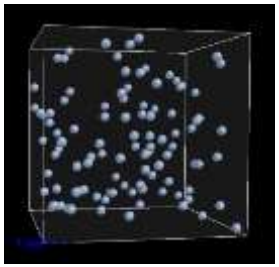
Gas

Liquid

Building of Gases and Liquids (II)

- Don't exceed ~1,000 atoms* total
  …or things may get very slow!

**atoms*, not molecules



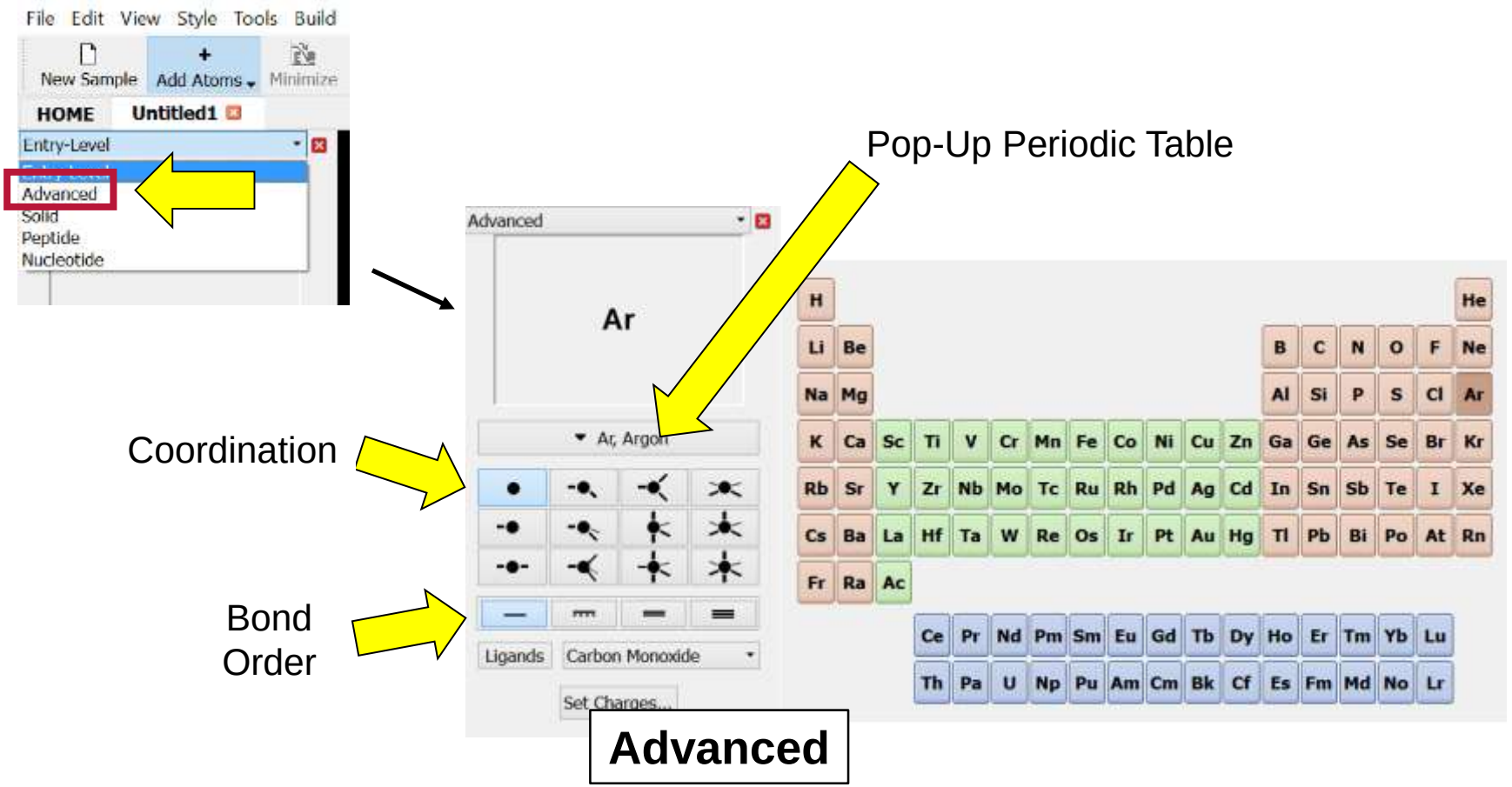
- *Argon* is excellent for
  Gas Laws / Kinetic Theory
  (computationally "cheap")

- Build Gases at ~10 atm (rather than ~1 atm)
  → More collisions, "better" (faster) equilibrium

- Build Liquids at slightly reduced density
  (such as 0.9 g/cm^3 instead of 1.0 g/cm^3)
  → More mobility, faster equilibrium

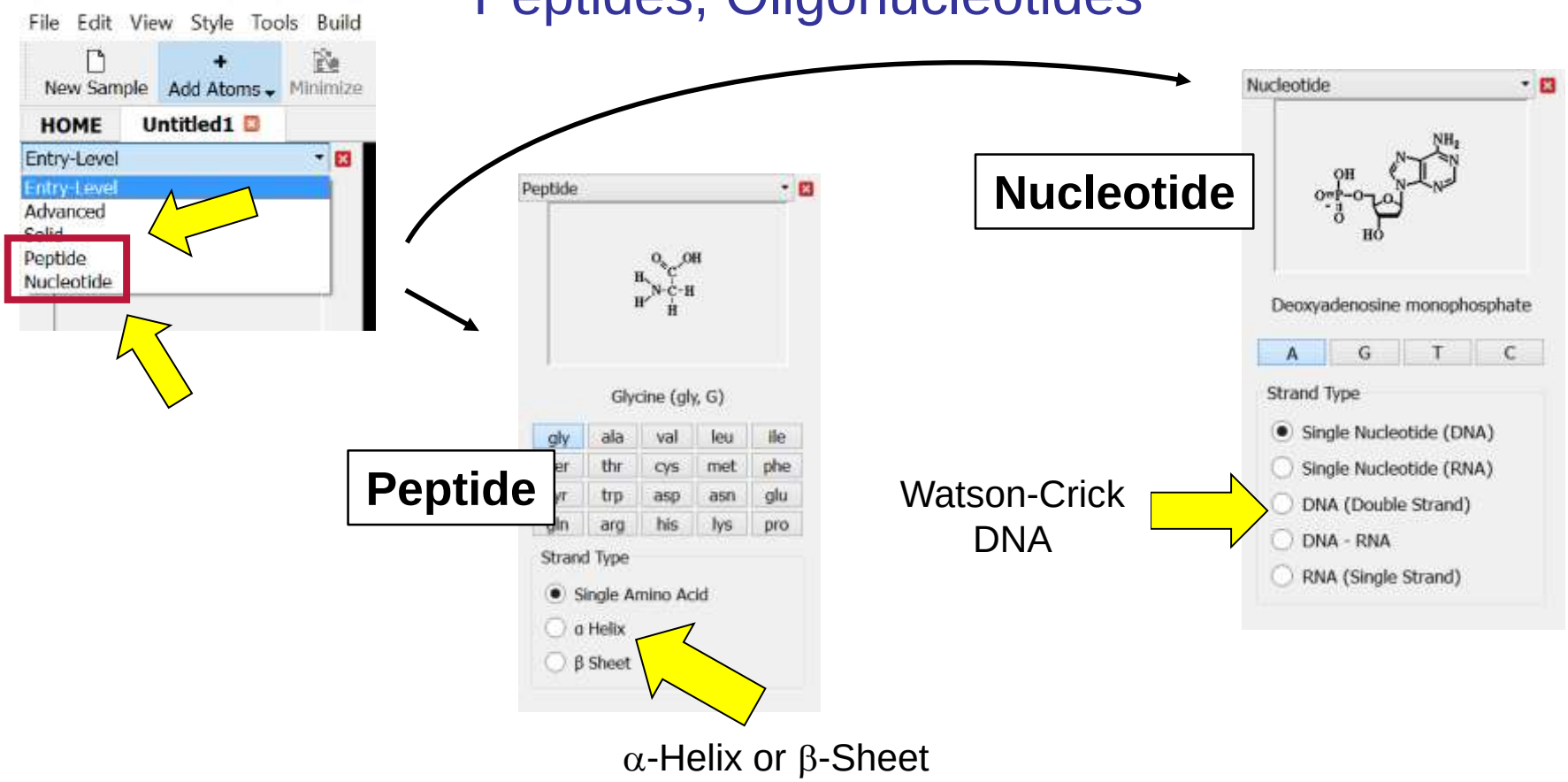
Advanced Building

Unusual Bond Orders, Inorganic Compounds, Complexes



Biopolymer Building

Peptides, Oligonucleotides



Peptide

Nucleotide

Watson-Crick DNA

α-Helix or β-Sheet

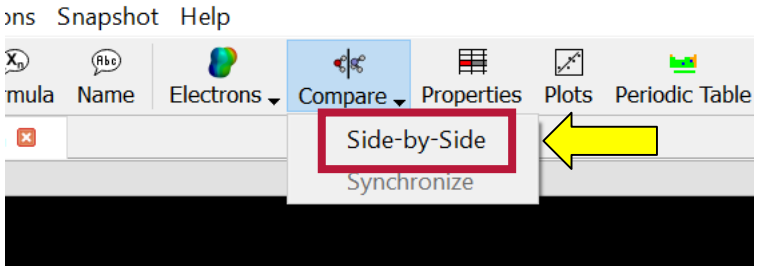
- Don't exceed ~30 amino acids / ~30 base pairs

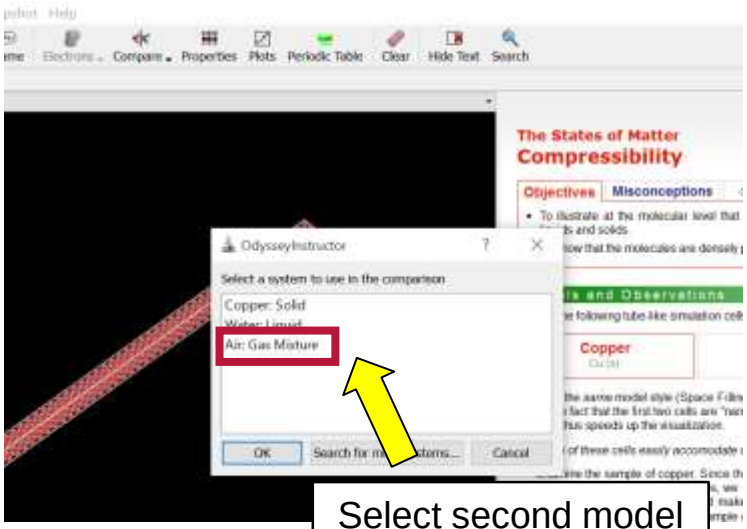
  …or things may get very slow!

Comparing

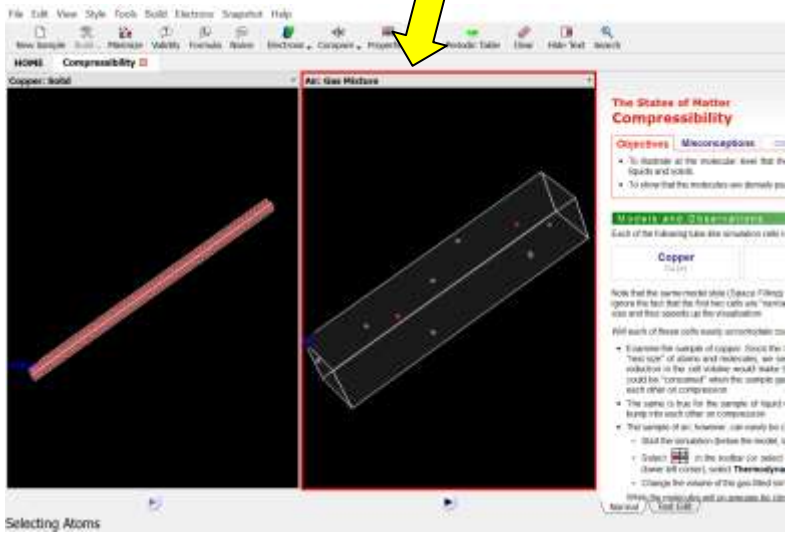
Showing Models Side-by-Side

Comparing Two Models from the Same Lab





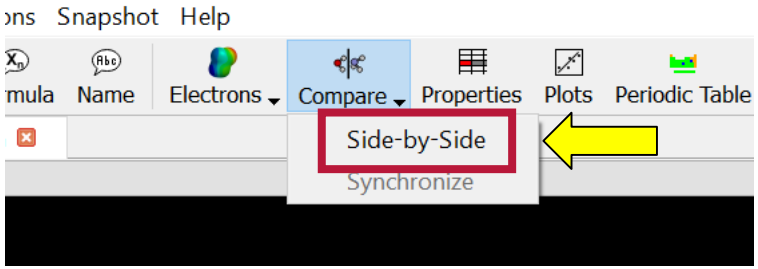
Select second model for the comparison



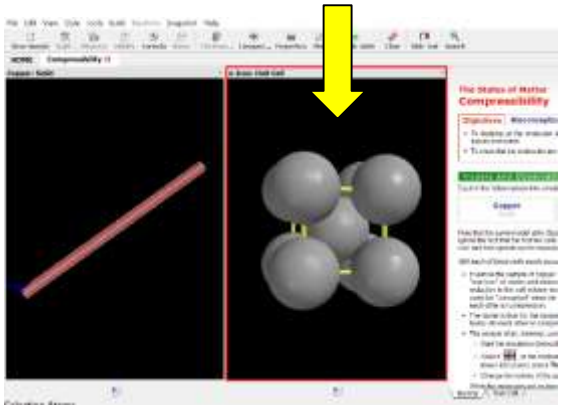
Models can be manipulated individually

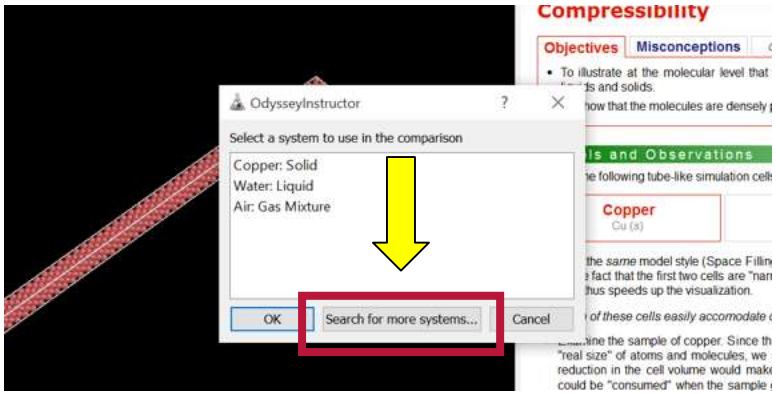
Choose “active” model (has **red frame** around it) by selecting its background

Getting the Comparison Model via Search

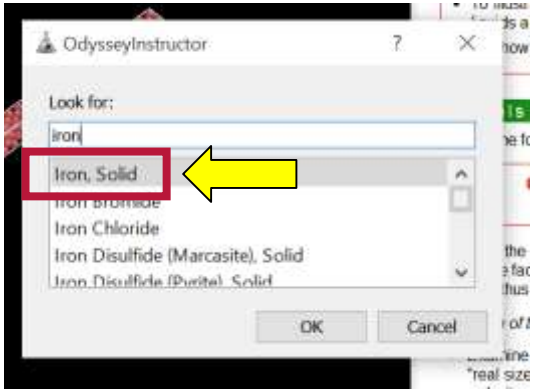


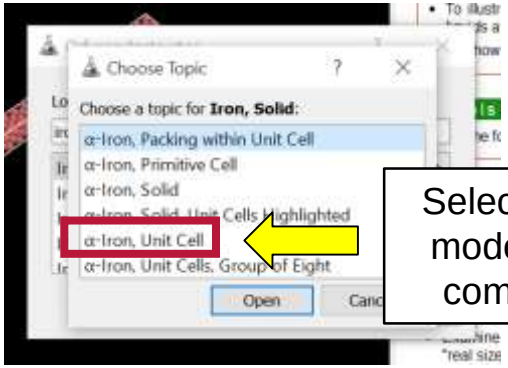
Second model initially shown on same scale (zoom is required)





Available for comparison: ~1,800 models

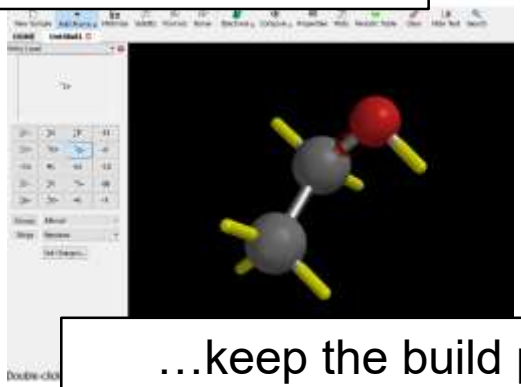




Select second model for the comparison

Comparing Two User-Built Models (I)

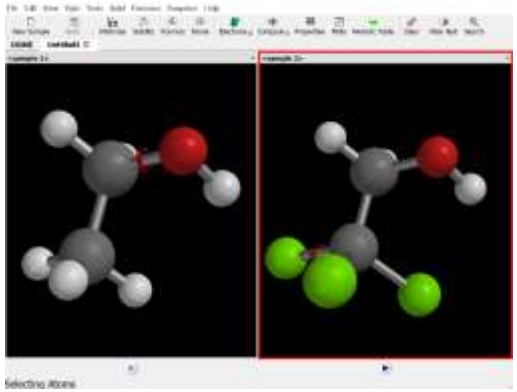
Build the first model…



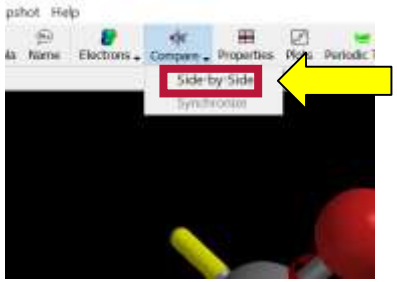
…keep the build panel **open!**
(if already closed, you **must** reopen it with *Build* → *Add Atoms*)

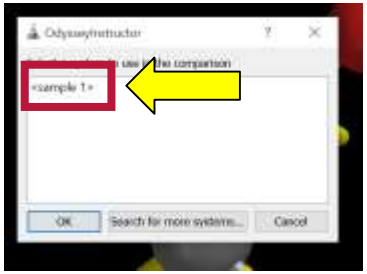
Suitable even for…

- ❑ simulation **cells**
- ❑ independent **dynamics** of both systems
- ❑ independent **electron** cloud calculations

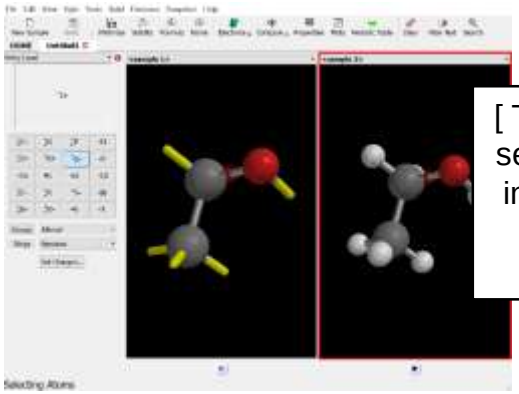


Modify the second model, finally close the build panel
(*Note:* Cannot reopen panel once closed)





Duplication Step

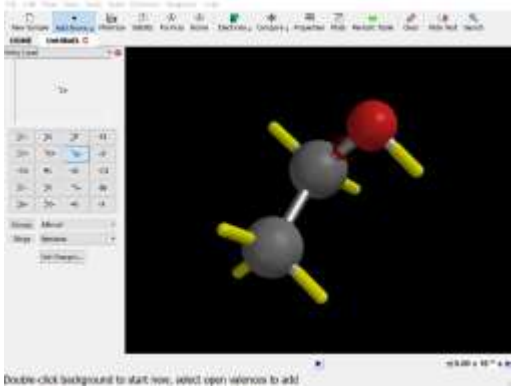


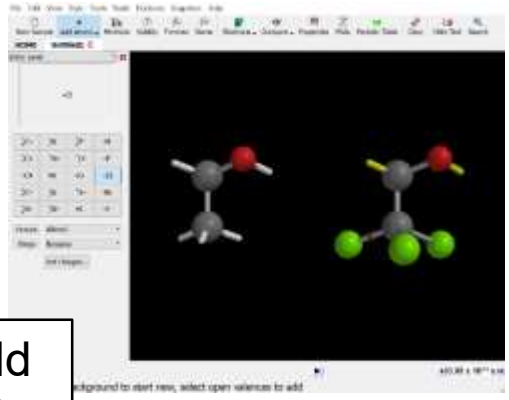
[The hydrogens of the second model will turn into yellow spokes as soon as a building block is selected]

ODYSSEY Molecular Explorer — Comparing Two User-Built Models (II)

Alternate Method

Build the first molecule…

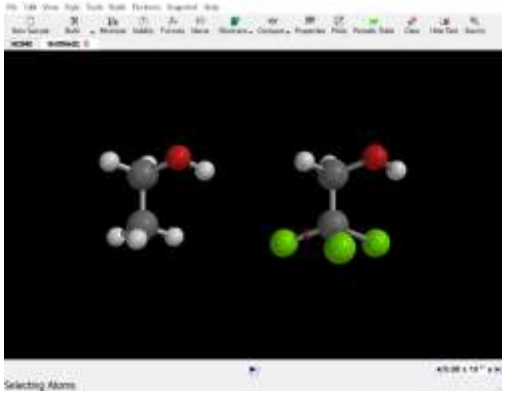




…and simply add another molecule to the **same** model

(double-tap/double-click on background to start the second molecule)

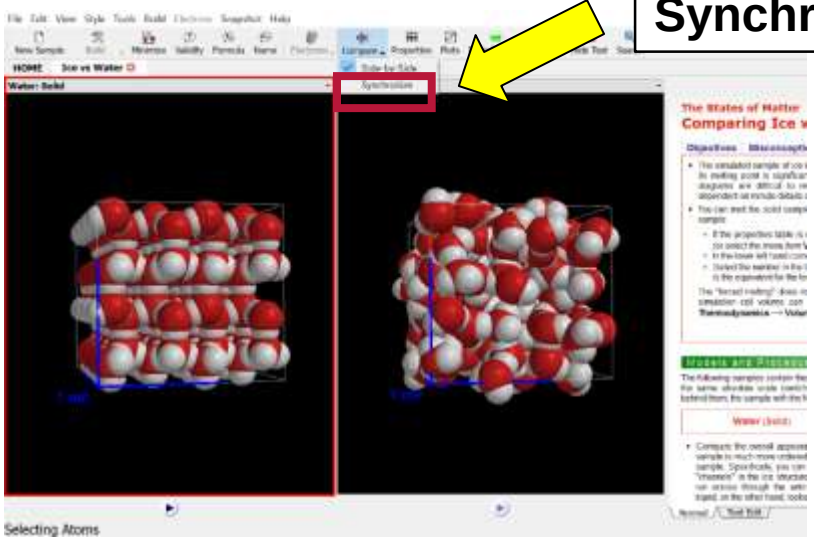
Close the build panel



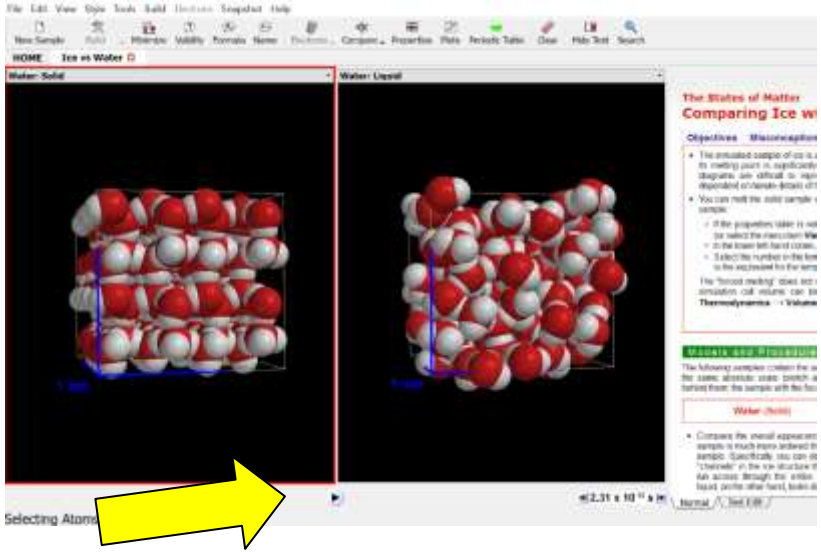
- ❑ Comparison of two simulation cells not possible
- ❑ Dynamics applies to the interacting **dimer** (!) of molecules, not the two molecules independently
- ❑ Electron cloud calculated for the **dimer** (!) of molecules, not the two molecules independently

Running Two Simulations at Once

Synchronize option



Calculating the dynamics of two systems at once invariably probes the limits of computational power → expect slow simulations



One dynamics toggle controls both simulations
(simulations progress at the same speed)