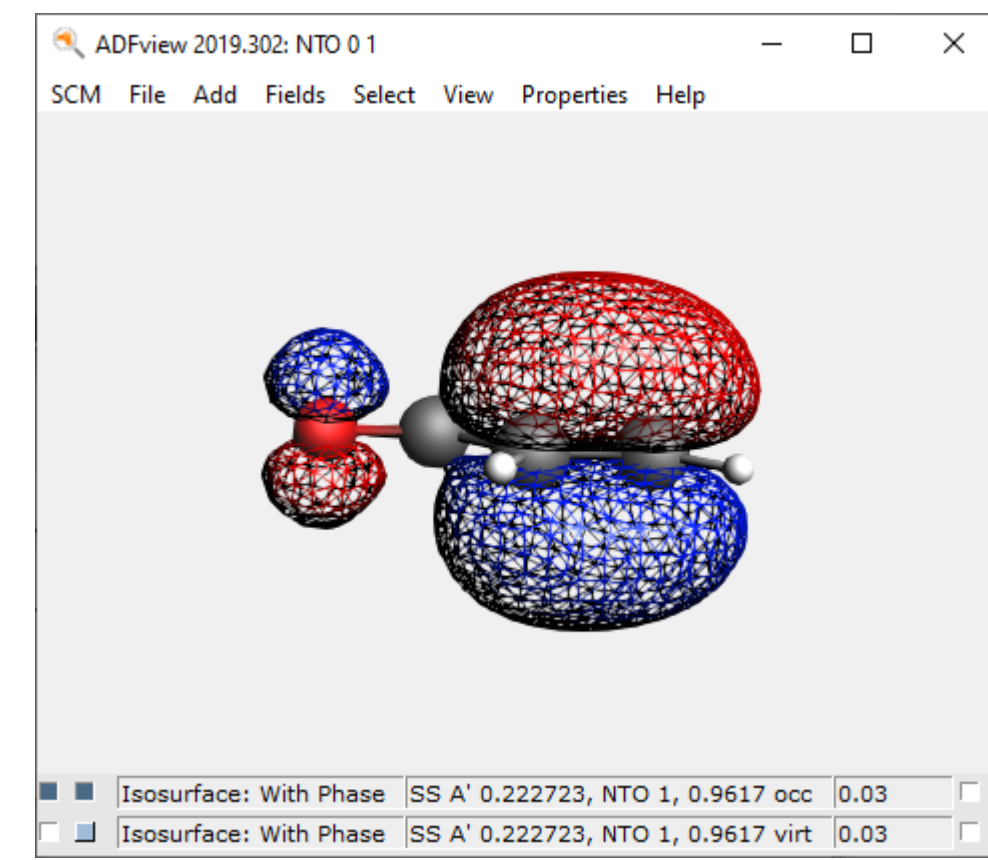
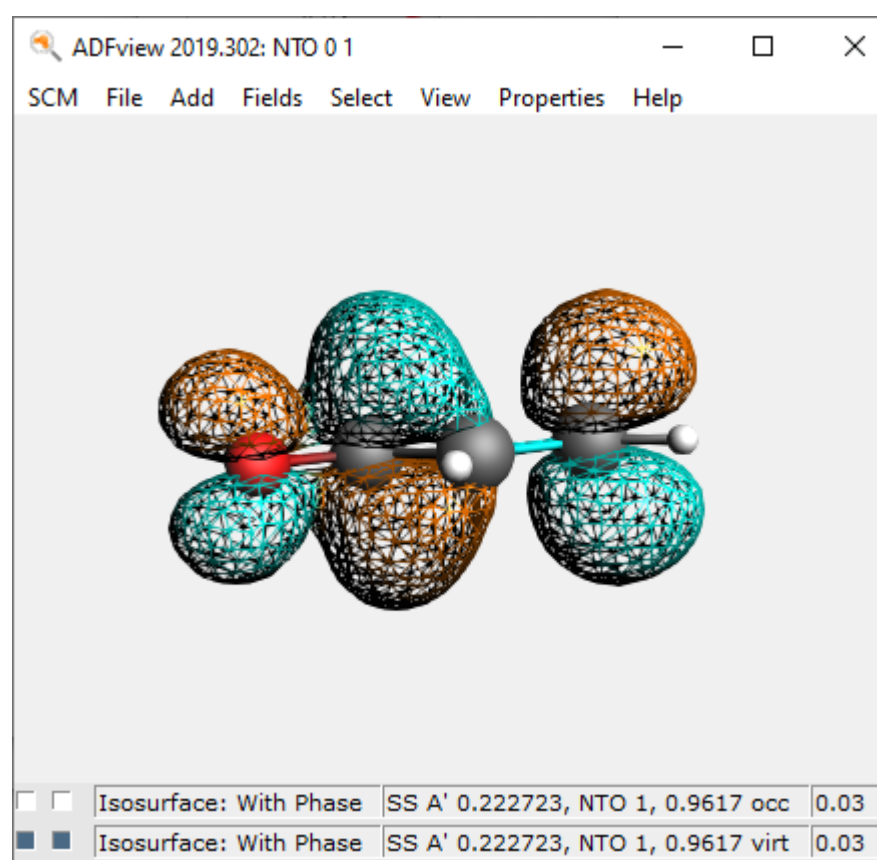
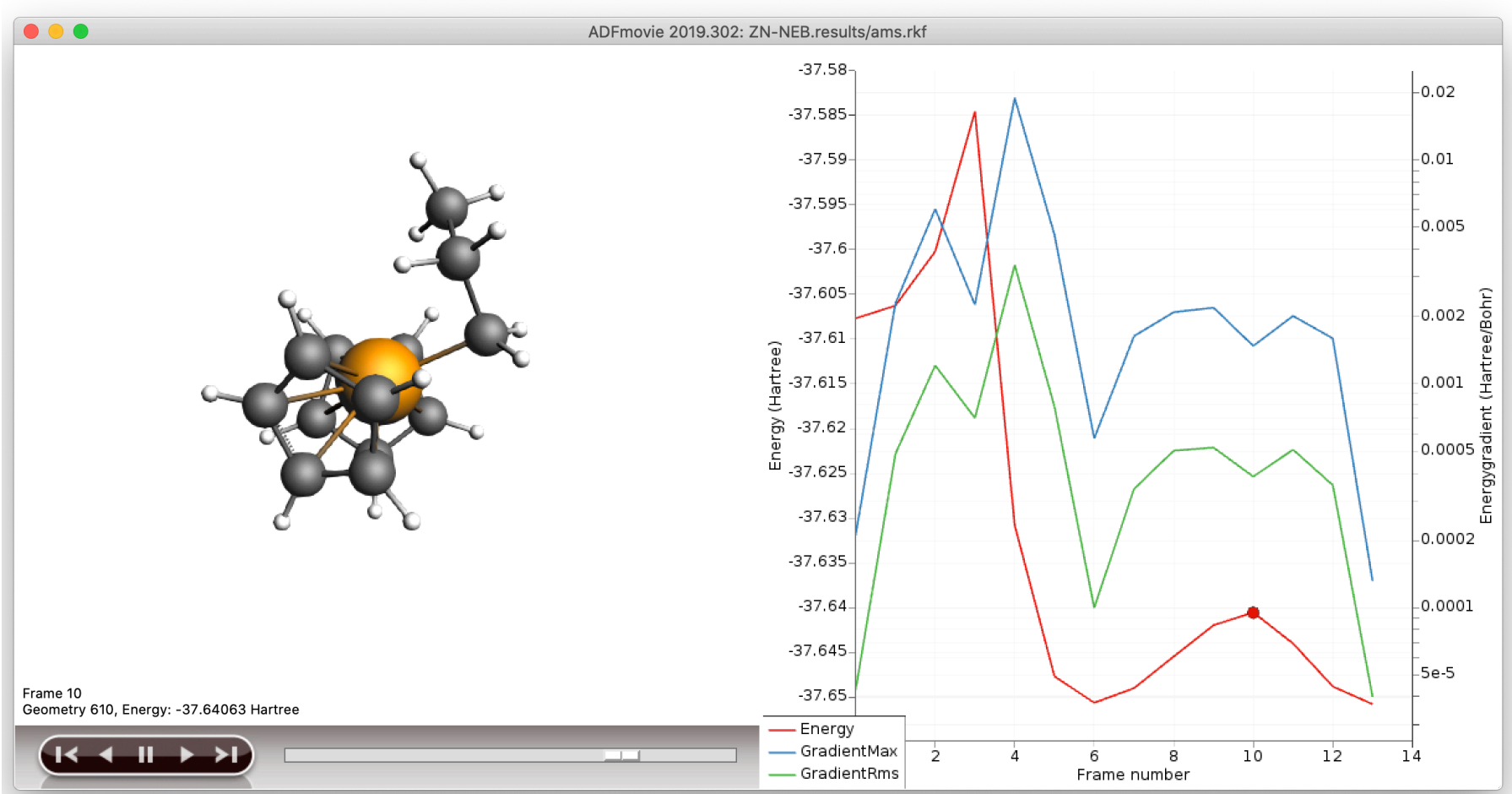
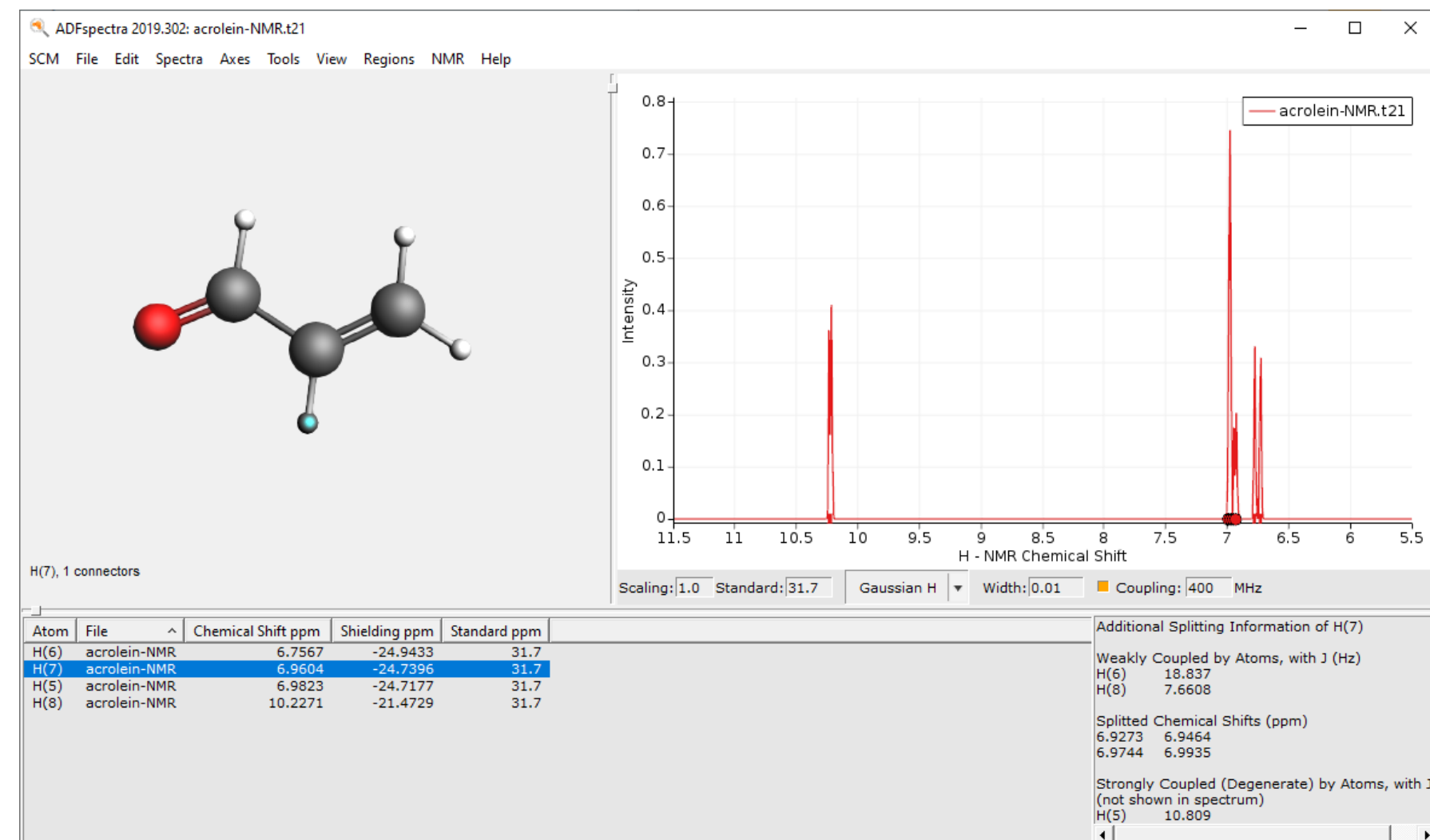
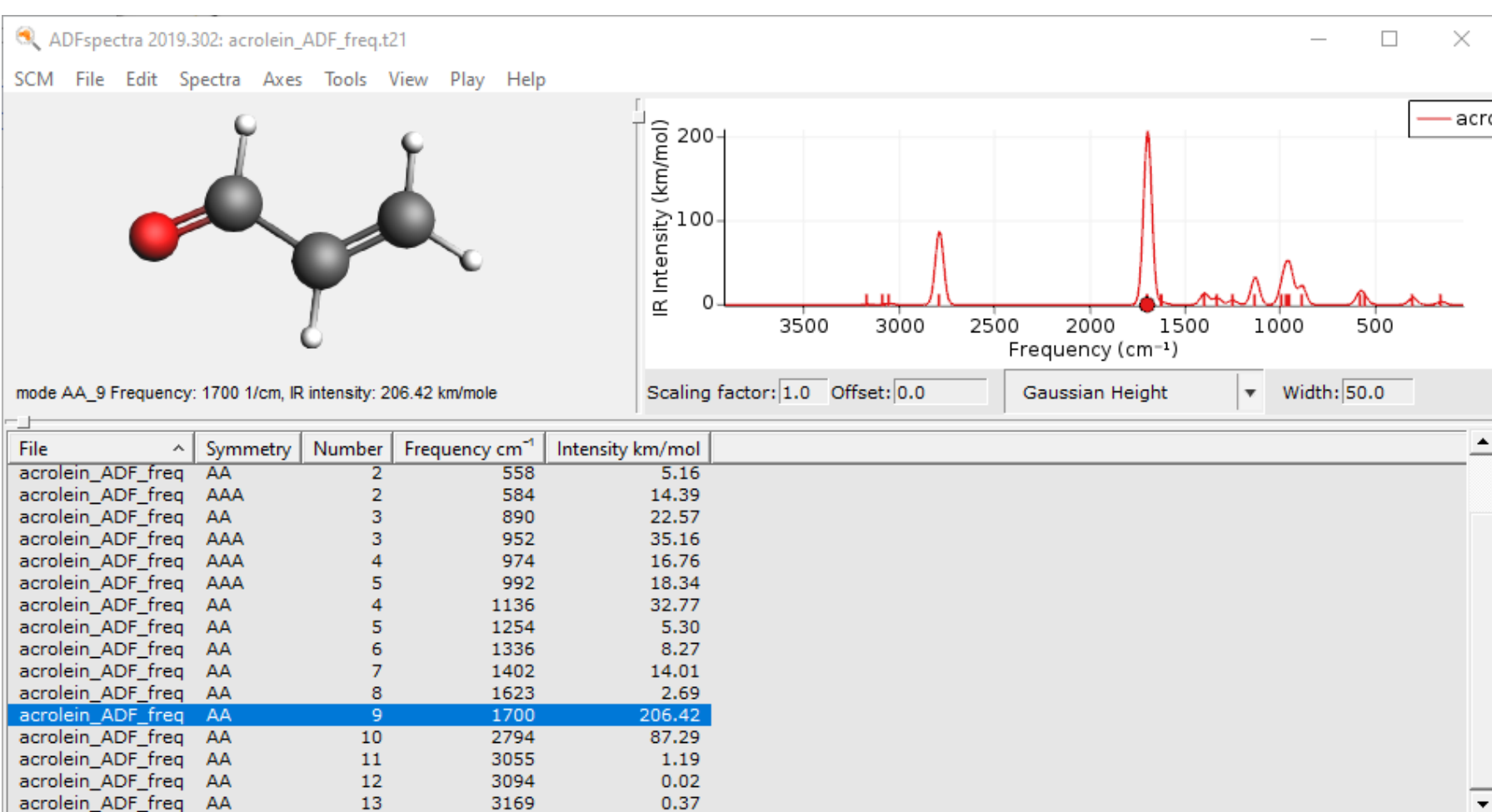


Hands-on exercise 1: molecules



Virtual Winter School on Computational Chemistry, 20 February 2020

Fedor Goumans, goumans@scm.com

Ole Carstensen, carstensen@scm.com

Thomas Soini, soini@scm.com

SCM support: support@scm.com

Getting started with the GUI

Starting ADFjobs: job bookkeeping tool

- Win: dbl-click desktop item
- Mac: open Application
- Linux: run `$ADFBIN/adfjobs`

- ADF is a bit separate concerning setting up tasks
- There is 'classic' ReaxFF besides ReaxAMS
 - Both will move to AMS driver – engine set up in 2020

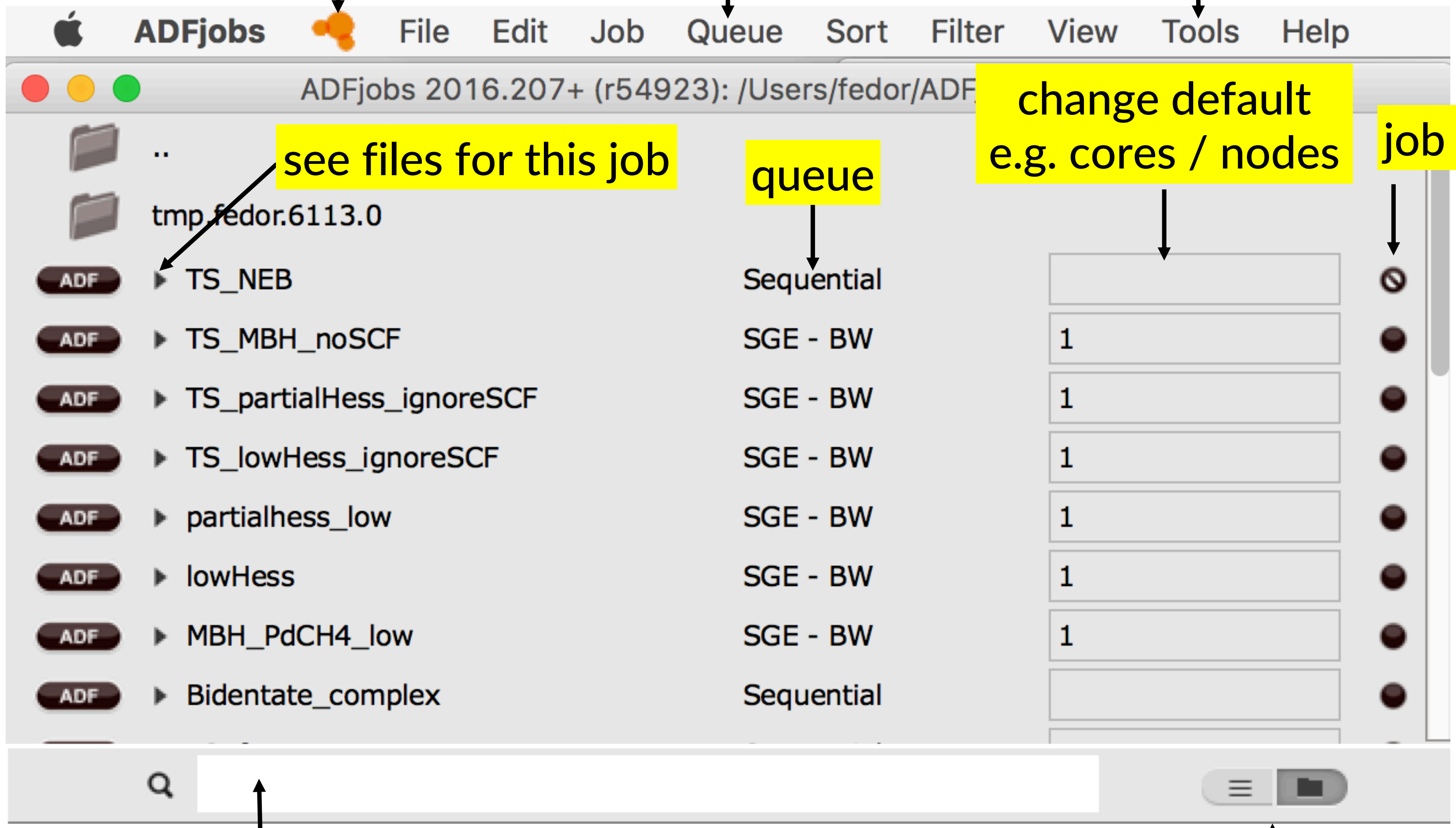
- Other GUI modules: (Input, View, Levels, Movie, Spectra, Band Structure, ADFTrain, Microkinetics, COSMO-RS, ...)
 - Can be opened by dbl-clicking '.exe' (Win) or opening e.g. '`$ADFBIN/adfinput`'

ADFjobs: job bookkeeping

switch GUI functionality

define & switch queues

reports & templates



see files for this job

queue

change default
e.g. cores / nodes

job status

search

all jobs / folder view

Basic calculations & settings

The screenshot shows the ADF software interface with the following annotations:

- switch modules**: Points to the top navigation bar containing 'ADF', 'Main', 'Model', 'Properties', 'Details', and 'MultiLevel'.
- job types & set up**: Points to the 'Task' dropdown menu.
- search**: Points to the search icon in the top right corner.
- job type**: Points to the 'Task' dropdown menu.
- charge/spin**: Points to the 'Total charge' and 'Spin polarization' input fields.
- functional & relativistic appr**: Points to the 'XC functional' and 'Relativity' dropdown menus.
- basis & numerical accuracy**: Points to the 'Basis set', 'Frozen core', and 'Numerical quality' dropdown menus.
- builder tools**: Points to the 'C O N H Cl X' toolbar.
- preoptimize**: Points to the star icon in the toolbar.
- symmetrize**: Points to the star icon in the toolbar.
- > = more details**: Points to the right-pointing arrow icons next to the dropdown menus.

Basic calculations & settings

The screenshot shows the ADF software interface with the following annotations:

- switch modules**: Points to the top navigation bar (ADF, Main, Model, Properties, Details, MultiLevel).
- job types & set up**: Points to the 'Task' dropdown menu.
- search**: Points to the search icon in the top right.
- job type**: Points to the 'Task' dropdown menu.
- charge/spin**: Points to the 'Total charge' and 'Spin polarization' input fields.
- functional & relativistic appr**: Points to the 'XC functional' and 'Relativity' dropdown menus.
- basis & numerical accuracy**: Points to the 'Basis set', 'Frozen core', and 'Numerical quality' dropdown menus.
- builder tools**: Points to the 'C O N H Cl X' toolbar.
- preoptimize**: Points to the star icon in the toolbar.
- symmetrize**: Points to the star icon in the toolbar.
- > = more details**: Points to the right-pointing arrow icons next to the dropdown menus.

GUI input editor controls

- ▶ Free rotation **left mouse button (LMB)** & drag
- ▶ In-plane rotation **ctrl + LMB** & drag
- ▶ In-plane shift **right mouse button (RMB)** & drag
- ▶ Zoom **mouse wheel / alt** & drag
- ▶ Area selection **shift + LMB**
- ▶ Deselect **LMB** on drawing space
- ▶ Undo **ctrl + z**
- ▶ Redo **shift + ctrl + z**
- ▶ View along x- / y- / z-axis **ctrl + 1 / ctrl + 2 / ctrl + 3**

GUI input editor controls

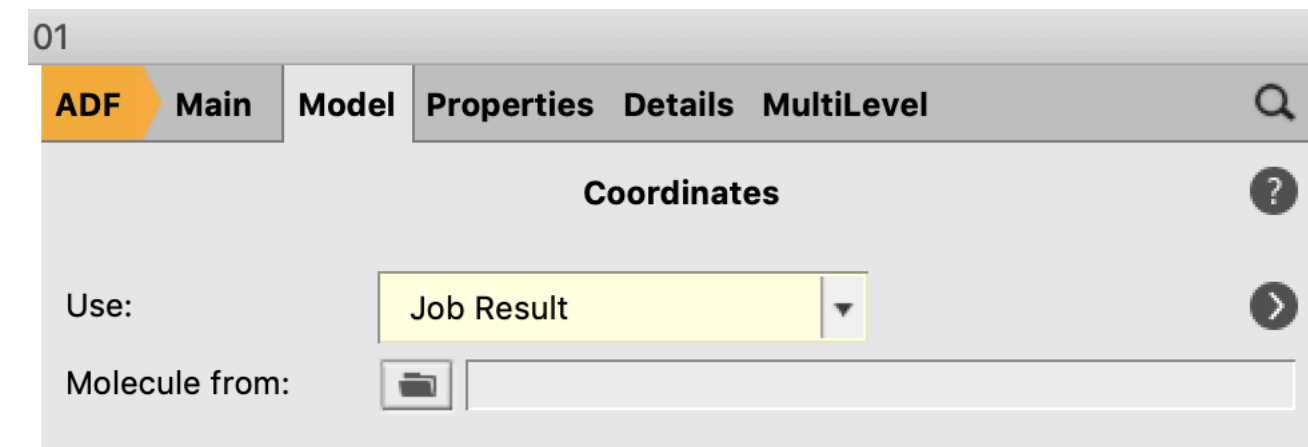
- ▶ Selection free rotation **LMB** & drag from a selected atom
- ▶ Selection in-plane rotation **ctrl** + **LMB** & drag from atom
- ▶ Selection in-plane shift (**shift** +) **RMB** & drag from atom
- ▶ Select all atoms **ctrl** + **A**
- ▶ Add hydrogen atoms **ctrl** + **E**
- ▶ Link selected atoms **ctrl** + **L**
- ▶ Delete selected atoms **del** / **backspace**

- ▶ More shortcuts: **Help** → **Shortcuts**

Using the GUI more efficiently

1. Chained jobs

- Model -> coordinates use Job results
- E.g. first do pre / partial optimization
- Can not be used to also read in Hessian
 - Python scripting could work (do check on nimag e.g.)



2. Preset

- If you always use same XC, basis set, relativity & quality, etc. you can save it:
 - File -> Save as preset (all fields different from default)
 - File -> Save as full preset (all input options)
- Load this: File -> Preset -> 'Your preset' on future jobs with the same setting

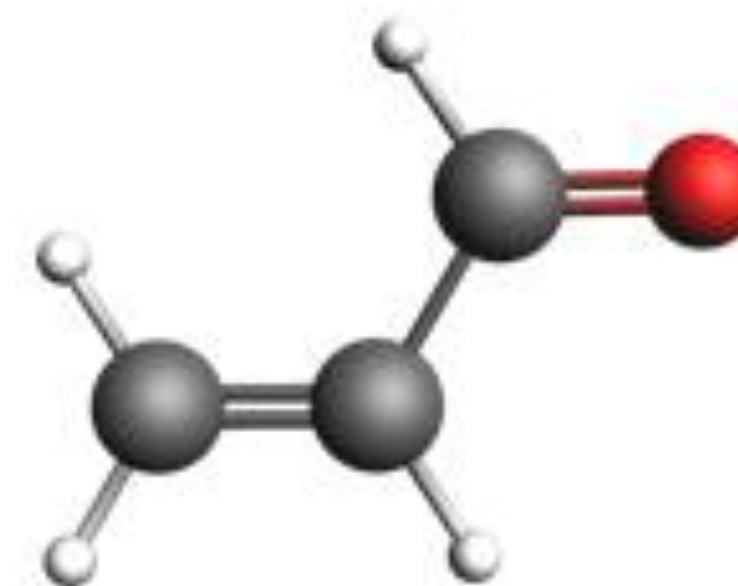
3. Adfprepare (& report)

- In adfjobs select a job, tools -> prepare
- Now you can run the same job but with different settings (e.g. basis set, xc, ...)
- With adfreport you can [build a report to visualize results](#) (e.g. distances)
- (also consider Python scripting with PLAMS)

Building molecules

www.scm.com/doc/Tutorials/GUI_overview/Building_Molecules.html

- Search molecules
- Import: InChI, SMILES, xyz, cif, pdb, ...
- Included library + building
- **Excercise:** Build acrolein / propenal
 - By searching for it in the GUI
 - By starting from the builder tools
 - use '2' for double bonds, Ctrl+E to add H atoms
 - By importing SMILES, InChI (e.g. from Wikipedia, PubChem or ChempSpider)
- Symmetrize (Cs), pre-optimize (UFF, MOPAC, DFTB)

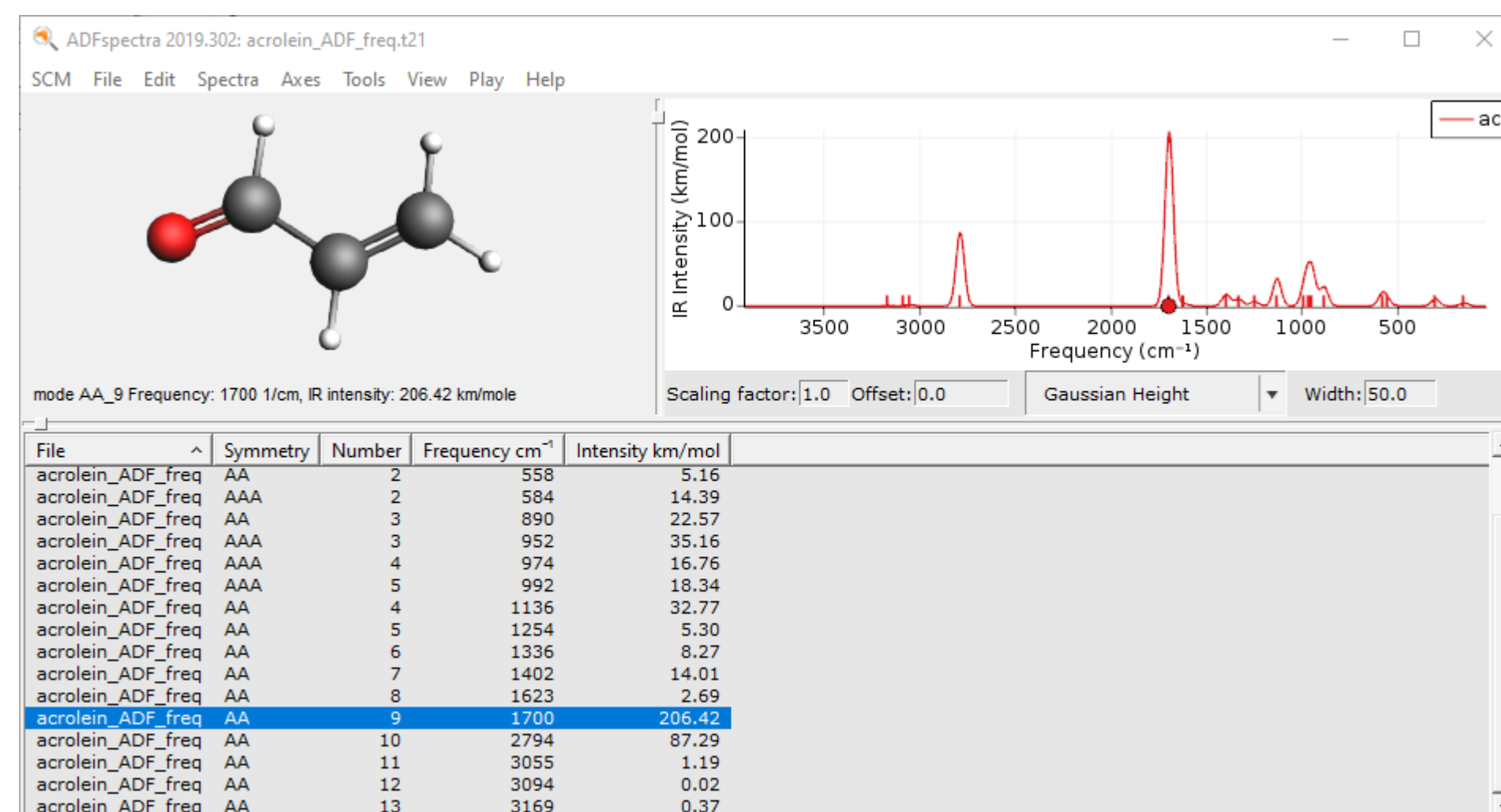
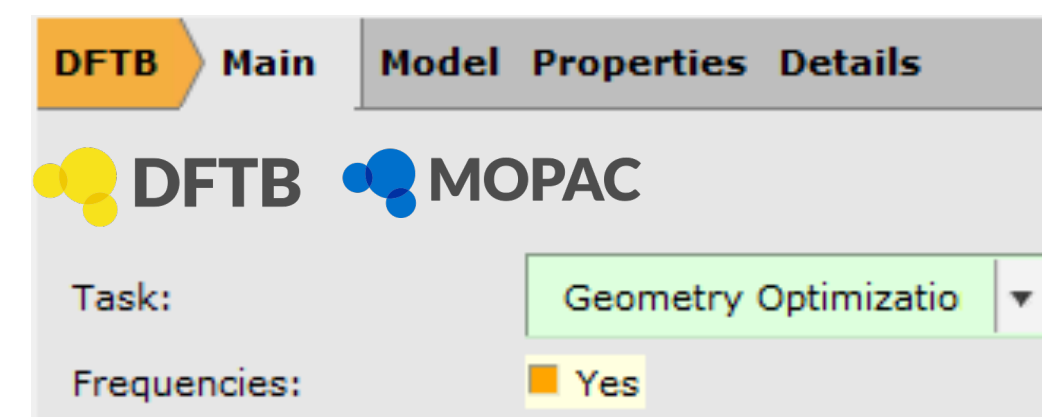
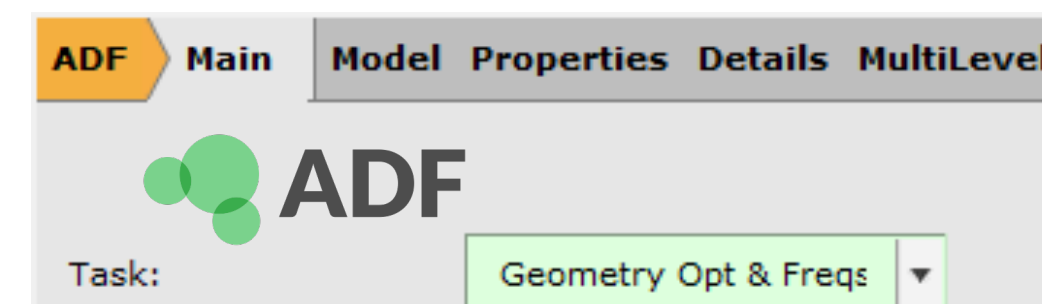


Spectra: IR

https://www.scm.com/doc/Tutorials/ADF/Vibrational_frequencies_and_IR_spectrum_of_ethane.html

• Excercise: Calculate & visualize frequencies

- Geometry needs to be optimized at same level as frequency calc.
- ADF (not yet part of AMS): Task = Geometry Opt & Freq
- MOPAC, DFTB: Task = Geometry Opt + Frequencies = Yes
- Try a few different methods:
 - ADF: PBE-D4/DZP + Scalar ([.adf](#))
 - DFTB: DFTB3-D3-BJ/3ob-3-1 ([.adf](#))
 - MOPAC
- Visualize: ADFSpectra; tweak broadening
- Compare to [NIST](#)



Spectra: UV/VIS

• Exercise:

- With ADF: calculate 10 allowed excitations
 - use SAOP model potential, DZP (or TZP), no core (.adf)
- See also [UV/VIS FAQ for tips](#)
- Go to spectra, change x-axis to nm
- Increase the line width to ~10
- Visualize the pi-pi* NTOs at ~205nm (click on NTO1)
- Visualize the MOs strongest Single Orbital Transition
- Compare to [NIST data](#)
 - Rerun with method 'sTDA' and tick TDA
 - Also try TD-DFT+TB (ADF)
 - and TDDFTB ([DFTB3/3ob-3-1](#), [GFN-xTB](#))
 - (can use the same PBE-D4 optimized geometry)

Task: Single Point

XC functional: Model:SAOP

Relativity: Scalar

Basis set: DZP

Frozen core: None

ADF Main Model Properties Details MultiLevel

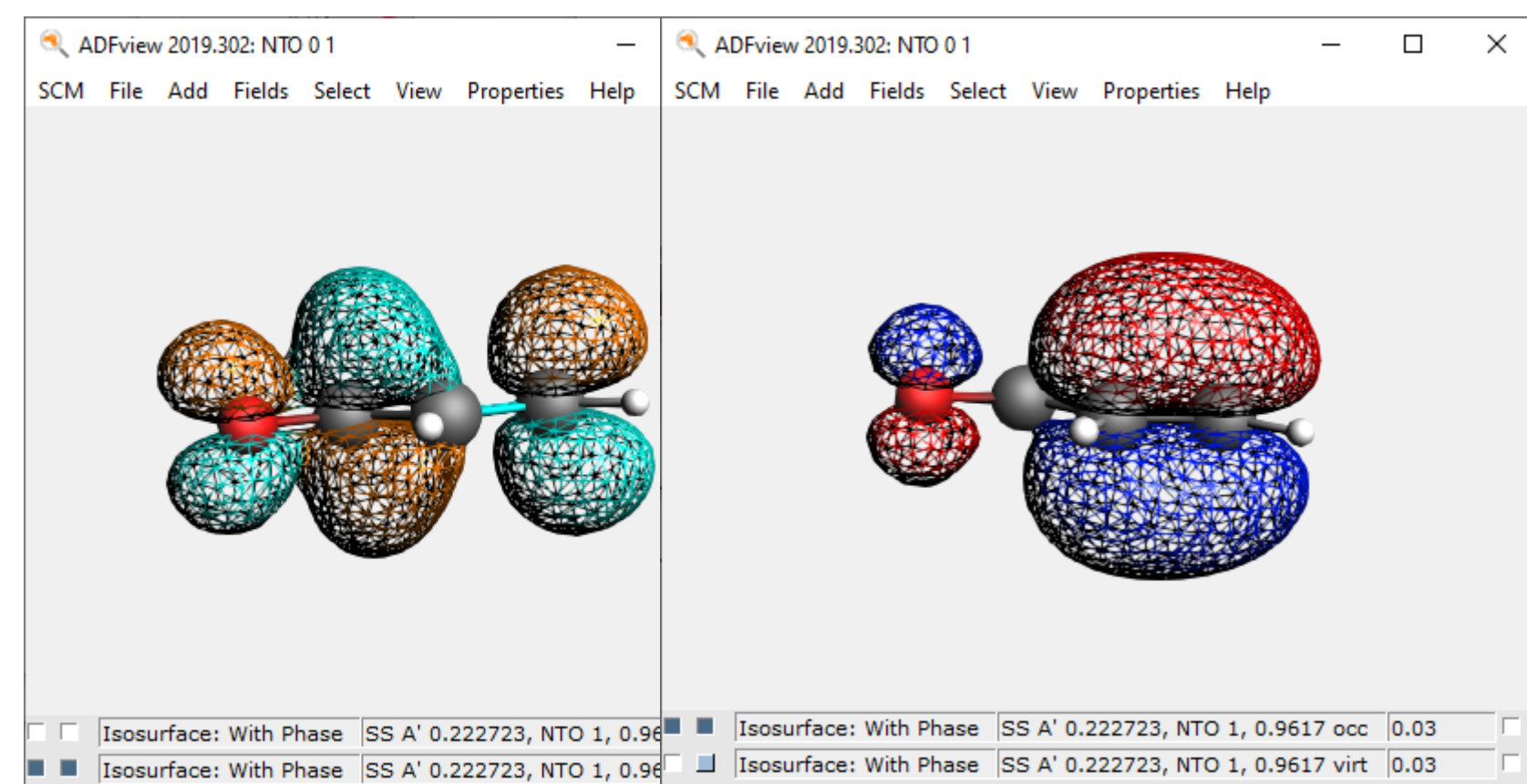
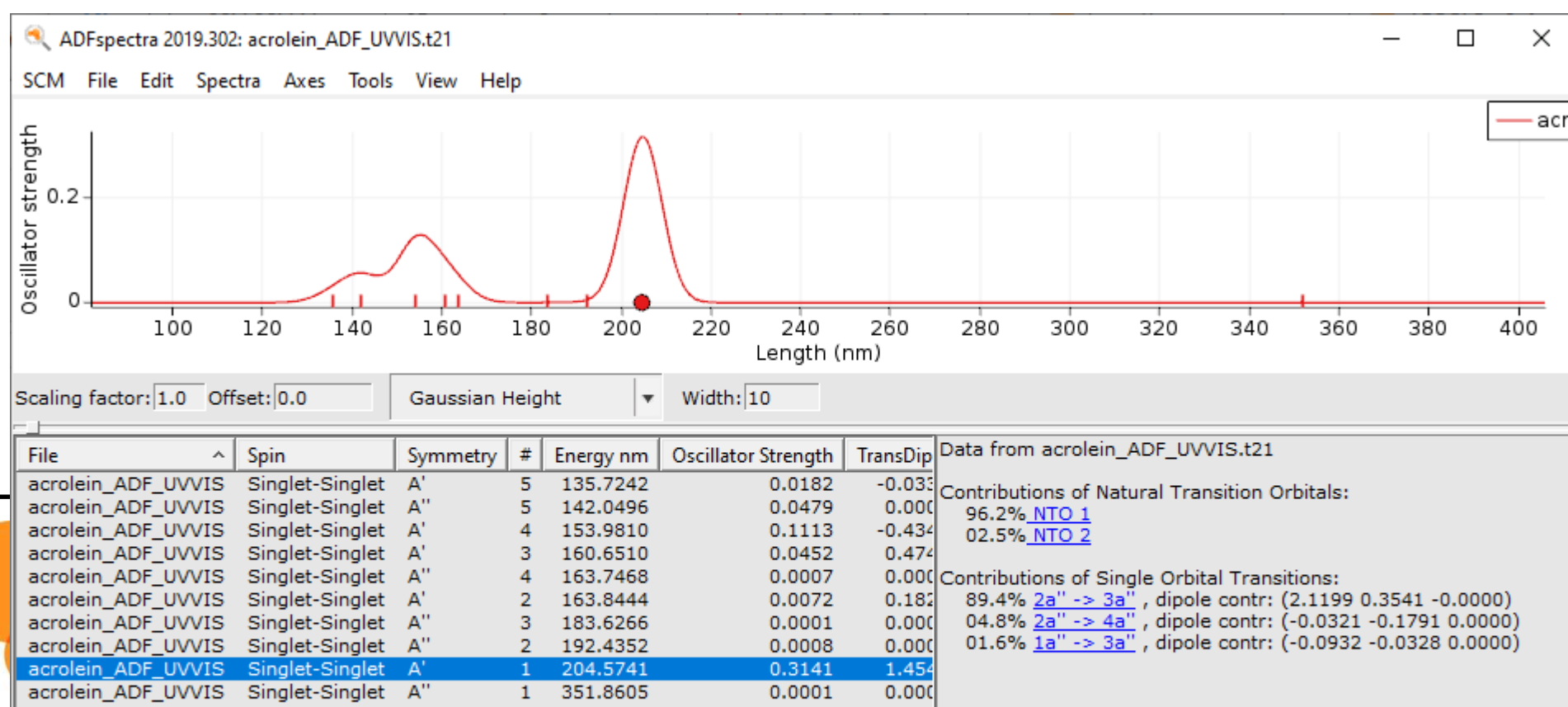
Excitations (UV/Vis), CD

Type of excitations: AllowedOnly

Method: Davidson

TDA: Yes

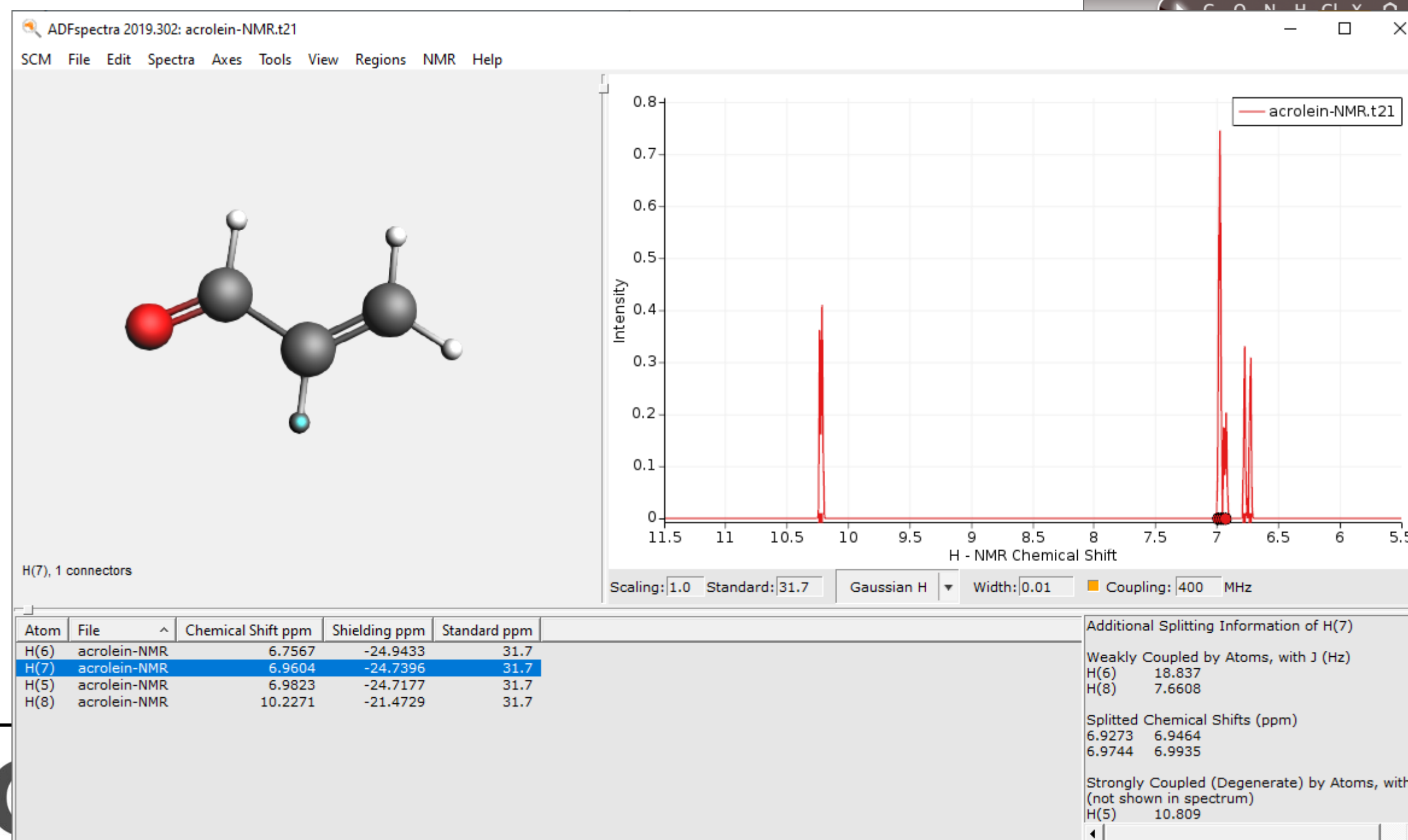
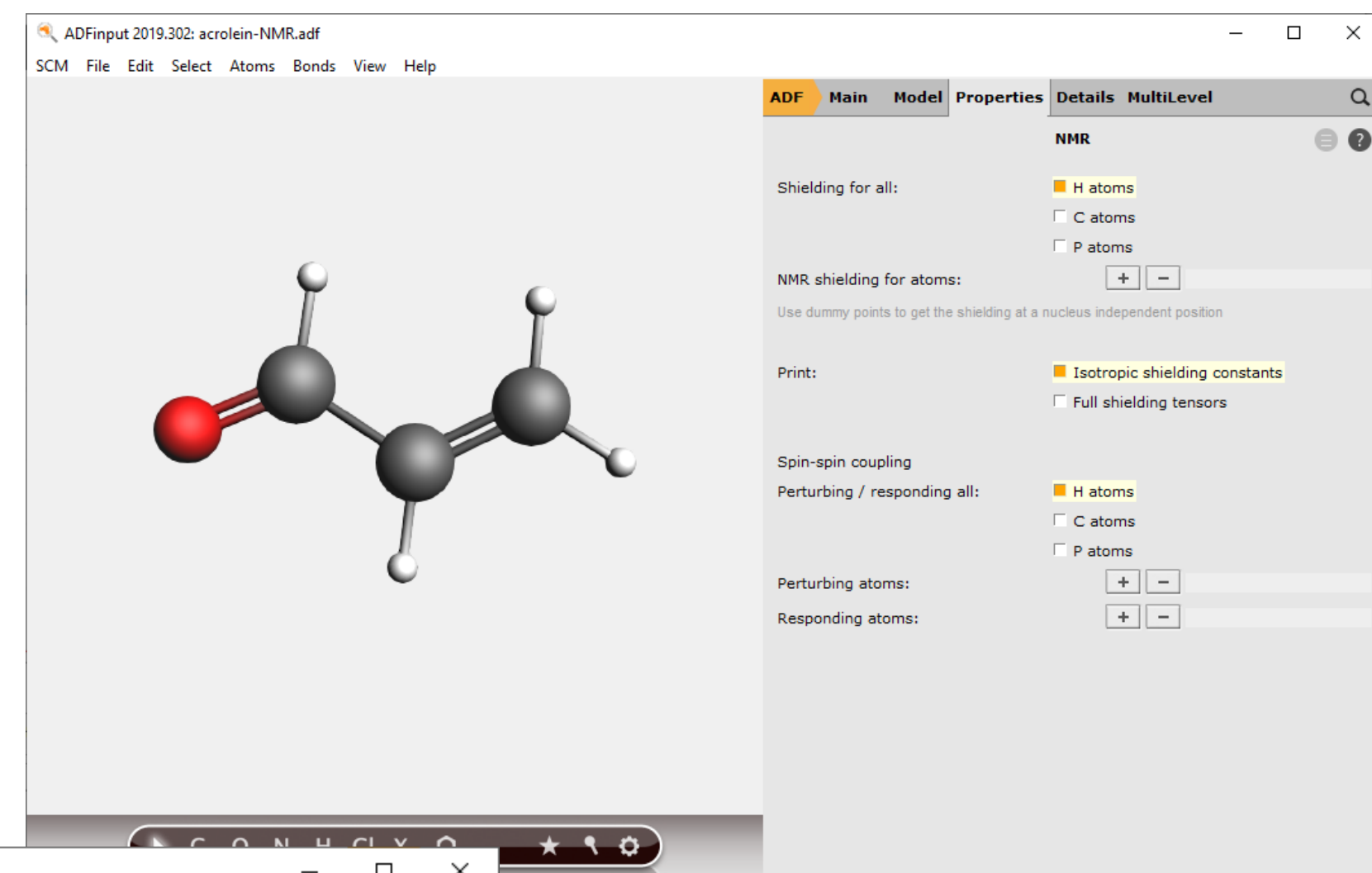
Number of excitations: 10



Spectra: NMR

- Exercise:

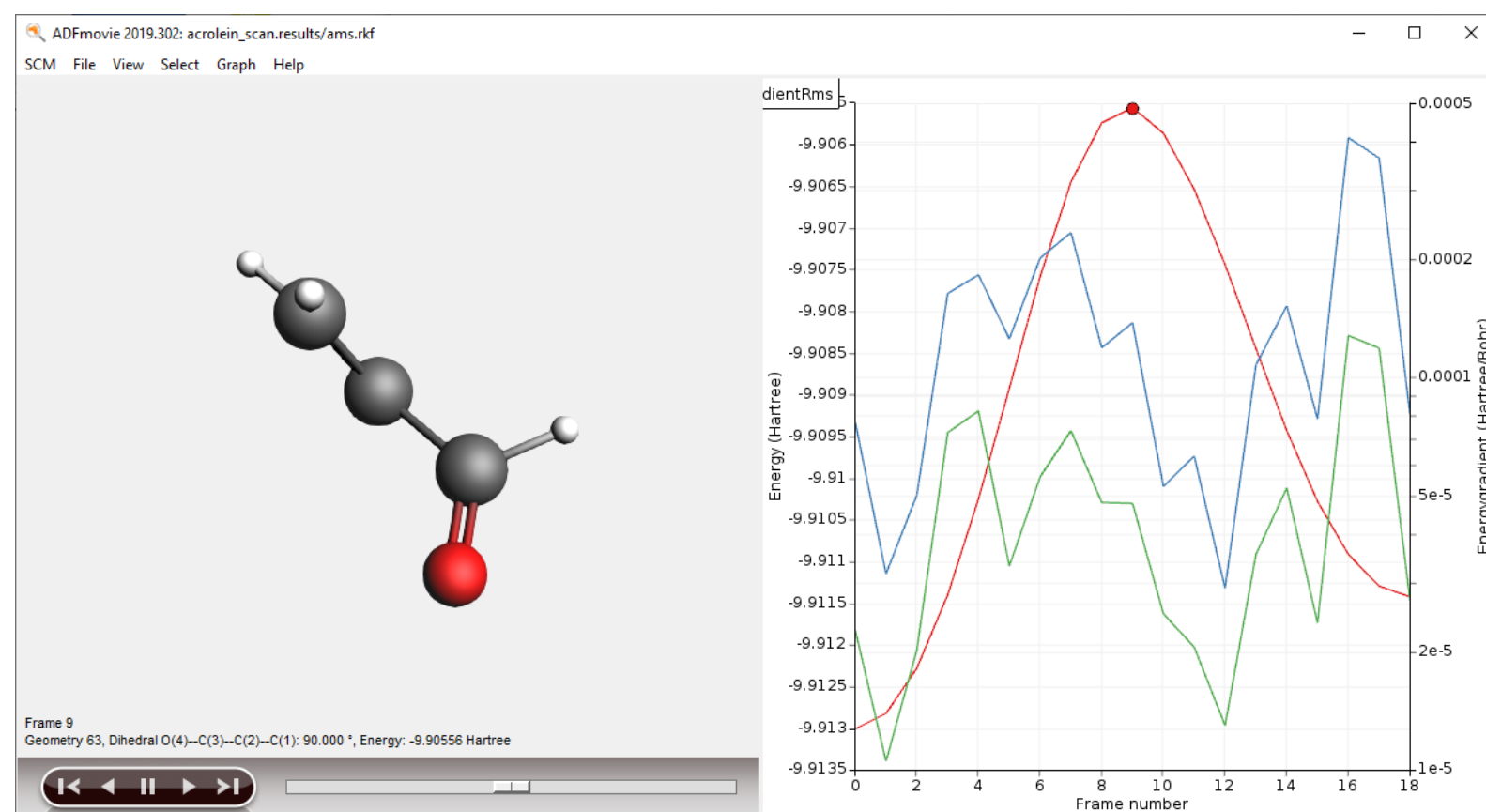
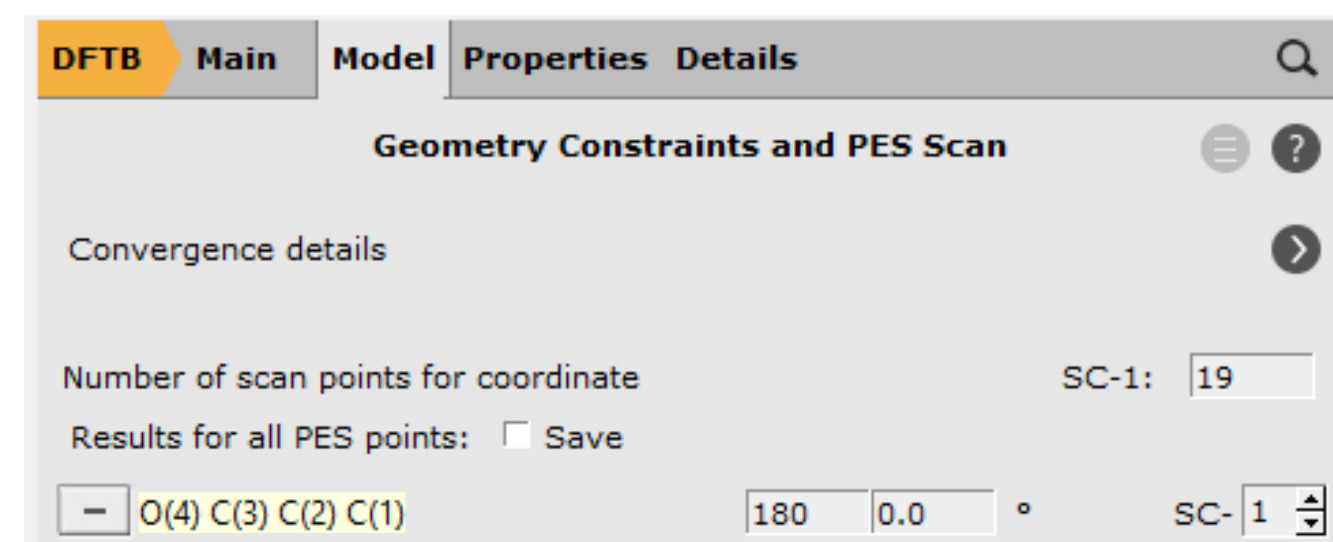
- See also [NMR FAQ for tips + advanced tutorials](#)
- Use PBE0 + TZP, Scalar, no core (.adf)
- Select Properties -> NMR
 - select shielding & coupling for all H
 - Set 400 MHz and tick coupling, [compare](#)
- Note the internal ref. uses different settings!
 - Recalculate TMS with same set up



PES: conformers, scan dihedral

- Exercises:

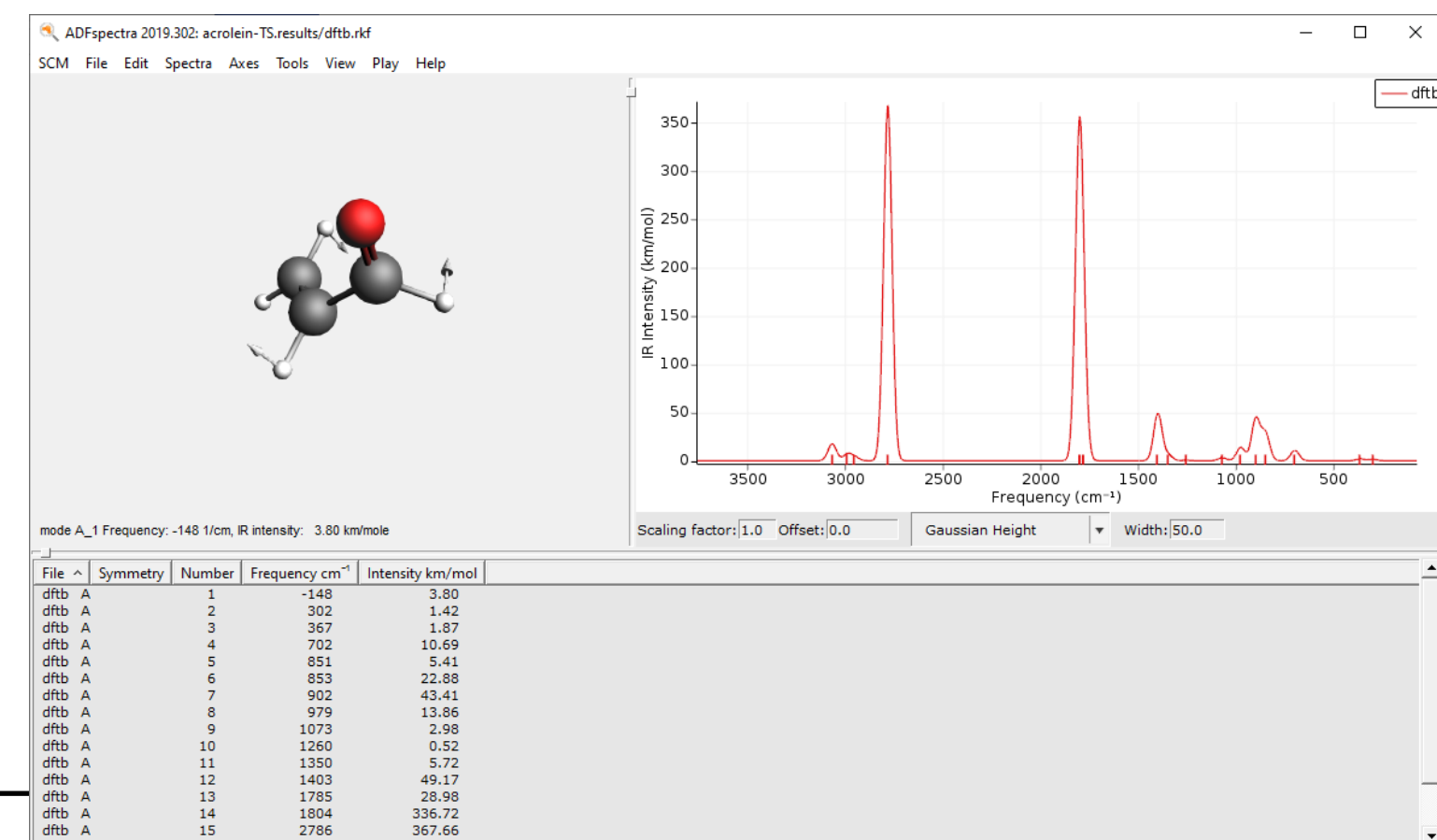
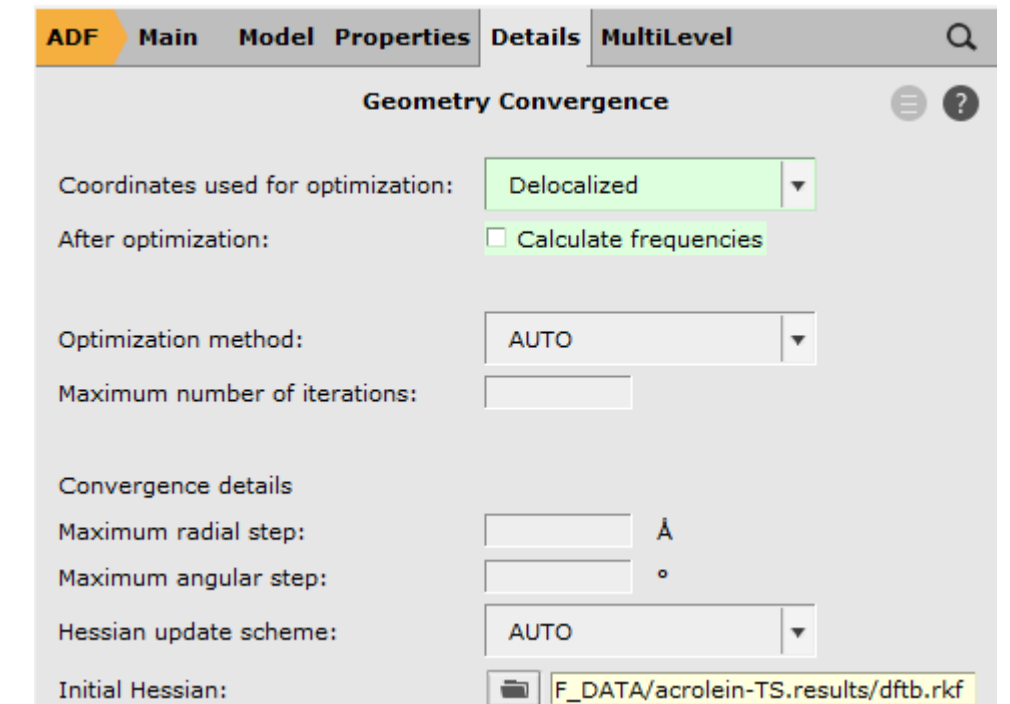
- Take any acrolein, switch the engine to Conformers, run, visualize -> ADFMovie
 - Does it find all conformers :) ? Maybe try a larger molecule?
 - Switch to, e.g. DFTB, and from Model -> Coordinates, Use: Selected File, select your.sdf
 - Do a frequency run on all geometries and visualize a Boltzmann-averaged spectrum
- Take a DFTB input, set task to PES Scan, click >
 - Select dihedral and scan in 19 points from 180-0 ([.adf](#))
 - Wait for calculation to finish -> ADFMovie
 - Select highest, save geometry (to import for TS search)



Transition State (I)

- Exercises:

- New DFTB input, DFTB3-D3-BJ/3ob-3-1
 - Import highest point from PES scan
 - Change Task: Transition State, and calculate frequencies ([.adf](#))
 - Leave all defaults and run, verify 1 imaginary mode
- Update geometry and switch to ADF
 - Change Task: Transition State, click >
 - Next to initial Hessian click again >
 - Choose the dftb.rkf from the DFTB TS as initial Hessian
 - On the main tab, choose Meta -> MN15L, DZP, no core ([.adf](#) – check restart file!)
 - Verify imaginary modes?
 - Can also use 'TSRC' if no lower-level Hessian

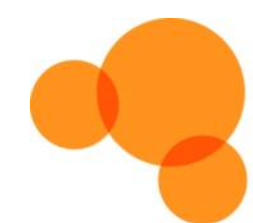


Quick thermodynamic properties

- Exercise:


- Open SCM -> COSMO-RS (no need to install database)
- In the SMILES input, put C=CC=O and Add
- Properties -> Pure compound
- Compare some properties (density, boiling point) (e.g. [Wikipedia](#))


Property		Unit
Boiling point	346.746	K
Critical pressure	51.21	bar
Critical temperature	524.603	K
Critical volume	0.195	L/mol
Liquid density	0.816	kg/L
Dielectric constant	10.985	
Absolute entropy (ideal gas)	309.848	J/(mol K)
Flash point	270.523	K
Gibbs energy of formation (ideal gas)	-111.468	kJ/mol
Net enthalpy of combustion	-1652.692	kJ/mol
Std. state enthalpy of formation	-188.906	kJ/mol
Enthalpy of fusion	17.129	kJ/mol
Enthalpy of formation (ideal gas)	-157.71	kJ/mol
Enthalpy of sublimation	49.534	kJ/mol
Melting point	213.82	K
Liquid molar volume	0.069	L/mol
Parachor	161.085	
Solubility parameter	10.098	$\sqrt{(\text{MPa})}$
Triple point temperature	213.778	K
Van der Waals area	91.576	\AA^2
Van der Waals volume	63.229	\AA^3

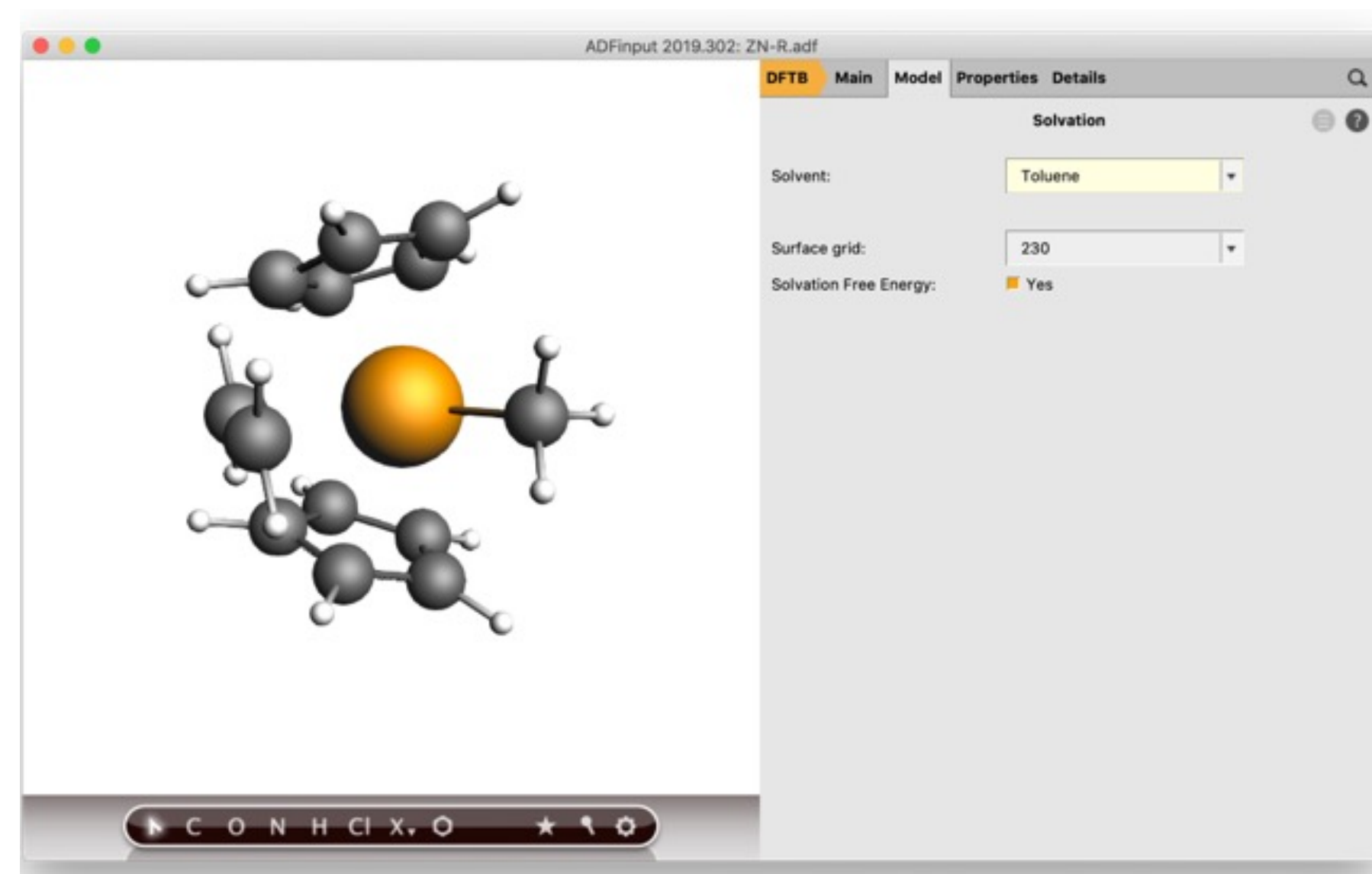
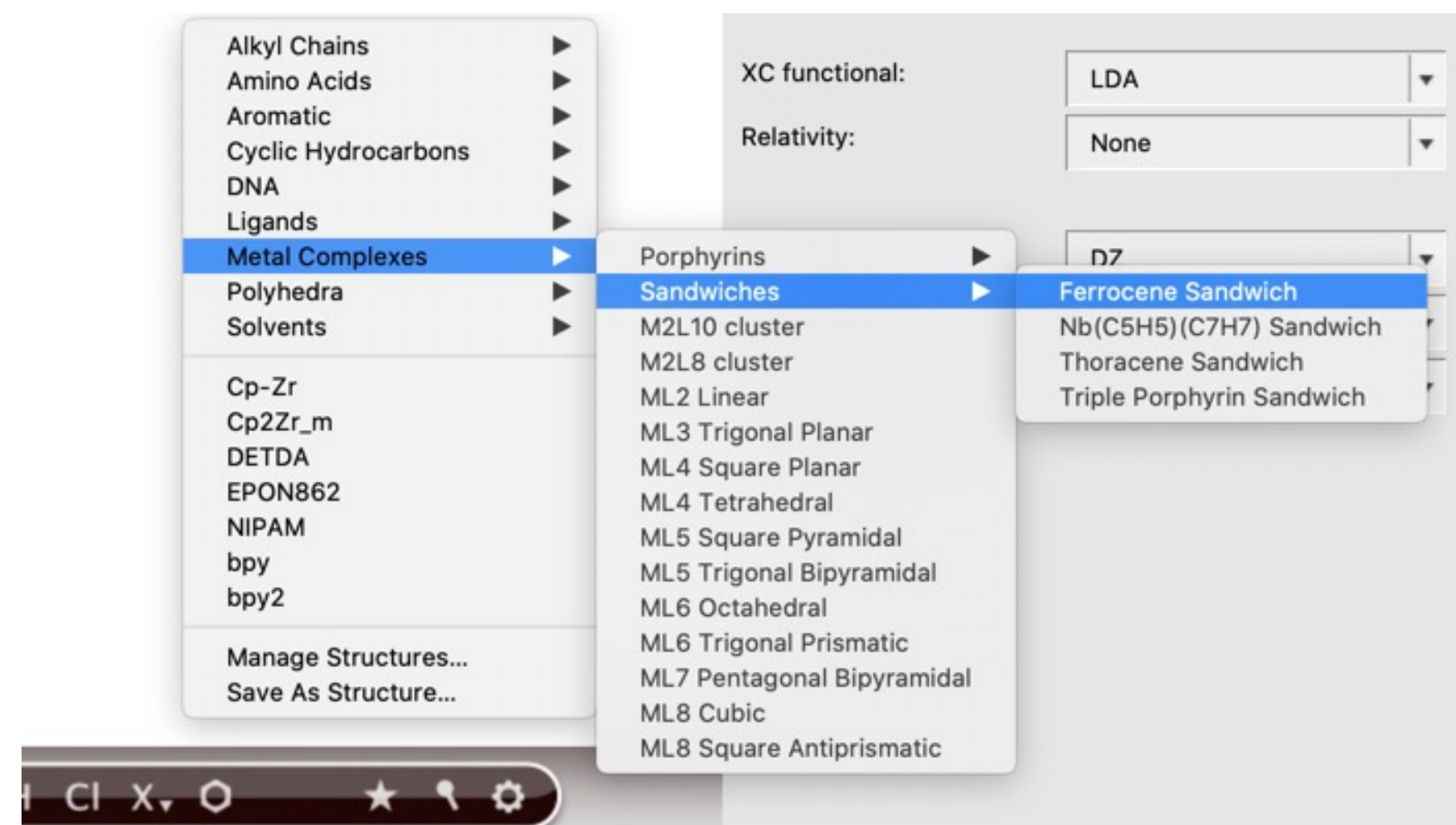


Transition State (II): Ziegler-Natta

- Exercises:

- New DFTB input, GFN-xTB
- Build Cp_2ZrMe^+
 - structure tool  => ferrocene
 - Right-click Fe -> Element -> Zr
 - Add C and replace by methyl
 - (Use dummies to change CpMCp angle)
 - Model -> Solvent -> Toluene
 - Add charge and optimize ([.adf](#))

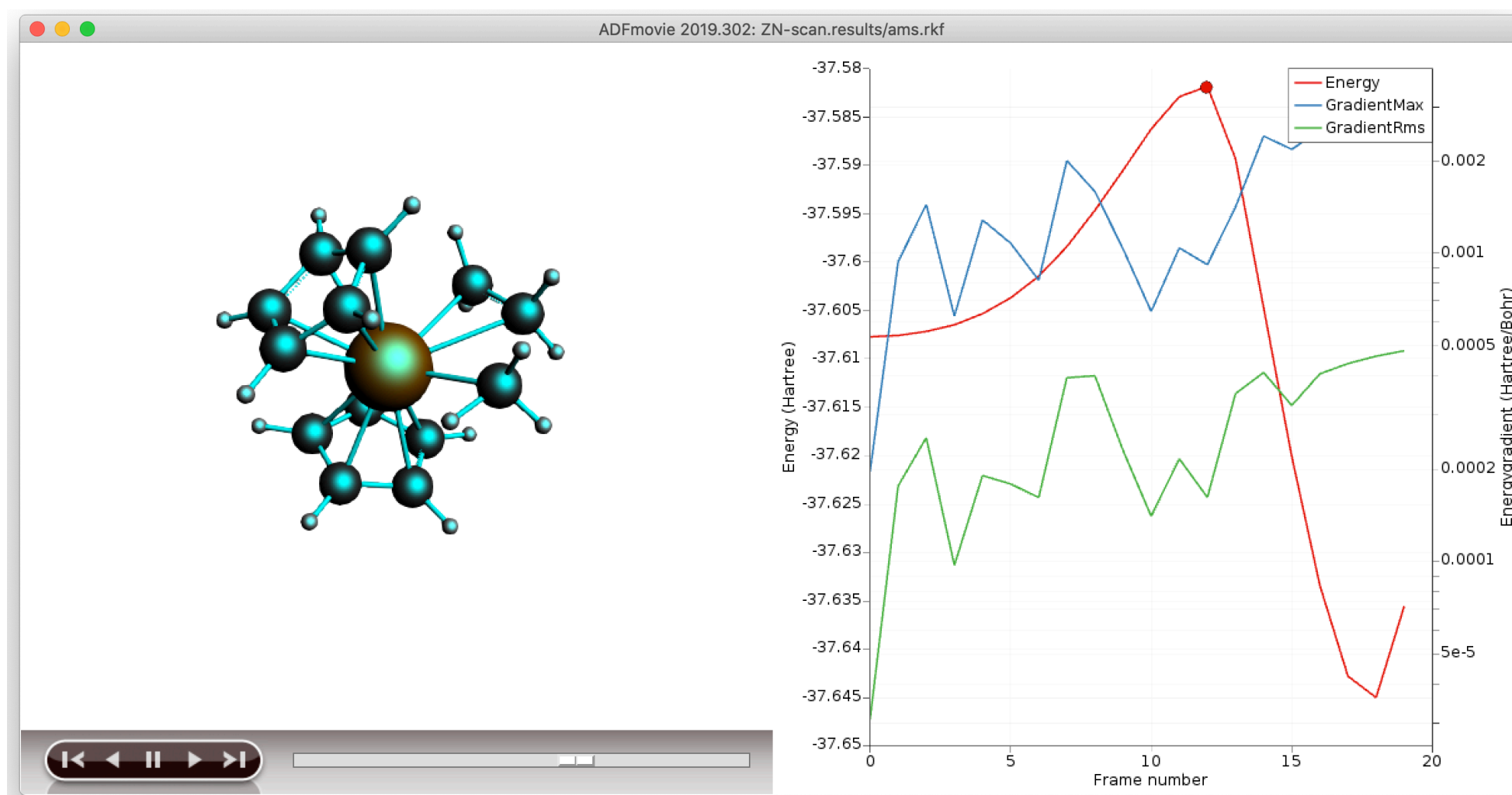
- Add ethene (use the )
 - Manipulate it in position
 - Right-click + drag = translate
 - Left-click + drag = rotate
 - Ctrl+M = select molecule
 - Remove dummies ([.adf](#))
 - Optimize



Transition State (II): Ziegler-Natta

- Exercise:

- Set up a PES scan, scanning 1 coordinate
 - Zr-C to 2.4 & C-C to 1.55
- Loosen the Convergence criteria by a factor of 5 ([.adf](#))
- When finished, open ADFMovie



The figure shows a screenshot of the ADF software interface, specifically the 'Geometry Constraints and PES Scan' panel. The panel is titled 'DFTB Main Model Properties Details'. Under 'Geometry Constraints and PES Scan', there are several options and settings:

- Convergence details: >
- Number of scan points for coordinate: SC-1: 10
- Results for all PES points: Save
- [-] C(28) Zr(1): 3.205 2.4 Å SC-1
- [-] C(29) C(25): 3.295 1.55 Å SC-1
- [+] All bonds in region: Auto_Genera
- [+] selected atoms (fix positions)
- [+] C(29) C(25) (distance)

At the bottom of the panel, convergence criteria are listed:

- Gradient convergence: 5.0e-3 Hartree/Å
- Energy convergence: 5.0e-5 Hartree
- Step convergence: 5.0e-3 Å

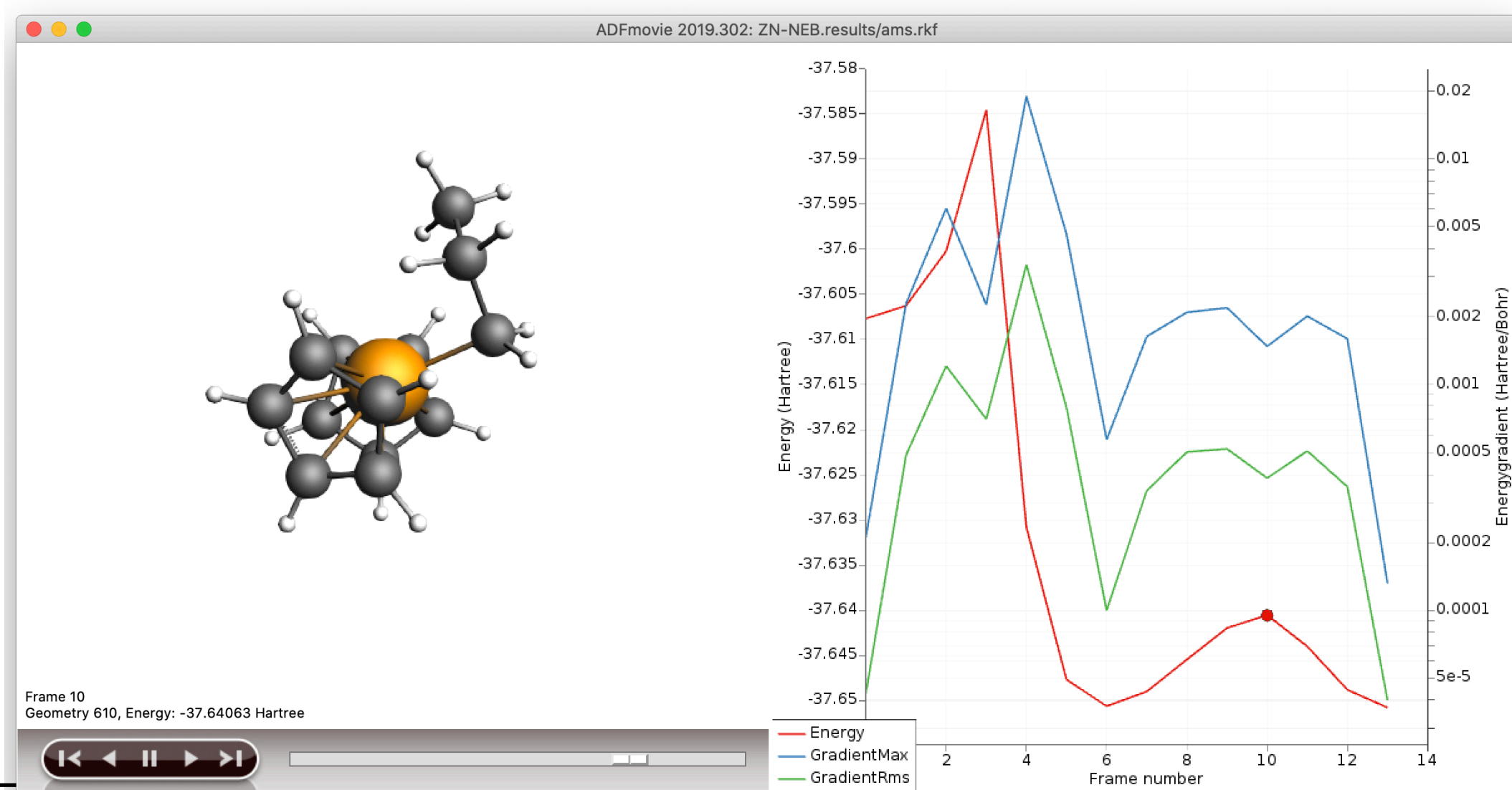
- Copy the highest energy structure (e.g. Ctrl+U), or save as structure
- Set up a TS run
 - make sure there are no constraints, and regular convergence
 - use a calculate Hessian as initial guess and calculate frequencies ([.adf](#))

Transition State (III): Ziegler-Natta

- Exercise:

- Optimize the product from the last PES scan point ([.adf](#))
- Rotate the Zr-C-C-H dihedral to ~ 0 (metallacycle Zr-C-C-H) & optimize ([.adf](#))
- Set up a climbing nudged elastic band calculation Task: NEB
- Choose this structure as final, the other product as intermediate, and R as initial (import structures from the ams.rkf) and choose 12 points
- Don't optimize R&P, relax convergence by factor 4* ([.adf](#))
- Open ADFMovie when finished
 - Which is the rate-determining step?

Number of images:	<input type="text" value="12"/>
Initial system:	<input type="text" value="Mol-3"/>
Final system:	<input type="text" value="Mol-1"/>
Intermediate system:	<input type="text" value="Mol-2"/>



* Tip: use NEB to get close to TS, then use Hessian-based optimization to find it

Transition States: Further considerations

- Reaction rates:

- Calculate ΔG^\ddagger : include H_{vib} , S (ADFoutput -> Other Properties -> Statistical Thermal Analysis)

Temp		Transl	Rotat	Vibrat	Total
----		-----	-----	-----	-----
298.15	Entropy (cal/mole-K):	42.601	31.219	51.511	125.331
	Internal Energy (Kcal/mole):	0.889	0.889	161.150	162.927
	Constant Volume Heat Capacity (cal/mole-K):	2.981	2.981	55.756	61.718
Summary of energy terms					
		hartree	eV	kcal/mol	kJ/mol
		-----	-----	-----	-----
	Bond Energy:	-37.588359904200161	-1022.8313	-23587.05	-98688.22
	Internal Energy:	0.259640981269797	7.0652	162.93	681.69
	pV/n = RT:	0.000944186013486	0.0257	0.59	2.48
	Enthalpy H:	-37.327774736916879	-1015.7404	-23423.53	-98004.06
	-T*S:	-0.059548659150599	-1.6204	-37.37	-156.34
	Gibbs free energy:	-37.387323396067480	-1017.3608	-23460.90	-98160.40

- Use harmonic TST as first approximation: $k = \exp(-G^\ddagger/RT)$
- Could also try [mircokinetics](#). More underway ([ReaxPro](#))

- Suggestions / troubleshooting

1. get close to TS: NEB, PES Scan, constrained opt, previous TS + change ligands (PLAMS script!),
2. get a good curvature (Hessian): pre-calc with GFN-xTB, MOPAC; partial Hessian
3. check final curvature / path: Frequency calculation, PES point characterization, [IRC](#)
4. Spurious imag. Freq.: displace along that mode (ADFMovie) & retry