

## Probing the Origins of Intermolecular Vibrational and Relaxational Dynamics in Organic Solids with CP2K

#### Michael Ruggiero

Department of Chemical Engineering and Biotechnology, University of Cambridge

CP2K Annual Users Meeting – Edinburgh

Email: mtr34@cam.ac.uk

#### **Outline**

- Introduction
  - Why do we care about vibrational dynamics?
  - Experimental and theoretical characterization
- Using CP2K to determine static (harmonic approx.) normal modes
- Using CP2K to determine vibrational spectra with molecular dynamics
  - The pros and cons of each
- Conclusions



- Intermolecular forces (IMFs) are a critical for understanding physical properties
- IMFs are typically weak compared to covalent bonds
  - Hydrogen Bonds
  - van der Waals
- Understanding how and why IMFs form important for describing physical observations



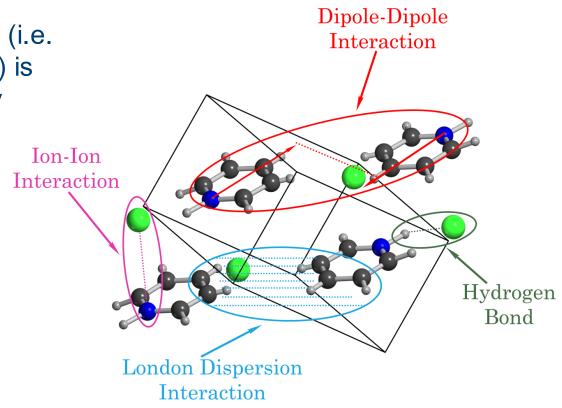




#### Vibrational Dynamics

Structural information (i.e. X-ray crystallography) is useful for qualitatively understanding the interactions between molecules/atoms

 But doesn't yield a complete picture



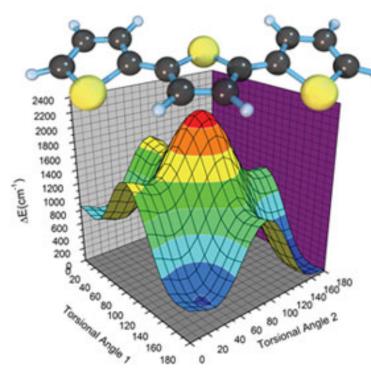
 But because vibrations depend on the <u>Curvature</u> of the potential energy surface, they are powerful for understanding the interaction strengths and nature

• 
$$F = ma = m\frac{\partial V^2}{\partial r^2} = -kx$$

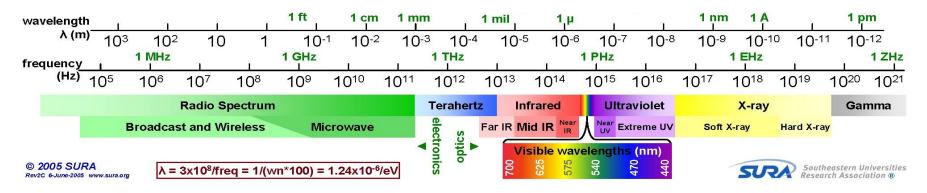
Quantum mechanically, solving the

Schrodinger equation yields the expression

$$E_n = \hbar\omega\left(n + \frac{1}{2}\right)$$



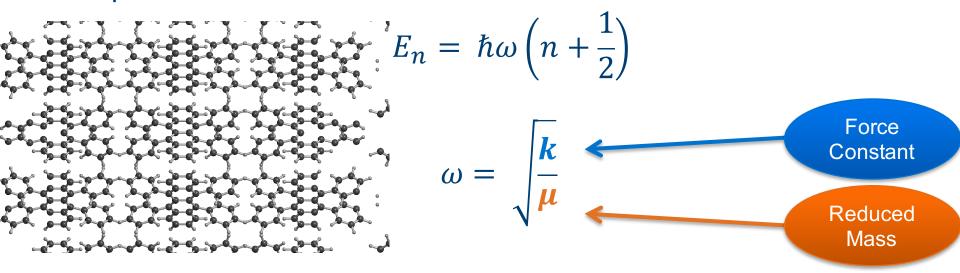
- So experimentally, we can use vibrational spectroscopy to understand the interactions in materials
  - Mid-IR, Raman
- For solids, terahertz time-domain spectroscopy is a low frequency version of mid-IR and is powerful for looking at solids





#### **Terahertz Vibrations**

Mode-types arise from the solution to the Schrödinger equation:

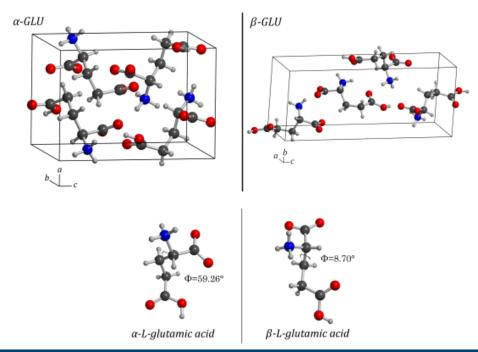


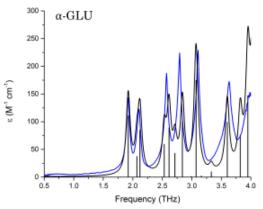
- Large amplitude vibrations transverse large areas of the potential energy surface
- Therefore, both the internal bond <u>AND</u> external intermolecular potentials are sampled!

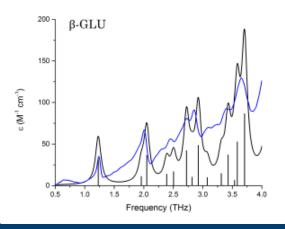


Unlike the mid-IR, there are no functional group specific vibrations at THz frequencies

- NEED a way of analyzing the spectra!
  - DFT and AIMD!



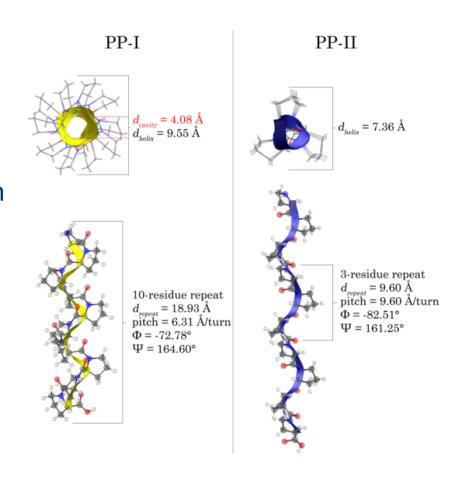






#### **Quick Example of Usefulness**

- Polyproline 'rigid' peptide that has been used to as a standard in biochemistry due to its uniform length and size.
- Two forms PP-I and PP-II, differ in their chirality
- Rigidity information not known nor easily obtained
  - AFM is v. difficult!



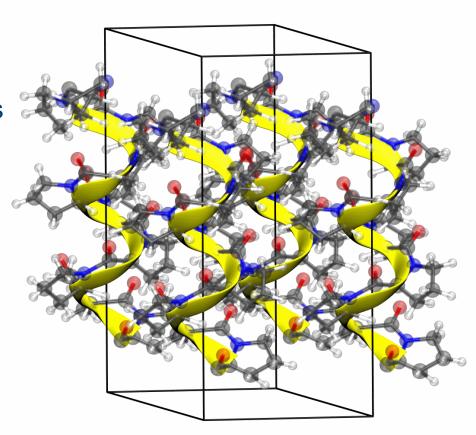
#### **Example**

- Calculation of low-frequency vibrations show that the modes are very 'spring' like
- Can use vibrational force constants and reduced masses to determine Young's moduli!

$$Y = \frac{\sigma}{\varepsilon} = \frac{FL_0}{A_0 \Delta L}$$

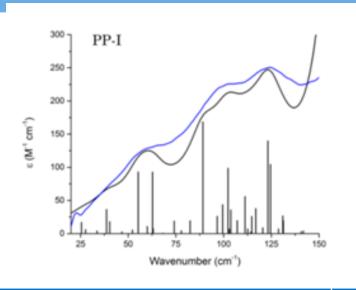
$$F = \underbrace{\frac{YA_0}{L_0}\Delta L}_{\text{Hooke's Law}} = \underbrace{\frac{YA_0}{L_0}}_{\text{Hooke's Law}}$$

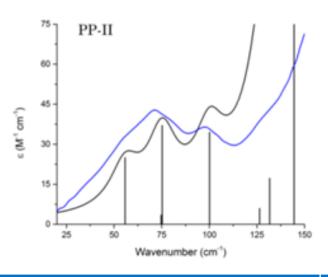
$$\therefore k = \frac{YA_0}{L_0}$$





#### **Example – Does it work?**

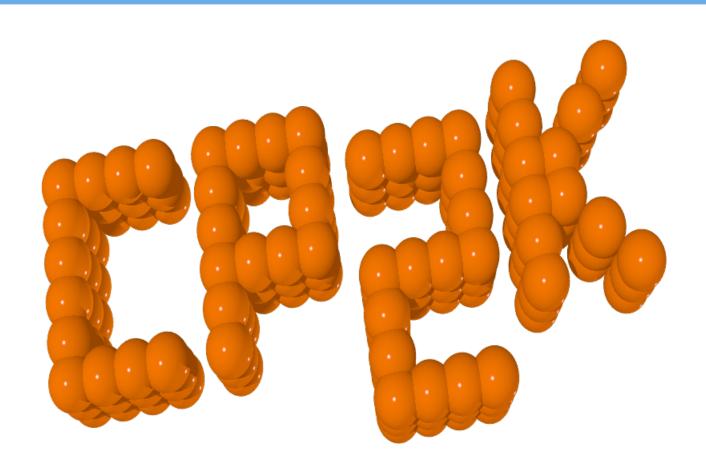




	Experimental			Calculated				Ab initio
	$\widetilde{\mathcal{V}}$	k	Y	$\widetilde{\mathcal{V}}$	k	μ	Y	Υ
PP-I	66.6	1.9	4.9 <u>+</u> 0.2	68.15	1.94	7.08	5.04	5.06
PP-II	98.1	3.8	9.6 <u>+</u> 0.1	100.1	3.91	6.62	9.82	10.57



#### So What Can We Do With CP2K?!



#### **Using DFT Methods to Characterise Dynamics**

#### Static DFT

- Harmonic approximation
- Gradient of P.E.S determined via finite differences (dx, dy, dz)
- Yields very detailed information
  - Normal mode frequencies, eigenvectors
- Integrated intensities can be easily determined with high accuracy

#### **AIMD**

- No explicit treatment of quantized vibrations
- Generates an overall vibrational spectra
- Yields lineshapes, intensities.
- No explicit normal mode treatment/calculation
- Can include temperature effects!



#### **Static DFT**

- Works by building a force constant matrix
  - Numerical displacements in all three coordinates for all atoms
    - 3N displacements

$$D_{IJ} = \frac{\partial^2 E}{\partial R_I \partial R_J}$$

 Force constant matrix (Hessian) is then diagonalized to yield eigenvectors and eigenvalues

#### So what does the INPUT look like?

Very similar to normal CP2K INPUT, but with an additional block(s)

```
&VIBRATIONAL_ANALYSIS
INTENSITIES
NPROC_REP 16
DX 0.001
&PRINT
    &PROGRAM_RUN_INFO ON
    &END
    &END
&END
```

```
&DFT

BASIS_SET_FILE_NAME ./BASIS_MOLOPT

POTENTIAL_FILE_NAME./GTH_POTENTIALS

&PRINT

&MOMENTS

PERIODIC FALSE

&END

&END
```



#### **Important considerations**

- Vibrational analyses should only be performed on well-optimized structures!
  - If not at a minimum in the P.E.S this will lead to imaginary modes!
- Tighter convergence criteria should be used!
  - EPS\_SCF < 10<sup>-9</sup> (or tighter!!) for best results
    - Especially for intensities!  $Z^* = \frac{\partial \mu}{\partial R} = \frac{\partial^2 E}{\partial R \partial \varepsilon} = \frac{\partial P}{\partial R}$
  - MAX\_FORCE should also be checked to ensure convergence
    - 1.0E-4 or smaller

#### **Output from Static DFT**

• Good output, no imaginary (negative) frequencies

VIBI	NORMAL MODES	- CARTESIAN DISPLACE	MENTS
VIB			
VIB	1	2	3
VIB Frequency (cm^-1)	340.444852	1036.860333	1096.247495
VIB Intensities	0.007659	0.005229	0.006011
VIB Red.Masses (a.u.)	1.067601	1.114971	7.032618
VIB Frc consts (a.u.)	0.000037	0.003299	0.026003
ATOM EL X	Y Z	X Y Z	X Y Z
1 C 0.	00 0.00 -0.00	0.08 -0.01 0.00	0.01 0.54 -0.00
2 0 -0.	00 -0.00 0.06	-0.01 0.05 -0.00	0.00 -0.44 0.00
3 H -0.	00 -0.00 -0.30	-0.08 -0.58 -0.00	-0.10 0.09 0.00
4 H 0.	00 -0.00 -0.88	-0.20 -0.59 0.00	0.05 -0.36 0.00
5 H -0.	22 0.04 0.10	-0.25 0.26 0.04	-0.07 0.42 0.05
6 н 0.	22 -0.04 0.10	-0.25 0.26 -0.04	-0.07 0.42 -0.05



#### **Bad output!**

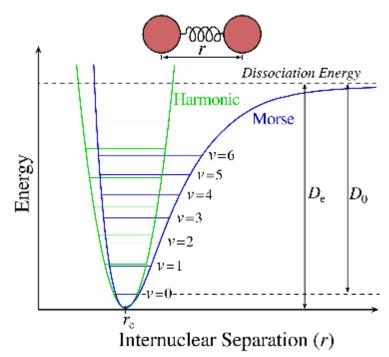
- Bad output! Negative modes!
  - Not in a global minimum!

```
VIBI
                            NORMAL MODES - CARTESIAN DISPLACEMENTS
VIB |
VIBI
                        -34.444852
                                            1036.860333
                                                                 1096.247495
VIB|Frequency (cm^-1)
VIB | Intensities
                          0.007659
                                               0.005229
                                                                    0.006011
VIB|Red.Masses (a.u.)
                          1.067601
                                               1.114971
                                                                    7.032618
VIB|Frc consts (a.u.)
                          0.000037
                                               0.003299
                                                                    0.026003
ATOM EL
                      Χ
                                                                      Y
                            Y
                                                                X
                                                                             Z
       C
                     0.00 0.00 -0.00
                                        0.08 -0.01 0.00
                                                               0.01 0.54 -0.00
                    -0.00 -0.00 0.06
                                         -0.01 0.05 -0.00
                                                               0.00 - 0.44
                                                                           0.00
                    -0.00 -0.00 -0.30
                                         -0.08 - 0.58 - 0.00
                                                              -0.10 0.09 0.00
      Η
                    0.00 -0.00 -0.88
                                         -0.20 - 0.59
                                                               0.05 -0.36 0.00
                                                      0.00
                    -0.22 0.04 0.10
                                         -0.25 0.26 0.04
      Η
                                                              -0.07 0.42 0.05
                     0.22 -0.04 0.10
                                         -0.25 0.26 -0.04
                                                              -0.07 0.42 -0.05
```



#### Ab initio MD

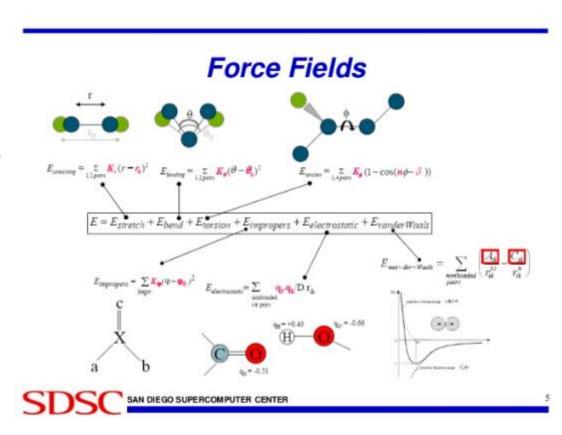
- The Harmonic Approx is great and has proven to give good results
- But it is only an approximation, and any deviations from harmonic behavior wont be accounted for
  - Anharmonicity
  - Thermal Effects
- MD can account for these!





#### ab initio Simulations - Molecular Dynamics

- Molecular dynamics (MD) calculations can be applied to very large systems
  - Proteins, 100,000s of atoms
- However traditional MD is a classical method
  - Newtonian mechanics and pre-built atomic 'force-fields'
- Leads to biased vibrational results!

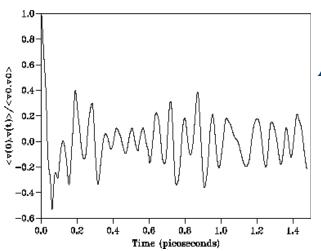




#### ab initio Simulations - Molecular Dynamics

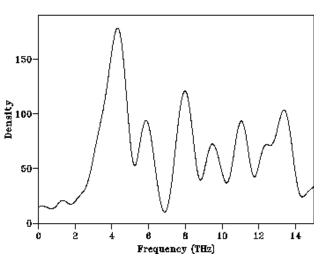
- The solution?
  - A dual DFT-MD approach (ab initio molecular dynamics, AIMD)
- Recalculate the quantum potential energy surface at each classical time-step

MD results can be used to calculate IR spectra



$$A(\omega) \propto \int \langle \mu(\tau)\mu(t+\tau) \rangle_{\tau} e^{-i\omega t} dt$$

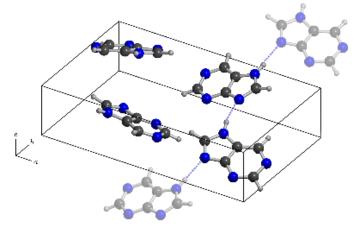
Fourier Transforming the dipole moment autocorrelation function

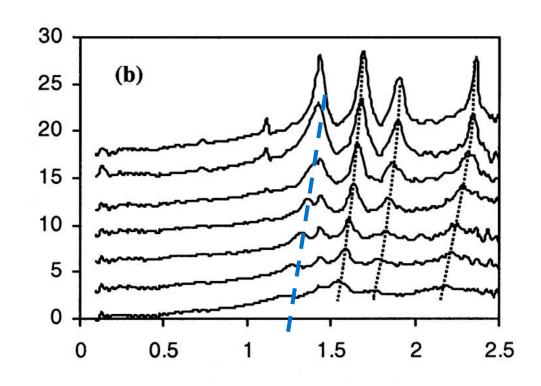


BC8 Silicon D.O.S. (500K)

#### **Example – Crystalline Purine**

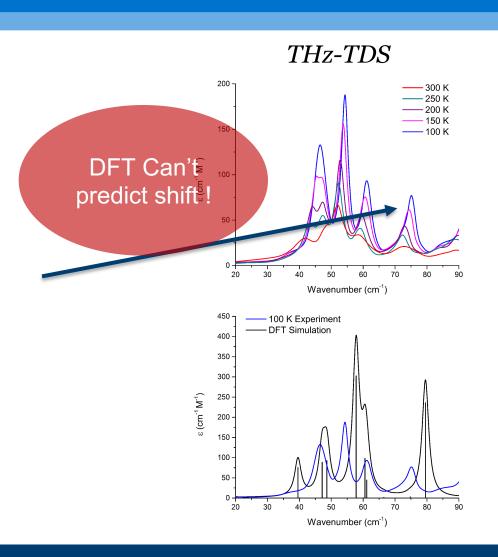
- Model system Purine
- Large changes in THz-TDS spectra as a function of temperature
  - Sign of anharmonicity



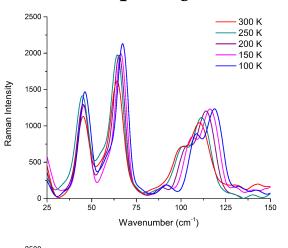


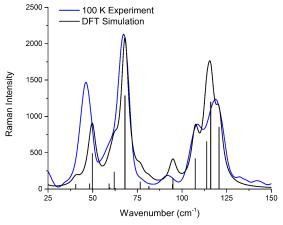
Shen, Y. C., P. C. Upadhya, E. H. Linfield, and A. Ga Davies. "Temperature-dependent low-frequency vibrational spectra of purine and adenine." *Applied Physics Letters* 82, no. 14 (2003): 2350-2352.

#### **New Data**



#### Low-Frequency Raman

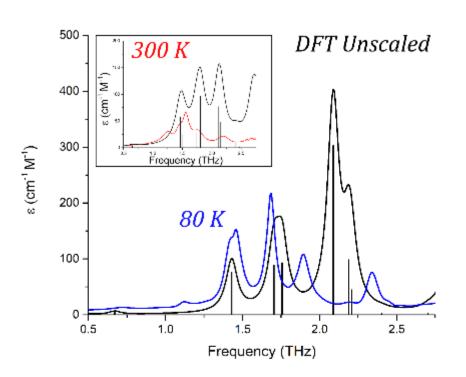


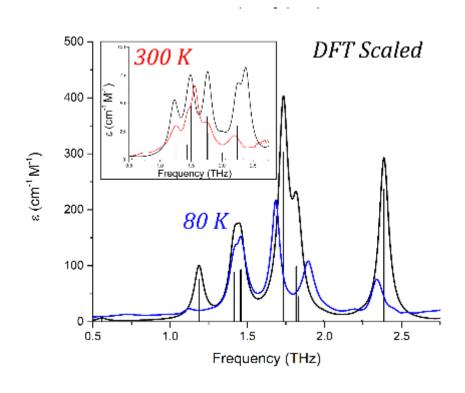




#### Is it reliable?

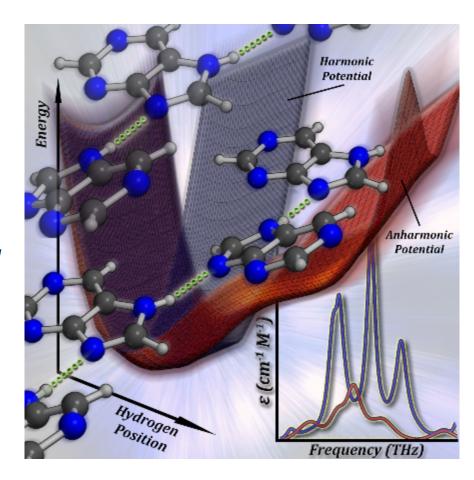
#### Solid-state DFT results

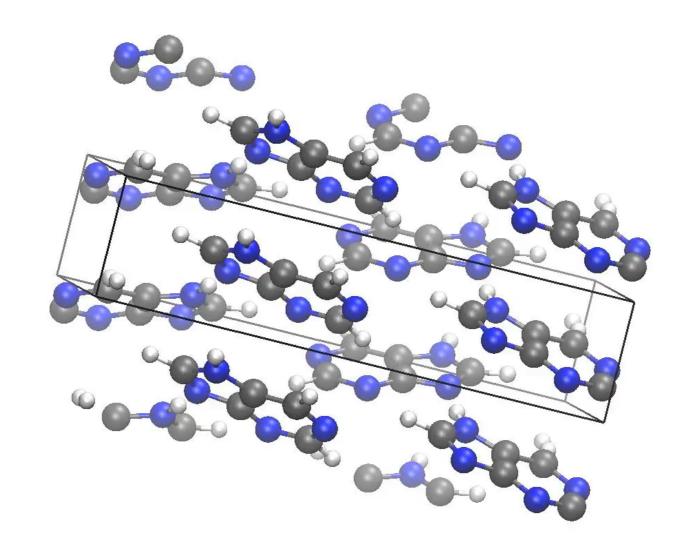




#### Is it reliable?

- DFT is good, but requires scaling and not all peak shifting is reproduced
  - Can account for structural anharmonicity, but not vibrational anharmonicity
- Solution: AIMD





#### How To?

- NVT Simulation, with the calculation of Wannier Functions at various intervals
  - Best is 0.5 fs time step, with WF calculation at every 5 steps (2.5 fs).

```
&LOCALIZE

METHOD CRAZY

MAX_ITER 2000

&PRINT

&WANNIER_CENTERS

IONS+CENTERS

FILENAME = wannierout.xyz

&EACH

MD 5

&END EACH

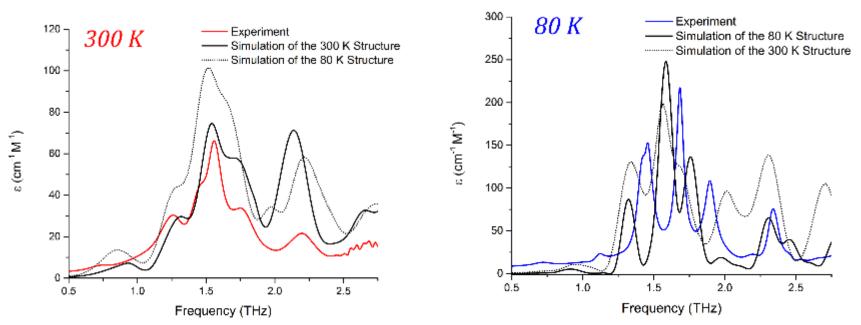
&END WANNIER_CENTERS

&END PRINT

&END LOCALIZE
```



#### **MD** of Purine



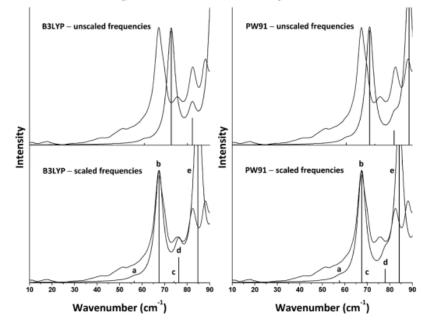
- Temperature dependencies are resolved without any scaling!
- Origins of temperature changes probed by performing the MD simulations on the 'reciprocal' structures
  - 300 K structure simulated at 80 K, and vice versa

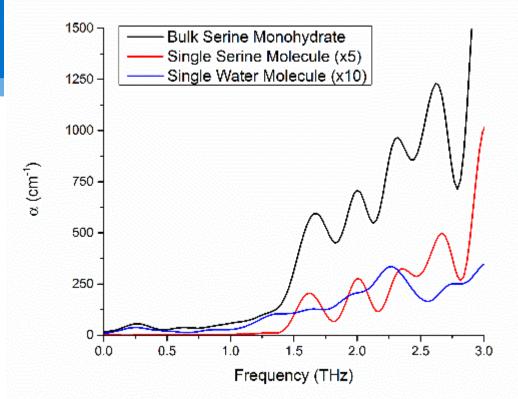
### **Contributions from Different Groups – Serine Monohydrate**

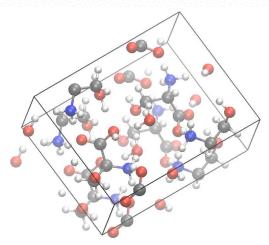
- Serine monohydrate is believed to exhibit anharmonicty
- DFT was shown to over-estimate vibrational frequencies by ~10%
- What specific atoms are contributing to the anharmonicity?

Investigating the Anharmonicity of Lattice Vibrations in Water-Containing Molecular Crystals through the Terahertz Spectroscopy of L-Serine Monohydrate

Matthew D. King, William D. Buchanan, and Timothy M. Korter\*







Investigating the Anharmonicity of Lattice Vibrations in Water-Containing Molecular Crystals through the Terahertz Spectroscopy of L-Serine Monohydrate

Matthew D. King, William D. Buchanan, and Timothy M. Korter\*

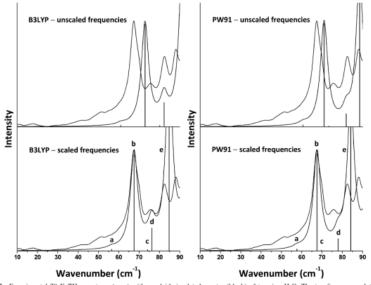
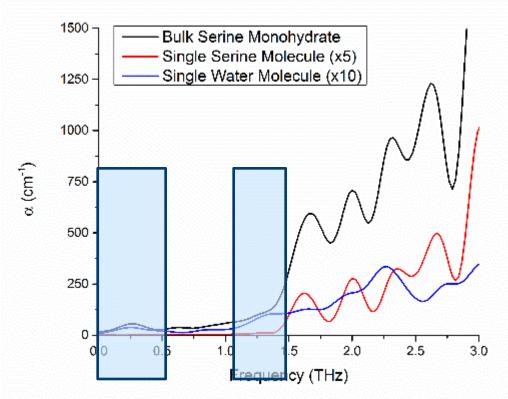


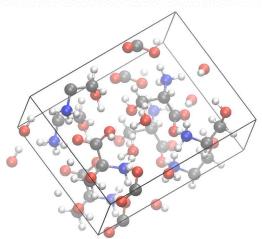
Figure 5. Experimental 78 K THz spectrum (gray) with overlaid simulated spectra (black) of t-serine  $H_2O$ . The top figures are plotted with unscaled vibrational frequencies and the bottom with the applied frequency scalars of 0.925 for B3LYP and 0.950 for PW91. An empirical full-width-half-maximum value of 4.30 cm<sup>-1</sup> was used in convolving Lorentzian line shapes for simulated spectra.

L-Serme-H <sub>2</sub> O			
mode freq, cm <sup>-1</sup>		mode description <sup>a</sup>	% H <sub>2</sub> O contrib <sup>b</sup>
a	61.0	serine: 100% ET along a-axis	18
		H <sub>2</sub> O: 75% ET along b-axis, 25% ER about b-axis	
b	72.9	serine: 75% ER about b- and c-axes, 25% Int (-NH3+ rotation)	20
		H <sub>2</sub> O: 100% ET along a-, b-, and c- axes	
c	80.1	serine: 75% ET along c-axis, 25% ER about b-axis	16
		H <sub>2</sub> O: 75% ET along c-axis, 25% ER about b- and c-axes	
d	82.3	serine: 25% ET along c-axis, 25% ER about a- and c-axes,	16
		50% Int (C <sub>1</sub> -C <sub>2</sub> , C <sub>3</sub> -O <sub>3</sub> torsions)	
		H2O: 50% ET along a- and c-axes, 50% ER about a-axis	
e	91.5	serine: 100% ER about b-axis	15
		H <sub>2</sub> O: 100% ET along a-axis	
f	98.9	serine: 75% ER about a-axis, 25% Int (C2-C3 torsion)	19
		H <sub>2</sub> O: 100% ET along a- and b-axes	
g	101.5	serine: 50% ER about c-axis, 50% Int (C <sub>1</sub> -C <sub>2</sub> , C <sub>3</sub> -O <sub>3</sub> torsions)	22
		H <sub>2</sub> O: 100% ET along b-axis	
h	105.8	serine: 50% ER about a-axis, 50% Int (C <sub>1</sub> -C <sub>2</sub> , C <sub>3</sub> -O <sub>3</sub> torsions)	26
		H <sub>2</sub> O: 100% ET along b-axis	
i	107.6	serine: 75% ER about b- and c-axes, 25% Int (C2-C3 torsion)	10
		H <sub>2</sub> O: 75% ET along a-, b-, and c-axes, 25% ER about a-, b-, and	
		c-axes	

<sup>&</sup>lt;sup>a</sup> ET = translation; ER = external rotation; Int = internal motion. <sup>b</sup> Percent of total atomic displacements due to motion of H<sub>2</sub>O molecules.







Investigating the Anharmonicity of Lattice Vibrations in Water-Containing Molecular Crystals through the Terahertz Spectroscopy of L-Serine Monohydrate

Matthew D. King, William D. Buchanan, and Timothy M. Korter\*

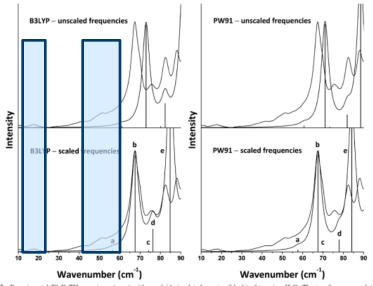


Figure 5. Experimental 78 K THz spectrum (gray) with overlaid simulated spectra (black) of t-serine H<sub>2</sub>O. The top figures are plotted with unscaled vibrational frequencies and the bottom with the applied frequency scalars of 0.925 for B3LYP and 0.950 for PW91. An empirical full-width-half-maximum value of 4.30 cm<sup>-1</sup> was used in convolving Lorentzian line shapes for simulated spectra.

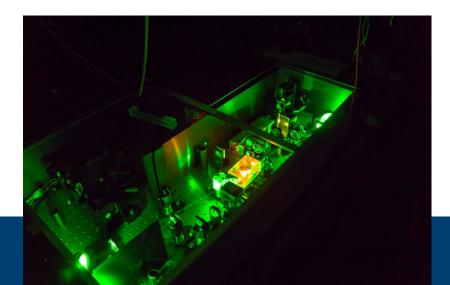
mode freq, cm <sup>-1</sup> a 61.0		mode description <sup>a</sup>	% H <sub>2</sub> O contrib <sup>b</sup>
		serine: 100% ET along a-axis	
		H <sub>2</sub> O: 75% ET along b-axis, 25% ER about b-axis	
b 72.9	72.9	serine: 75% ER about b- and c-axes, 25% Int (-NH <sub>3</sub> + rotation)	20
		H <sub>2</sub> O: 100% ET along a-, b-, and c- axes	
C	80.1	serine: 75% ET along c-axis, 25% ER about b-axis	16
		H <sub>2</sub> O: 75% ET along c-axis, 25% ER about b- and c-axes	
d	82.3	serine: 25% ET along c-axis, 25% ER about a- and c-axes,	16
		50% Int (C <sub>1</sub> -C <sub>2</sub> , C <sub>3</sub> -O <sub>3</sub> torsions)	
		H <sub>2</sub> O: 50% ET along a- and c-axes, 50% ER about a-axis	
e	91.5	serine: 100% ER about b-axis	15
		H <sub>2</sub> O: 100% ET along a-axis	
f 98.	98.9	serine: 75% ER about a-axis, 25% Int (C2-C3 torsion)	19
		H <sub>2</sub> O: 100% ET along a- and b-axes	
g	101.5	serine: 50% ER about c-axis, 50% Int (C <sub>1</sub> -C <sub>2</sub> , C <sub>3</sub> -O <sub>3</sub> torsions)	22
		$H_2O$ : 100% ET along b-axis	
h	105.8	serine: 50% ER about a-axis, 50% Int (C <sub>1</sub> -C <sub>2</sub> , C <sub>3</sub> -O <sub>3</sub> torsions)	26
		$H_2O$ : 100% ET along b-axis	
i	107.6	serine: 75% ER about b- and c-axes, 25% Int (C <sub>2</sub> -C <sub>3</sub> torsion)	10
		H <sub>2</sub> O: 75% ET along a-, b-, and c-axes, 25% ER about a-, b-, and	
		c-axes	

<sup>&</sup>lt;sup>a</sup> ET = translation; ER = external rotation; Int = internal motion. <sup>b</sup> Percent of total atomic displacements due to motion of H<sub>2</sub>O molecules.



#### Conclusions

- Analysing spectroscopic data, especially low-frequency spectra, via DFT methods
- Generates a picture of intermolecular energy landscape
- Static DFT calculations (in the harmonic approx.) give very detailed info, but lack temperature/anharmonic information
- MD calculations fill in the gaps





#### **Acknowledgements**

#### **Terahertz Applications Group**

J. Axel Zeitler - PI
Daniel Markl – Postdoctoral Fellow



#### **External Collaborators**

Stephen R. Elliott Marcin Krynski Iain Bethune Alessandro Erba Timothy Korter



(Cambridge, UK)
(Cambridge, UK)
(EPCC, UK)
(University of Turin, IT)
(Syracuse University, USA)







Email: mtr34@cam.ac.uk

# Thank you for your attention!

