

Molecular Dynamics Simulations in the School of Chemistry



Philip Camp



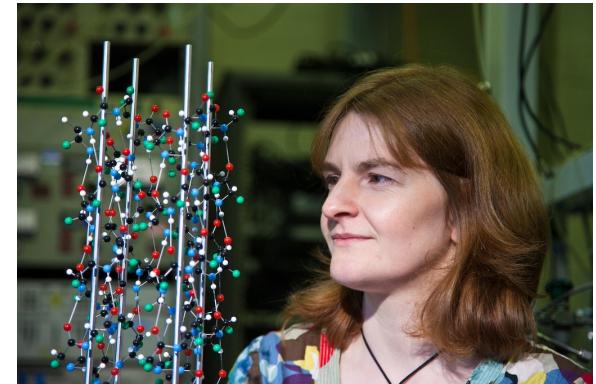
Fernanda Duarte



Adam Kirrander



Julien Michel



Carole Morrison

Research themes

1. Reaction dynamics and electron/X-ray scattering

Adam Kirrander

2. Solid-state structure and dynamics

Carole Morrison

3. Catalysis

Fernanda Duarte

4. Molecular liquids and biomolecular systems

Philip Camp, Julien Michel, Carole Morrison

5. Soft matter

Philip Camp

Simulation methods

1. Few-atom quantum dynamics

Adam Kirrander

2. Ab-initio and Car-Parrinello molecular dynamics

Carole Morrison

3. Quantum mechanics/molecular mechanics

Fernanda Duarte

4. Classical atomistic molecular dynamics

Philip Camp, Julien Michel, Carole Morrison

5. Coarse-grained dynamics

Philip Camp



length/time

1. Adam Kirrander: Reaction dynamics

- Few-atom quantum dynamics

Andrés Moreno, Darren Bellshaw, Nikola Zotev, Maria Tudorovskaya, and Minas Stefanou



The Leverhulme Trust



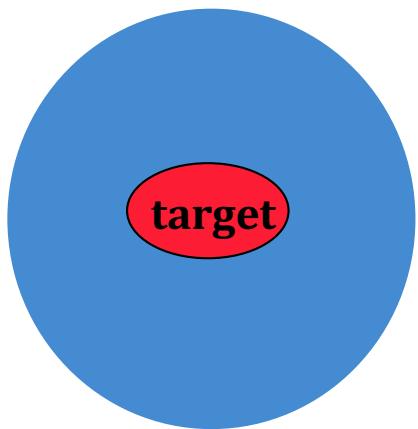
THE CARNEGIE TRUST
FOR THE UNIVERSITIES OF SCOTLAND



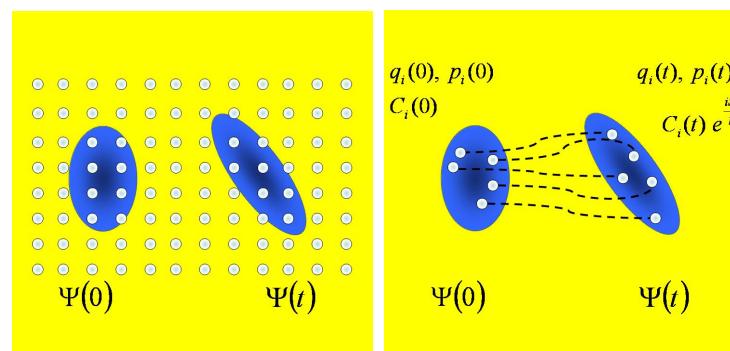
1. Adam Kirrander: Reaction dynamics

- Interpreting ultrafast X-ray (XFEL) and electron diffraction measurements to generate ‘molecular movies’

scattering theory



grid-based methods
 $N \lesssim 20$ atoms



semi-classical dynamics

$$\hbar \rightarrow 0$$

$$\Psi = \sum_k c_k g_k(\bar{\mathbf{q}}_t, \bar{\mathbf{p}}_t)$$

accuracy

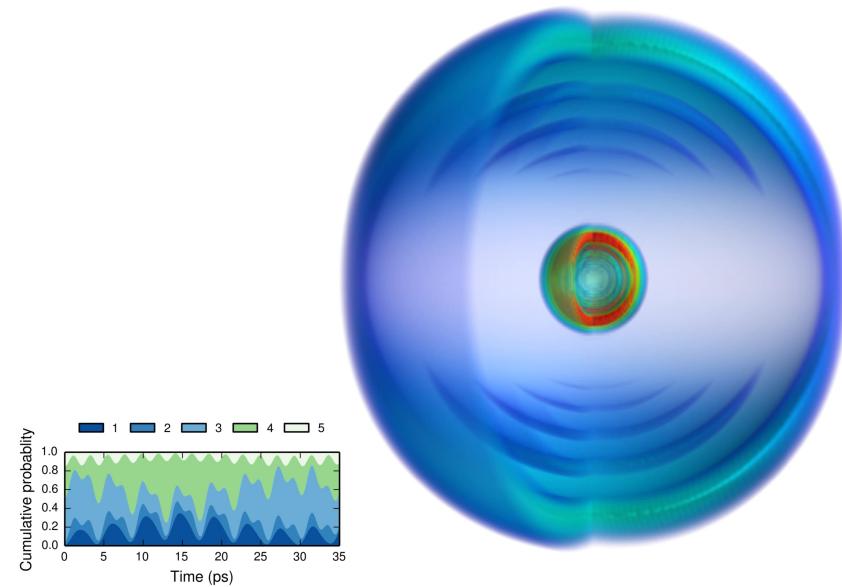


number of atoms

1. Adam Kirrander: Reaction dynamics

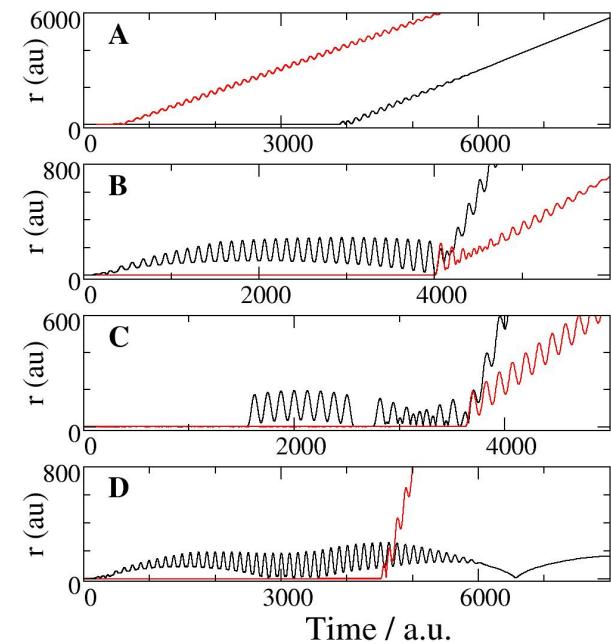
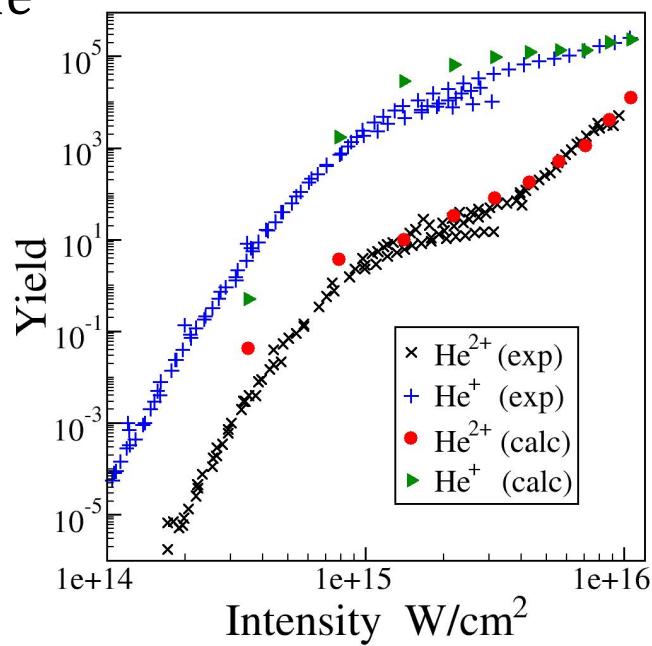
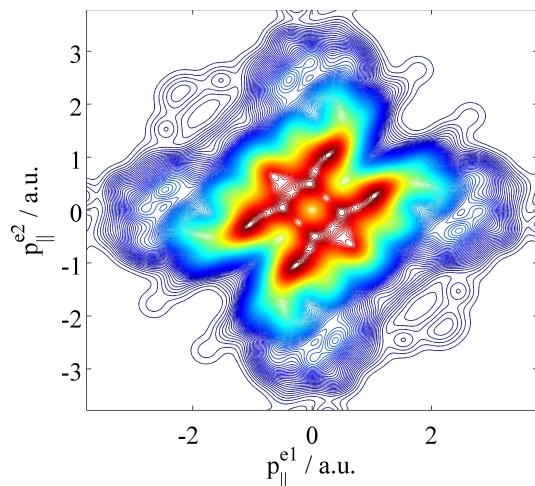
Electron dynamics in argon

Phys. Rev. Lett. **112**, 043002 (2014)



Double ionisation of He

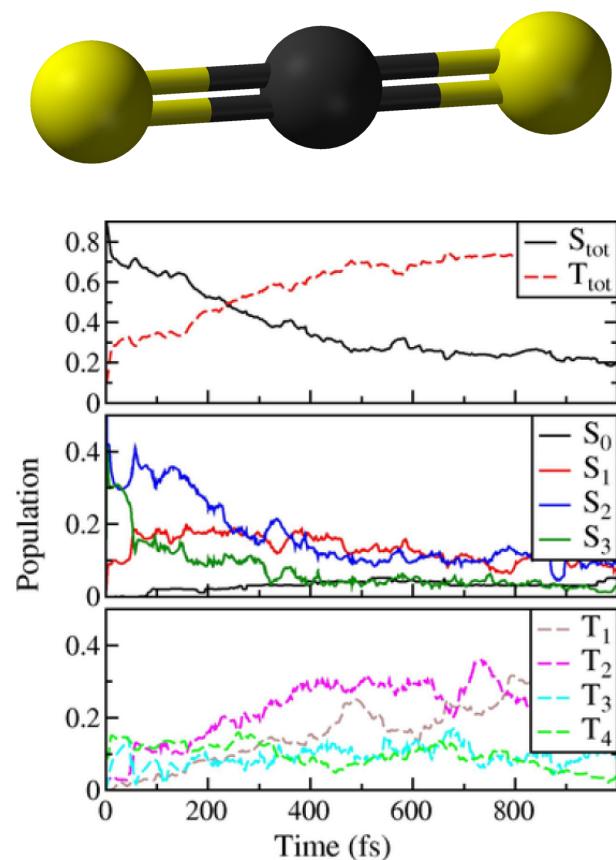
Phys. Rev. A **84**, 033406 (2011)



1. Adam Kirrander: Reaction dynamics

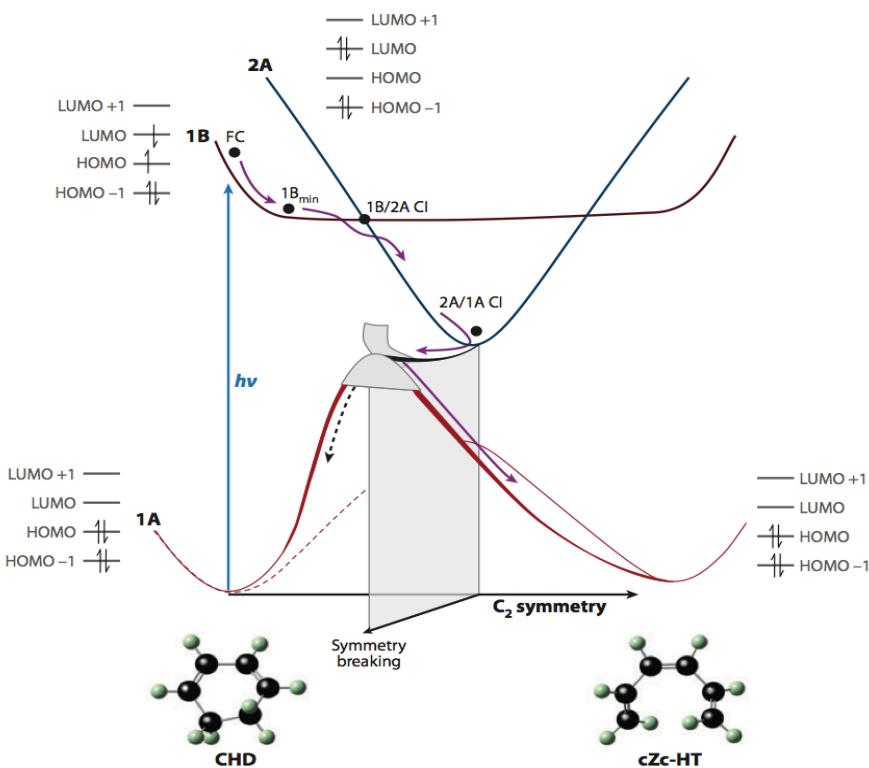
Efficient dissociation of CS_2
promoted by spin-orbit coupling
 $\text{CS}_2 + h\nu \rightarrow \text{CS}(\text{X}) + \text{S}({}^1\text{D}_1 \text{ or } {}^3\text{P})$

Chem. Phys. Lett. (in press)



1,3-cyclohexadiene ring-opening

Phys. Rev. Lett. **114**, 255501 (2015)

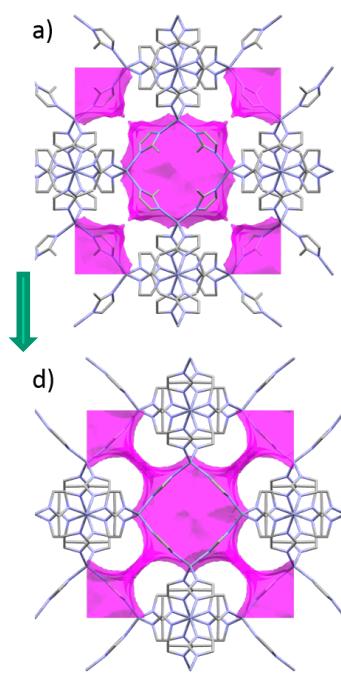
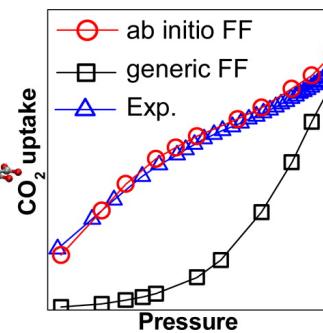
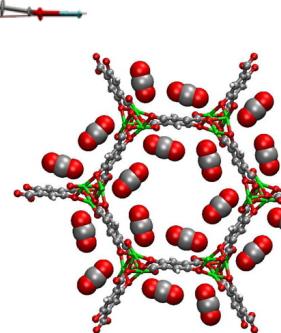
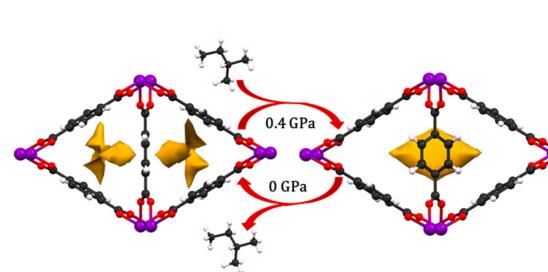
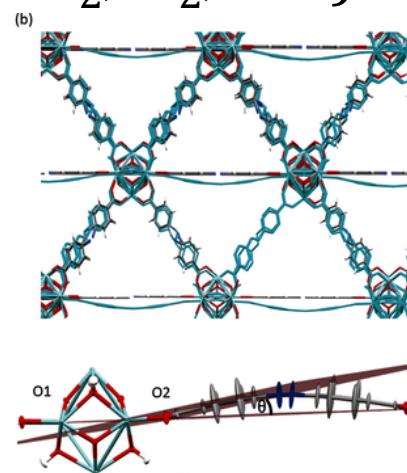
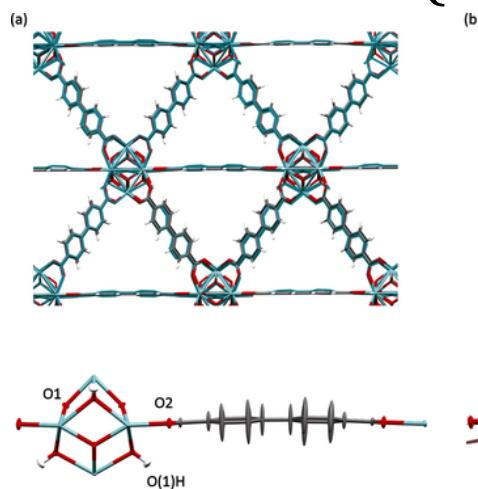


2. Carole Morrison: Solid-state structure and dynamics

- **Ab-initio and Car-Parrinello molecular dynamics**

Stephen Moggach, Tina Düren, Claire Hobday, and Jonathan Richardson

- Combining experiment and theory to understand solid-state structure, reaction dynamics, and adsorption of small molecules (CO_2 , H_2 , etc.)



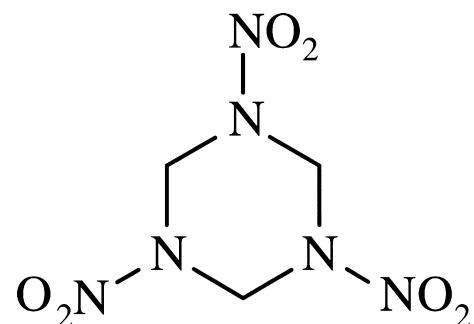
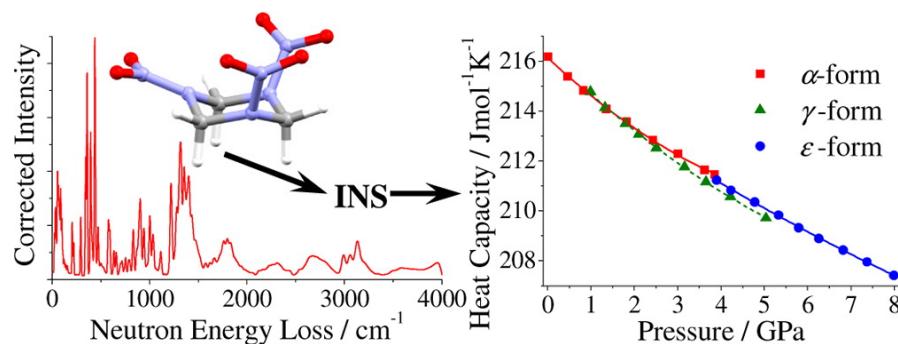
J. Am. Chem. Soc. **135**, 15763 (2013)
Angew. Chem. Int. Ed. **128**, 2447 (2016)
Chem. Mater. **28**, 466 (2016)
Nature Chem. (in press)

2. Carole Morrison: Solid-state structure and dynamics

- **Ab-initio and Car-Parrinello molecular dynamics**

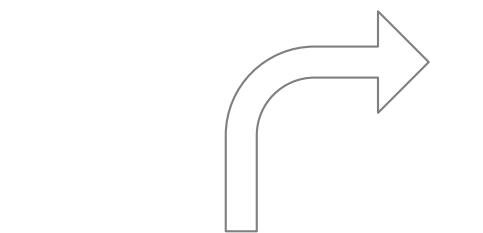
Colin Pulham and Adam Michalchuk

- Predicting impact sensitivities of energetic materials from first-principles phonon calculations

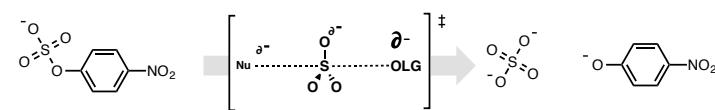
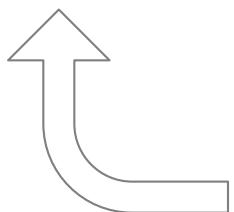
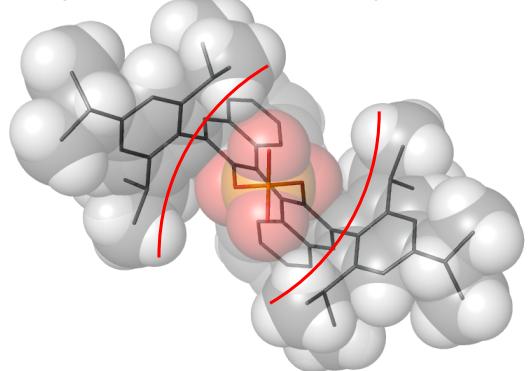


3. Fernanda Duarte: Catalysis

- Quantum mechanics/molecular mechanics

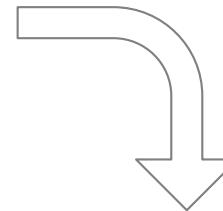


New Models for
Asymmetric Catalysis

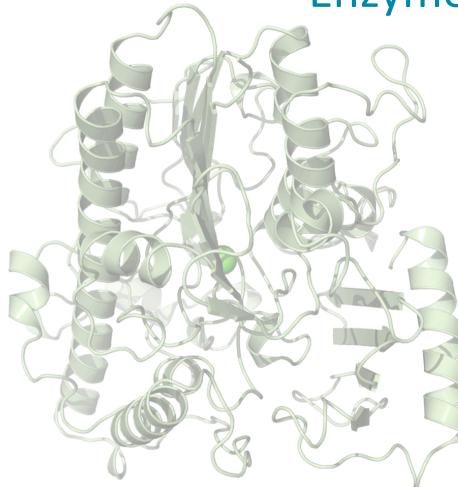


Reaction Mechanism

BBA - General Subjects **1850**, 954 (2015)



Enzyme Catalysis



QM/MM
DFT
EVB

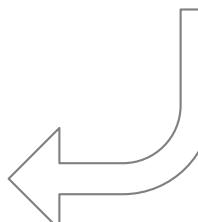
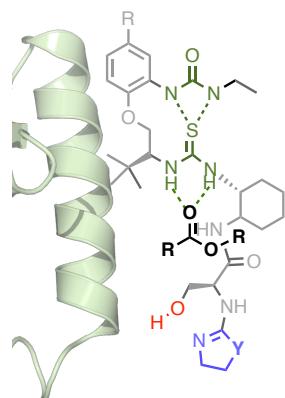
```
infile = open(title,"r")
inlines = infile.readlines()
getATOMS(self,inlines)

class getdata:
    def __init__(self,F,file):
        if not os.path.exists(file):
            print ("\\nFATAL ERROR: Input file [%s] does not exist" % file)
        self.REASONABLE = True
        self.ATOMS = []
        self.REASONABLE = True
        for i in range(0,len(inlines)):
            if not is_number(inlines[i].split("#")[0]):
                print "FATAL ERROR: input [%s] is not a number" % inlines[i]
                sys.exit(1)
            atomid = int(inlines[i].split("#")[0])
            self.ATOMS.append(atomid)

    def getATOMS(self,inlines):
        self.REASONABLE = True
        for i in range(0,len(inlines)):
            if not is_number(inlines[i].split("#")[0]):
                print "FATAL ERROR: input [%s] is not a number" % inlines[i]
                sys.exit(1)
            atomid = int(inlines[i].split("#")[0])
            self.ATOMS.append(atomid)

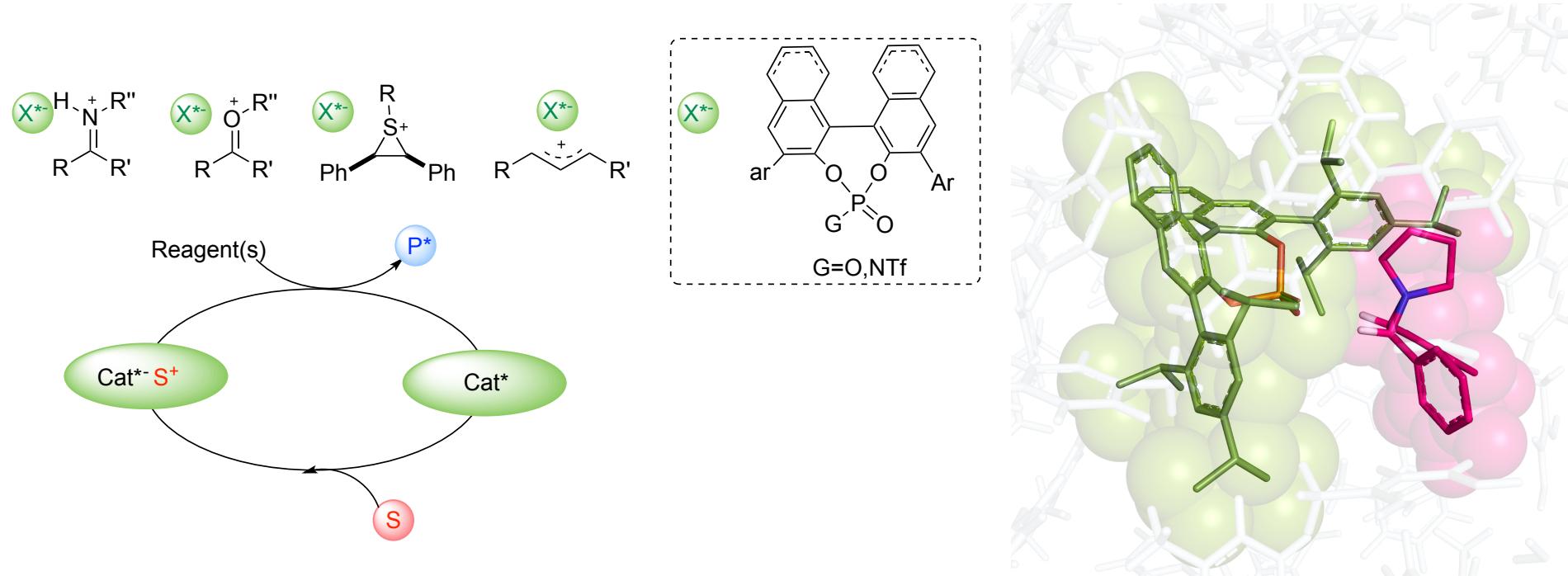
infile = open(file,"r")
inlines = infile.readlines()
getATOMS(self,inlines)
```

Biomimetic Catalysis



3. Fernanda Duarte: Asymmetric catalysis

- From mechanistic understanding to prediction

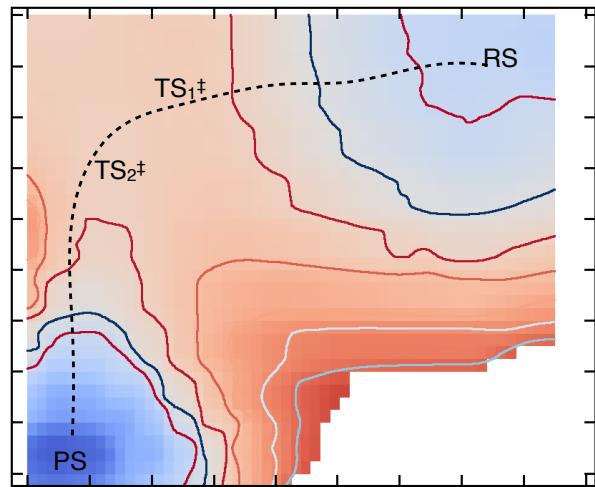


- Most new drugs are marketed as single enantiomers
- Catalyst discovery remains a trial-and-error process

3. Fernanda Duarte: Biomimetic catalysis

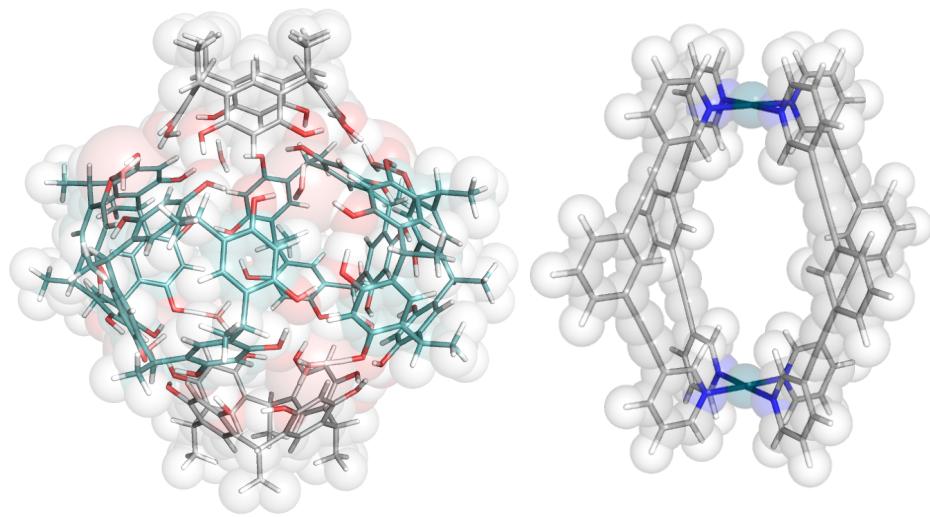
Angew. Chem. Int. Ed. **53**, 8246 (2014)
Angew. Chem. Int. Ed. ASAP (2017)

Reaction Mechanism



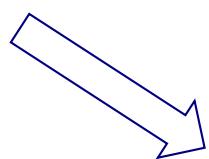
Understanding the
fundamental chemistry

Supramolecular Chemistry



Exploring Physical / Dynamic
properties

Mechanistic Insights

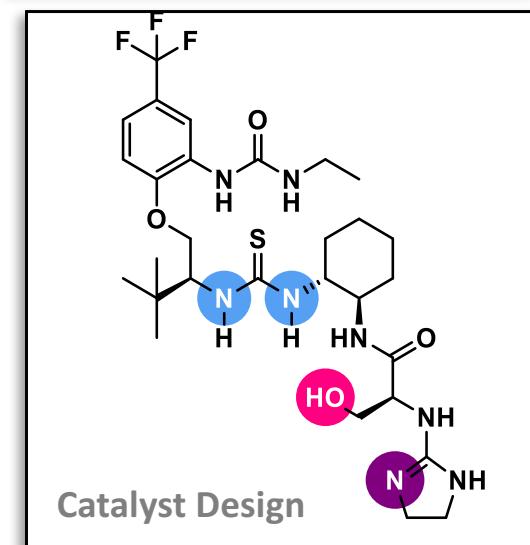
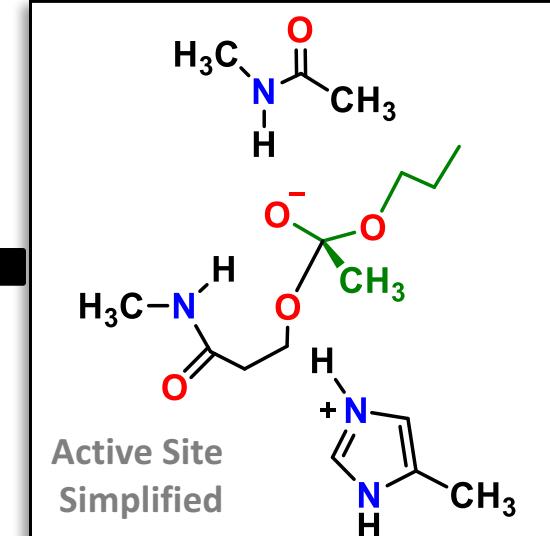
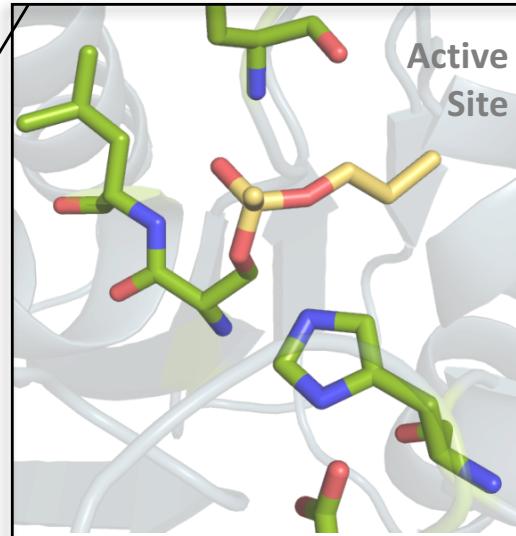
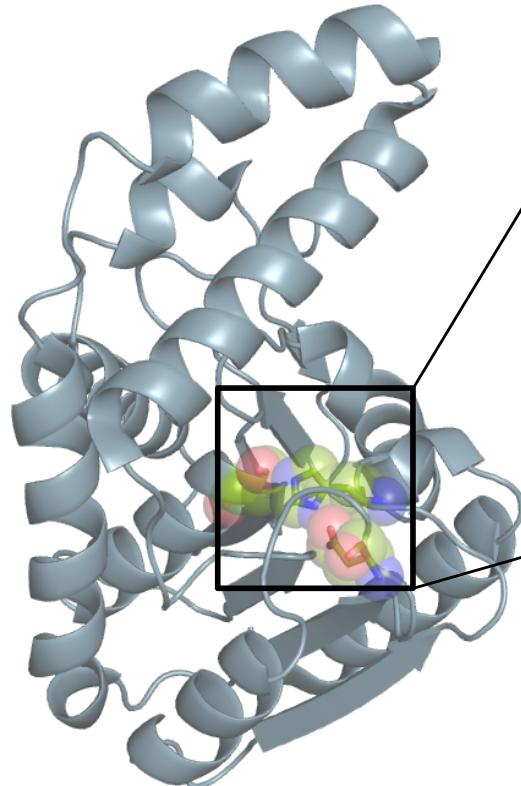


New Scaffolds

Self-Assembled “Nanzyme”

3. Fernanda Duarte: Biomimetic/enzyme catalysis

- Using natural scaffolds to introduce catalysis – learning from Nature



Code snippet illustrating the process of reading input files and extracting atom IDs:

```
infile = open(file, "r")
inlines = infile.readlines()
getATOMS(self, inlines)

class getdataData: #Read atoms number from a data
    def __init__(self, file):
        if not os.path.exists(file):
            print ("\nFATAL ERROR: Input file [%s] does not exist" % file)

    def getATOMS(self, inlines):
        self.REFATOMID = []
        for i in range(0,len(inlines)):
            if not is_number(inlines[i].split("#")):
                print ("FATAL ERROR: input '%s' is not a number" % inlines[i])
                sys.exit(1)
            else:
                self.REFATOMID.append(int(inlines[i].split("#")[0]))
```

Properties

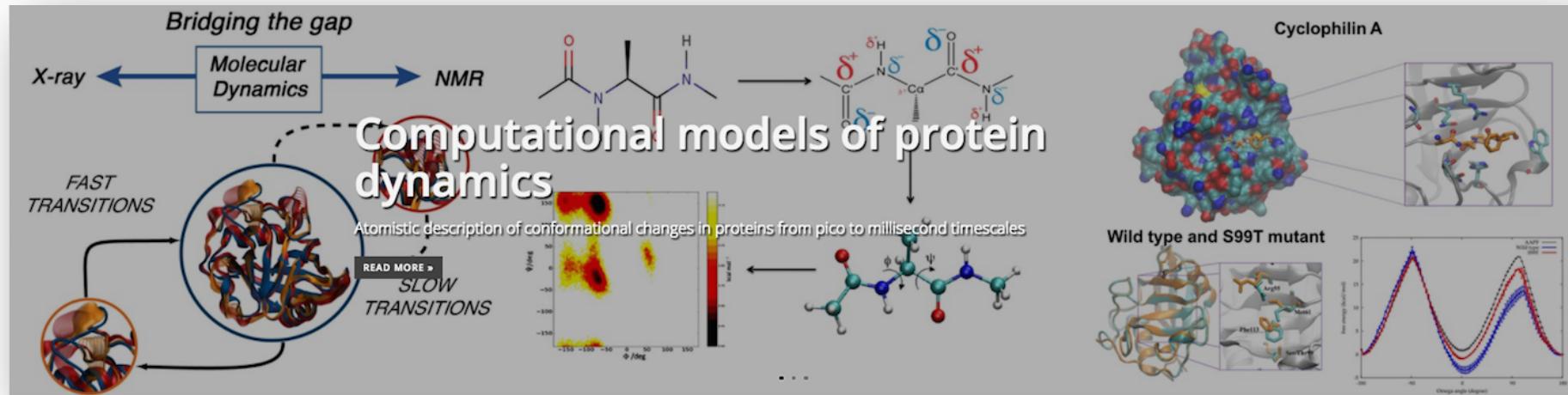
```
infile = open(file,"r")
inlines = infile.readlines()
getATOMS(self, inlines)
```

4. Julien Michel: Biomolecular systems

- Classical atomistic molecular dynamics



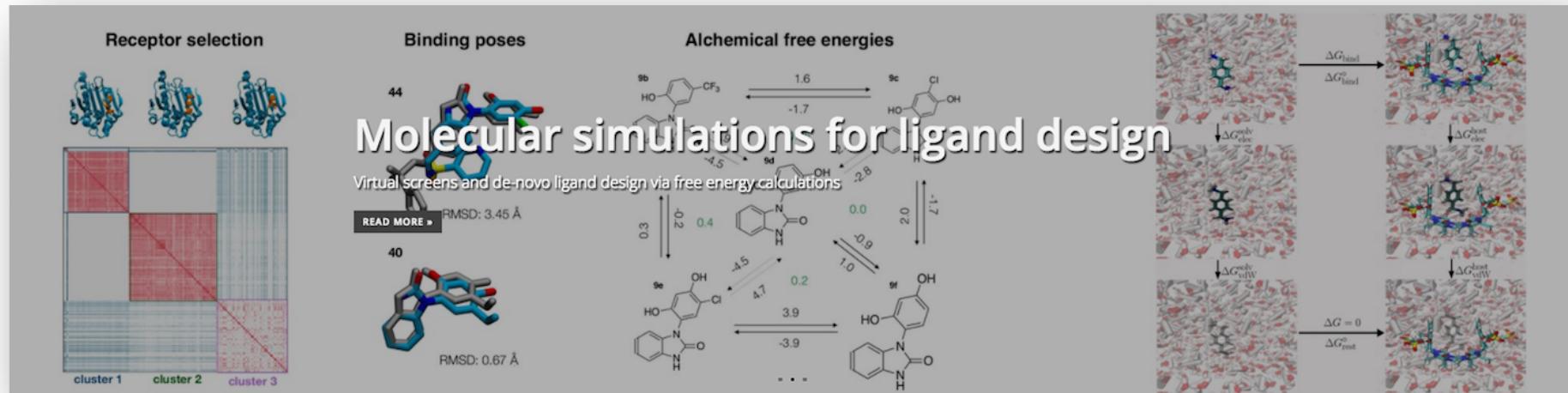
4. Julien Michel: Biomolecular systems



Atomic level description of protein structure and dynamics (picosecond to millisecond) via classical molecular dynamics simulation methods and back-calculation of experimental observables (e.g. NMR spectra)

PLoS Comput. Biol. **11**, e1004282 (2015)

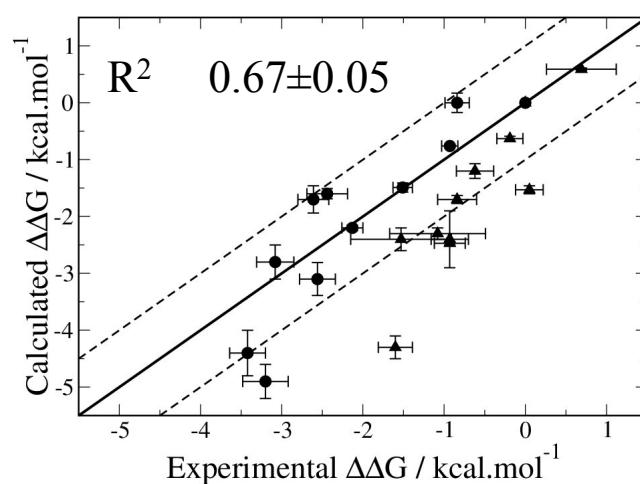
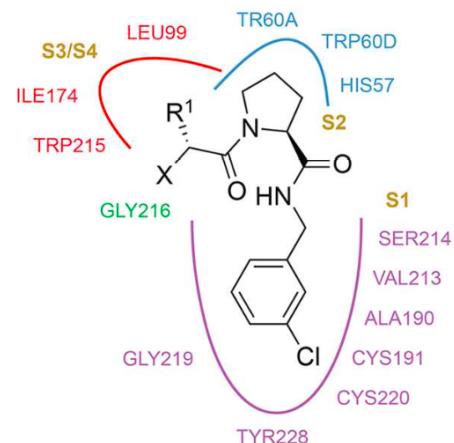
4. Julien Michel: Biomolecular systems



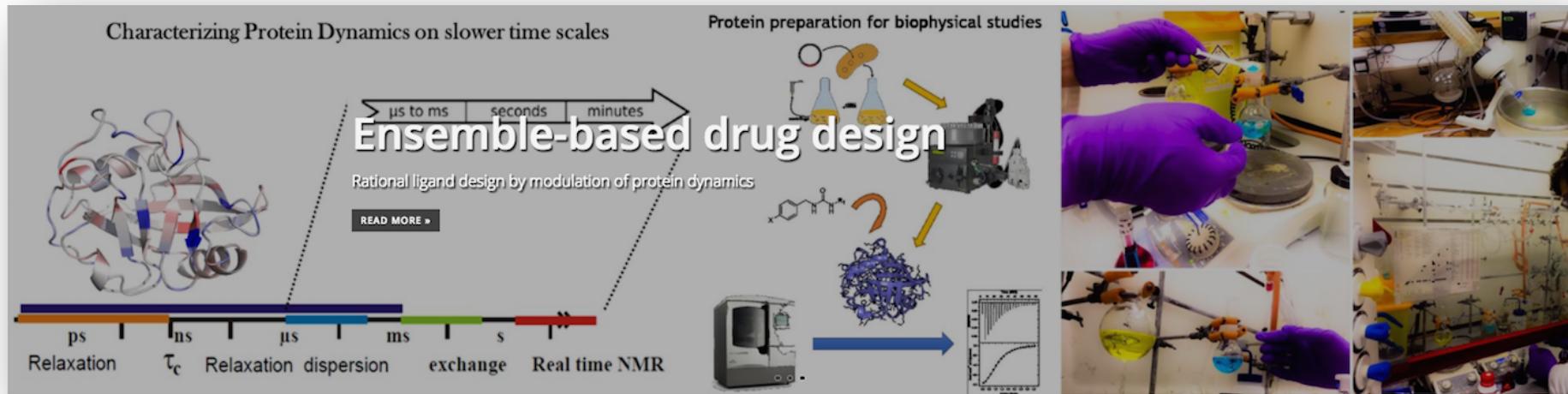
- Molecular simulation algorithms for next-generation computer-aided drug design technologies

Prediction of binding energies for thrombin ligands by molecular dynamics alchemical free energy calculations

J. Phys. Chem. B **120**, 5340 (2016)

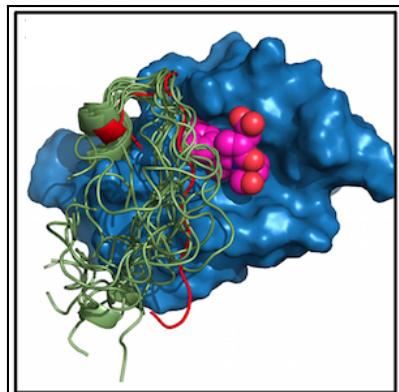


4. Julien Michel: Biomolecular systems

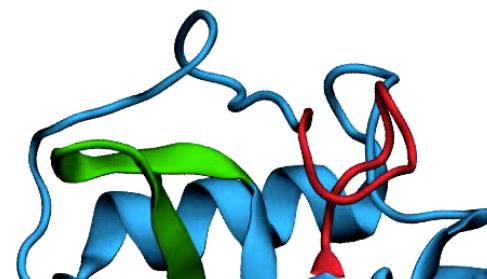


- Combination of molecular modelling, organic synthesis, and biophysical assays methods to deliver improved ligands for challenging drug targets via modulation of protein dynamics

MDM2 lid dynamics (cancer)



Cyclophilins loops dynamics (viral infections, neurodegenerative diseases)

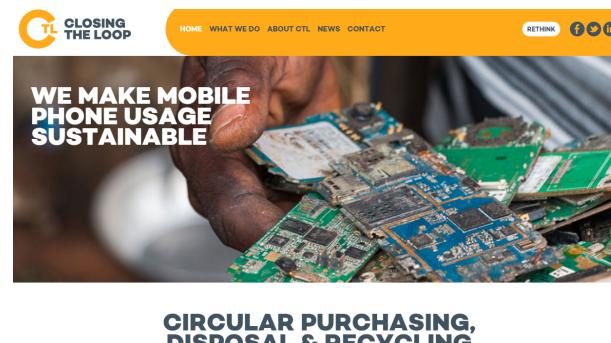
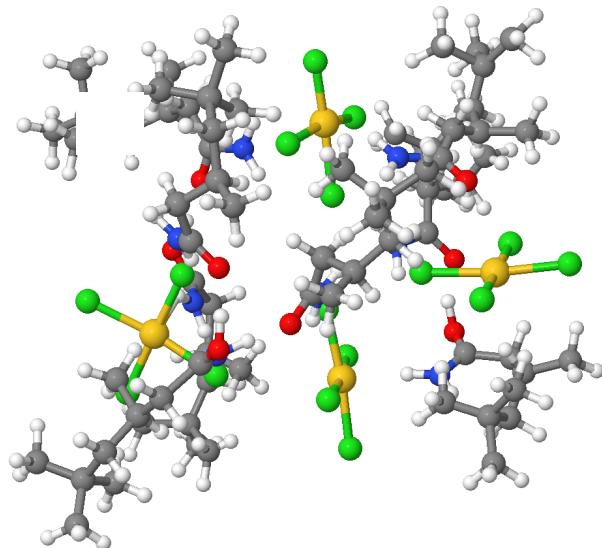


4. Carole Morrison: Molecular liquids

- **Ab-initio and classical molecular dynamics**

Jason Love, Mary Healy, Peter Tasker, Innis Carson, Rebecca Nicolson, Euan Doidge, and Jamie Hunter

- Urban mining – recovering wealth from waste electronics
- Designing and understanding sustainable processes to recover, e.g., gold (selectively!) from printed circuit boards



Angew. Chem. Int. Ed. **55** 12436 (2016)
Infinite Magazine (UoE/ERI) Issue 14, October 2015

4. Philip Camp: Molecular liquids

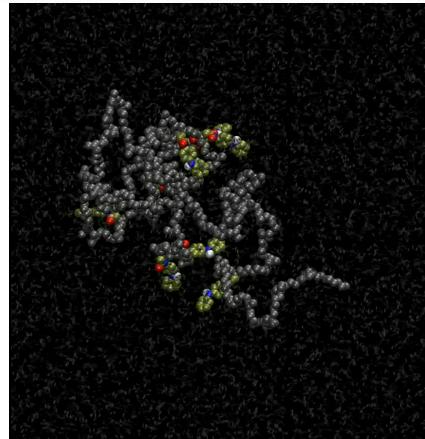
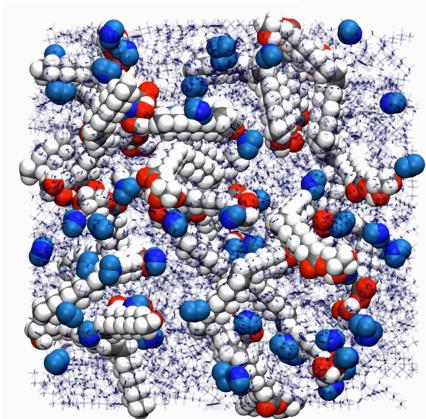
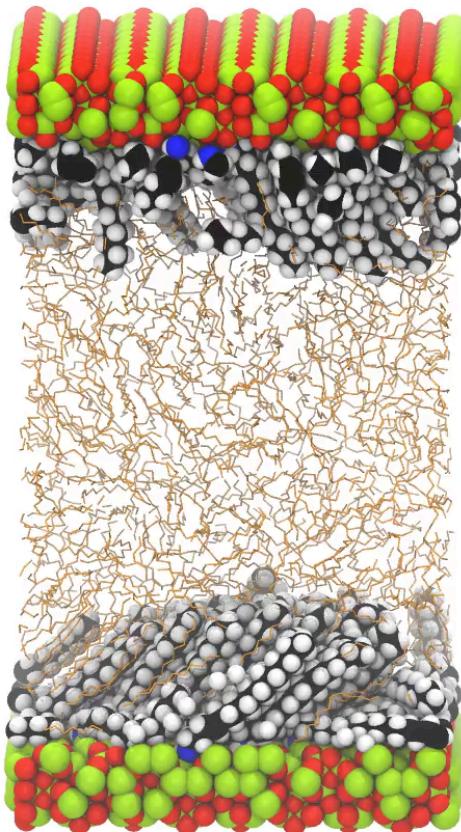
- Classical molecular dynamics



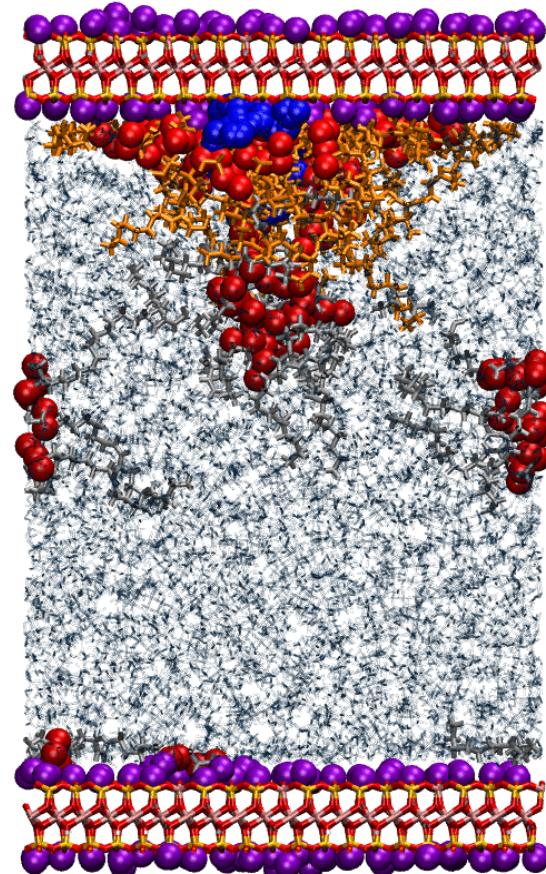
4. Philip Camp: Molecular liquids

- Self-assembly, adsorption, and friction in lubricants

Rui Apóstolo and Georgia Tsagkaropoulou



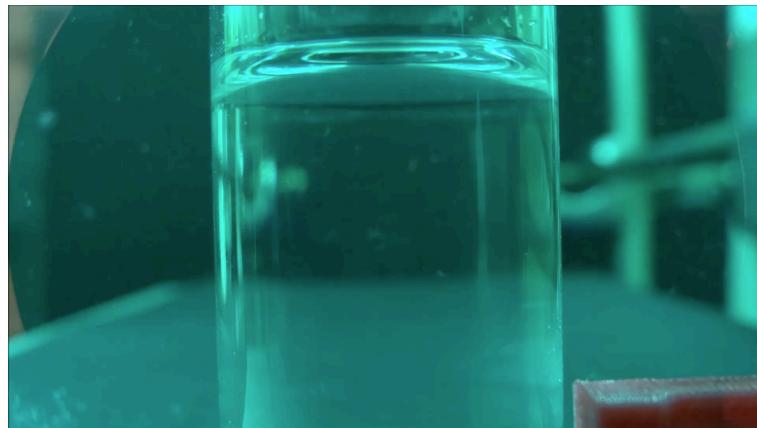
Langmuir **30**, 186 (2014)
J. Phys. Chem. B **55** 12436 (2015)
Phys. Chem. Chem. Phys. **17**, 5248 (2015)
Langmuir **32**, 7707 (2016)



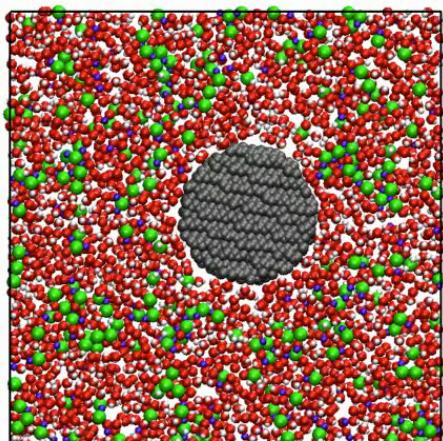
4. Philip Camp: Molecular liquids

- Non-photochemical laser-induced nucleation
Andrew Alexander and Julien Sindt

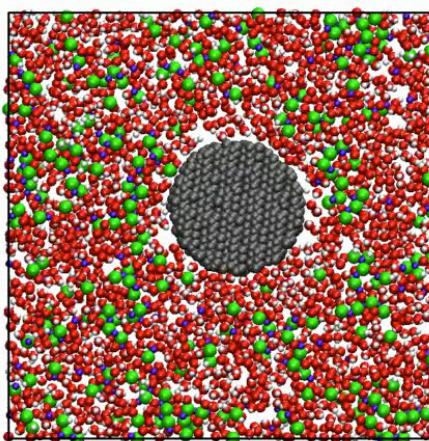
J. Phys. Chem. B **118**, 9404 (2014)



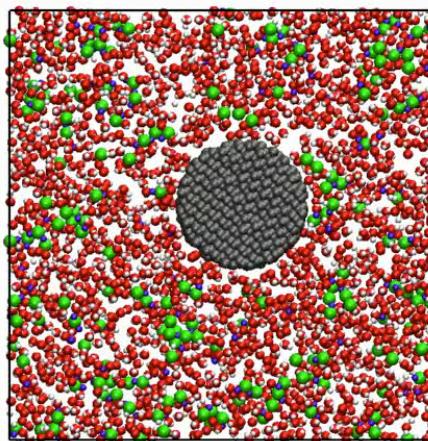
- Nanoparticle heating in aqueous salt solutions



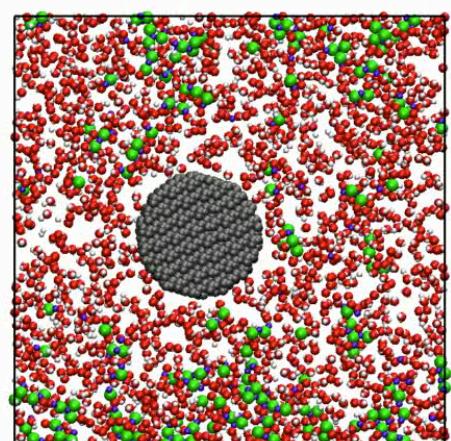
equilibrium



$t = 0.0\text{--}0.1 \text{ ns}$



$t = 0.9\text{--}1.0 \text{ ns}$



$t = 2.3\text{--}2.4 \text{ ns}$

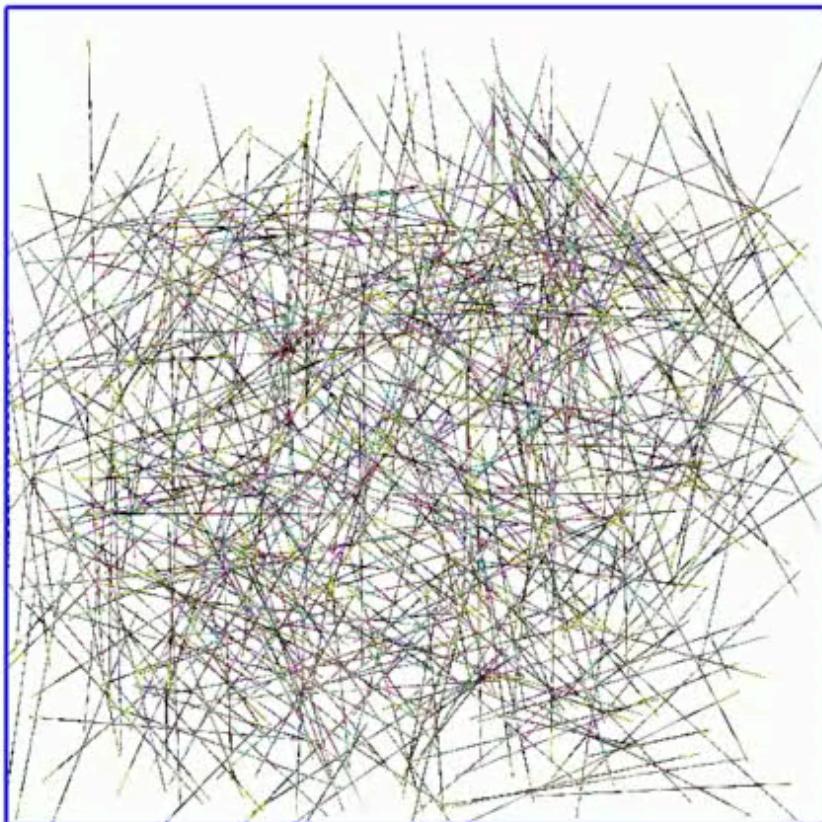
5. Philip Camp: Soft matter

- **Coarse-grained dynamics**

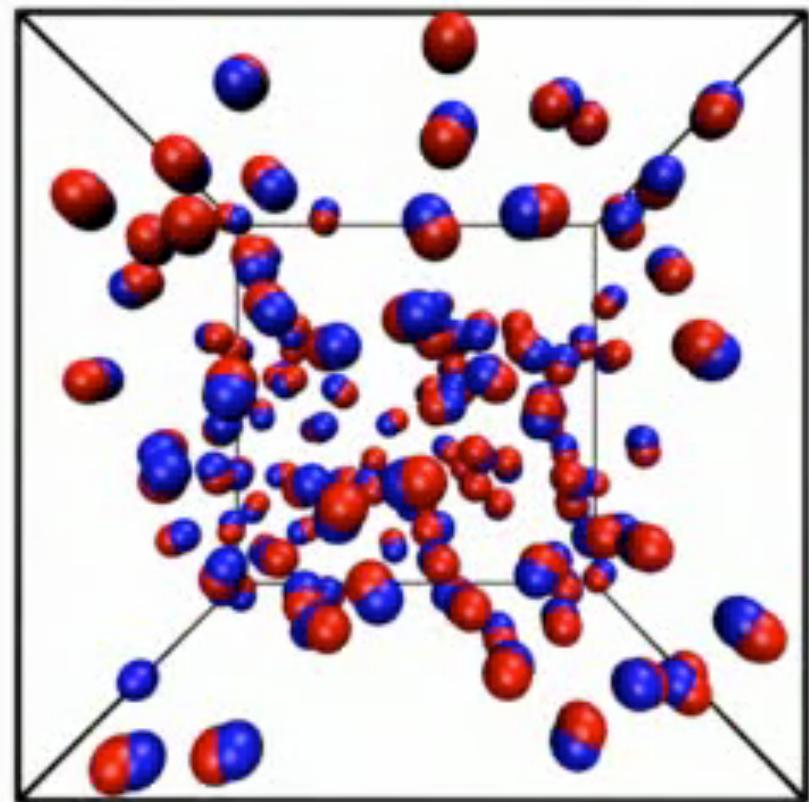
Fabio Nudelman and Julien Sindt

Collagen fibril formation

Aggregation kinetics



Magnetic colloids
AC field-induced hyperthermia



Phys. Rev. E **93**, 063117 (2016)

MD Simulations in the School of Chemistry

1. Few-atom quantum molecular dynamics

Adam Kirrander

2. Ab-initio and Car-Parrinello molecular dynamics

Carole Morrison

3. Quantum mechanics/molecular mechanics

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