

*Biosimulation for drug discovery
across multiple length-scales –
from enzymes to organs*

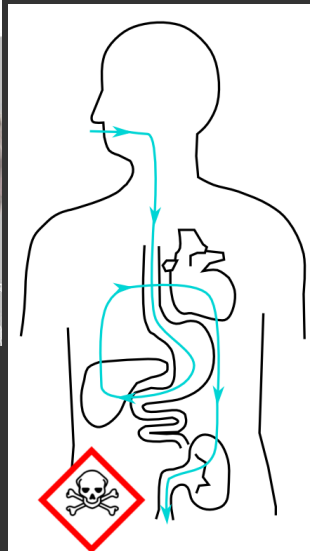
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Visit your “in silico GP”

Rebecca Wade, HITS,
Heidelberg

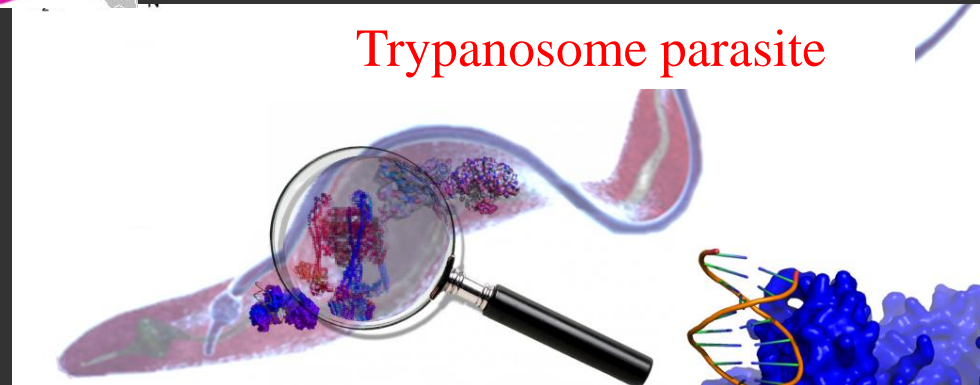


Medication against neglected parasitic tropical diseases.

Simulate the drug from intake to action at target to elimination

Consider host (human) and parasite from the atomistic level upwards

Trypanosome parasite



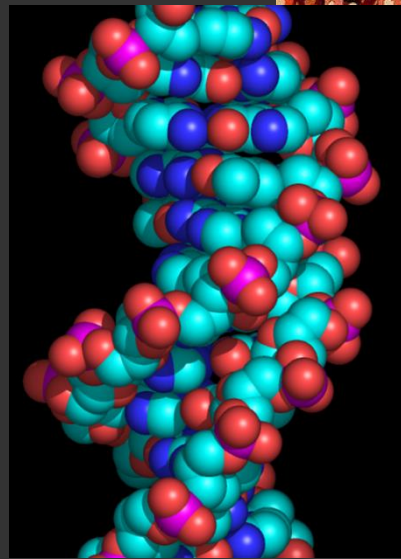
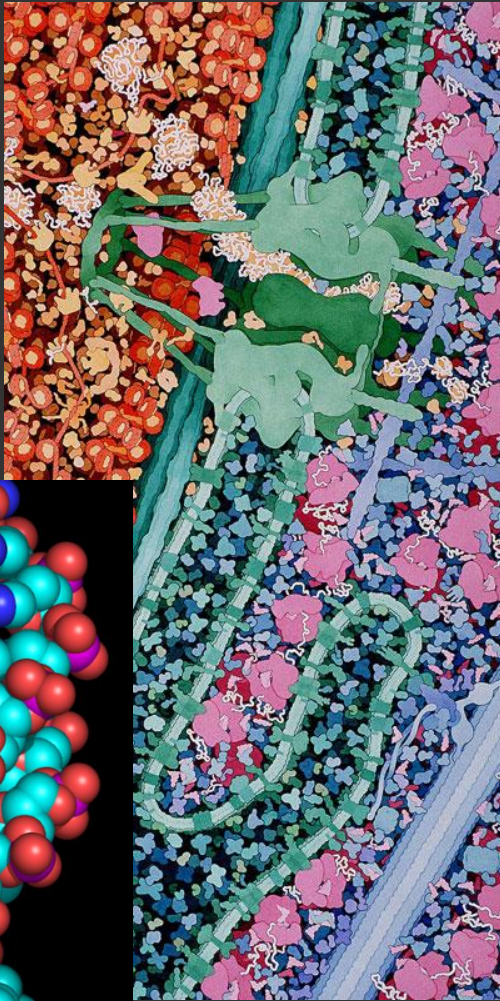
Molecular Biology

Human cell: $>10\mu\text{m}$

Human genome: 3 billion
(3000 Mb/ 3×10^9) base pairs
3m long

Ribosome (makes proteins
from RNA): 30nm

Hormone molecule/ Antibiotics/
Other drugs: 1-5nm



$2\text{nm} = 2\times 10^{-9}\text{ m} =$
 0.0000002 cm



Time and length-scales in Cell Divison

Quantum

100 atoms,
1nm, 100fs

Atomic

10,000 atoms
10nm, 100 μ s

Molecular

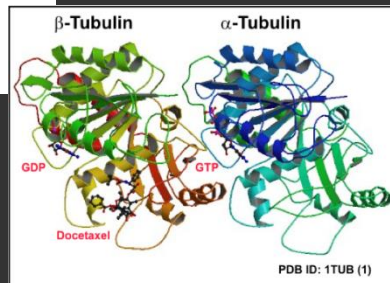
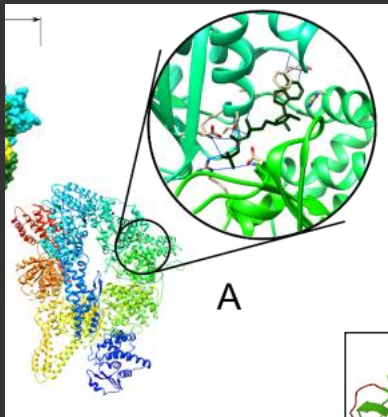
100nm, ms

Cellular

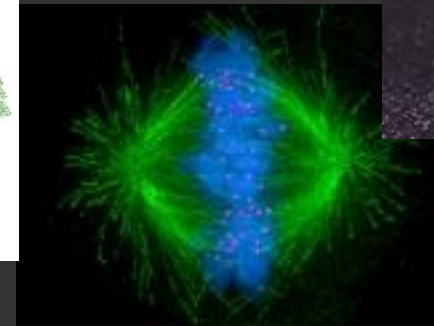
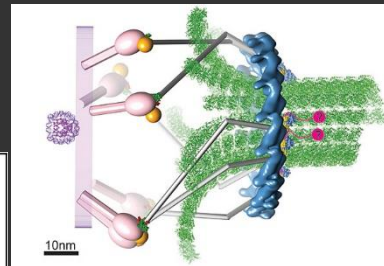
10^{14} atoms,
1 μ m, 30 mins

Macroscopic

1m
100 years



Unseen



Microtubules green, chromosomes (DNA) in blue (Eva nogales)



Burning
fuel (ATP
hydrolysis)

Molecular
recognition

Molecular
self-
assembly

Cell
division

Tissue/organ
growth

Multiscale Modelling of CYP450 drug metabolism

- **Coarse-grained MD**

Build model of protein in the membrane

Study orientation of protein in membrane

- **Atomistic MD**

Relaxation

Explore conformations of protein and binding modes of drugs

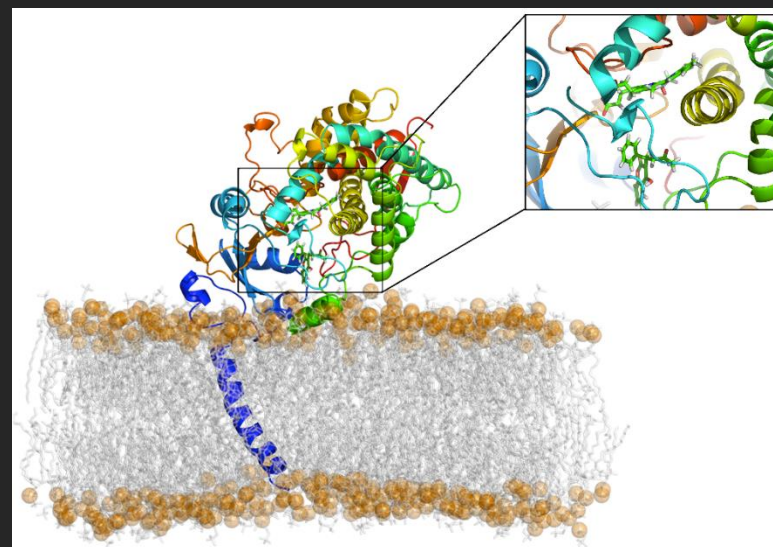
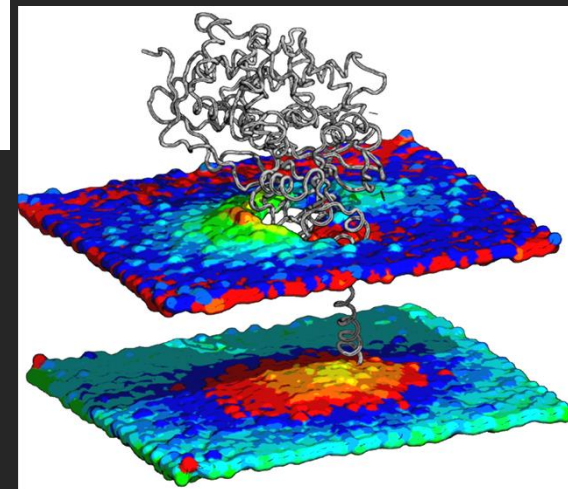
- **QM/MM**

Model reactions of drugs in P450s

(e.g. Lonsdale *et al.* *JACS* 2013; PLoS *Comp. Biol.* 2014)

Amaro and Mulholland, *Nature Reviews Chemistry* 2018

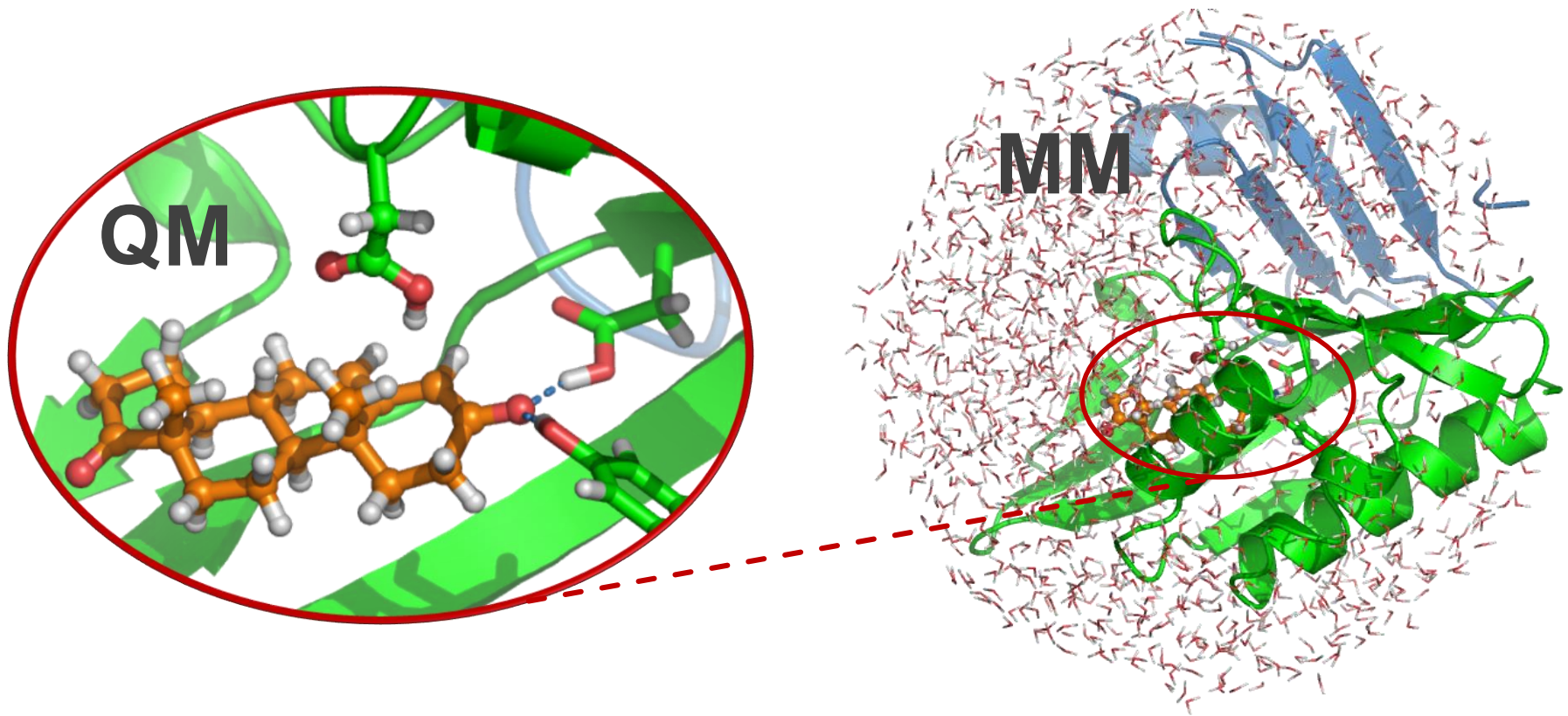
CCPBioSim



Scripts will be available on ccpbiosim.ac.uk

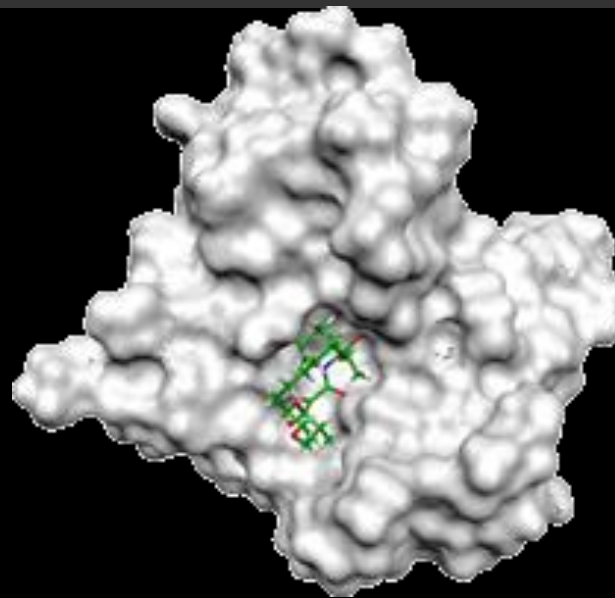
QM/MM Enzyme Reaction Modelling

Use QM only for region where bonding changes, and molecular mechanics (MM) for the surroundings



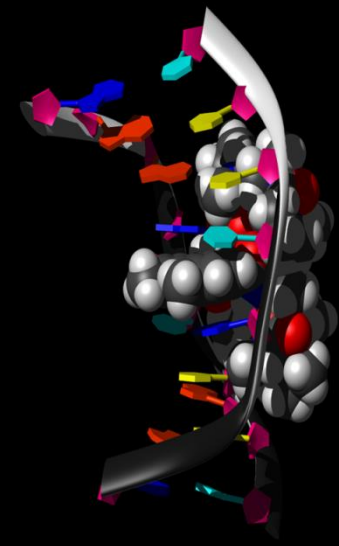
Molecular Recognition and Drug Design

Molecular recognition uses shape and chemical complementarity to convey metabolic information



Amprenavir/HIV protease

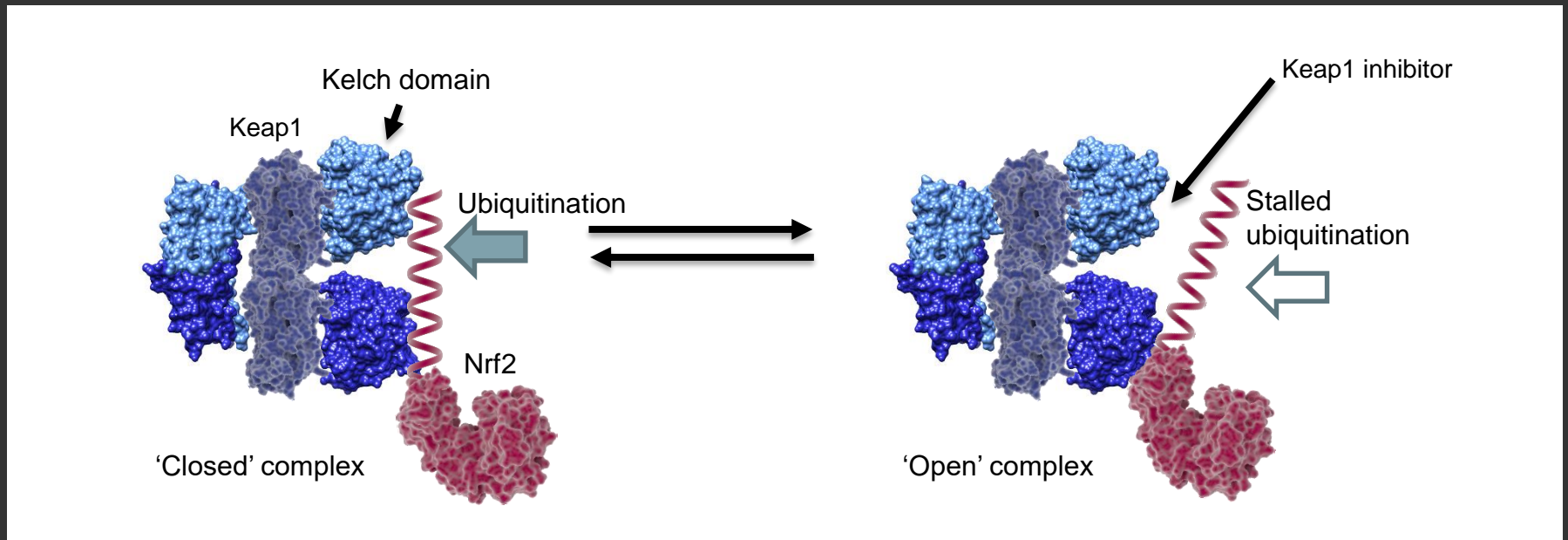
Actinomycin D/ DNA



But biomolecules (and the solvent) are always moving....

Inhibition of the Keap1-Nrf2 Interaction

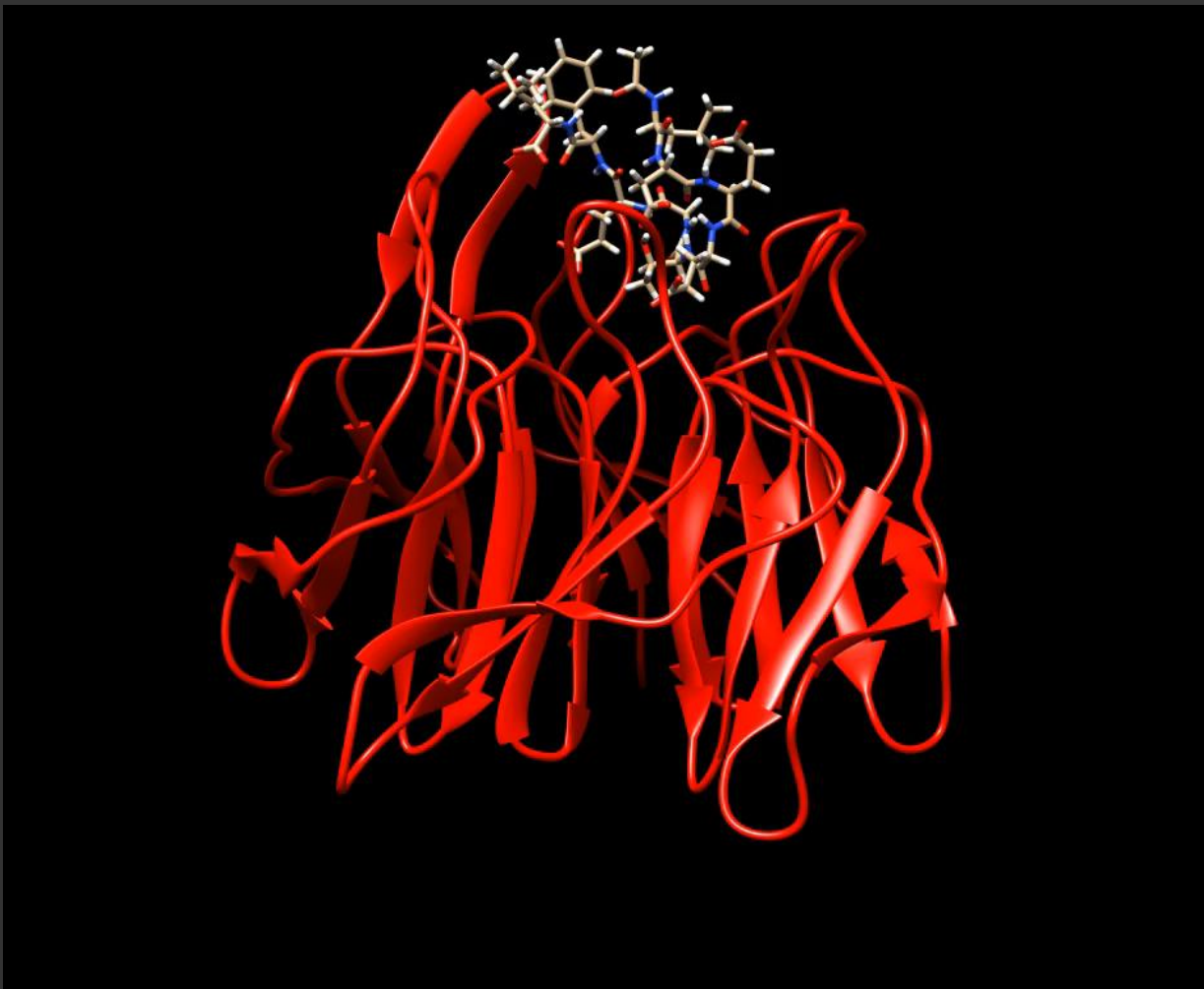
Nrf2 (red) is a transcription factor that increases the expression of a range of antioxidant, cytoprotective and anti-inflammatory genes



Concentrations are kept low by ubiquitination (facilitated by Keap1 (blue)), but this can be blocked with small molecules.

Therapeutic applications are in neurodegenerative conditions (*e.g.* Parkinson's & Alzheimer's diseases) and inflammatory conditions.

The bound form of Nrf2 Peptides



Limitations of MD for Molecular Recognition

Accuracy of empirical MD forcefields (MM improving – or use QM!!)

Dynamics and entropy (finite simulation timescales, ensemble averages)

Understanding the experimental data (e.g. environmental conditions, pH, salt etc)

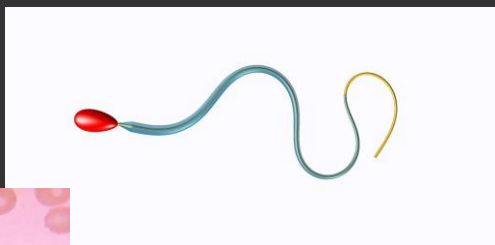


<https://uk.pcmag.com/networking-communications-software/16824/what-is-cloud-computing>

The Axoneme ~ A Macromolecular Machine

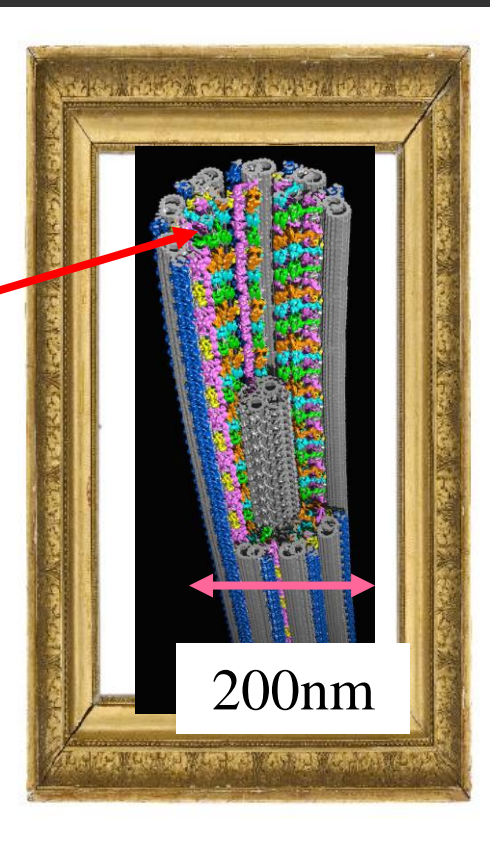
Hermes Gadelha, York

Sperm



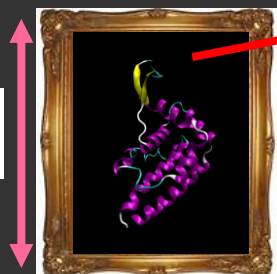
16 dyneins in 96nm repeat
9 MT doublets
 $50-100 \times 96\text{nm} = 5-10\mu\text{m}$
 6×10^8 atoms (non solvent)

Axoneme



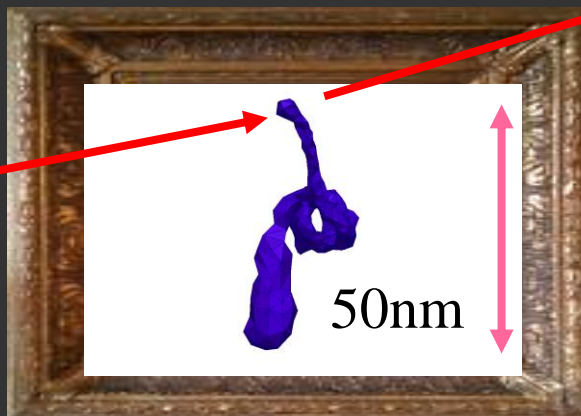
Cryo-ET Nicastro lab

Trypanosomes



10nm

Dynein MTBD



50nm

Dynein Motor

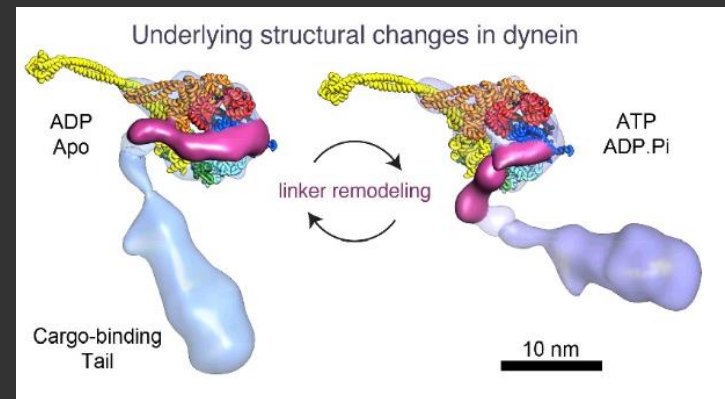
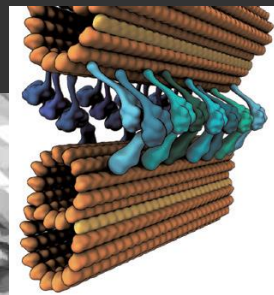
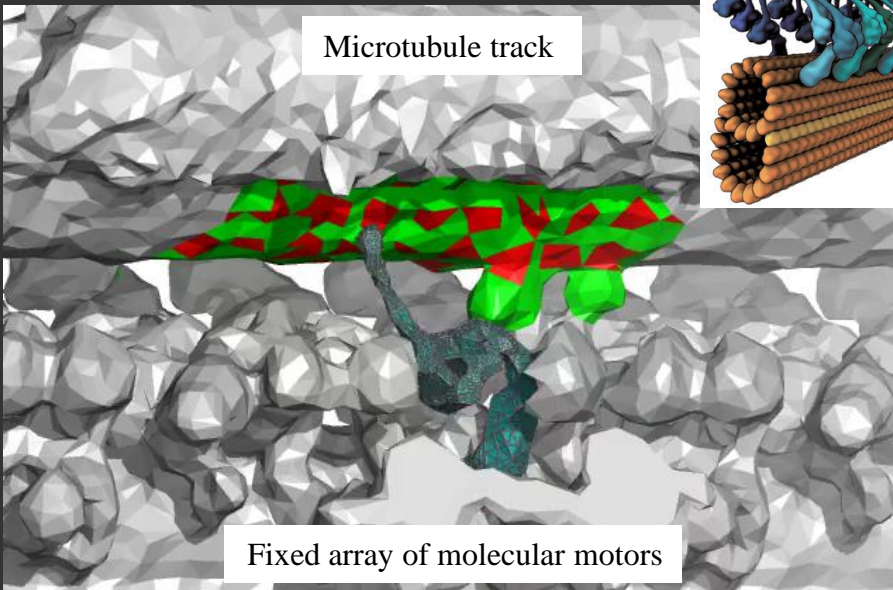
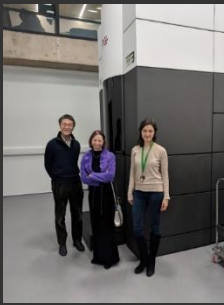
~1 million atoms in water (no tail)

How do we identify the best protein-protein interactions to target to inhibit the action of the axoneme?

FFEA of Flagellar Dynein in Situ

Dock 3D cryoEM of dynein into 3D tomogram of the axoneme

~1 μ s FFEA shows dynamics *in situ*.



Red

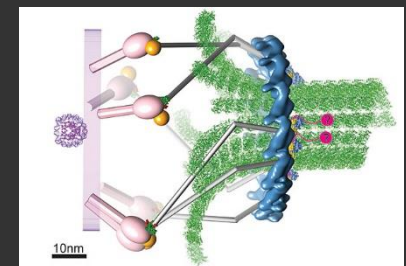
Cyan

Cryo-tomography:
Bui et al, J Cell Biol
198, 913, 2012

CryoEM:
Burgess *et al Nature*
(2003) 421, 715; Roberts
et al, Structure (2012), 20
1670

FFEA of dynein mechano-chemical cycle

<http://ffea.bitbucket.io/>
Solernou et al, PLoS Comp. Bio 2018

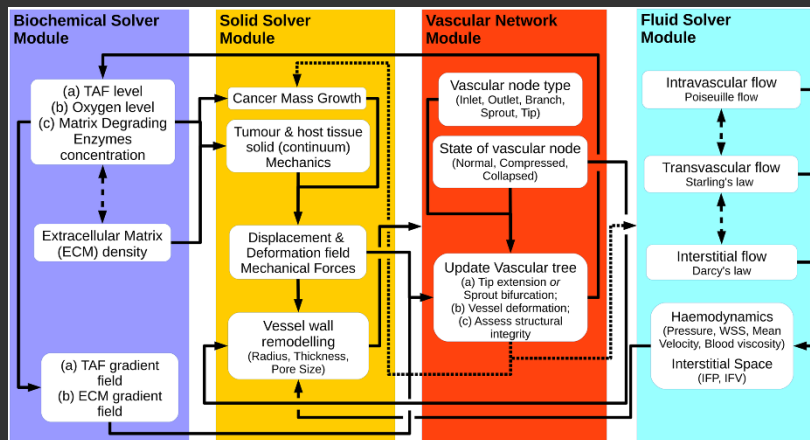
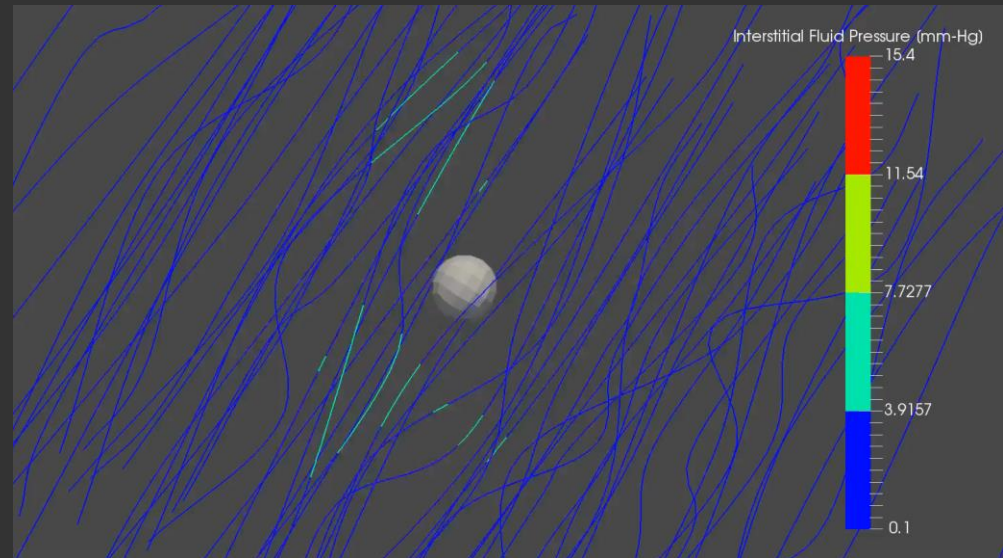


Tumour Angiogenesis

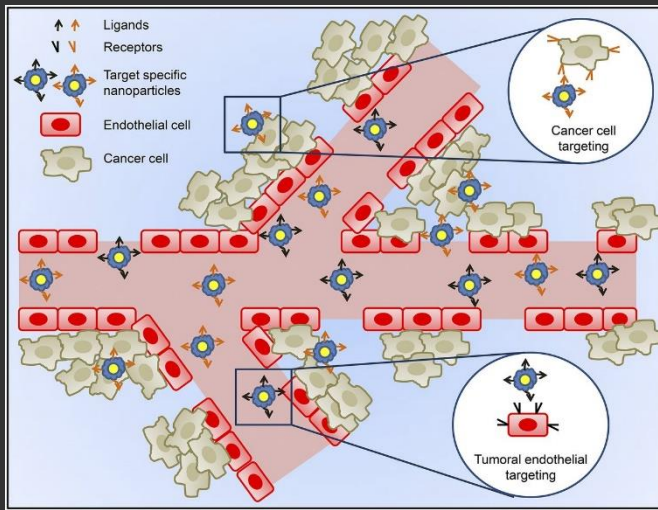


Vavourakis et al Plos Comp Bio 2017

Finite Element models of solid tumours show the pattern of blood flow, and the difficulty of delivering chemotherapies *in situ*

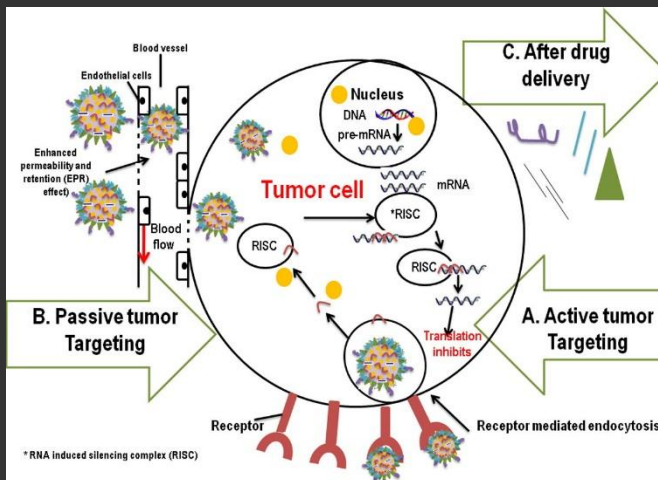


Why do we need Multi-scale?



Many orders of magnitude difference in size between target/drug and patient

Active biological processes (e.g. endocytosis) still poorly understood



Coupling between different time and length-scales

Save The Date

4th CCPBioSim/CCP5 Manchester Multiscale Conference

Dates: 30 March – 1 April 2020

Venue: Manchester Conference Centre

Invited Speakers:

- Maria Fyta (Stuttgart, Germany)
- Frauke Gräter (Heidelberg, Germany)
- Syma Khalid (Southampton, UK)
- Horst Lillig (Greifswald, Germany)
- Céline Merlet (Toulouse, France)
- Irina Paci (Victoria, Canada)
- Lars Pastewka (Freiburg, Germany)
- Anđela Šarić (UCL, UK)

Registration will be announced on the CCPBioSim website, our mailing list and our twitter account (@ccpbiosim).

www.ccpbiosim.ac.uk/multiscale2020

