

# DNA damage from first principles

**Jorge Kohanoff**

Atomistic Simulation Centre  
School of Maths and Physics  
Queen's University Belfast  
Northern Ireland  
UK

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# Queen's University Belfast Northern Ireland



# The Atomistic Simulation Centre

## Queen's University Belfast, Northern Ireland



Tchavdar Todorov



Daniel Dundas



Myrta Grüning



Gareth Tribello



Lorenzo Stella



Jorge Kohanoff

# Contents

- Introduction
- Low-energy electrons
  - Electronic capture
  - C-O bond cleavage in nucleotides
  - Strand breaks in polynucleotides
  - Electronic capture in aminoacid-DNA
- Conclusions
- (Shock waves)



# Radiation damage of biological systems

- Radiation causes lesions to any biomolecule, especially **DNA**

- **Directly**

- Ionization (X-rays, UV)
- Impact fragmentation

- **Indirectly** by generating reactive species

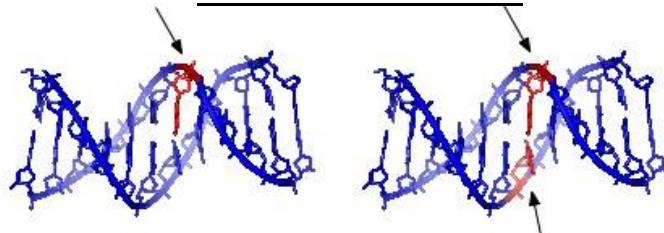
- Low-energy electrons by ionization
- free radicals: e.g.  $\text{OH}^\bullet$  from water

- **Thermo-mechanically**

## Types of DNA Damage

- Base Damage
- Single Strand Breaks
- Double Strand Breaks
- Clustered Damage

### Strand Breaks



SSB

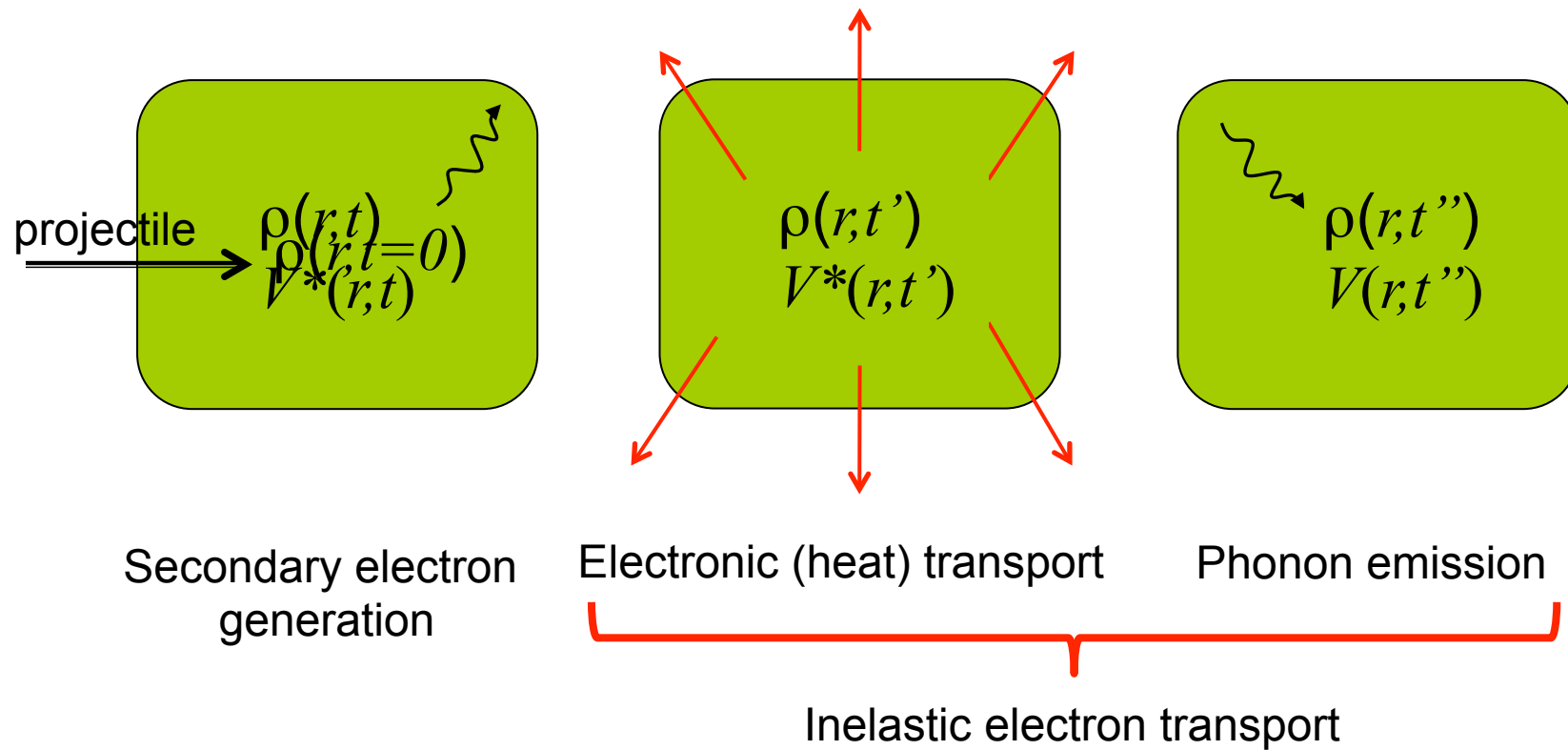
DSB

Low-energy electrons (1-20 eV) cause SSB and DSB in **plasmid DNA**

B. Boudaïffa et al, *Science* 287, 1659 (2000)

P. Swiderek, *Angew. Chem. Int. Ed.* 45, 4056 (2006)

# The irradiation process



# Multiscale phenomenon

- **Secondary electron generation (TDDFT-Ehrenfest)**

- A. A. Correa, J. Kohanoff, E. Artacho, D. Sánchez-Portal, and A. Caro, *Non-adiabatic forces in ion-solid interactions: the initial stages of radiation damage*, Phys. Rev. Lett. **108**, 213201 (2012).
- M. Ahsan Zeb, J. Kohanoff, D. Sánchez-Portal, A. Arnau, J. I. Juaristi, and E. Artacho, *Electronic stopping power in gold: The role of d electrons and the H/He anomaly*, Phys. Rev. Lett. **108**, 225504 (2012).

- **Inelastic transport (Beyond Ehrenfest)**



- **Capture/localization (Ground state DFT)**

- **Chemical stage: strand breaks (Ground state DFT)**

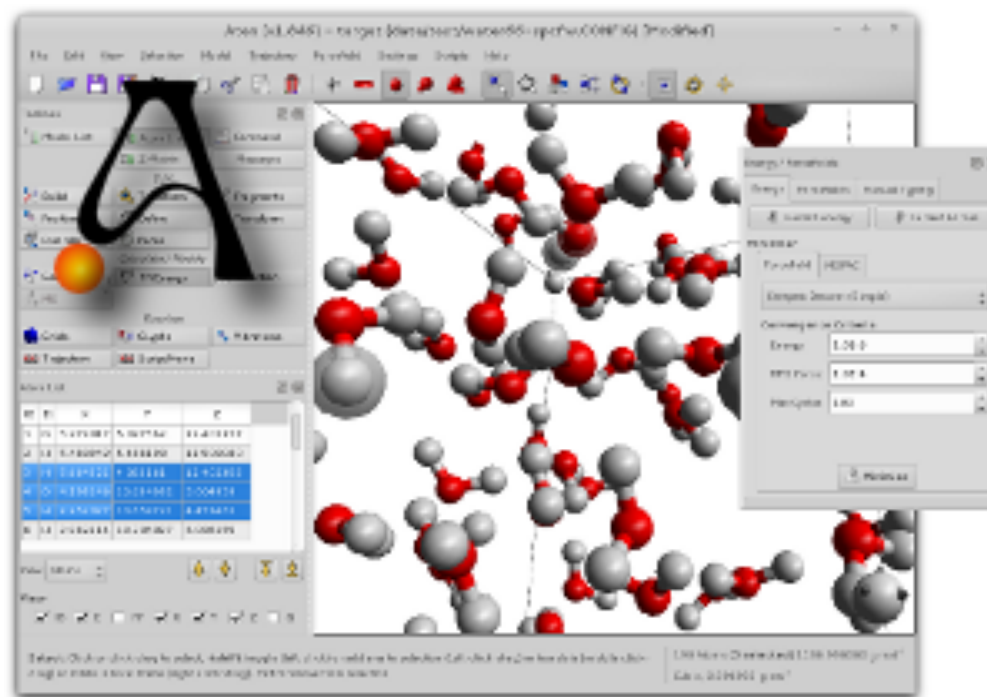
...

- **Radiobiological effects**

# Damage due to low-energy electrons

- **Ab initio molecular dynamics simulations**
  - Quickstep module of **CP2K**
  - Electronic structure via DFT (**GGA-PBE + VDW, higher level**)
  - **GTH** pseudopotentials
  - **GPW** method, **TZVP-GTH** basis set
  - Up to **1,000 atoms** and **10 ps** (HECToR) **10,000 atoms**
  - **Spin density** shows excess (unpaired) electron
- **REALISTIC ENVIRONMENT + THERMAL FLUCTUATIONS**
  - Increasingly large solvated DNA fragments

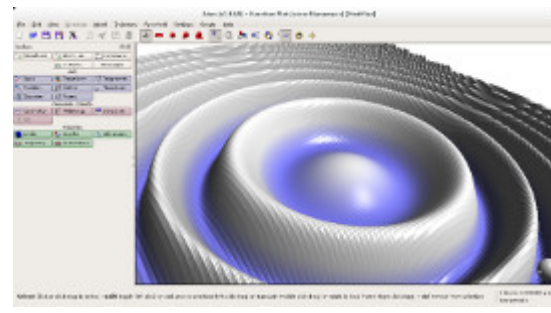
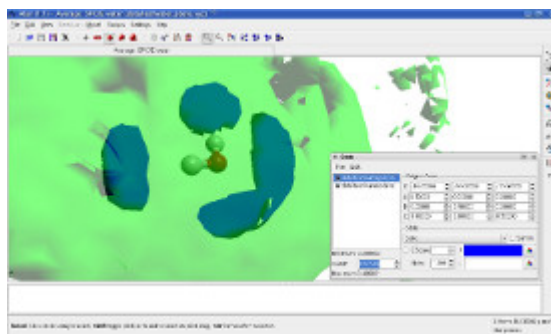
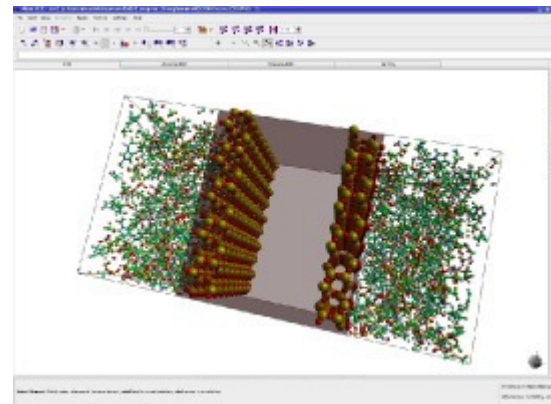
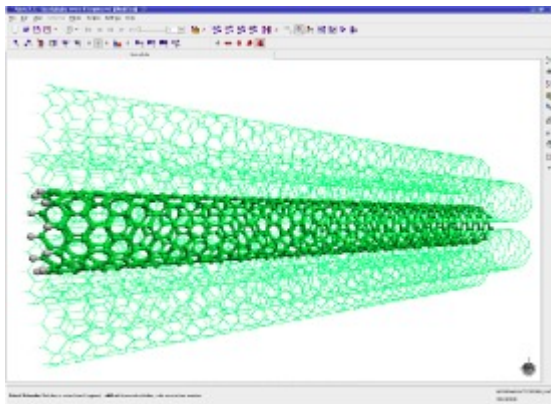
# Molecular builder and visualiser: Aten ([www.projectaten.org](http://www.projectaten.org)) by Tristan Youngs (RAL – former QUB)



It generates input files for many codes, e.g. quantum-esspresso, Siesta, DL\_POLY, MOPAC, ... **Do we want CP2K as well? (Ask Tristan)**



# Molecular builder and visualiser: Aten ([www.projectaten.org](http://www.projectaten.org)) by Tristan Youngs (RAL – former QUB)



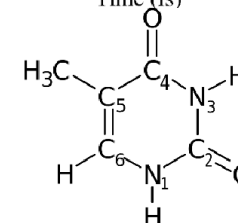
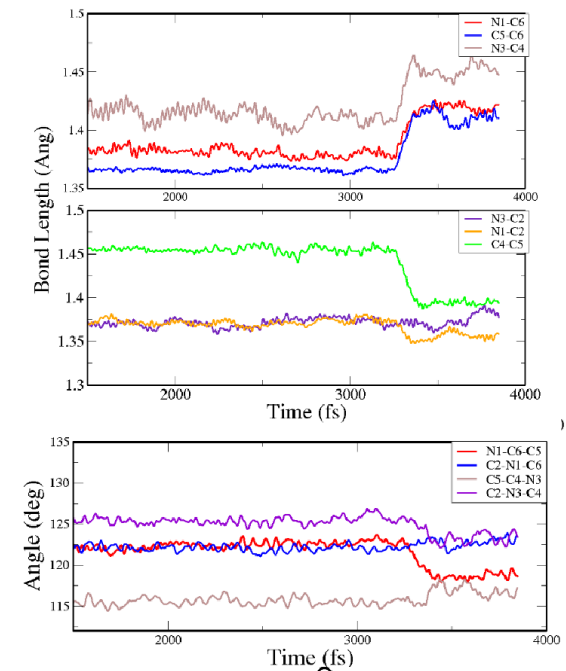
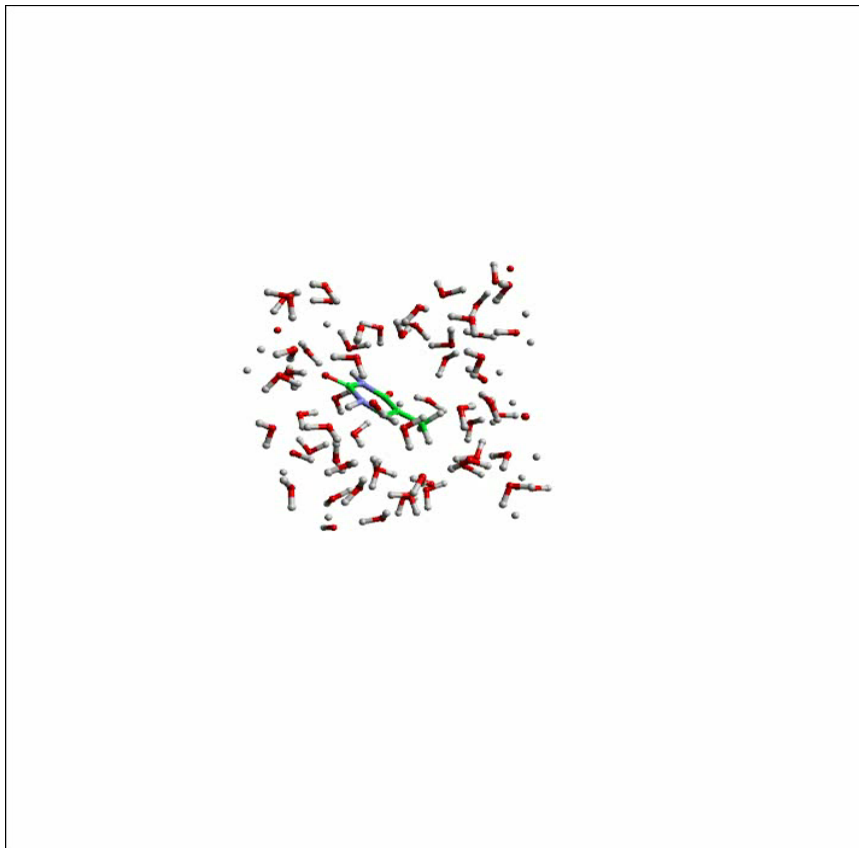


# Electron localization

# Nucleobases: Thymine

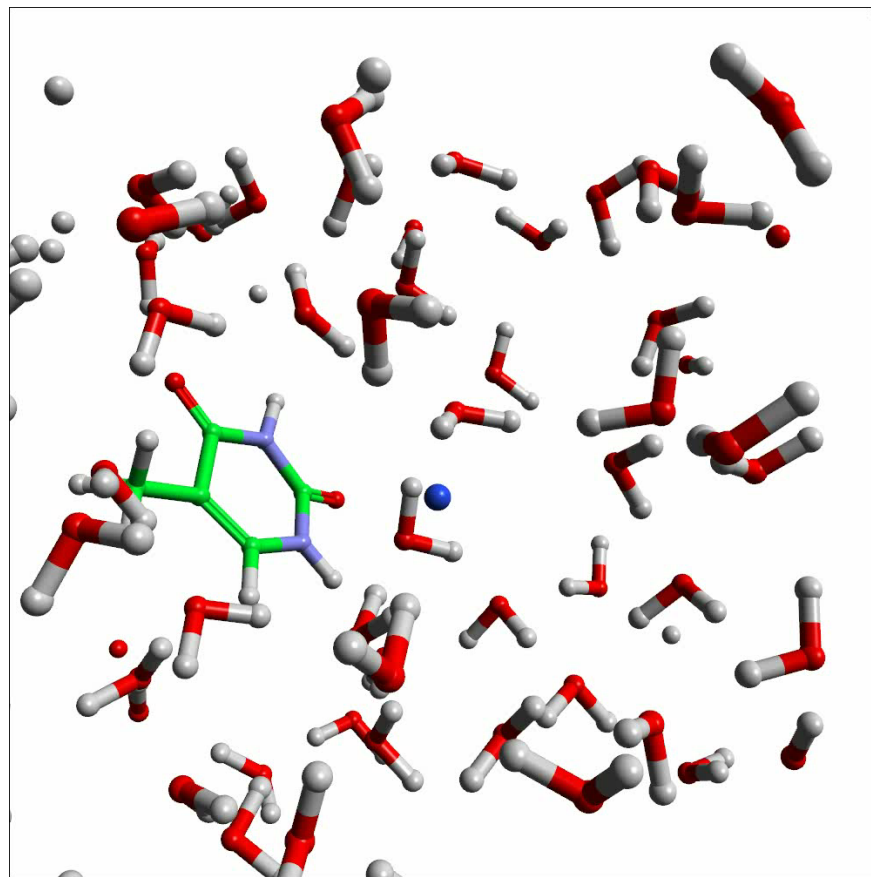
## First-principles Molecular Dynamics Simulations

M. Smyth and J. Kohanoff, Phys. Rev. Lett. **106**, 238108 (2011)



# Nucleobases vs cavity

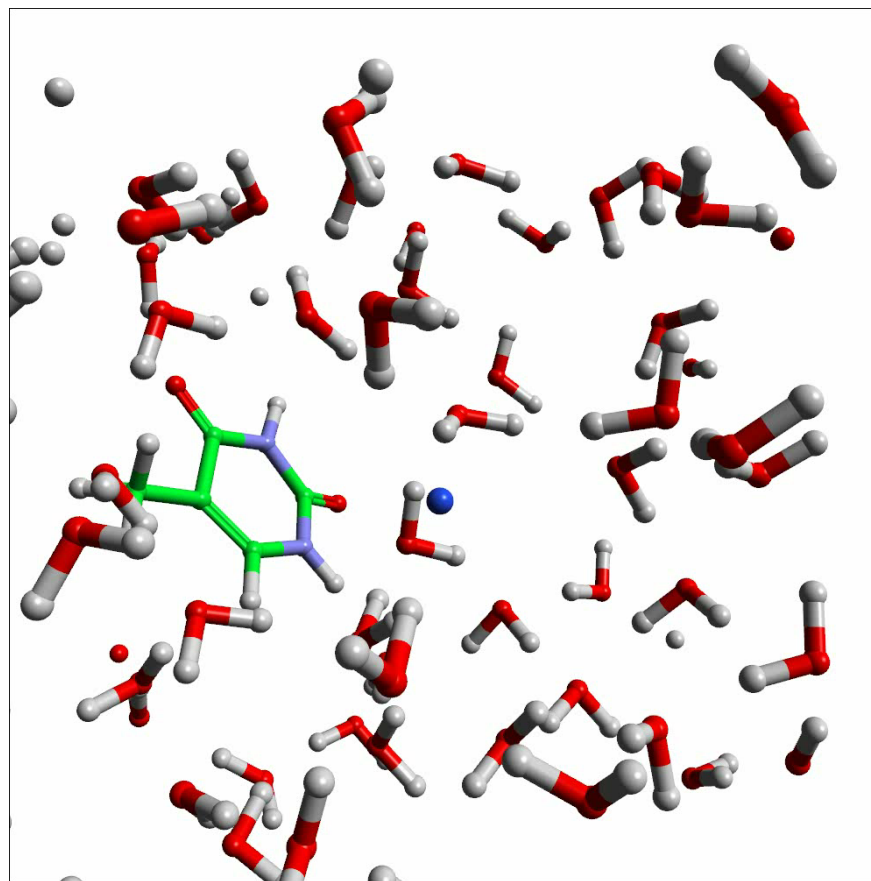
## Self-interaction



PBE

# Nucleobases vs cavity

## Self-interaction

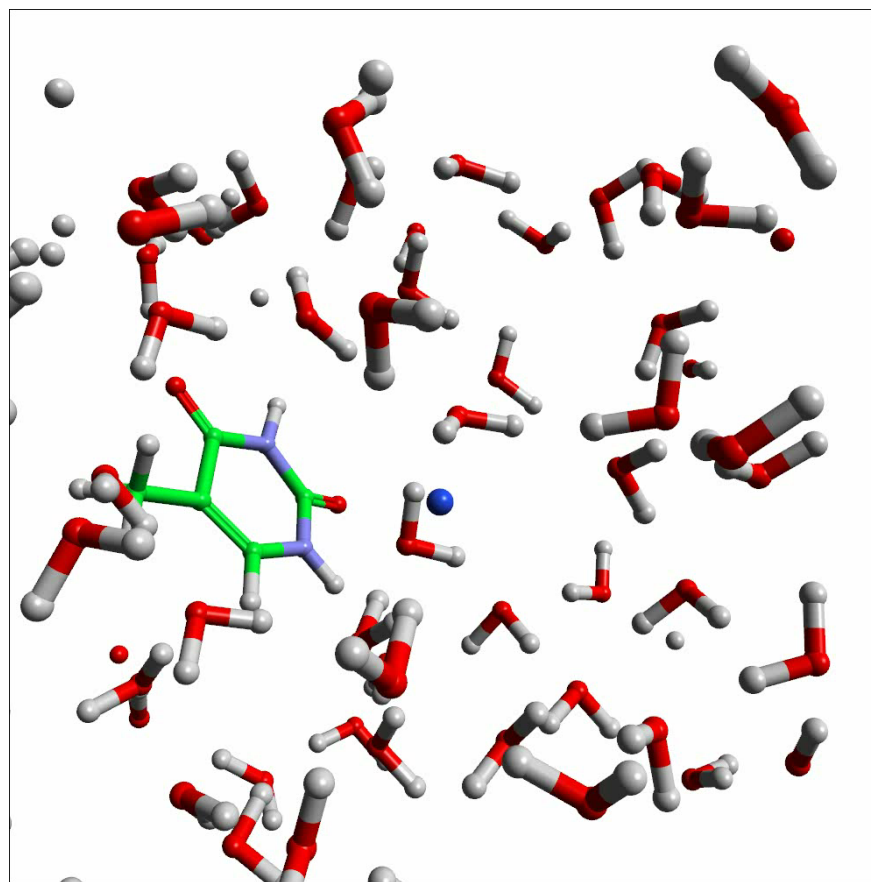


SIC  
 $a=0.2, b=0$



# Nucleobases vs cavity

## Self-interaction

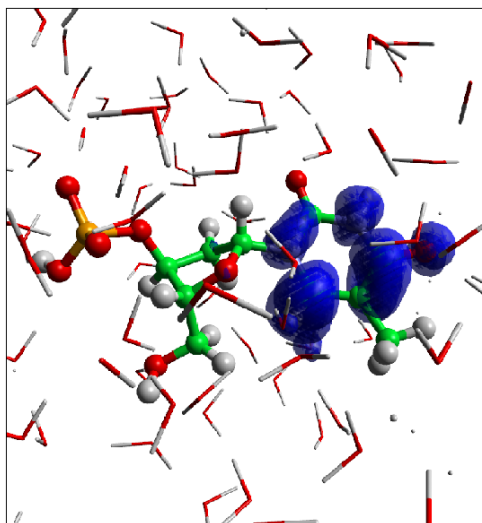


SIC  
 $a=0.8, b=0.5$

# Nucleotides: dTMP

## First-principles constrained Molecular Dynamics

M. Smyth and J. Kohanoff, J. Am. Chem. Soc. **134**, 9122 (2012)



**Excess electron still localized in the base**

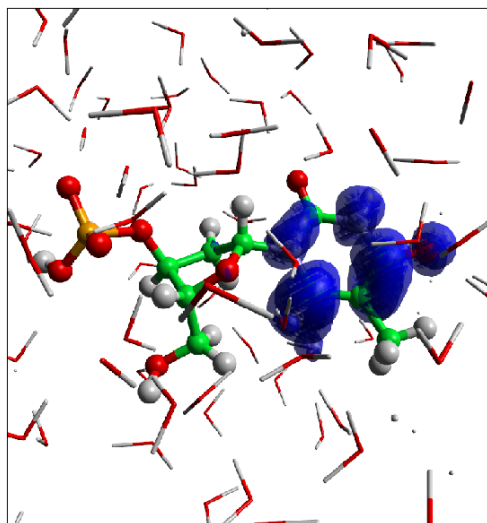
## Strand breaks

- Don't occur spontaneously
- Rare event
- **Constrained MD simulations:** stretch bond and compute free energy by integrating the potential of mean force. *Equilibration and statistics.*

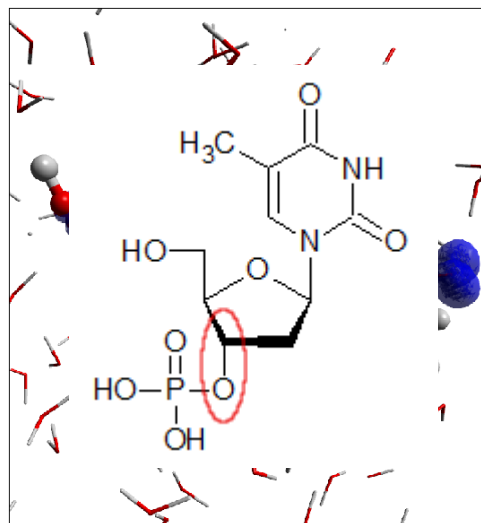
# Nucleotides: dTMP

## First-principles constrained Molecular Dynamics

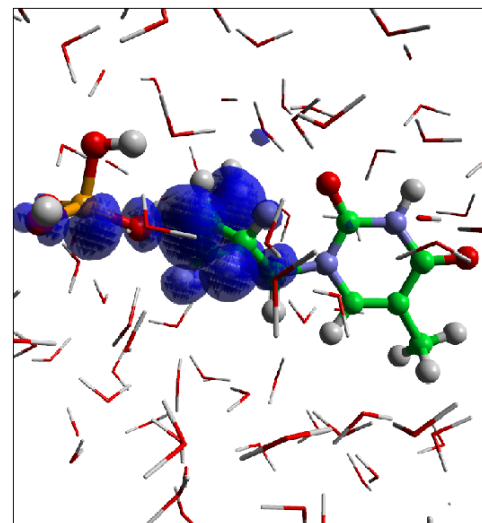
M. Smyth and J. Kohanoff, J. Am. Chem. Soc. **134**, 9122 (2012)



GS



TS



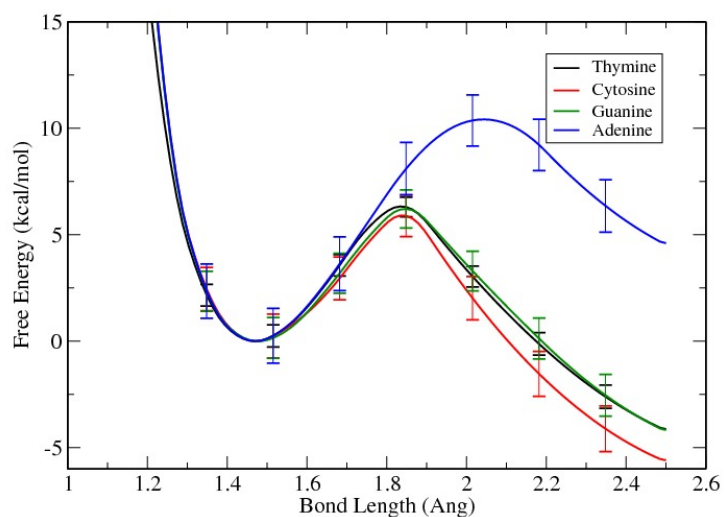
PS

**By stretching the C<sub>3'</sub>-O<sub>3'</sub> phosphodiester bond, the excess electron is transferred from the base to the sugar**

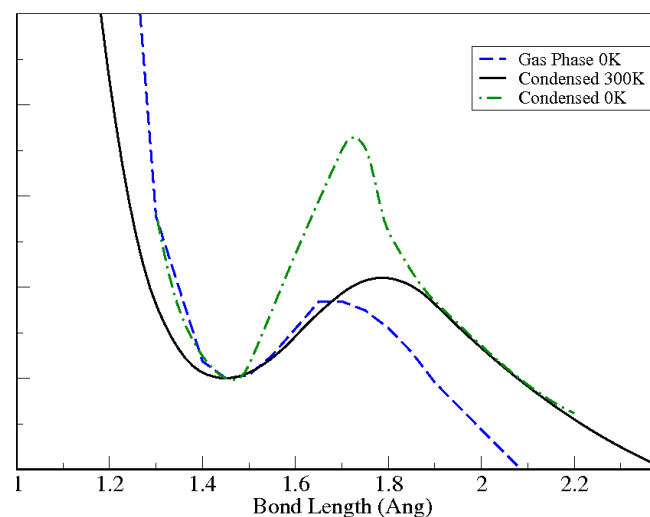
# Single Strand Breaks

## $C_3'-O_3'$ phosphodiester bond cleavage in nucleotides

M. Smyth and J. Kohanoff, J. Am. Chem. Soc. **134**, 9122 (2012)



**Gas Phase**



**From Gas to Condensed Phase**

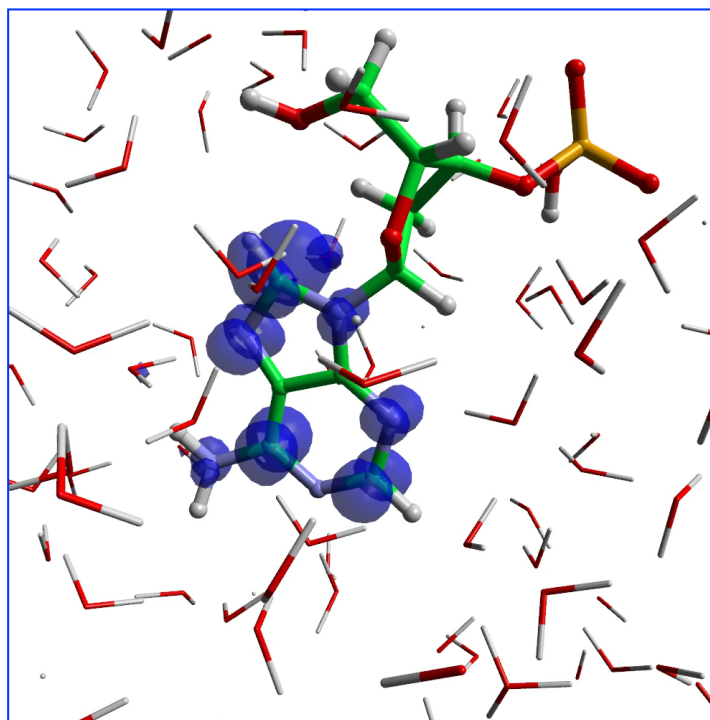
- **Barriers are about 5 kcal/mol  $\Rightarrow$  spontaneous SSB is feasible**
- **Environmental fluctuations are crucial to lower the barriers**



# Nucleotides: dAMP

## First-principles constrained Molecular Dynamics

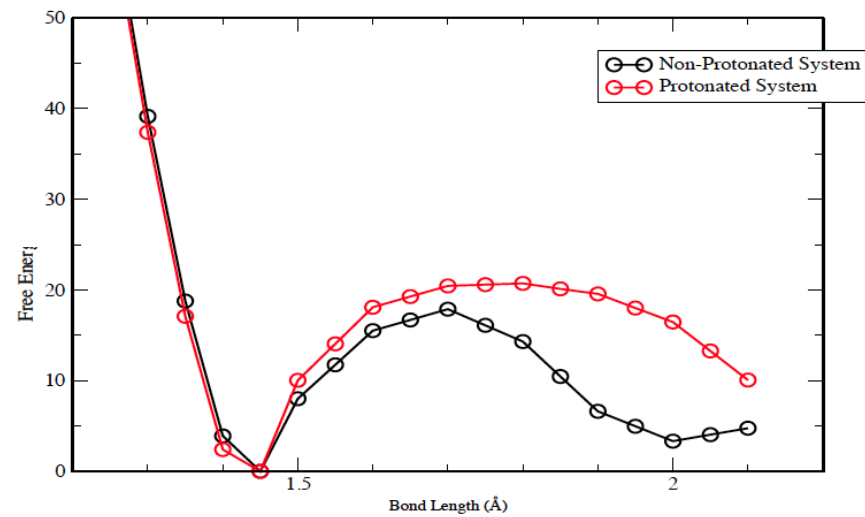
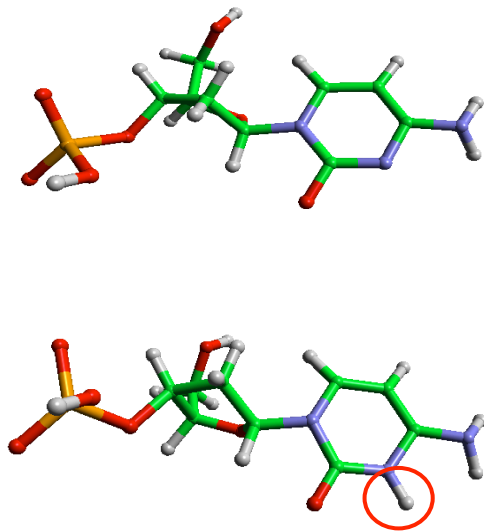
M. Smyth and J. Kohanoff, *J. Am. Chem. Soc.* **134**, 9122 (2012)



**Protonation**

# Protonation vs strand break in dCMP

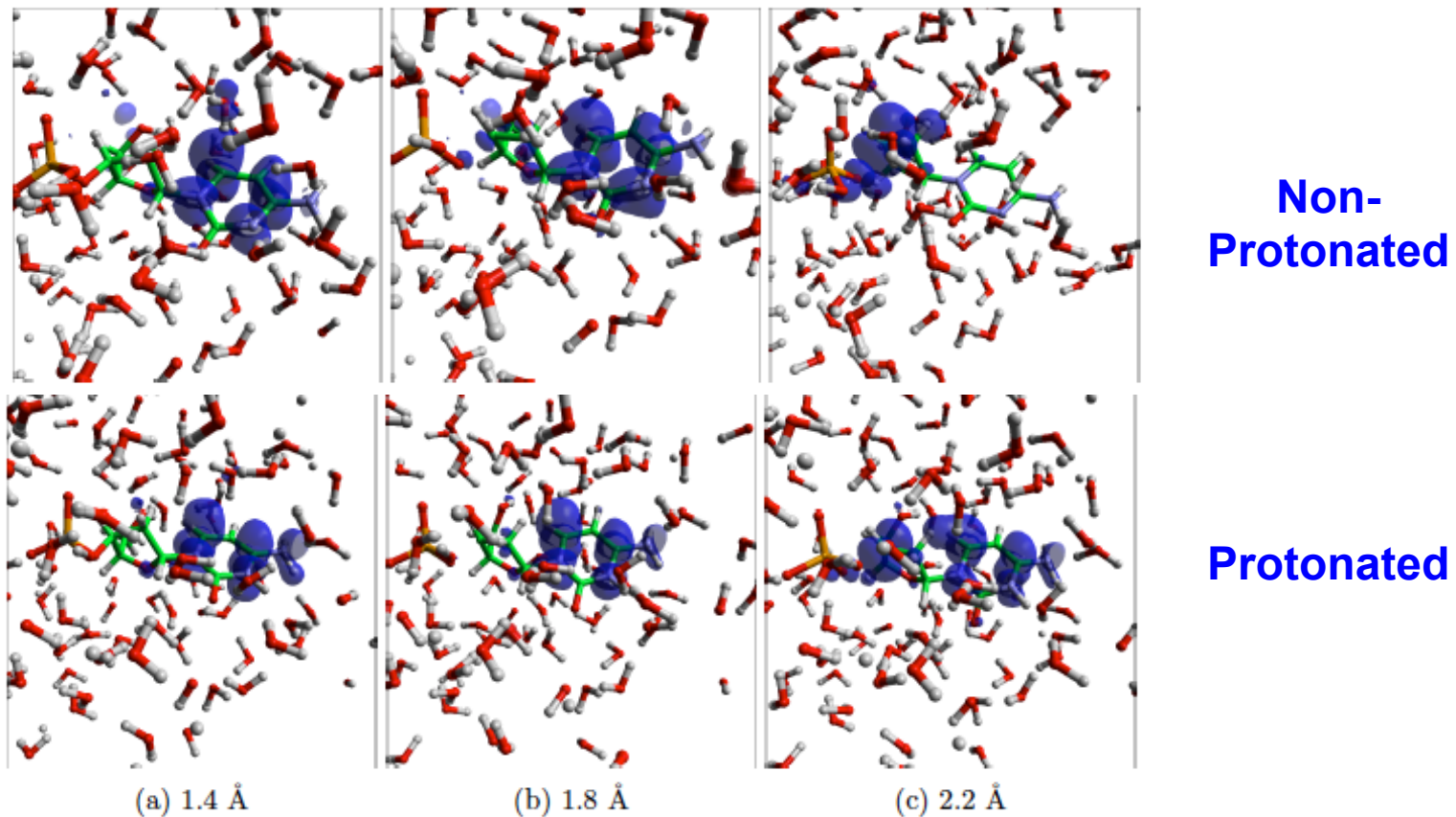
M. McAllister, M. Smyth, G. Tribello, and J. Kohanoff (unpublished)



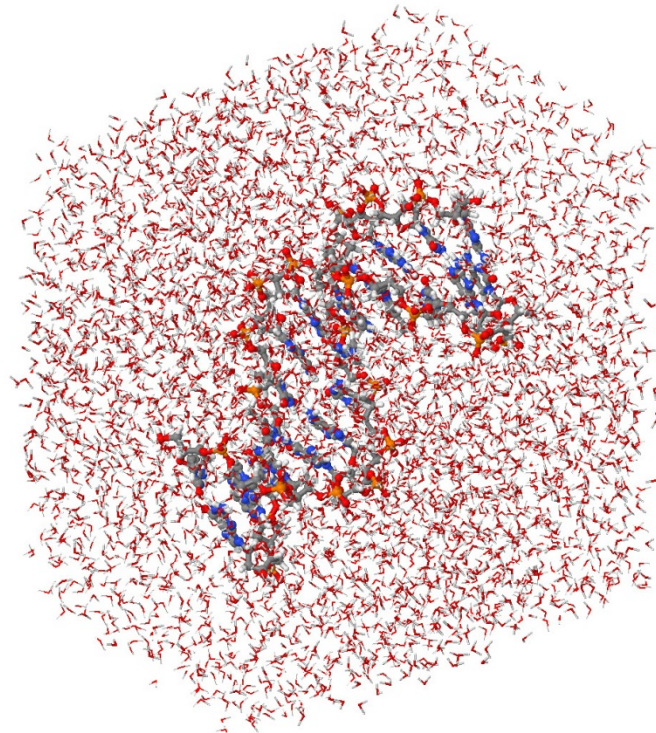
**Experimentally, LEE in dAMP and dCMP do not lead to bond cleavage**

# Protonation vs strand break in dCMP

M. McAllister, M. Smyth, G. Tribello, and J. Kohanoff (unpublished)



# Towards reality: larger DNA fragments

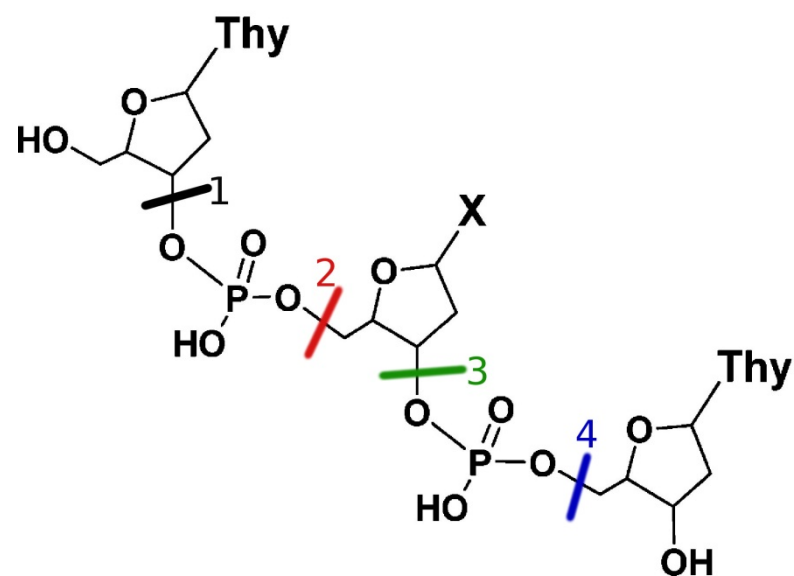


- **Are there specific sequences that favour strand breaks?**
- **Role of base pairing (duplex DNA)**

# Trinucleotides

## TXT

Z. Li, P. Cloutier, L. Sanche and J. R. Wagner, JACS **132**, 5422 (2010)



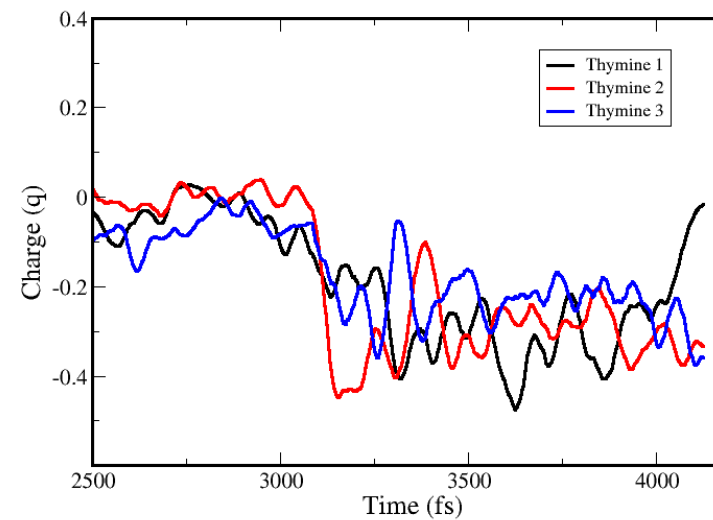
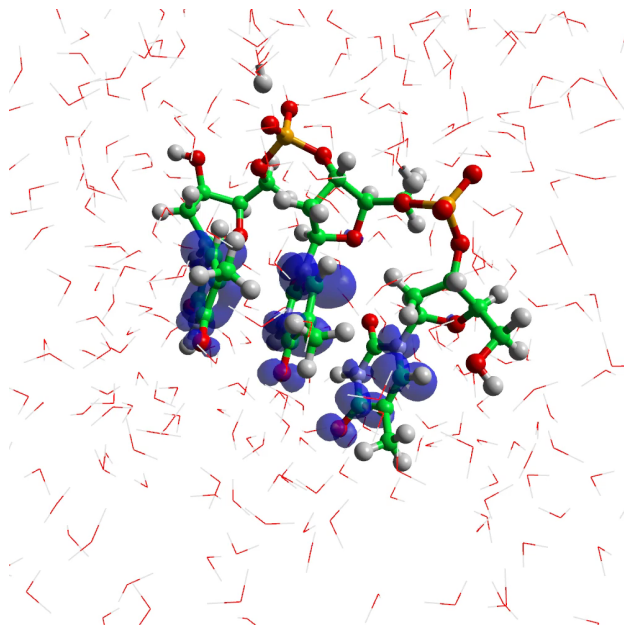
There are 4 possible bonds to break  
Experiment suggests **1** (C<sub>3'</sub>-O<sub>3'</sub>) for TTT



# Trinucleotides

## TTT

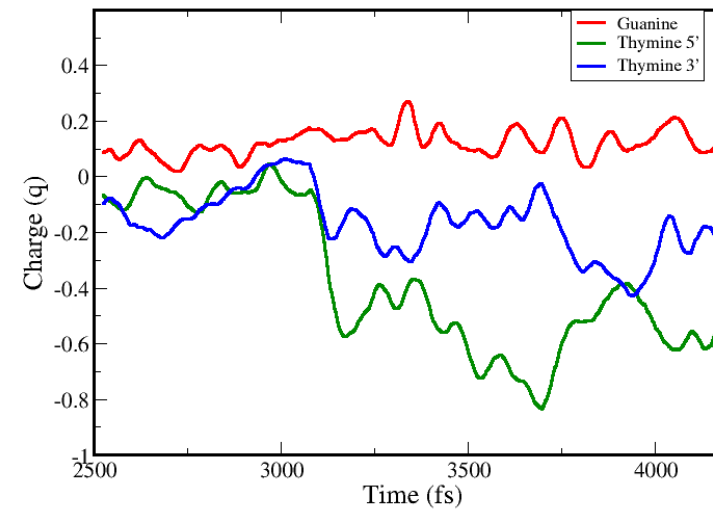
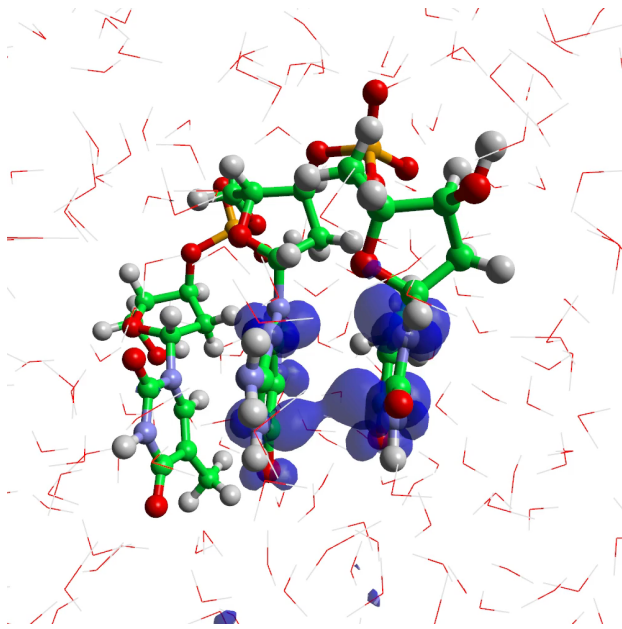
L. Bouëssel du Bourg, M. Smyth and J. Kohanoff (unpublished)



**Excess electron fluctuates between the three Thymines**

# Trinucleotides TGT

L. Bouëssel du Bourg, M. Smyth and J. Kohanoff (unpublished)



**Excess electron fluctuates between the two Thymines**

**Self-interaction corrected approaches. Hybrids?**

# Metadynamics



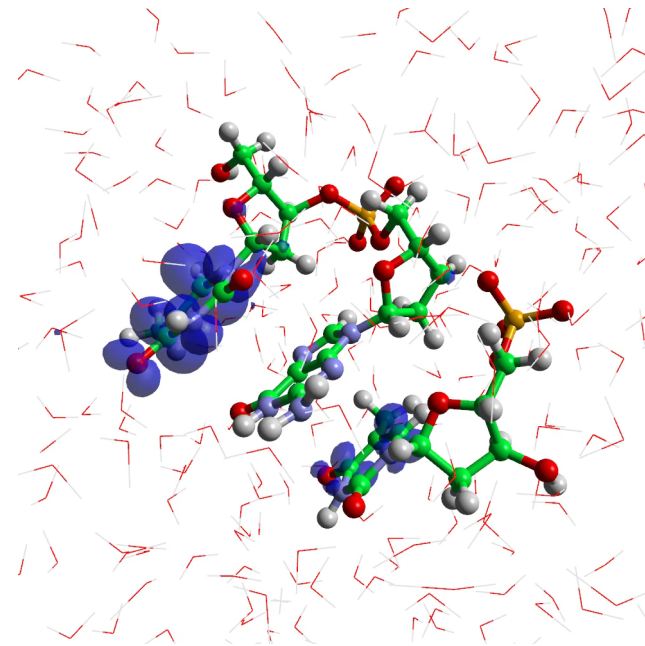
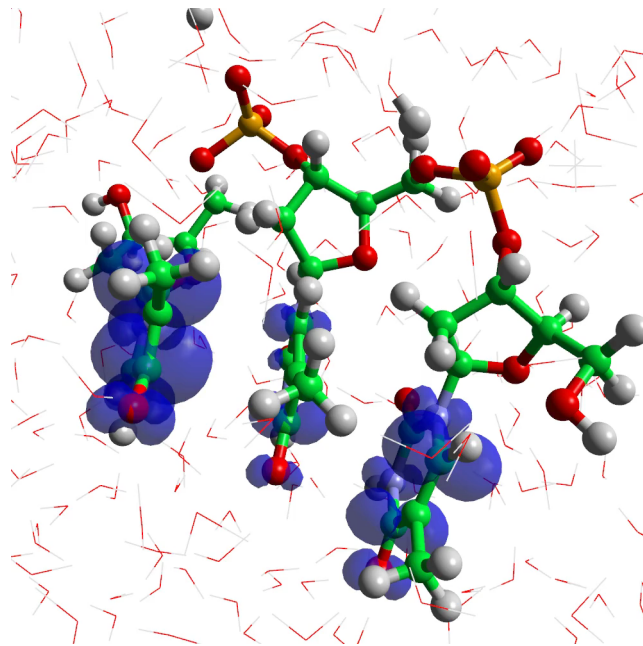
Which path will the system take?  
Constrain product of *switching functions* for the 4 bonds

**PLUMED** ([www.plumed-code.org](http://www.plumed-code.org)): interface with CP2K?

# Trinucleotides via metadynamics

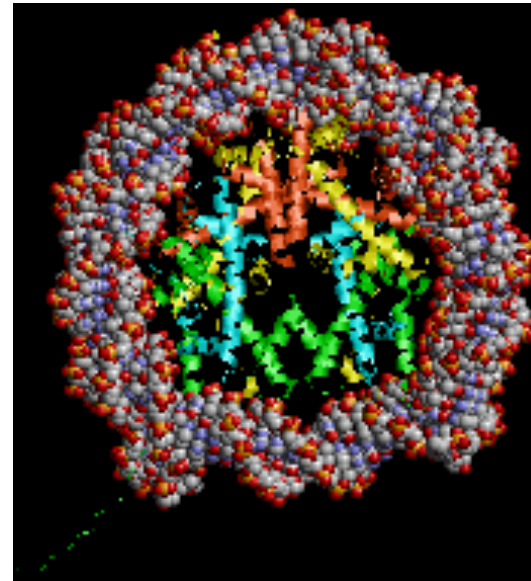
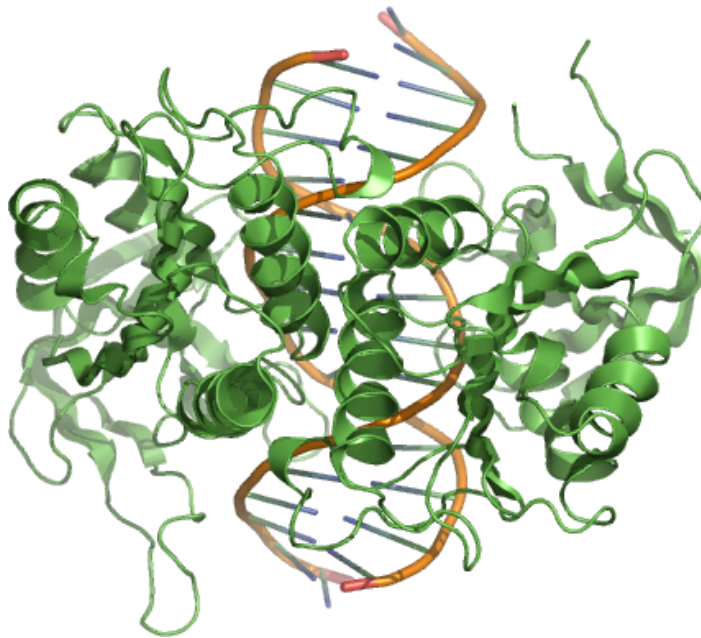
## TTT vs TGT

L. Bouëssel du Bourg, M. Smyth, G. Tribello and J. Kohanoff (unpublished)



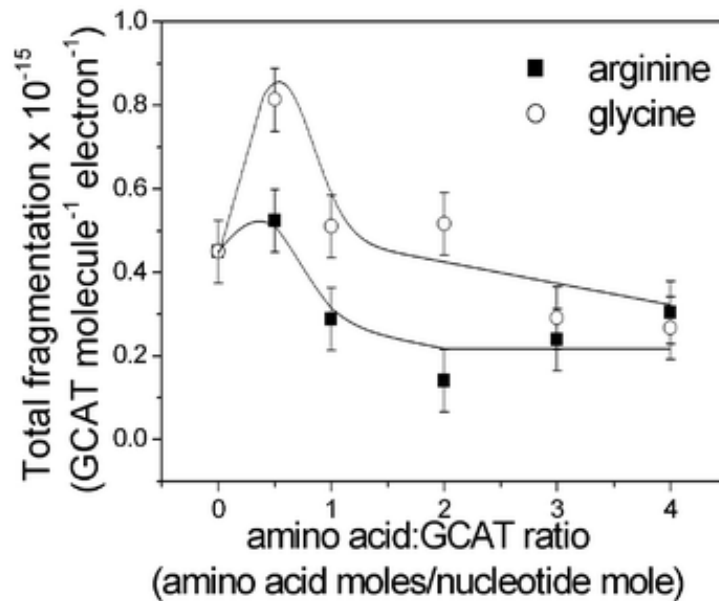
**Strand breaks seem to occur in different places depending on sequence**

# Towards reality: DNA in the nuclear cell environment

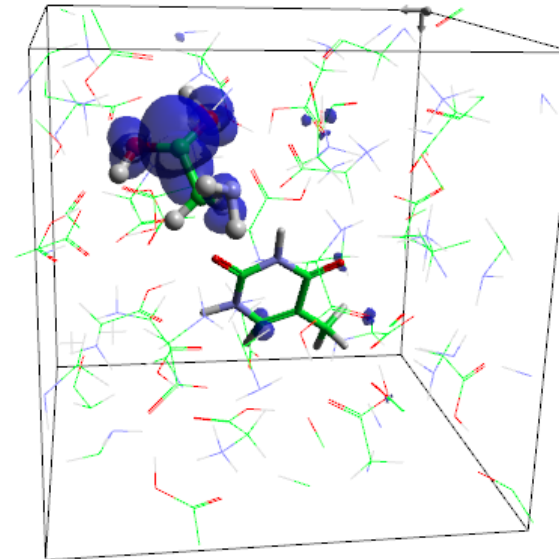


**Does the proximity of histones protect DNA against electron attachment and radical attack? If so, how?**

# A first attempt: The protective role of Glycine



*S. Ptasinska, Z. Li, N. J. Mason and L. Sanche,  
Phys. Chem. Chem. Phys., 2010, 12, 9367*

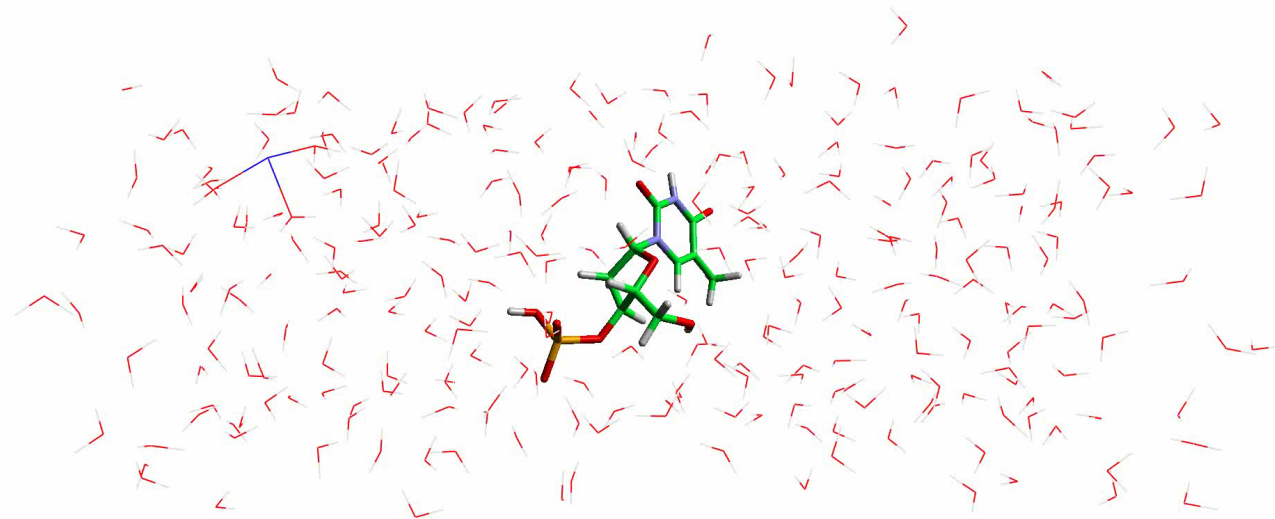


*Bin Gu, M. Smyth and J. Kohanoff  
(unpublished): Thy in pure Gly*

**Depending on whether it is in the canonical or zwitterion form,  
Glycine can be more attractive than Thymine for electrons**

# Shock waves: nucleotide in water

Alberto Fraile and JK (unpublished)

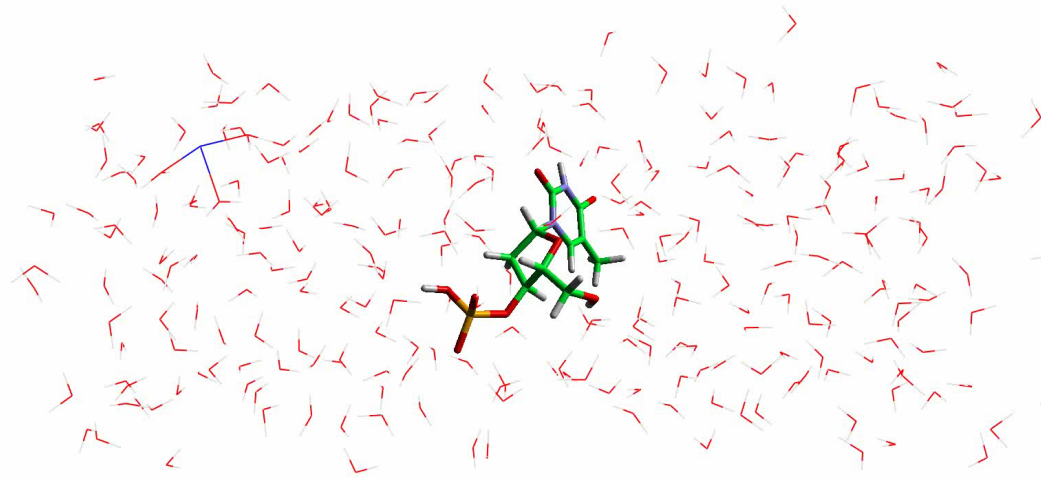


**CP2K,  $v=10$  km/s, single shock**



# Shock waves: nucleotide in water

Alberto Fraile and JK (unpublished)

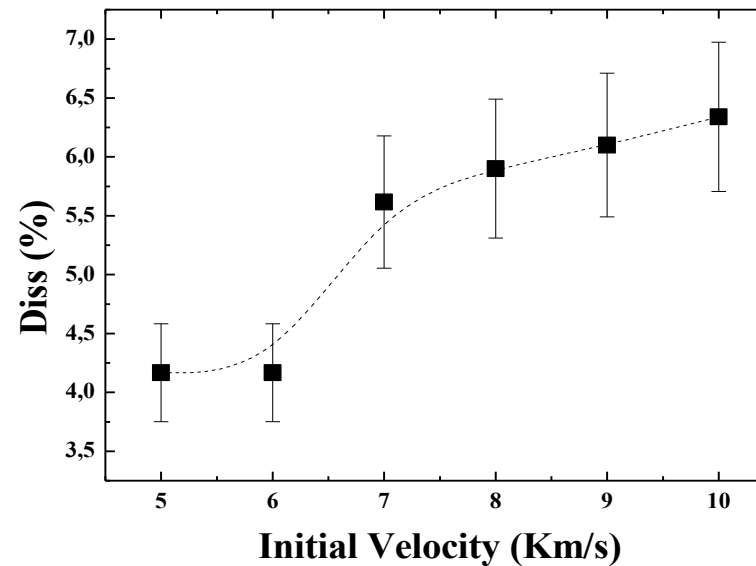
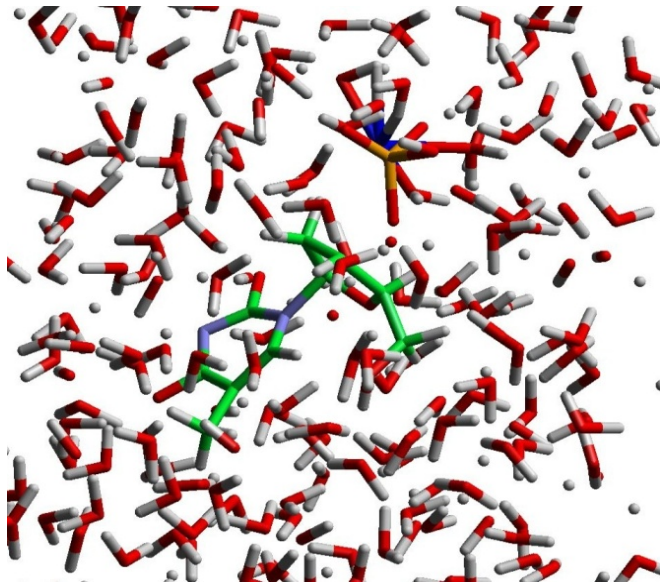


**CP2K,  $v=10$  km/s, MSST (Hugoniot)**



# Water dissociation: enhanced acidity

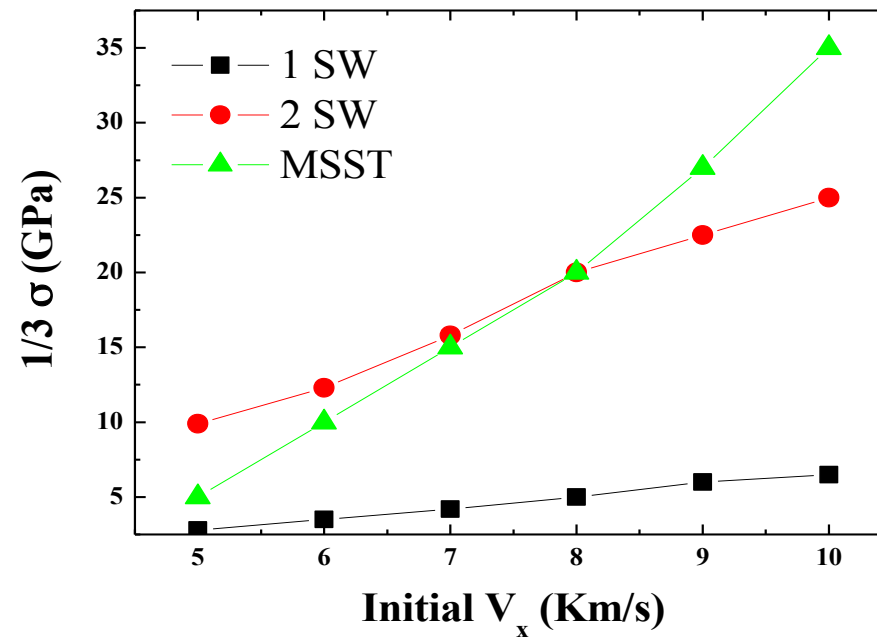
Alberto Fraile and JK (unpublished)



**Protons from dissociated water are free to react with the nucleotide**

# Pressures generated in SW

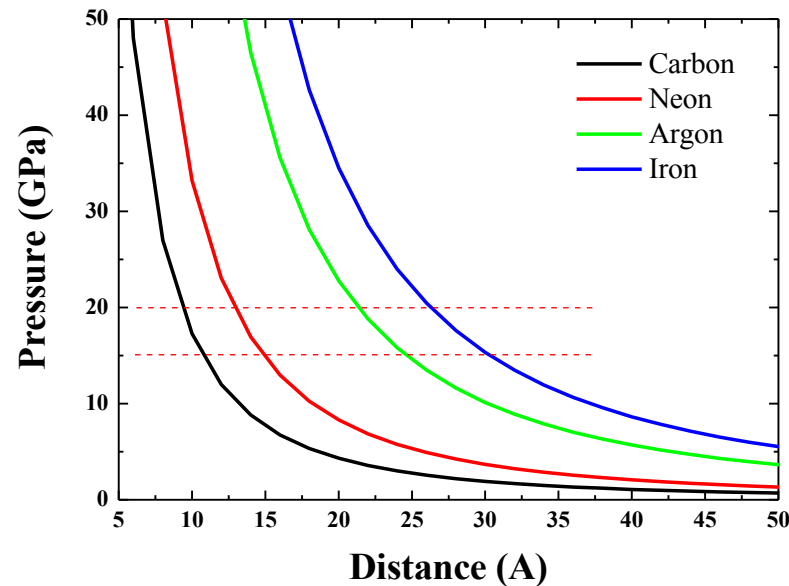
Alberto Fraile and JK (unpublished)



**CP2K-MSST. Pressures from 5 to 35 Gpa  
with v between 5 and 10 km/s**

# Shock waves: nucleotide in water

Alberto Fraile and JK (unpublished)



- **Damage happens at pressures above 15-20 GPa**
- **Protons don't produce any damage**
- **Carbon ions must come closer than 10 Å**
- **Only heavy ions produce damage via shock waves**

## Summary

- When secondary electrons reach zero kinetic energy (vertical attachment), it **localizes in the nucleobases in times  $\approx 15-25$  fs.**
- **No time to create a cavity** as in pure water (time scale  $\sim 1.5$  ps)
- **Nucleotides** are stable in water, but **excess electrons weaken the C-O (phosphodiester) bond** between ribose and phosphate.
- At ambient conditions **solvated nucleotides** can spontaneously cleave ( $\sim 5$  kcal/mol barriers), thus leading to **strand breaks**, competing with **protonation**, which stabilizes the backbone.
- Tri- and tetra-nucleotides. **Bond cleaved depends on sequence.**
- Neighbouring **aminoacids**, as present in chromatin, can physically and chemically **shield DNA**, thus **reducing the chances of damage.**

# Wish list for CP2K

- Integrate the following features:
  - Molecular editor (e.g. aten)
  - Force field for MD equilibration
  - PLUMED for free energies
  - Force field fitting procedure(s)
- Further developments:
  - Real-time electron dynamics beyond Ehrenfest
  - Resonant electronic states
  - Radicals
- Manual !!
  - Tutorials linked to manual sections (e.g. HFX, QMMM, etc)

## Collaborators

- Maeve Smyth (QUB → Cardiff)
- Lila Bouëssel du Bourg (ENS-Paris)
- Maeve McAllister (QUB)
- Gareth Tribello (QUB)
- Bin Gu (NUIST, China)
- Alberto Fraile (Madrid → Crete)

