



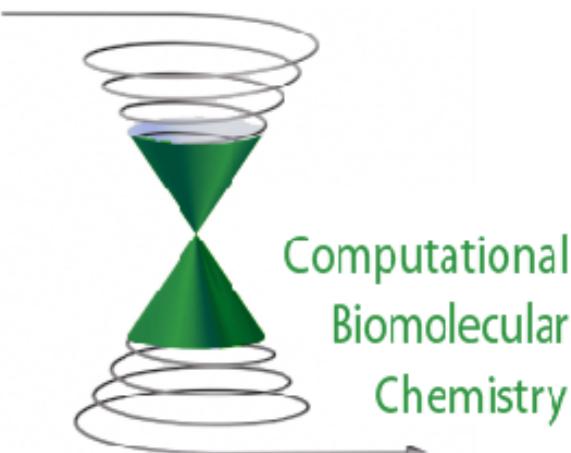
Observe while it happens: catching photochemistry in the act with computer simulations

Gerrit Groenhof

Department of Chemistry & Nanoscience Center
University of Jyväskylä
Finland



www.foksuk.nl/betacanon



Why observe while it happens?

"Everything that living things do can be understood in terms of the jiggling and wiggling of atoms."



Richard Feynman

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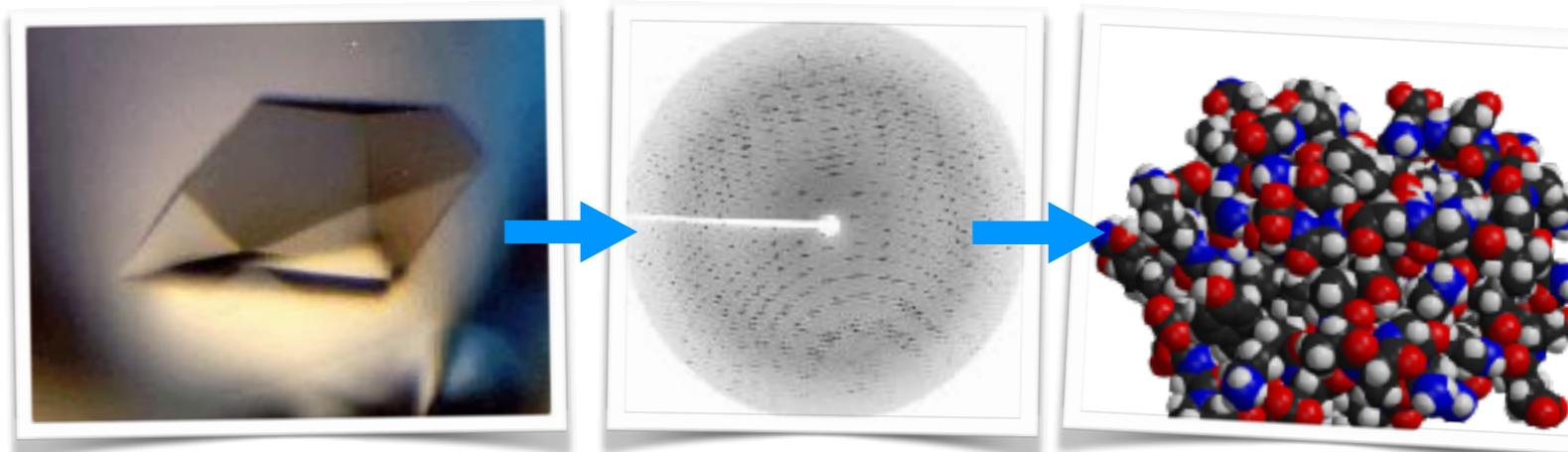


Richard Feynman

Why is that so difficult?

experiment cannot access the relevant length- and timescales simultaneously

spacial resolution: Å (10^{-10} m) 



x-ray
crystallography

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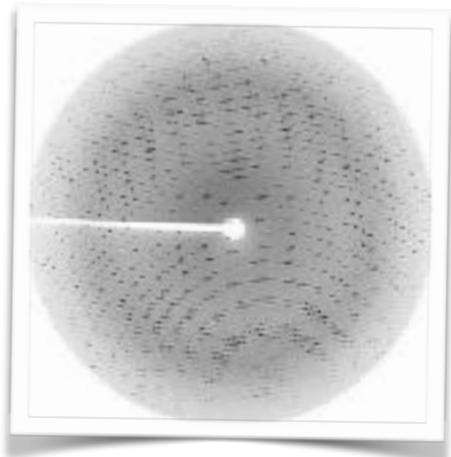
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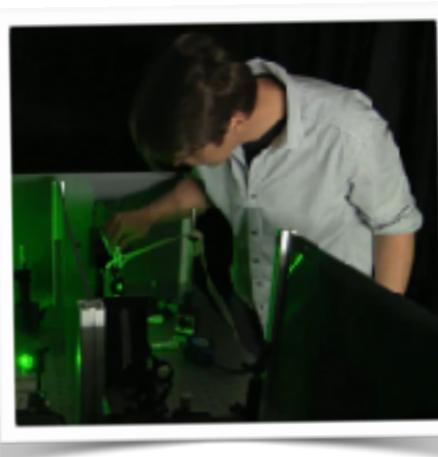
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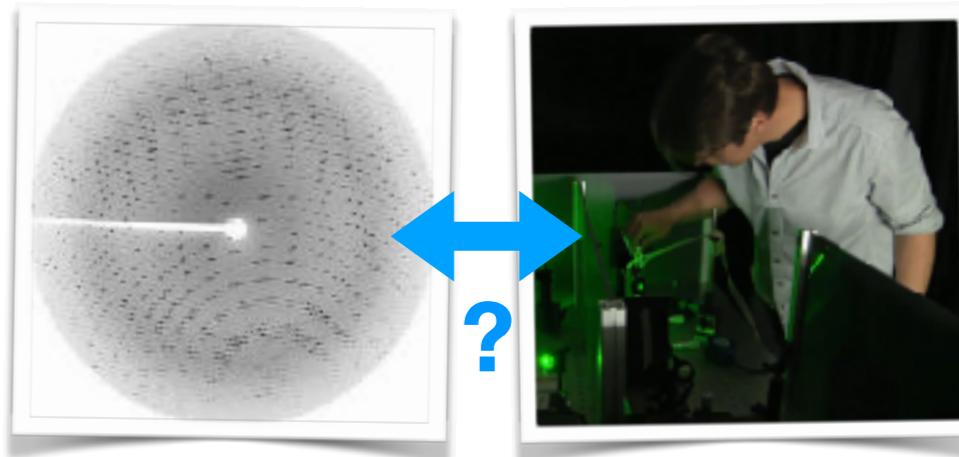
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fs time & Å spacial resolution 



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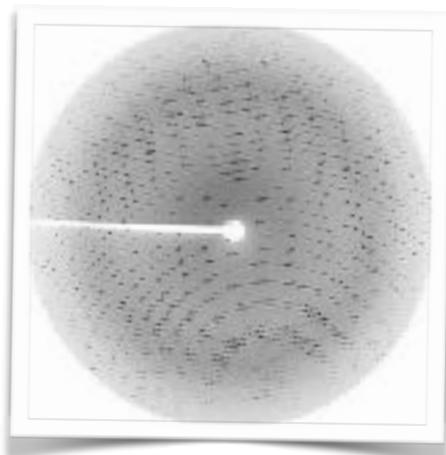
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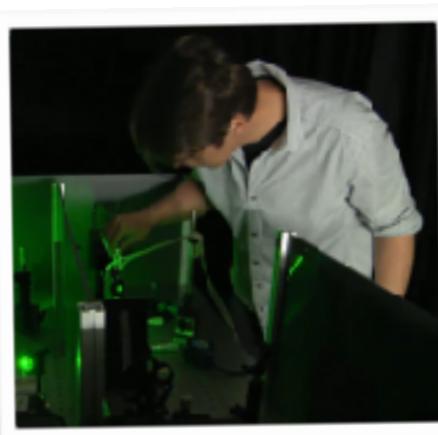
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spectroscopy

What can we do instead?

molecular dynamics computer simulations



Sisu.csc.fi: 1688 TFlop/s

Molecular dynamics simulations

classical nuclei

$$\mathbf{F}_i = -\nabla_{\mathbf{R}_i} V(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) = m_i \frac{d^2}{dt^2} \mathbf{R}_i$$



Isaac Newton

Molecular dynamics simulations

classical nuclei

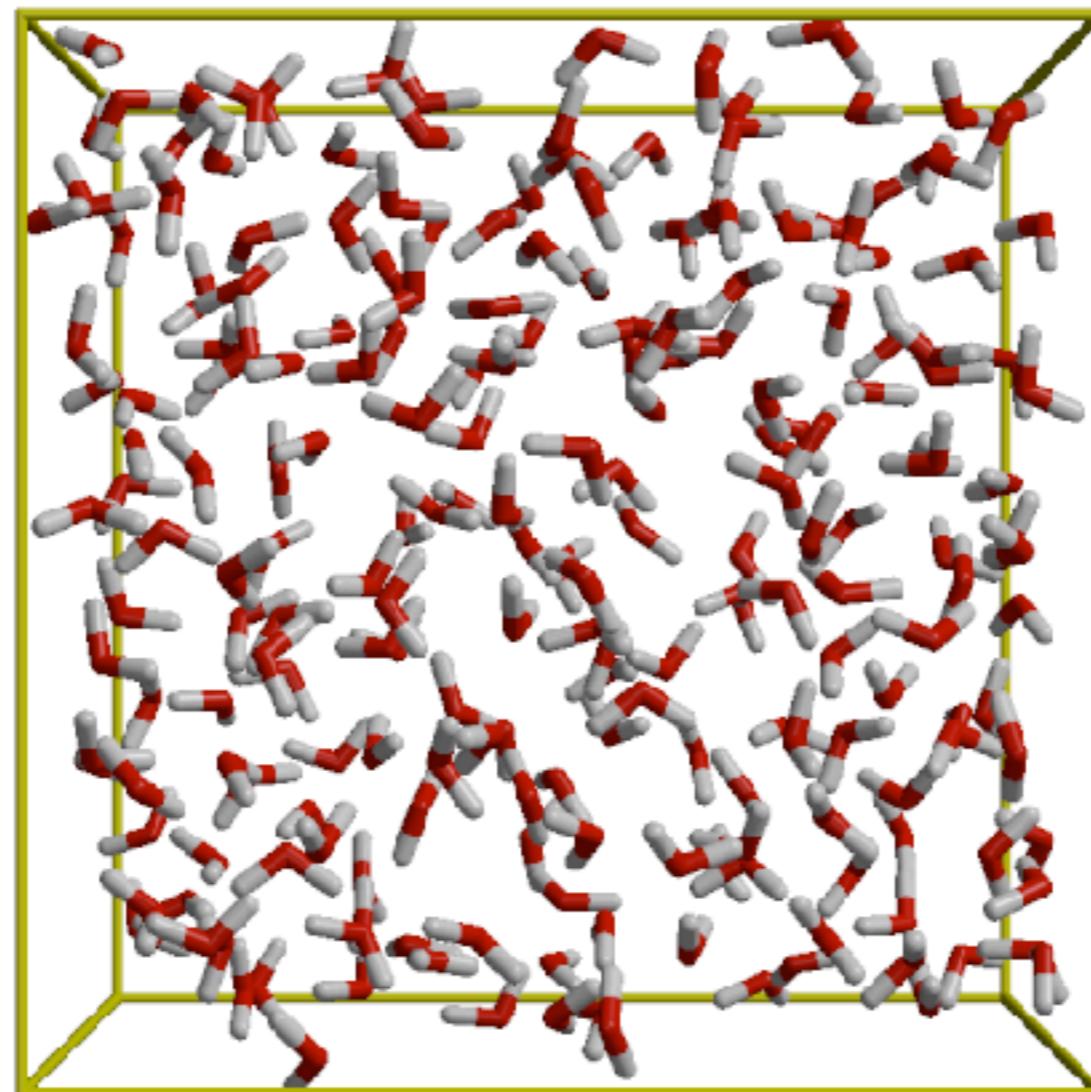
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Isaac Newton

trajectory

jiggling & wiggling



Molecular dynamics simulations

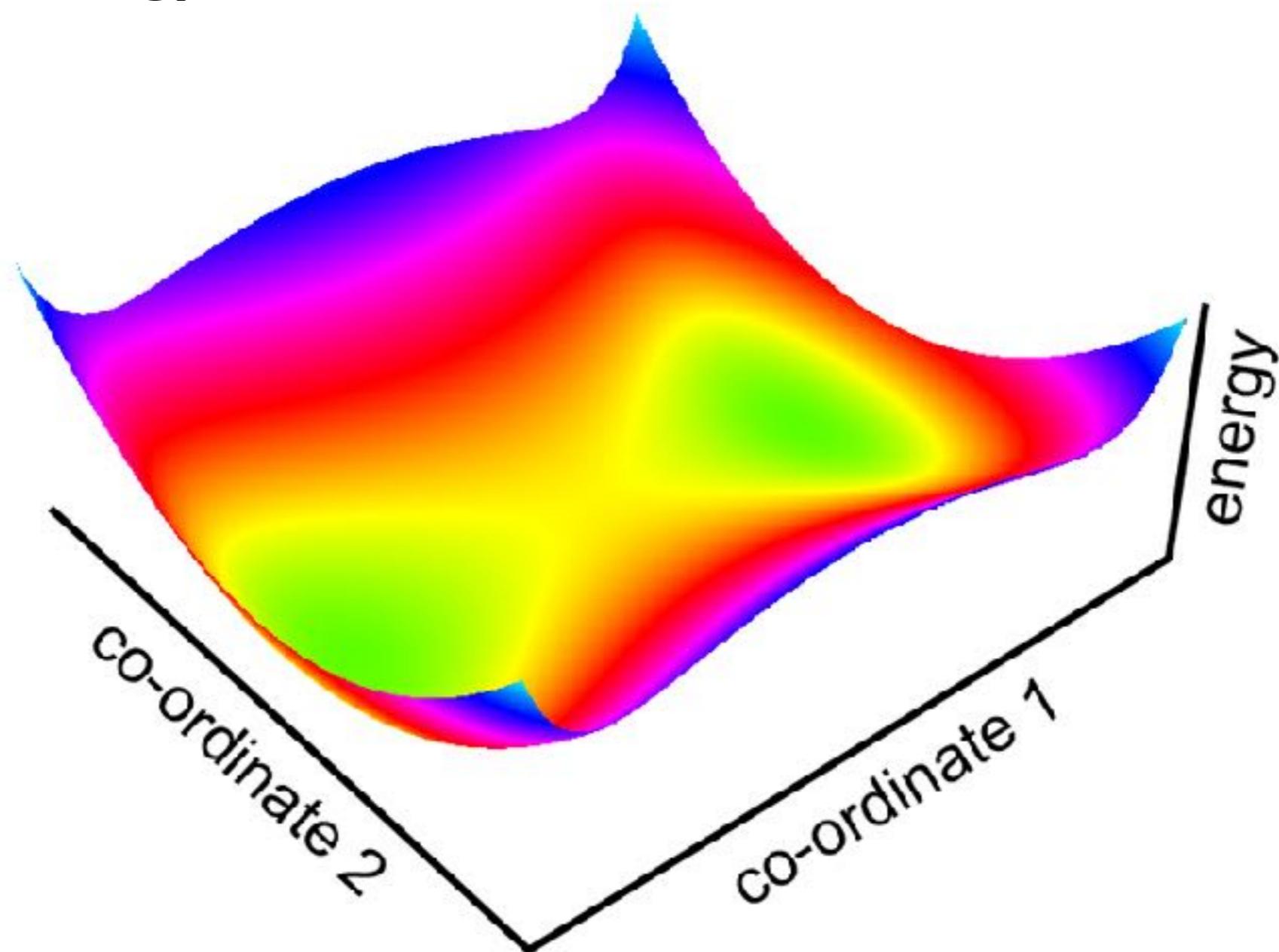
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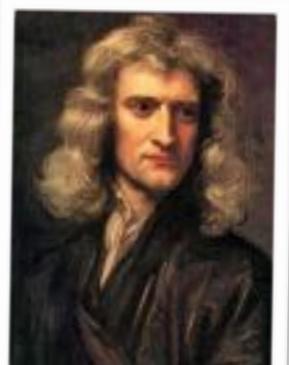
potential energy surface



Molecular dynamics simulations

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Isaac Newton

potential energy surface

quantum mechanics (QM)

explicit electrons

$$V^{\text{QM}}(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) =$$



Erwin Schrödinger

$$\langle \Psi_e(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_n) | \hat{H}_e(\mathbf{R}_1, \mathbf{R}_2, \dots, \mathbf{R}_N) | \Psi_e(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_n) \rangle$$

Molecular dynamics simulations

classical nuclei

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Isaac Newton

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molecular mechanics (MM)

approximate the effect of electrons by empirical functions with parameters

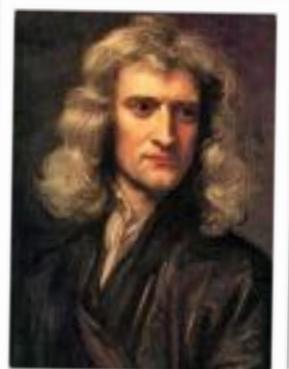
$$V^{\text{MM}}(R_1, R_2, \dots, R_N) = \sum_k v_k(R_i, R_j, R_k, R_l; \{p_k\})$$

or combination of both

Molecular dynamics simulations

classical nuclei

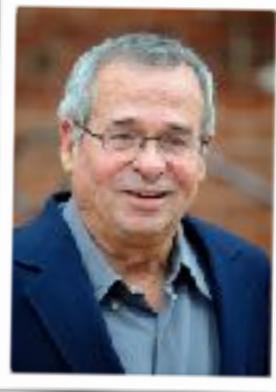
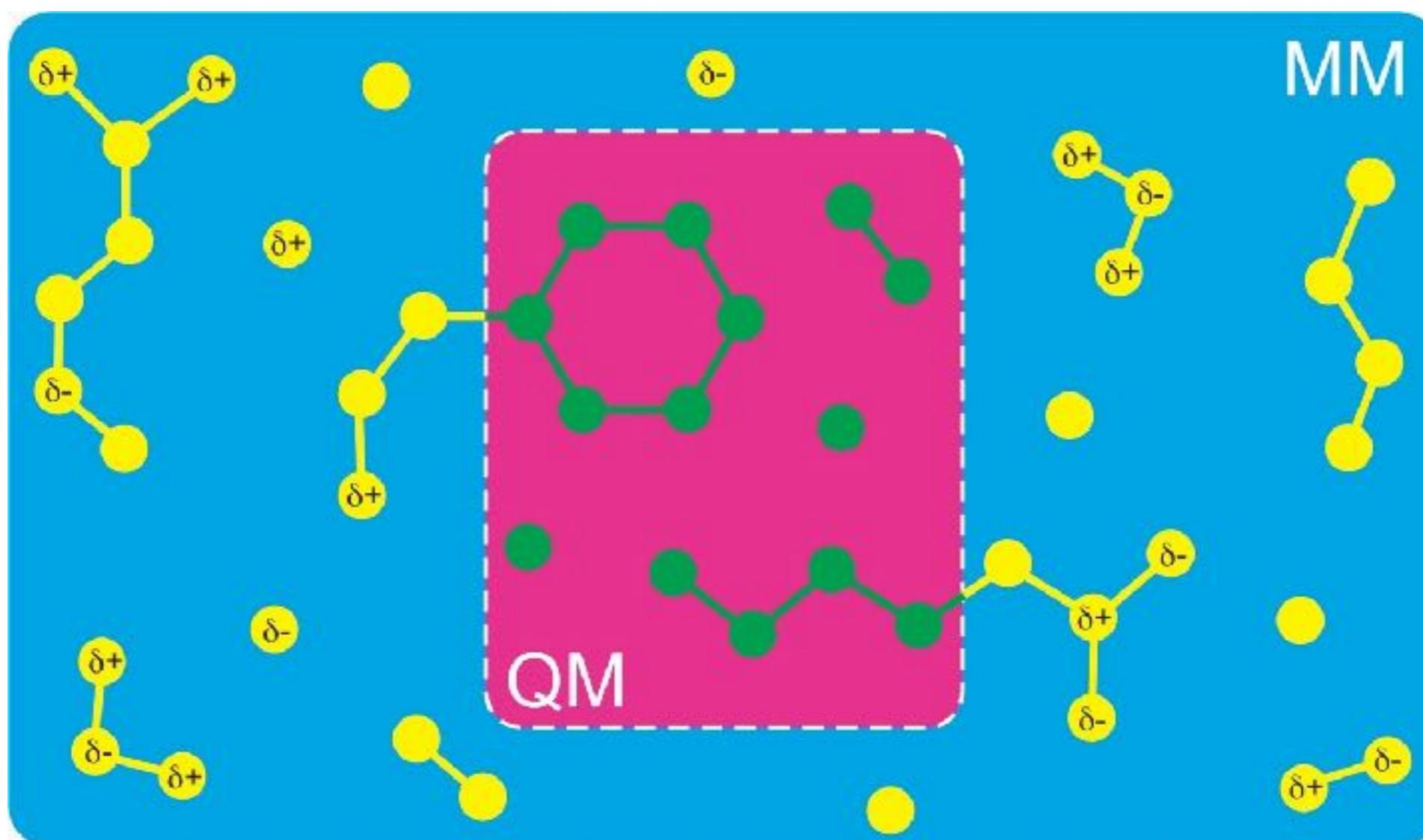
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Isaac Newton

potential energy surface

quantum mechanics/molecular mechanics (QM/MM)



Arieh
Warshel



Michael
Levitt

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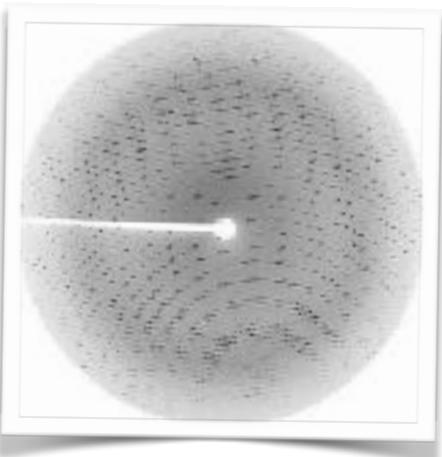
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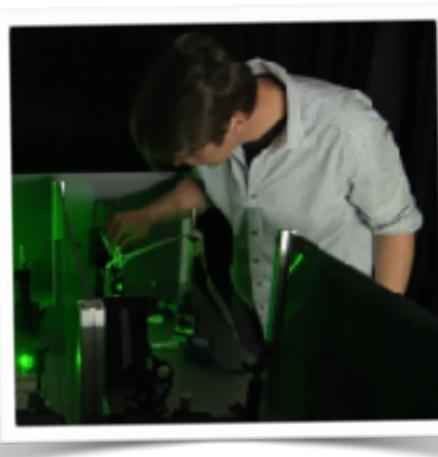
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time resolution: femtoseconds (10^{-15} s) 

fs time & Å spacial resolution 



x-ray
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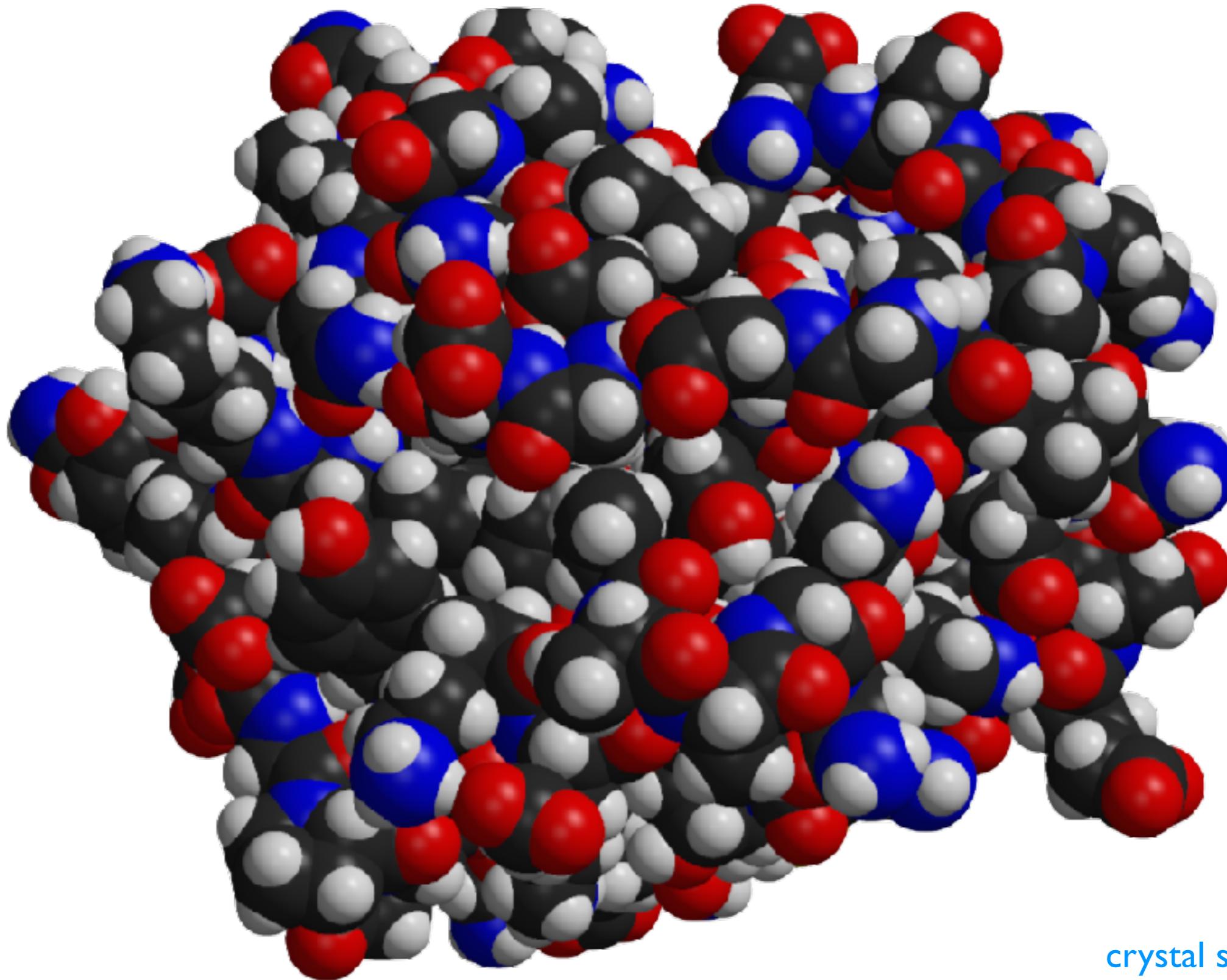
accuracy? 



Sisu.csc.fi: 1688 TFlop/s

Observe while it happens until 2015

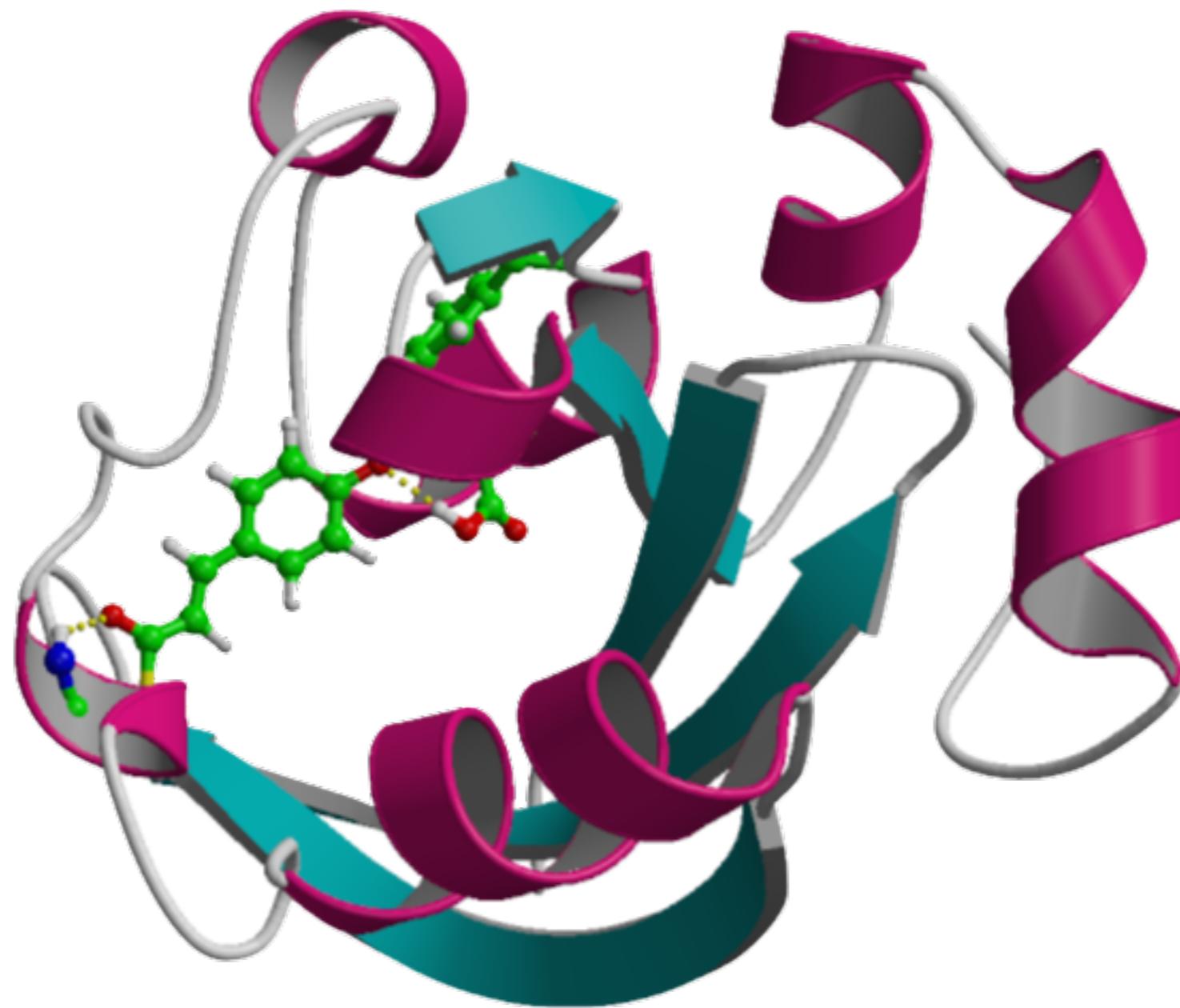
MD simulation of photoactive yellow protein



crystal structure: 2PHY

Observe while it happens until 2015

MD simulation of photoactive yellow protein

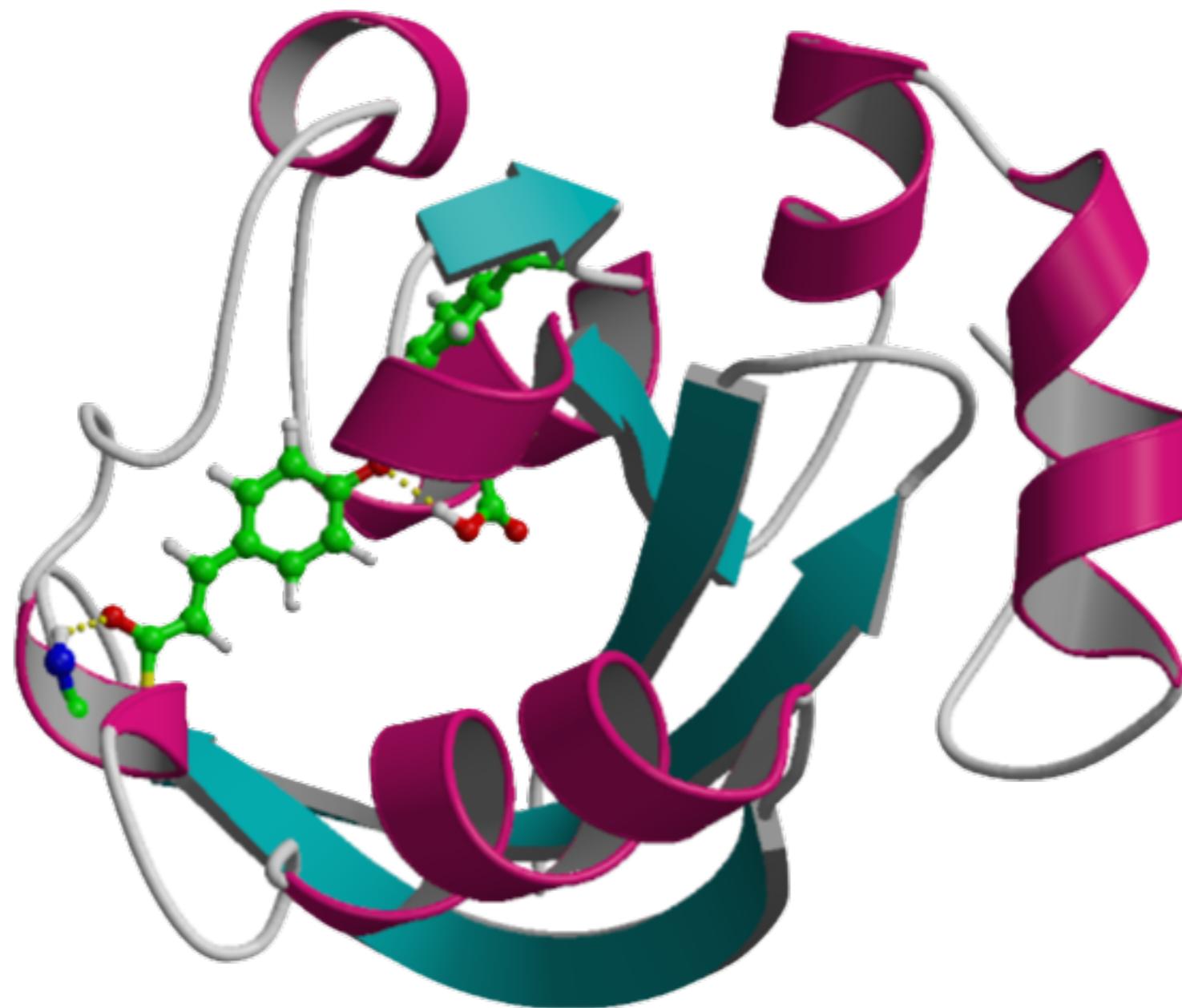


crystal structure: 2PHY

Observe while it happens until 2015

photoreceptor (“eye”) in *halorhodospira halophila*

detect and respond to blue light



crystal structure: 2PHY

Photoactive yellow protein

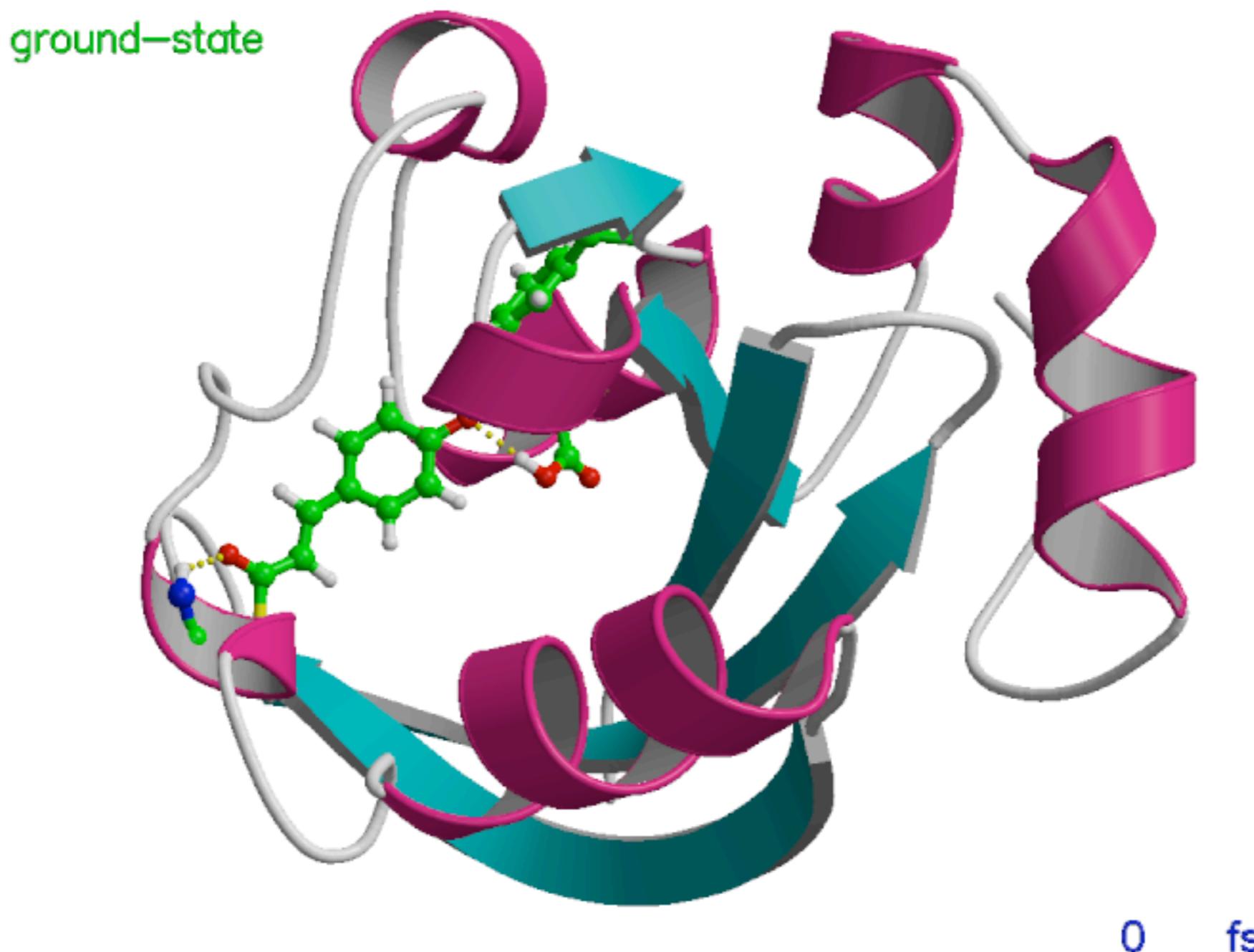
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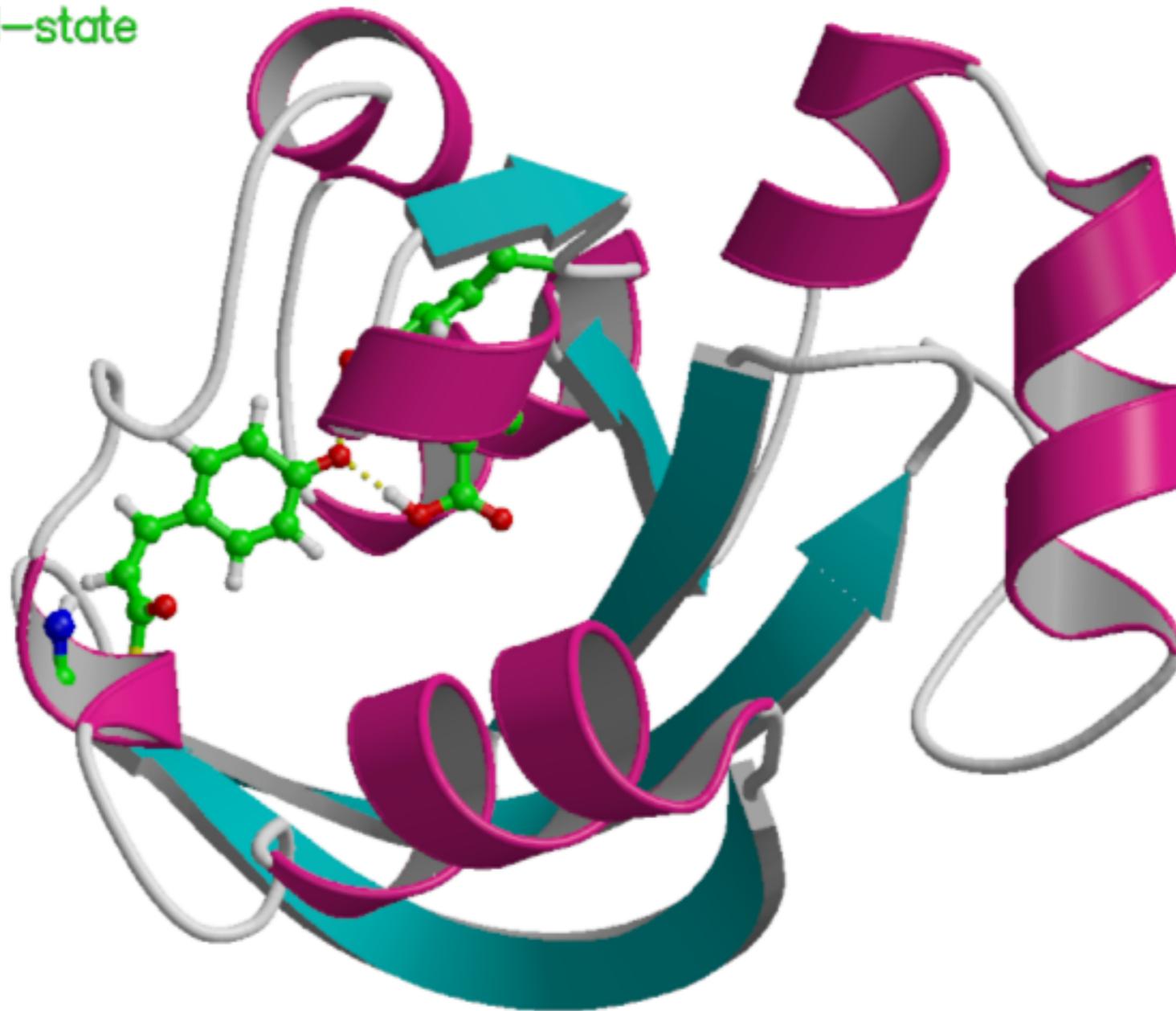
all atom simulation of photoactive yellow protein



Observe while it happens until 2015

all atom simulation of photoactive yellow protein

ground-state



2466 fs

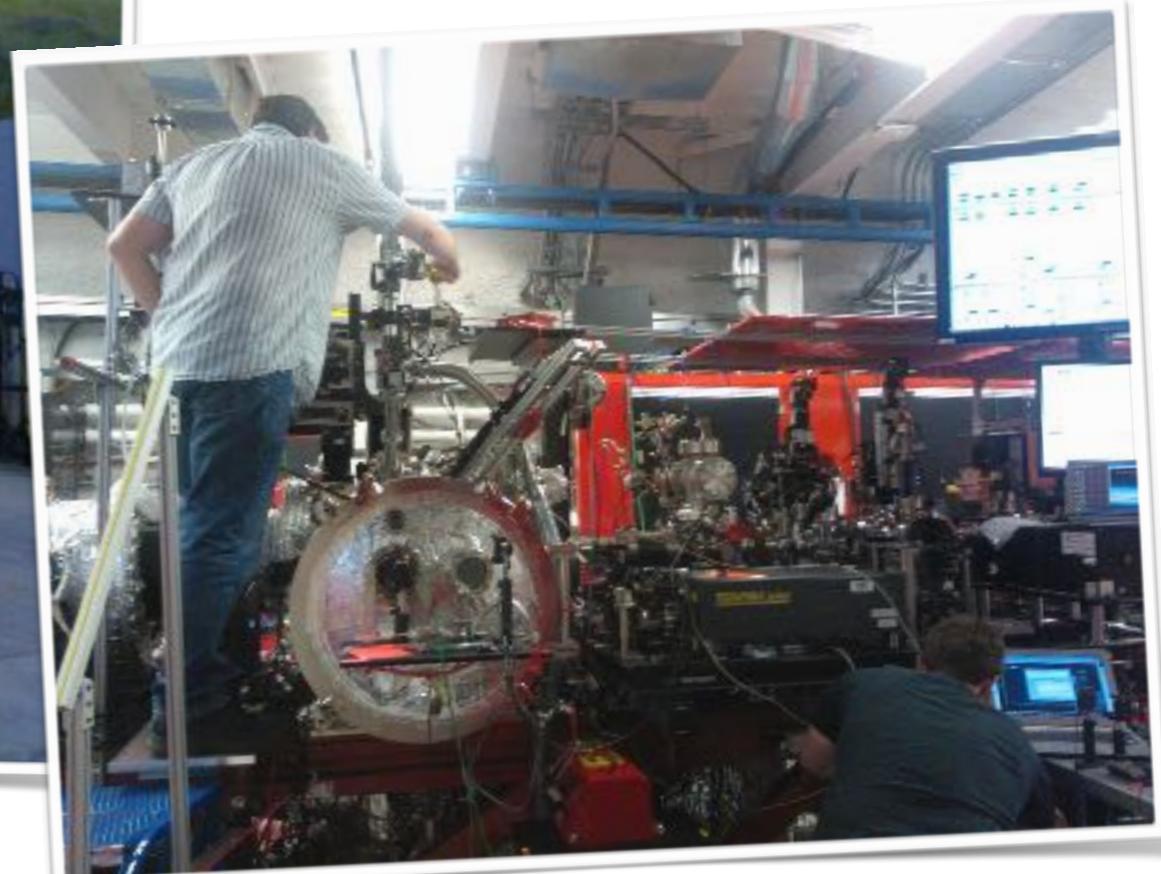
but hey, this is just a model...

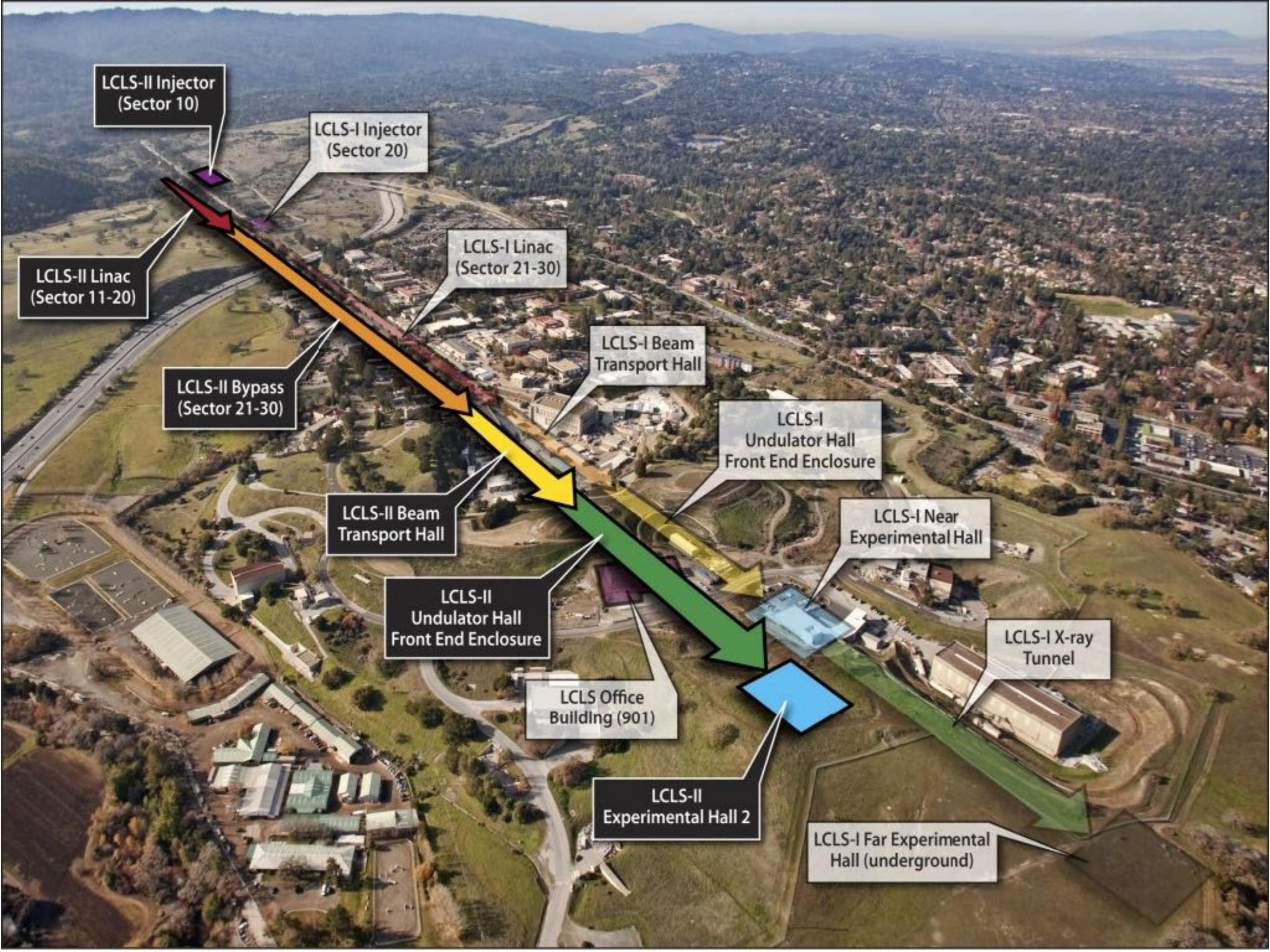
difficult to verify validity, until now

Femtosecond time-resolved x-ray diffraction free electron lasers

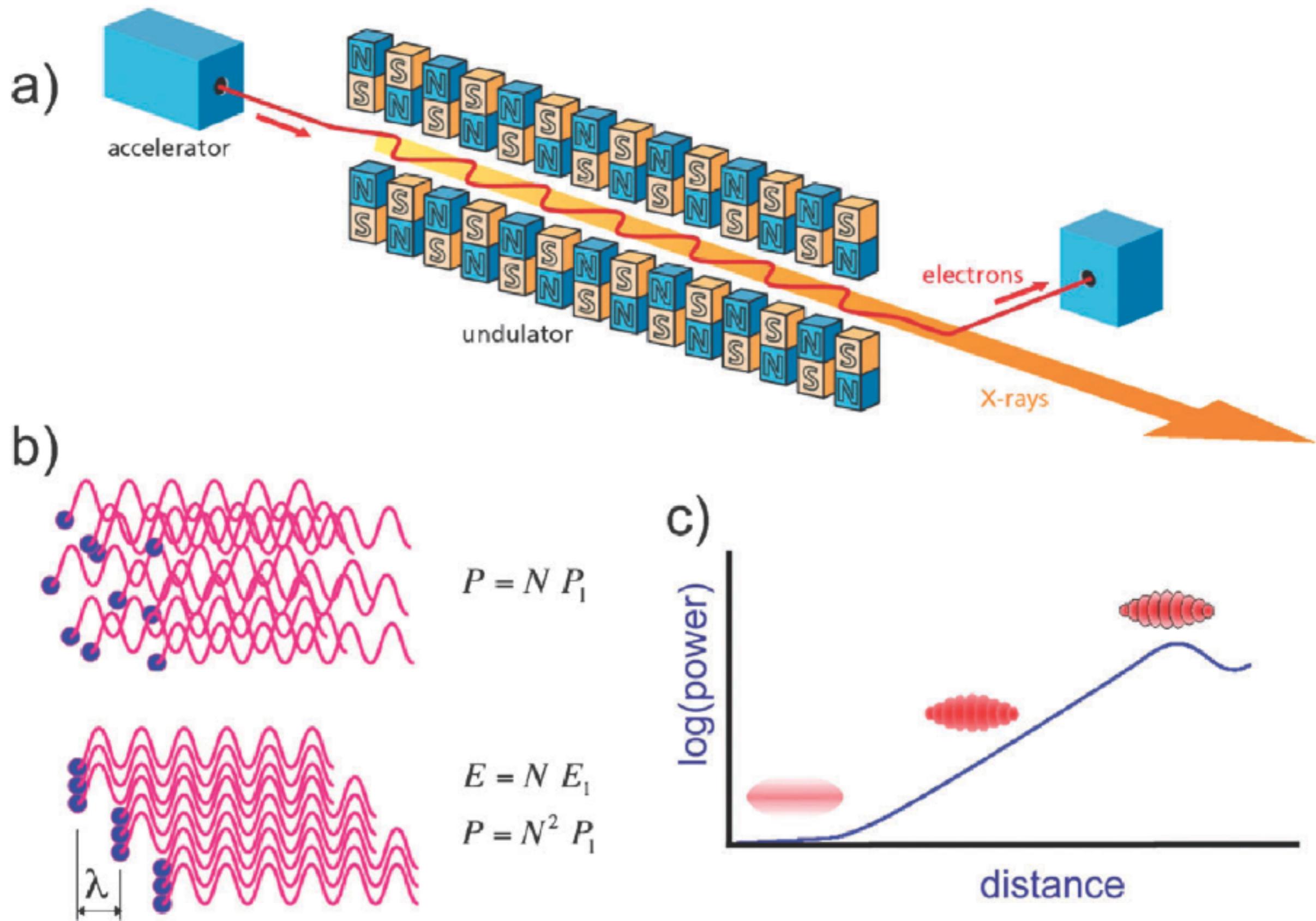
Linear Coherent Light Source in Stanford

Coherent X-ray Imaging (CXI)





Free electron laser

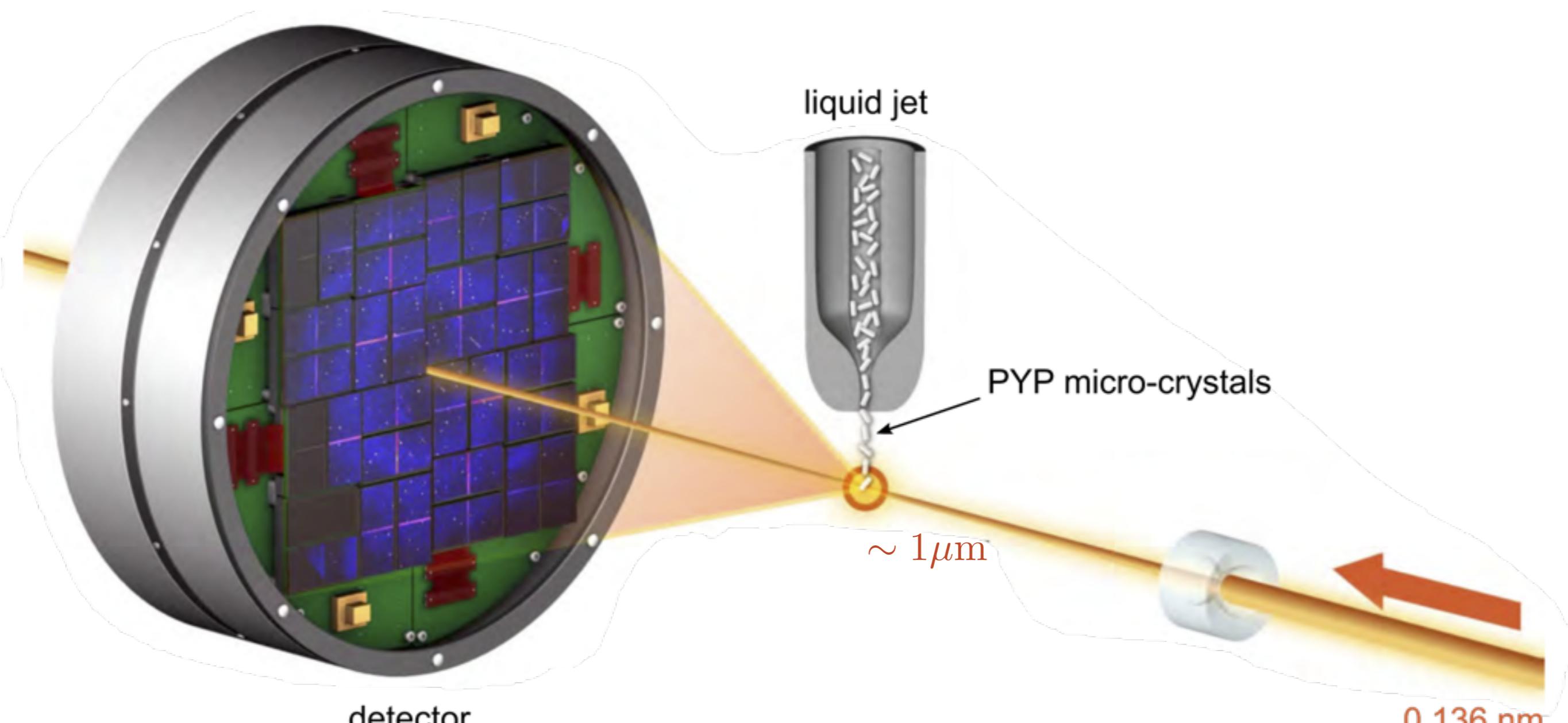


Serial femtosecond x-ray crystallography

difficult and destroy

outrun radiation damage

nano crystals

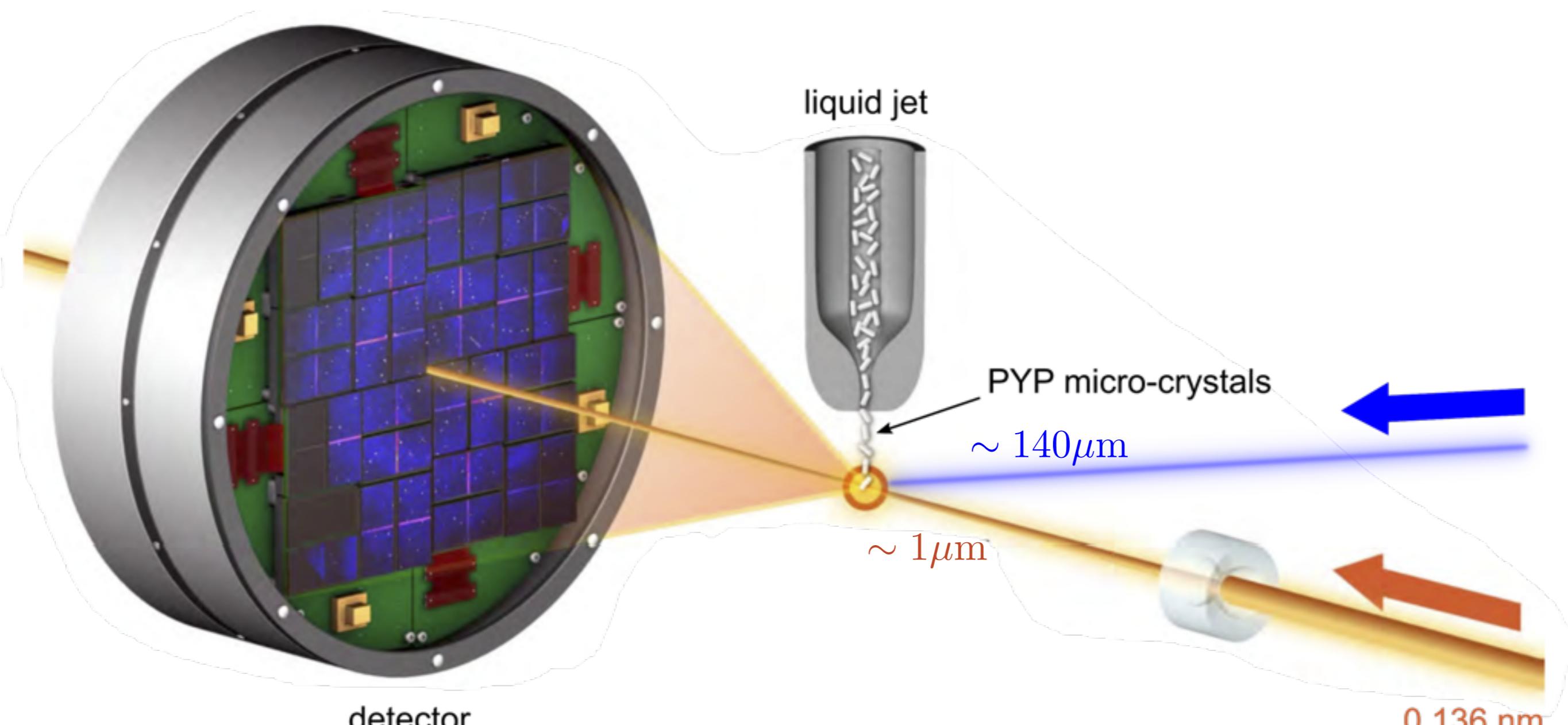


Serial femtosecond x-ray crystallography

diffract and destroy

time-resolved: pump-probe

synchronization: timing tool

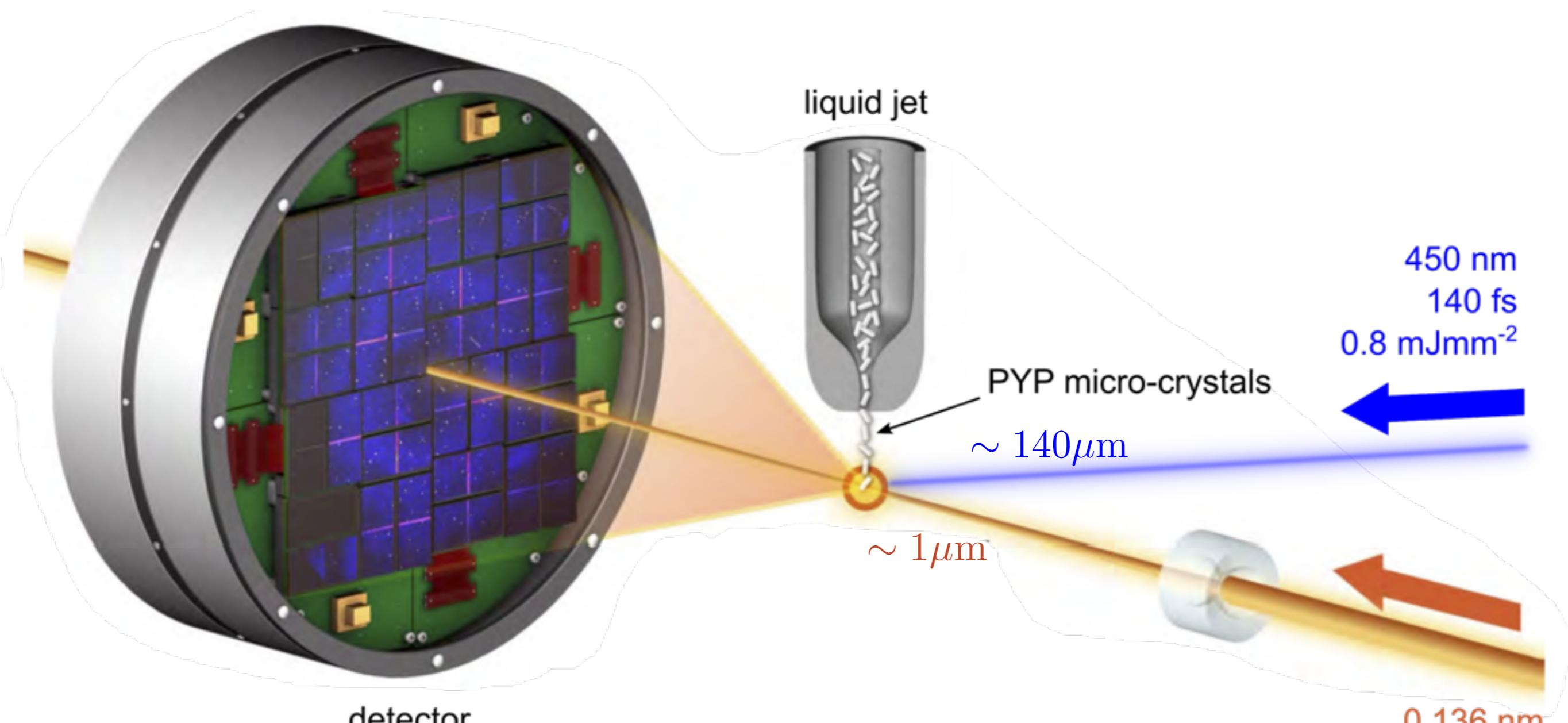


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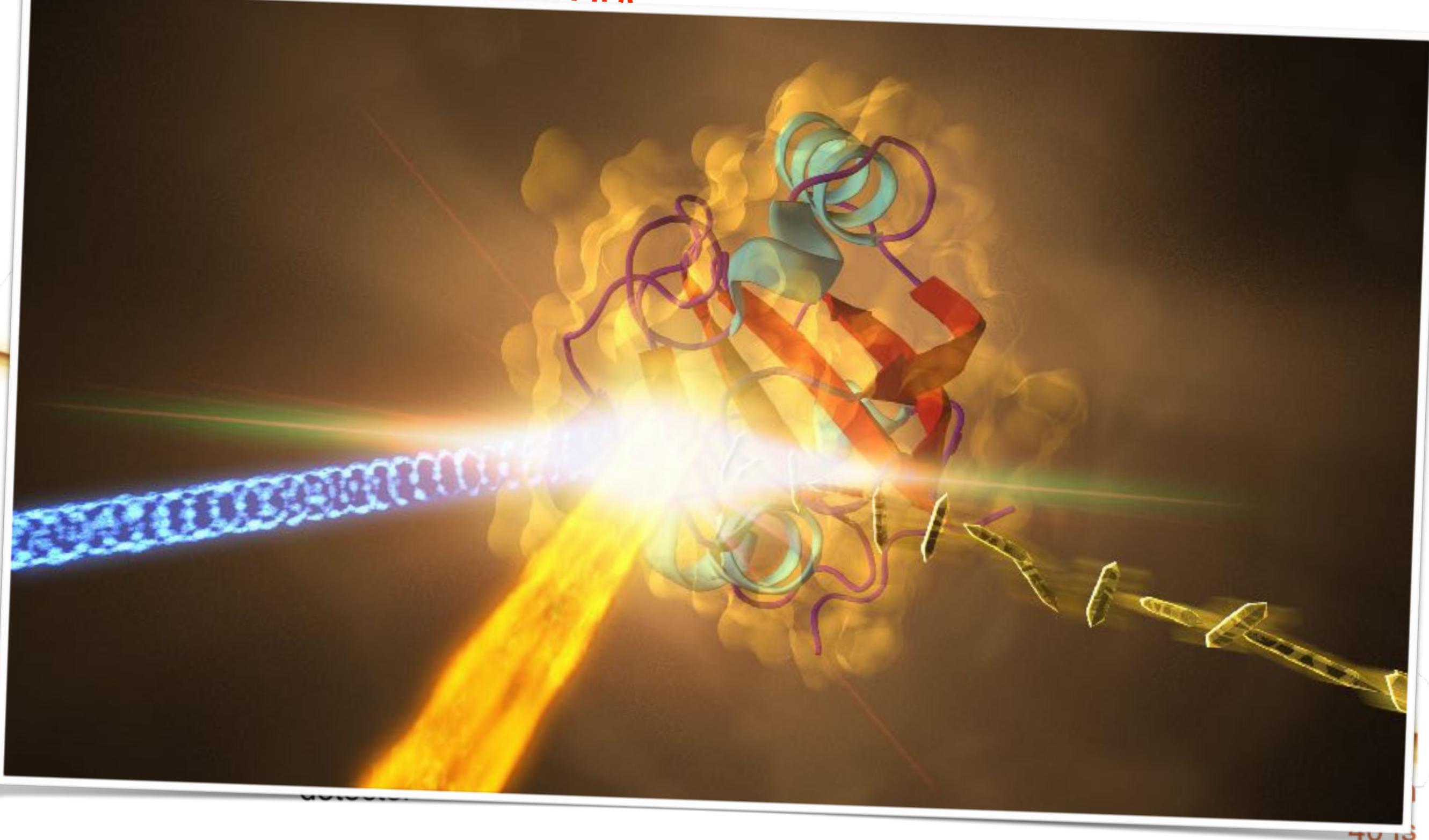
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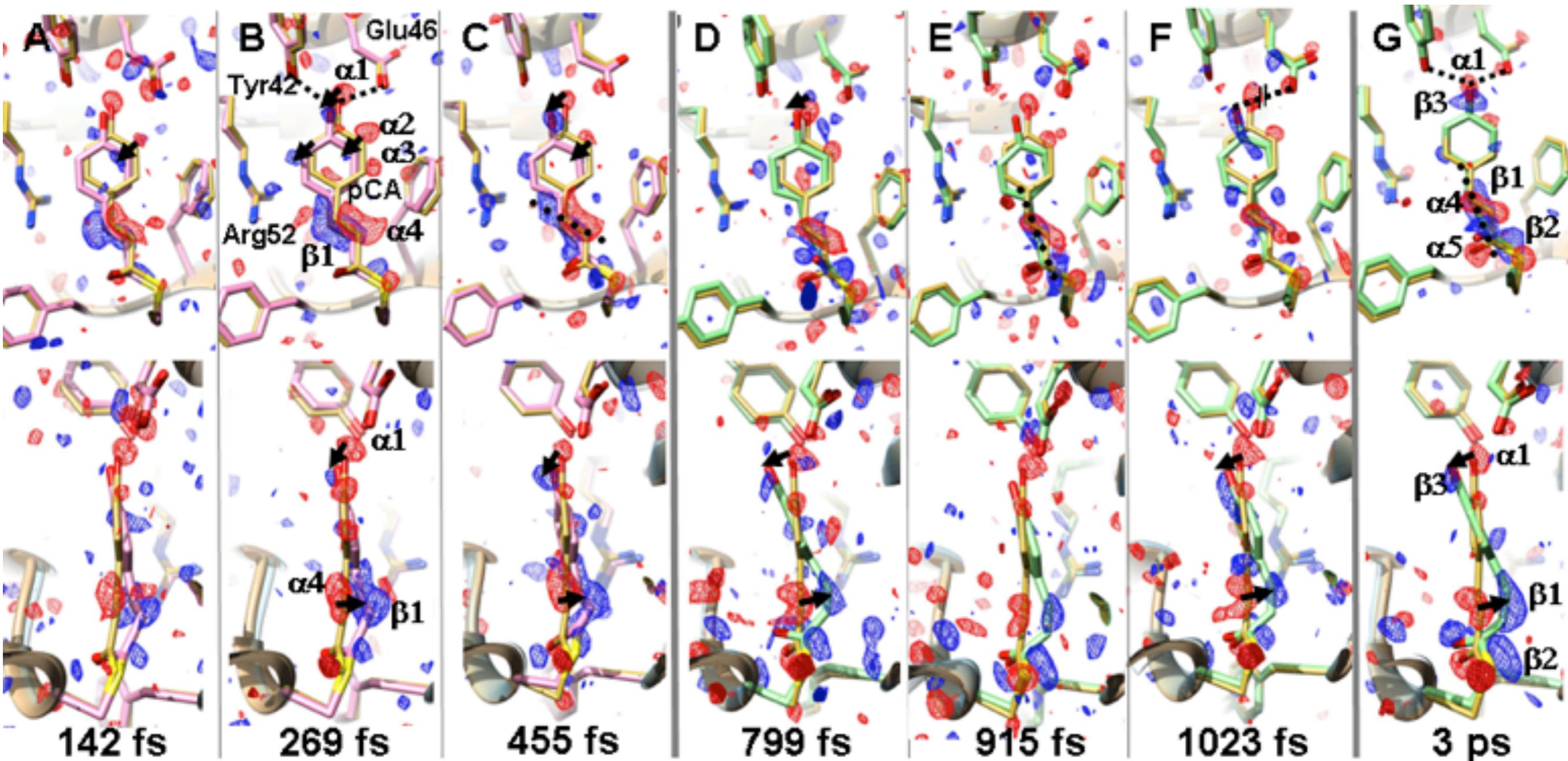
• ~~laser-pump-probe~~



Serial femtosecond x-ray crystallography

indexing, timing tool sorting, merging & refinement

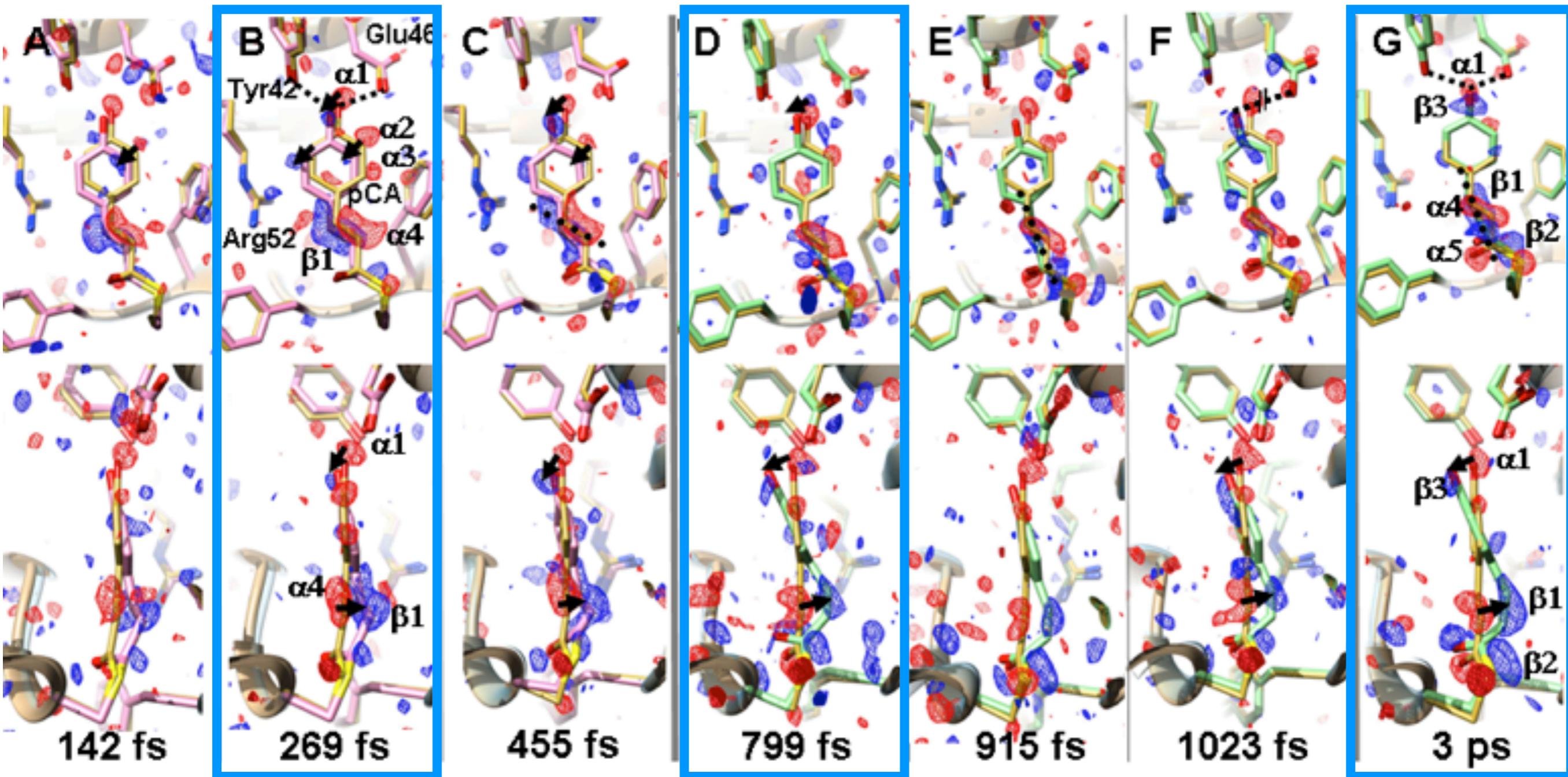
seven difference density maps from 100 femto- to 3 picosecond



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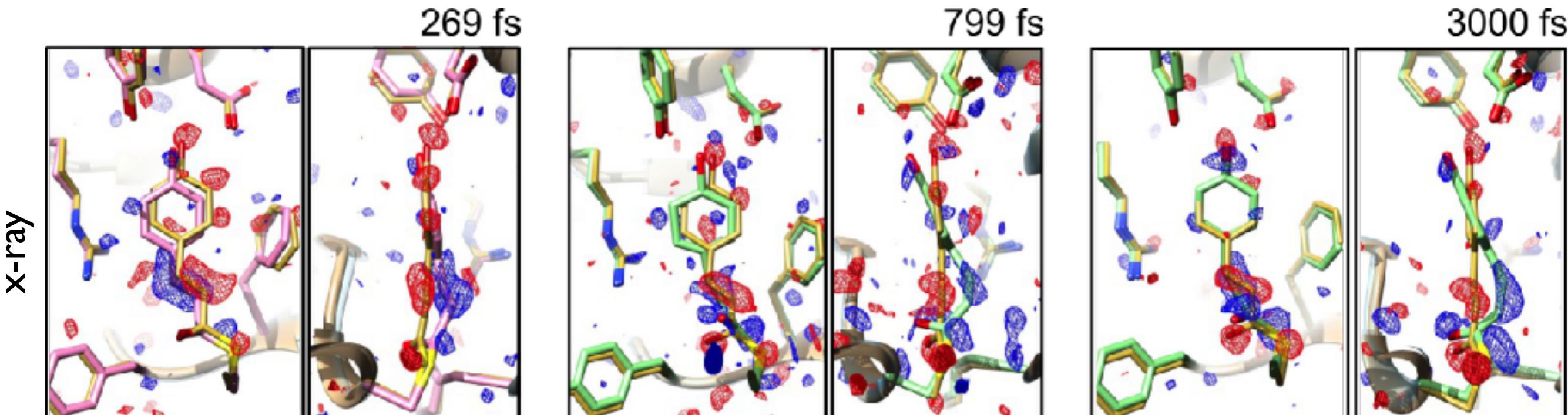
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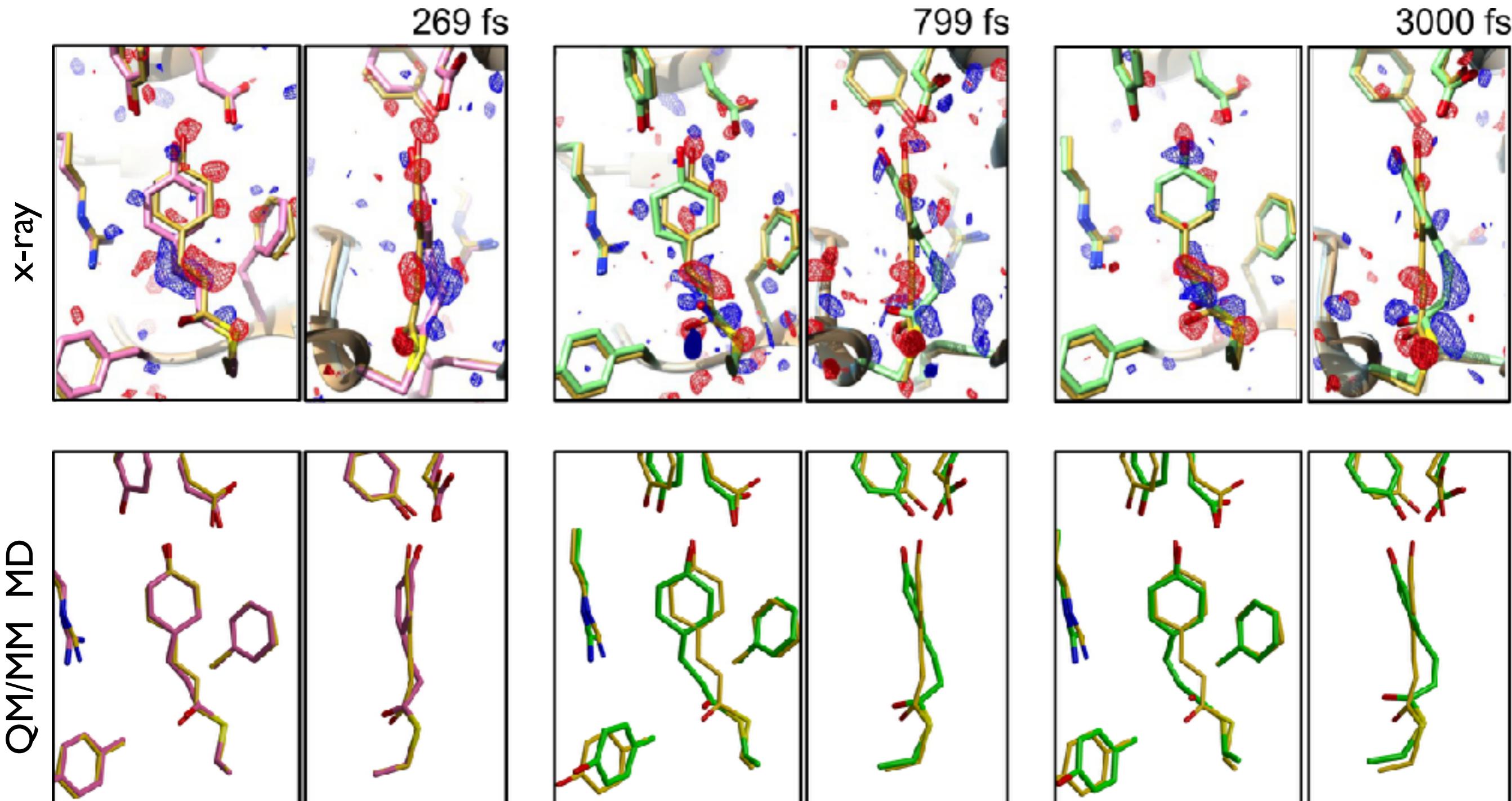
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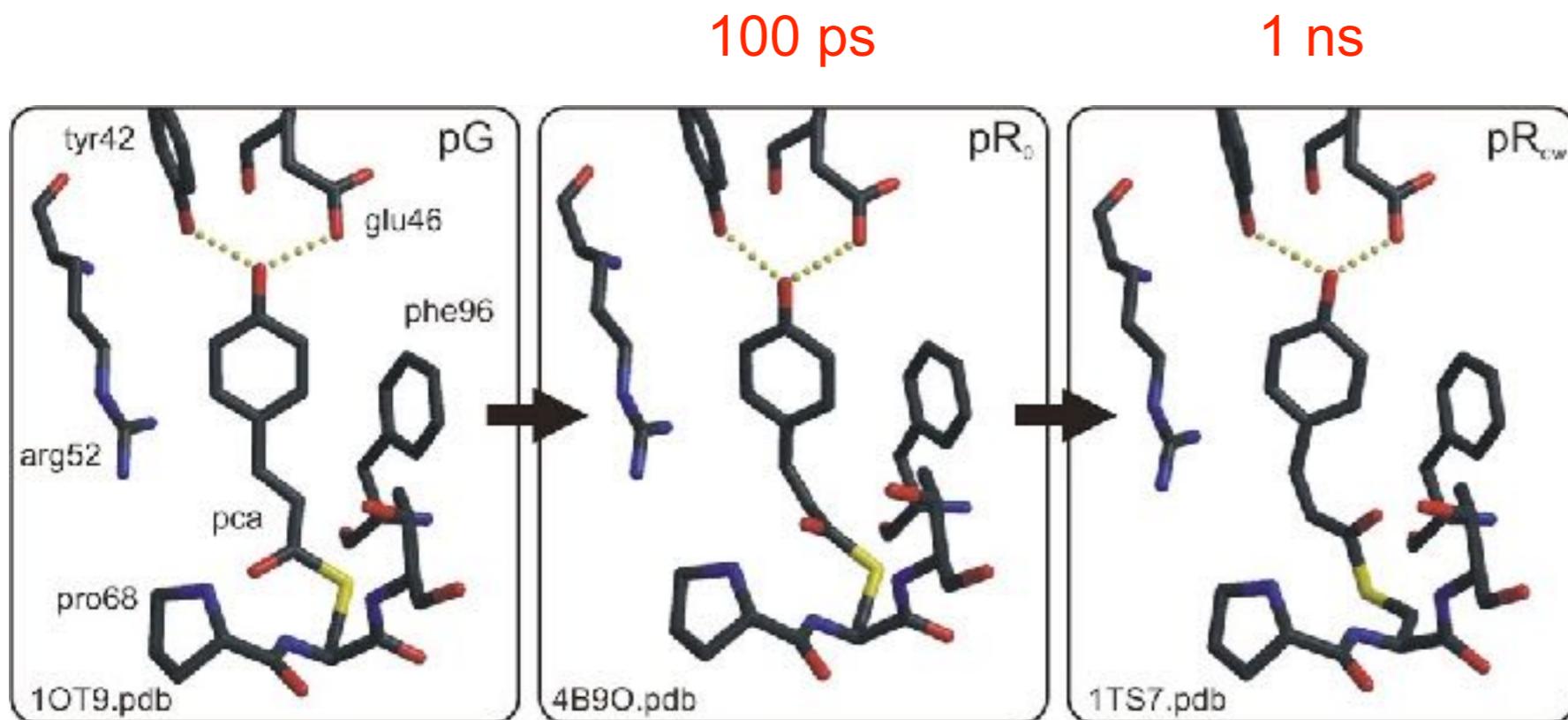
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From picosecond to nanosecond

previous x-ray diffraction studies @ synchrotrons

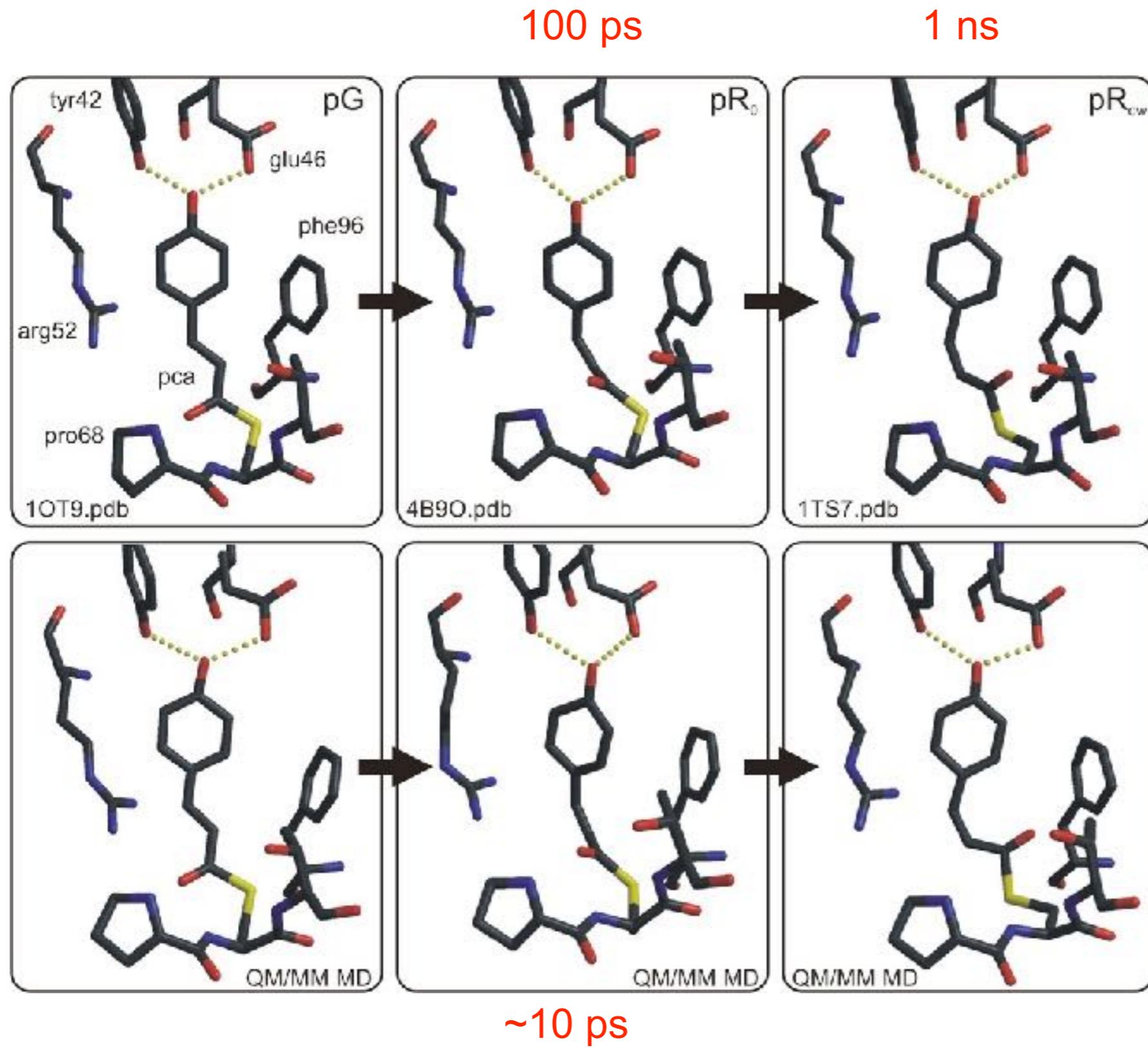


Schotte et al.
PNAS 107 (2012) 76

Ihee et al.
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MD simulations
CAS(10,9)/6-31G*/Amber03

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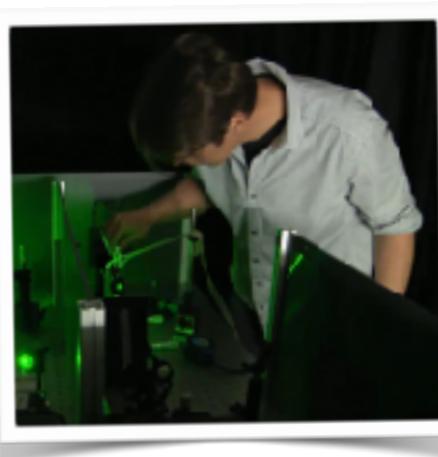
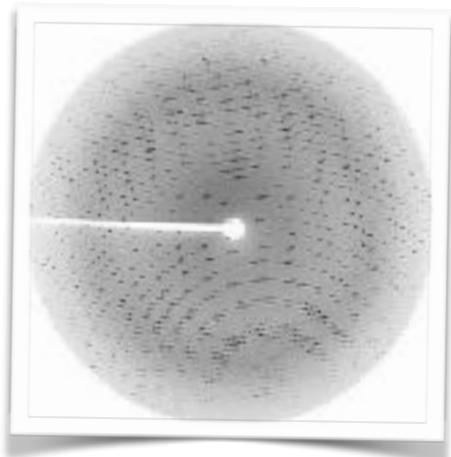
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fs time & Å spacial resolution



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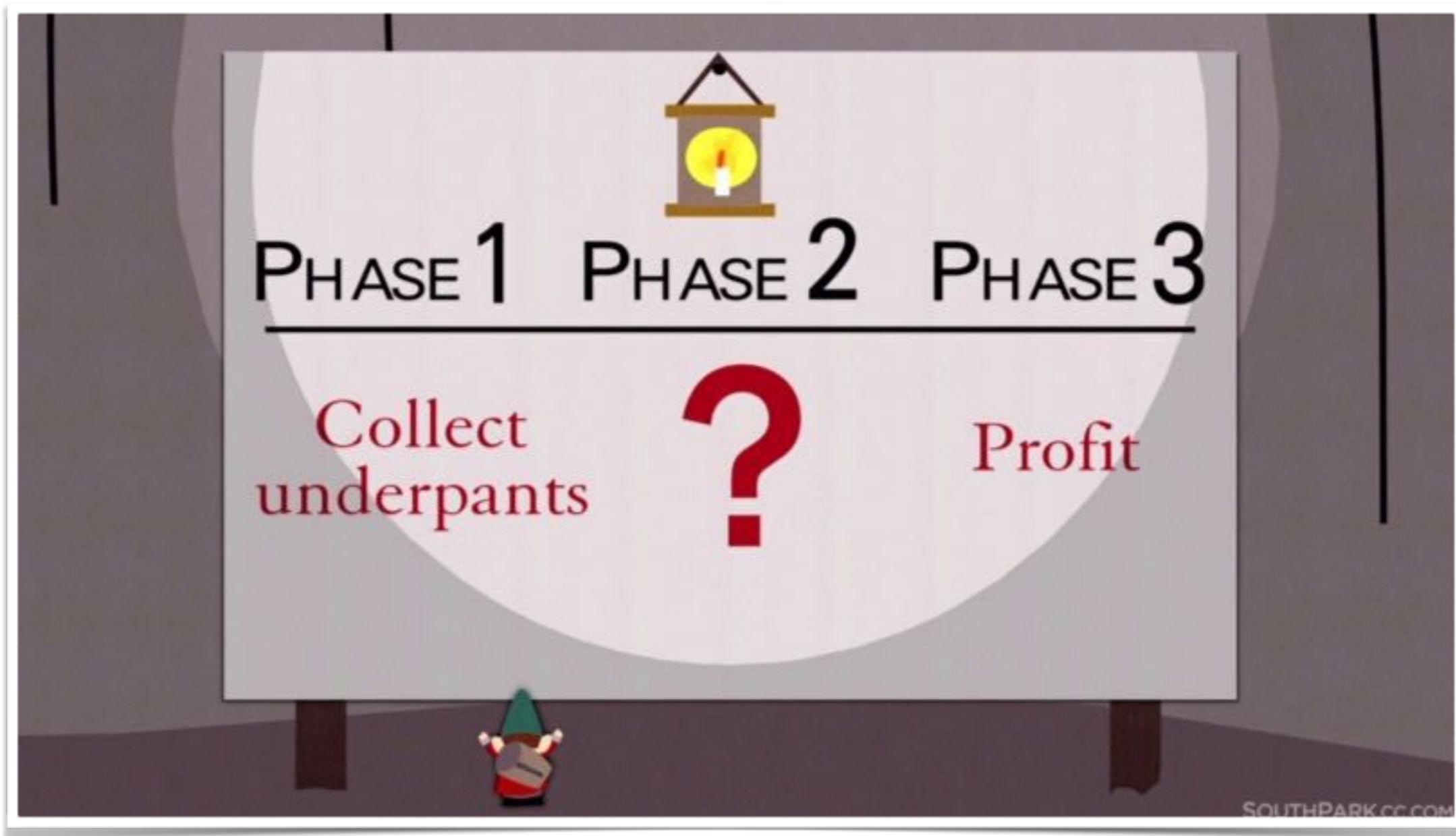
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Sisu.csc.fi: 1688 TFlop/s

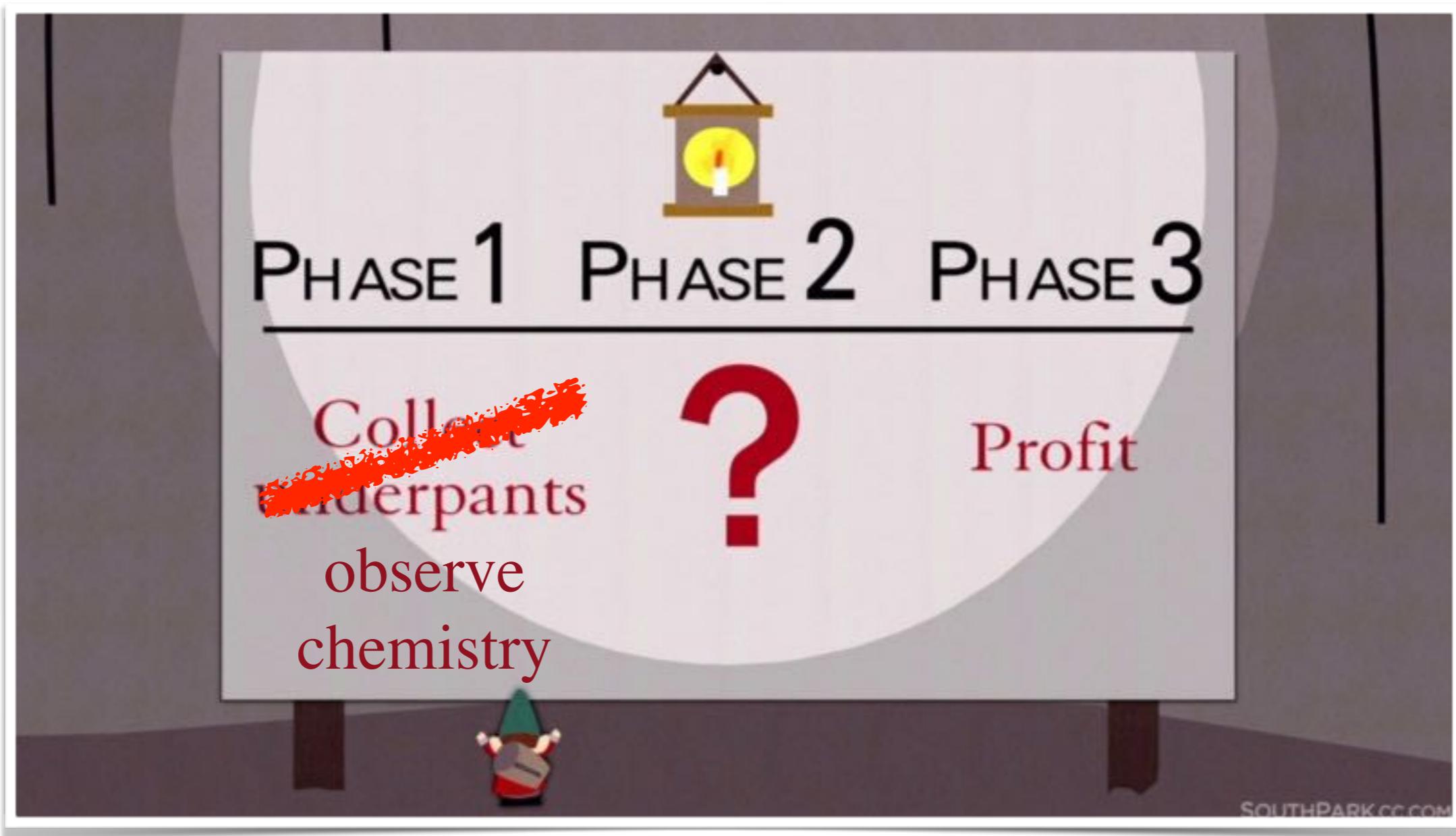
The bigger picture \$\$\$

South Park's Underpants Gnomes' Profit Plan



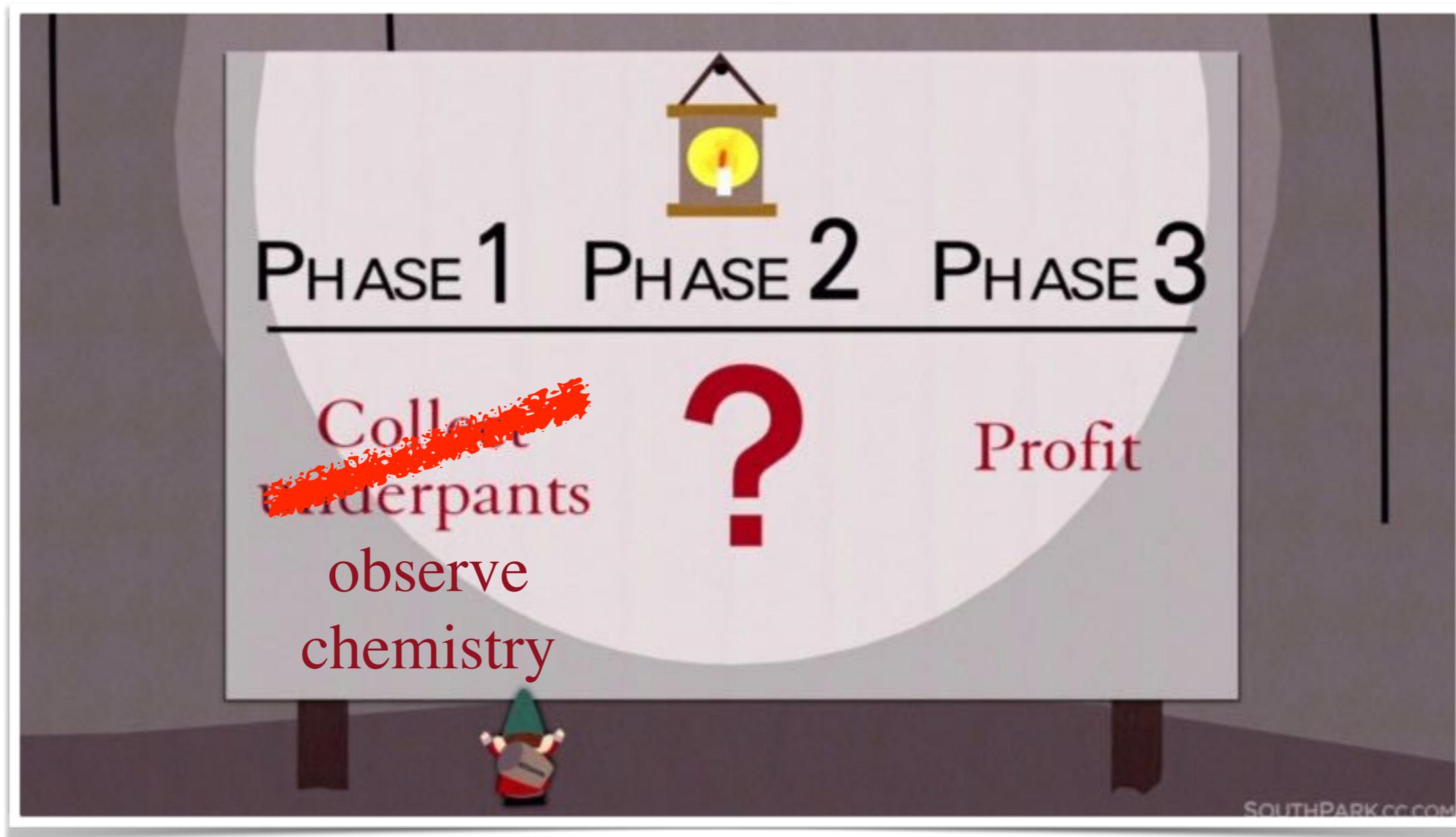
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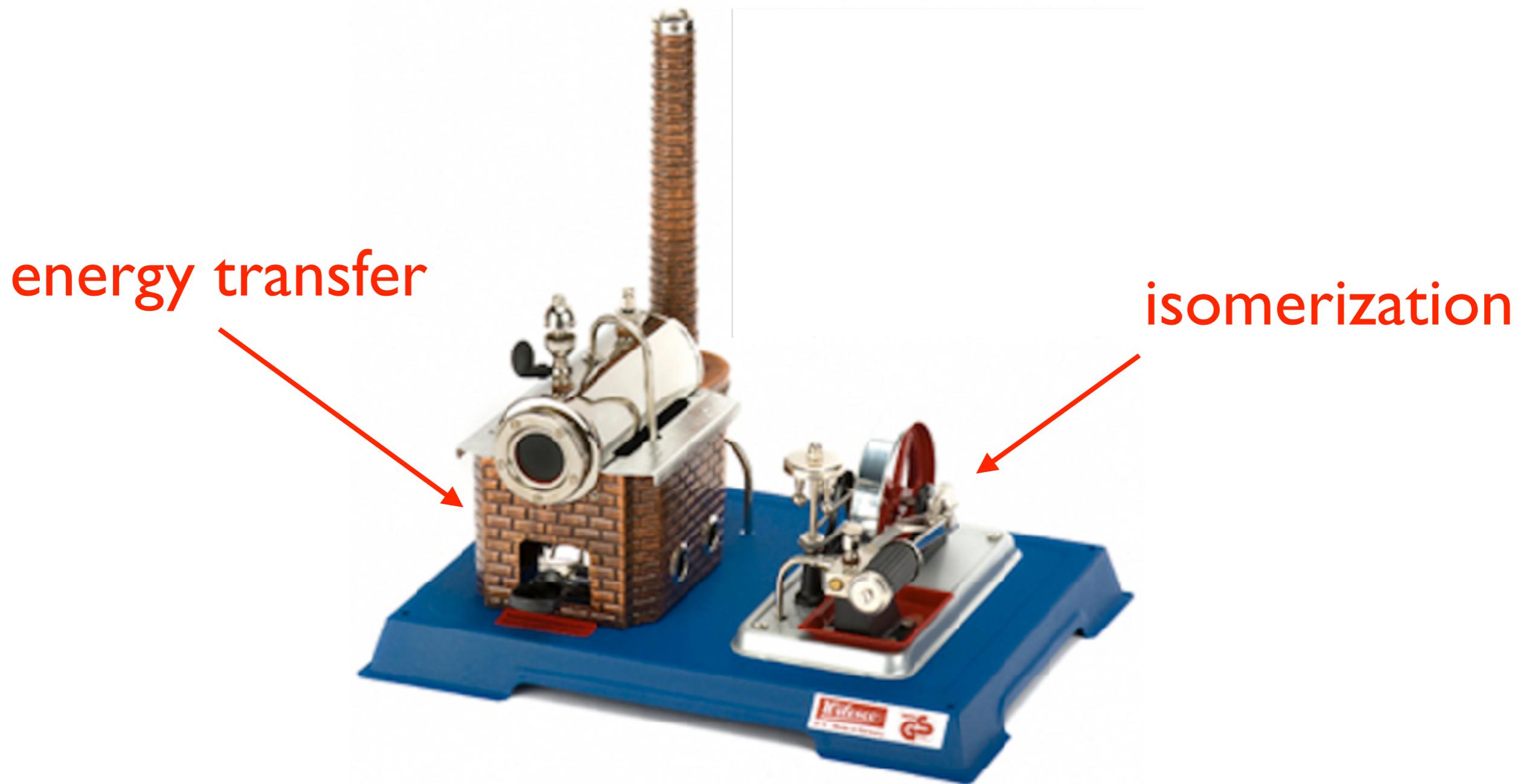
South Park's Underpants Gnomes' Profit Plan



our Phase 2 strategy
manipulate chemistry

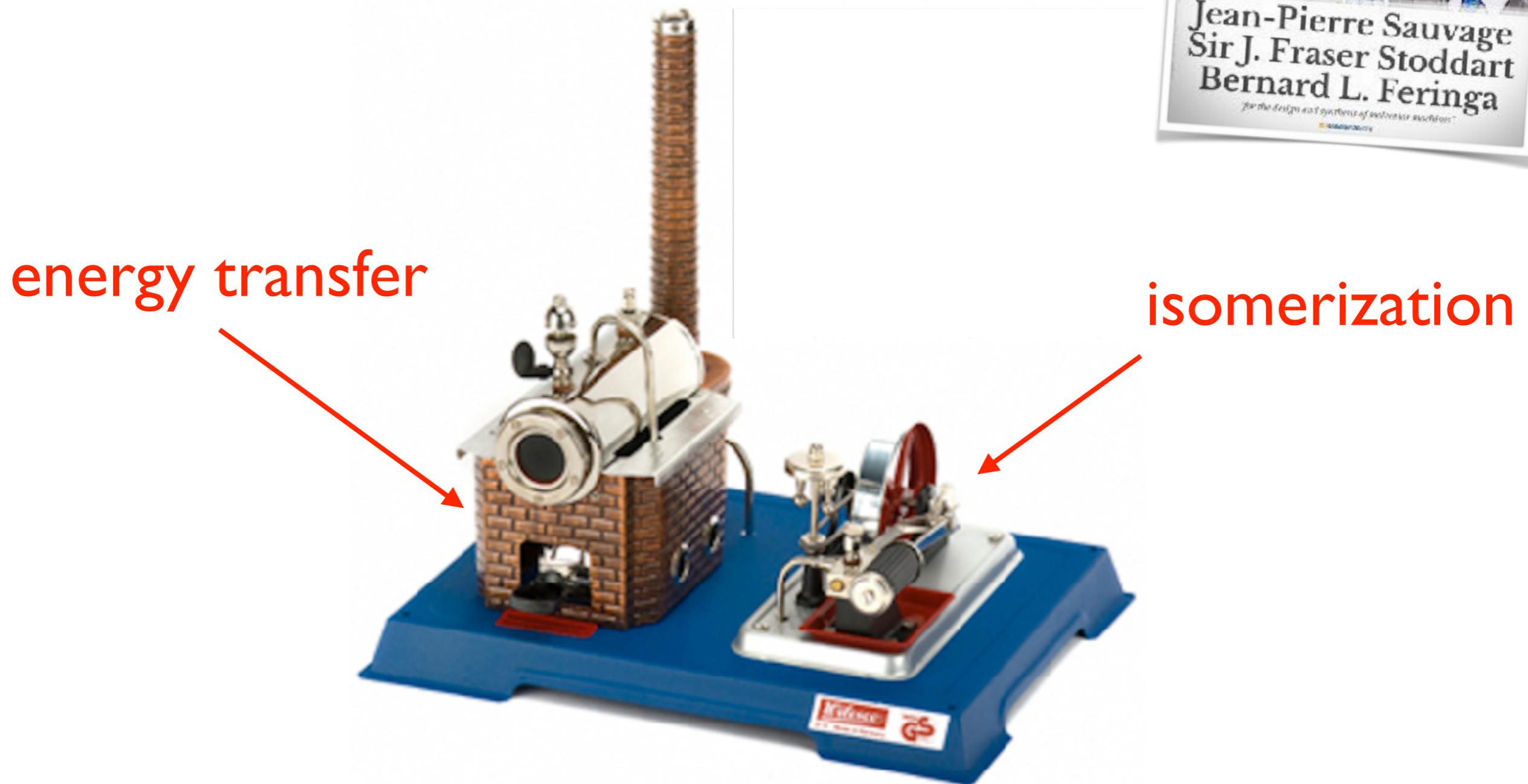
Our ultimate goal

light-fuelled artificial molecular machines



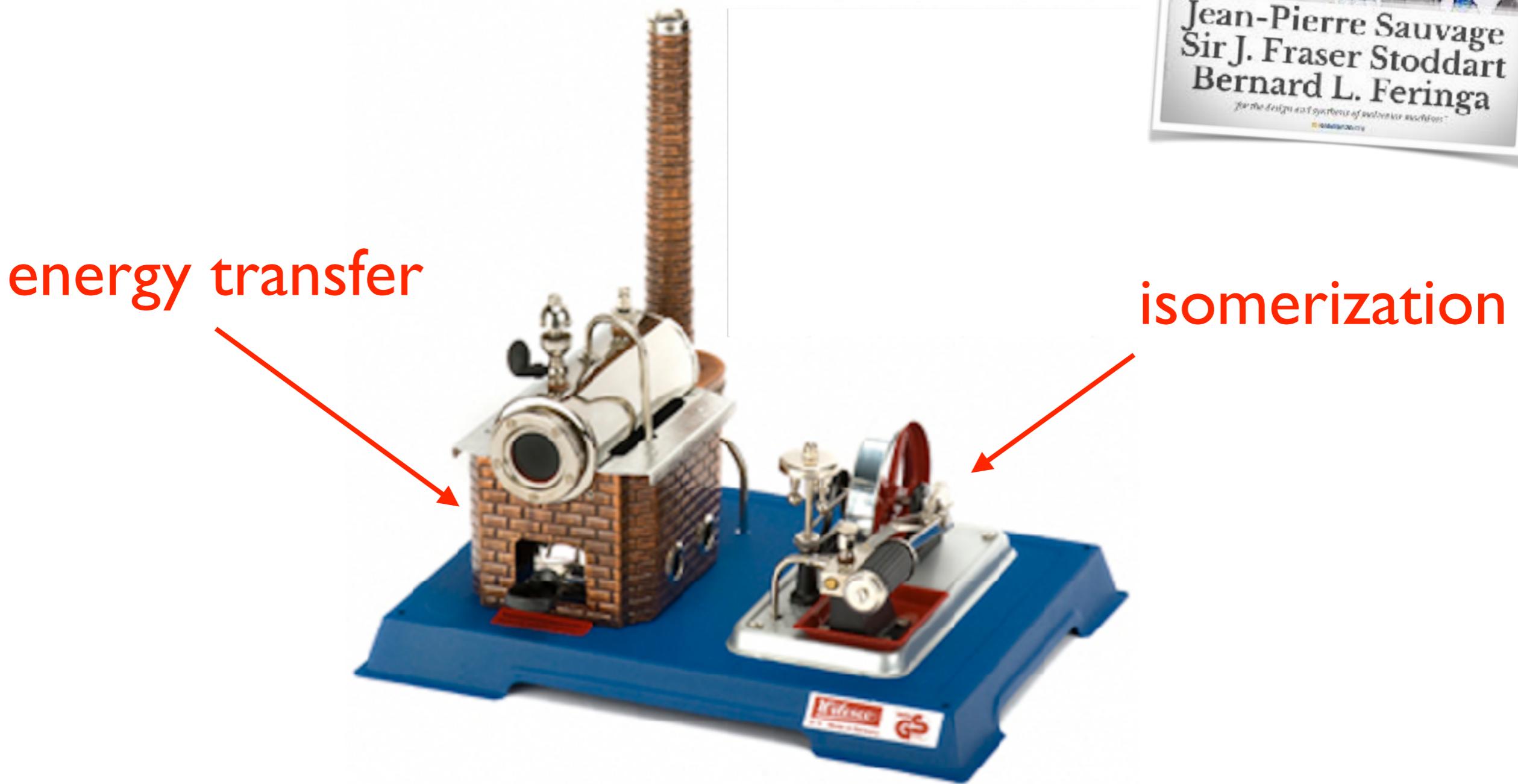
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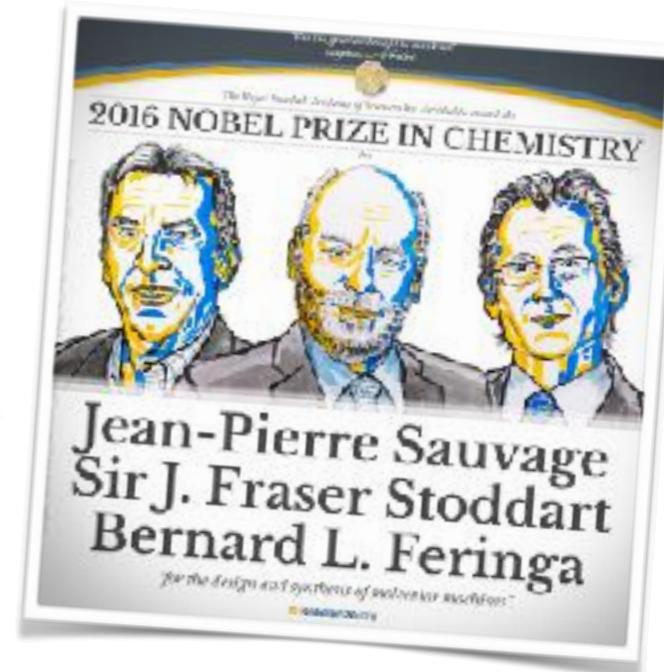


Our ultimate goal

light-fuelled artificial molecular machines



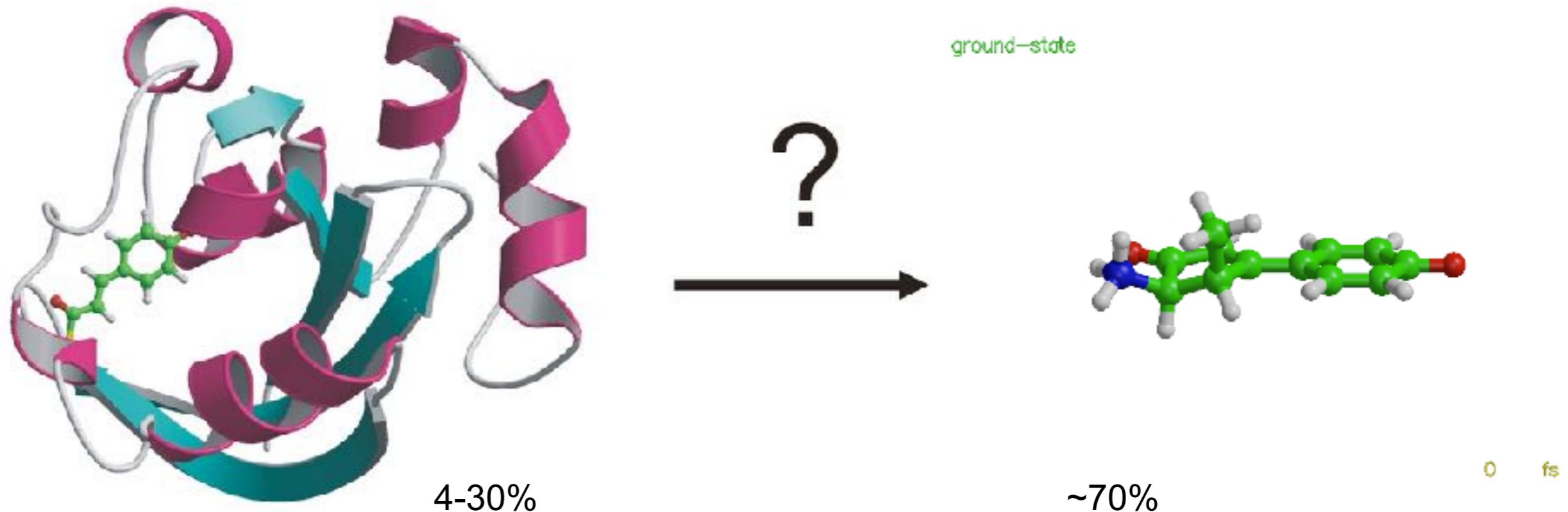
complete understanding of photochemistry required
control & design



Get inspired by nature

e.g. photo-isomerization in photoactive yellow protein

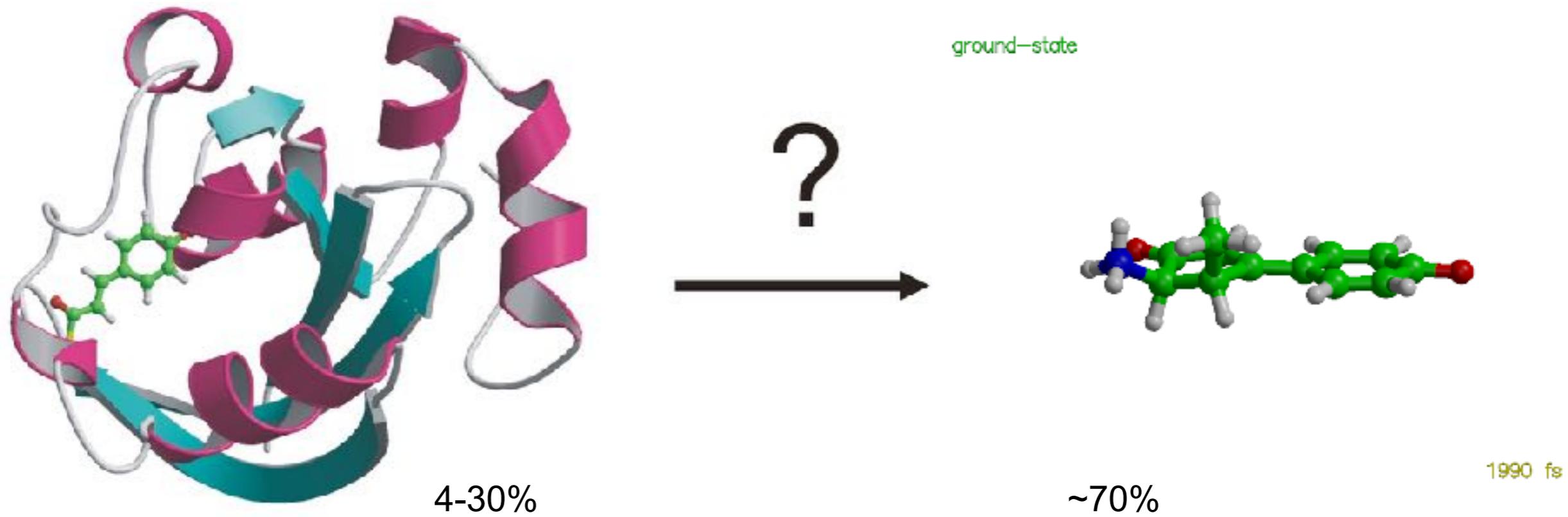
learn & mimic the effect of the protein environment



Get inspired by nature

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learn & mimic the effect of the protein environment



seemed like a good idea at first, but

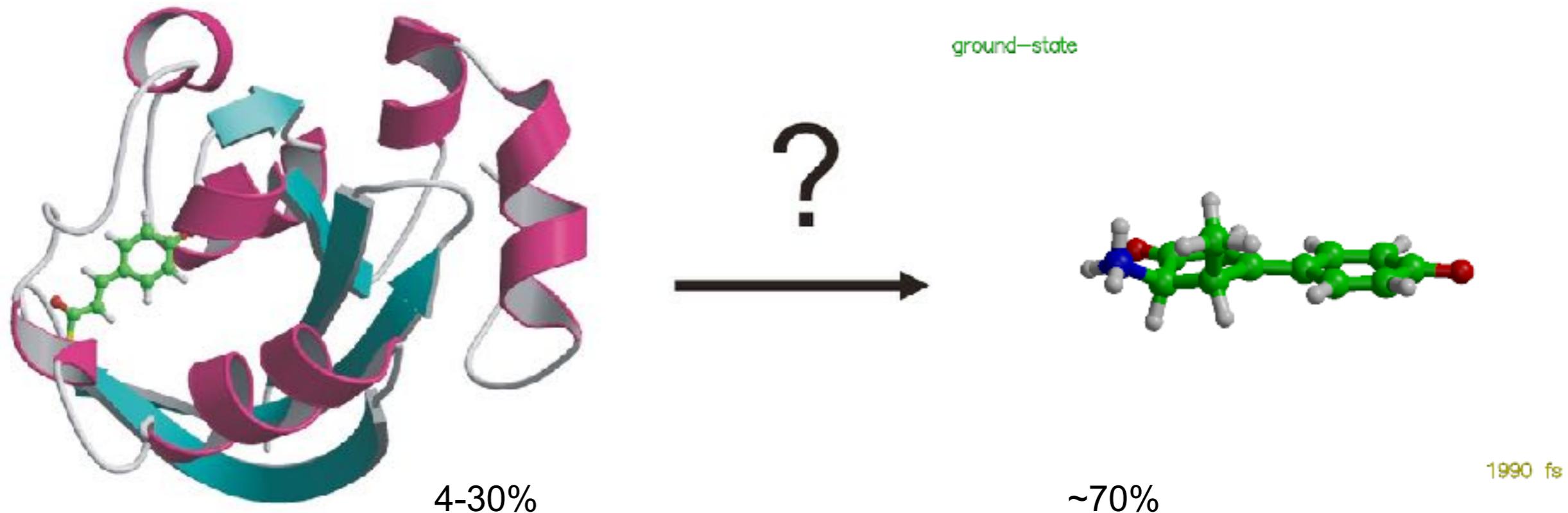
difficult to improve functionality

difficult to transfer functionality

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e.g. photo-isomerization in photoactive yellow protein

learn & mimic the effect of the protein environment



seemed like a good idea at first, but

difficult to improve functionality

difficult to transfer functionality

try something else instead!



with Jussi Toppari

Manipulating photo-chemistry

Green Fluorescent Protein (Ser65Thr/His148Asp)

ultra-fast excited-state proton transfer



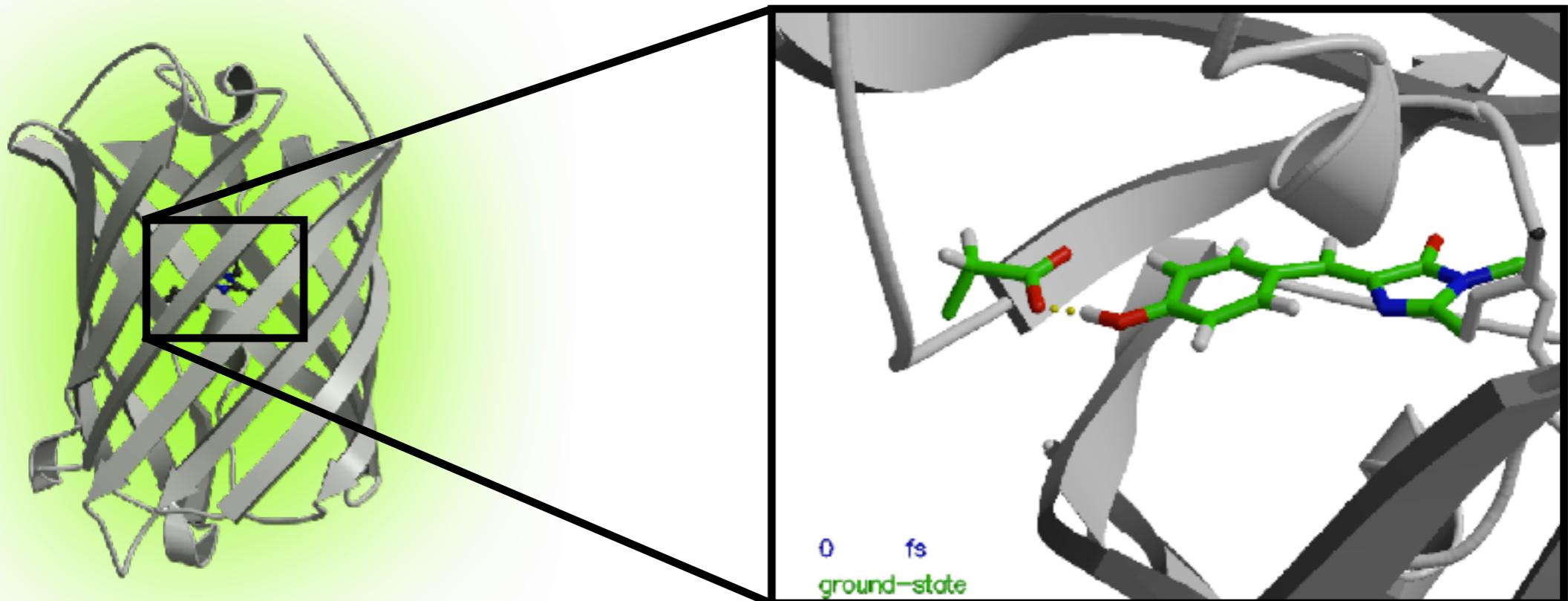
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Calvin
Luk

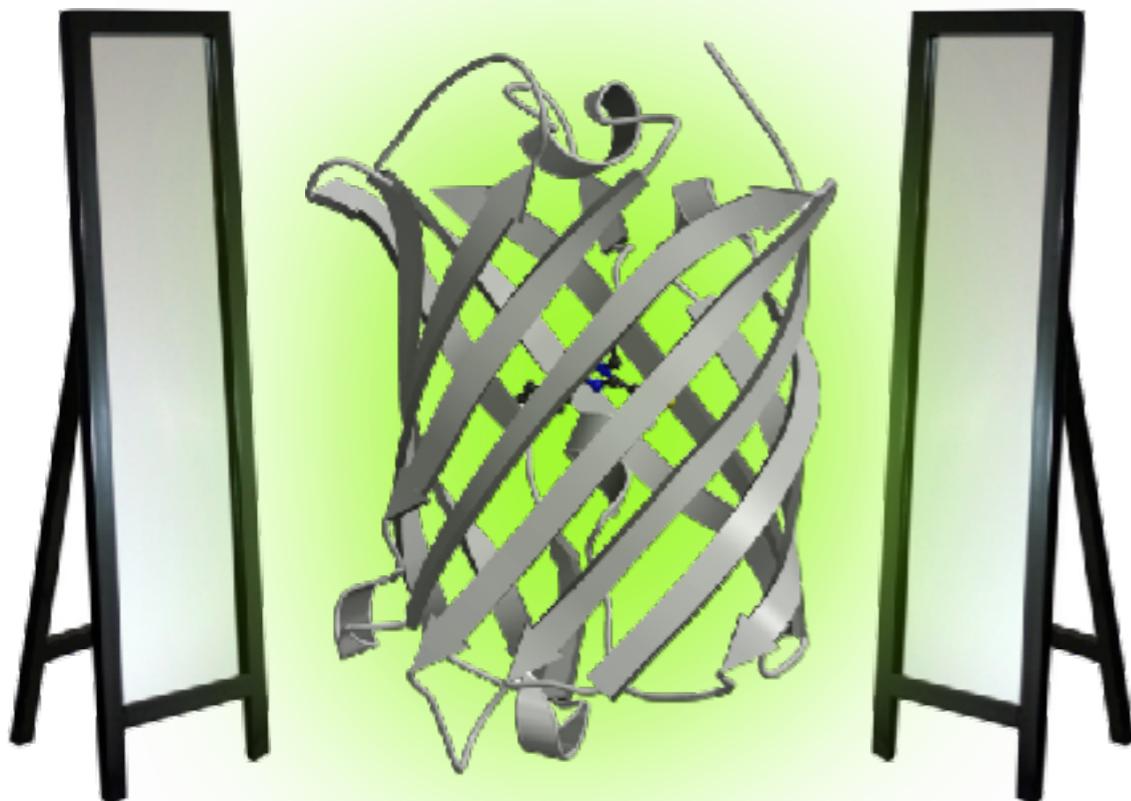


CASSCF(6,6)/3-21G//Amber03

Manipulating photo-chemistry with mirrors

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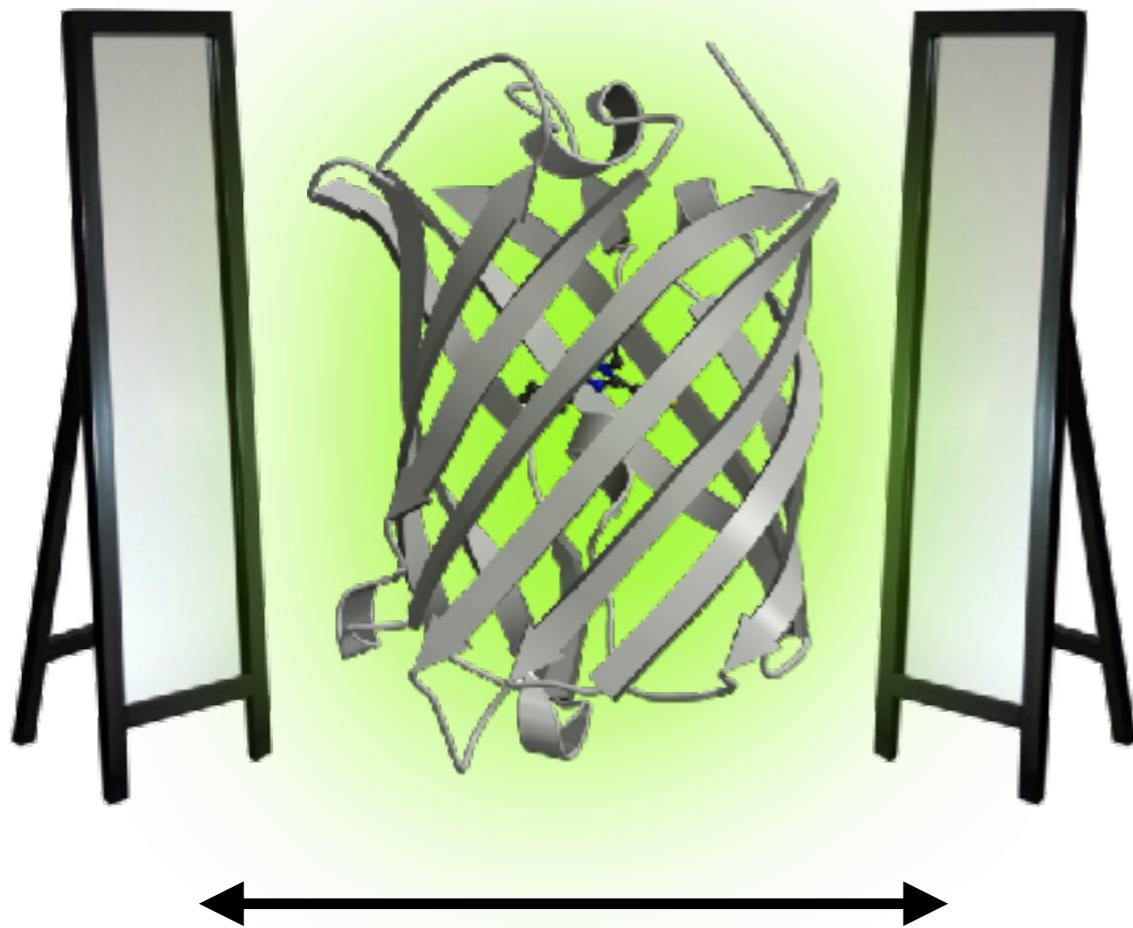
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$$\frac{1}{2} \lambda_{\max}$$

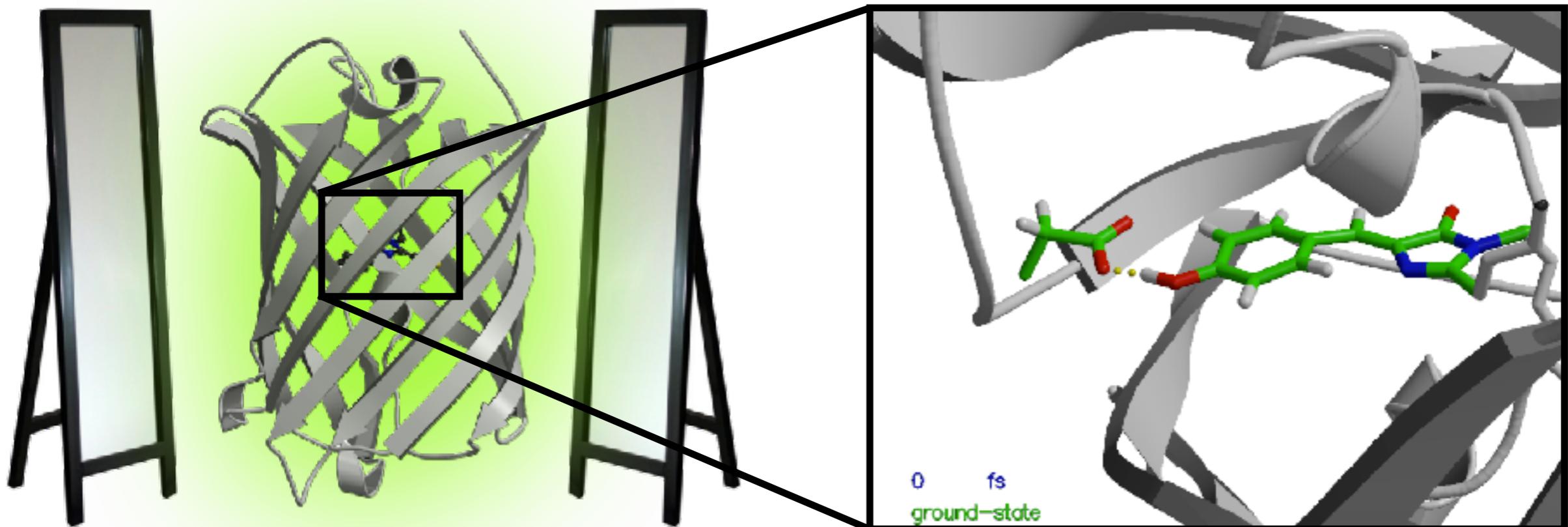
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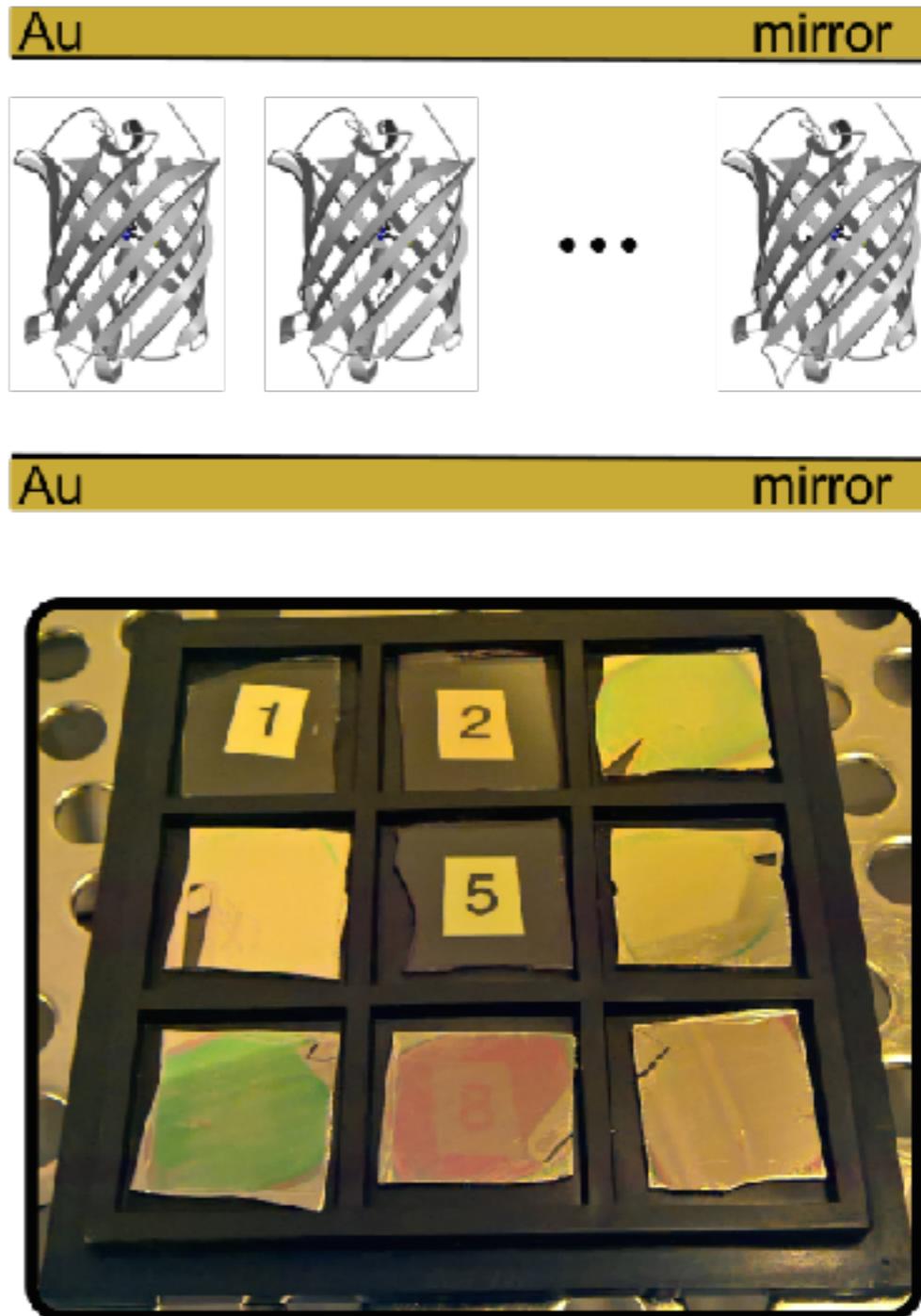
Manipulating photo-chemistry with mirrors

Green Fluorescent Protein

excited-state proton transfer



=



Mikael
Kautto



Satu
Mustalahti

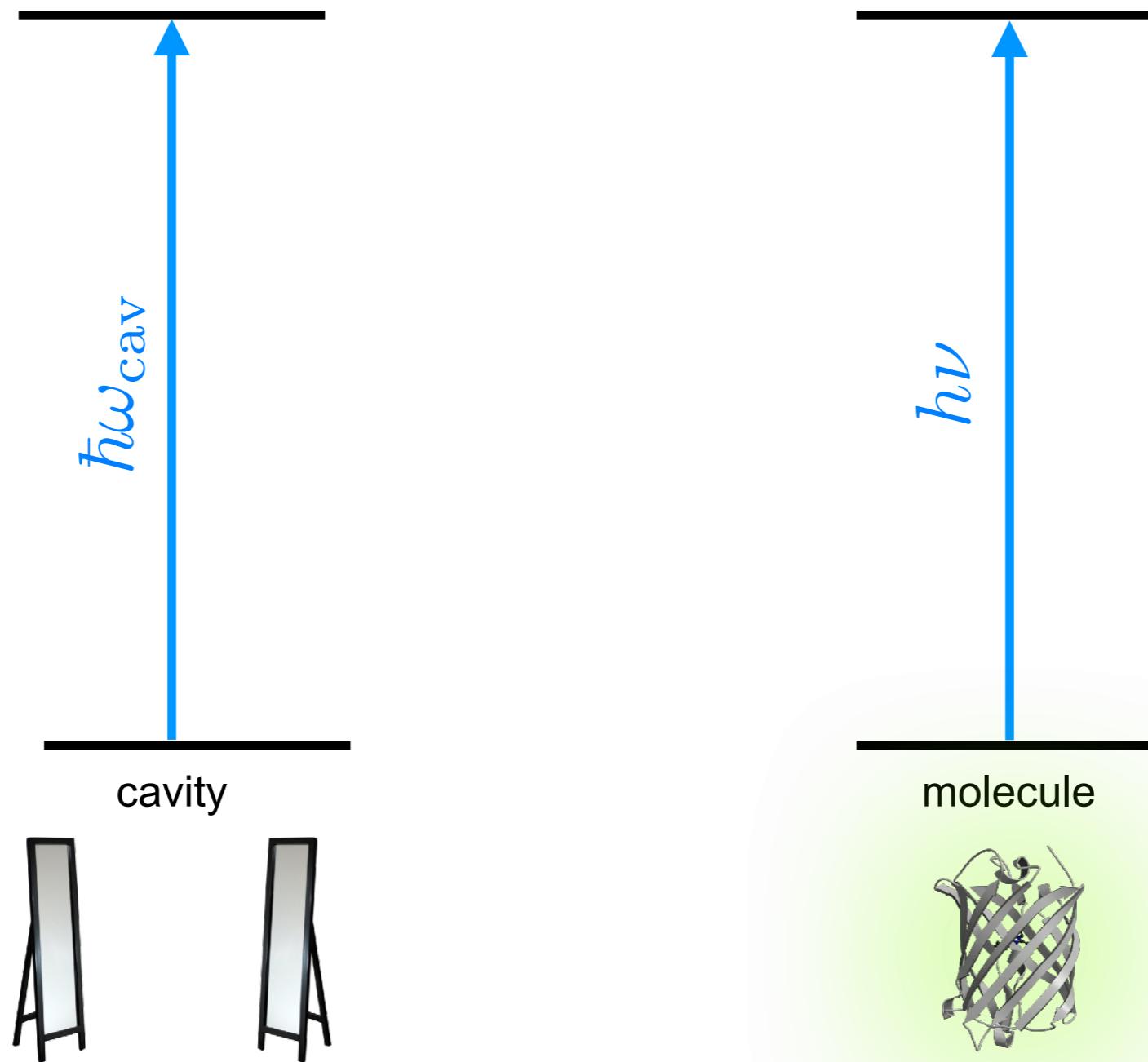


Eero
Hulkko

Why does the photochemistry change?

strong coupling with confined light (cavity QED)

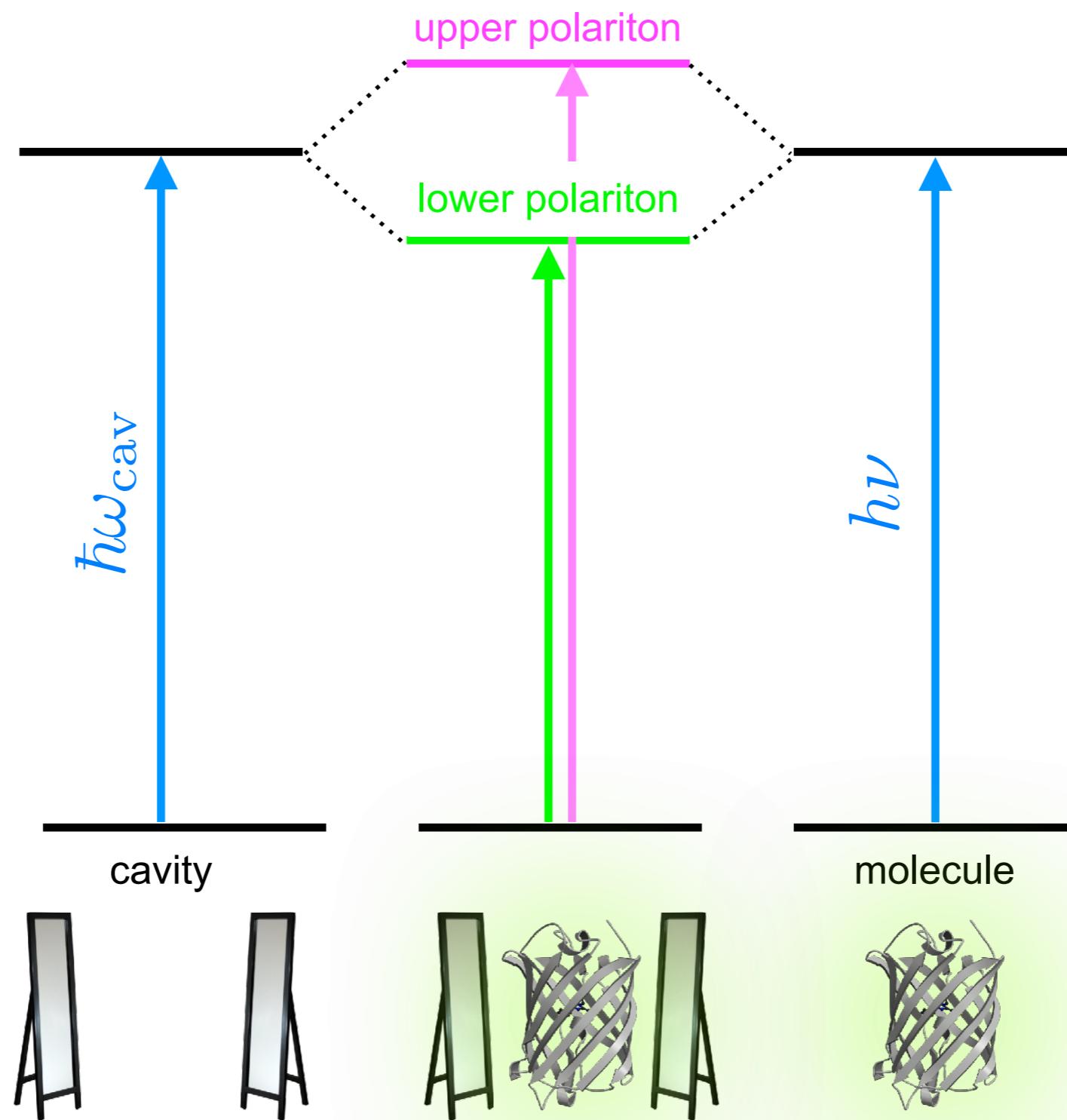
light-matter hybrid states: polaritons



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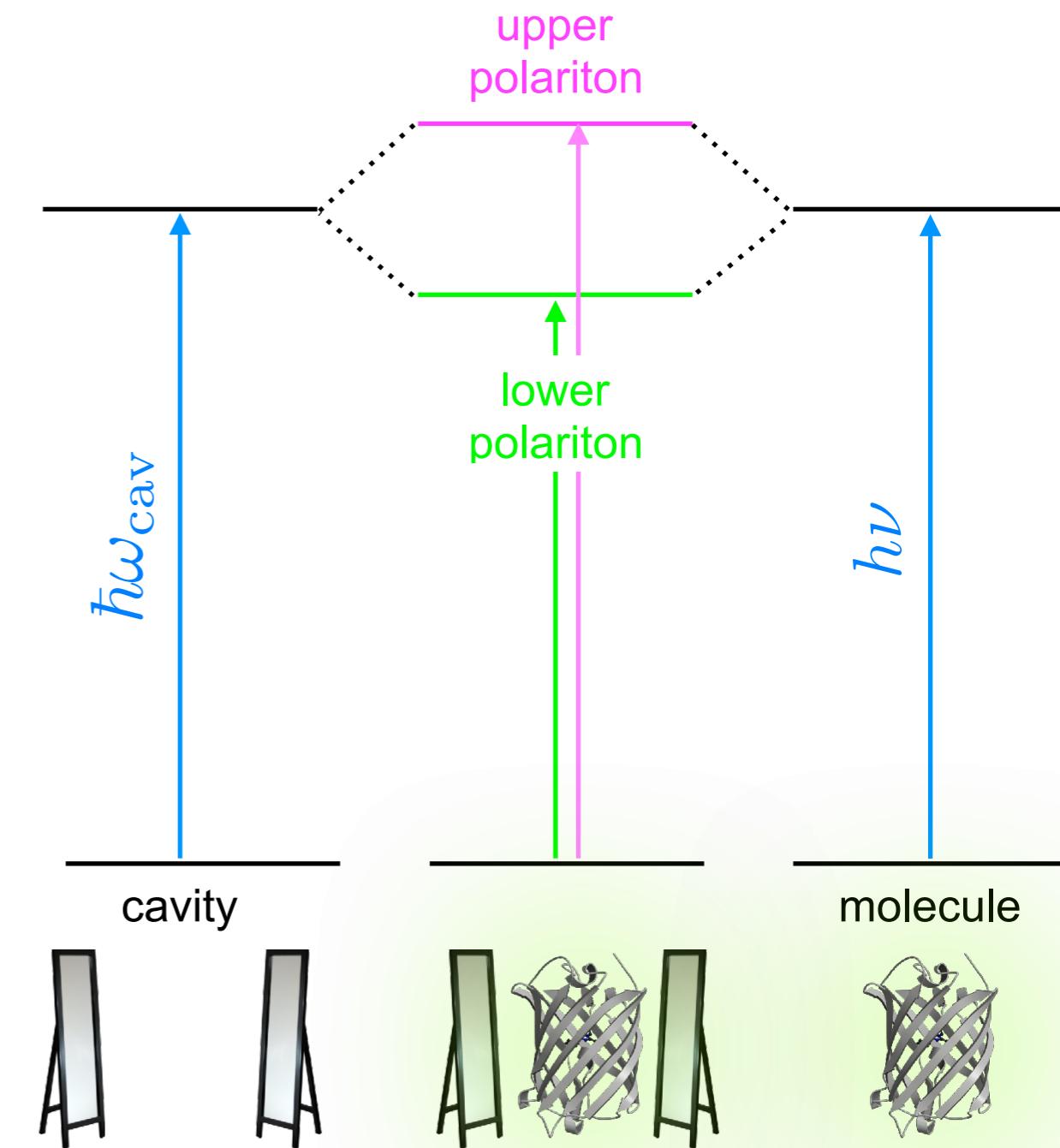


Why does the photochemistry change?

strong coupling with confined light (cavity QED)

light-matter Hamiltonian for one protein (Jaynes-Cummings)

$$\mathbf{H}^{\text{cav}} = \begin{pmatrix} H_{11} & H_{21} \\ H_{12} & H_{22} + \hbar\omega_{\text{cav}} \end{pmatrix}$$



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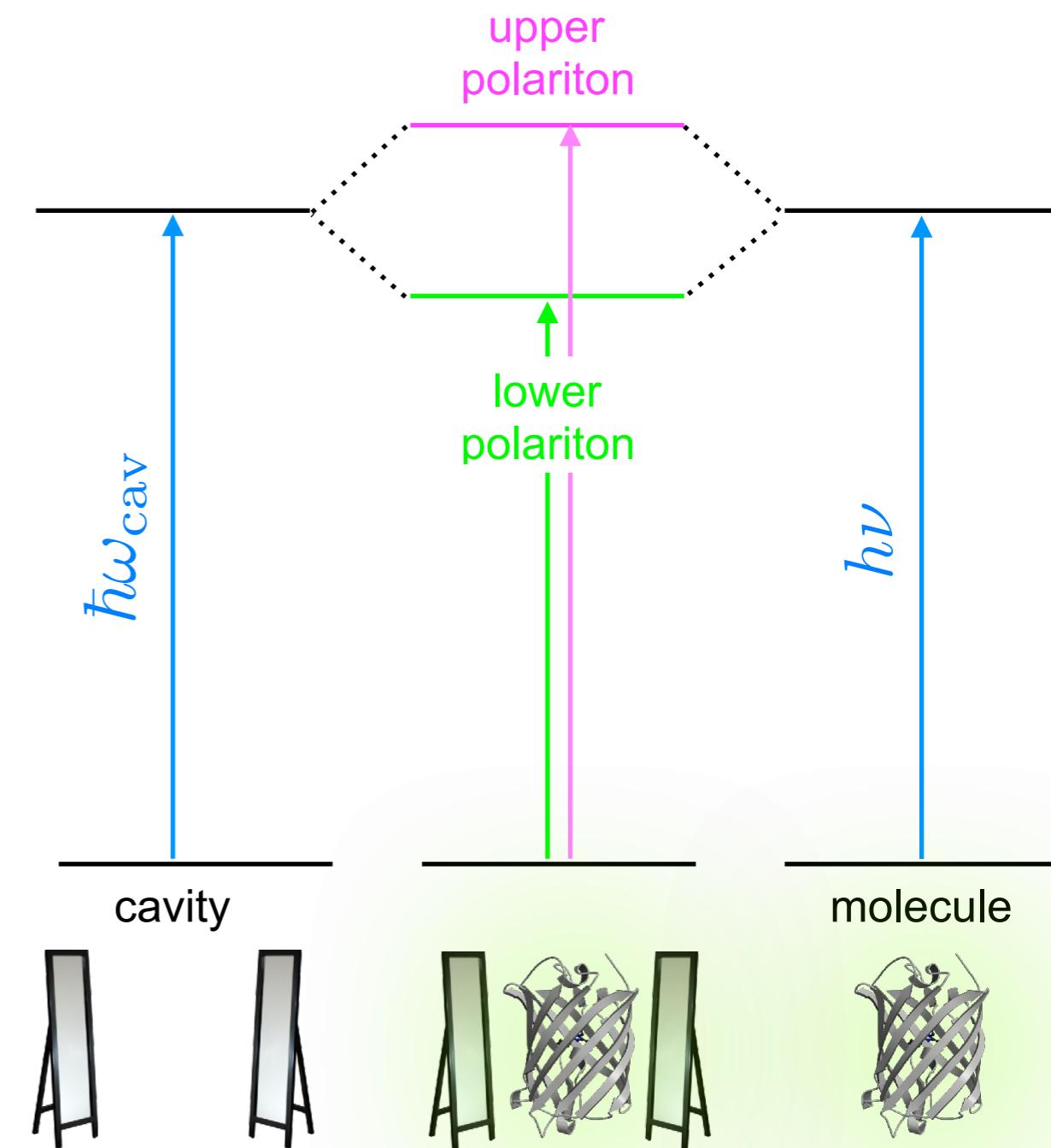
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with matrix elements

$$H_{11} = \langle \text{[protein]}^\star | \hat{H} | \text{[protein]} \rangle \langle 0|0\rangle$$

$$H_{22} = \langle \text{[protein]} | \hat{H} | \text{[protein]} \rangle \langle 1|1\rangle$$



Why does the photochemistry change?

strong coupling with confined light (cavity QED)

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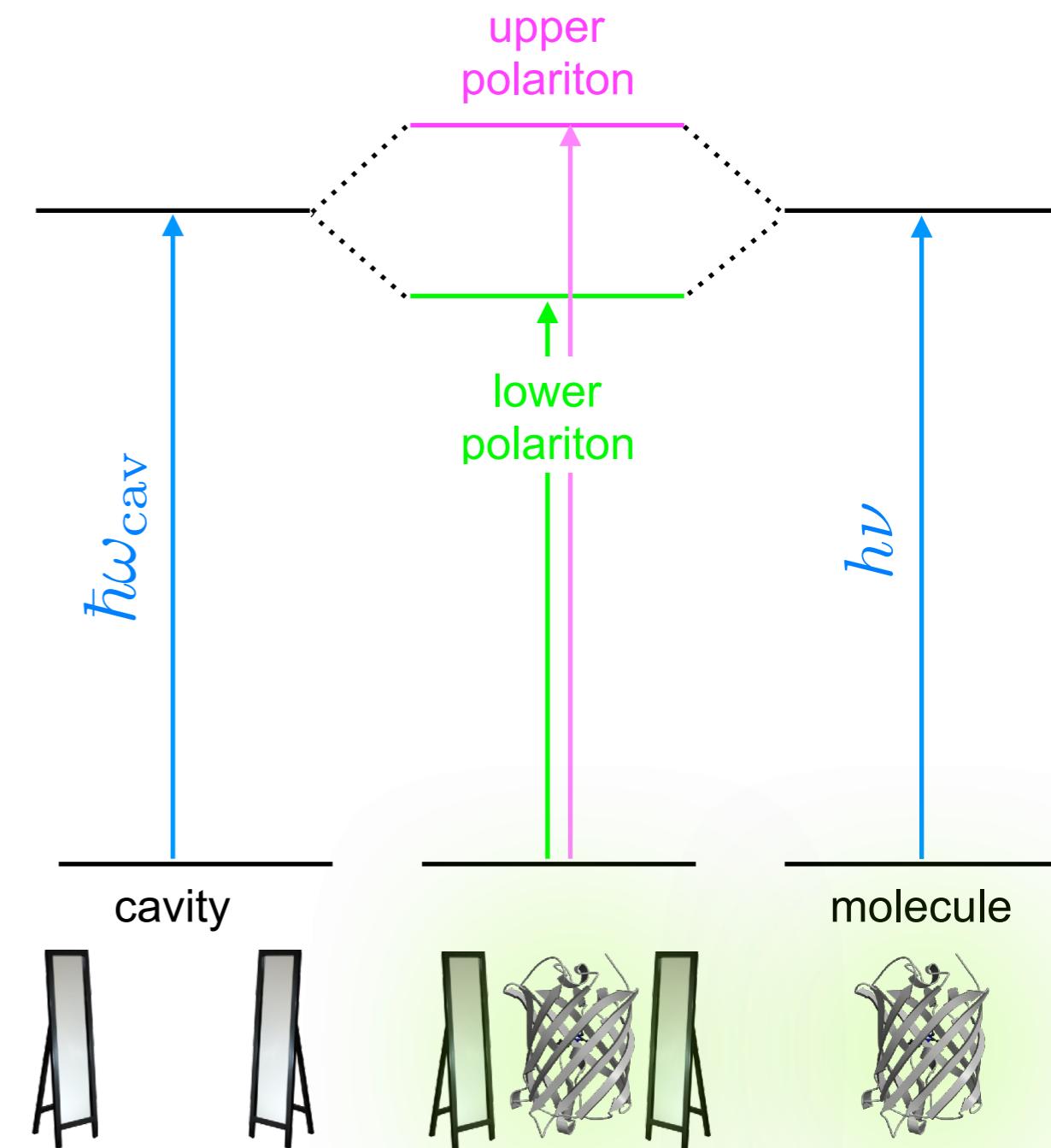
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with matrix elements

$$H_{11} = \langle \text{[protein]}^\star | \hat{H} | \text{[protein]} \rangle \langle 0 | 0 \rangle$$

$$H_{22} = \langle \text{[protein]} | \hat{H} | \text{[protein]} \rangle \langle 1 | 1 \rangle$$

$$H_{12} = H_{21} = |\langle \text{[protein]}^\star | \hat{\mu} | \text{[protein]} \rangle| \sqrt{\hbar\omega_{\text{cav}} / \epsilon_0 V_{\text{cav}}}$$



Why does the photochemistry change?

strong coupling with confined light (cavity QED)

light-matter Hamiltonian for one protein (Jaynes-Cummings)

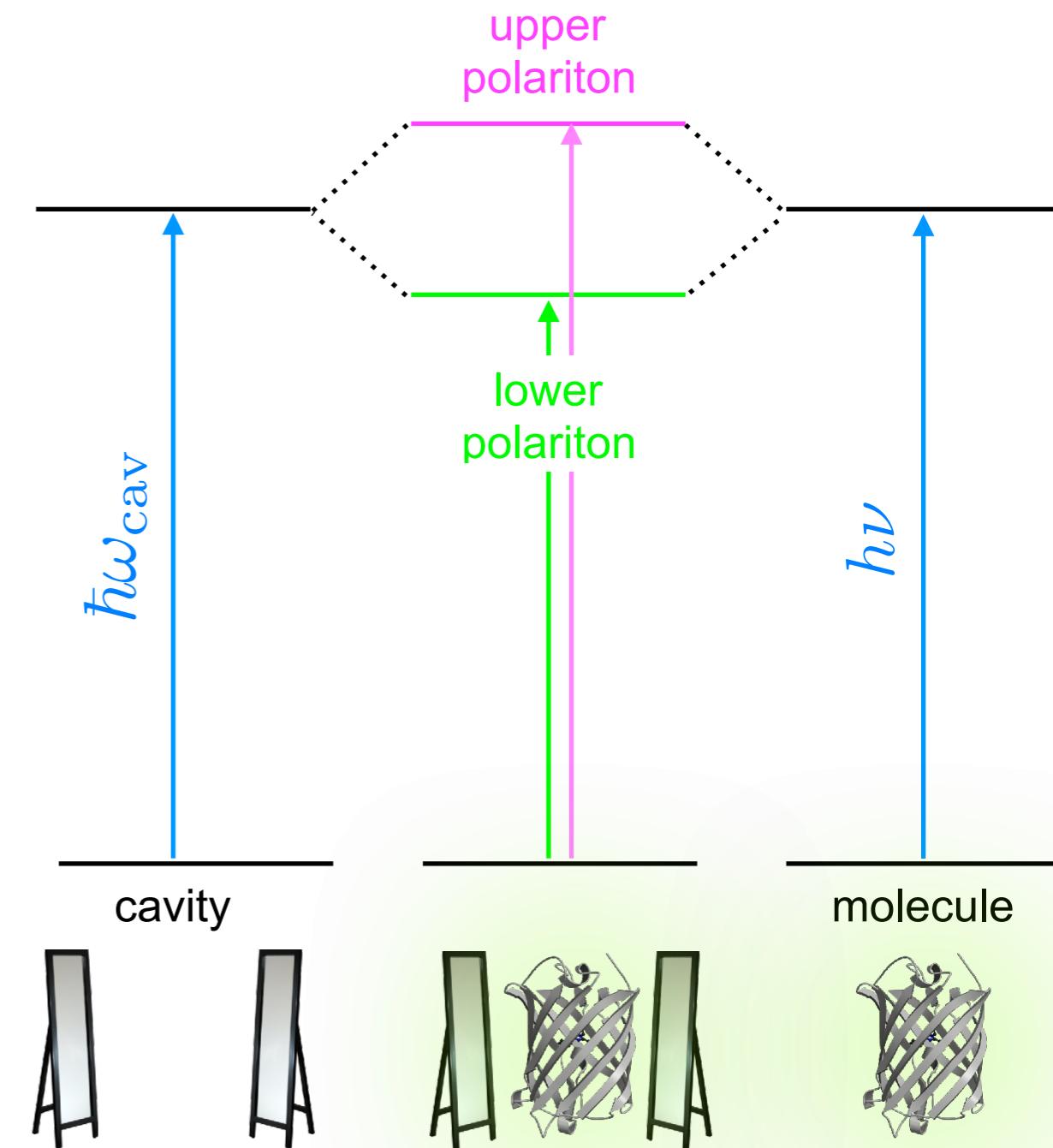
$$\mathbf{H}^{\text{cav}} = \begin{pmatrix} H_{11} & H_{21} \\ H_{12} & H_{22} + \hbar\omega_{\text{cav}} \end{pmatrix}$$

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$$H_{11} = V_{S_1}(\mathbf{R})$$

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$$H_{12} = H_{21} = |\boldsymbol{\mu}_{S_0 \rightarrow S_1}^{\text{TDM}}(\mathbf{R})| \sqrt{\hbar\omega_{\text{cav}}/\epsilon_0 V_{\text{cav}}}$$



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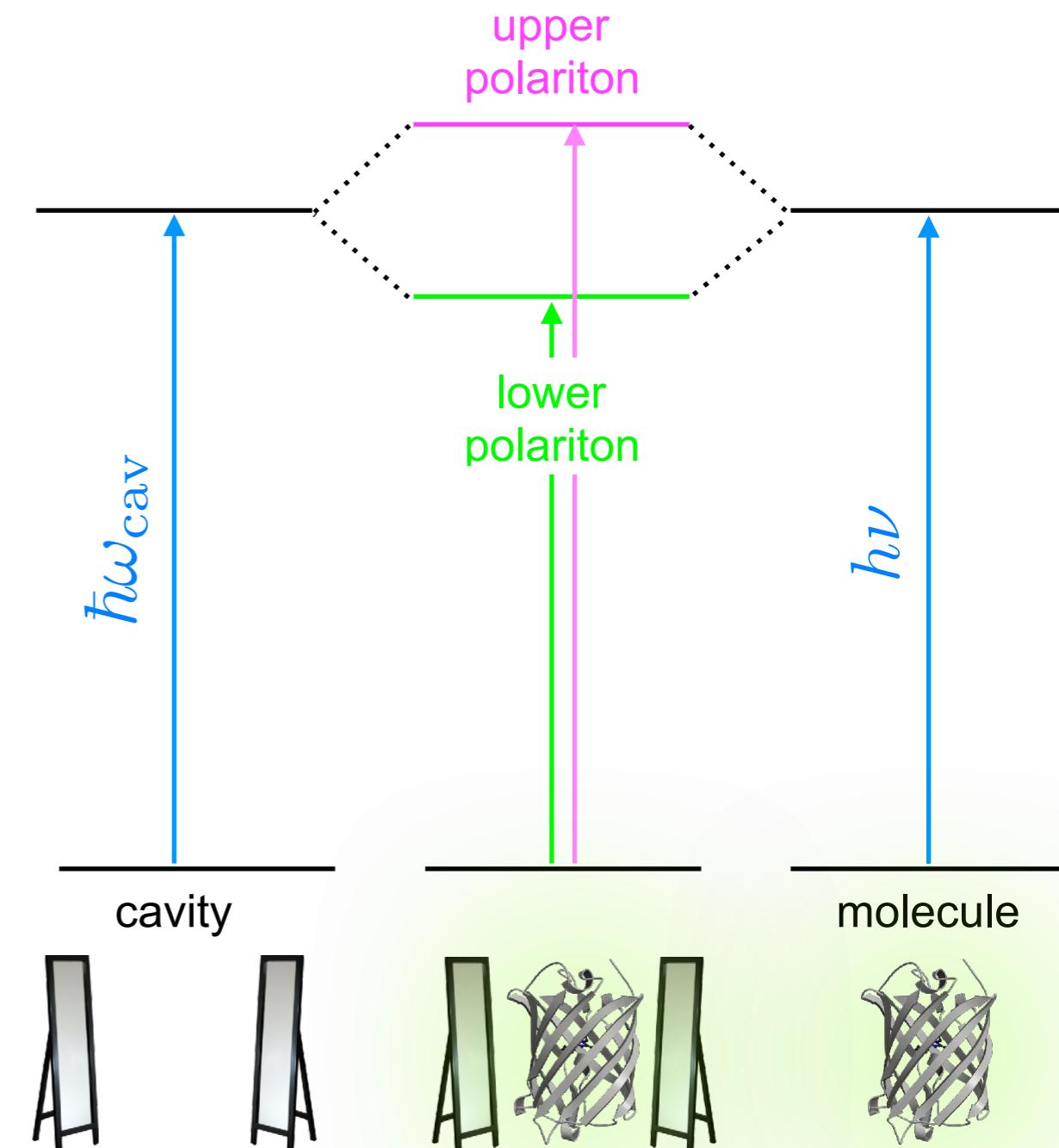
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and solution

$$\Psi^K = \beta_1^K | \text{protein}_1^\star \rangle | 0 \rangle + \alpha^K | \text{protein}_2^\star \rangle | 1 \rangle$$

$$|\beta_1^K|^2 + |\alpha^K|^2 = 1$$

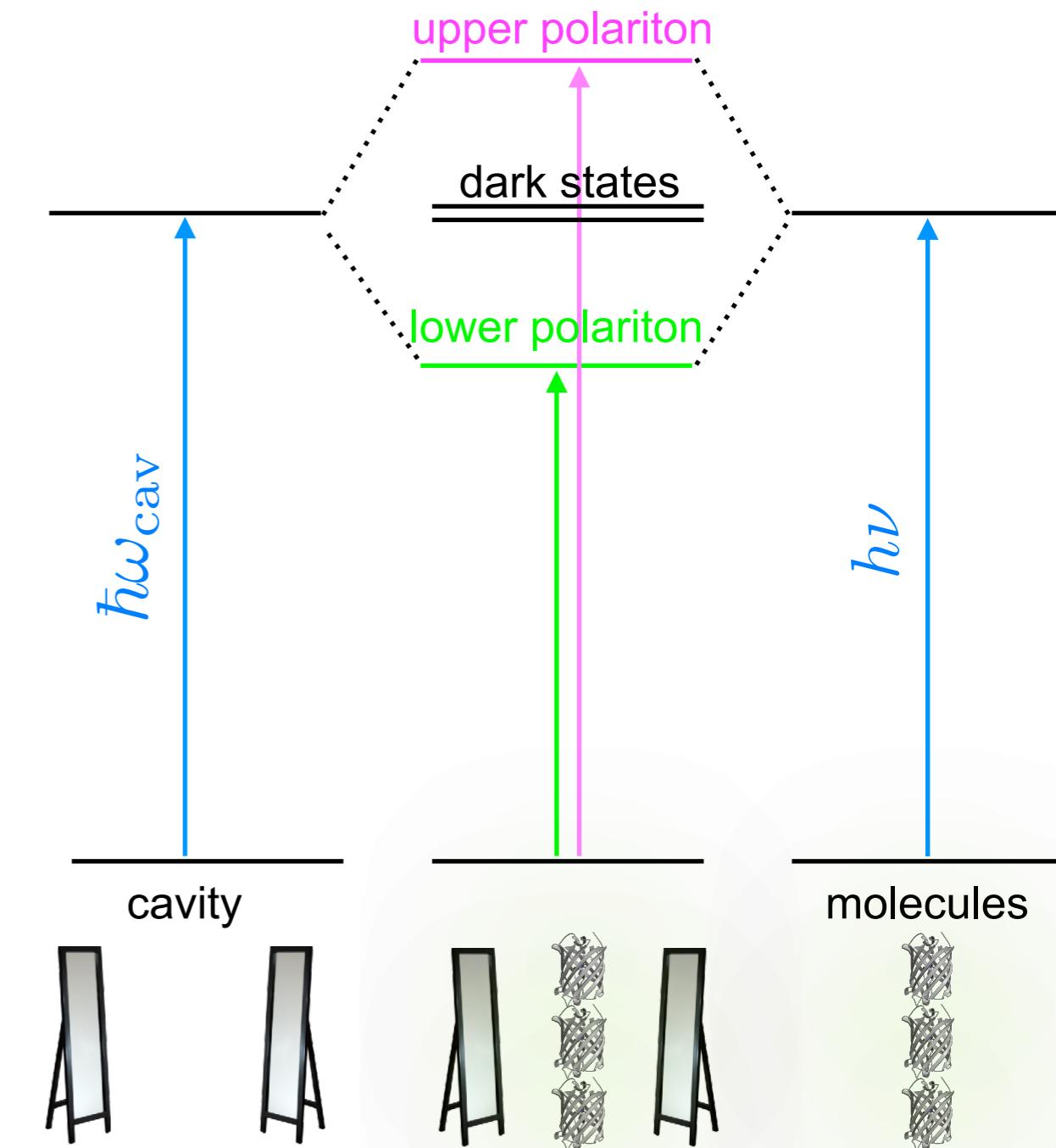


Why does the photochemistry change?

strong coupling with confined light (cavity QED)

light-matter Hamiltonian for three proteins (Tavis-Cummings)

$$\mathbf{H}^{\text{cav}} = \begin{pmatrix} H_{11} & 0 & 0 & H_{41} \\ 0 & H_{22} & 0 & H_{42} \\ 0 & 0 & H_{33} & H_{43} \\ H_{14} & H_{24} & H_{34} & H_{44} + \hbar\omega_{\text{cav}} \end{pmatrix}$$



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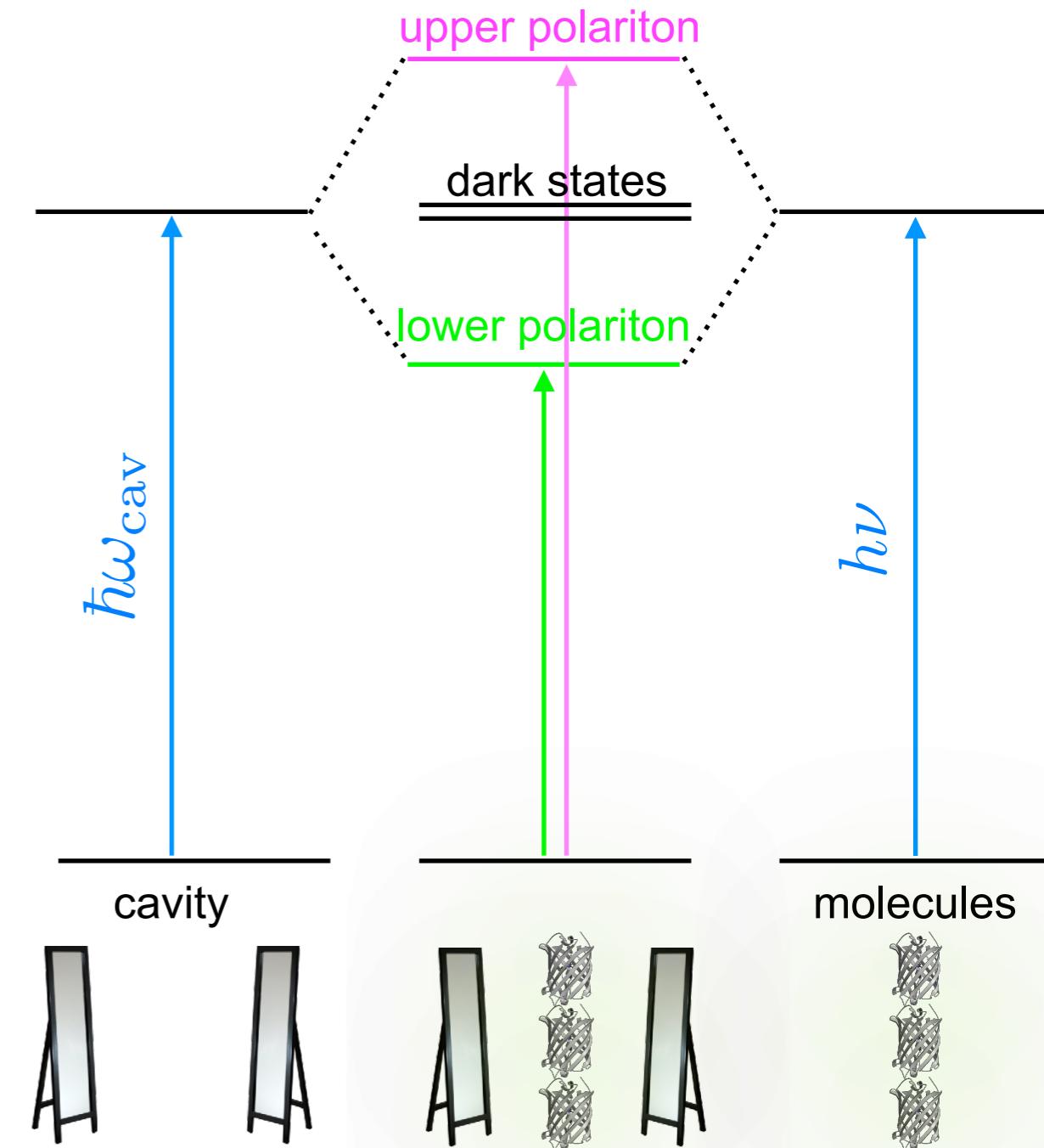
with matrix elements

$$H_{11} = \langle \text{protein}_1 | \hat{H} | \text{protein}_1 \rangle \langle 0 | 0 \rangle$$

$$H_{22} = \langle \text{protein}_2 | \hat{H} | \text{protein}_2 \rangle \langle 0 | 0 \rangle$$

$$H_{33} = \langle \text{protein}_3 | \hat{H} | \text{protein}_3 \rangle \langle 0 | 0 \rangle$$

$$H_{44} = \langle \text{molecules} | \hat{H} | \text{molecules} \rangle \langle 1 | 1 \rangle$$



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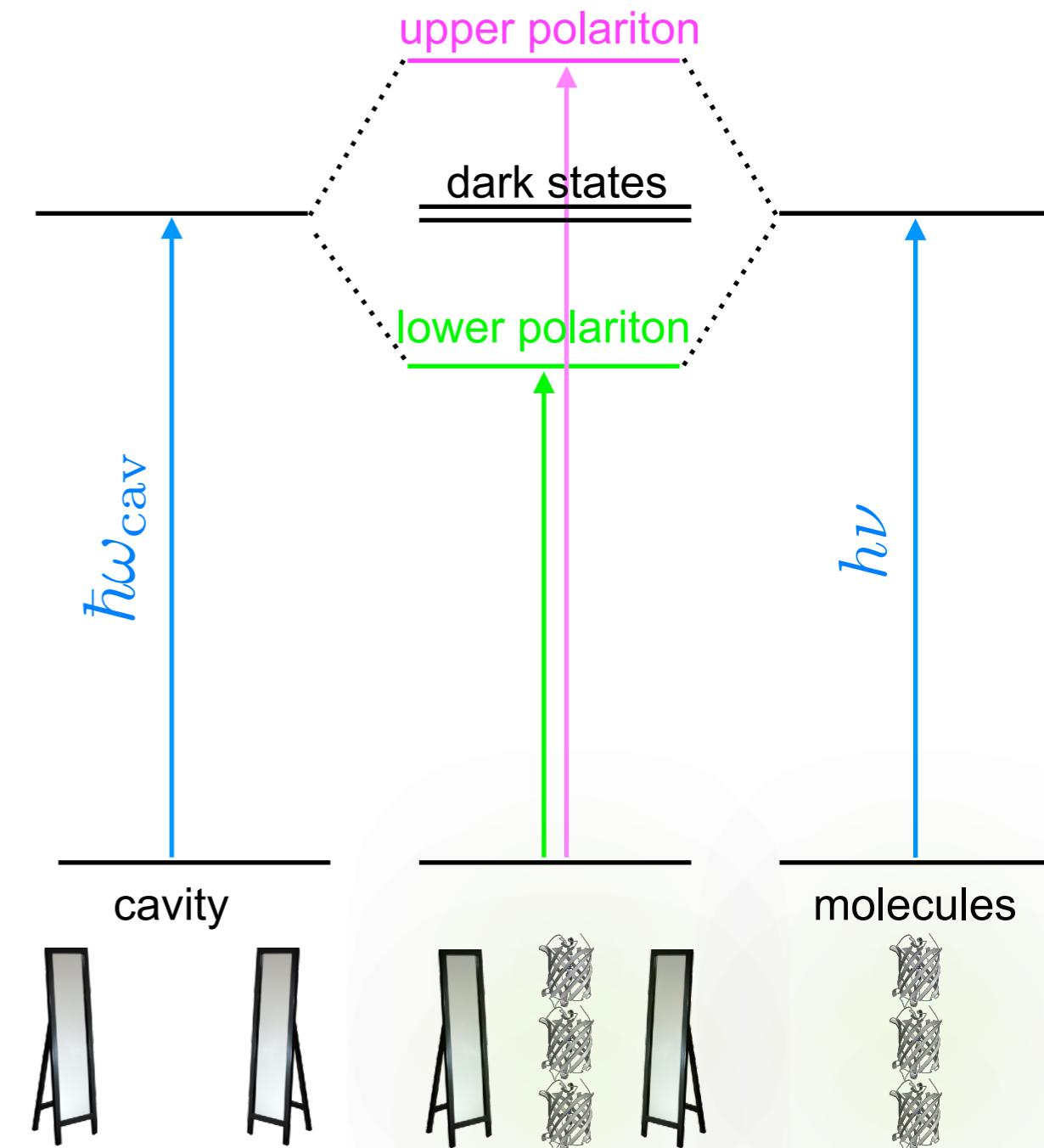
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$$H_{4i} = H_{i4} = |\langle \text{protein}_i | \hat{\mu} | \text{molecules} \rangle| \sqrt{\hbar\omega_{\text{cav}} / \epsilon_0 V_{\text{cav}}}$$



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with matrix elements

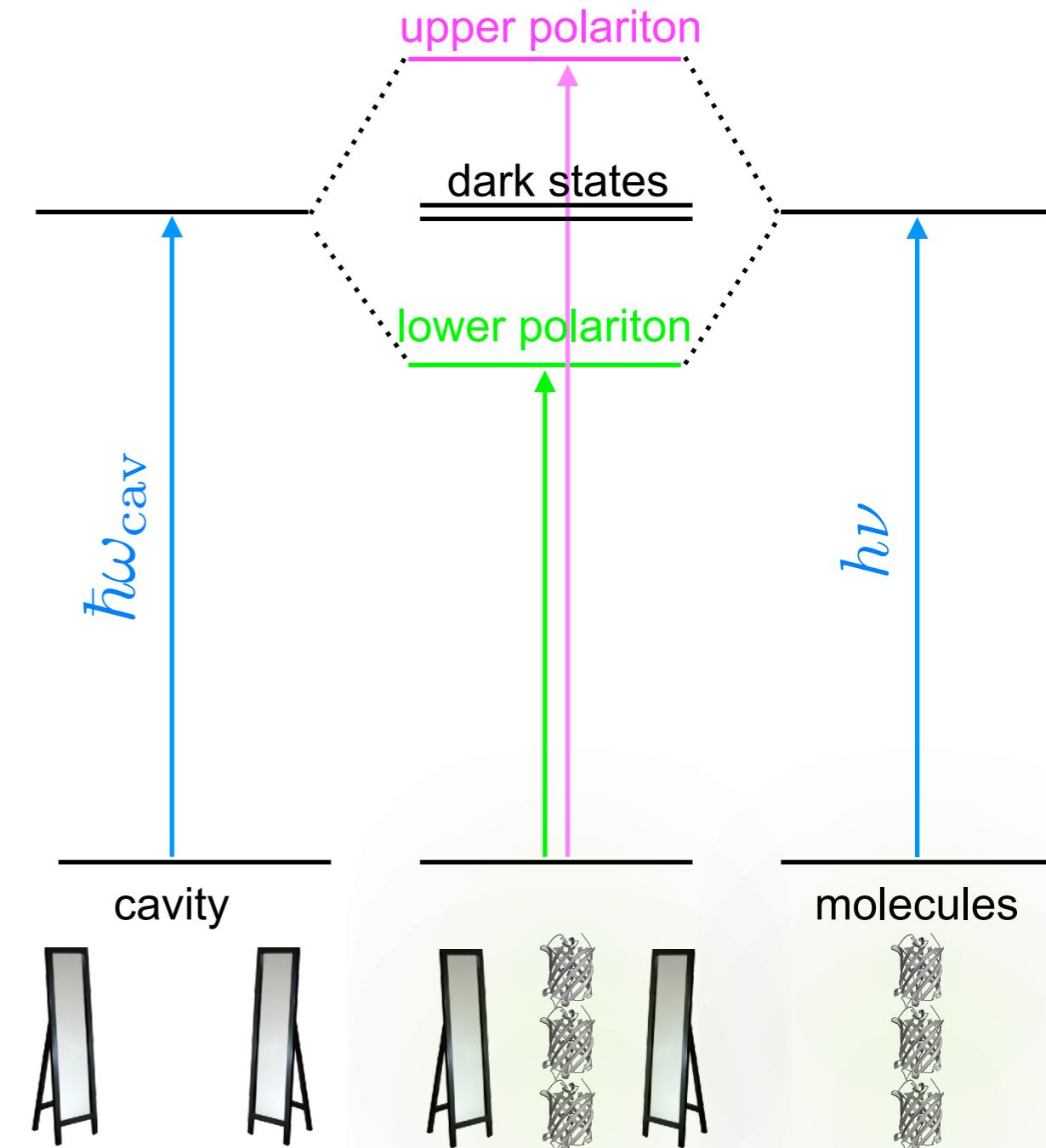
$$H_{11} = V_{S_1}(\mathbf{R}_1) + V_{S_0}(\mathbf{R}_2) + V_{S_0}(\mathbf{R}_3)$$

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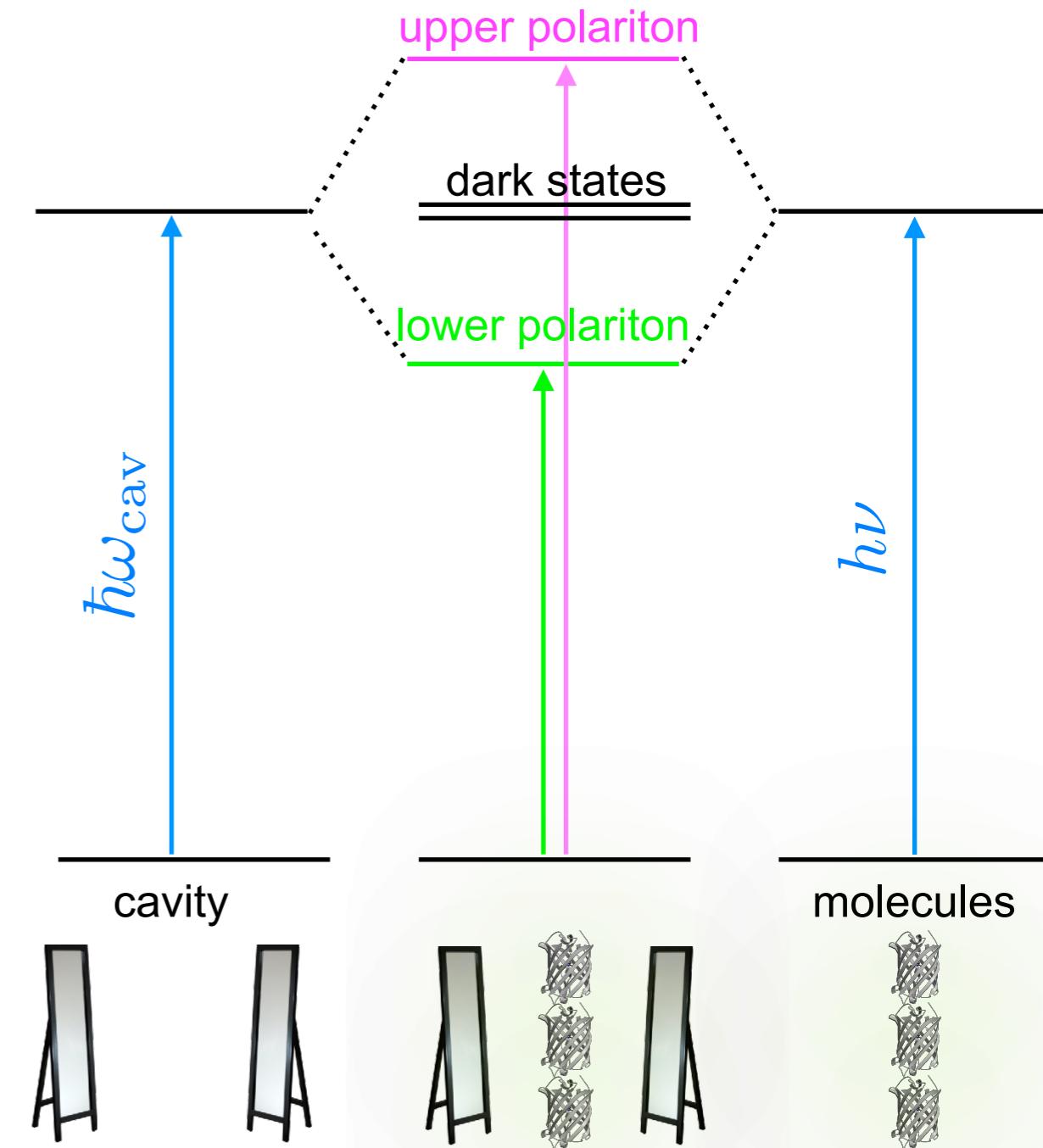


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with matrix elements

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$$\Psi^K = \beta_1^K | \text{protein 1}^\star \text{protein 2} \text{protein 3} \rangle |0\rangle + \beta_2^K | \text{protein 1} \text{protein 2}^\star \text{protein 3} \rangle |0\rangle + \beta_3^K | \text{protein 1} \text{protein 2} \text{protein 3}^\star \rangle |0\rangle + \alpha^K | \text{protein 1} \text{protein 2} \text{protein 3} \rangle |1\rangle$$

Why does the photochemistry change?

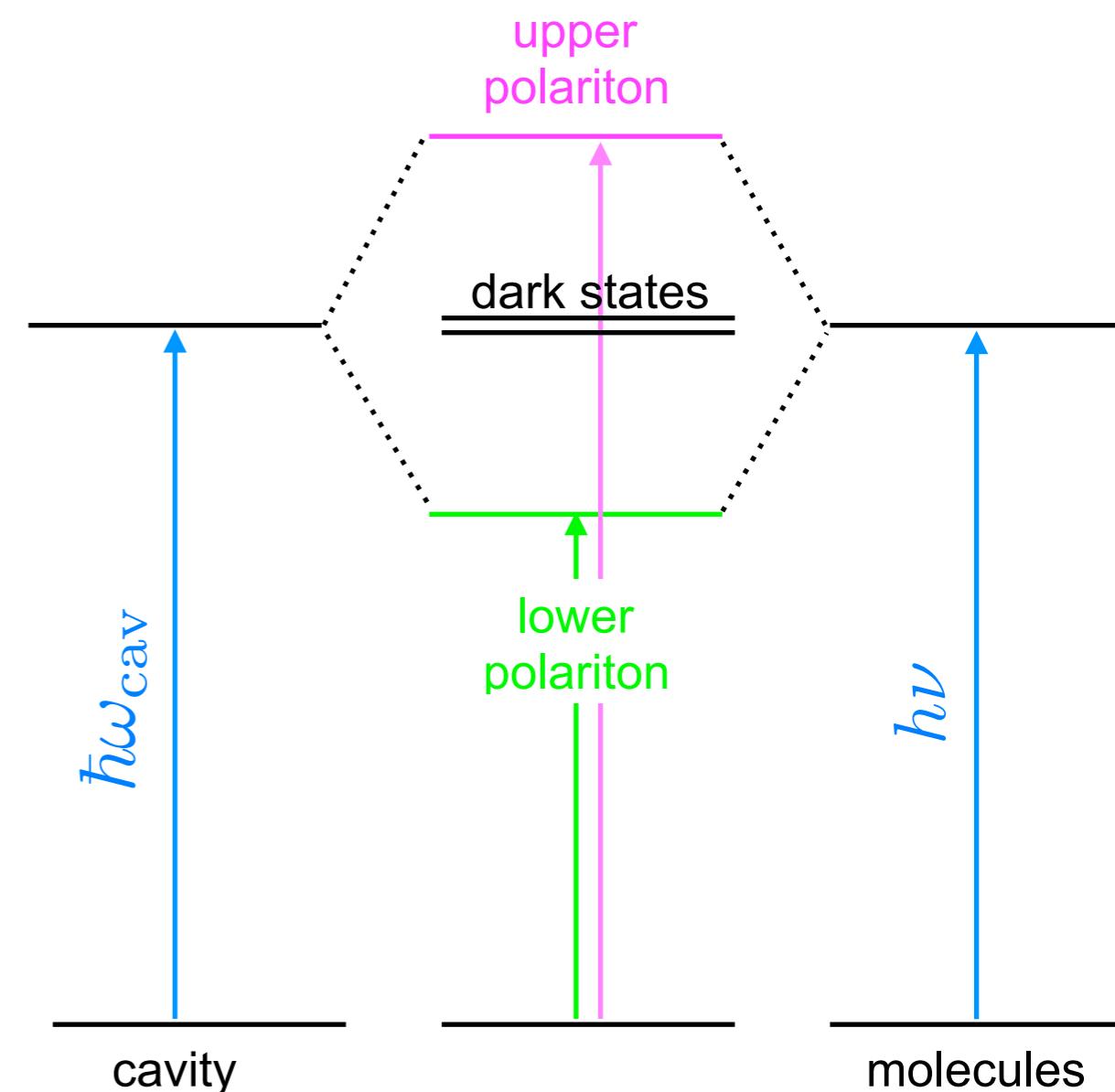
strong coupling with confined light (cavity QED)

two bright polaritons

$$\Psi^K = \beta_1^K | \text{[molecule]}\star\rangle|0\rangle + \beta_2^K | \text{[molecule]}^\star\text{[light]}\rangle|0\rangle + \beta_3^K | \text{[light]}^\star\text{[molecule]}\rangle|0\rangle + \alpha^K | \text{[molecule]}\star\rangle|1\rangle$$

Rabi splitting

$$\hbar\Omega^{\text{Rabi}} \propto \sqrt{N/V_{\text{cav}}}$$



Why does the photochemistry change?

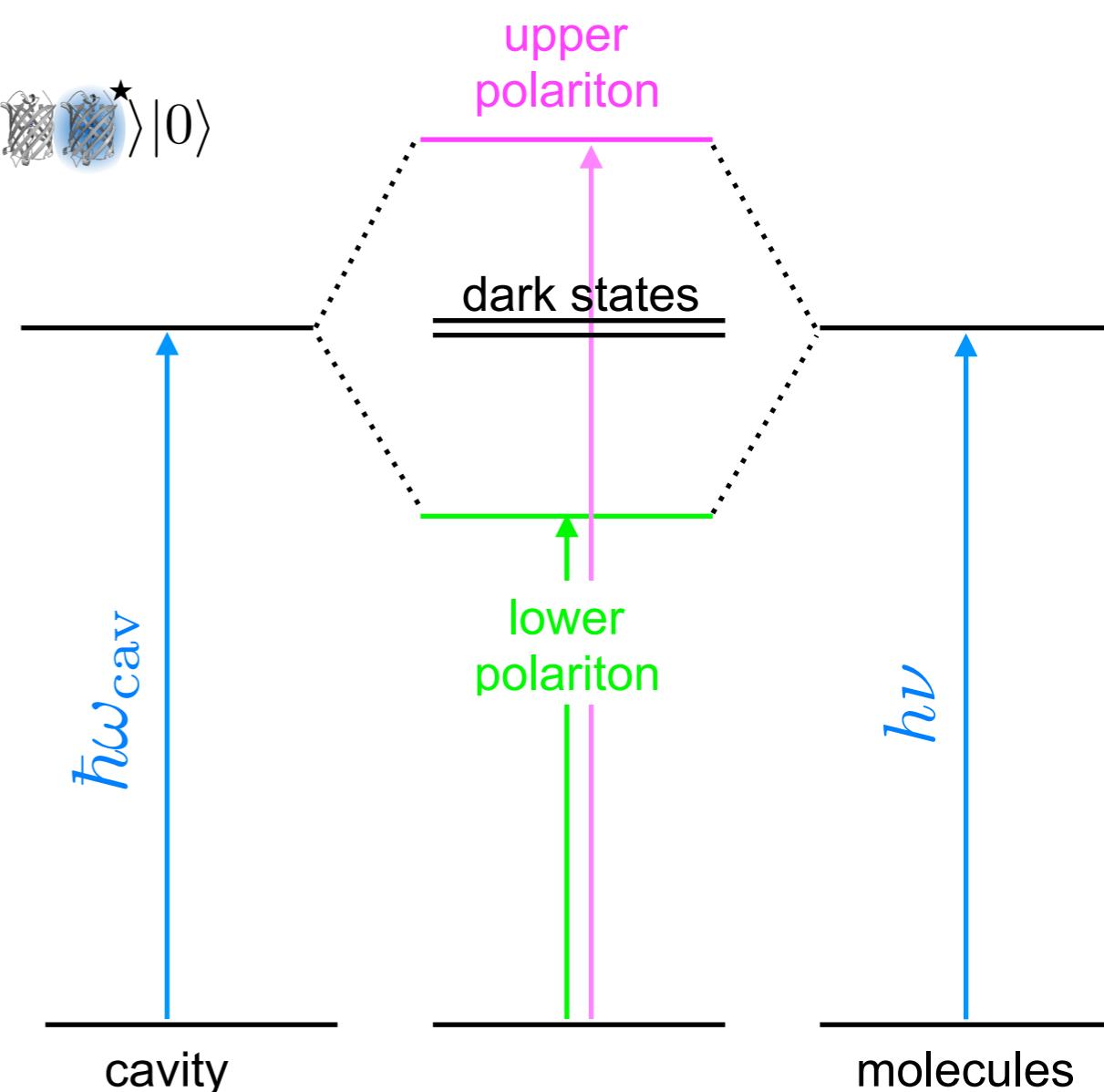
strong coupling with confined light (cavity QED)

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$$\Psi^K = \beta_1^K | \text{diagram with 1 star} \rangle |0\rangle + \beta_2^K | \text{diagram with 2 stars} \rangle |0\rangle + \beta_3^K | \text{diagram with 3 stars} \rangle |0\rangle + \alpha^K | \text{diagram with 4 stars} \rangle |1\rangle$$

two dark states (in general $N-1$)

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double peak spectrum

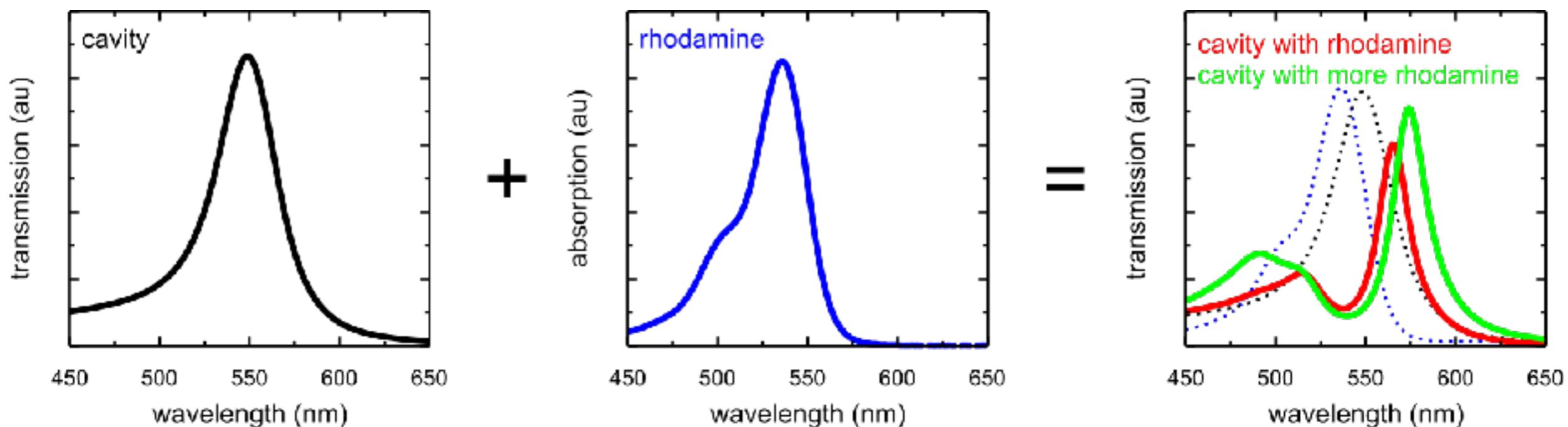
example: cavity with rhodamine 6G



Mikael
Kautto



Eero
Hulkko



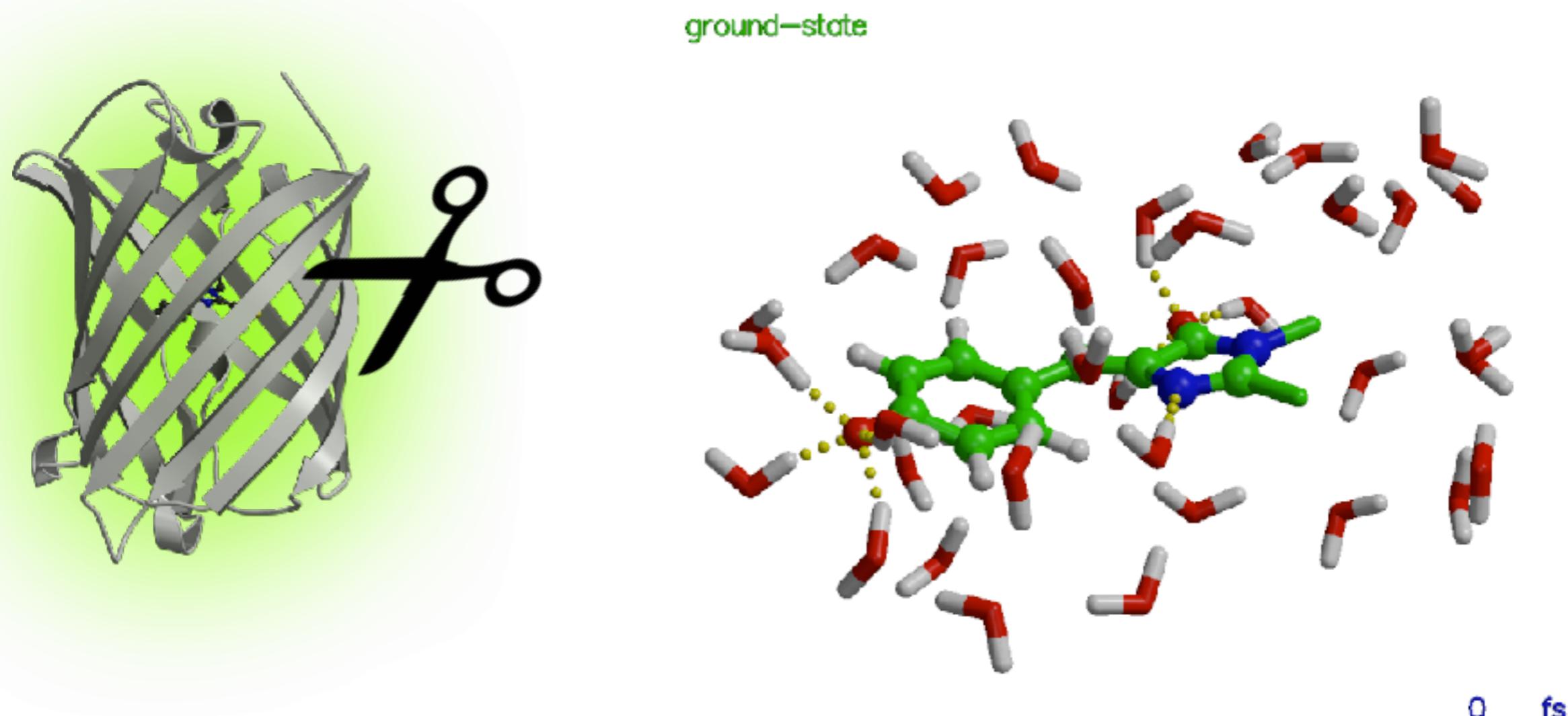
Manipulating photo-chemistry with mirrors

GFP chromophore in water

no fluorescence: dark



Dmitry
Morozov



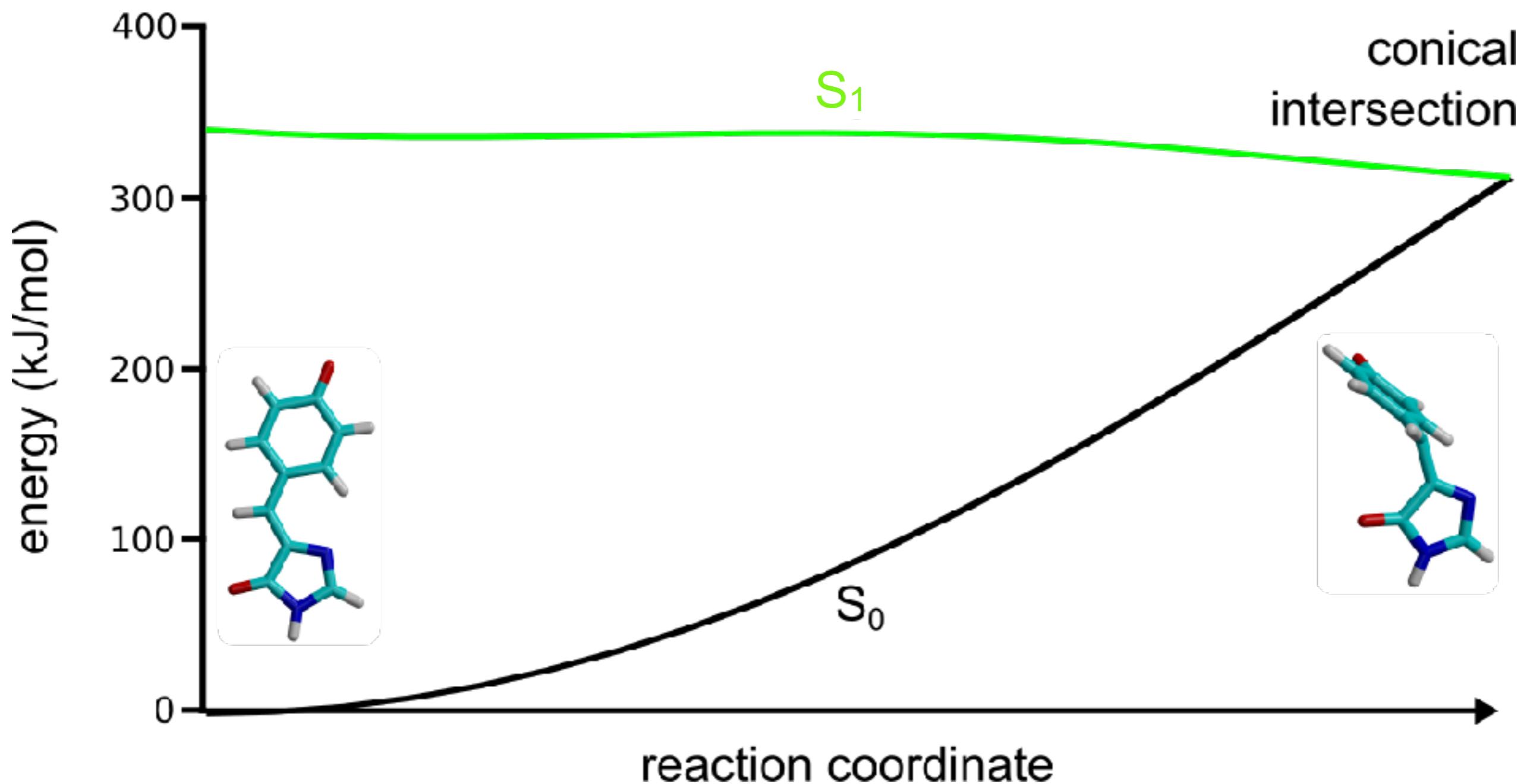
CASSCF(6,6)/3-21G//SPC

CASSCF(12,11)/cc-pVDZ//EFP

Manipulating photo-chemistry with mirrors

GFP chromophore in water

no fluorescence: dark

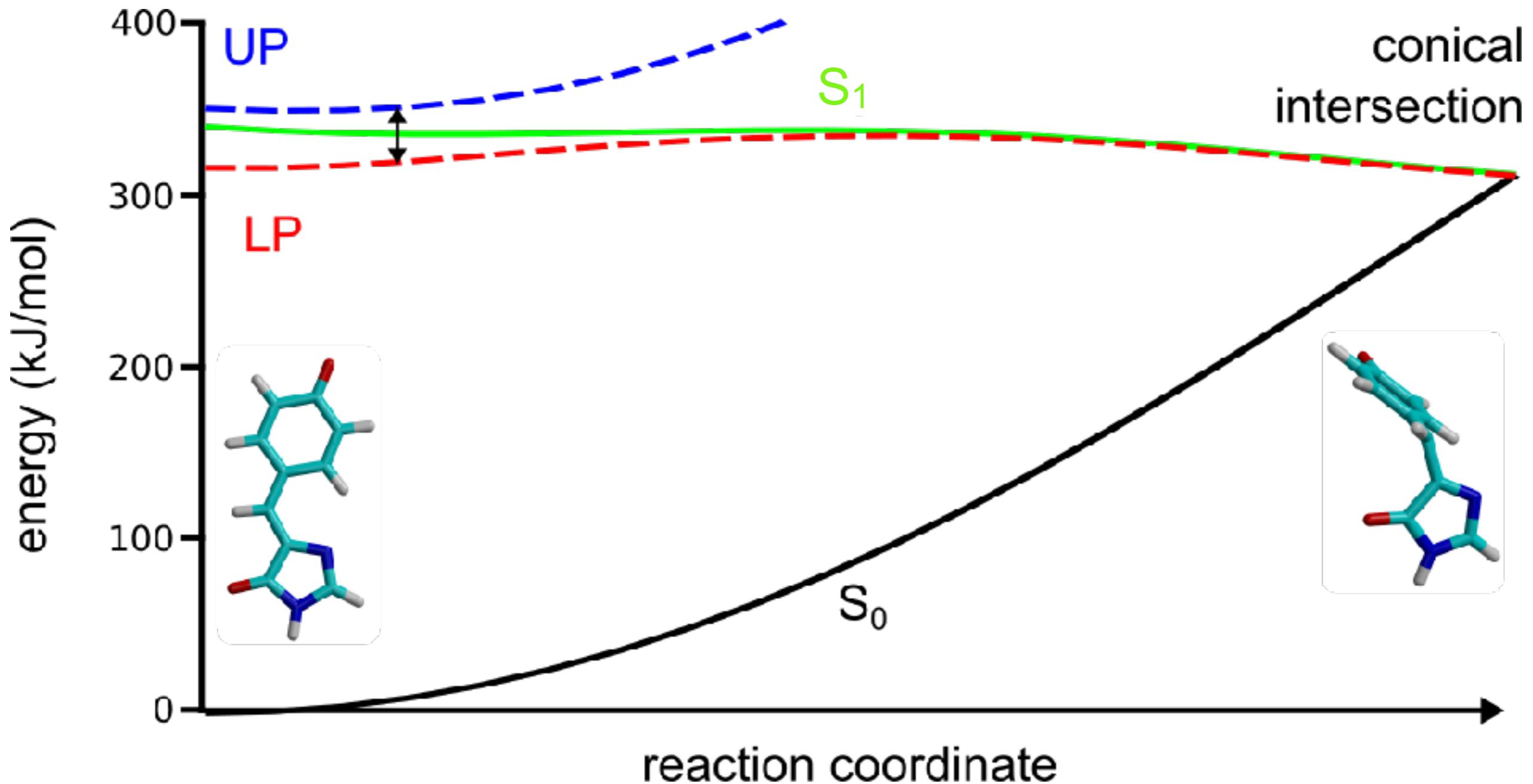


Manipulating photo-chemistry with mirrors

one GFP chromophore in water in a cavity

strong coupling to confined light?

minimum on lower polariton surface

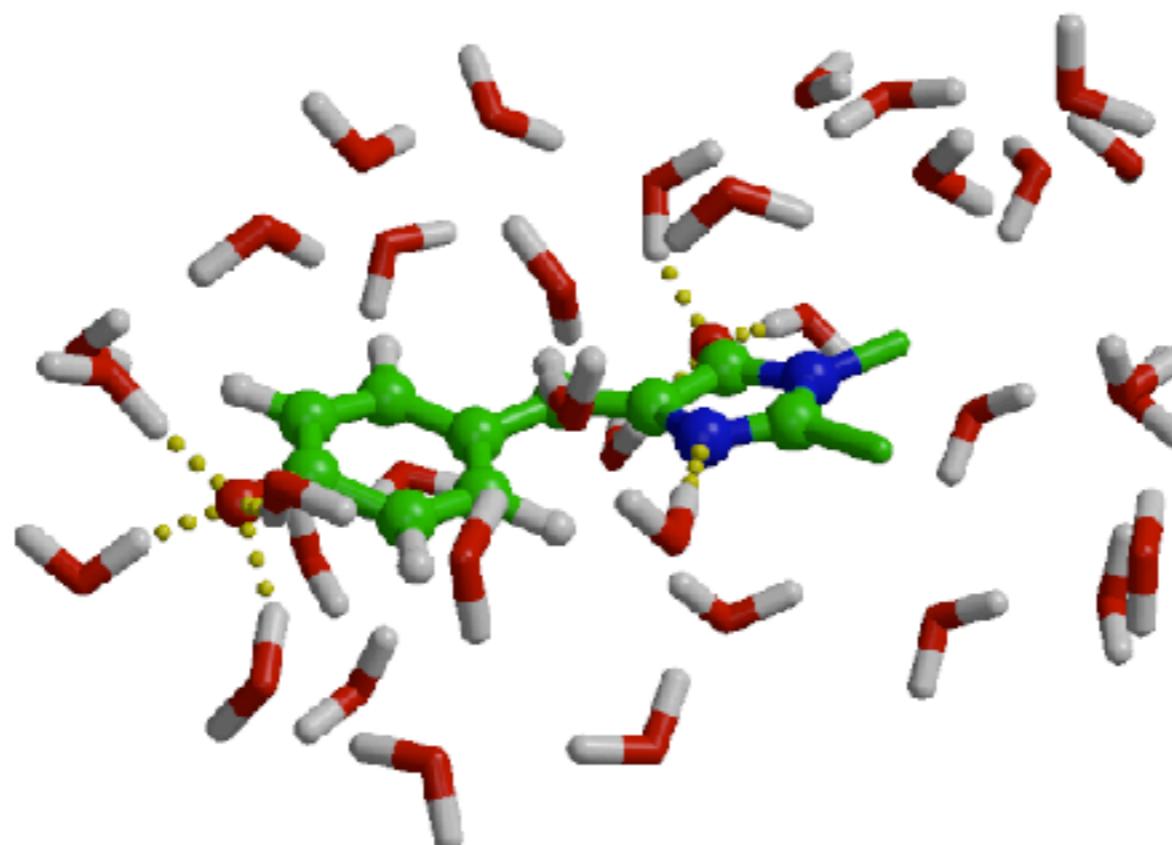


Manipulating photo-chemistry with mirrors

one GFP chromophore in water in a cavity

no fluorescence: dark

ground-state



0 fs

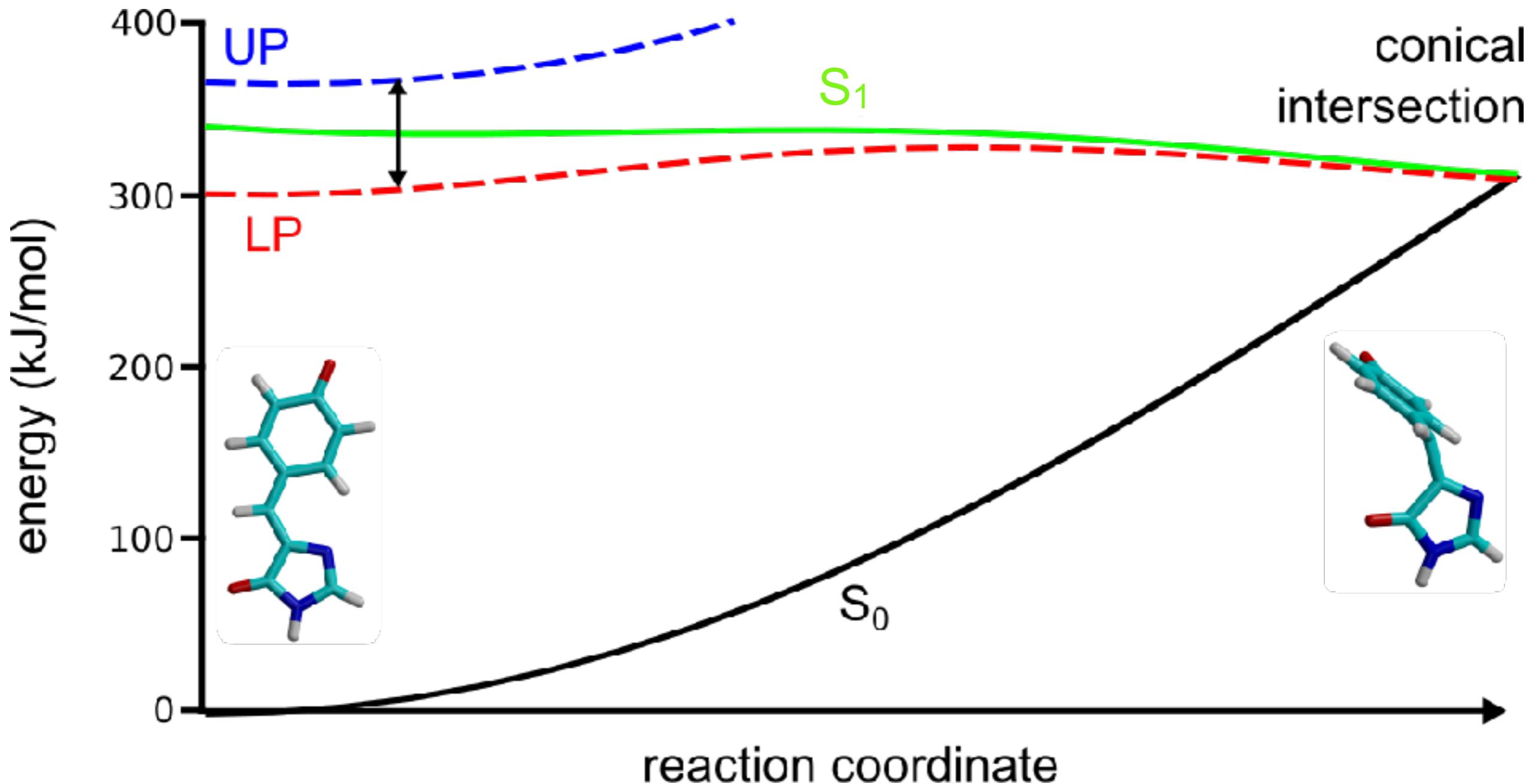
$$\frac{1}{2}\lambda_{\max}$$

Manipulating photo-chemistry with mirrors

four GFP chromophores in water in a cavity

two times stronger coupling with confined light

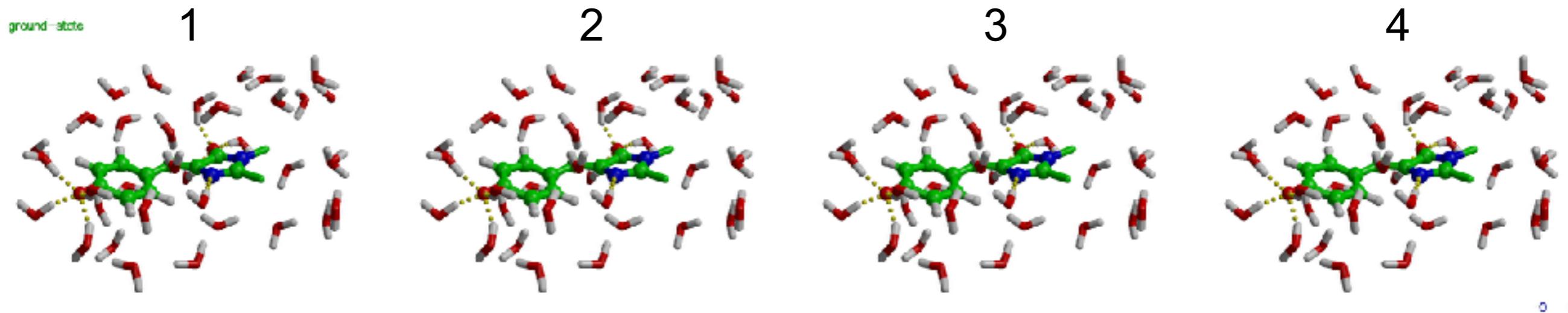
deeper minimum on lower polariton surface



Manipulating photo-chemistry with mirrors

four GFP chromophores in water in a cavity

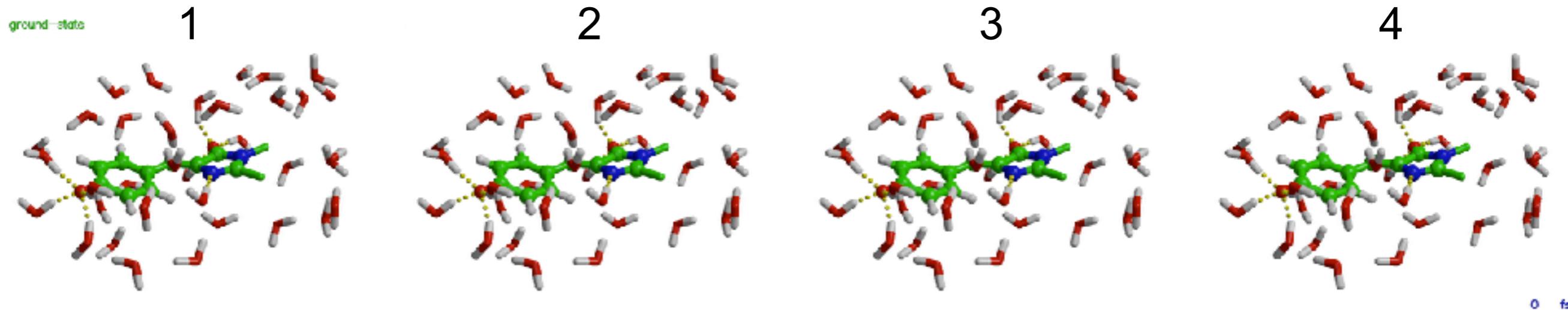
trapped: fluorescence



Manipulating photo-chemistry with mirrors

four GFP chromophores in water in a cavity

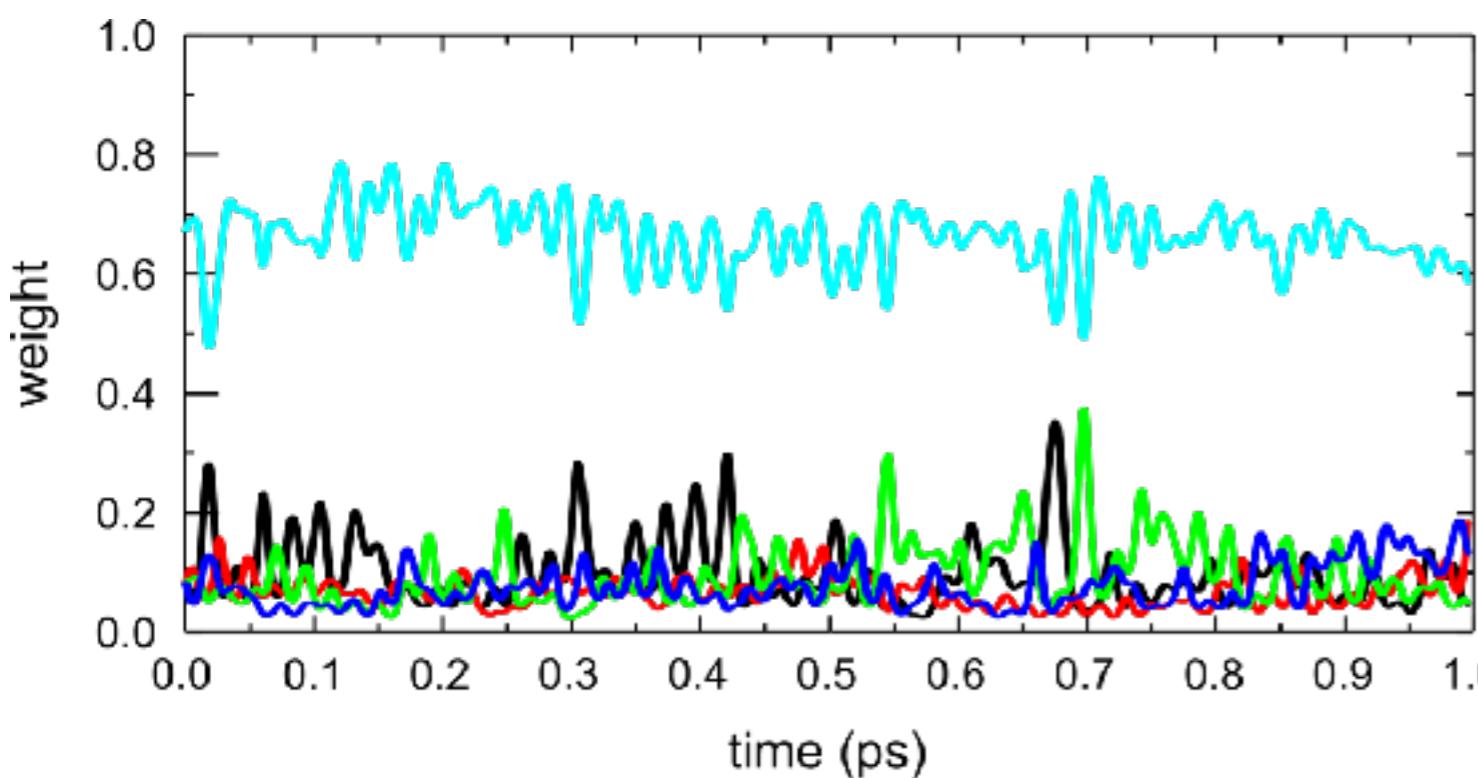
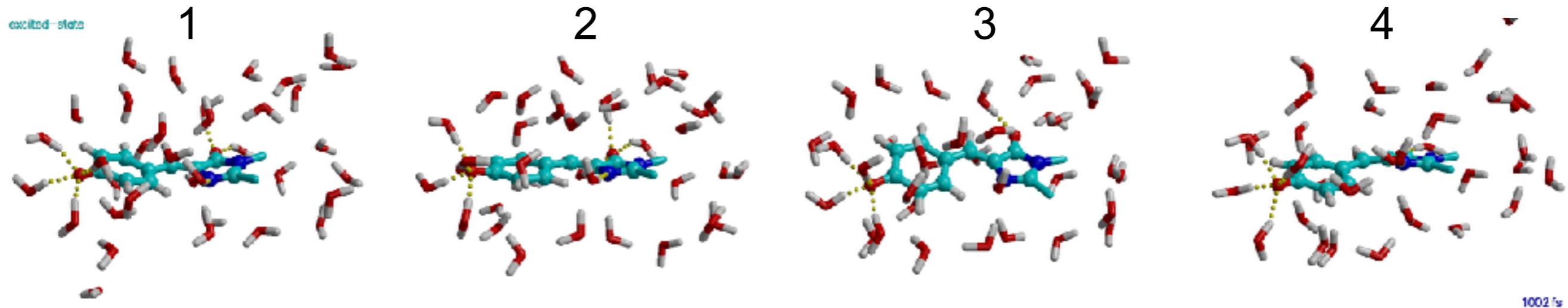
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Manipulating photo-chemistry with mirrors

four GFP chromophores in water in a cavity

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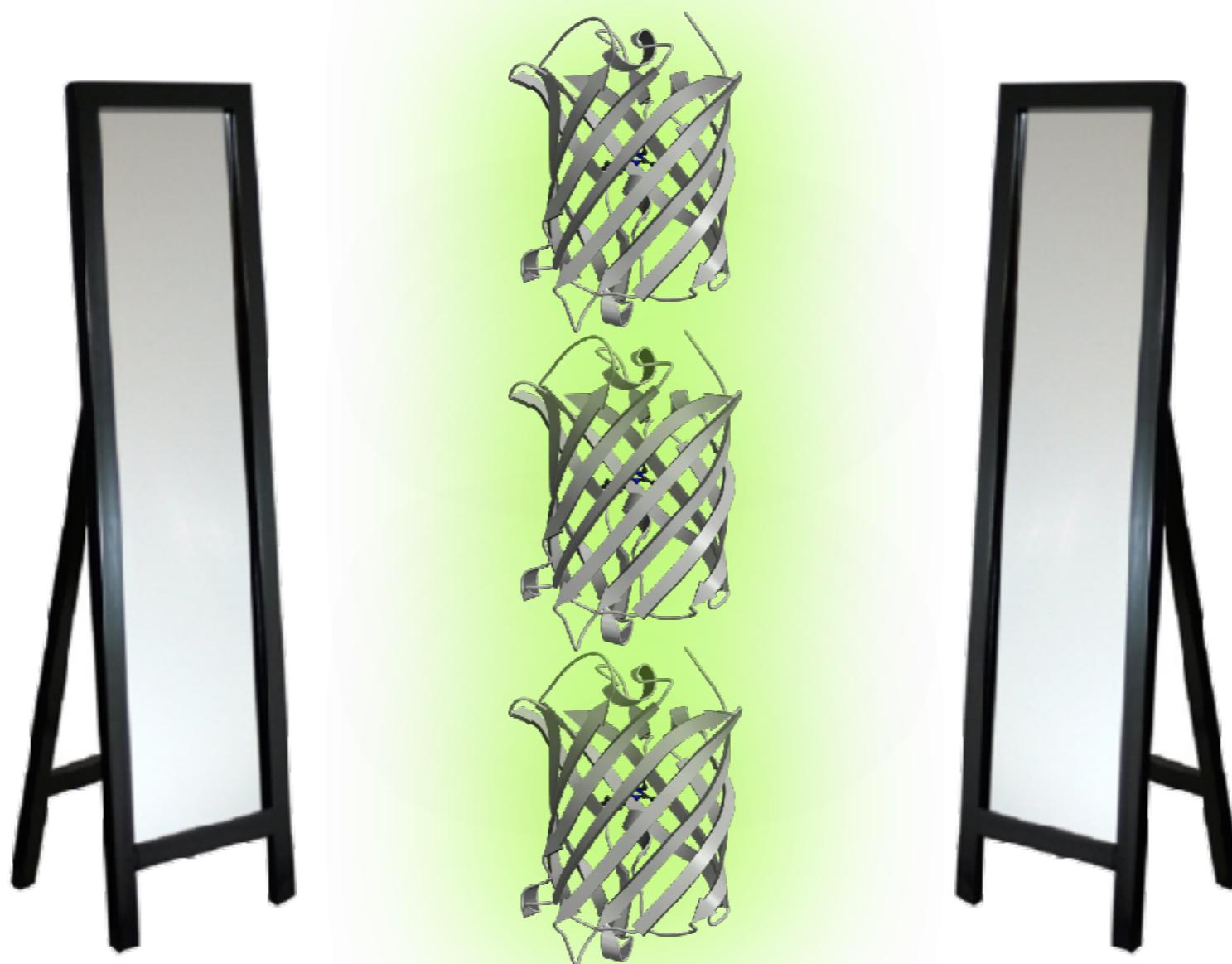
$$\Psi^{\text{LP}} = +\beta_1^{\text{LP}} |1^*234\rangle|0\rangle$$
$$+\beta_2^{\text{LP}} |12^*34\rangle|0\rangle$$
$$+\beta_3^{\text{LP}} |123^*4\rangle|0\rangle$$
$$+\beta_4^{\text{LP}} |1234^*\rangle|0\rangle$$
$$+\alpha^{\text{LP}} |1234\rangle|1\rangle$$

Manipulating photo-chemistry with mirrors

summary

cavity “QED”/MM

simulations of molecules under strong coupling with confined light



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new photocatalysis paradigm?

re-shaping potential energy surface

control of photo-chemical reactions

Ebbesen & coworkers: *Angew. Chem. Int. Ed.* 51 (2012) 1592–1596

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Angew. Chem. Int. Ed. 55 (2016) 6202–6206

Nature Materials 14 (2015) 1123–1129

Coles et al. *Nature Materials* 13 (2014) 712–719

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challenges

cavity lifetimes

dielectric mirrors

interpretation of cavity spectra

optical filtering

Acknowledgements



Dmitry
Morozov



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Kautto



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Luk



Oleg
Blyednov



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Jussi
Toppari



Siim
Pikker



Eero
Hulkko



Aili
Asikainen



Vaibhav
Modi



Tero
Heikkilä

support (Euros, FLOPs & photons)

Simulating molecules in cavity

QED matrix elements

independent molecules interacting with cavity photon

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Free electron laser

SLAC

laser parameters

Table 1 | Design and typical measured parameters for both hard (8.3 keV) and soft (0.8–2.0 keV) X-rays. The ‘design’ and ‘hard’ values are shown only at 8.3 keV. Stability levels are measured over a few minutes.

Parameter	Design	Hard	Soft	Unit
Electrons				
Charge per bunch	1	0.25	0.25	nC
Single bunch repetition rate	120	30	30	Hz
Final linac e^- energy	13.6	13.6	3.5–6.7	GeV
Slice [†] emittance (injected)	1.2	0.4	0.4	μm
Final projected [†] emittance	1.5	0.5–1.2	0.5–1.6	μm
Final peak current	3.4	2.5–3.5	0.5–3.5	kA
Timing stability (r.m.s.)	120	50	50	fs
Peak current stability (r.m.s.)	12	8–12	5–10	%
X-rays				
FEL gain length	4.4	3.5	~1.5	m
Radiation wavelength	1.5	1.5	6–22	\AA
Photons per pulse	2.0	1.0–2.3	10–20	10^{12}
Energy in X-ray pulse	1.5	1.5–3.0	1–2.5	mJ
Peak X-ray power	10	15–40	3–35	GW
Pulse length (FWHM)	200	70–100	70–500	fs
Bandwidth (FWHM)	0.1	0.2–0.5	0.2–1.0	%
Peak brightness (estimated)	8	20	0.3	$10^{32} *$
Wavelength stability (r.m.s.)	0.2	0.1	0.2	%
Power stability (r.m.s.)	20	5–12	3–10	%

*Brightness is photons per phase space volume, or photons $\text{s}^{-1} \text{mm}^{-2} \text{mrad}^{-2}$ per 0.1% spectral bandwidth.

[†]‘Slice’ refers to femtosecond-scale time slices and ‘projected’ to the full time-projected (that is, integrated) emittance of the bunch.

Simulating molecules in cavity

QED matrix elements

independent molecules interacting with cavity photon

$$H_{11} = V_{S_1}(\mathbf{R}_1) + V_{S_0}(\mathbf{R}_2) + V_{S_0}(\mathbf{R}_3)$$

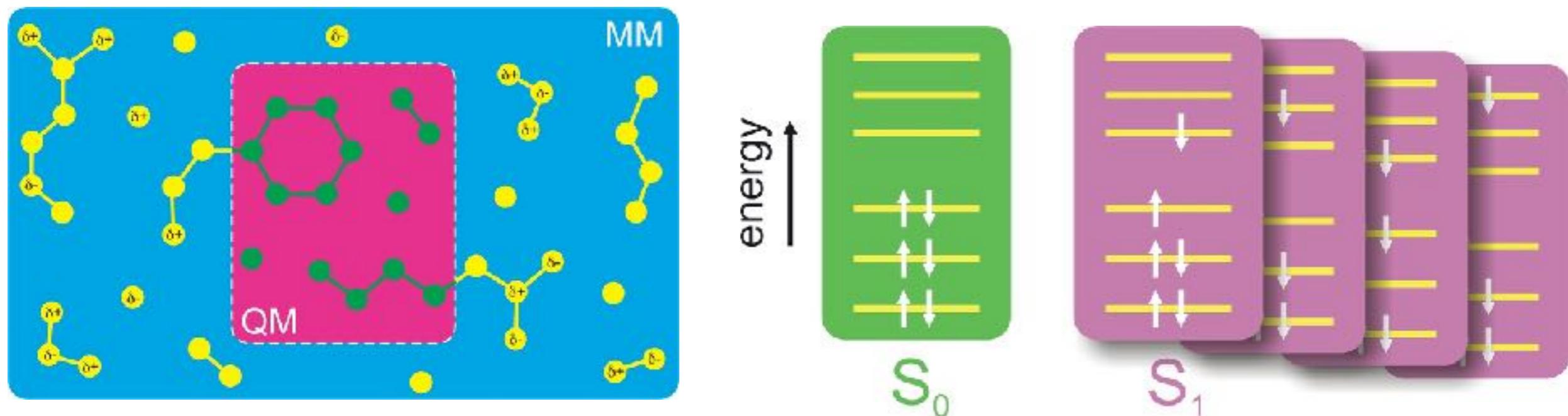
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QM/MM energies in ground (S_0) and excited (S_1) states



Simulating molecules in cavity

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Jussi
Toppuri



Johannes
Feist

diagonalize

two ‘bright’ delocalised polariton states $N-1$ ‘dark’ states

$$\Psi^K = \beta_1^K | \text{Diagram 1} \rangle |0\rangle + \beta_2^K | \text{Diagram 2} \rangle |0\rangle + \beta_3^K | \text{Diagram 3} \rangle |0\rangle + \alpha^K | \text{Diagram 4} \rangle |1\rangle$$

Hellmann-Feynman forces on the atoms: on-the-fly molecular dynamics

$$\mathbf{F}_i^K = -\langle \Psi^K | \nabla_{\mathbf{x}_i} \mathbf{H}^{\text{cav}} | \Psi^K \rangle$$

transitions between states: surface hopping



Calvin
Luk

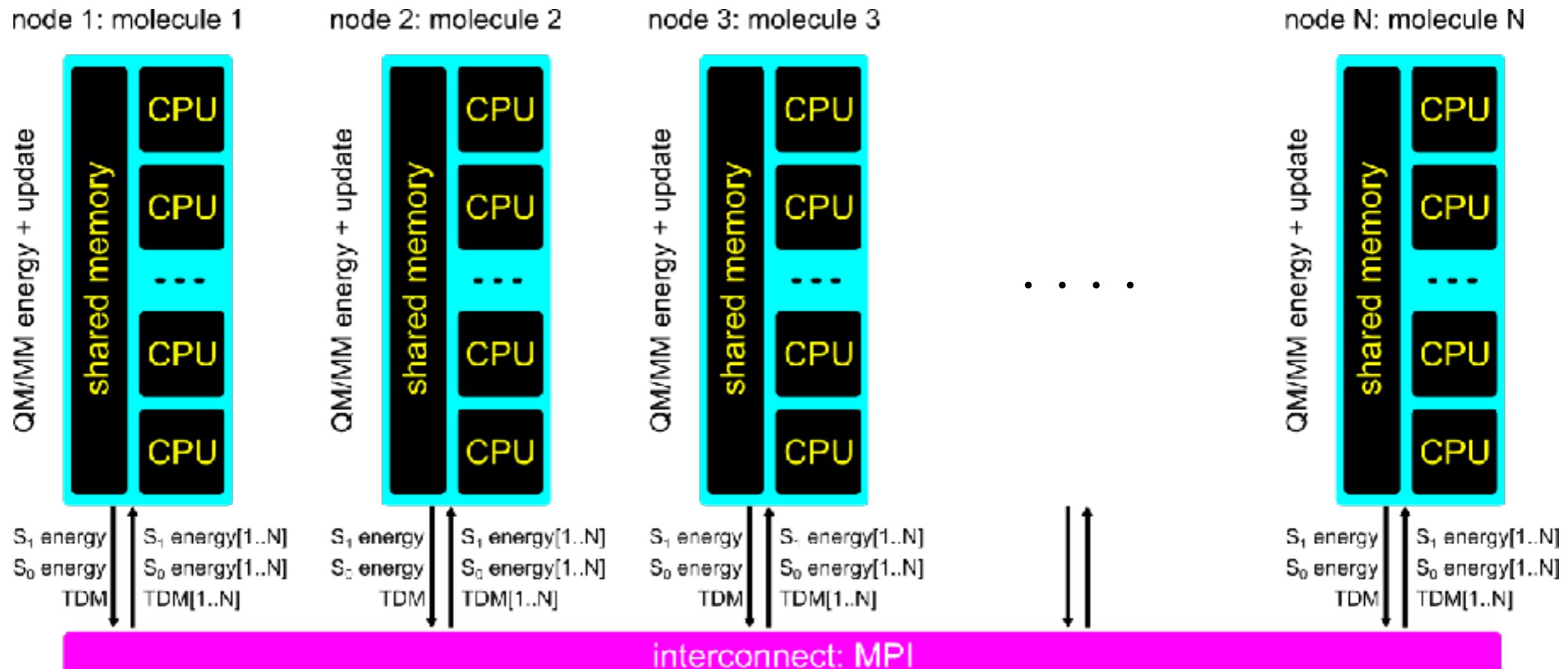
Simulating molecules in cavity

implementation in Gromacs

linear scaling cavity “QED”/MM

Gromacs 4.5 uses as many MPI nodes as there are molecules

Gaussian09 uses all shared memory threads on node



Simulating molecules in cavity

implementation in Gromacs

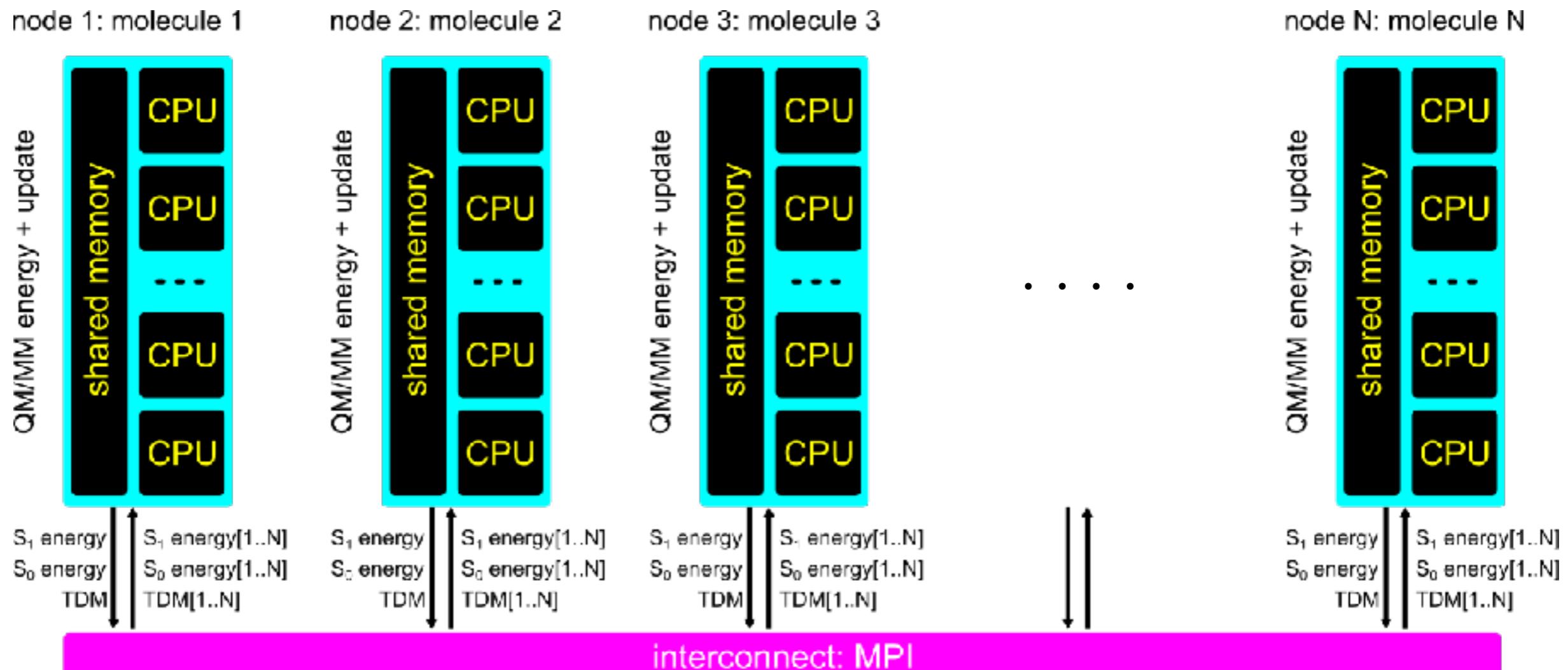
linear scaling cavity “QED”/MM



Sisu.csc.fi: 1688 TFlop/s

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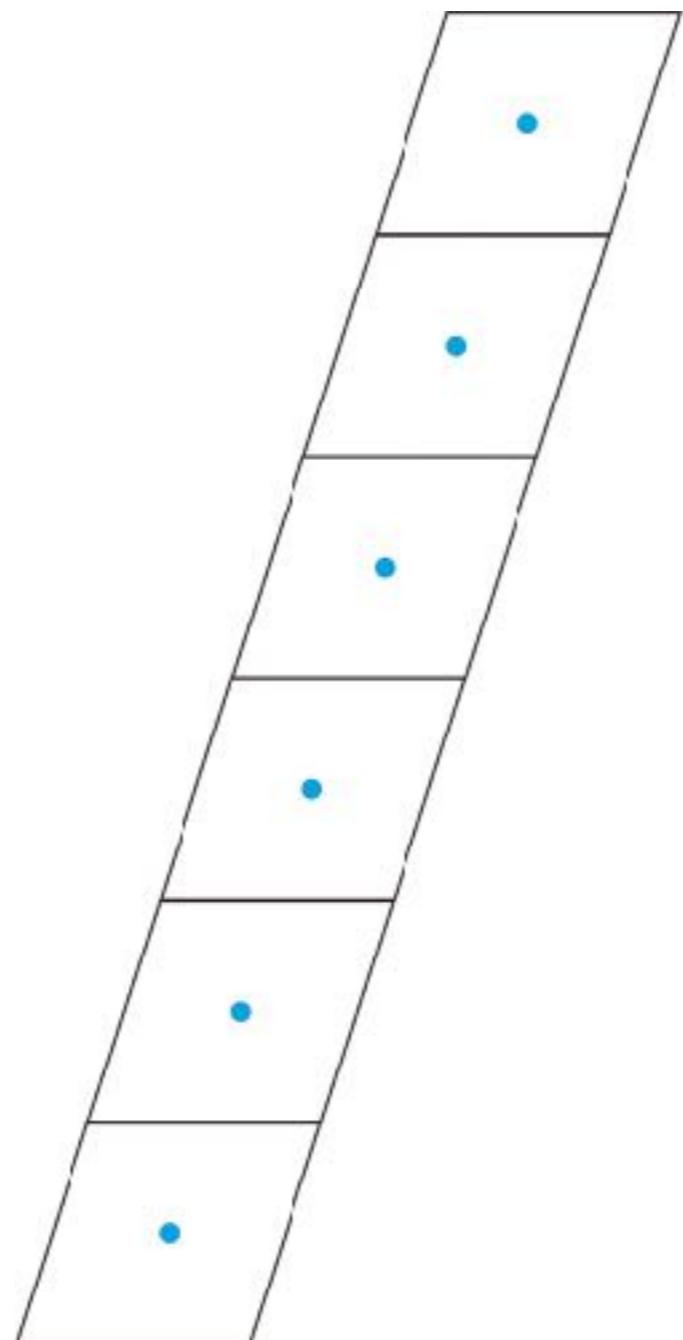
new world record?

43,200 QM / 17,700,800 MM atoms on 1,600 nodes (38,400 CPUs)

X-ray crystallography

scattering from one atom in the unitcell

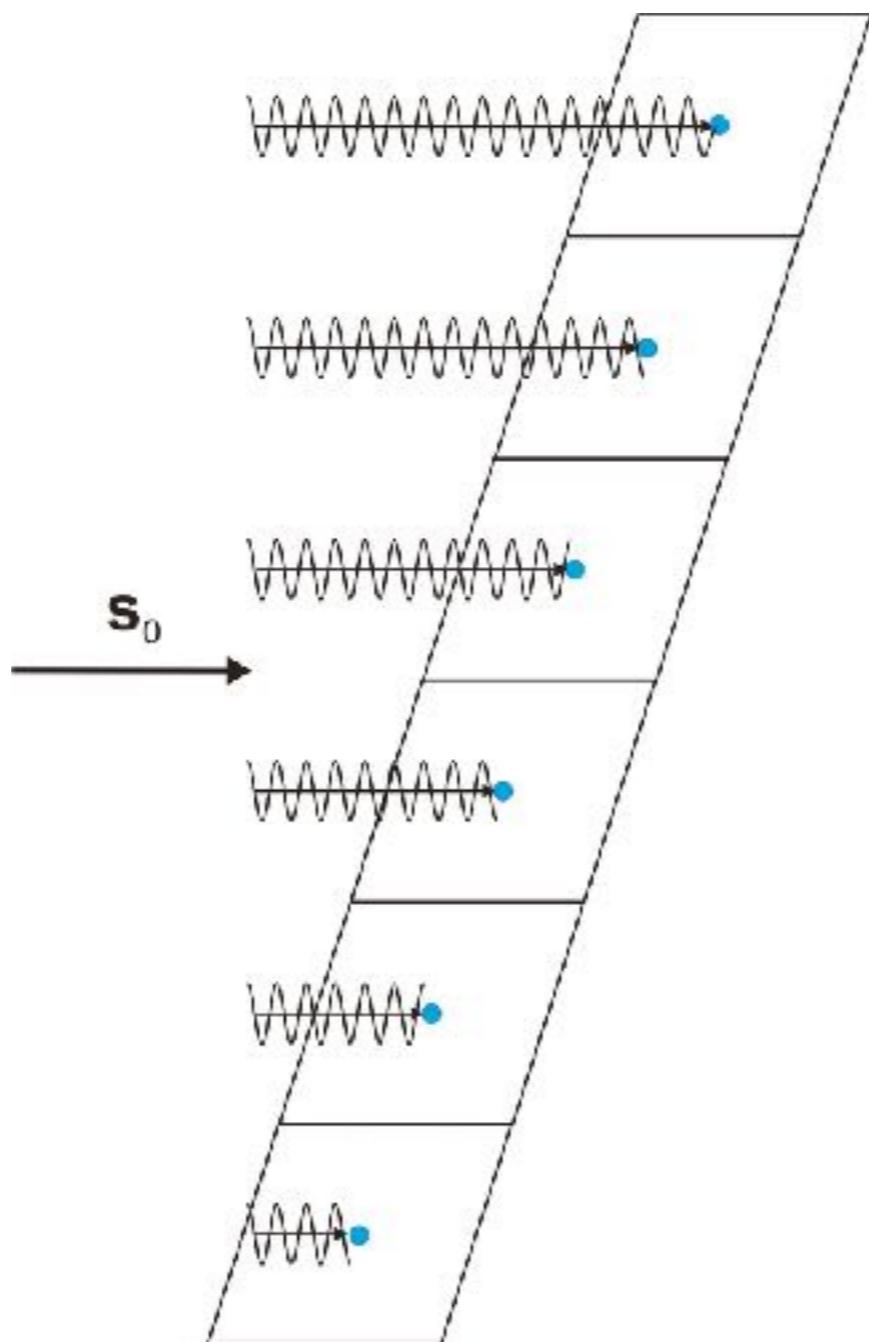
crystal (i.e lattice of unitcells)



X-ray crystallography

scattering with one atom in the unitcell

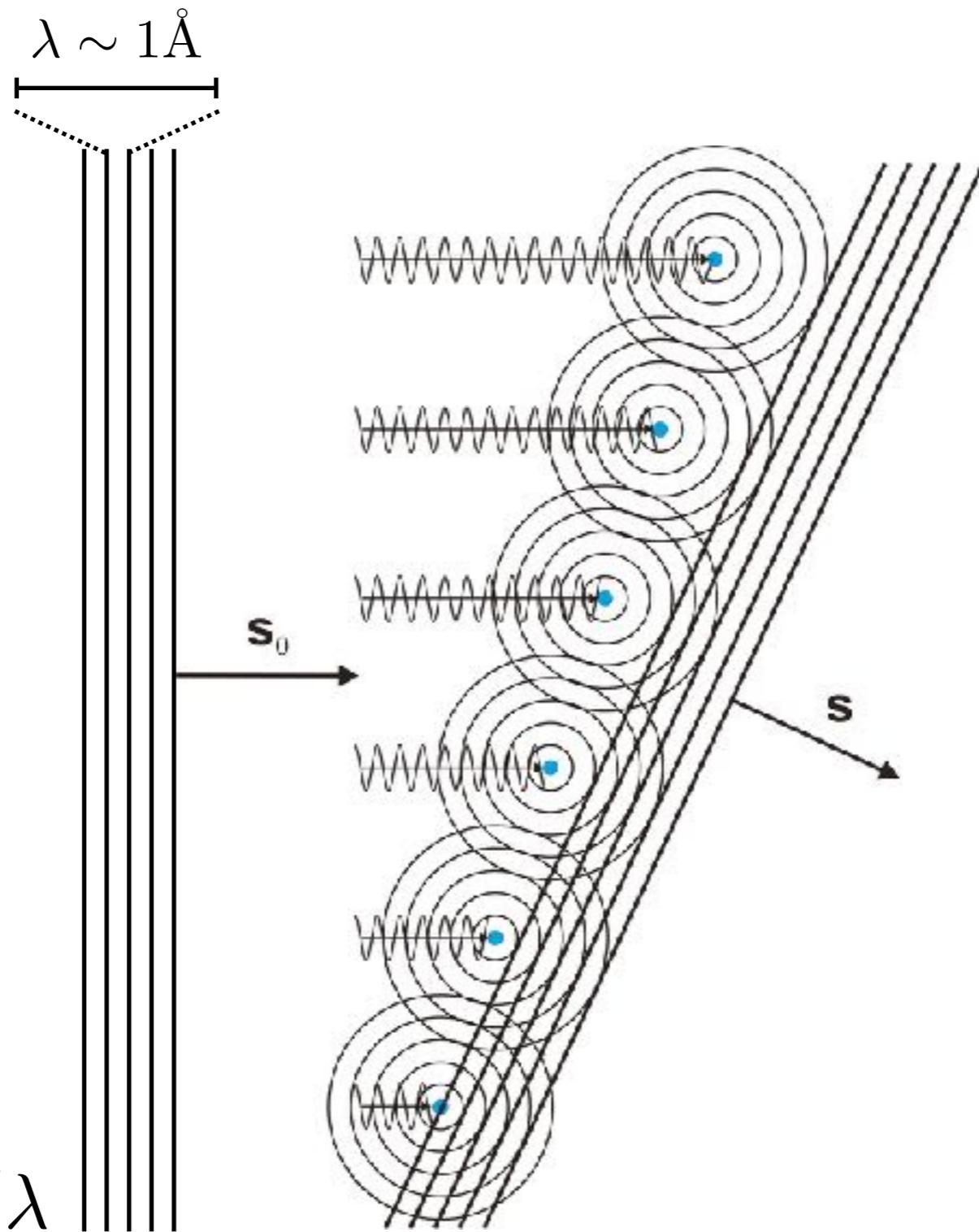
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X-ray crystallography

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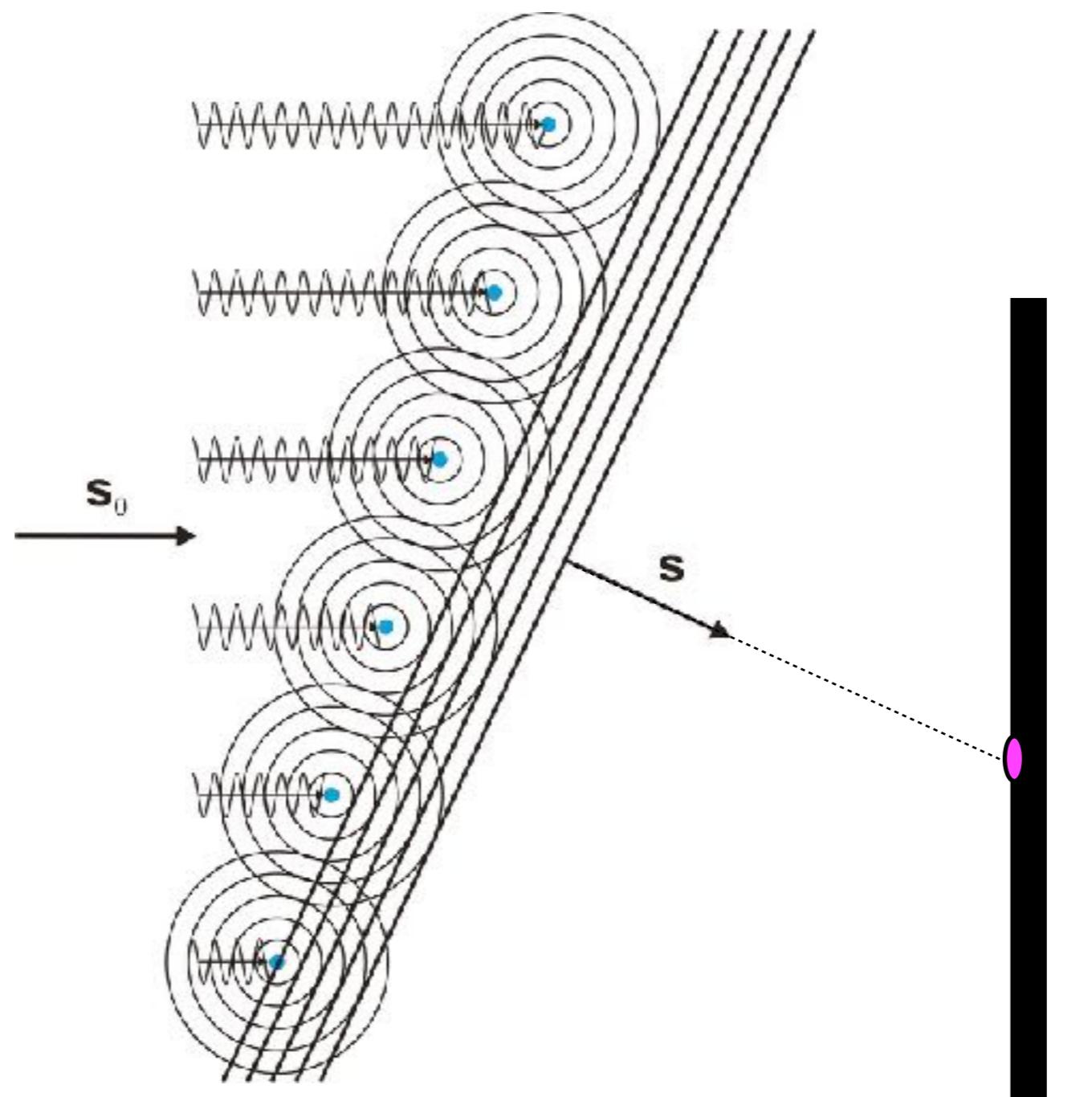
scattering vector

$$\mathbf{S} \equiv (\mathbf{s} - \mathbf{s}_0)/\lambda$$

X-ray crystallography

scattering with one atom in the unitcell

crystal (i.e lattice of unitcells)



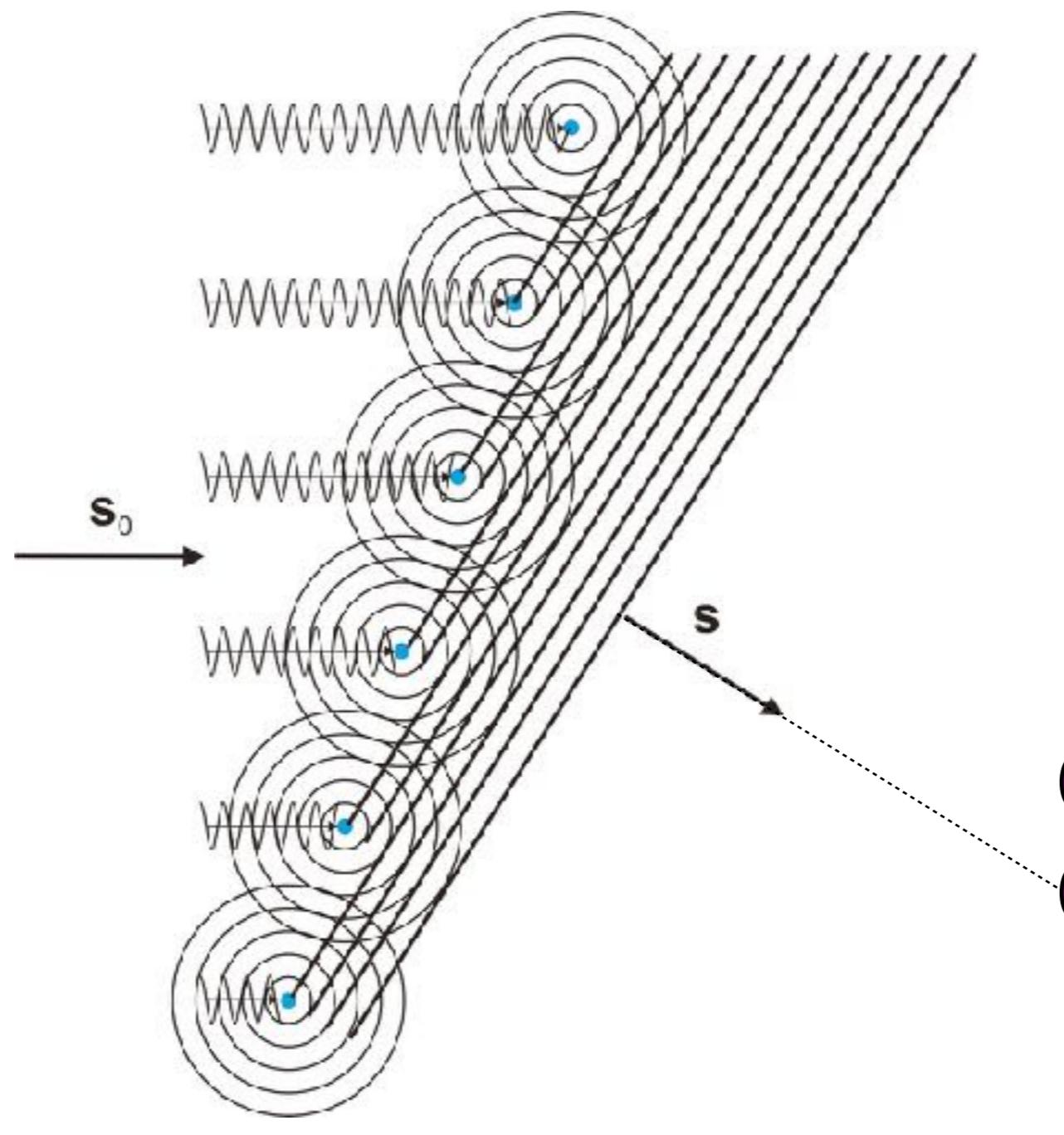
scattering vector

$$\mathbf{S} \equiv (\mathbf{s} - \mathbf{s}_0)/\lambda$$

X-ray crystallography

scattering with one atom in the unitcell

crystal (i.e lattice of unitcells)



scattering vector

$$\mathbf{S} \equiv (\mathbf{s} - \mathbf{s}_0)/\lambda$$

far away detector (not to scale)

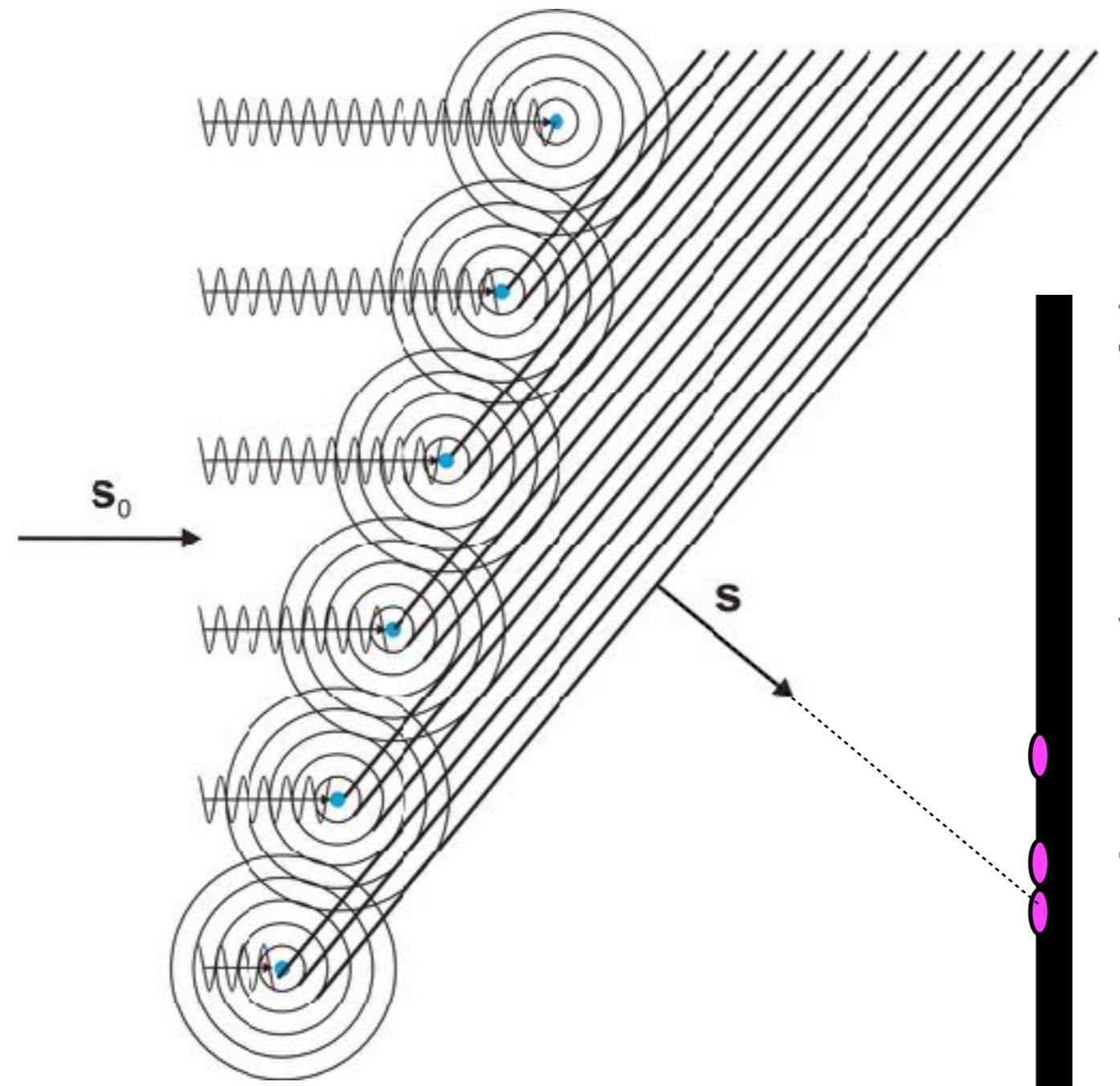
X-ray crystallography

scattering with one atom in the unitcell

crystal (i.e lattice of unitcells)

discrete scattering spots: diffraction

reflections



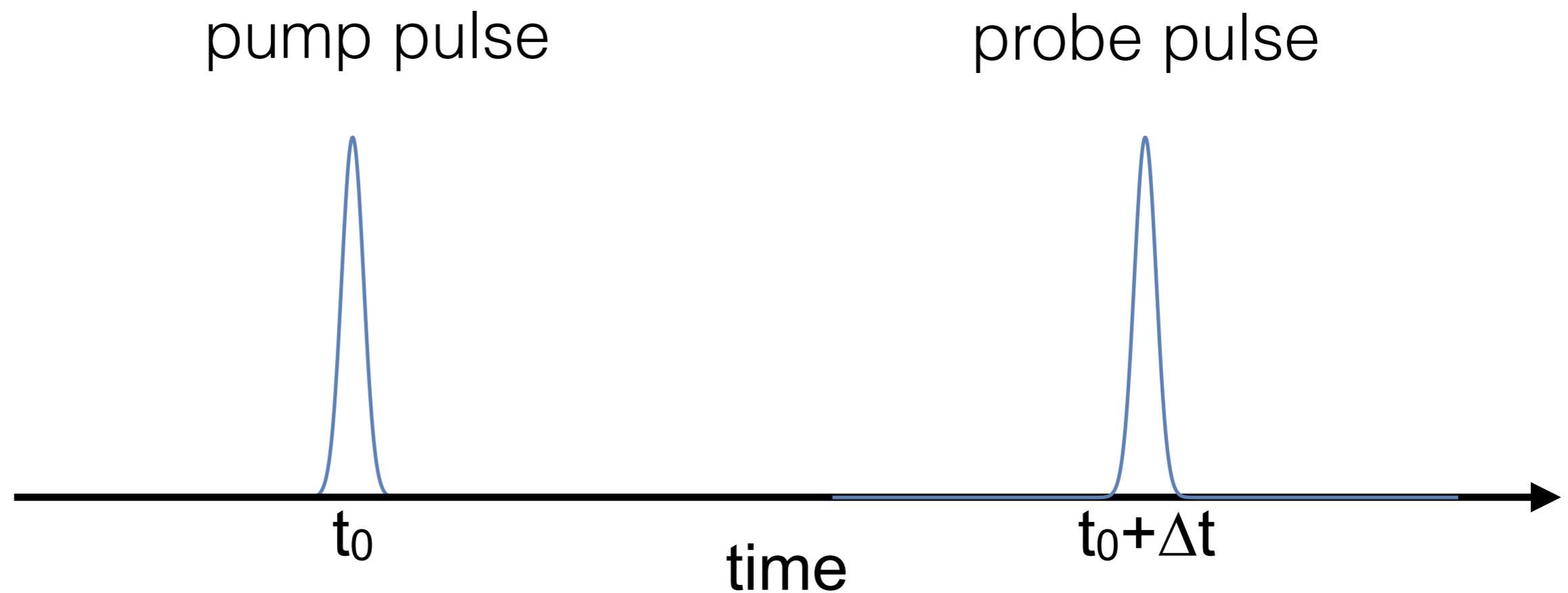
scattering vector

$$\mathbf{S} \equiv (\mathbf{s} - \mathbf{s}_0)/\lambda$$

far away detector (not to scale)

Time-resolved spectroscopy

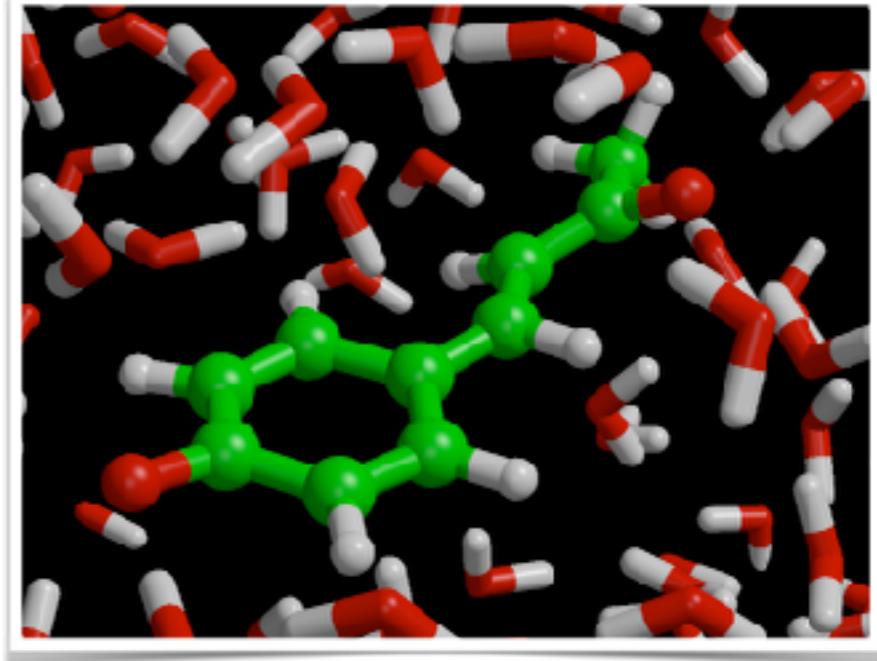
linear pump-probe spectroscopy



Time-resolved spectroscopy

linear pump-probe spectroscopy

idealised example: PCK in water

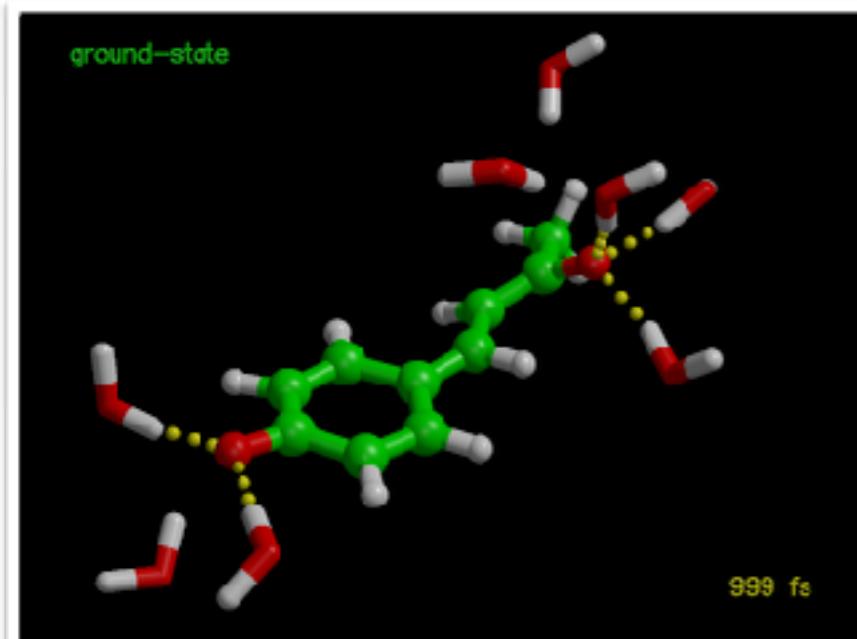
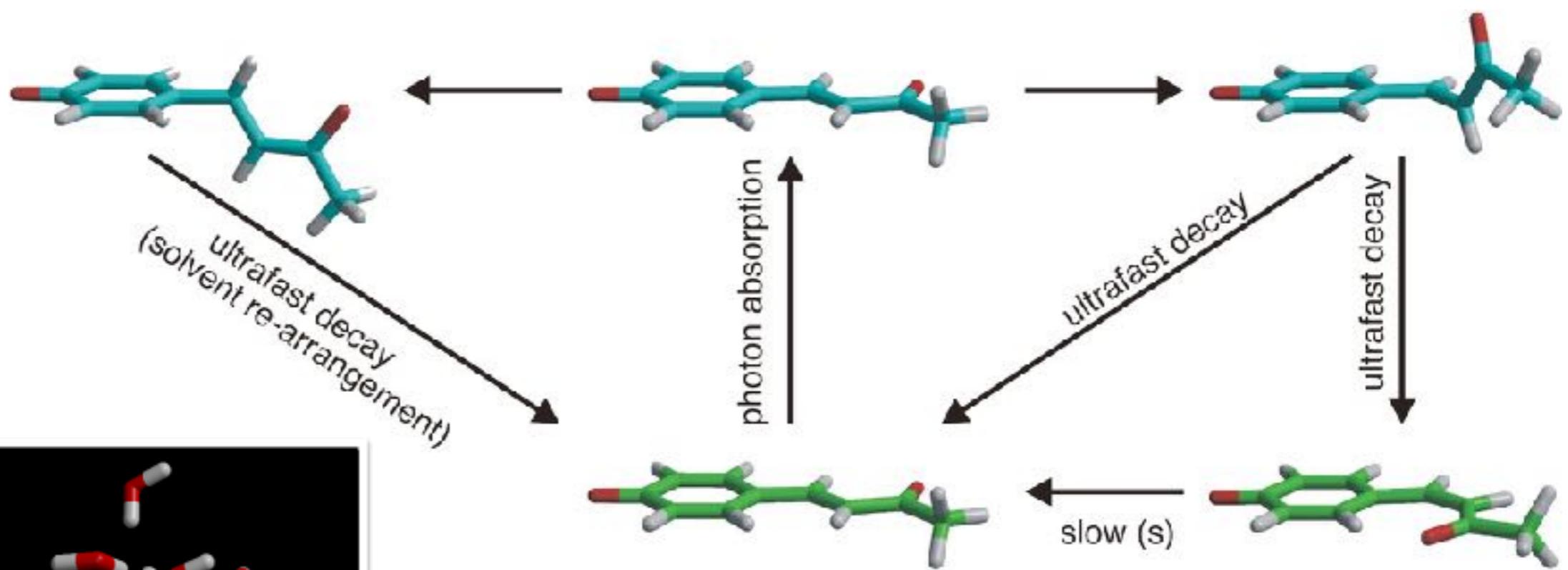
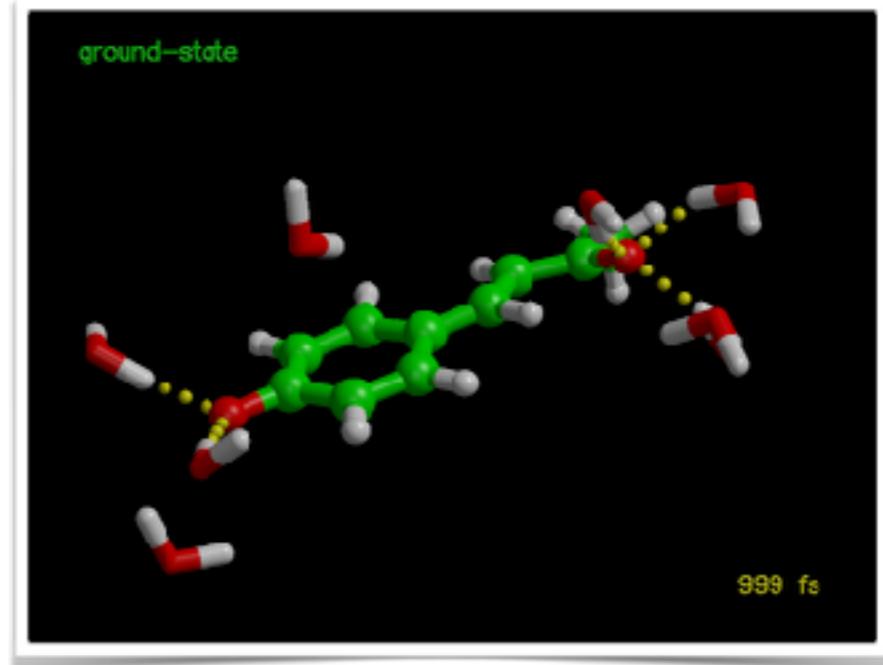


Time-resolved spectroscopy

linear pump-probe spectroscopy

idealised example: PCK in water

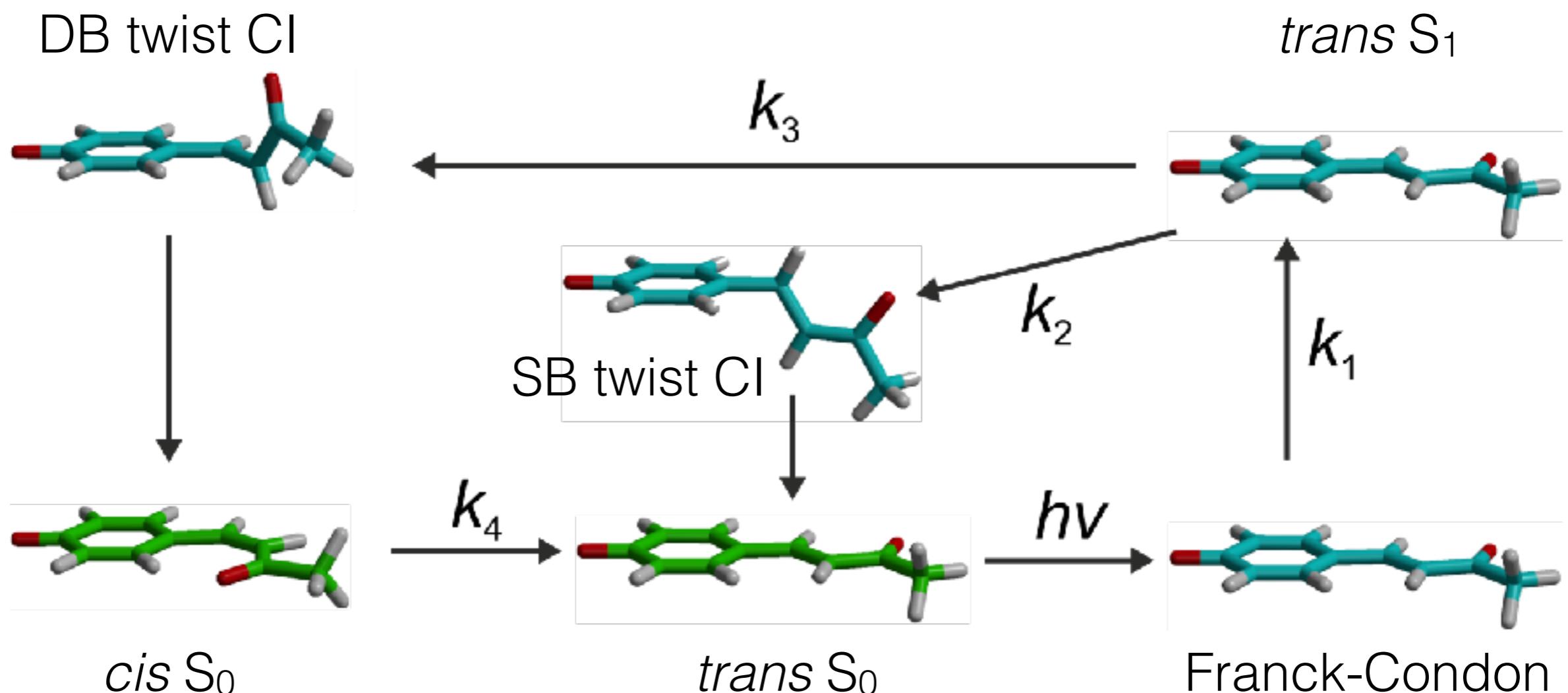
assuming our simulations are correct ;-)



Time-resolved spectroscopy

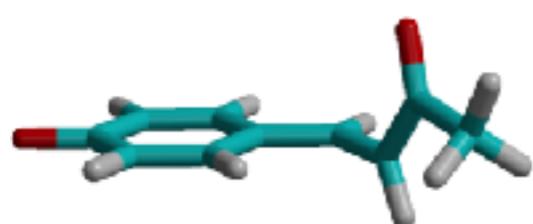
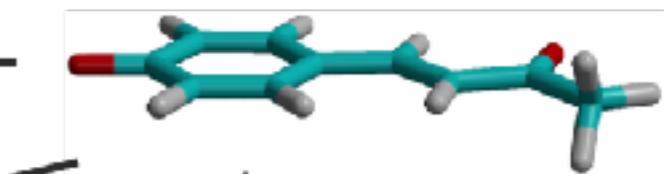
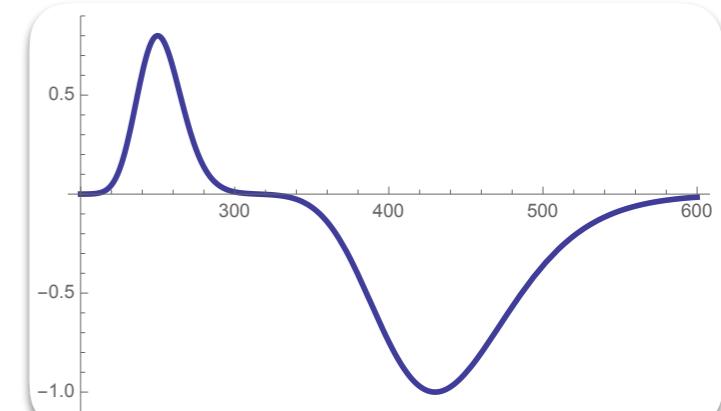
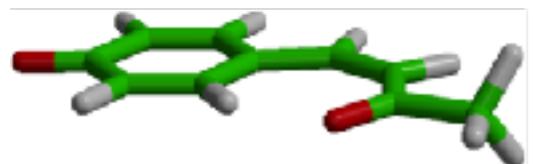
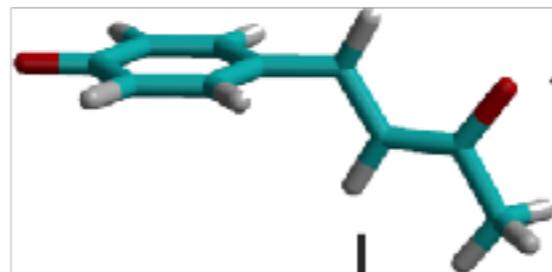
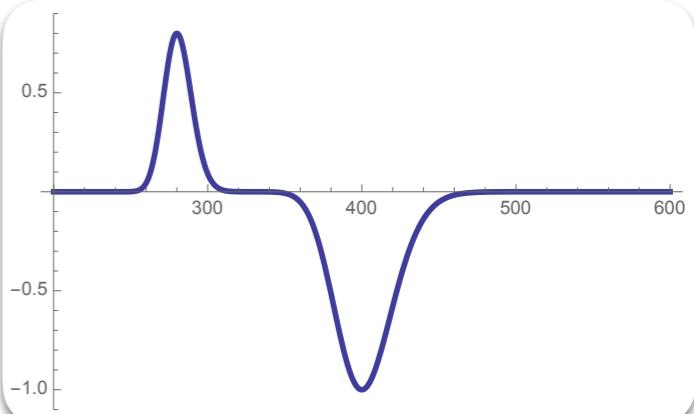
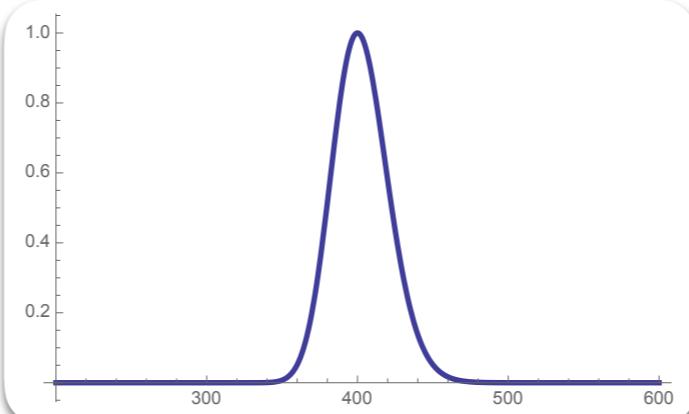
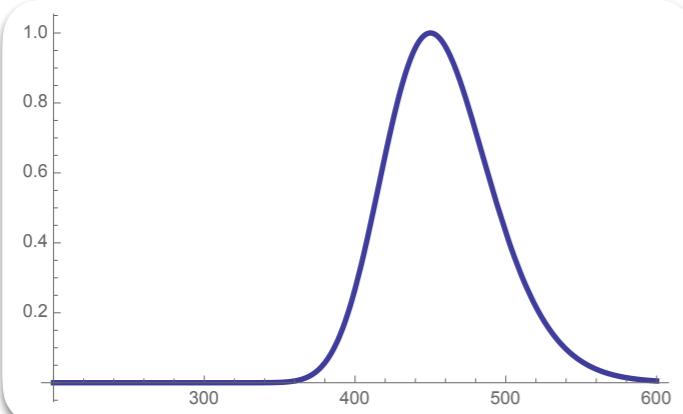
note: different orientation of reaction scheme!

horizontal excitation ;-)



Time-resolved spectroscopy

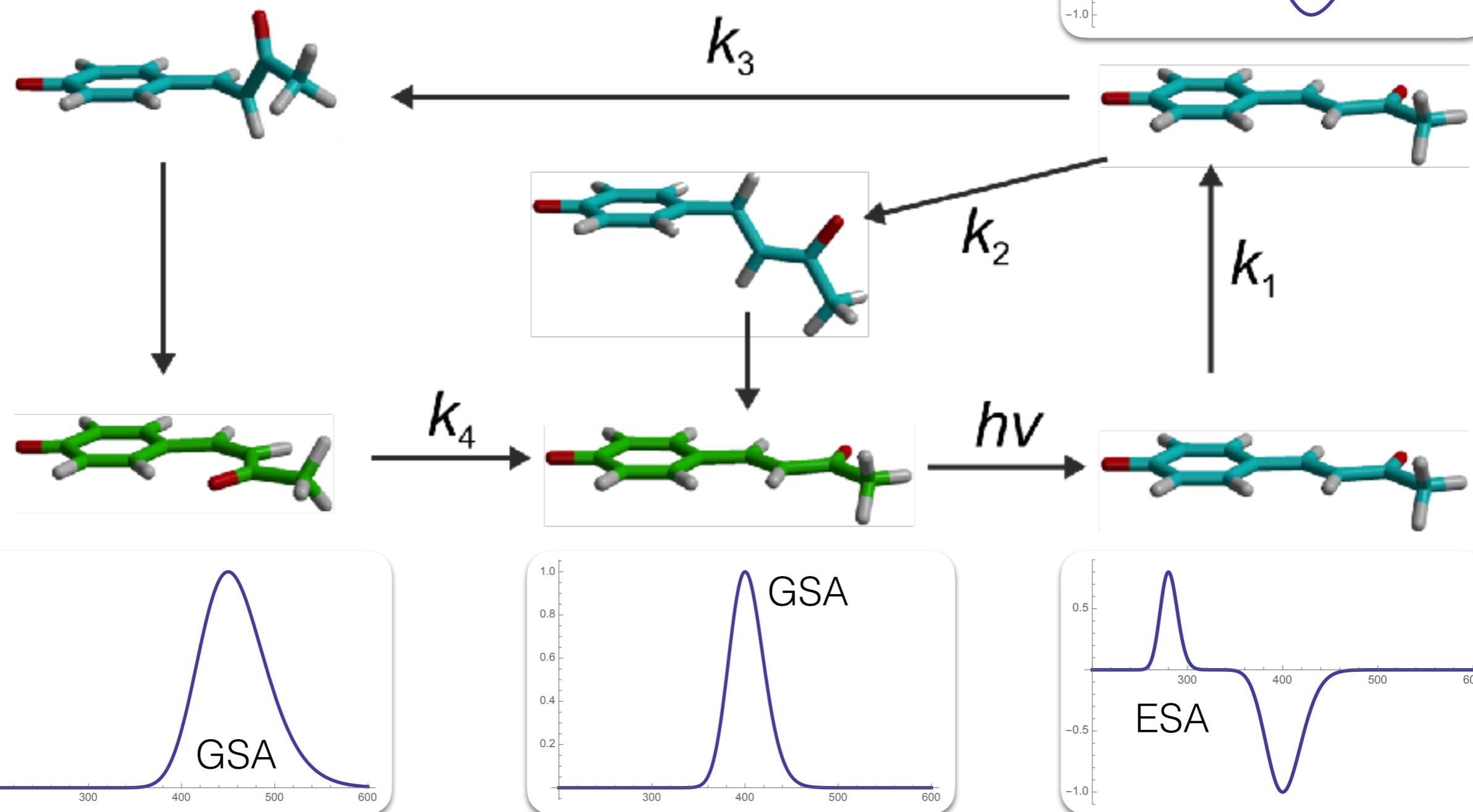
intermediates are species with own spectrum:

 k_3  k_2 k_1  k_4 $h\nu$ 

Time-resolved spectroscopy

intermediates are species with own spectrum:

ground/excited state absorption

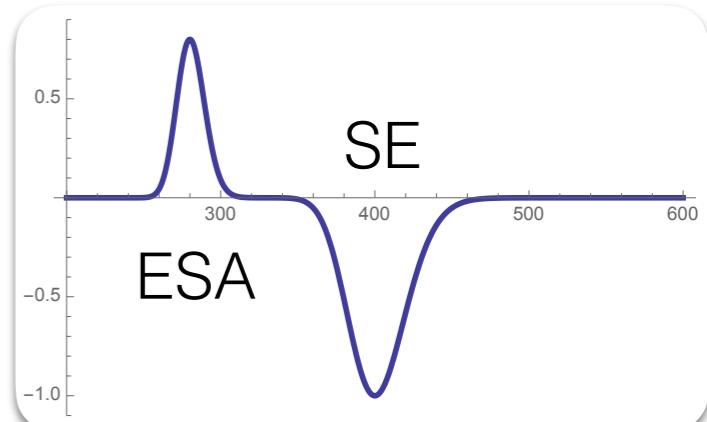
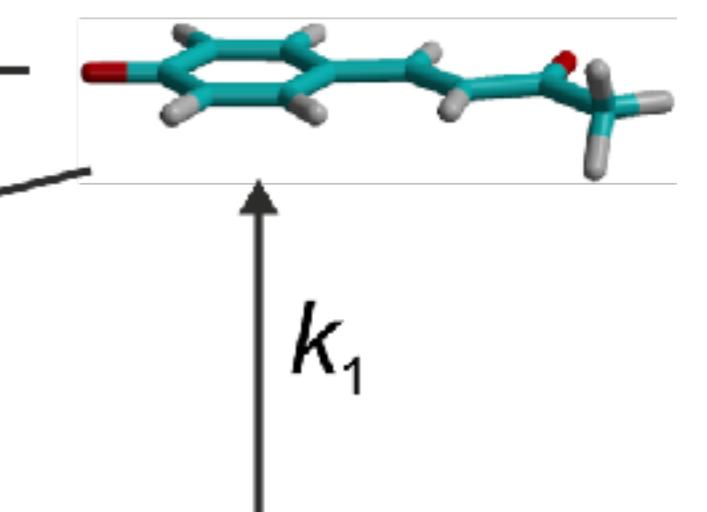
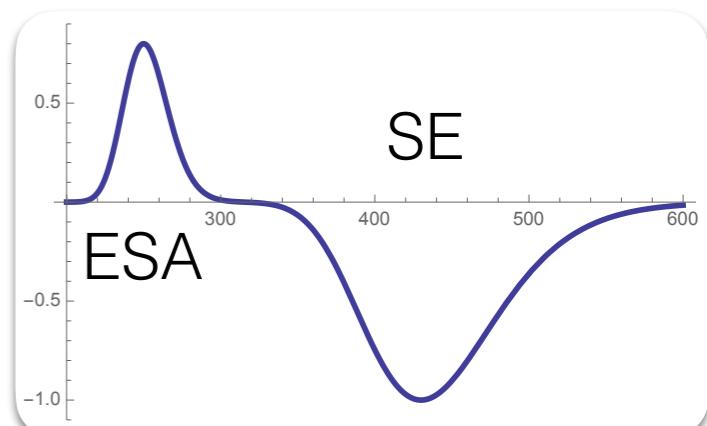
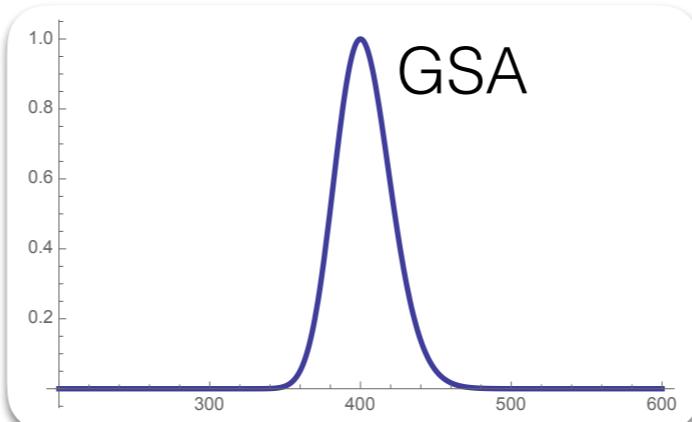
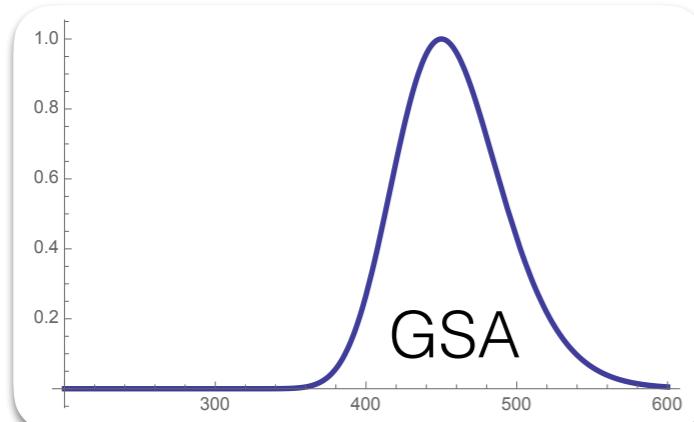
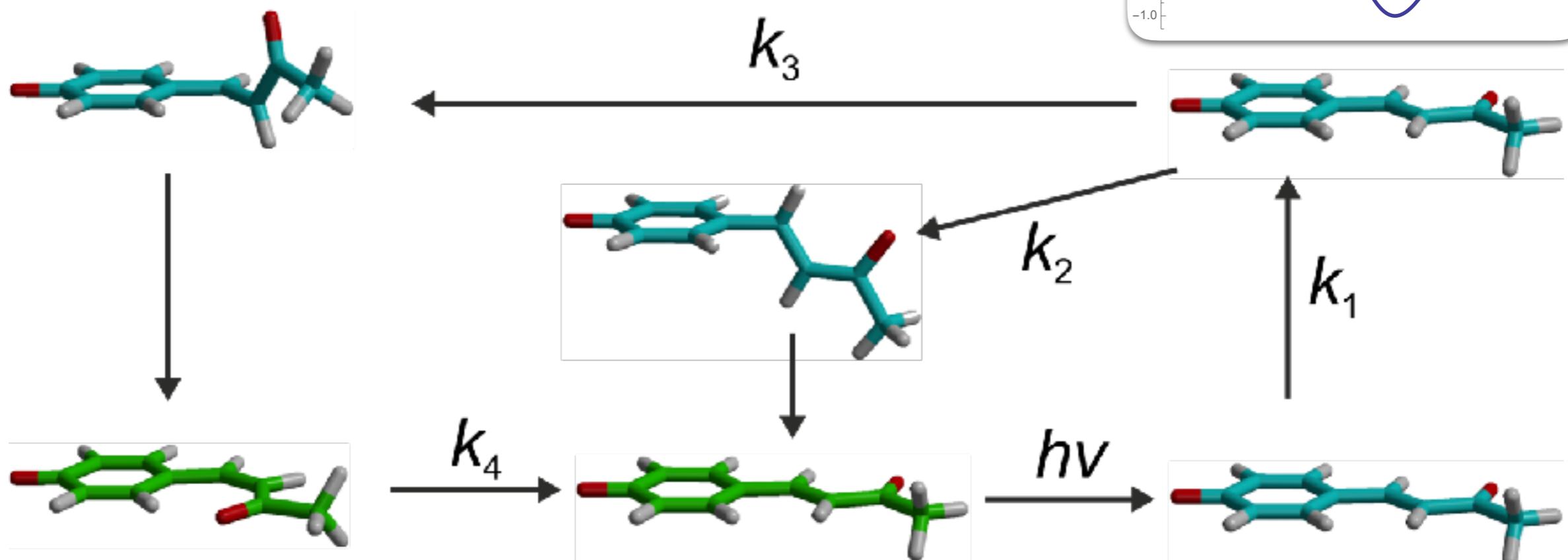


Time-resolved spectroscopy

intermediates are species with own spectrum:

ground/excited state absorption

stimulated emission



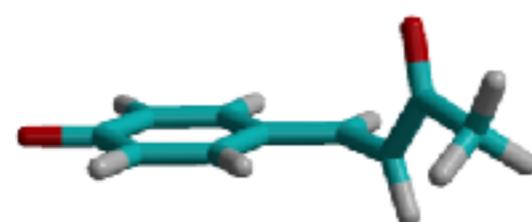
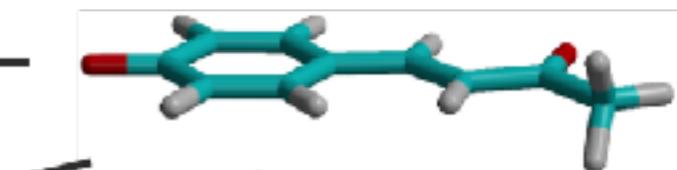
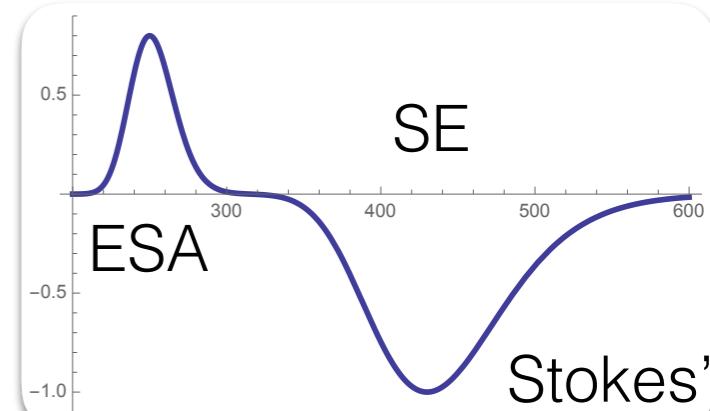
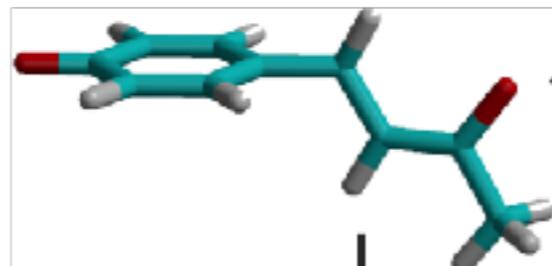
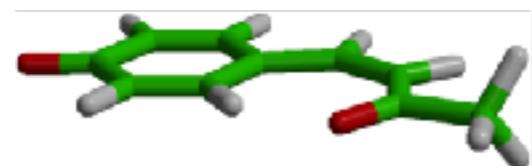
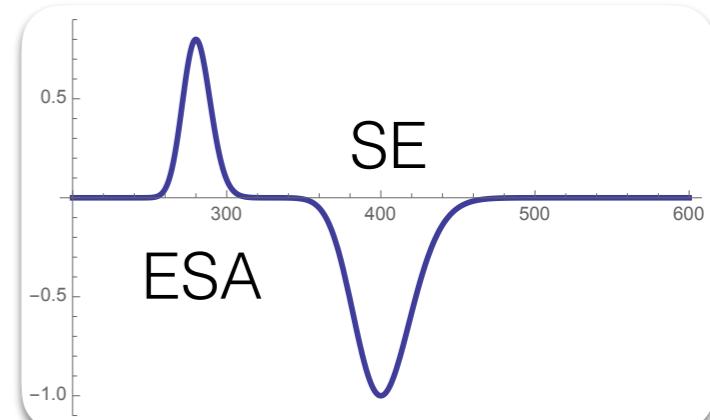
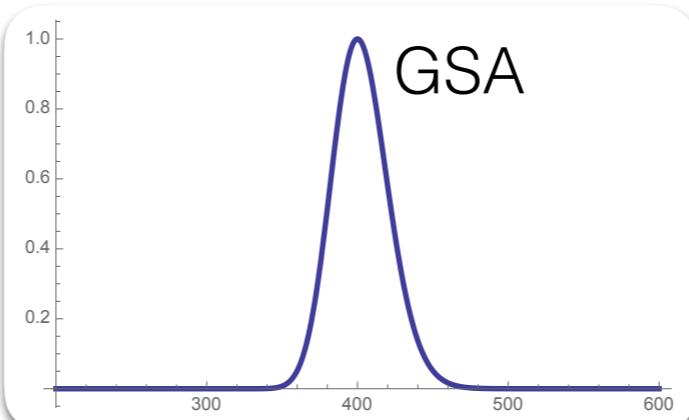
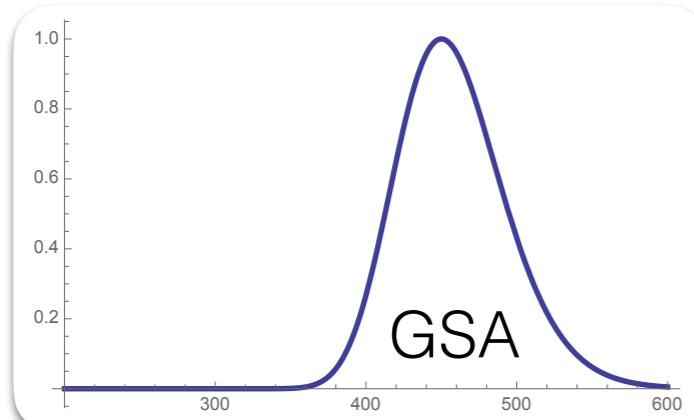
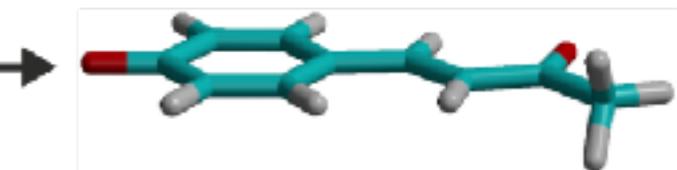
Time-resolved spectroscopy

intermediates are species with own spectrum:

ground/excited state absorption

stimulated emission

Stokes' shift

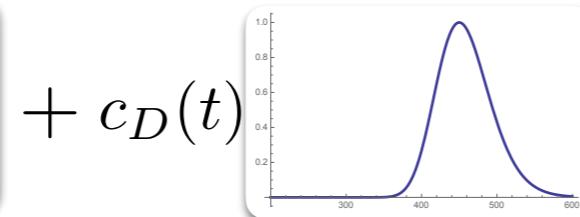
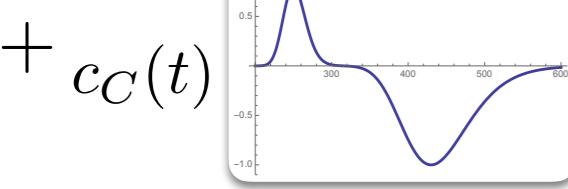
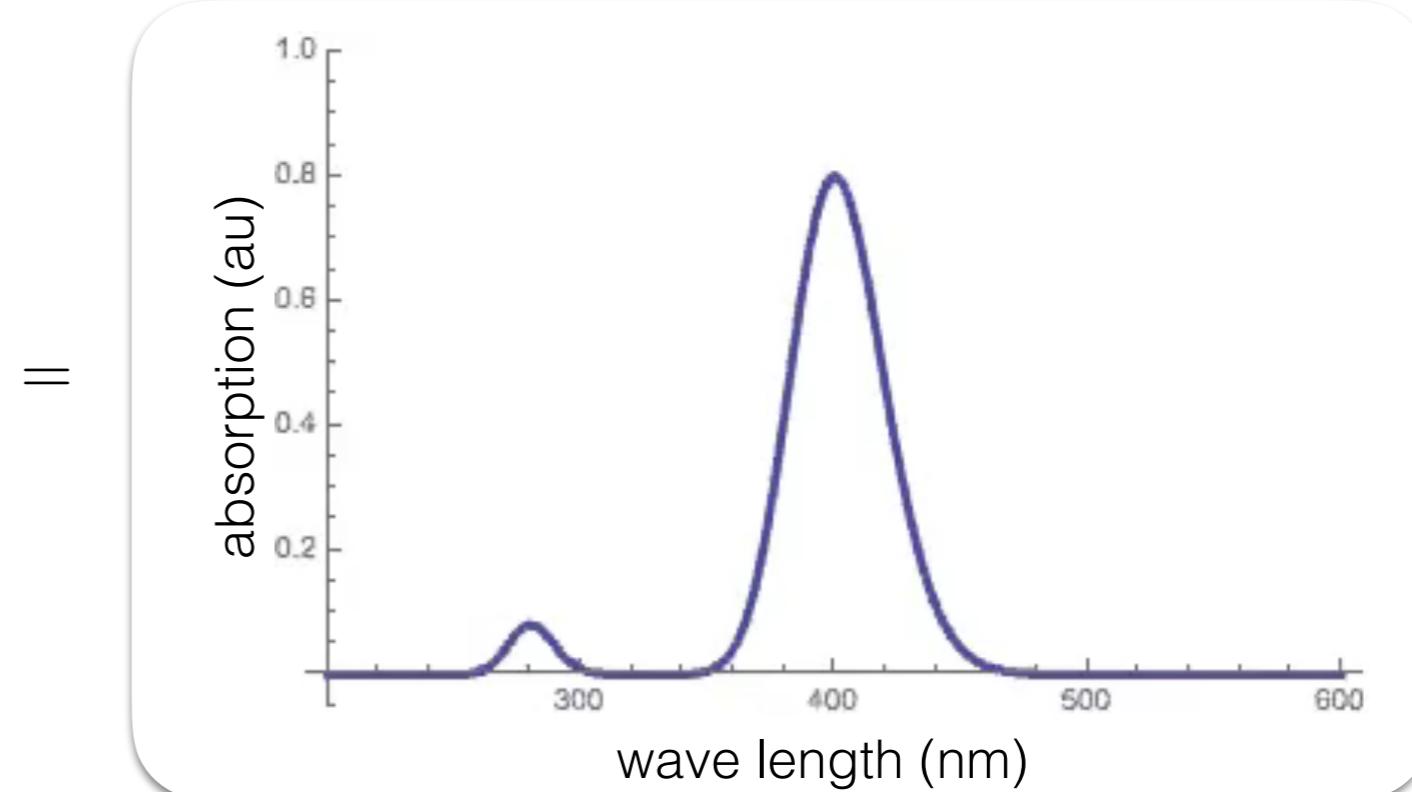
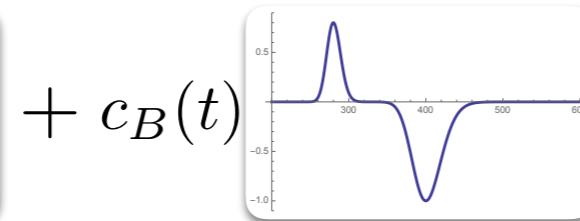
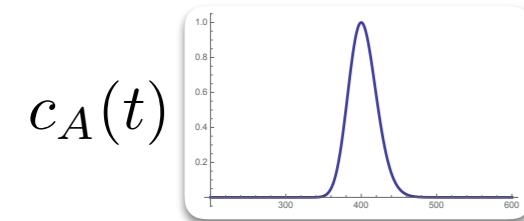
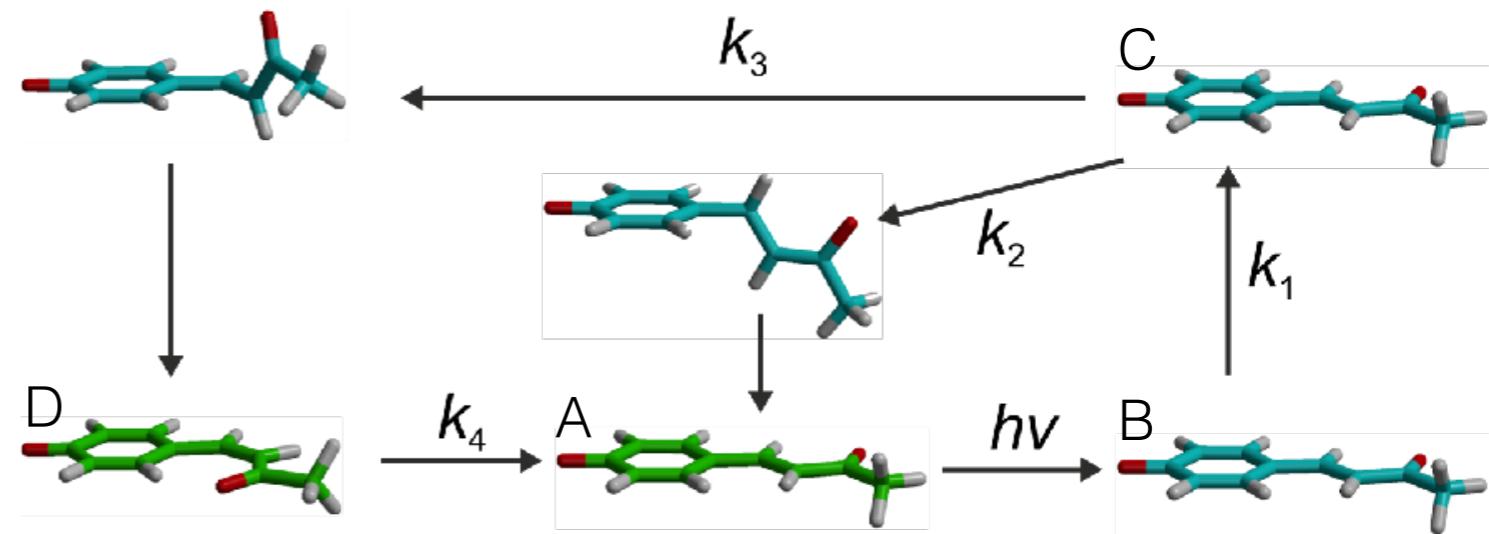
 k_3  k_1  k_2  k_4 $h\nu$ 

Time-resolved spectroscopy

time-dependent spectrum

linear superposition of SAS

$$S(\lambda, t) = \sum_i c_i(t) s_i(\lambda)$$



the problem

from atomistic model to spectral signal: easy

from spectral signal to atomistic model: difficult

heavily underdetermined optimisation problem