

PAUL SCHERRER INSTITUT



Dr. Jörg Standfuss :: Group Leader :: Laboratory of Biomolecular Research

# Watching the release of a photopharmacological drug over fourteen orders of magnitude in time

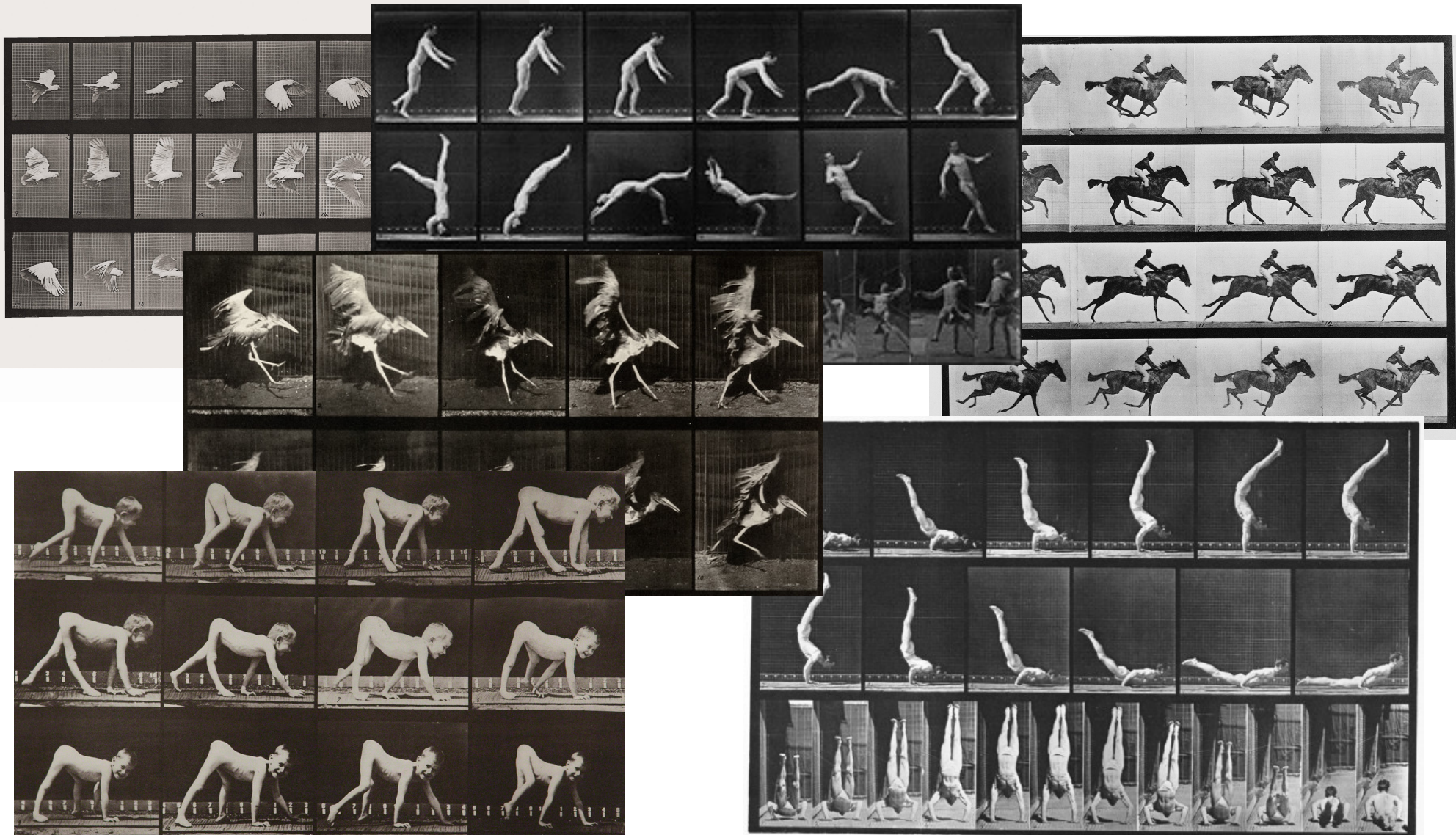
Leaps meets Life Sciences, May 2023



# Human And Animal Locomotion Photographs

“Eadweard Muybridge, 1887”

*Temporal snapshots allow the study of dynamic-function relationships*





# Time-resolved structural biology group

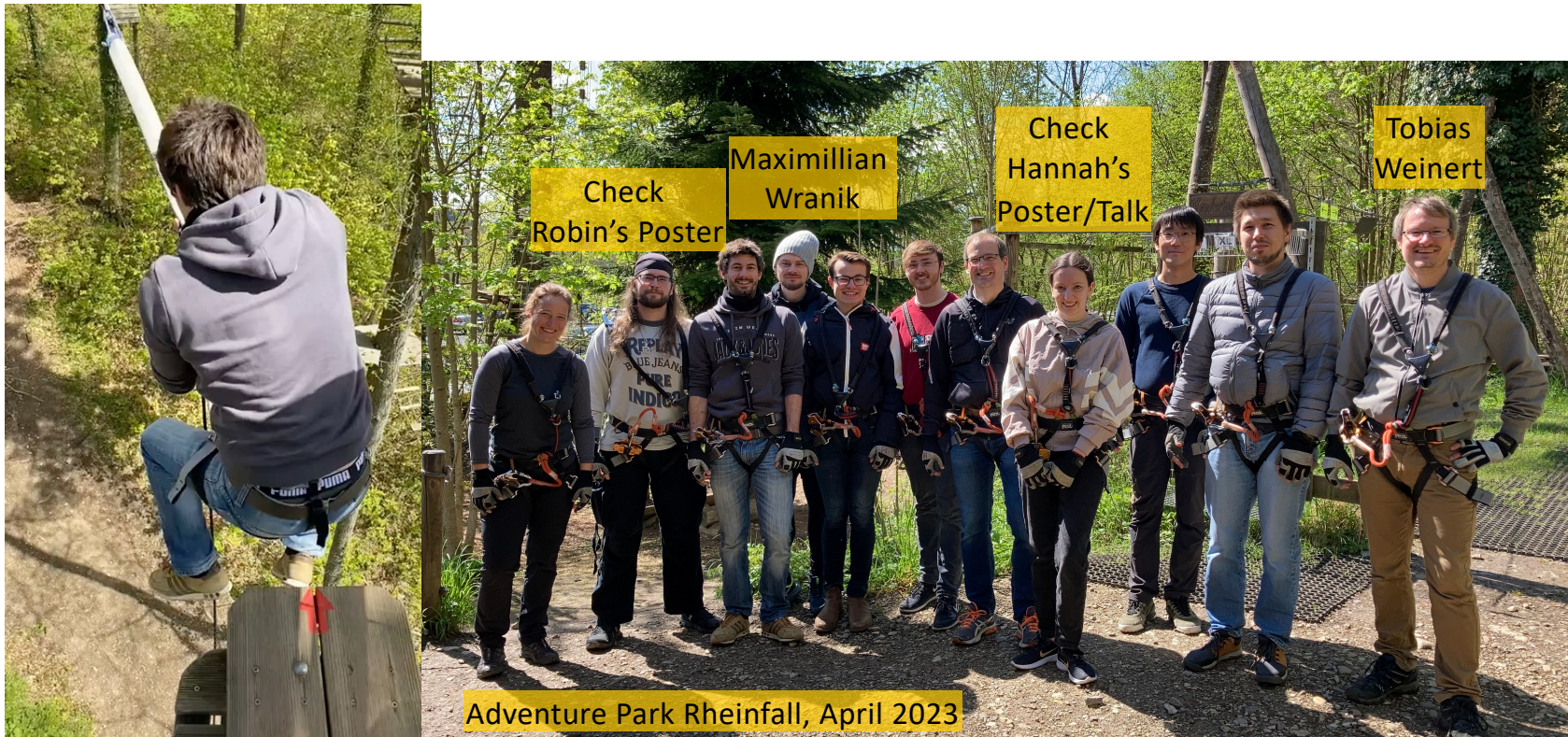
@ Laboratory of Biomolecular Research, PSI

**Members:** Hannah Glover, Robin Stipp, Peter Seidel, Georgii Khusainov, Thomas Mason, Melissa Carrillo, Matthias Mulder, Sina Hartmann, Quentin Bertrand, Yasushi Kondo, Fabienne Stierli, Michal Kepa, Tobias Weinert, Jörg Standfuss

**Former Members:** Max Wranik, Przemek Nogly, Antonia Furrer, Dan James, Petr Skopintsev, Demet Kekilli, Kathrin Jäger, Dardan Gashi, Steffen Brünle

## Mission statement:

**We include time as a fourth dimension in structural biology to resolve transient conformational states important for protein function.**





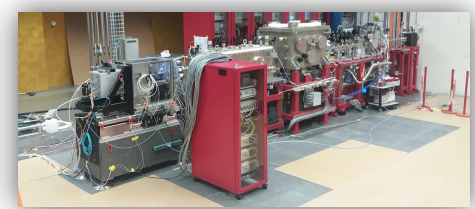
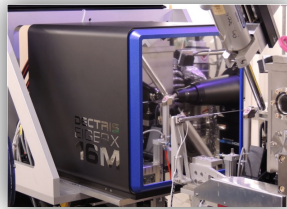
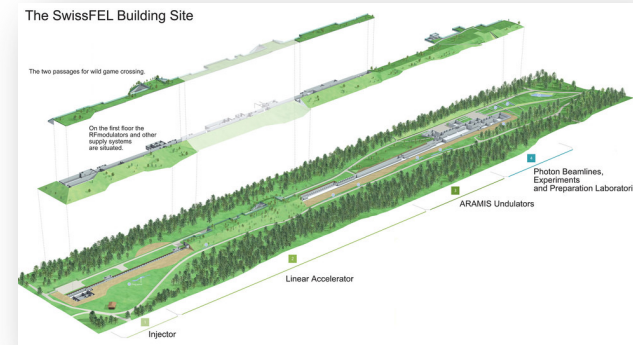
# “High-speed cameras” at the PSI

Swiss Light Source and Swiss X-ray Free Electron Laser

## SLS (& SLS 2.0)



## SwissFEL



Macromolecular crystallography

X06SA PXI  
X10SA PXII  
X06DA PXIII  
SwissFEL  
MX

Macromolecular crystallography:  
MAD, SAD, large unit cells, small crystals,  
spectroscopy, screening, multi-axis go-  
niometer, ...

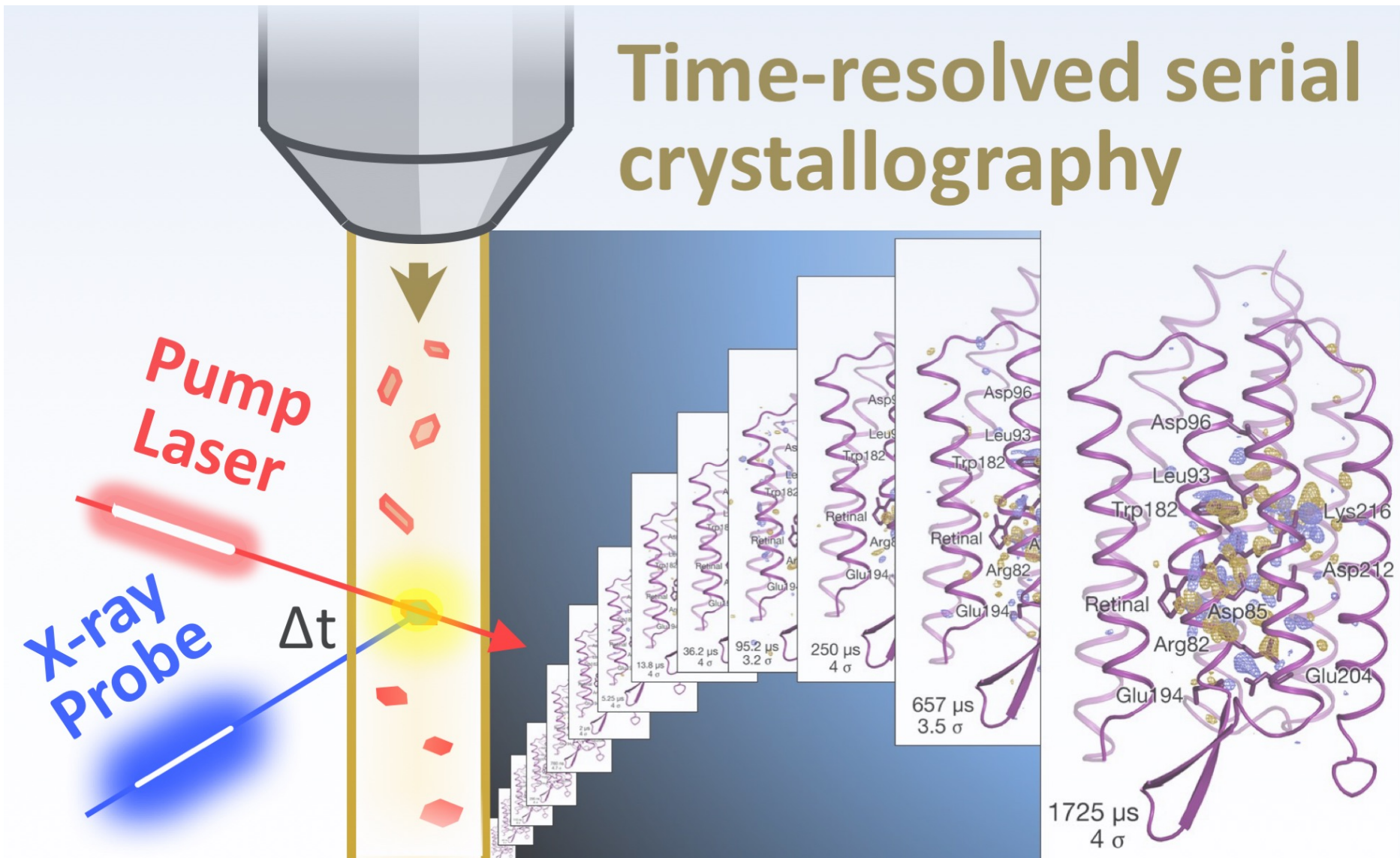
1. experimental station Alvra
2. experimental station Bernina
3. experimental station Cristallina

Collaboration: F. Dworkowski, M. Wang  
and co-workers

C. Milne, J. Beale, C. Bacellar,  
and co-workers



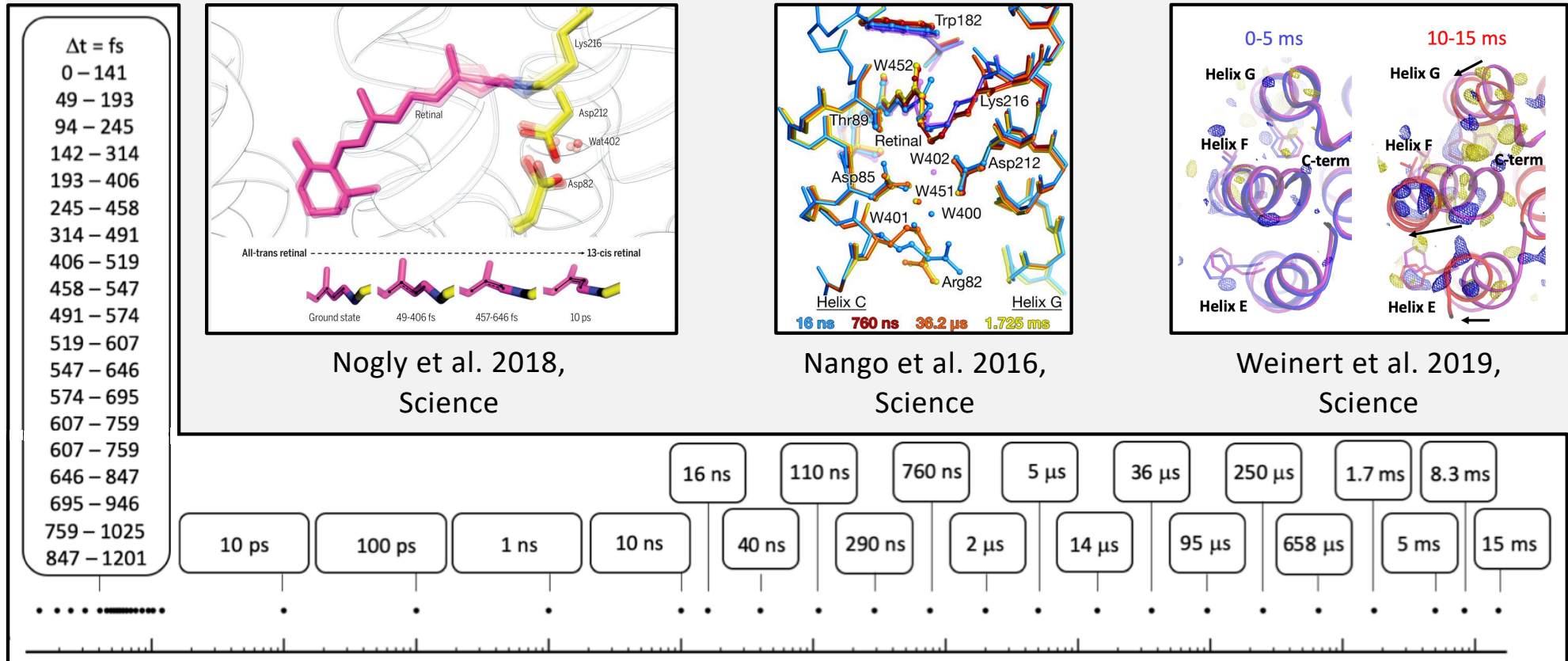
# Bringing time-resolved measurements to the molecular scale





# Pioneering works at synchrotrons and X-ray lasers

*Learning and establishing technology abroad before bringing it to PSI*



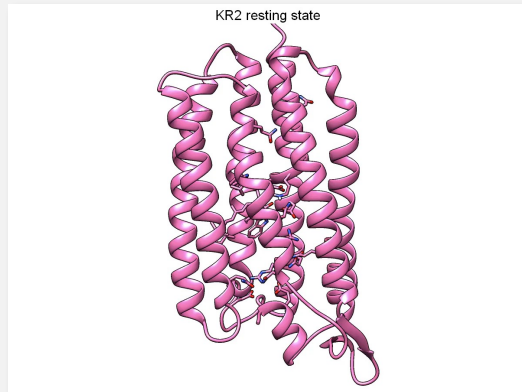
## Light-driven proton pump bacteriorhodopsin

- Largest structural dynamics data resource available for any protein
- The (nearly) whole pumping cycle resolved from isomerization to proton release and re-uptake



# First user experiments at SwissFEL

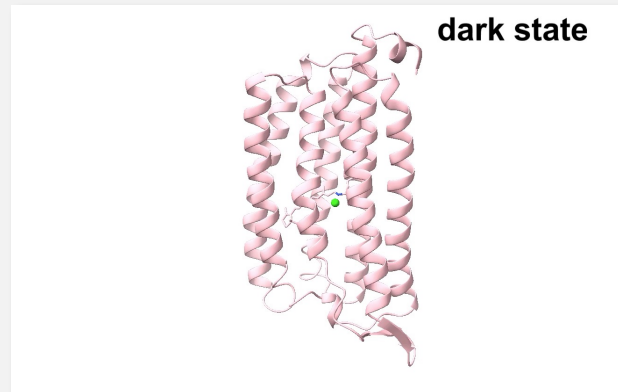
*Rhodopsins pave the way into a dynamic future for structural biology*



Skopintsev *et al.*, 2020,  
Nature

## Sodium pumping rhodopsin

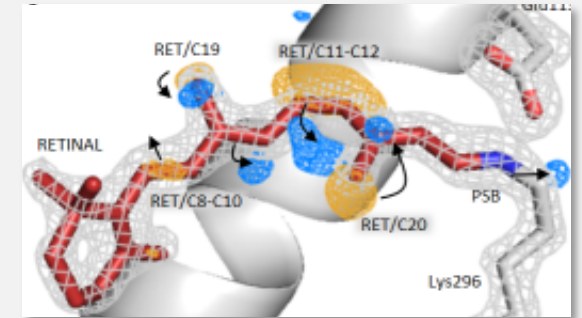
- Ten molecular snapshots of **sodium** transport **out of the cell**
- Next-generation **optogenetic tool**



Mous *et al.*, 2022,  
Science

## Chloride pumping rhodopsin

- SwissFEL and SLS resolves **chloride** transport **into the cell**
- Electrostatic gates **explain transport**  
**Nice seeing you Sandra!!**



Gruhl *et al.*, 2023,  
Nature

## Visual GPCR rhodopsin

- Molecular snapshots of the **early events in vision**
- **GPCR activation**  
**Great talk Valerie!!**

Collaboration Nogly & Schertler



# Dynamics in Drug Discovery

*Perhaps using the right kind of experiments these questions can be addressed*

- **Binding and drug design:** Protein-ligand interactions are best described by dynamic induced-fit or conformational selection mechanisms and not a simplistic key-and-lock.
- **Binding kinetics:** Protein dynamics influence the rate at which a drug molecule binds to its target protein and the residence time of the drug at the binding site.
- **Allosteric regulation:** Protein dynamics are critical for transmitting allosteric signals from a drug binding site to distant sites affecting protein function.
- **Drug resistance:** Mutations can alter protein dynamics, reducing the effectiveness of a drug.
- **Mechanisms of drug action:** Conformational changes in receptors, transporters, channels or kinases can explain drug action in detail.



## **X-ray lasers allow us to observe structural changes in a wide temporal window**

Blink of an eye = 0.1 s

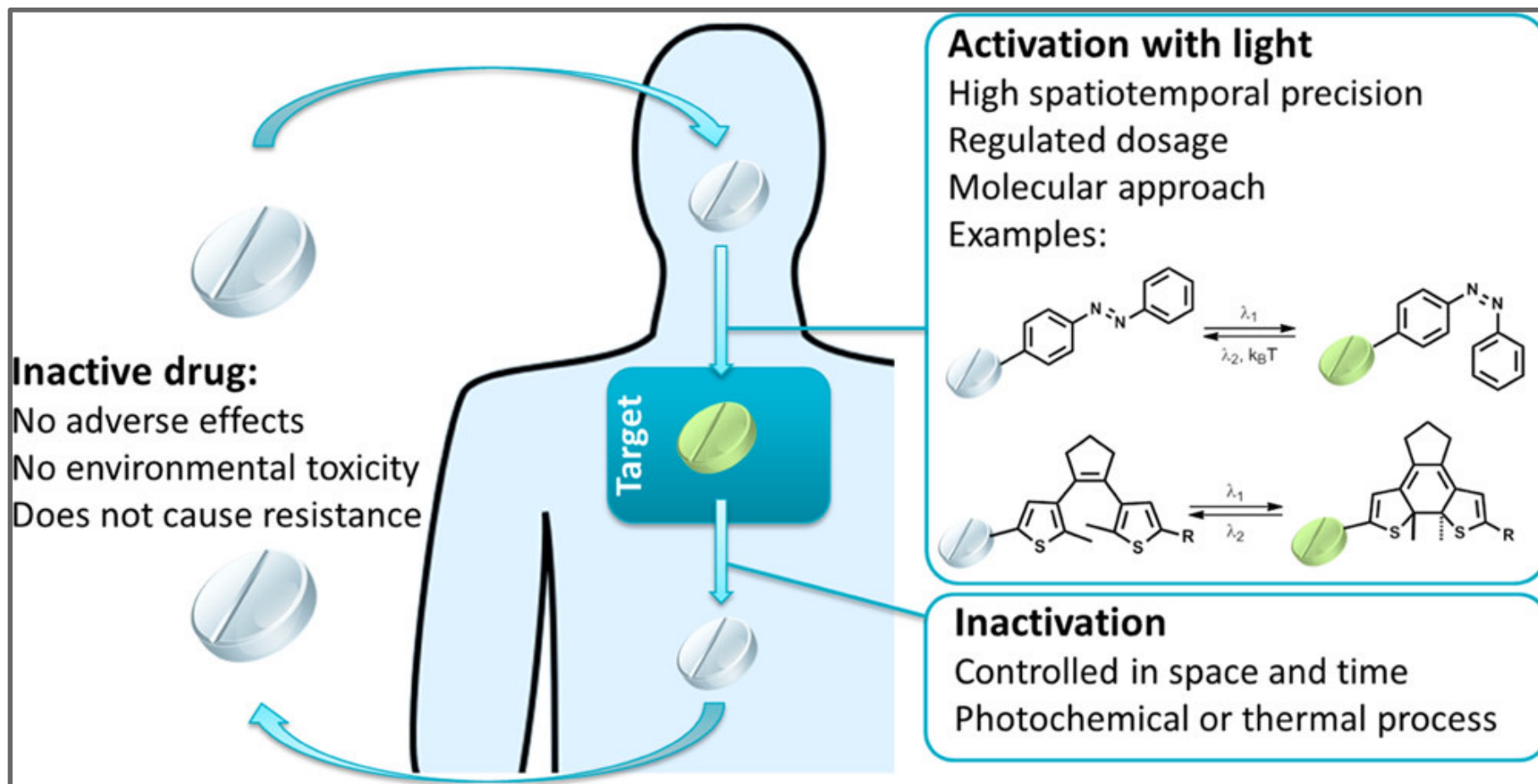
Photocycle = 0.01 s

Retinal excitation = 0.000 000 000 000 1 s

**-> But drug targets don't have photoswitches!  
...or do they?**

# The field of photopharmacology

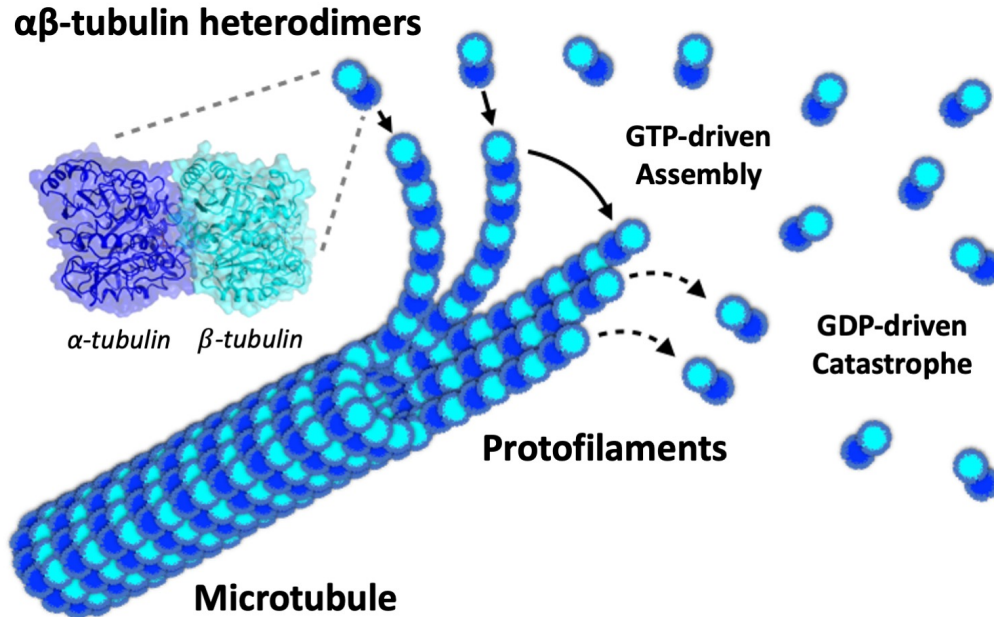
*Allows for remote spatial and temporal control of bioactivity by light*



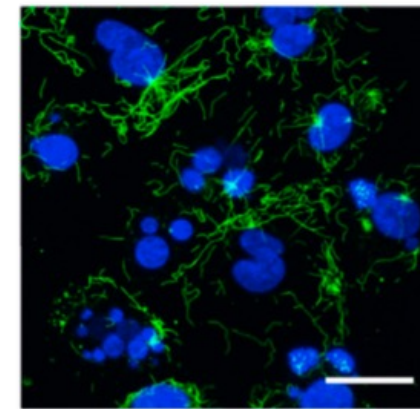
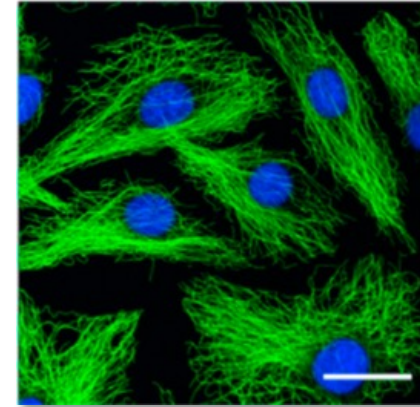
Taken from: W. Velema, W. Szymanski & B. Feringa (2014)



## Target of interest:



## Photopharmacology:



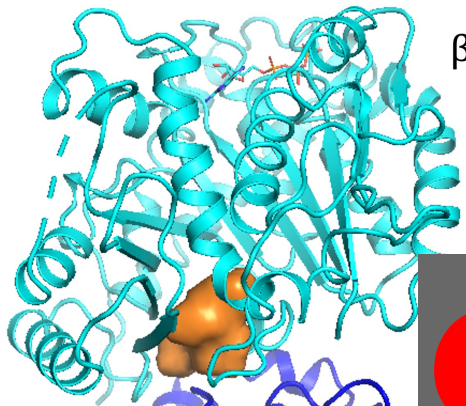
## Tubulin binding drugs:

- Kill cancer cells (Taxol chemotherapy)
- Reduce inflammation (Colchicine)
- Lower Covid-19 death rate (Sabizabulin)

# Microtubule dynamics: Colchicine binding site

*Selection of small molecule drugs under development*

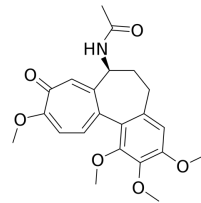
## $\alpha\beta$ -tubulin heterodimer



$\beta$ -tubulin

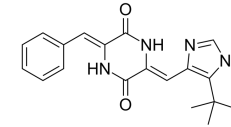
# Off-target effects

### How it started:



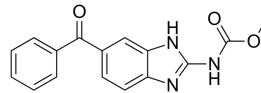
**Colchicine**  
Gout pain  
FDA approved

### Where we go:

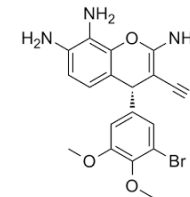


**Plinabulin**  
Lung cancer  
Clinical phase 3

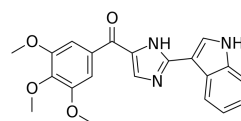
$\alpha$ -tubulin



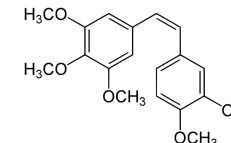
**Mebendazole**  
Worm infections  
FDA approved



**Crolibulin**  
Thyroid cancer  
Clinical phase 2



**Sabizabulin**  
Covid-19  
FDA approved



**Combretastatin A4**  
Prostate cancer  
Multiple clinical trials



# Prototypical azobenzene photoswitch

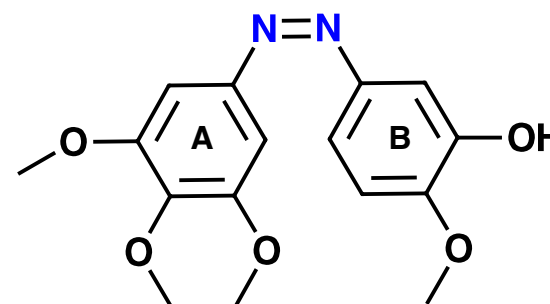
*Azo-combretastatin A4, a photoswitchable anti-cancer compound*

## Natural source



**Combretastatin A4** is a promising anti-cancer drug candidate from the bark of the South African bushwillow (a **medical plant of the Zulu**).

## Photochemical affinity switch



*cis*-azo-CA4



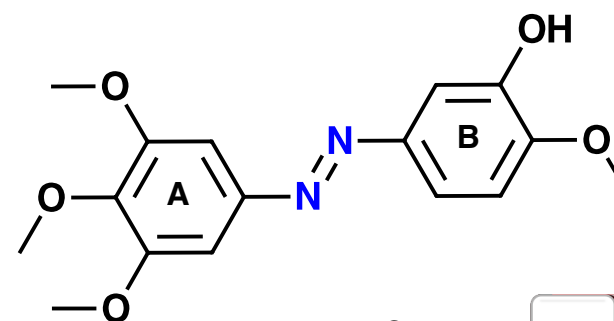
Synthesis with  
azobenzene motif



$\lambda = 450$  to  
530 nm



$\lambda = 350$  to  
430 nm



*trans*-azo-CA4



# A couple of night shifts later

*A big !!!THANK YOU!!! to everyone at SLS and SwissFEL*

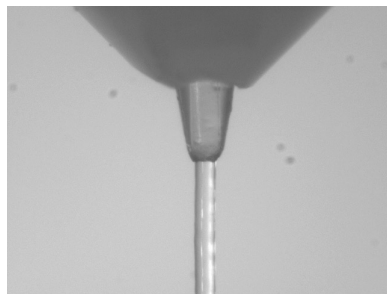
## A few shifts at SLS



## Crystal enthusiasts



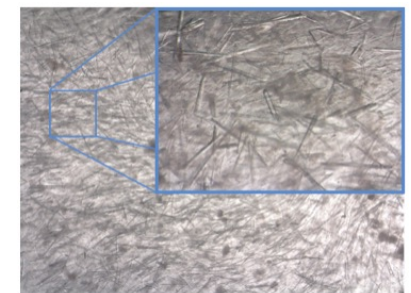
## HE Cellulose



## A few shifts at SwissFEL



## Microcrystals

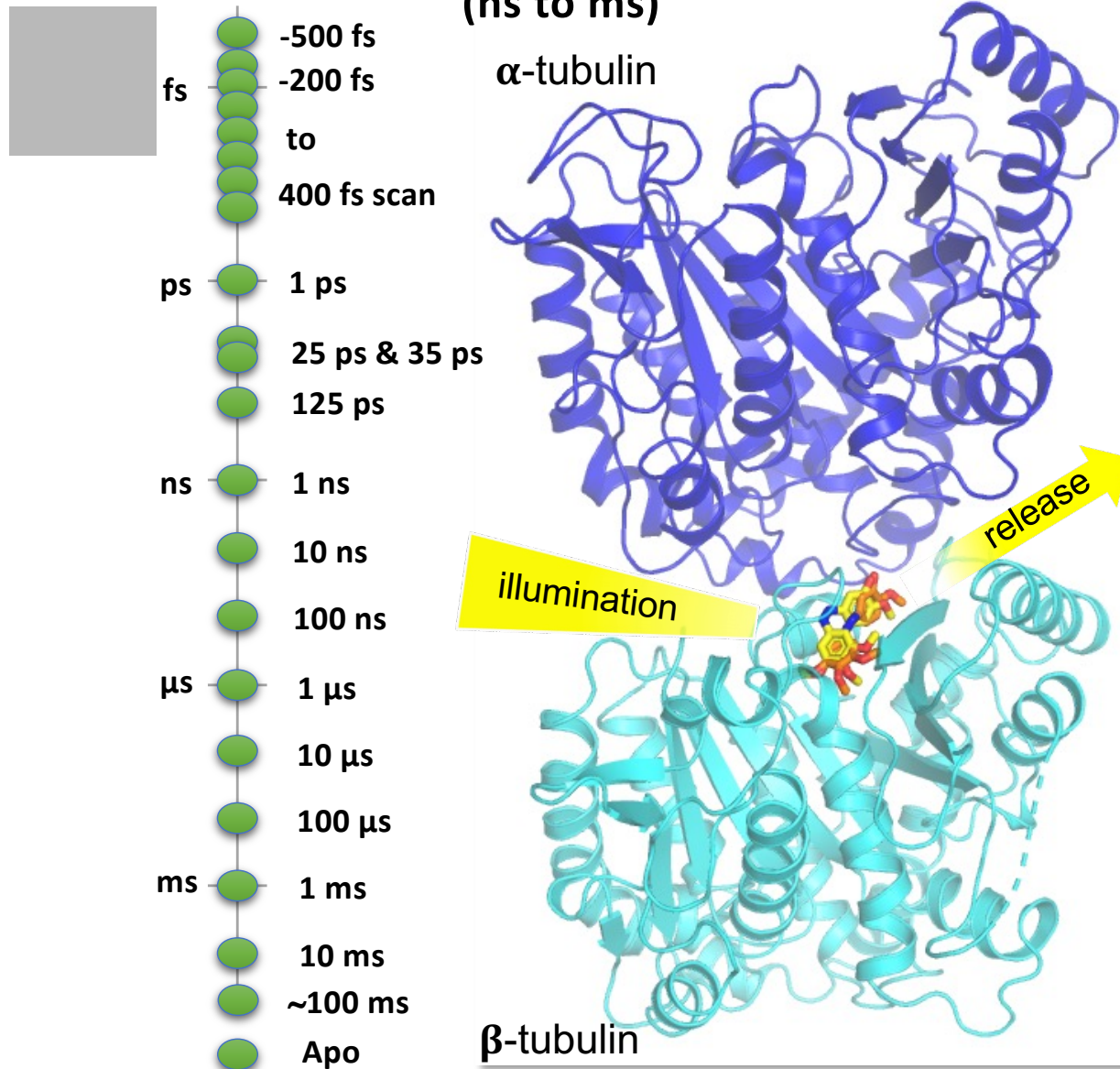




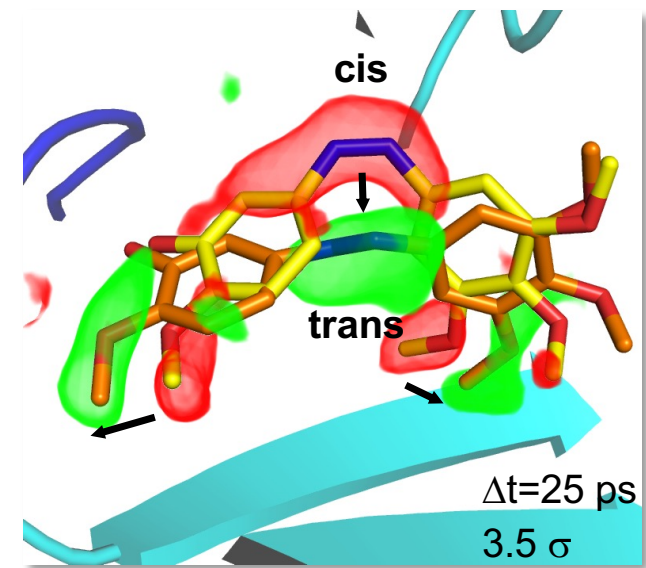
# Molecular snapshots of drug release

*Using synthetic photoswitches for time-resolved crystallography*

## Mechanisms of Drug Action (ns to ms)



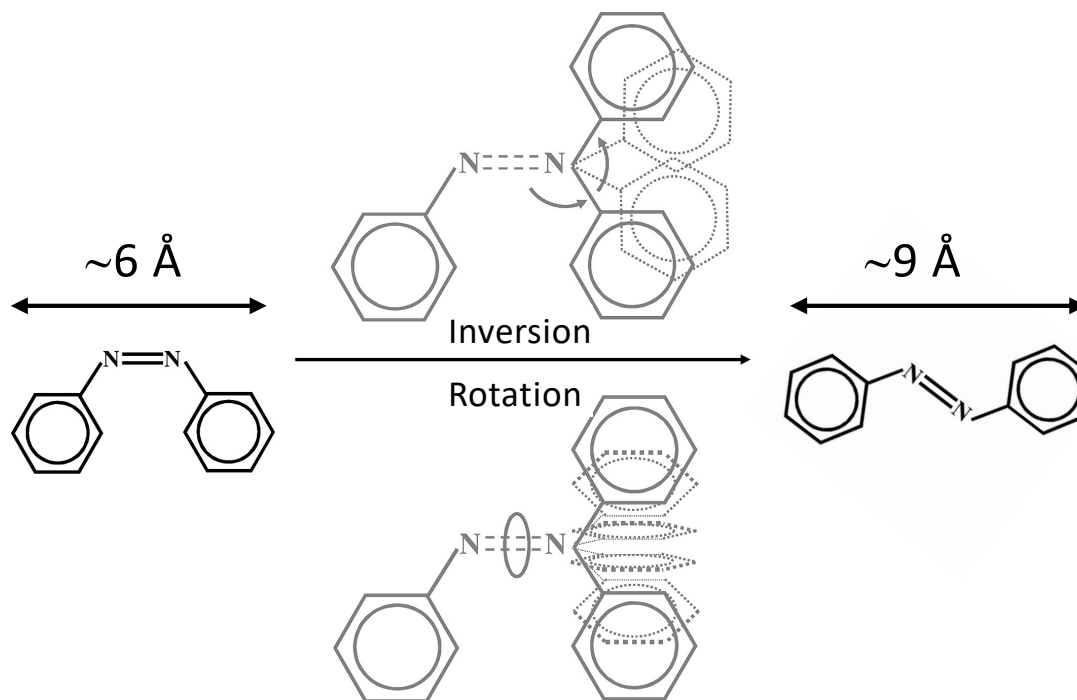
## Azobenzene Photochemistry (fs to ps)



>2.000.000 patterns, 1.7 Å resolution  
Ligand-protein interactions at  
**near-atomic resolution** over  
**fourteen orders of magnitude** in time

Photon energy is translated into mechanical energy  
via a transition in molecular shape!

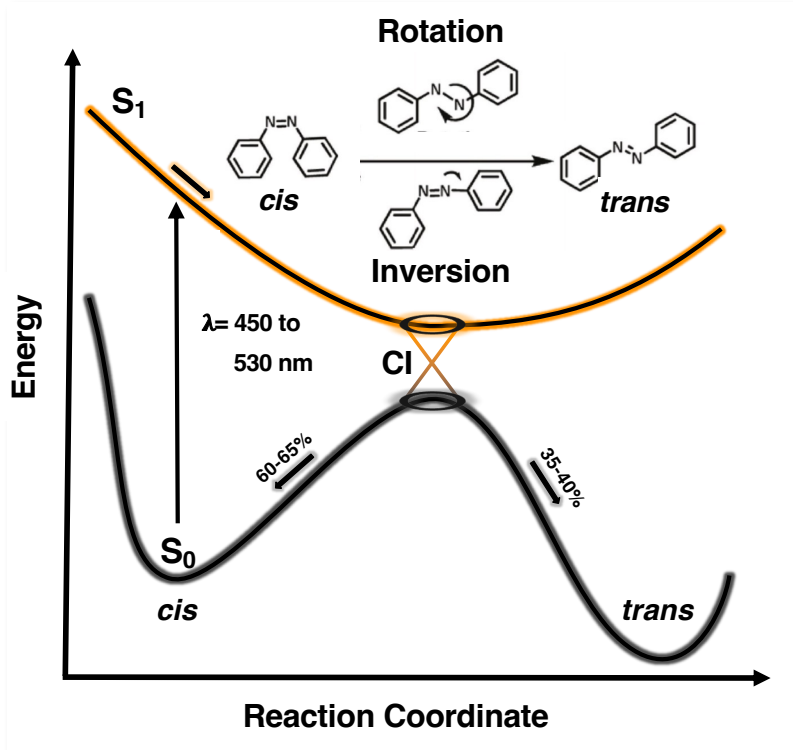
... but the mechanisms remain controversial



From: Conti et al., *JACS*, 2008

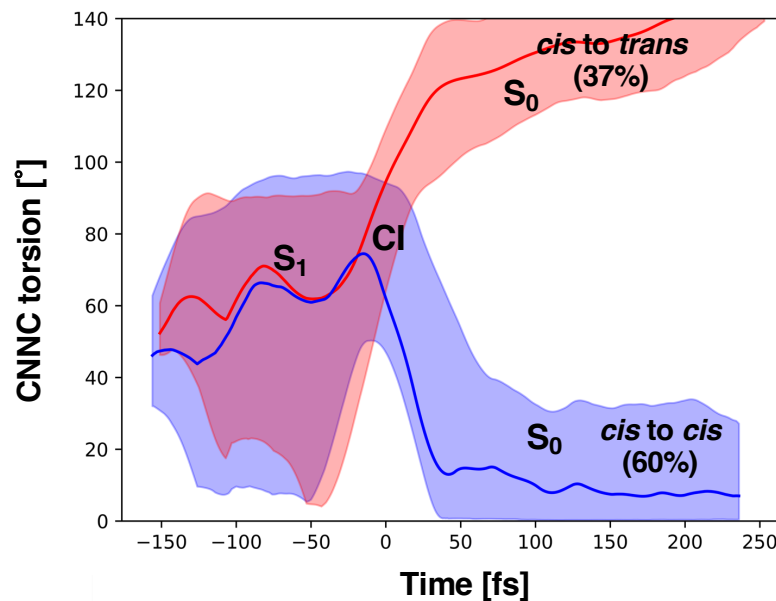


### Potential Energy Diagram

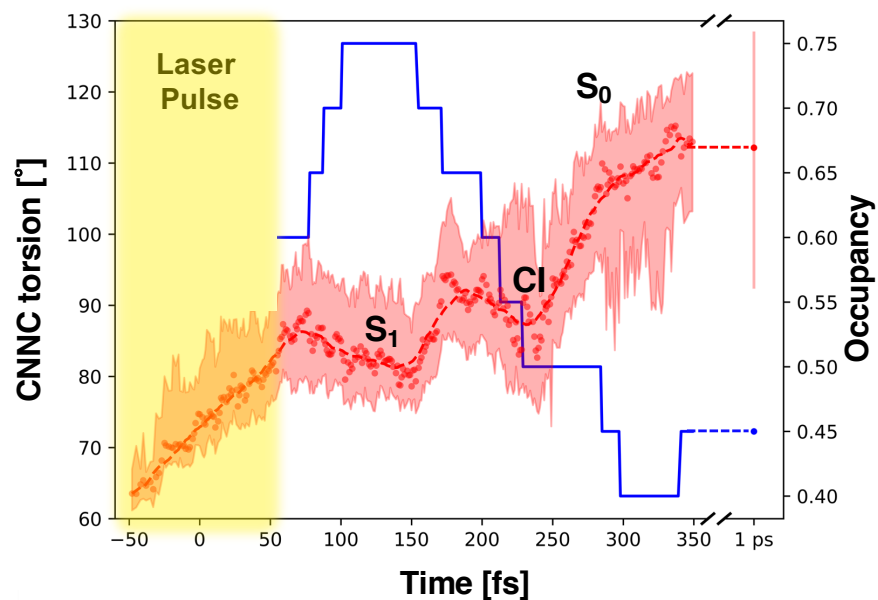


Collaboration Schapiro group  
Hebrew University Jerusalem

### Quantum Chemical Simulation



### Femtosecond Structural Photochemistry

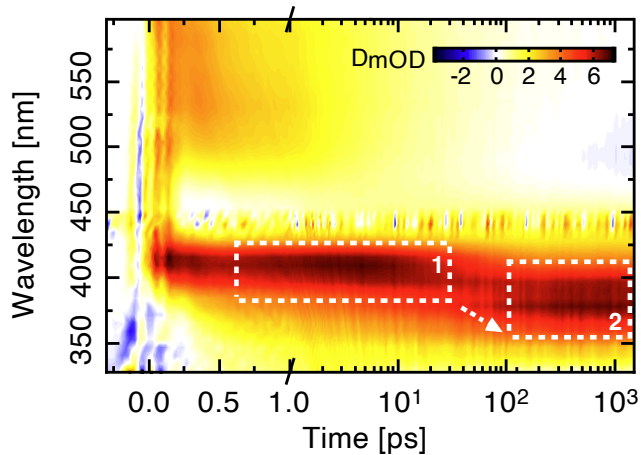


# Ultrafast Photoreaction of a Molecular Switch

*But the reaction is not finished within femtoseconds*

## Time-resolved absorption spectroscopy

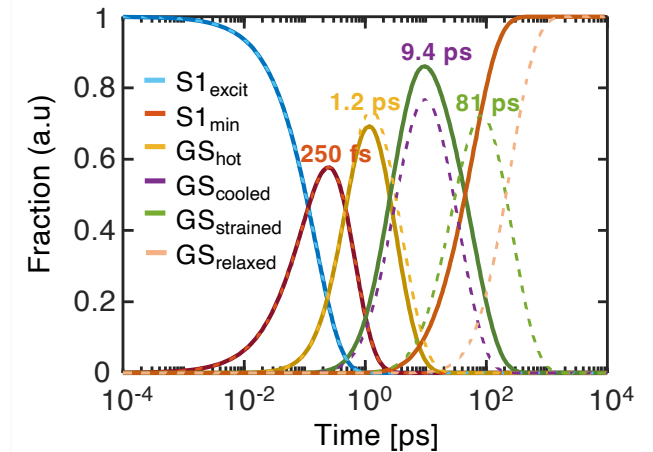
### Azo-CA4 tubulin



### Lifetimes

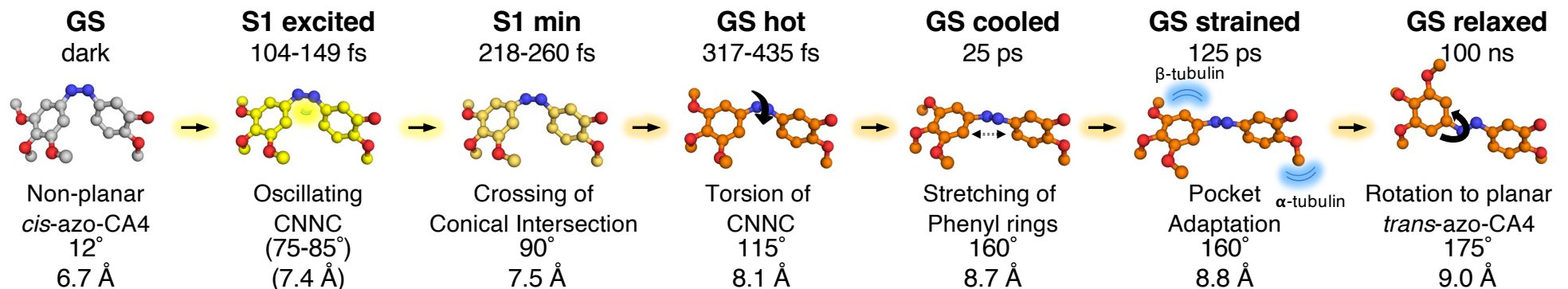
	Azo-CA4 solution	Azo-CA4 tubulin
$\tau_1$	0.15	0.15
$\tau_2$	0.45	0.45
$\tau_3$	2.8	3.6
$\tau_4$	X	35
$\tau_5$	59	240

### Populations



Collaboration Wachtveitl group, University of Frankfurt

## Time-resolved structural biology

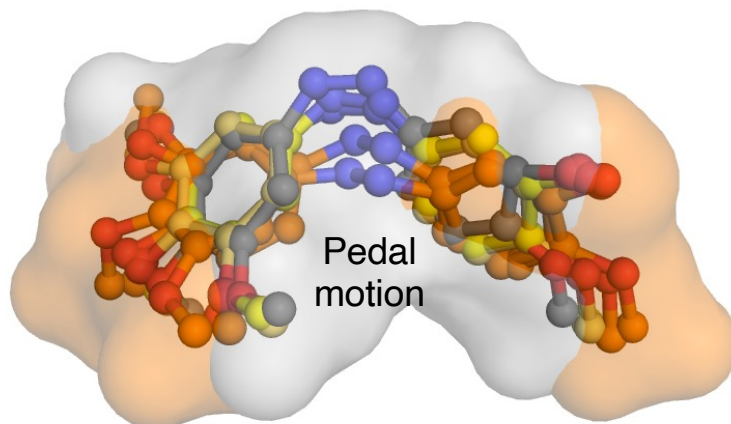


# Ultrafast Photoreaction of a Molecular Switch

*Two principal steps characterize the photoreaction*

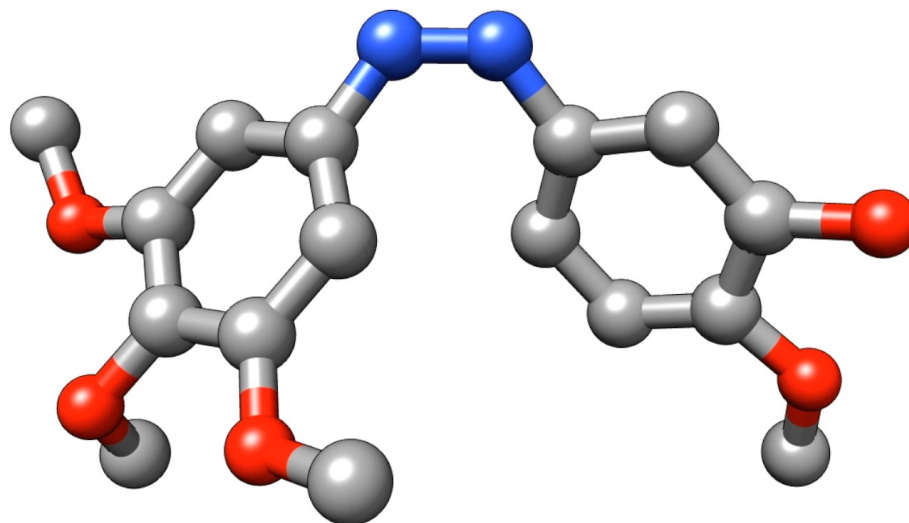
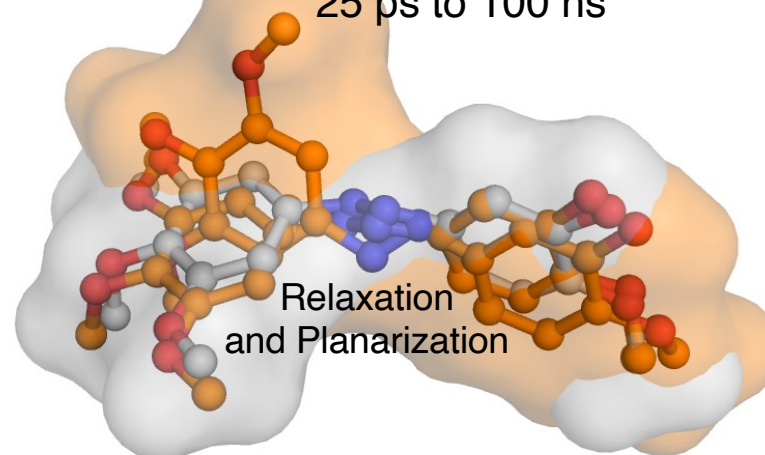
## First Torsion!

Dark to 25 ps



## Then Rotation!

25 ps to 100 ns

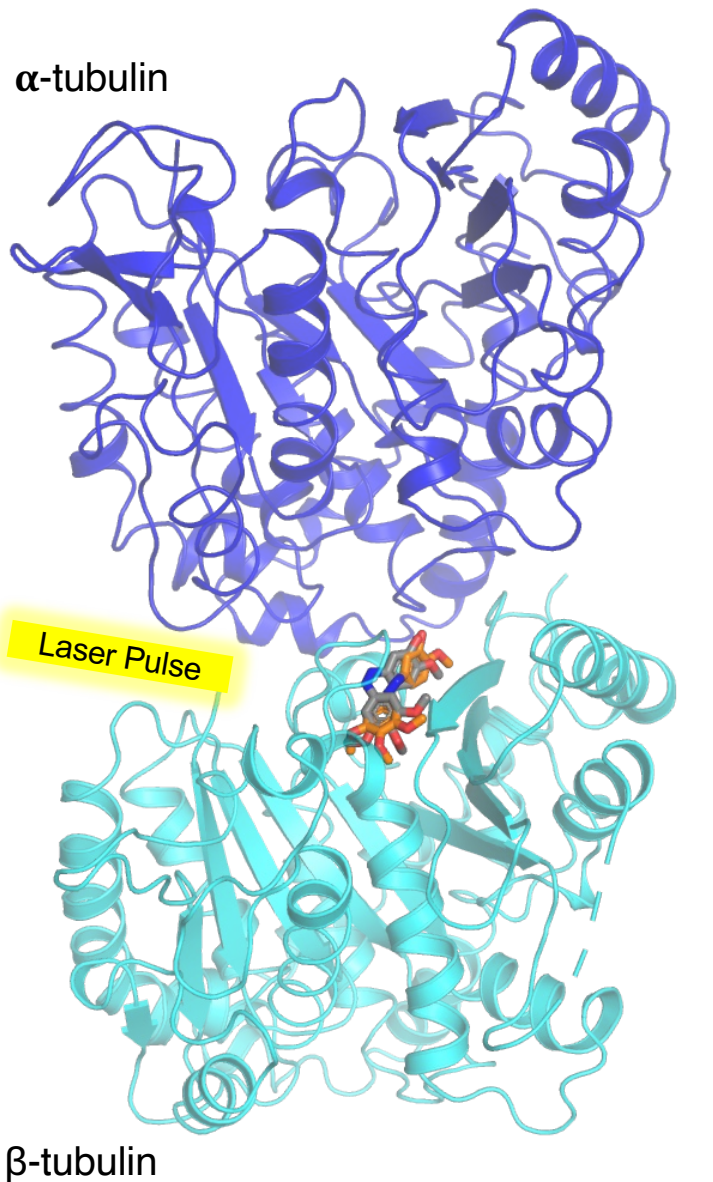




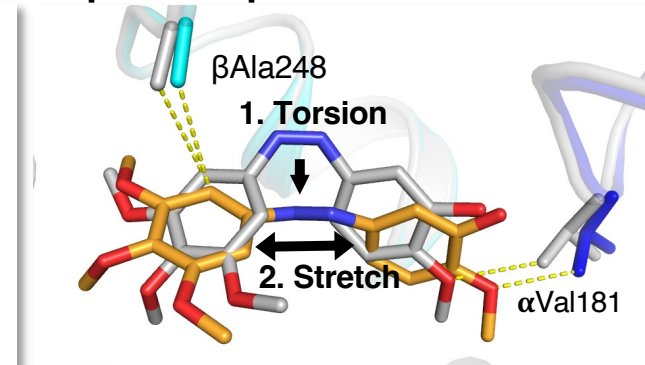
# Photoreaction in context of tubulin

*Protein environment constrains the early ligand response*

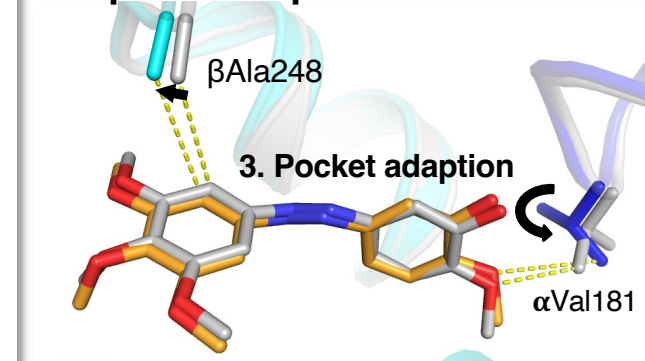
## Tubulin heterodimer



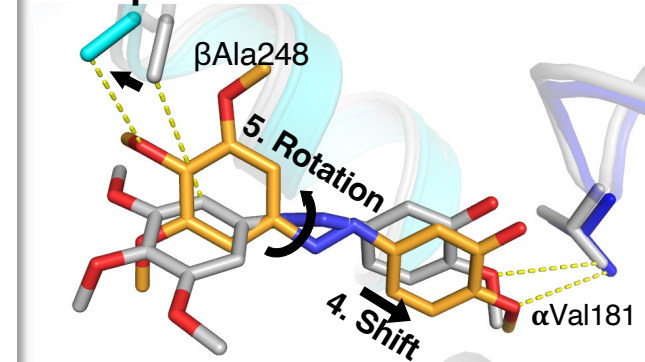
## 0 ps to 25 ps – Isomerized



## 25 ps to 125 ps – Cooled

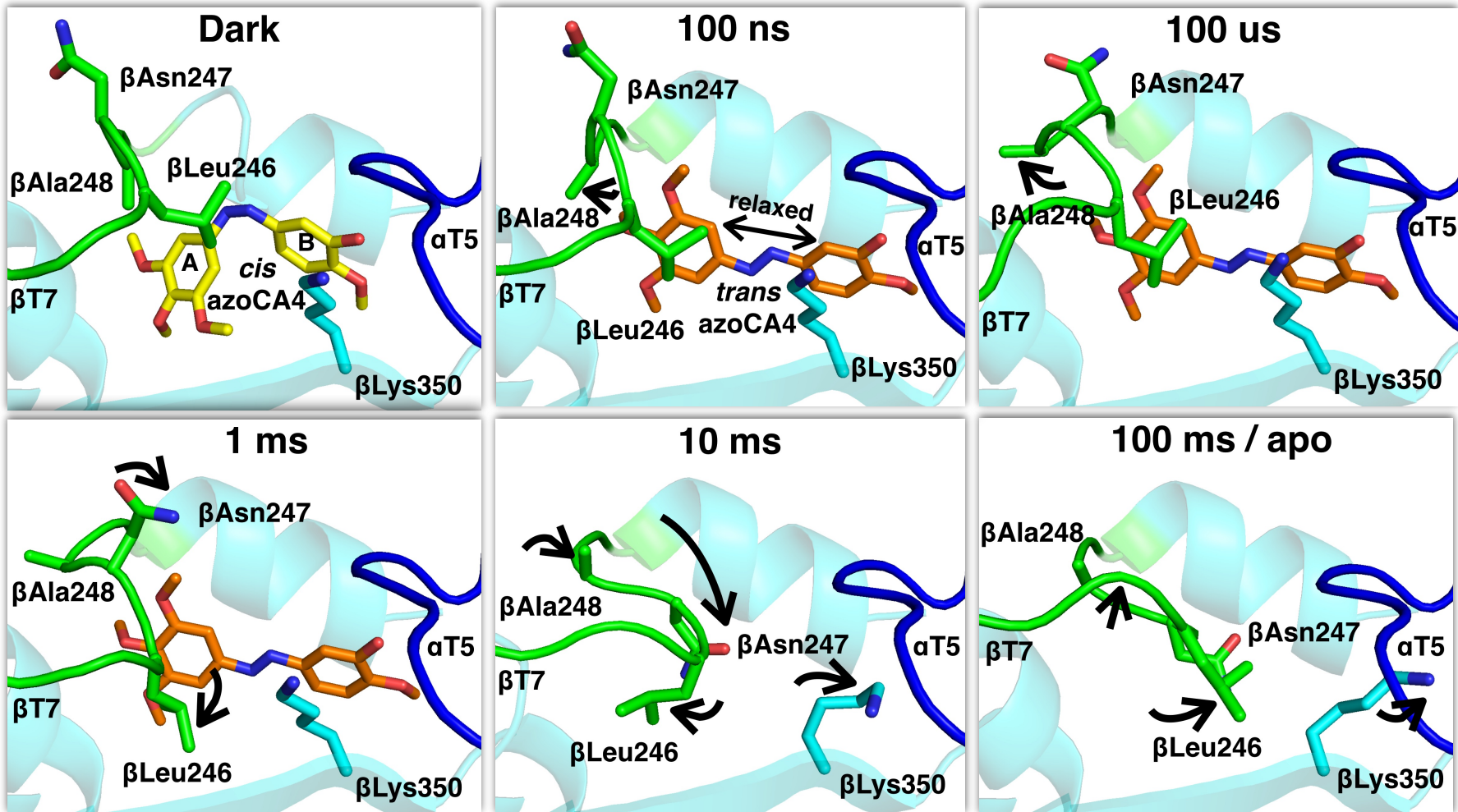
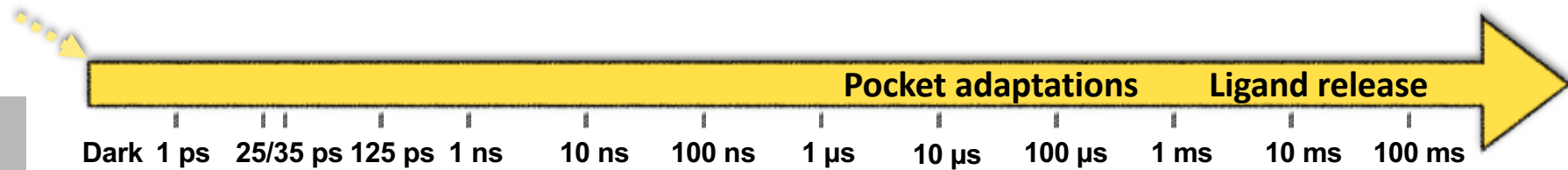


## 125 ps to 100 ns – Relaxed



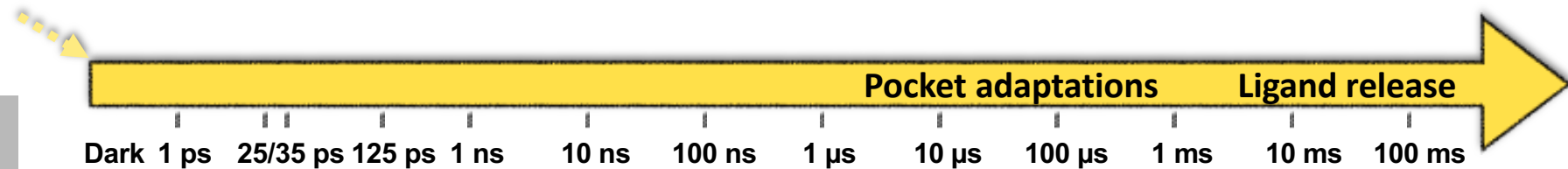
# Binding pocket adaptations in the microseconds

*Movements of the  $\beta$ T7 gating loop lead to azo-CA4 release*

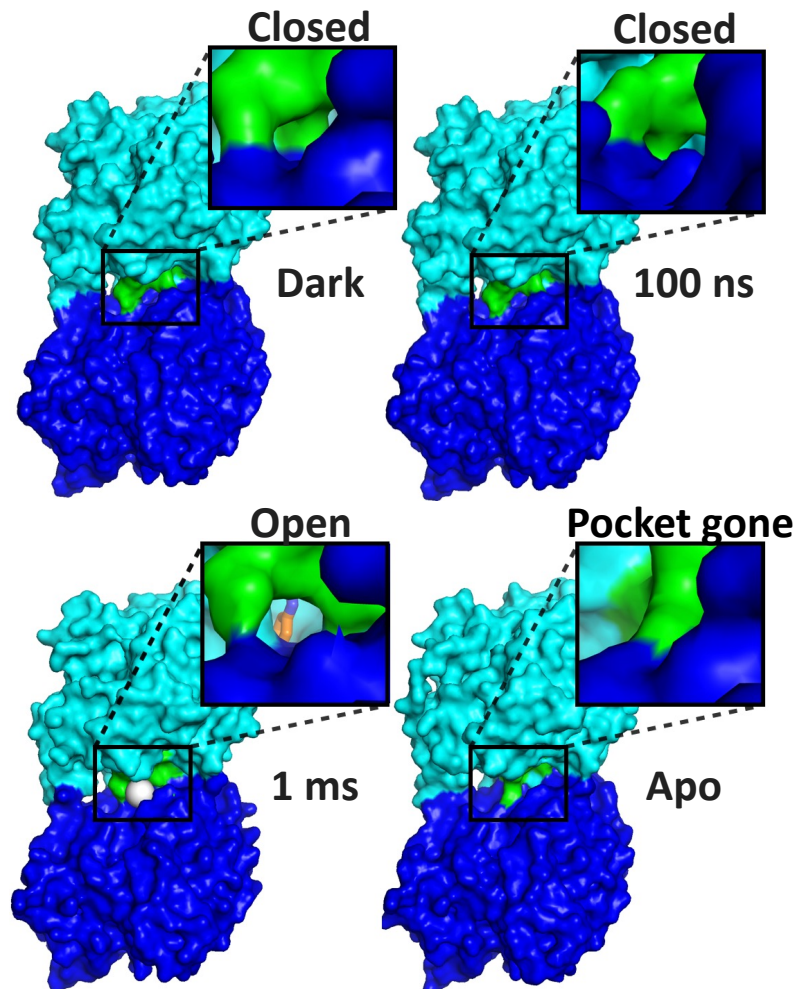


# Molecular mechanism of ligand release

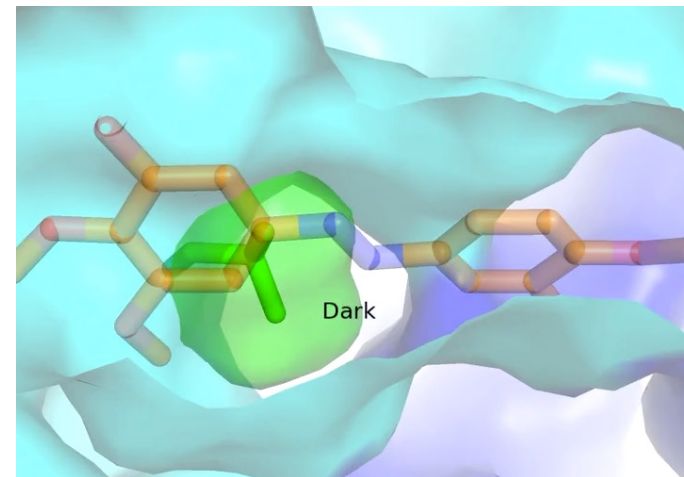
*Rearrangements of  $\beta T7$  loop open ligand release pathway*



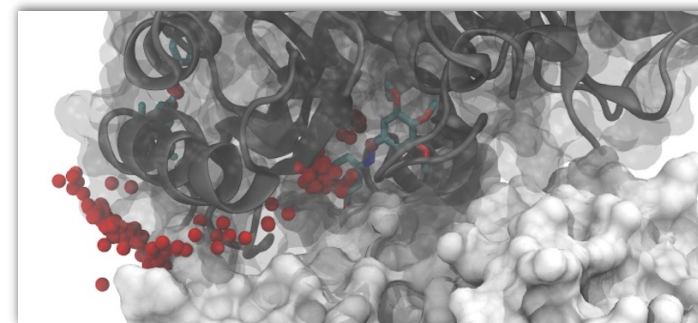
## Release in the milliseconds



## Role Leu246



## Molecular dynamic simulations

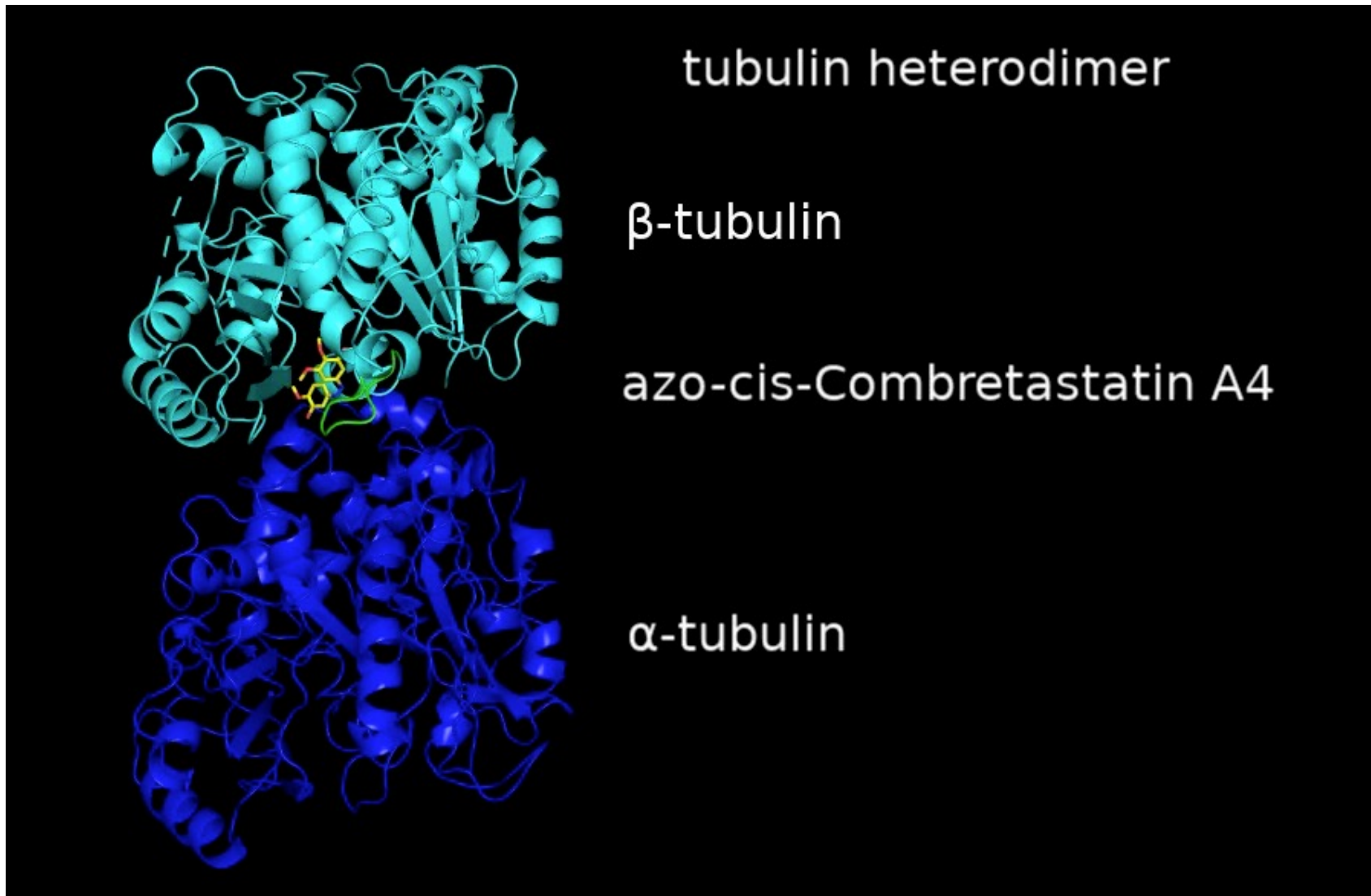
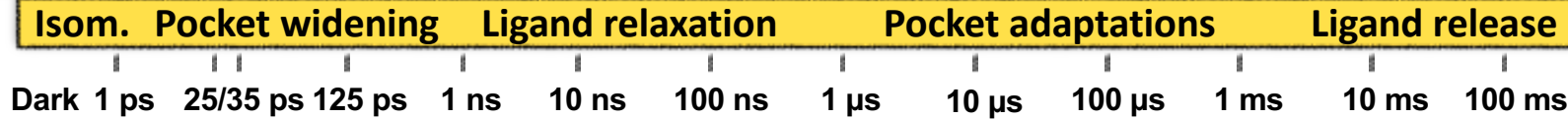


Simulations from Cavalli group, University of Bologna



# Drug release “The Movie”

*Dynamics within the colchicine site targeted by gout, cancer and covid-19 drugs*

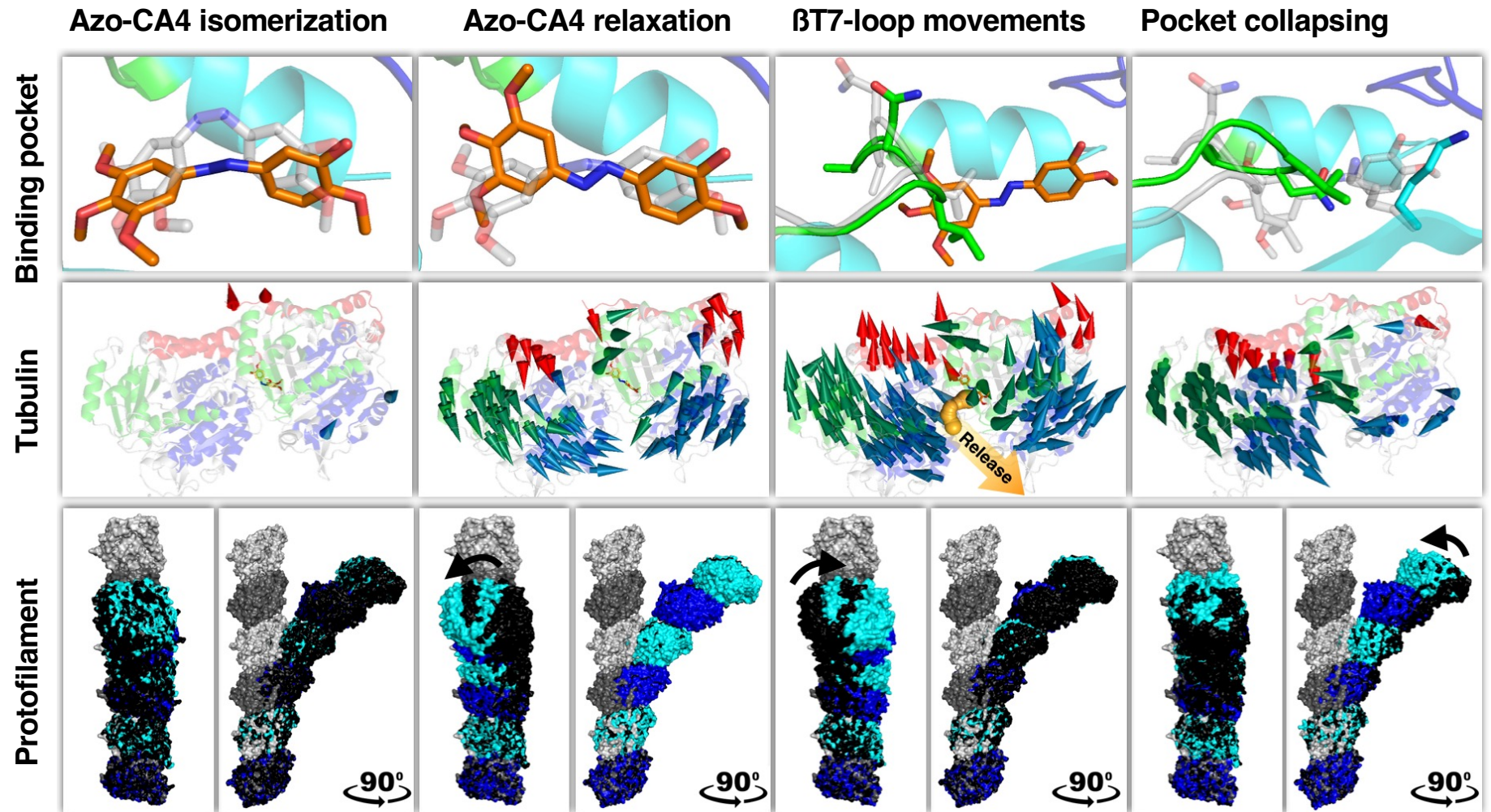


A solid grey square is positioned to the left of the main text, serving as a decorative element or a bullet point indicator.

**But can we learn something about the  
molecular mechanisms of drug action?**

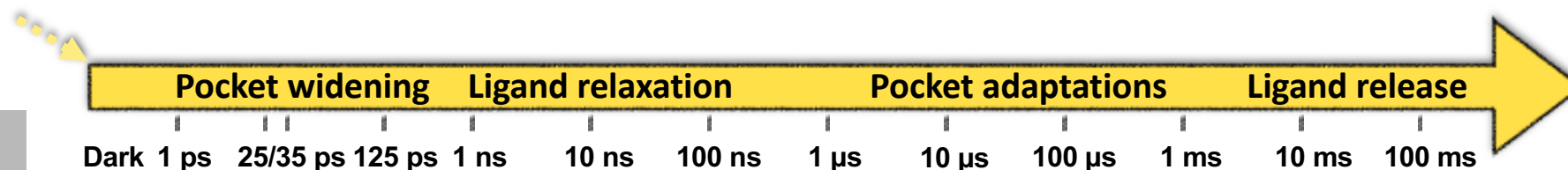
# Global tubulin rearrangements

*Local changes in the binding pocket have global impact on tubulin*





# Why watch protein-drug interactions dynamics?



## Insights for drug development approaches:

Photopharmacology

Expanding binding pocket

Metastable trans binding pose

Not a simple Key and Lock



Optimizing  
"residence time"

## Intermediate states for simulations:

Verifying QM/MM of early photochemistry

Opening of ligand release pathway at 1 ms



Milliseconds  
out of reach  
Experimental  
verification

## Methodological proof of concept:

Watch molecular motions in a wide range of targets with highest temporospatial resolution.



Diffusion based  
methods versatile, but  
slow

# Acknowledgments:

## Time-resolved structural biology:

**Max Wranik**, Hannah Glover, Robin Stipp, Peter Seidel, Georgii Khusainov, Thomas Mason, Melissa Carrillo, Matthias Mulder, Sina Hartmann, Quentin Bertrand, Yasushi Kondo, Fabienne Stierli, Michal Kepa, **Tobias Weinert**, Jörg Standfuss



Christmas Party, December 2022

## Main PSI collaborators:

**Macromolecular Crystallography (SLS):**  
Meitian Wang and co-workers

**Alvra Experimental Station (SwissFEL):**  
Chris Milne, Camilla Bacellar and co-workers

**Membrane Protein Structural Biology (Bio):**  
Gebhard Schertler and co-workers

**Biomolecular Complexes (LBR):**  
Michel Steinmetz and co-workers

## External collaborators:

**LeadXpro AG (Park Innovaare)**  
Michael Hennig and co-workers

**Ultrafast Spectroscopy Group (Uni. Frankfurt)**  
Josef Wachtveitl and co-workers

**Institute of Chemistry (Uni. Jerusalem)**  
Igor Schapiro and co-workers

**Data Science and Computation (Uni. Bologna)**  
Andrea Cavalli and co-workers