







Horizon 2020 European Union Funding for Research & Innovation

# Computational Screening of Fluorescent Protein Mutants

Dmitry Morozov

dmitry.morozov@jyu.fi

Vaibhav Modi

vaibhav.modi@aalto.fi

Gerrit Groenhof

gerrit.x.groenhof@jyu.fi

#### Fluorescent proteins

Osamu Shimomura, Martin Chalfie and Roger Tsien, Nobel Prize in Chemistry 2008



Chromophore



Could be reversibly photo-switchable



### Applications

The GFP-family proteins is widely used as a marker because of its very useful properties such as: high stability, minimal toxicity, non-invasive detection and the ability to fluoresce without specific equipment



#### Variety of fluorescent proteins





#### Excitation and Emission Characteristics of Fluorescent Proteins

Fluorescent Protein	Excitation Wavelength (nm)	Emission Wavelength (nm)
wtGFP	395/475	510
ECFP	433	475
EGFP	488	507
EYFP	513	527
DsRed	558	583
B-PE	545/565	575
R-PE	410/545/565	578
APC	650	660

**Development of task-specific FPs** 



#### FluProCAD Workflow Overview



# Application I: Predicting Structures

- Pairwise RMSD for each structure
- Group neighbors within cut-off threshold
- Largest group forms a cluster and eliminated from the pool of M structures
- Iterate until pool is empty



### rsGreen0.7 protein mutants

#### <u>Objectives</u>

Starting structure



rsGreen0.7 (eGFP variant) PDB: 4XOW

#### • Prepare mutant structures

- •Classical MD equilibration
- •Clusterization of the trajectory
- •Blind check MD against crystal structures

#### <u>Mutants</u>

- 1. K206A
- 2. K206A/F145H
- 3. K206A/F145M
- 4. K206A/H148G
- 5. K206A/E222G
- 6. K206A/E222V

In total 14 mutants have been modelled



#### Stability of the structures



8

### Stability of the structures





### Stability of the structures



#### Application II: Thermodynamic properties prediction



#### Thermodynamic properties:

- wt-GFP vs 4 mutants: S65T, F64L, A206K and S65T/F64L (eGFP)
- Molecular Dynamics to refine crystal structure
- **GROMACS** + **PMX** for free energy evaluation of dimerization and folding
- Blind prediction of mutant properties with unknown structure





#### Structures of the mutants





## Free energies of dimerization and folding

GFP MUTANTS	ΔΔG (kcal/mol)	
	Folding	Dimerization
S65T	6.399 (±0.8393)	-8.241 (±0.9198)
F64L	-3.726 (±0.2041)	-1.955 (±0.4097)
A206K	3.457 (± 0.1529)	10.481 (± 0.5241)
eGFP	10.125	-4.789
(F64L/S65T)	(± 0.2927)	(± 0.6471)

- <u>F64L</u>: improved stability
- <u>A206K</u>: Prefers to be in monomeric form
- Validated MM-MD models against known crystal structures.
- Predict solution structures for (un)-known mutants with no crystallographic data (K206A).



#### Why A206K prefer to be monomer?







#### Application III: Photochemical Properties



#### Spectra of wtGFP and 4 mutants



#### Outlook: excited state reactions



#### **GROMACS + CP2K**

Ultra-fast proton transfer in GFP mutant <u>S65T/H148D</u>.

**QM subsystem** : Chromophore + Asp148

Method: TD-DFT

Functional: PBE

Basis: DZVP-MOLOPT-GTH

**Software:** GROMACS-CP2K



## Summary

- MD simulations + Clustering predicts solution structures for FP mutants (avGFP: 4 mutants and rsGreen0.7: 14 mutants)
- Free energy calculations predicted effect of mutations on folding and dimerization
- Evaluated the effect of mutations on photochemical properties
- Local database for MM and QM/MM parameters
- Automated setup of free energy and QM/MM calculations
- Computational mutagenesis protocol for fluorescent proteins



#### Acknowledgements





Prof. Peter Dedecker

Dr. Elke De Zitter

Prof. Jeremy Harvey











Funded by the European Union Horizon2020 program Grant agreement No.675728



19