

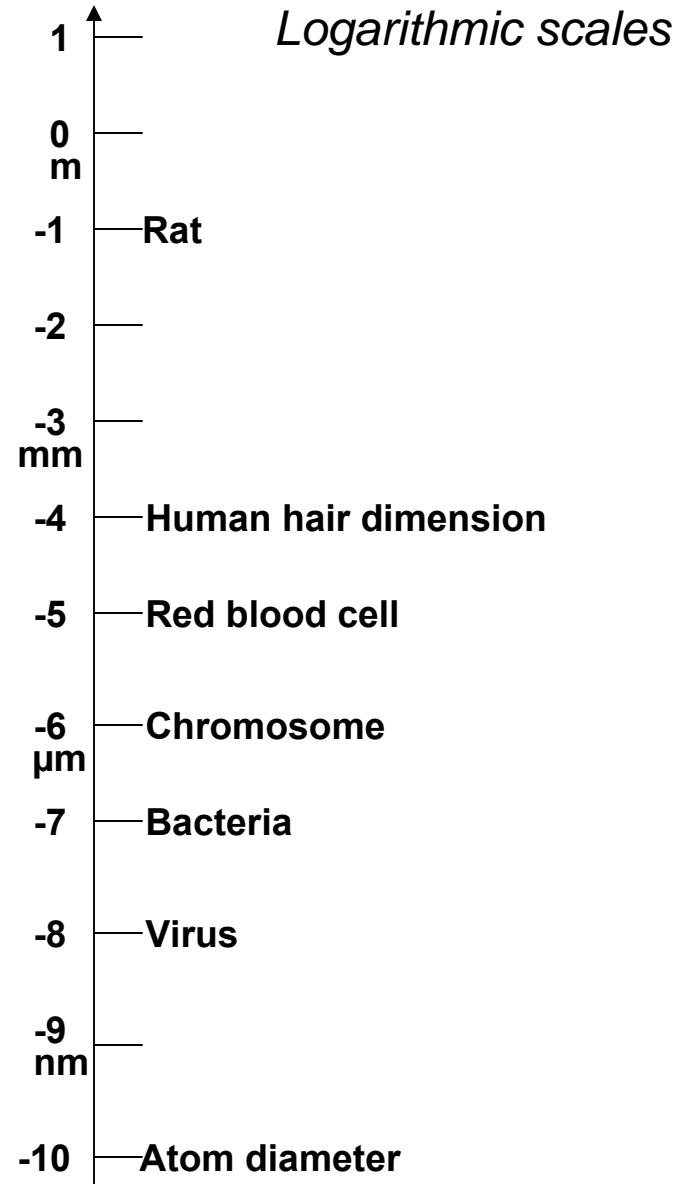
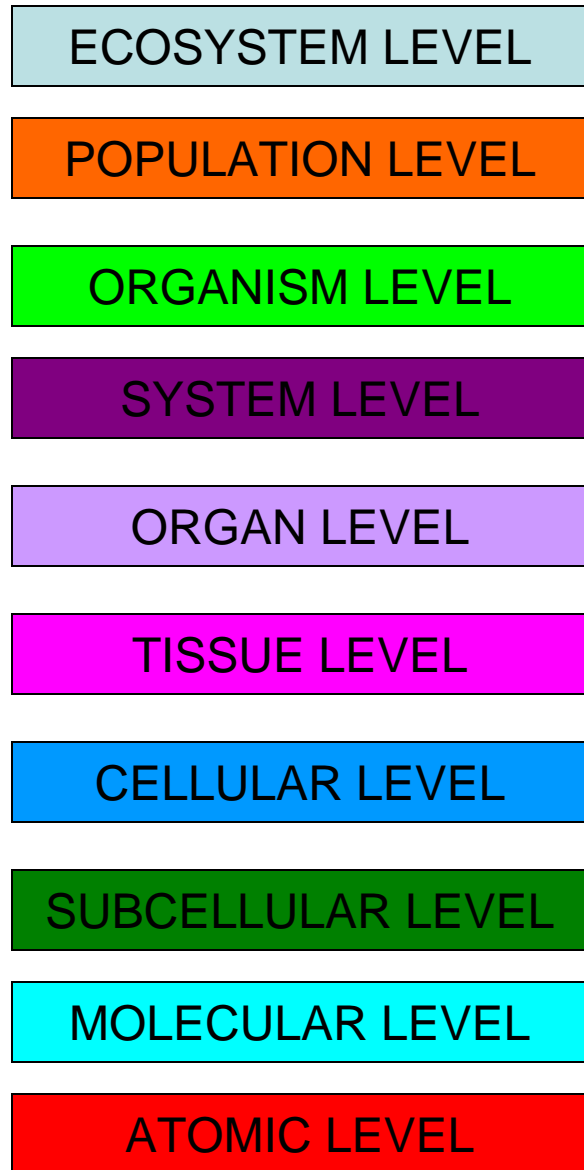
*Multiscale Approach to Protein
Engineering in Bioluminescence
Probe Design*

Yi Mao
Department of Mathematics
Michigan State University



“Kinetic Description of Multiscale Phenomena” Workshop
CSCAMM, University of Maryland March 2-5, 2009

Multiscale in Biology



Mathematics $\xrightarrow{\text{Data analysis}}$ **Biology**

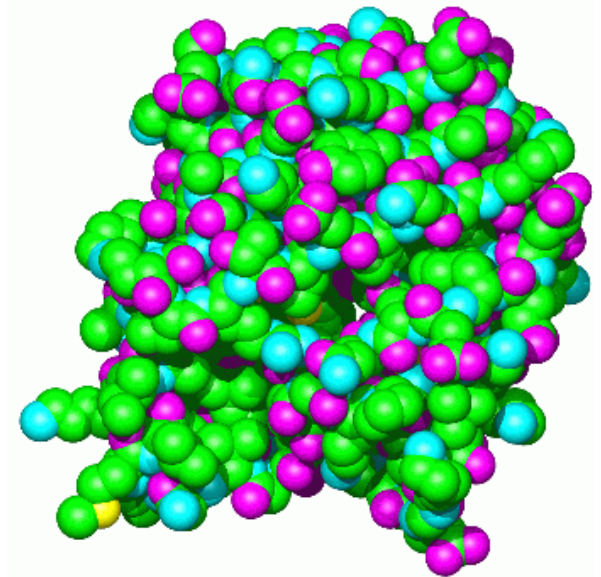
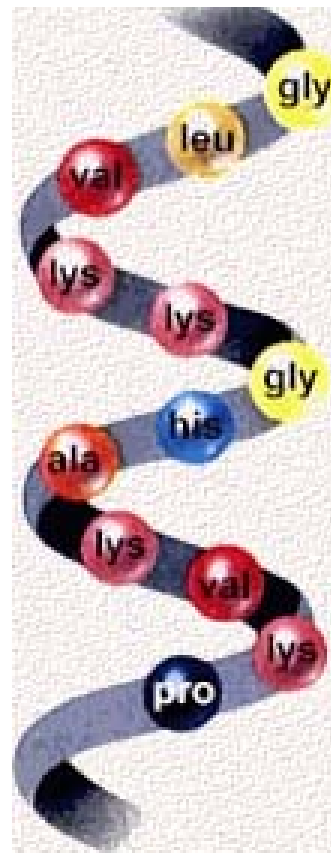
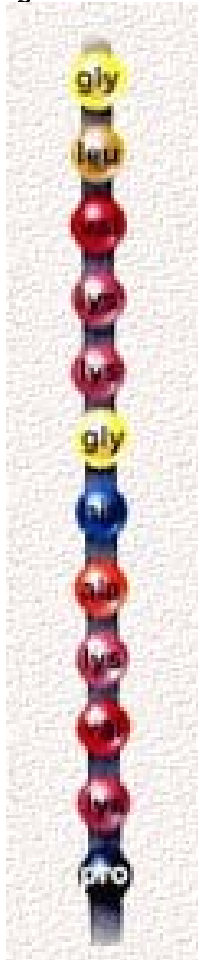
Challenge to deal with heterogeneity

**Mathematics Is Biology's Next Microscope,
Only Better;**

**Biology Is Mathematics' Next Physics,
Only Better**

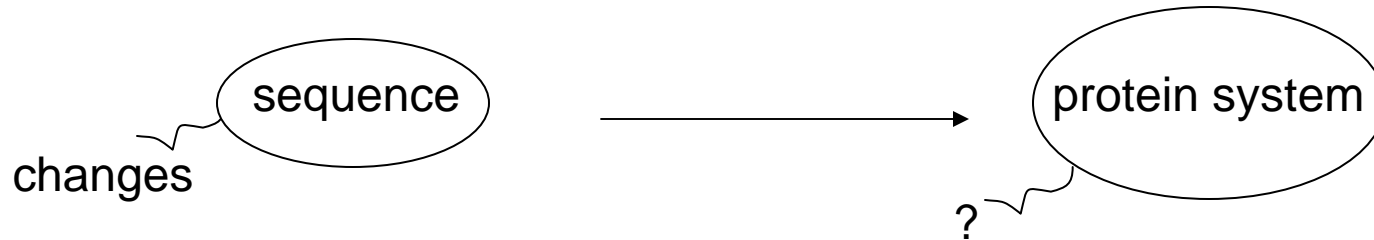
Protein Structure

- Primary structure
- Secondary structure
- Tertiary structure



Perturbation experiments in biology:

Mutation



Responses to mutation:

- no responses or localized responses
- cascading effects

Protein Engineering

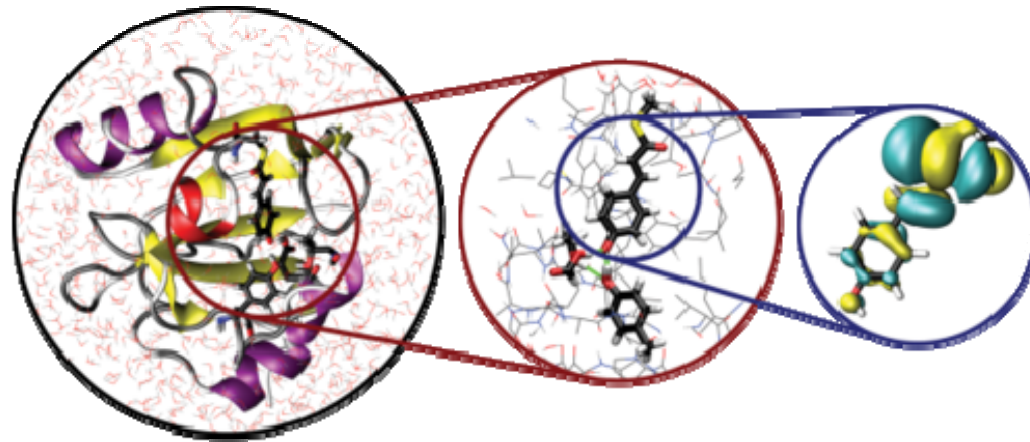
Goal: find the sequence → desired properties

Idea: alter the sequence → alter the properties

Methods:

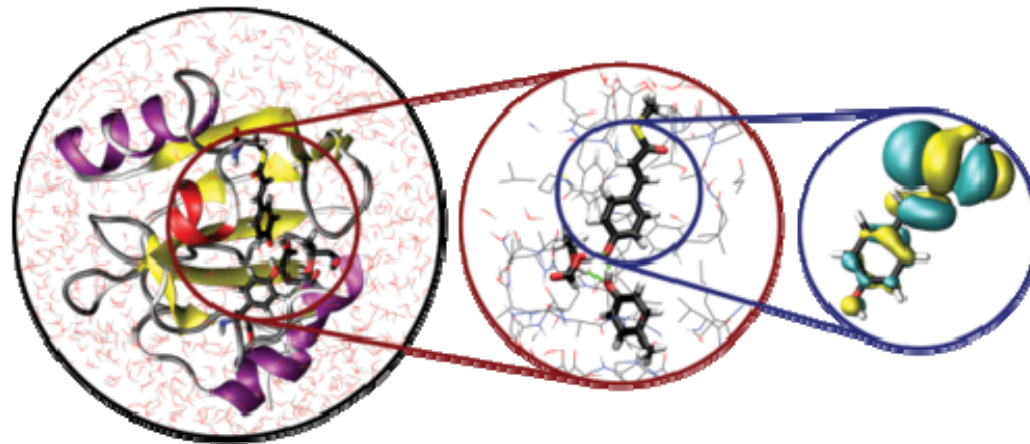
- rational design
- directed evolution

Multiscale Modeling for Proteins



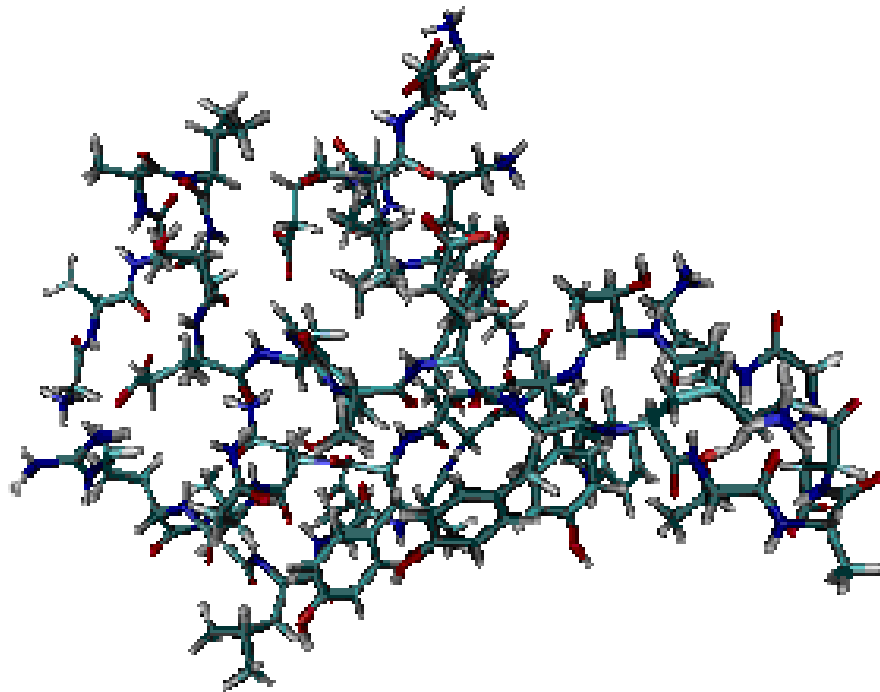
Multiscale Modeling for Proteins

“zoom-in” does NOT work!

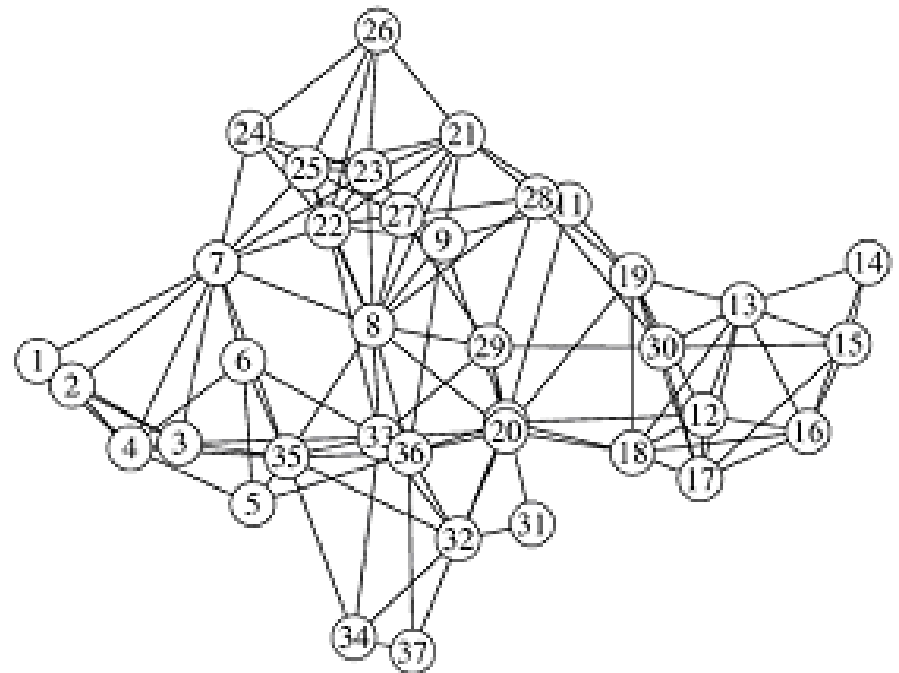


Multiscale Modeling for Proteins

- A **whole-system** study at all scales
- **Multiscale**: different resolutions



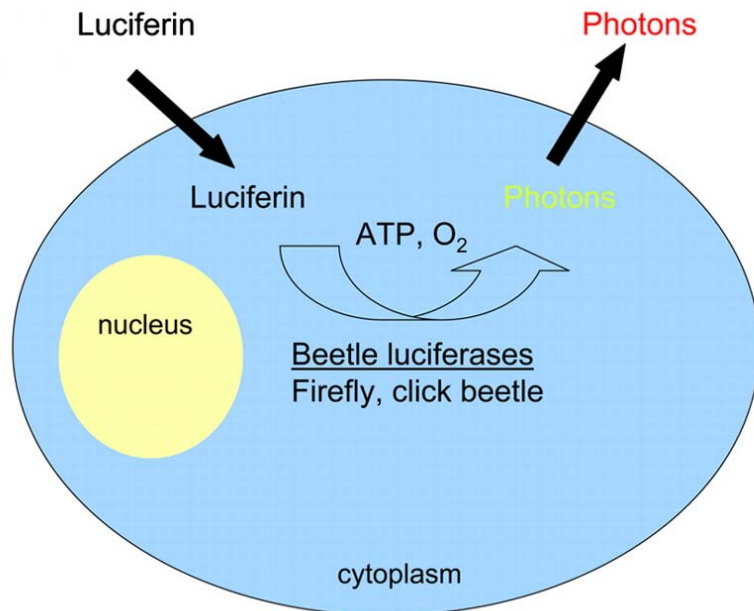
atomistic model
(QM/MM)



network model
(simplified potential)

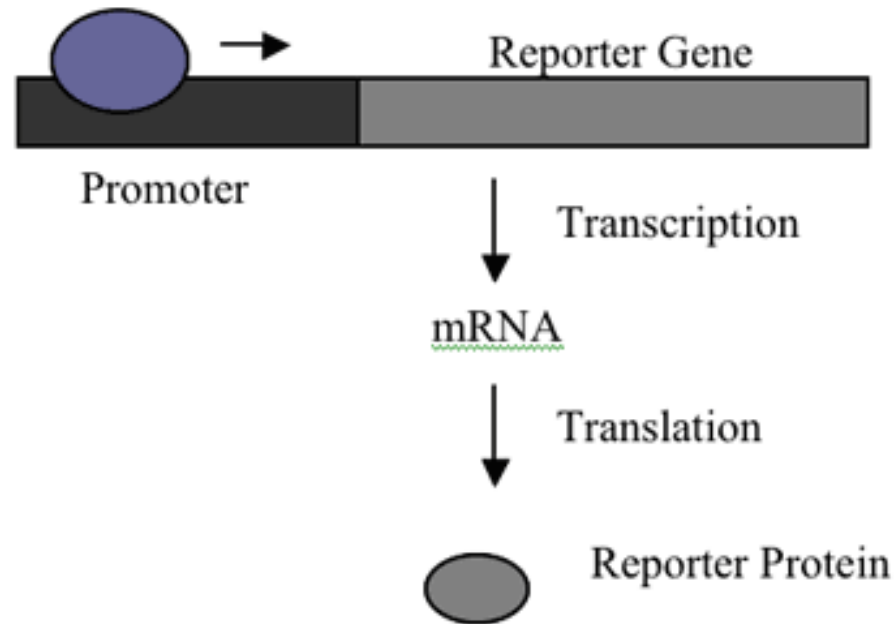
Bioluminescence

- conversion of chemical energy into light

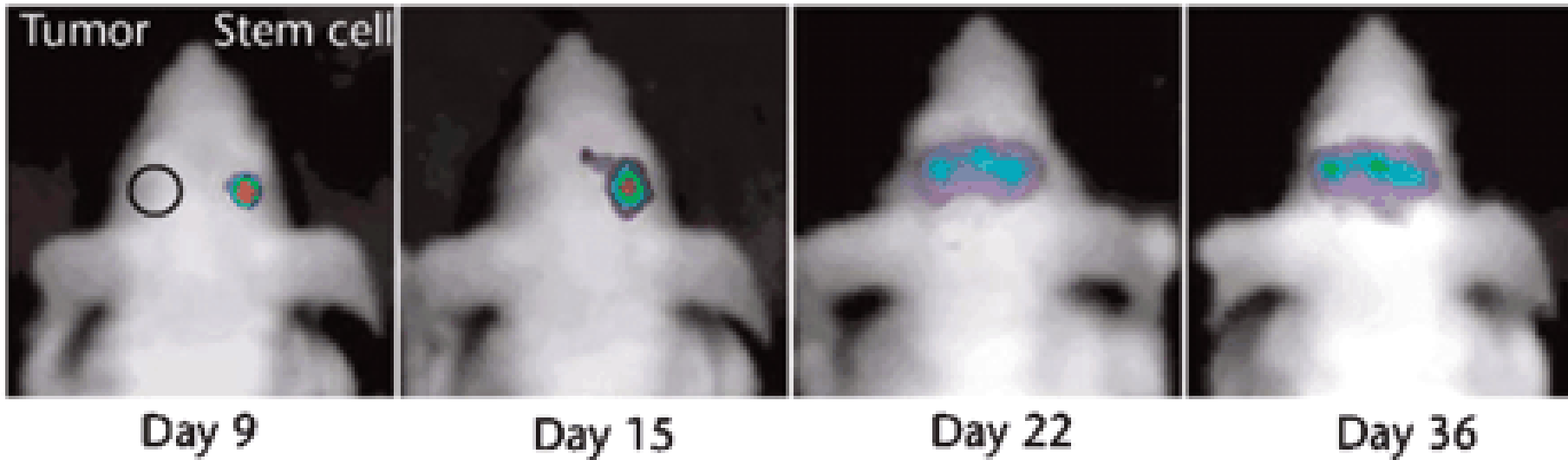


Bioluminescence Reporter Gene Imaging

Insert the reporter gene to the gene of interest to create a gene fusion.



Example of Bioluminescence Imaging



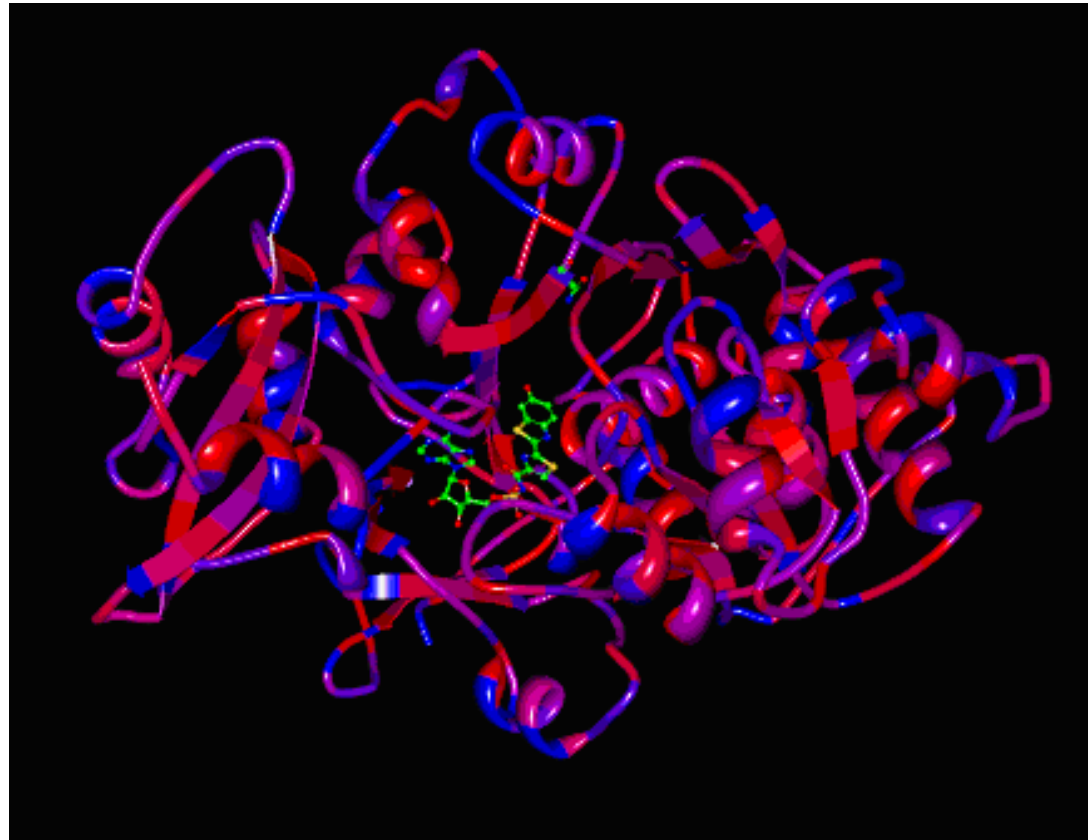
Migration of neural progenitor stem cells (labeled with the luciferin) across the midline towards an implanted brain cancer in a mouse.

A Dzik-Jurasz, *British Journal of Radiology* (2003) **76**, S98-S109

Challenge:

How to achieve Red Emission of Bioluminescence?

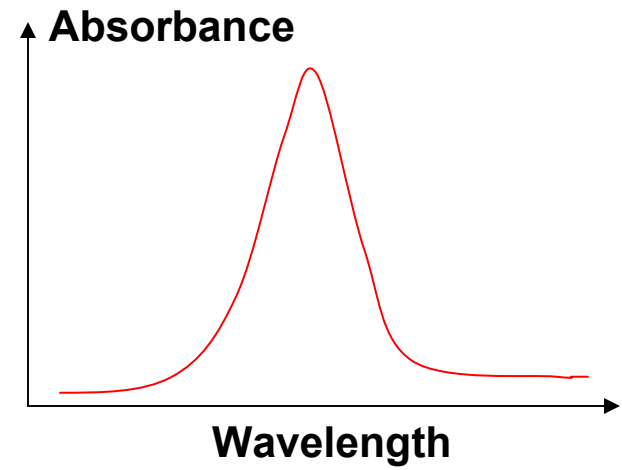
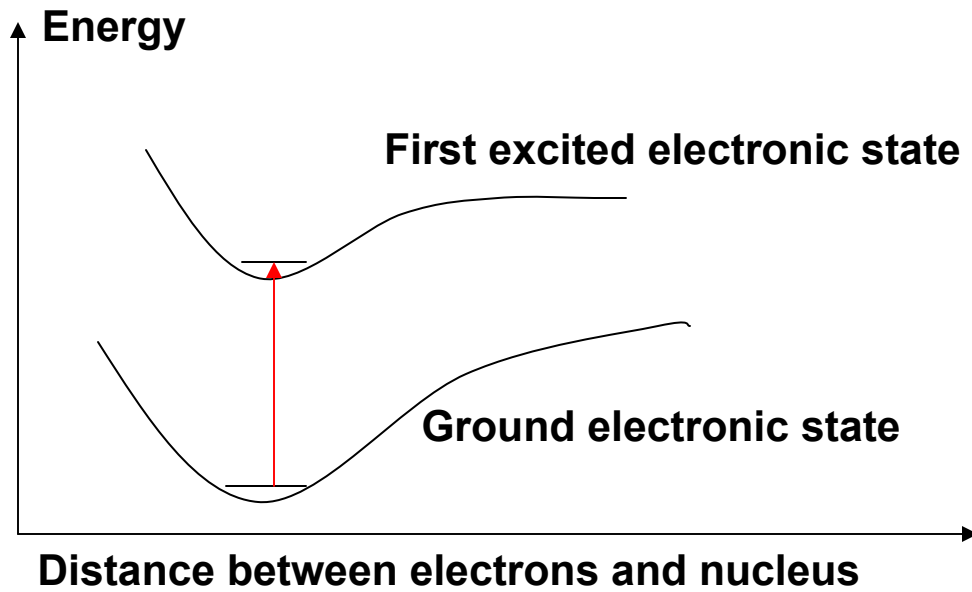
Luciferase•DLSA complex



Luciferase (protein): catalyst, 539 residues, 8451 atoms

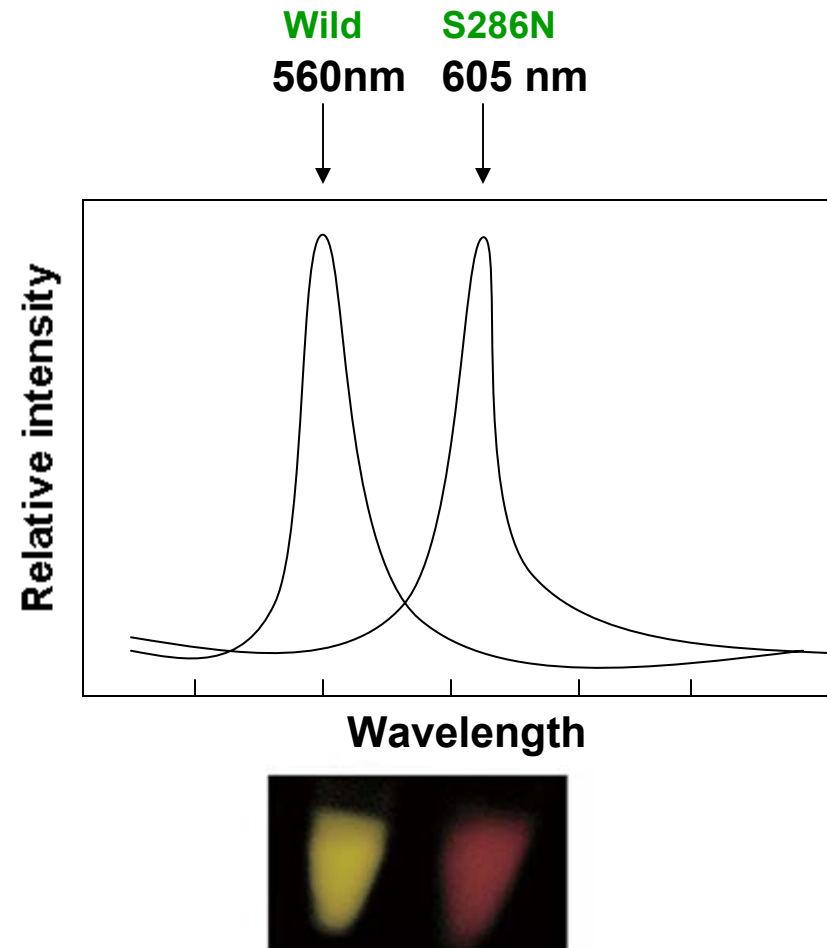
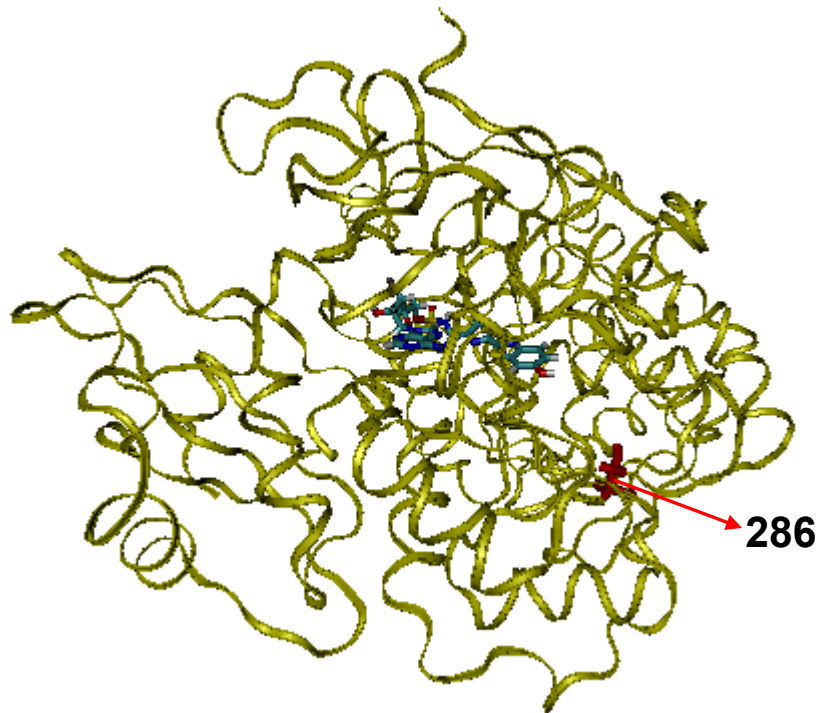
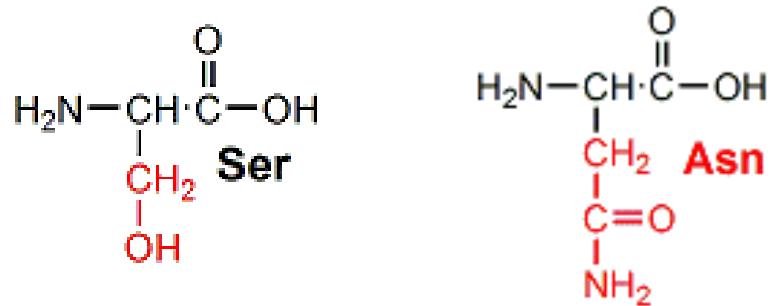
DLSA: light emitter, 58 atoms

Excitation of DLSA



Luciferase: Spectral Shift

Mutation at site 286: Ser → Asn



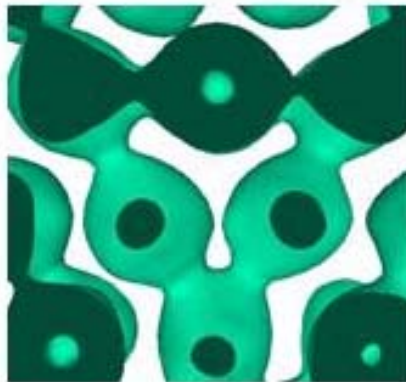
Nakatsu et al., *Nature* 440, p 372-376, 2006

Goal

- At the **atomic** level, explain the physical origin of the spectral shift caused by mutation.
- At the **sequence** level, design the system (luciferase) with desired optical property.

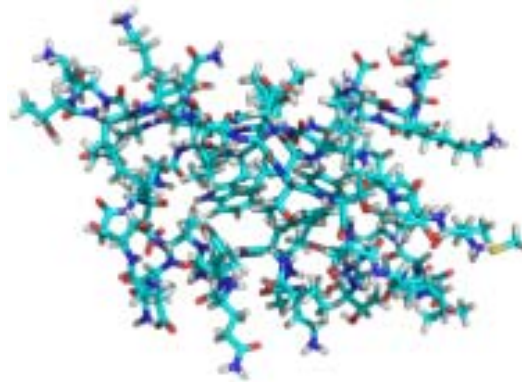
The matter of scale

scale of electrons



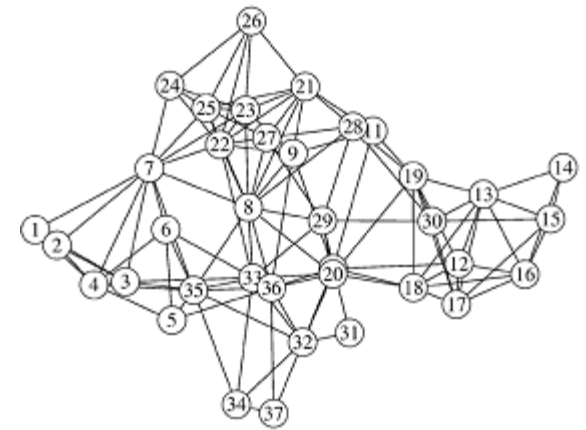
1 Å

scale of atoms



1 nm

scale of aggregates



10 nm

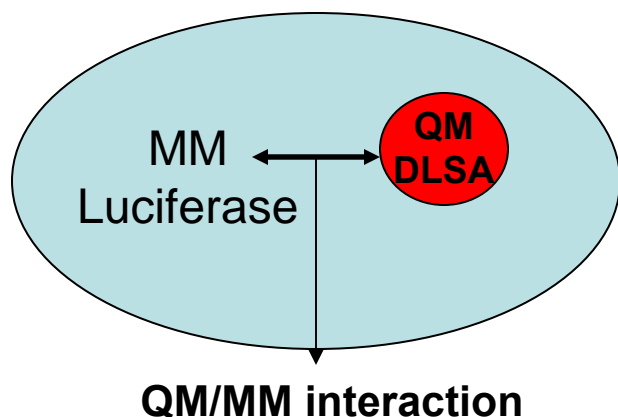
Quantum mechanics
(DLSA)

Molecular Dynamics
(protein)

Reduced Modeling
(protein/DLSA)

Hybrid Quantum Mechanical/Molecular Mechanical

(QM/MM) Approach



QM: $\hat{H}\psi = E\psi$

MM: $F = -\partial\hat{H}/\partial\mathbf{q}$

Hamiltonian: $\hat{H}_{\text{total}} = \hat{H}_{\text{QM}} + \hat{H}_{\text{MM}} + \hat{H}_{\text{QM/MM}}$

$$\hat{H}_{\text{QM}} = -\frac{1}{2} \sum_i \nabla_i^2 + \sum_{ij} \frac{1}{r_{ij}} - \sum_{i\alpha} \frac{Z_\alpha}{r_{i\alpha}} + \sum_{\alpha\beta} \frac{Z_\alpha Z_\beta}{r_{\alpha\beta}}$$

$$\hat{H}_{\text{QM/MM}} = -\sum_{iM} \frac{q_M}{r_{iM}} + \sum_{\alpha M} \frac{Z_\alpha q_M}{R_{\alpha M}} + \sum_{\alpha M} \left(\frac{A_{\alpha M}}{R_{\alpha M}^{12}} - \frac{B_{\alpha M}}{R_{\alpha M}^6} \right)$$

$$\hat{H}_{\text{MM}} = \sum_{\text{bonds}} k_r (r - r_0)^2 + \sum_{\text{angles}} k_\theta (\theta - \theta_0)^2$$

$$+ \sum_{\text{dihedrals}} k_\phi [1 + \cos(n\phi + \phi_0)]$$

$$\sum_{\text{atom}M} \sum_{M \neq N} \left\{ 4\epsilon_{M,N} \left[\left(\frac{\sigma_{MN}}{r_{MN}} \right)^{12} - \left(\frac{\sigma_{MN}}{r_{MN}} \right)^6 \right] + \frac{q_M q_N}{4\pi\epsilon_0 r_{MN}} \right\}$$

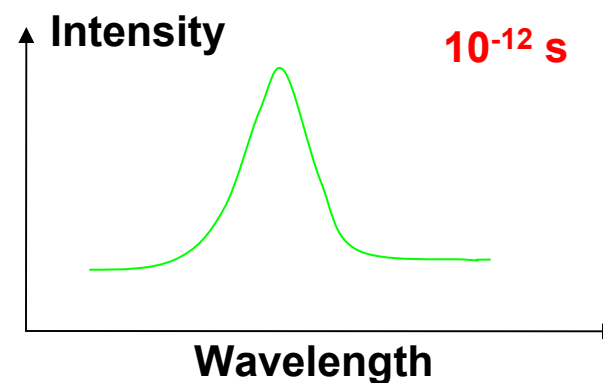
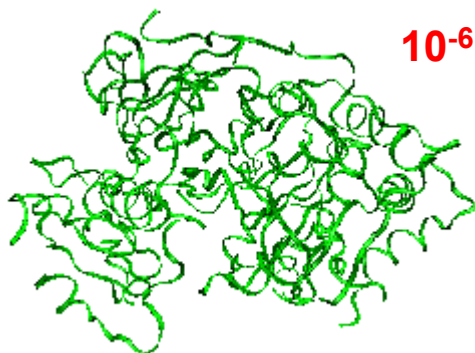
α, β : QM nuclei i, j : QM electron M, N : MM atoms

QM/MM Procedure

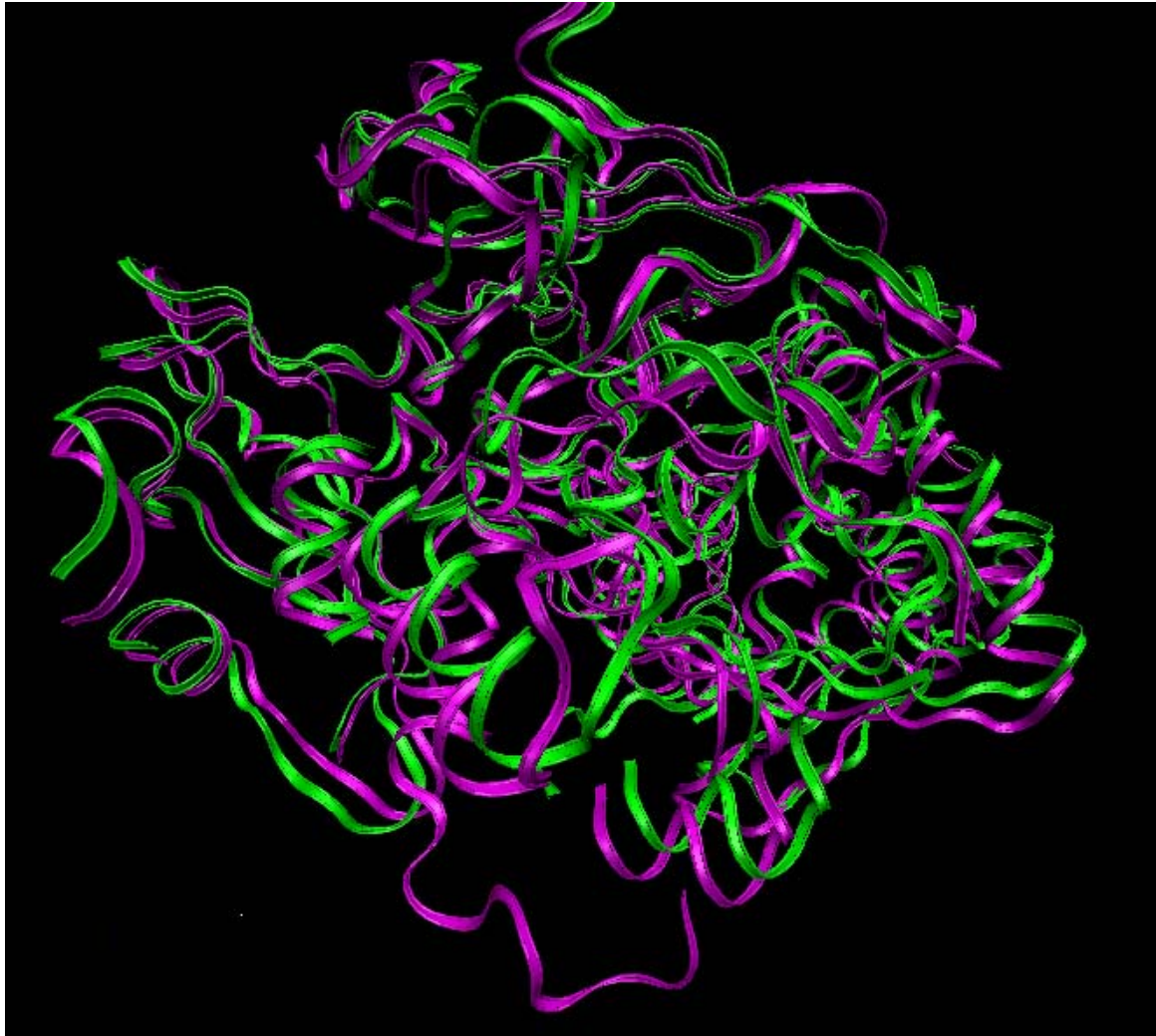
performed by ONIOM program (Gaussian 03)

- Start with the crystal structures
- The ground state is optimized at the ONIOM-EE (B3LYP/6-31G*:AMBER) level
- The $S_0 \rightarrow S_1$ excitation energy is computed by TDDFT/B3LYP/6-31G*:AMBER based on the optimized ground state structure

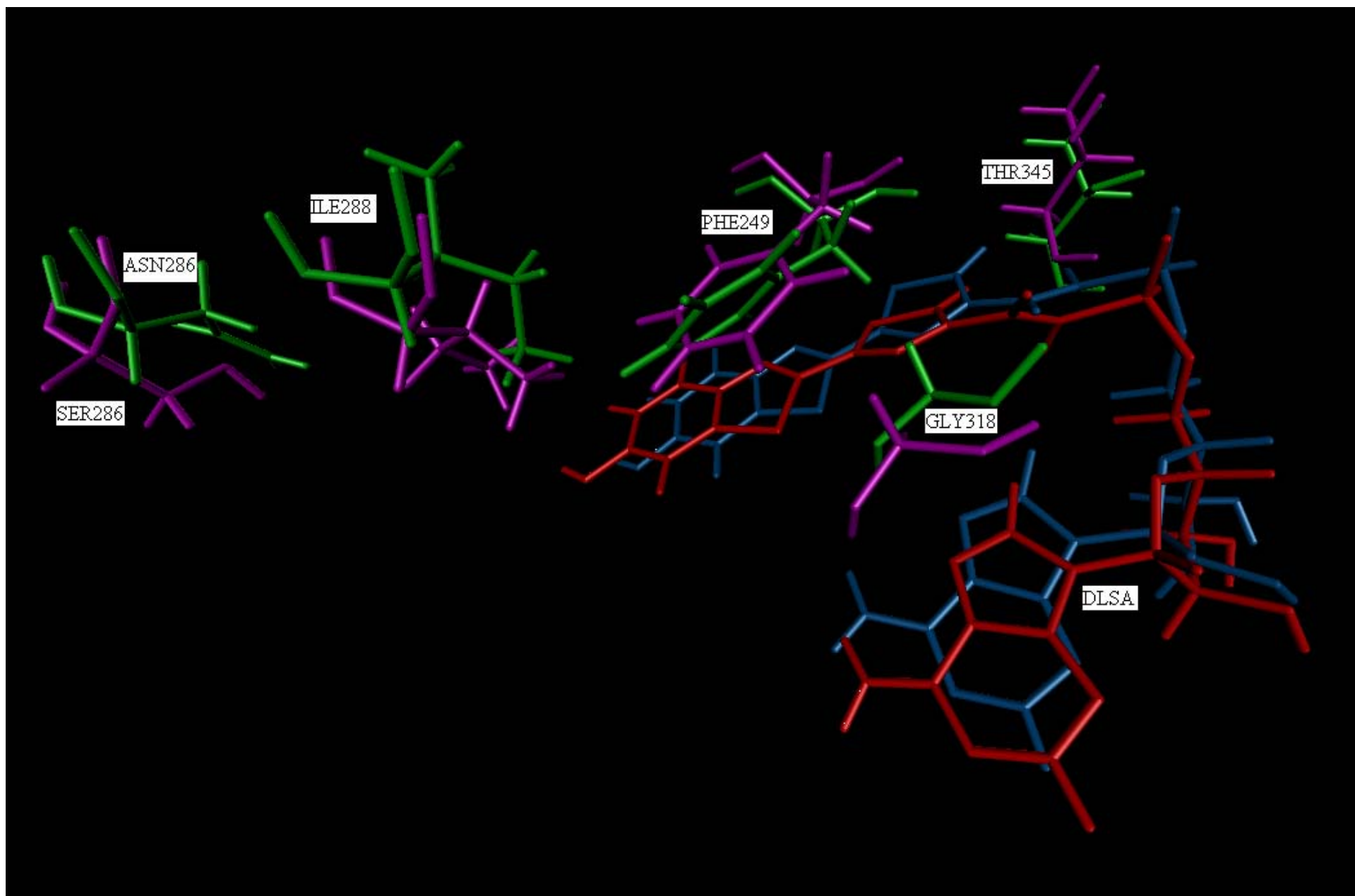
Assumption: time for structural relaxation \gg time for electron excitation

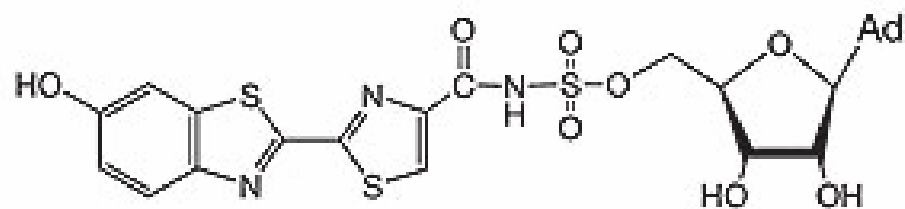


Global Structural Change Caused by Mutation S286N



— wild-type
— S286N mutant

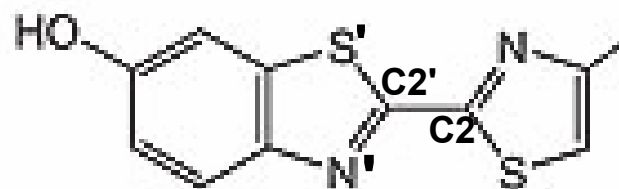




5'-O-[N-(dehydroluciferyl)-sulfamoyl]adenosine (DLSA)



| | C2'-C2 | C2'-N' | C2-S' | C2-N | C2-S | S'-C2'-C2-S | N'-C2'-C2-N |
|--------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|
| WT | 1.4486Å | 1.3073Å | 1.7614Å | 1.3074Å | 1.7649Å | 159.47° | 163.60° |
| S286N | 1.4483Å | 1.3101Å | 1.7604Å | 1.3098Å | 1.7661Å | 172.39° | 174.00° |



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Luciferase Multicolor Bioluminescence Mechanism

- The effect of the protein environment is on the relative angle of two rings of DLSA through van der Waals contacts.
- A more planar two rings of DLSA leads a spectral red-shift.

The Calculated Emission Spectra

| | Calculated | Experimental Data |
|---------------------------|------------|-------------------|
| Wild-type luciferase | 589 nm | 560 nm |
| Mutant (S286N) luciferase | 611 nm | 605 nm |