Day 2

Bridging Structure and Function, Experiments and Computations

Pemra Doruker

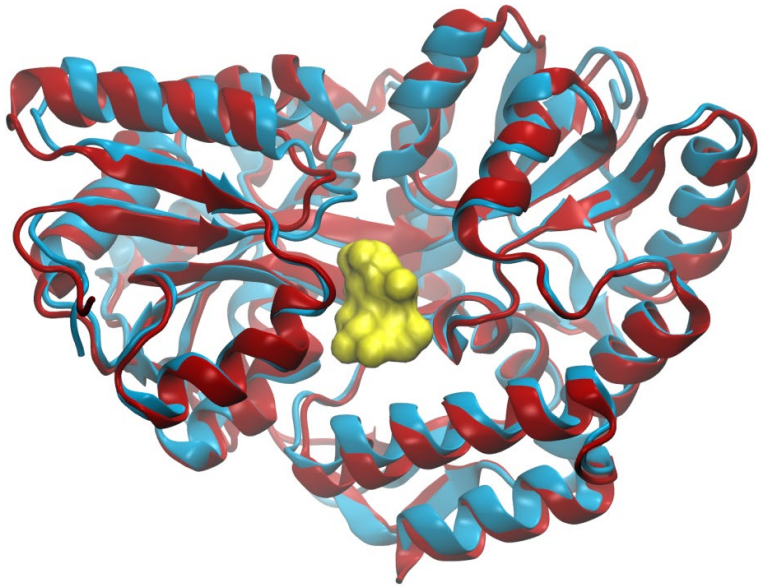
Department of Computational and Systems Biology
School of Medicine, University of Pittsburgh, Pittsburgh, PA 15260

Summary

1. Theory
   a. Gaussian Network Model (GNM)
   b. Anisotropic Network Model (ANM)
   c. Resources/Servers/Databases (ProDy, DynOmics)
2. Bridging Sequence, Structure and Function
   a. Ensemble analysis using the ANM
   b. Combining sequence and structure analyses – signature dynamics
   c. Allosteric communication – sensors and effectors
3. Membrane proteins and druggability
   a. Modeling environmental effects using elastic network models
   b. Modeling & simulations of Membrane Proteins with ENMs for lipids
   c. Druggability simulations

Proteins exploit pre-existing soft modes for their interactions

Structural changes involved in protein binding correlate with intrinsic motions in the unbound state

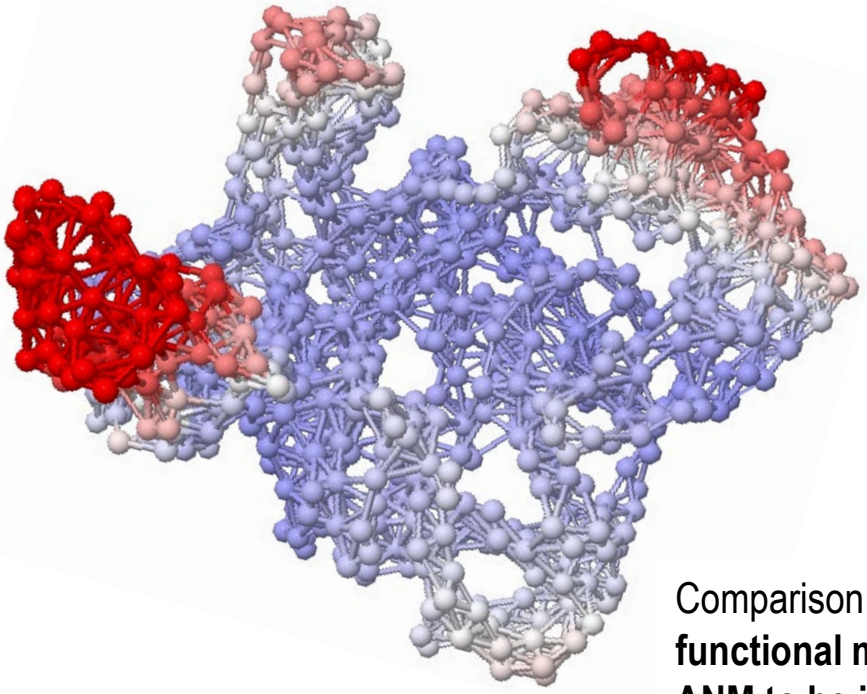


maltodextrin binding protein
Unbound/Bound

Dror Tobi & I. Bahar (2005) *PNAS* 102:18908-18913

Allosteric changes in conformation

Elastic Network Models are particularly useful for exploring the cooperative motions of large multimeric structures

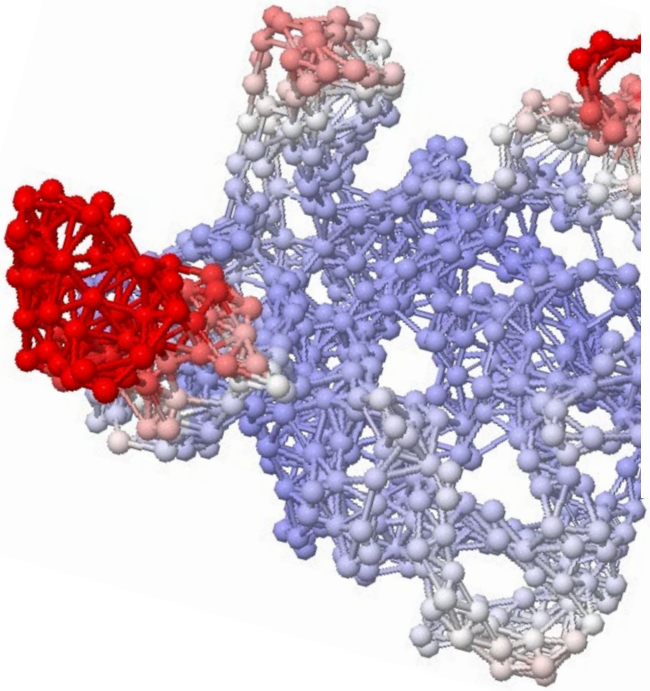


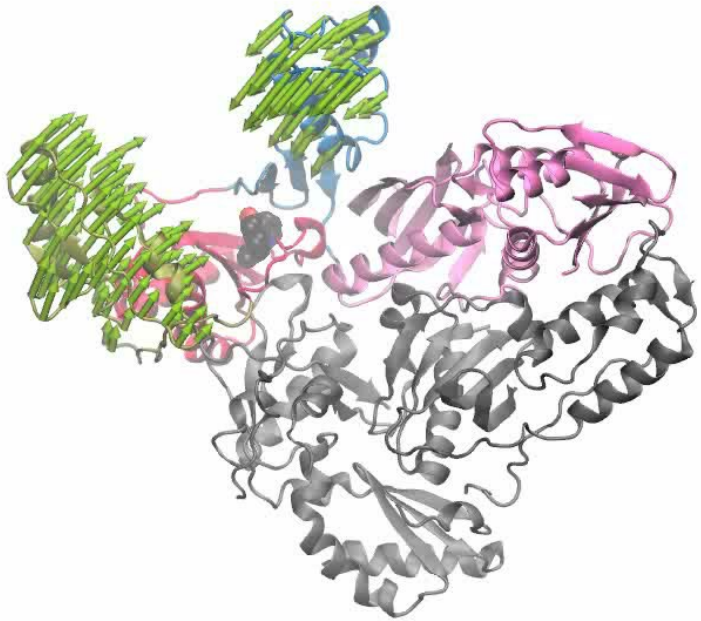
HIV Reverse Transcriptase (RT)
Red: most mobile
Blue: most constrained

Comparison with experimental data shows that **the functional movements are those predicted by the ANM to be intrinsically encoded by the structure**

Allosteric changes in conformation

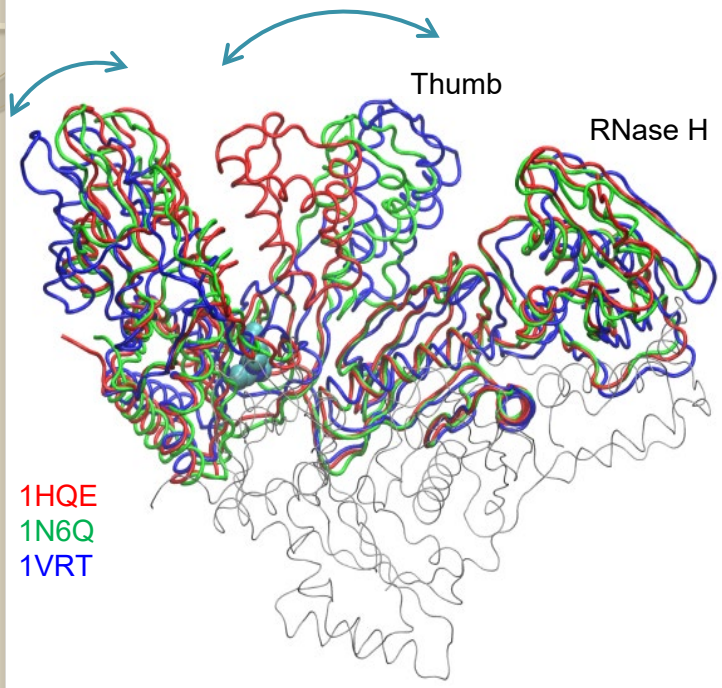
Elastic Network Models are particularly useful for exploring the cooperative motions of large multimeric structures



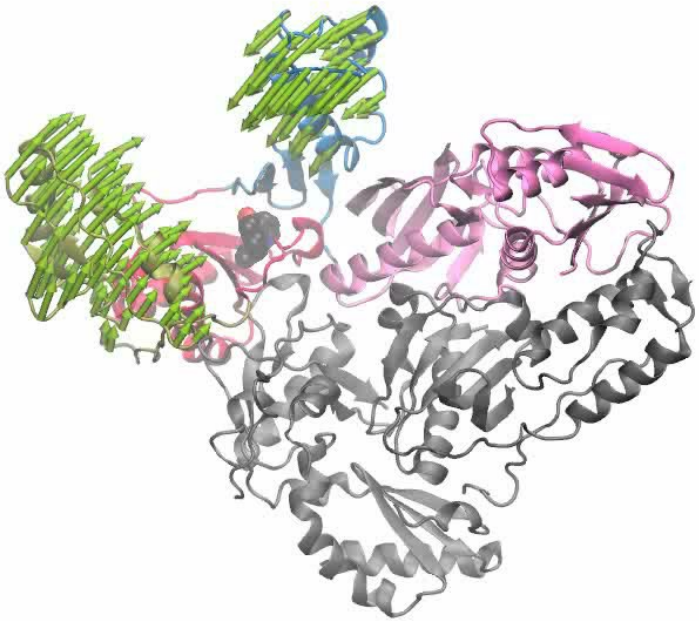


Comparison with experimental data shows that **the functional movements are those predicted by the ANM to be intrinsically encoded by the structure**

Induced Dynamics or Intrinsic Dynamics?



Experiments



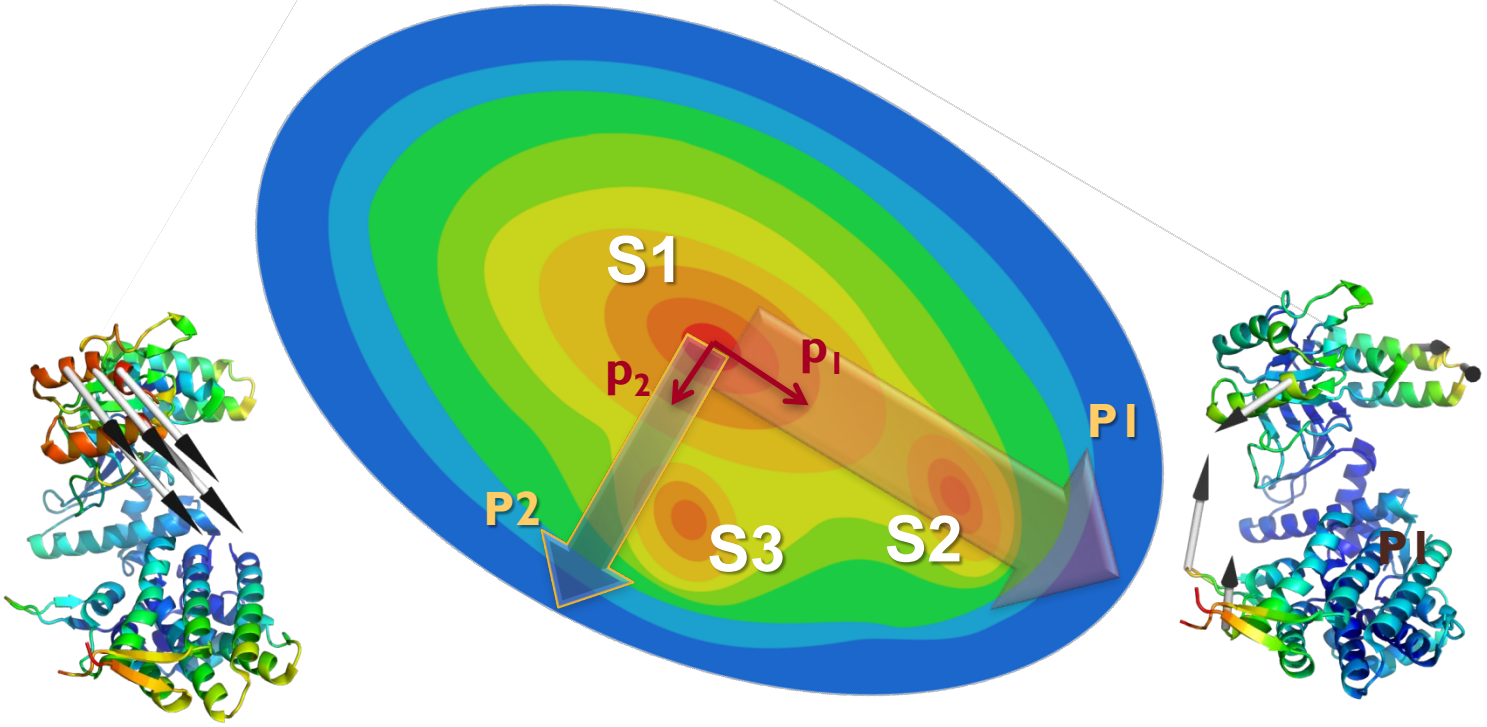
Theory

http://www.youtube.com/watch?v=1OUzdzm68YY

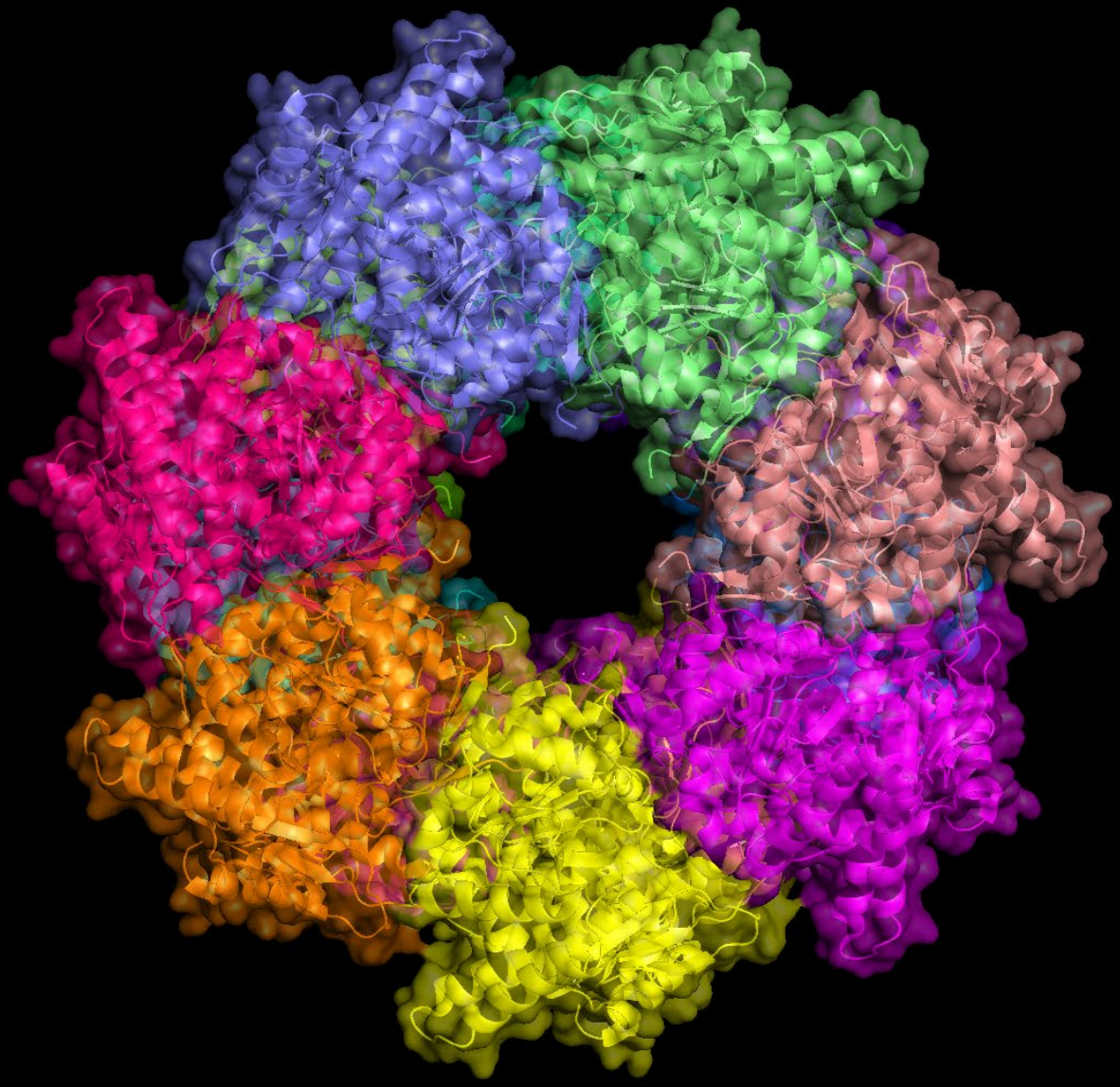
References:

Bakan & Bahar (2009) PNAS **106**, 14349-54.

Substates may be identified along soft modes

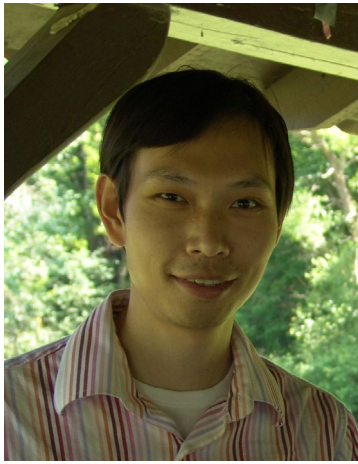


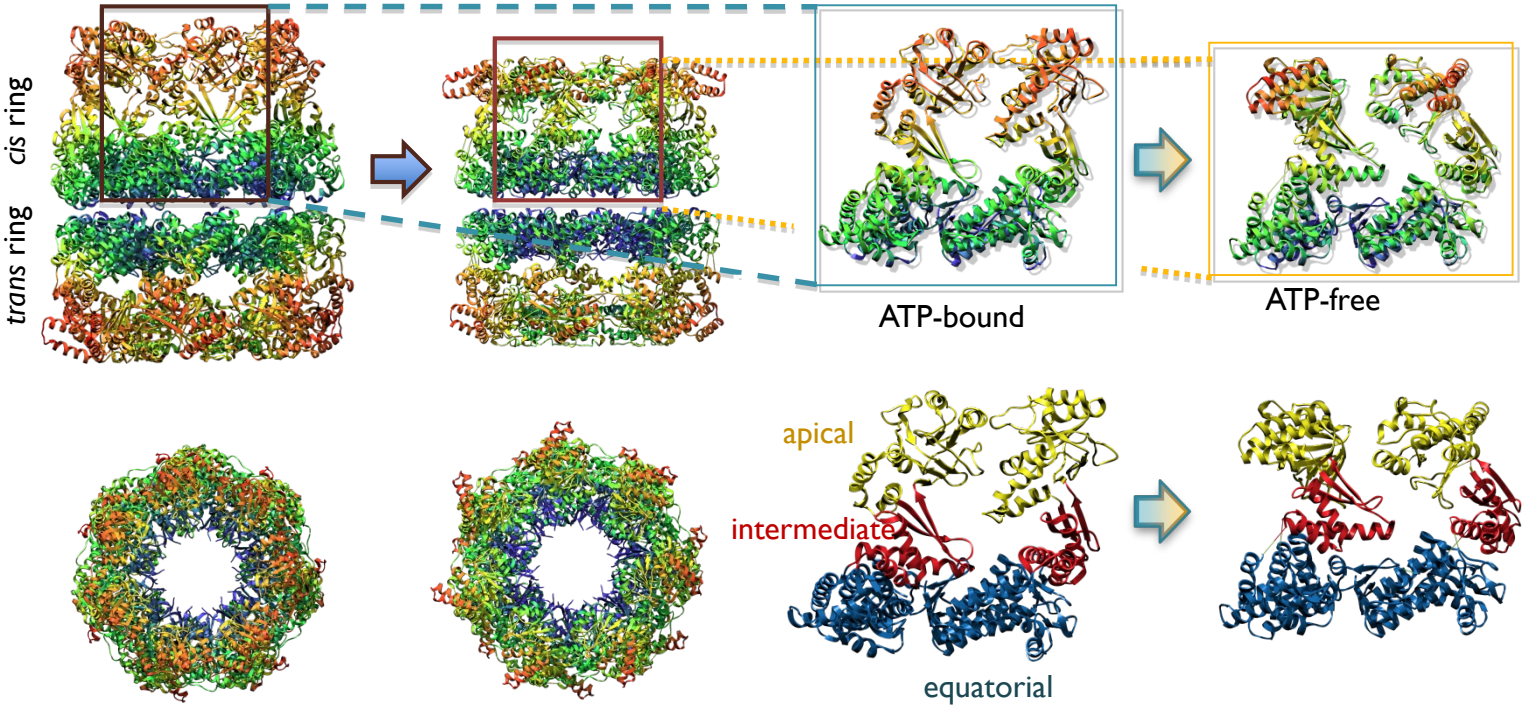
Bacterial chaperonin GroEL: an allosteric machine



GroEL Allosteric Dynamics

Passage between the R and T states





See...

Z Yang, P Marek and I Bahar, *PLoS Comp Biology* 2009

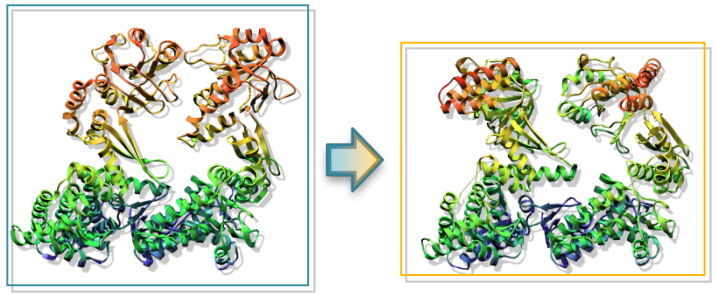
Computations

ANM yields a series of 3N dimensional **deformation vectors**

Mode 1 (slowest mode)
Mode 2
Mode 3
….
Mode 3N-6 (fastest mode)

Given by ANM eigenvectors $\mathbf{v}_1$, $\mathbf{v}_2$, $\mathbf{v}_3$, …. $\mathbf{v}_{3N-6}$, with respective frequencies proportional to κ_1, κ_2, κ_3,…. κ_{3N-6}

Experiments



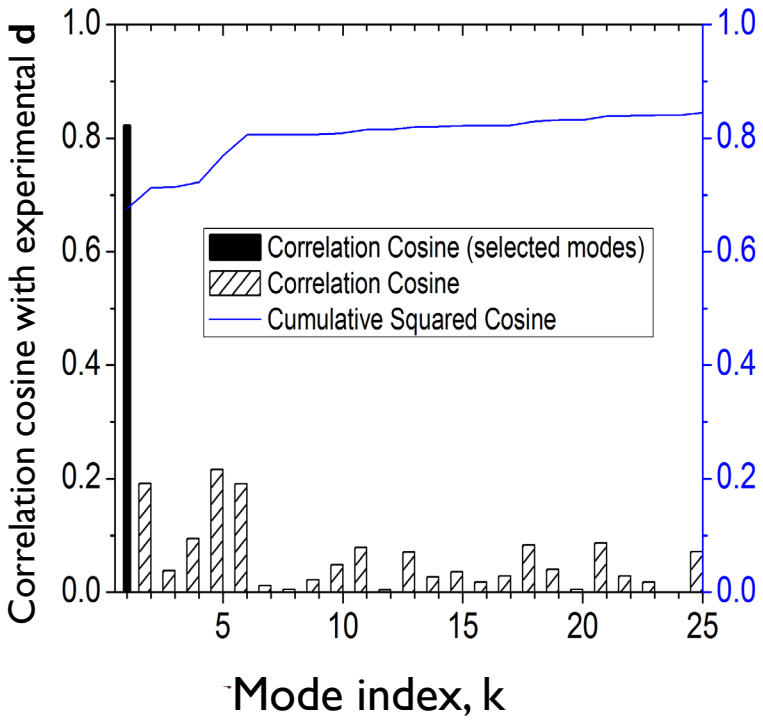
$$\mathbf{d} = [\Delta x_1 \;\; \Delta y_1 \;\; \Delta z_1 \;\ldots\;\; \Delta z_N]^T$$

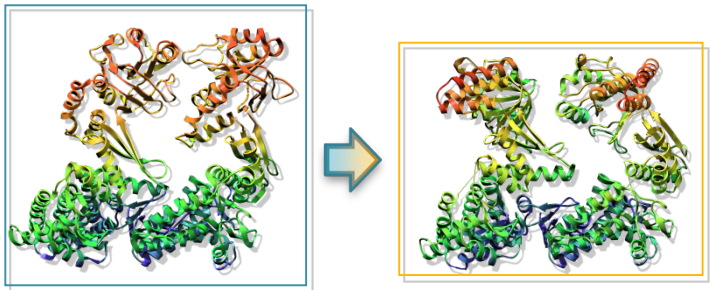
See...

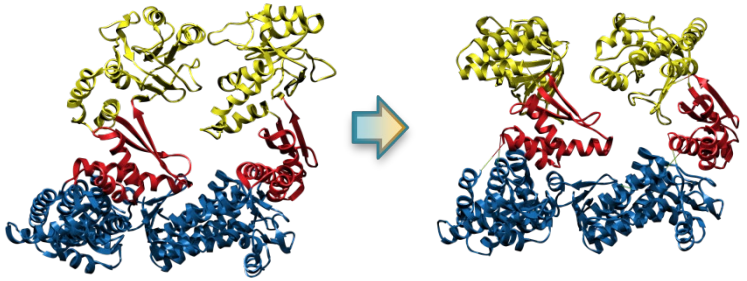
Z Yang, P Marek and I Bahar, *PLoS Comp Biology* 2009

What is the overlap between computations and experiments?

Correlation cosine between $\mathbf{v}_k$ and $\mathbf{d}$







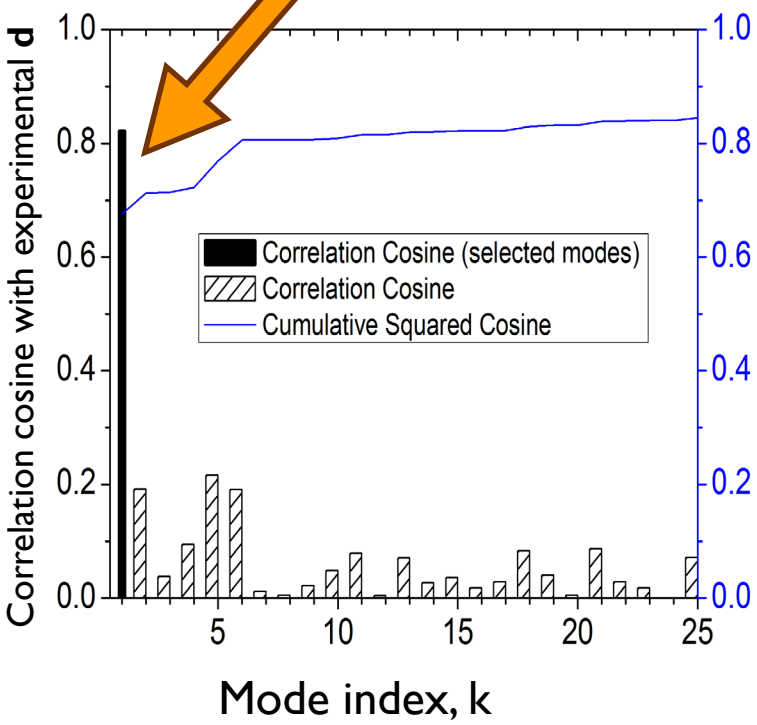
$$\mathbf{d} = [\Delta x_1 \;\; \Delta y_1 \;\; \Delta z_1 \;\ldots\; \Delta z_N]^T$$

See...

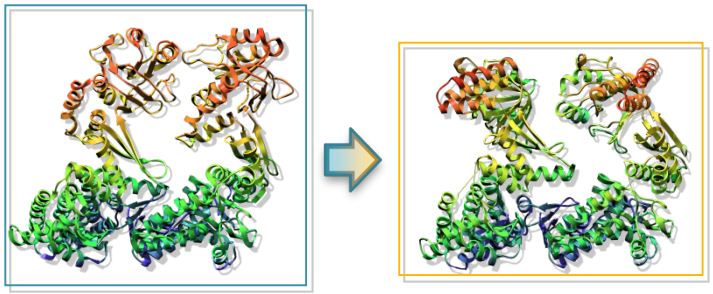
Z Yang, P Marek and I Bahar, *PLoS Comp Biology* 2009

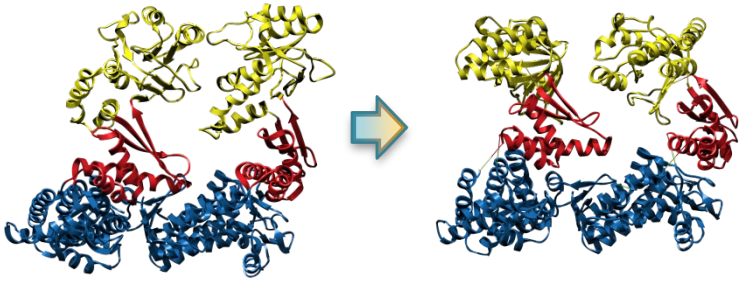
The softest mode enables the passage R → T

(with a correlation of 0.81)



$$CO(m) = \sqrt{\sum_{k=1}^{m} \left(\boldsymbol{v}^{(k)} \cdot \boldsymbol{d} / |\boldsymbol{d}|\right)^2}$$





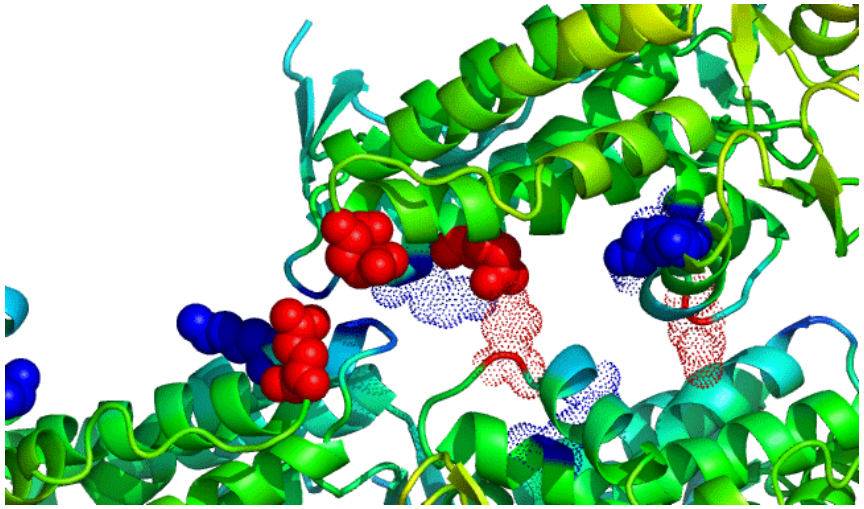
$\mathbf{d} = [\Delta x_1 \;\; \Delta y_1 \;\; \Delta z_1 \;\ldots\;\; \Delta z_N]^T$

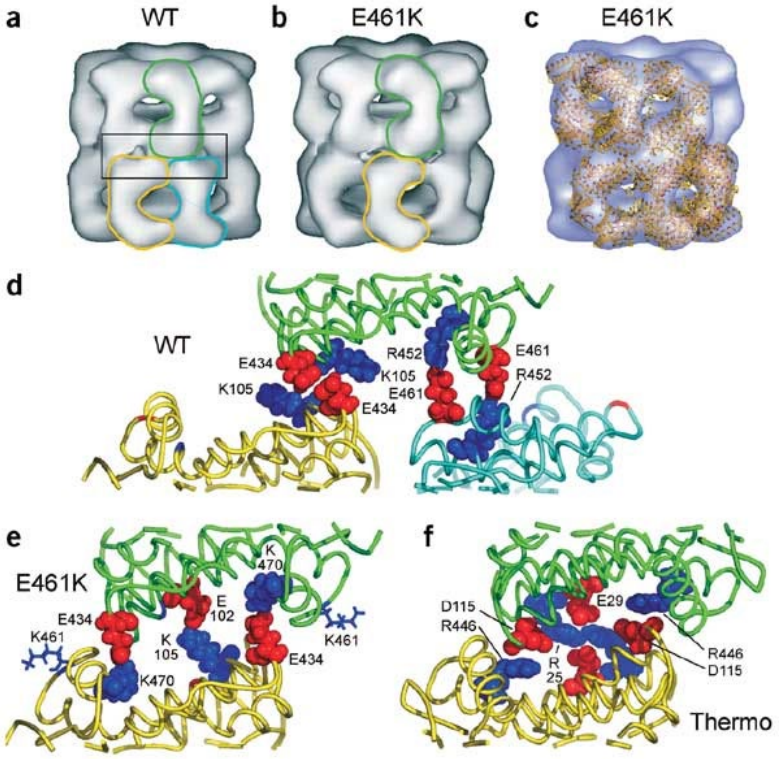
See...

Z Yang, P Marek and I Bahar, *PLoS Comp Biology* 2009

Mutations may stabilize conformers along soft modes – which may be impair function

E461 mutant is a deformed structure along mode 1





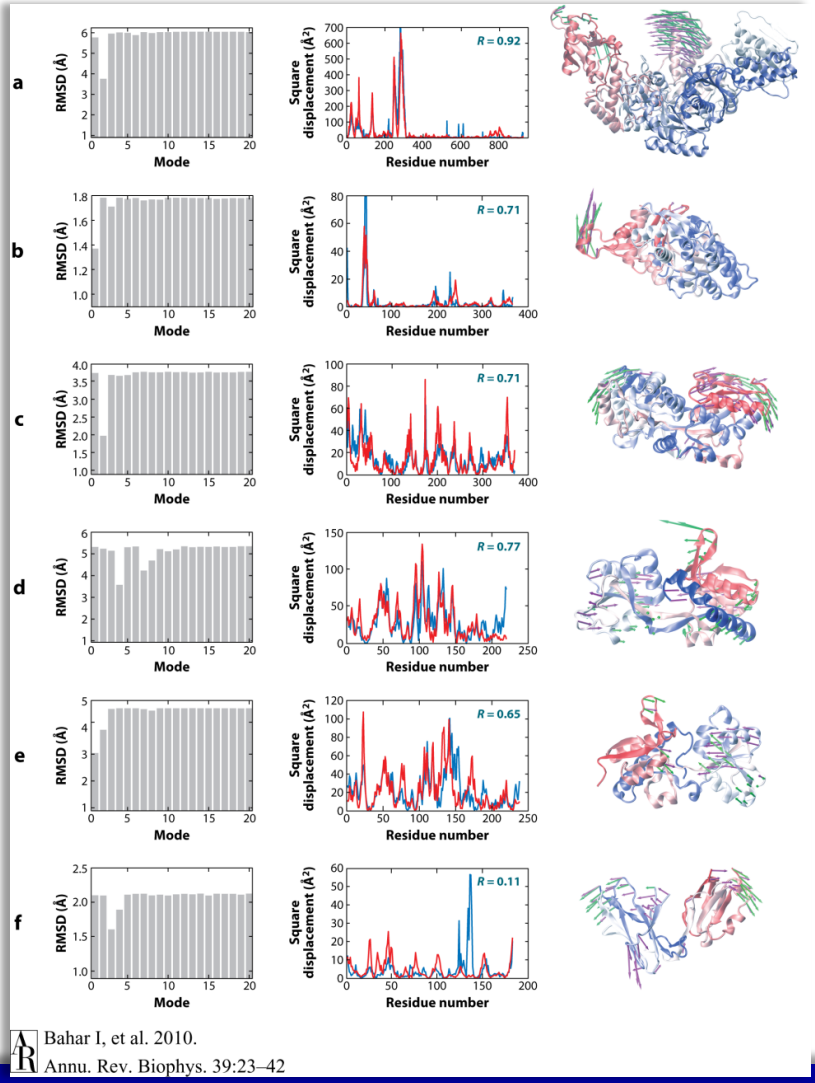
E461K mutation causes disruption of inter-ring transfer of ATP-induced signal (Sewell et al NSB 2004)

Yang et al. *Mol Biosyst* 2008

Experimentally observed structural changes are usually reconfigurations along soft modes

- Correlation cosine of 0.75 ± 0.15 between one of the softest modes and the experimentally observed change in structure

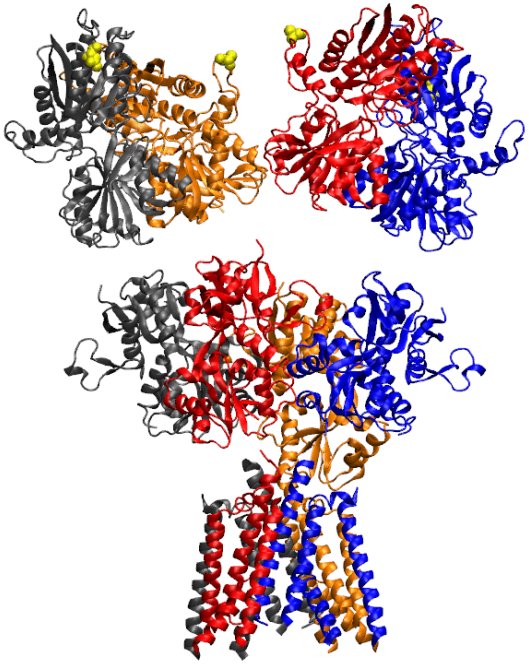
- Significant decrease in RMSD between the endpoints upon moving along a single soft mode (out of 3N-6 modes)



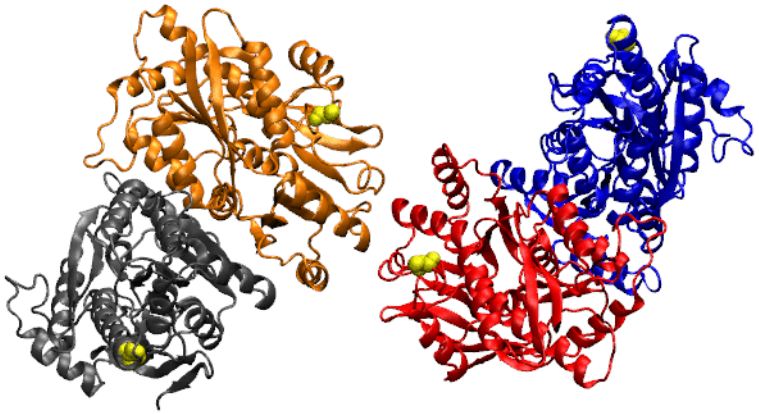
Bahar I, et al. 2010.
Annu. Rev. Biophys. 39:23–42

See...

Allosteric transition of AMPAR



Side view



Top view

The trajectory was generated with adaptive-ANM (aANM) using the first 30 modes
Initial: N-shaped (PDB id: 4uqj) → Target: O-shaped (PDB id: 5ide) AMPAR

Summary

1. Theory
   a. Gaussian Network Model (GNM)
   b. Anisotropic Network Model (ANM)
   c. Resources/Servers/Databases (ProDy, DynOmics)

2. Bridging Sequence, Structure and Function
   a. **Ensemble analysis using the ANM**
   b. Combining sequence and structure analyses – signature dynamics
   c. Allosteric communication – sensors and effectors

3. Membrane proteins and druggability
   a. Modeling environmental effects using elastic network models
   b. Modeling & simulations of Membrane Proteins with ENMs for lipids
   c. Druggability simulations

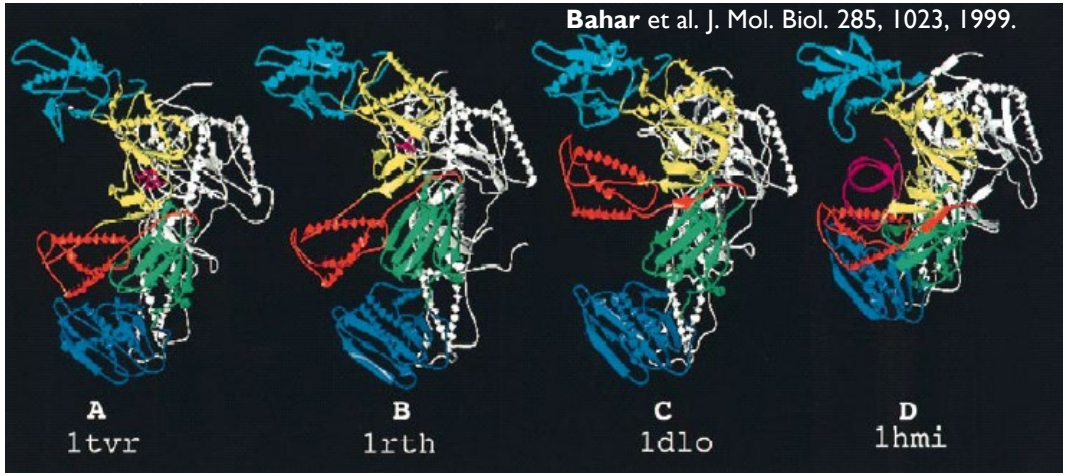
A better comparison:

Consider more than 2 end points for a given structure, but all the known structures for a given protein, or the structurally resolved

Ensemble of structures

Dynamics inferred from known structures

Comparison of static structures available in the PDB for the same protein in different form has been widely used is an indirect method of inferring dynamics.

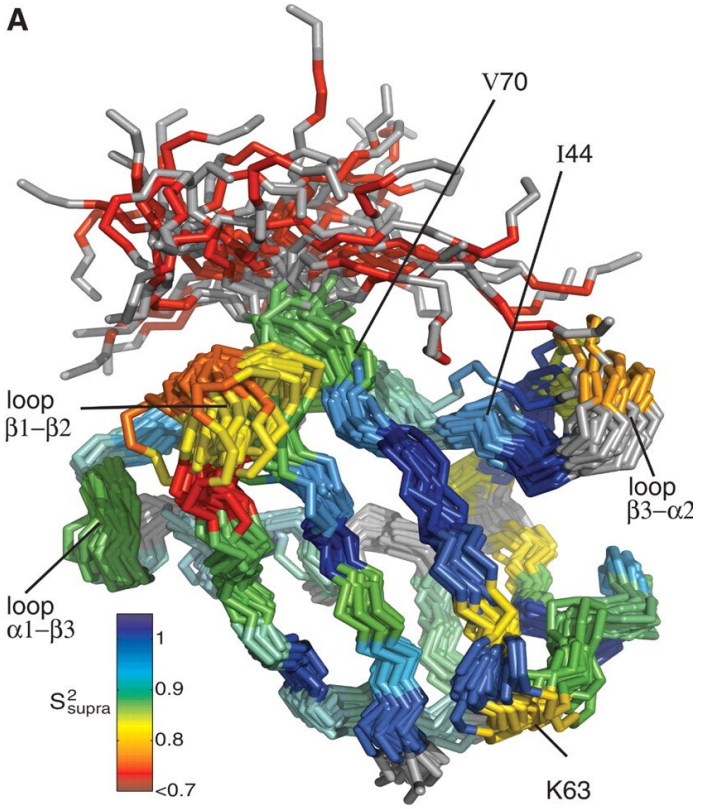


Different structures resolved for HIV-1 reverse transcriptase (RT)

RESEARCH ARTICLES

Recognition Dynamics Up to Microseconds Revealed from an RDC-Derived Ubiquitin Ensemble in Solution

Oliver F. Lange, ..., Jens Meiler, Helmut Grubmüller, Christian Griesinger, **Bert L. de Groot**



The ensemble covers the complete structural heterogeneity observed in 46 ubiquitin crystal structures, mostly complexes with other proteins.

- **Conformational selection, rather than induced-fit** explains the molecular recognition dynamics of ubiquitin.

- **A concerted mode** accounts for molecular recognition heterogeneity

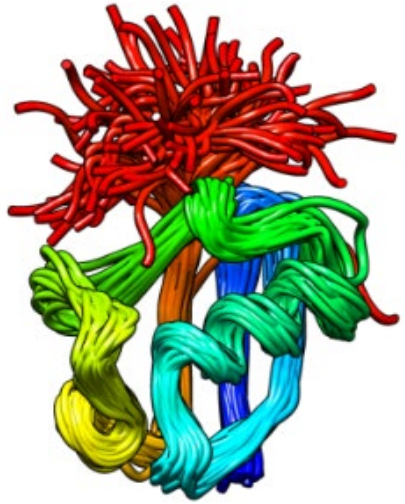
Reference

Lange et al. (2008) *Science* 320:1471 - 1475

Ensembles of structures

- Structural changes accompanying substrate (protein) binding

- Structural changes induced by, or stabilized upon, ligand binding

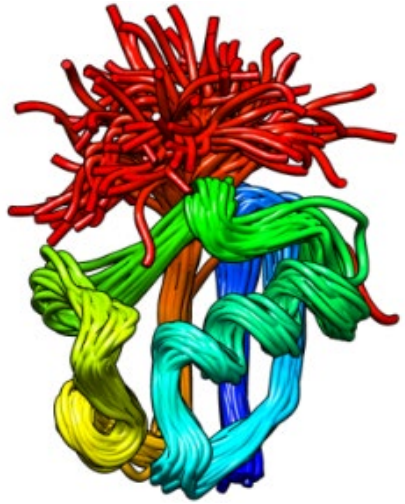


Ubiquitin
140 structures
1732 models

Ensembles of structures

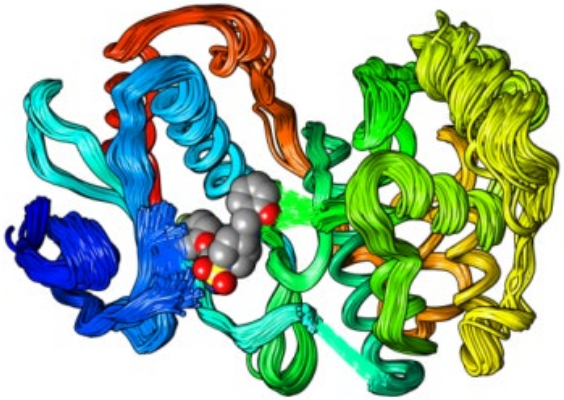
- Structural changes accompanying substrate (protein) binding

- Structural changes induced by, or stabilized upon, ligand binding

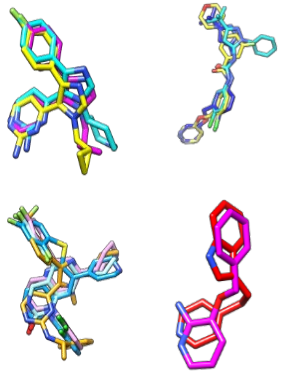


Ubiquitin
140 structures
1732 models

p38 MAP kinase
(**182 structures**)

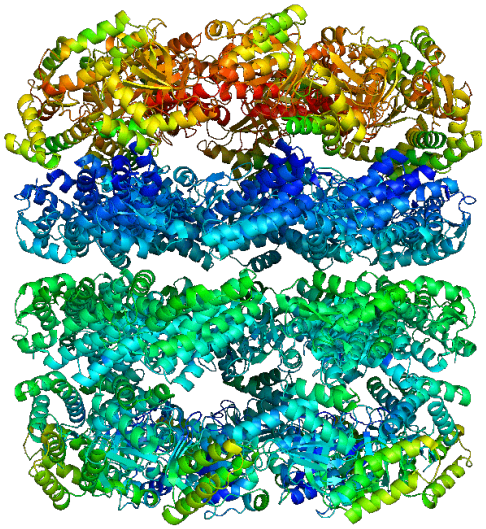


p38 inhibitors



Ensembles of structures

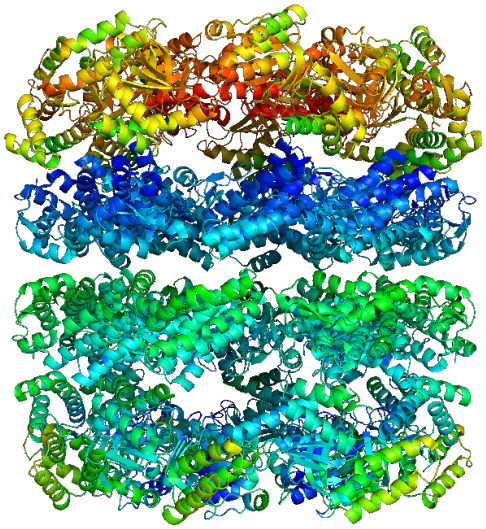
- Structural changes accompanying substrate (protein) binding
- Structural changes induced by, or stabilized upon, ligand binding
- Alternative conformations sampled during allosteric cycles



Yang et al. *PLoS Comp Biol* 2009

Ensembles of structures

- Structural changes accompanying substrate (protein) binding
- Structural changes induced by, or stabilized upon, ligand binding
- Alternative conformations sampled during allosteric cycles



Yang et al. *PLoS Comp Biol* 2009

What is Ensemble Analysis?

Principal component analysis

Input:

An ensemble of structures for a given protein

- NMR models (~40)
- X-ray structures resolved under different conditions (ligand-bound/unbound, different stages of molecular machinery or transport cycle
- MD snapshots/frames

Output:

Principal modes of conformational changes

- variations/differences between NMR models
- rearrangements/changes under different functional states
- dynamics/fluctuations observed in simulations

What is Ensemble Analysis?

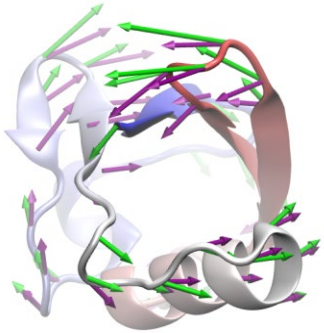
Principal component analysis

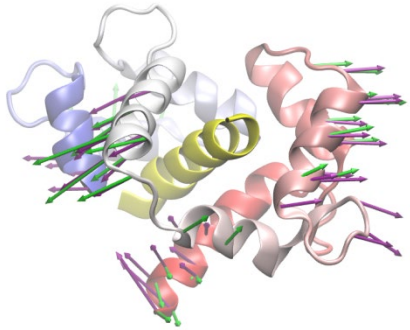
- ANM analysis
- Select a representative structure (e.g. with minimal RMSD from others)
- Theoretical
- Decompose either $\mathbf{H}$ or $\mathbf{C}$ into a series of modes (3N-6 eigenvectors)

PCA

- Superimpose/align the structures
- Experimental
- Decompose it into a series of modes of covariance (3N-6 eigenvectors)

Global motions inferred from theory and experiments

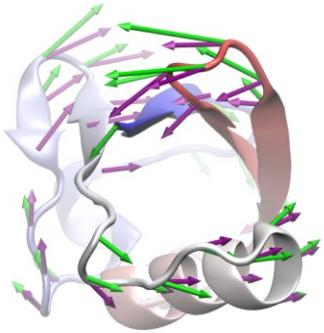


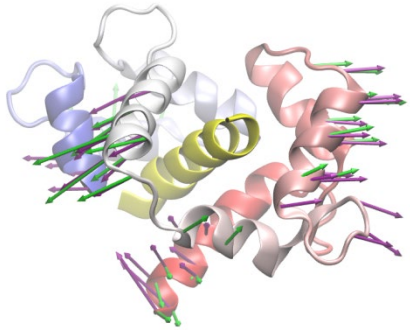


→ PCA of the ensemble of resolved structures

→ ANM analysis of a single structure from the ensemble

Global motions inferred from theory and experiments





The intrinsic dynamics of enzymes plays a dominant role in determining the structural changes induced upon inhibitor binding

Ahmet Bakan and Ivet Bahar[1]

Department of Computational Biology, School of Medicine, University of Pittsburgh, 3064 BST3, 3501 Fifth Avenue, Pittsburgh, PA 15213

Reference:

*Bakan & Bahar (2009) PNAS **106**, 14349-54*

Covariance matrix (NxN)

$$C = \begin{pmatrix} \langle \Delta R_1 \cdot \Delta R_1 \rangle & \langle \Delta R_1 \cdot \Delta R_2 \rangle & \dots & \dots & \langle \Delta R_1 \cdot \Delta R_N \rangle \\ \langle \Delta R_2 \cdot \Delta R_1 \rangle & \langle \Delta R_2 \cdot \Delta R_2 \rangle & & & \\ \dots & & & & \\ \dots & & & & \\ \langle \Delta R_N \cdot \Delta R_1 \rangle & & & & \langle \Delta R_N \cdot \Delta R_N \rangle \end{pmatrix} = \Delta R \, \Delta R^T$$

ΔR = N-dim vector of instantaneous fluctuations ΔR_i for all residues ($1 \leq i \leq N$)

$\langle \Delta R_1 \cdot \Delta R_1 \rangle$ = ms fluctuation of site 1 averaged over all *m* snapshots.

Covariance matrix (3Nx3N)

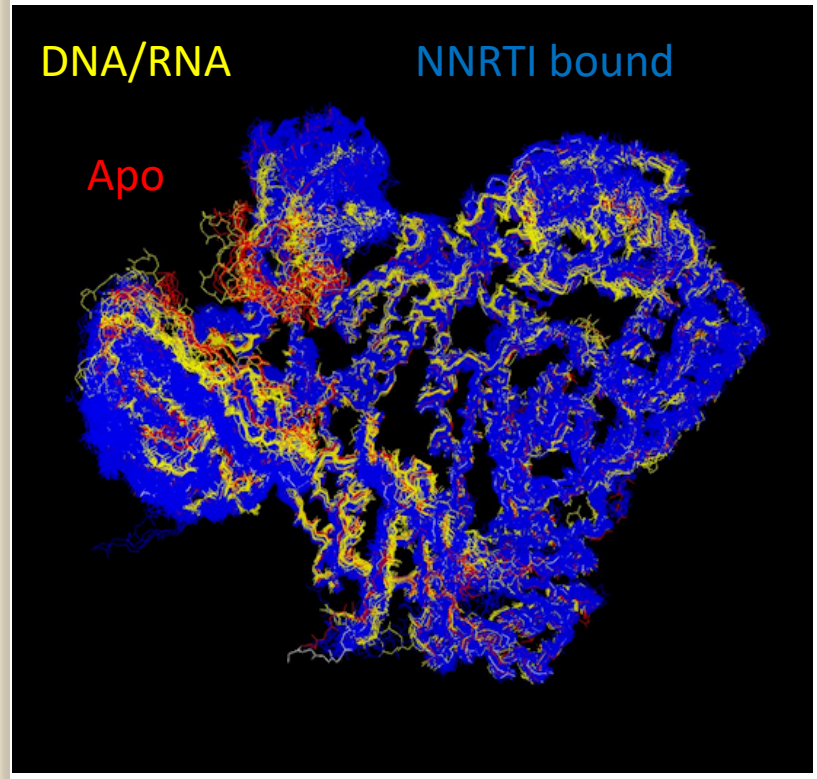
C_{3N} =

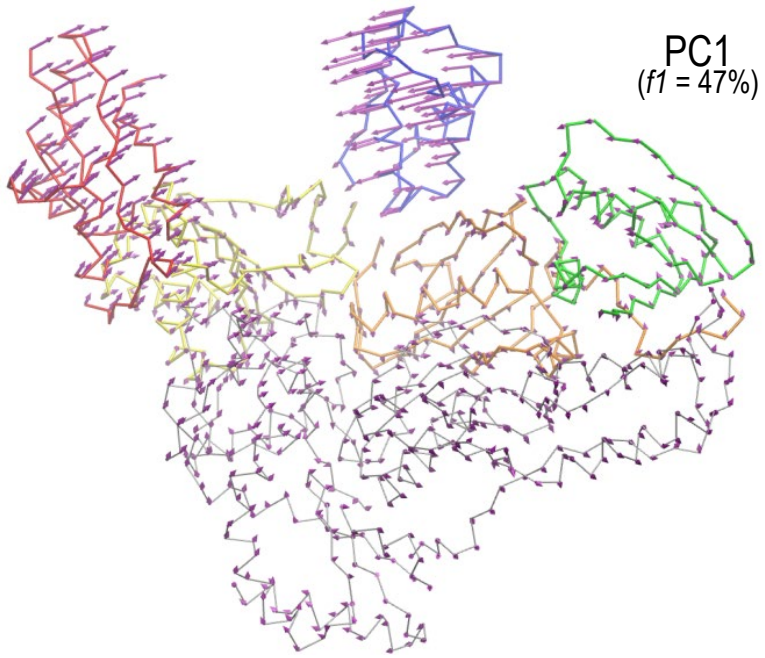
C_{11}	C_{21}	C_{13}		C_{1N}
C_{12}	C_{22}			
C_{N1}				C_{NN}

3N x 3N

$\langle \Delta X_1 \Delta X_2 \rangle$	$\langle \Delta X_1 \Delta Y_2 \rangle$	$\langle \Delta X_1 \Delta Z_2 \rangle$
$\langle \Delta Y_1 \Delta X_2 \rangle$	$\langle \Delta Y_1 \Delta Y_2 \rangle$	$\langle \Delta Y_1 \Delta Z_2 \rangle$
$\langle \Delta Z_1 \Delta X_2 \rangle$	$\langle \Delta Z_1 \Delta Y_2 \rangle$	$\langle \Delta Z_1 \Delta Z_2 \rangle$

Principal Component Analysis (PCA)

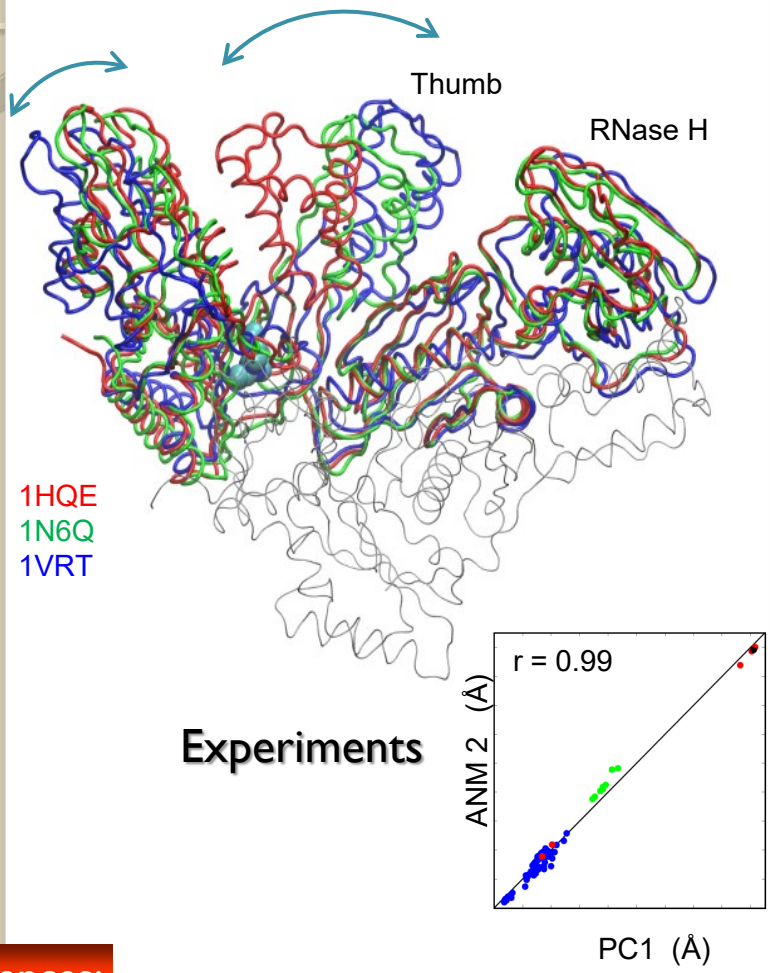




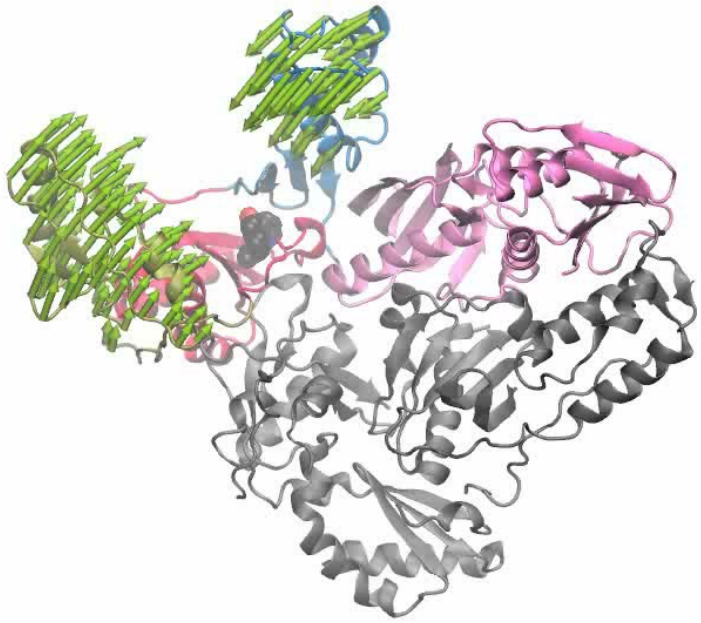
$$\mathbf{C}^{(ij)} = \begin{bmatrix} \langle \Delta x_i \Delta x_j \rangle & \langle \Delta x_i \Delta y_j \rangle & \langle \Delta x_i \Delta z_j \rangle \\ \langle \Delta y_i \Delta x_j \rangle & \langle \Delta y_i \Delta y_j \rangle & \langle \Delta y_i \Delta z_j \rangle \\ \langle \Delta z_i \Delta x_j \rangle & \langle \Delta z_i \Delta y_j \rangle & \langle \Delta z_i \Delta z_j \rangle \end{bmatrix}$$

$$\mathbf{C} = \mathbf{PSP}^T = \sum_{i=1}^{3N} \sigma_i \; \boldsymbol{p}^i \boldsymbol{p}^{iT}$$

Soft modes enable functional movements



Experiments



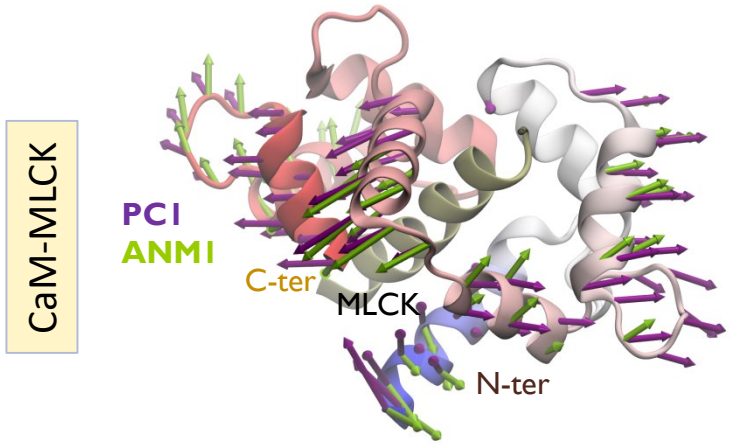
Theory

http://www.youtube.com/watch?v=1OUzdzm68YY

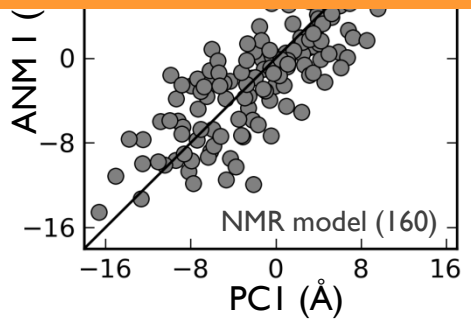
References:

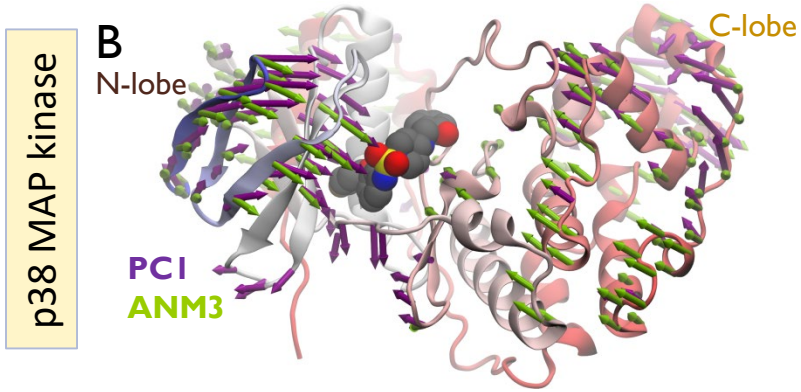
Bakan & Bahar (2009) PNAS **106**, 14349-54.

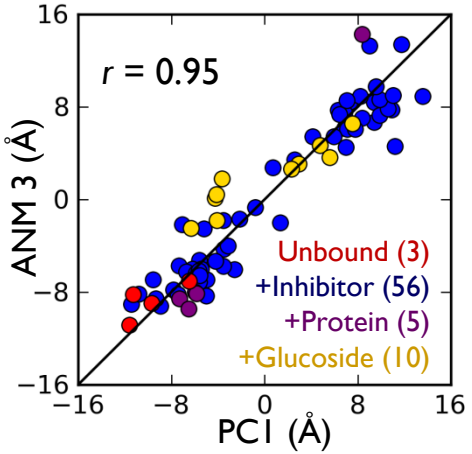
Experimental structures (for a given protein) are mainly variants along soft modes



Pre-existing paths







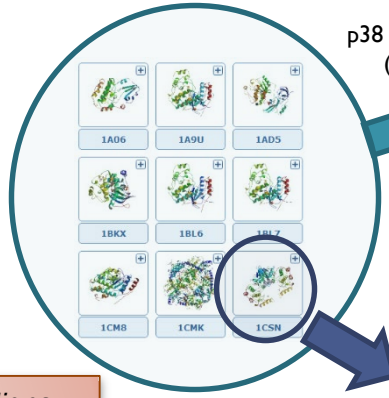
Meireles L, Gur M, Bakan A, Bahar I (2011) Pre-existing soft modes of motion uniquely defined by native contact topology facilitate ligand binding to proteins *Protein Science* **20**: 1645-58.

ProDy for exploring conformational space

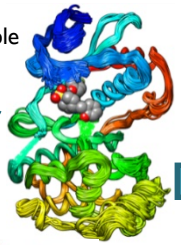
Protein Dynamics Analysis in Python

User inputs a protein sequence

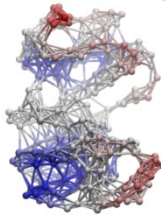
```
>1A9U:A|PDBID|CHAIN
GSSHHHHHHSSGLVPRGSHMSQER
PTFYRQELNKTIWEVPERYQNLSPV
GSGAYGSVCAAFDTKTGLRVAVKK
LSRPFQSIIHAKRTYRELRLLKHMKH
ENVIGLLDVFT.....
```



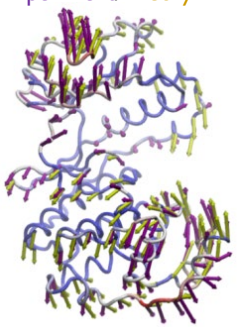
p38 ensemble (PCA)



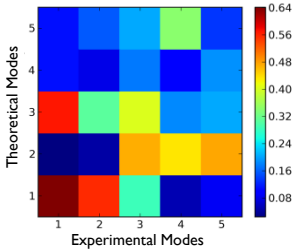
p38 network model (ANM)



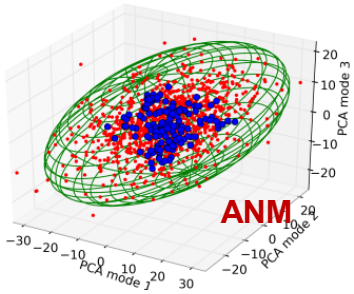
Experiment/Theory



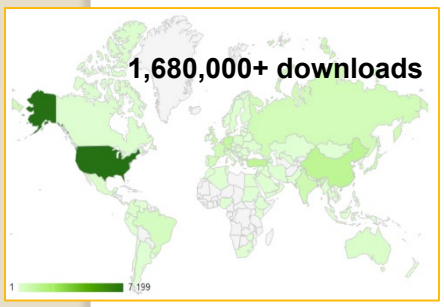
Overlap table



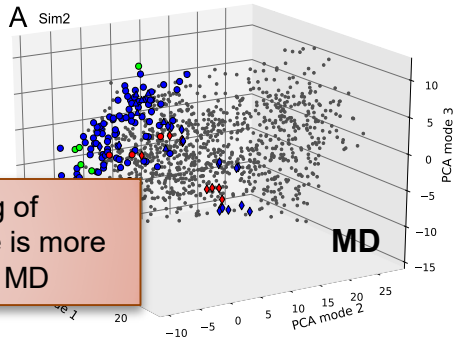
User can compare experimental and theoretical models



ProDy *identifies*, *retrieves*, *aligns,* and *analyzes (PCA)* structures that match the input sequence



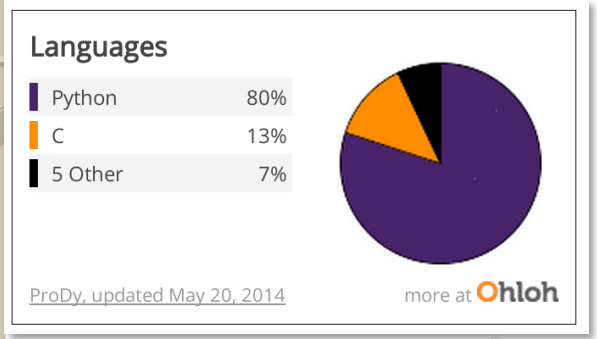
Source http://www.google.com/analytics/



ProDy-ANM sampling of conformational space is more complete than that of MD

User can sample an ensemble of conformations along ANM modes for docking simulations

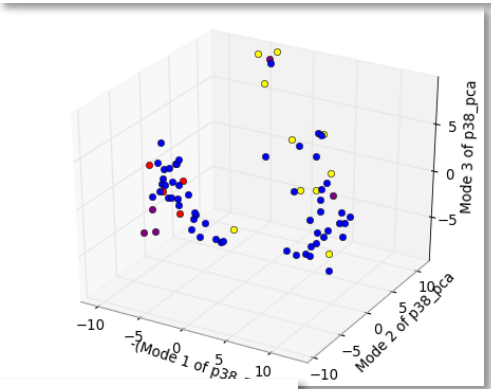
ProDy: An Interactive Tool

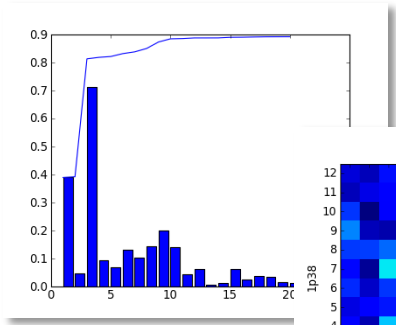


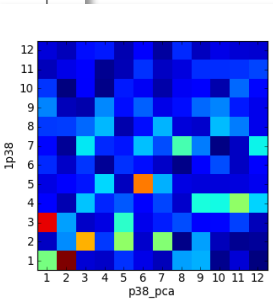
matplotlib

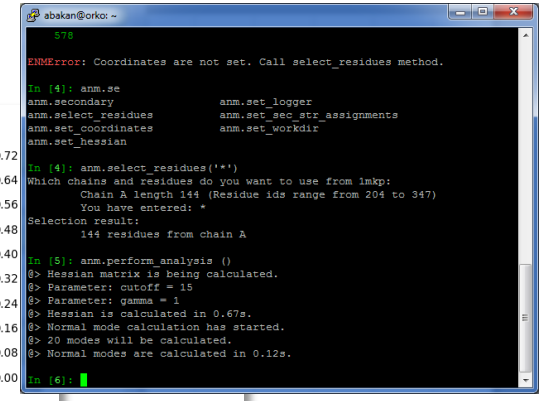
NumPy

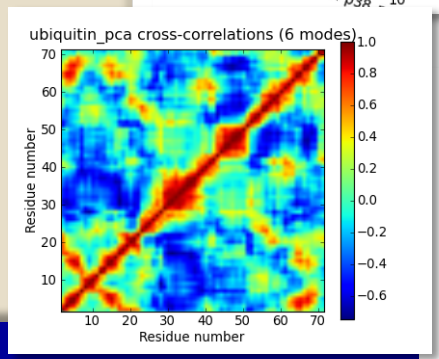
IP[y]: IPython
Interactive Computing

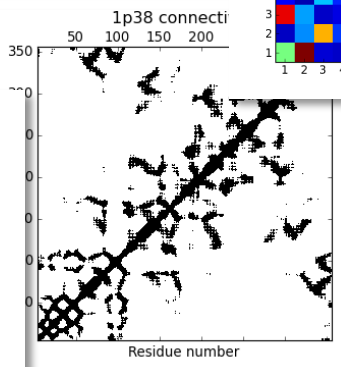


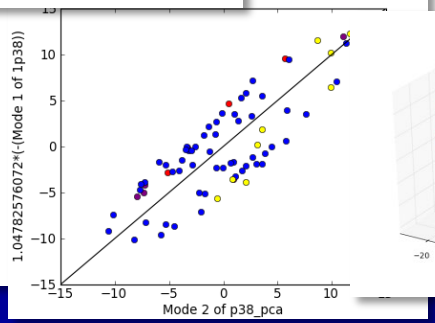


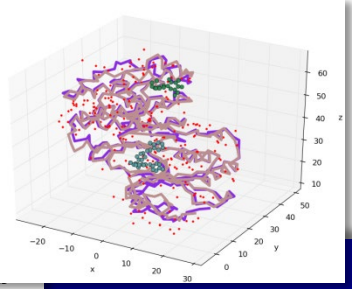








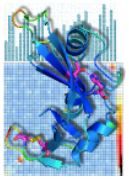




Suite of tools

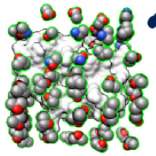
ProDy
Protein Dynamics & Sequence Analysis

Elastic Network Model (ANM/GNM) Analysis
Principal component analysis of experimentally resolved structures



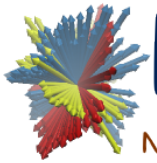
Evol
Bridging Evolution & Dynamics

Multiple Sequence Alignment
Sequence conservation
Correlated Mutations



DruGUI
Druggability Suite for VMD

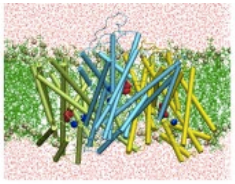
Computational Drug Discovery
Binding Site Prediction
Affinity Estimation



NMWiz
Normal Mode Wizard for VMD

A VMD plugin
Visualization of collective motions
Animations/movies

Suite of tools



membrANM

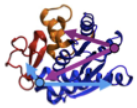
Membrane Anisotropic Network Model

Modeling coupled protein-lipid dynamics
Useful for membrane proteins

PRS

Perturbation-Response Scanning

Propagation allosteric signals
Effector and sensor residues



coMD

Collective Molecular Dynamics

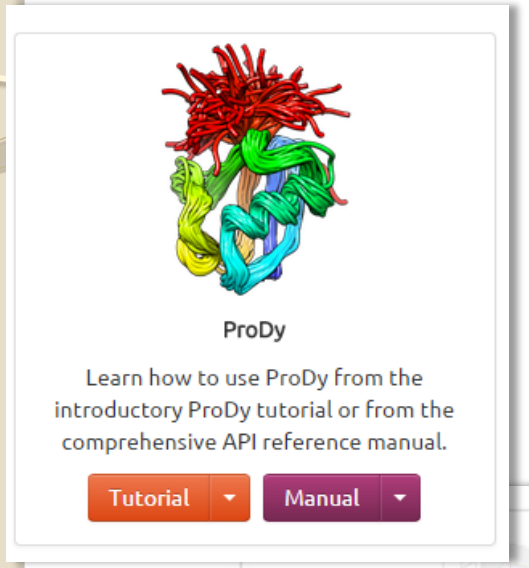
ENM guided MD simulations
Efficient sampling of energy landscape

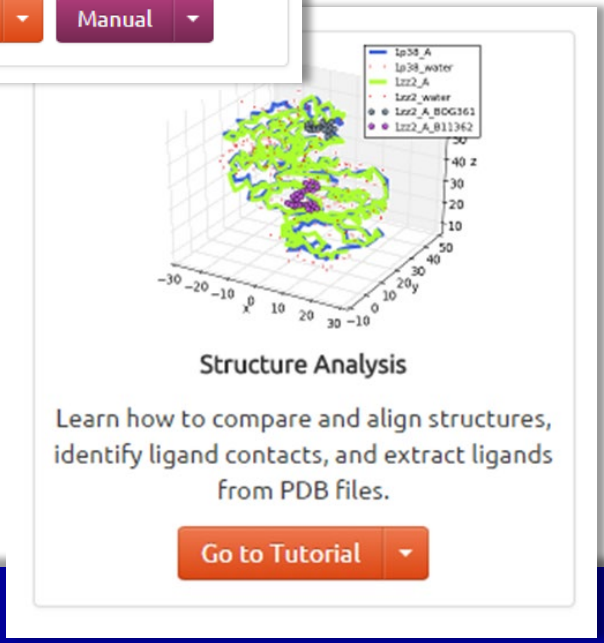
SignDy

Signature Dynamics of Families

Shared global ENM mode profiles and departures from them, dynamics-based trees

Tutorials: ProDy & Structure Analysis





- Retrieving PDB Files
- BLAST-Searching the PDB
- Constructing Biomolecular Assemblies
- Determining functional motions
- Aligning and Comparing Structures
- Identifying Intermolecular Contacts

Major advantages of ProDy:

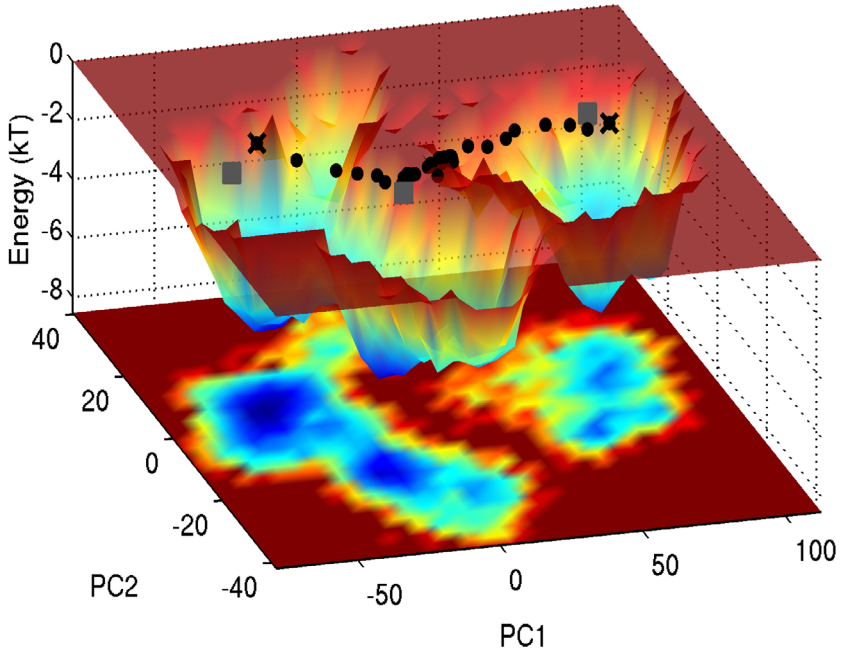
- Simplicity
- Visualizing the global dynamics
- Applicability to large systems
- Assessing cooperative motions
- Efficiency – immediate results
- Relevance to observables, to functional mechanisms & allostery

Caveats

- Low resolution approach
- No specific interactions
- Lack of atomic details
- Linear theory – applicable near an energy minimum
- not a tool for structure prediction (could be used for refinement)

Hybrid methods to overcome caveats ANM-guided atomistic simulations

coMD
Collective Molecular Dynamics

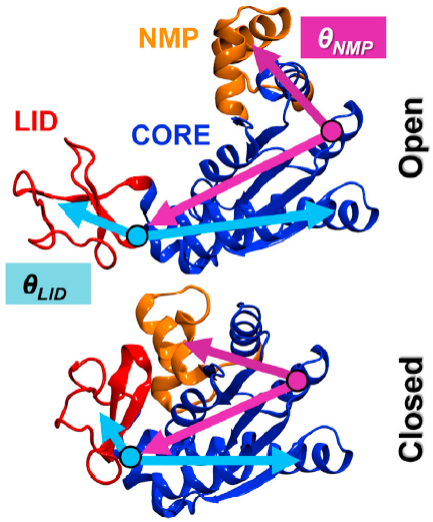


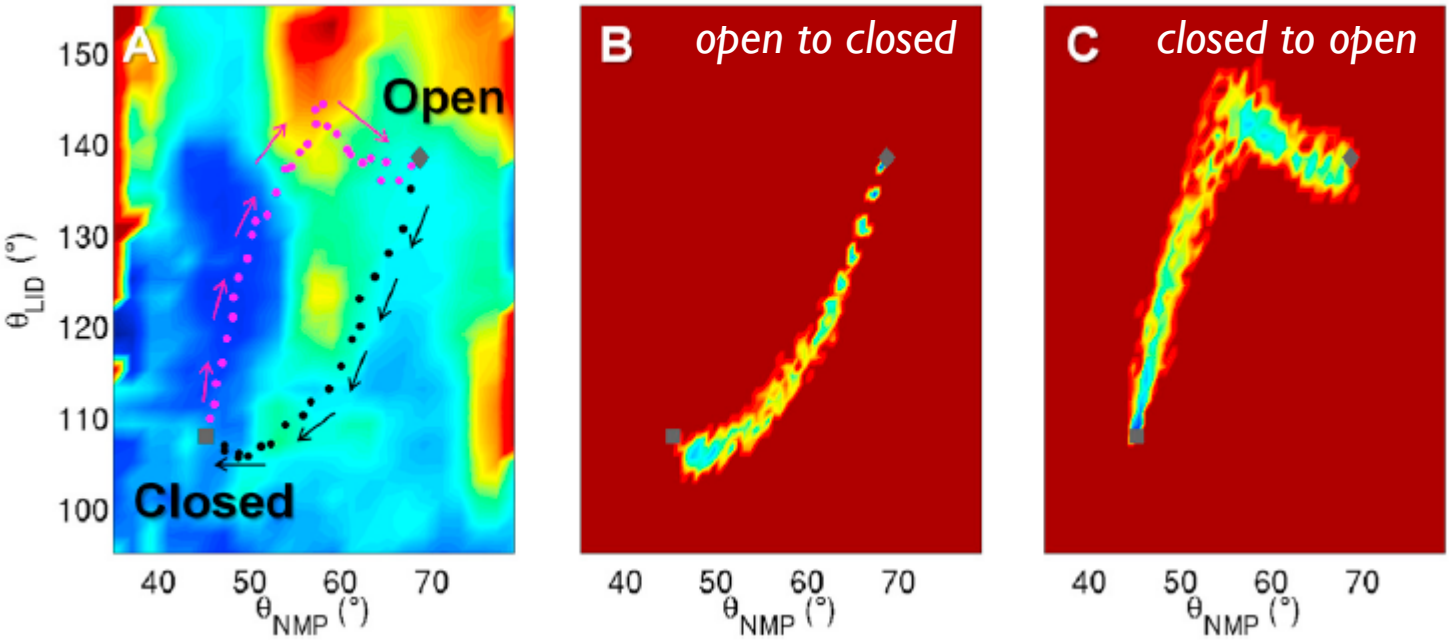
ANM-guided transition pathways

- Isin B, Schulten K, Tajkhorshid E, Bahar I (2008) *Biophysical J* 95: 789-803.
- Yang Z, Májek P, Bahar I (2009) *PLoS Comput Biol* 5: e1000360.
- Gur M, Madura JD, Bahar I (2013) *Biophys J* 105:1643-52
- Das A, Gur M, Cheng MH, Jo S, Bahar I, Roux B (2014) *PLoS Comput Biol* 10: e1003521

coMD trajectories proceed along the minima of free energy landscape

coMD transition pathways for adenylate kinase





Gur, Madura, Bahar, *Biophys J.* (2013) 105, 1643-1652

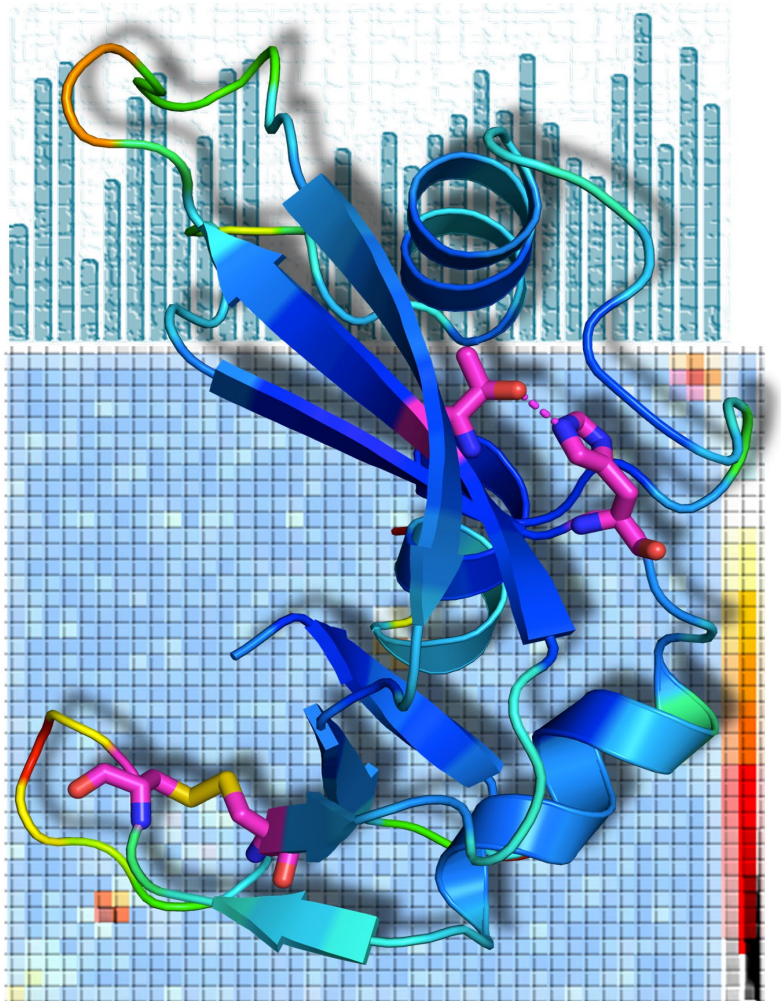
Summary

1. Theory
   a. Gaussian Network Model (GNM)
   b. Anisotropic Network Model (ANM)
   c. Resources/Servers/Databases (ProDy, DynOmics)

2. Bridging Sequence, Structure and Function
   a. Ensemble analysis using the ANM
   b. Combining sequence and structure analyses – signature dynamics
   c. Allosteric communication – sensors and effectors

3. Membrane proteins and druggability
   a. Modeling environmental effects using elastic network models
   b. Modeling & simulations of Membrane Proteins with ENMs for lipids
   c. Druggability simulations

Evol



Dr. Ying Liu

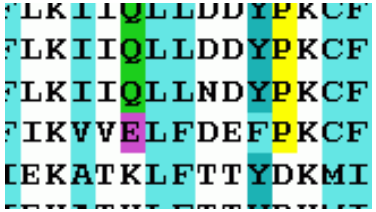
MBE MOLECULAR BIOLOGY AND EVOLUTION

Liu Y, Bahar I (2012) Sequence Evolution Correlates with Structural Dynamics *Mol Biol Evol* 29(9):2253-2263

Questions:

- Are key mechanical sites (e.g. hinges) conserved?
- Is there any correlation between sequence variability and structural dynamics?
- How does the structure ensure substrate specificity *and* conformational adaptability?

Sequence evolution
an information-theoretic approach



Residue index (up to *N*)

i					*i*+5		*i*+7		*i*+9	
	R				E		V		N	
	E				K		V		N	
	K				E		V		N	
	R				D		V		S	
	D				K		V		S	
	D				K		V		S	
	E				R		V		S	

conserved

correlated mutations

Information entropy (Shannon, 1951)

$$S(i) = \sum_{x_i=1}^{20} P(x_i) \log \frac{1}{P(x_i)}$$

Mutual information (MI)

$$\mathrm{I}(i,j) = \sum_{x_i=1}^{20} \sum_{y_j=1}^{20} P(x_i, y_j) \log \frac{P(x_i, y_j)}{P(x_i) P(y_j)}$$

for correlated mutations analysis (CMA)

K, R: + charge; E, D: - charge → salt bridge

Mutual Information
without the influence of phylogeny

MIp - to eliminate random noise and phylogenetic components

$$\mathrm{MI_p}\,(i,j) = \mathrm{I}(i,j) - \mathrm{APC}(i,j)$$

	R				E		V		N	
	E				K		V		N	
	K				E		V		N	
	R				D		V		S	
	D				K		V		S	
	D				K		V		S	
	E				R		V		S	

Average product correction

$\mathrm{APC}(i,j) = [\ \langle \mathrm{I}(i) \rangle \langle \mathrm{I}(j) \rangle\ ]\ /\ \langle \mathrm{I}(i,j) \rangle$

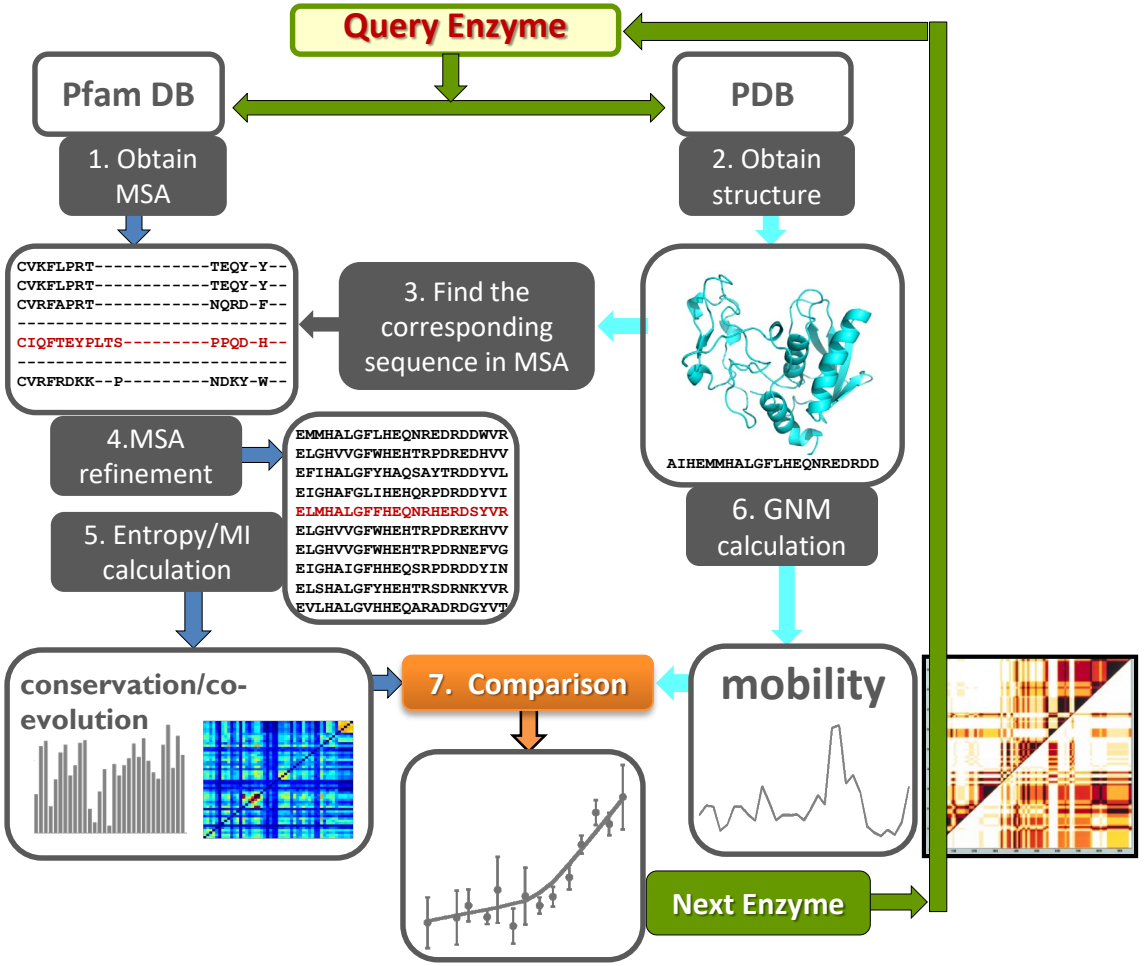
$\langle \mathrm{I}(i) \rangle$: the mean mutual information of column i

$\langle \mathrm{I}(i,j) \rangle$: average over all MI values

$$\langle \mathrm{I}(i) \rangle = \sum_{j=1, j \neq i}^{N} \mathrm{I}(i,j)/N$$

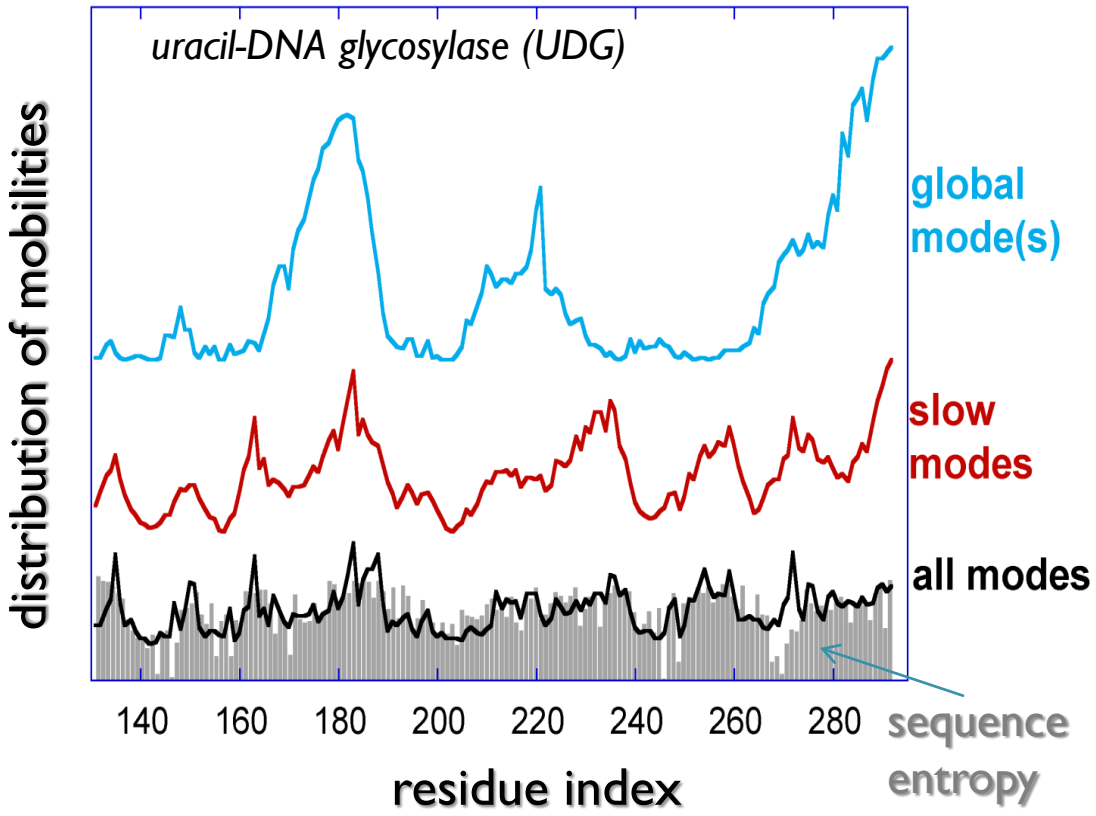
MBE MOLECULAR BIOLOGY AND EVOLUTION

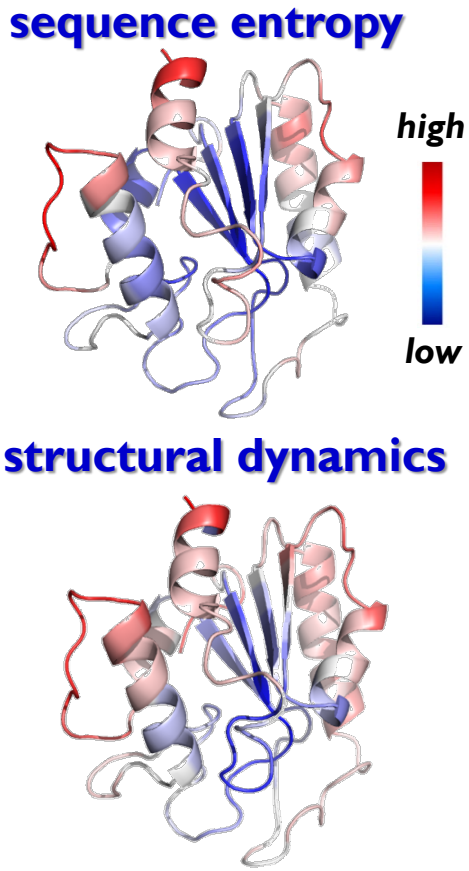
A systematic study of a set of enzymes



Liu Y, Bahar I (2012) "Sequence Evolution Correlates with Structural Dynamics" *Mol Biol Evol 9, 2253-63*

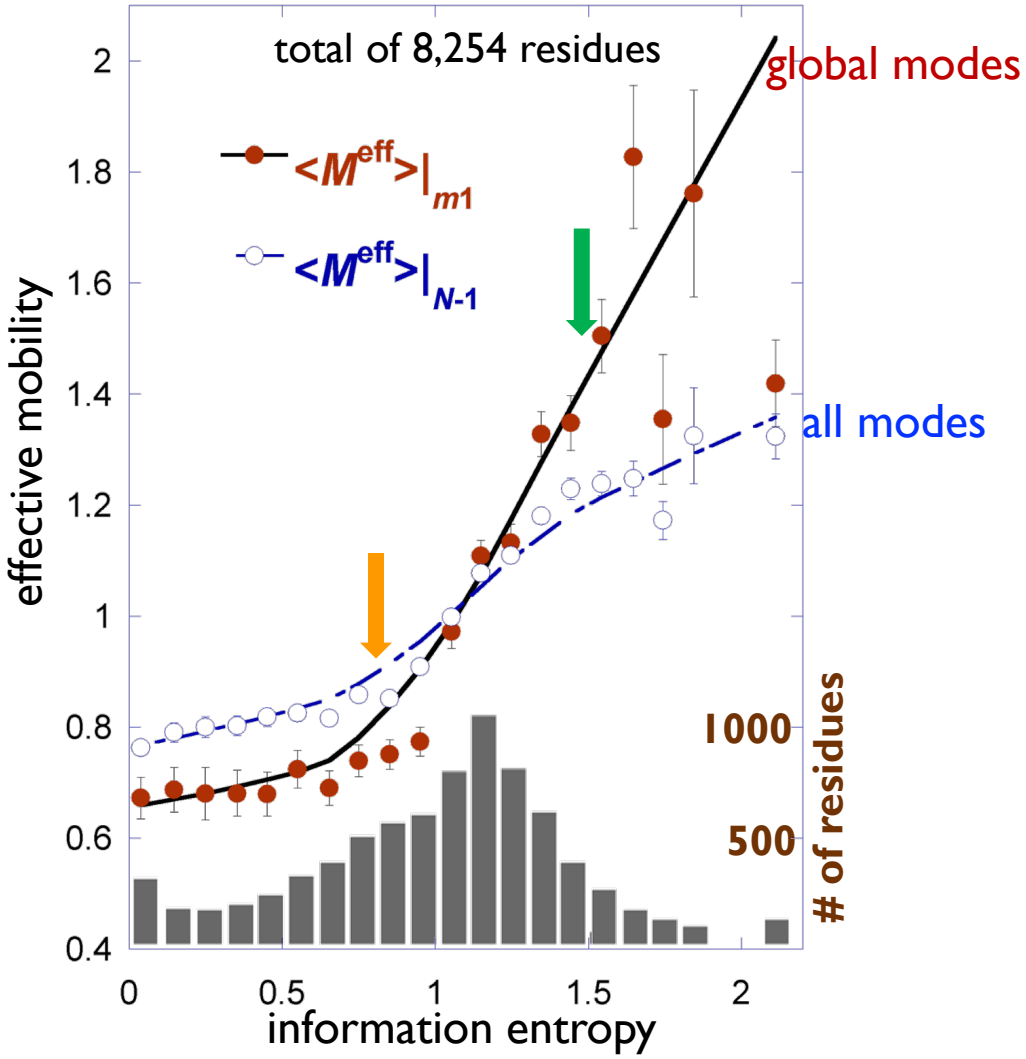
Correlation between sequence entropy & conformational mobility





Liu Y, Bahar I (2012) "Sequence Evolution Correlates with Structural Dynamics" *Mol Biol Evol 9, 2253-63*

Mobility increases with sequence entropy

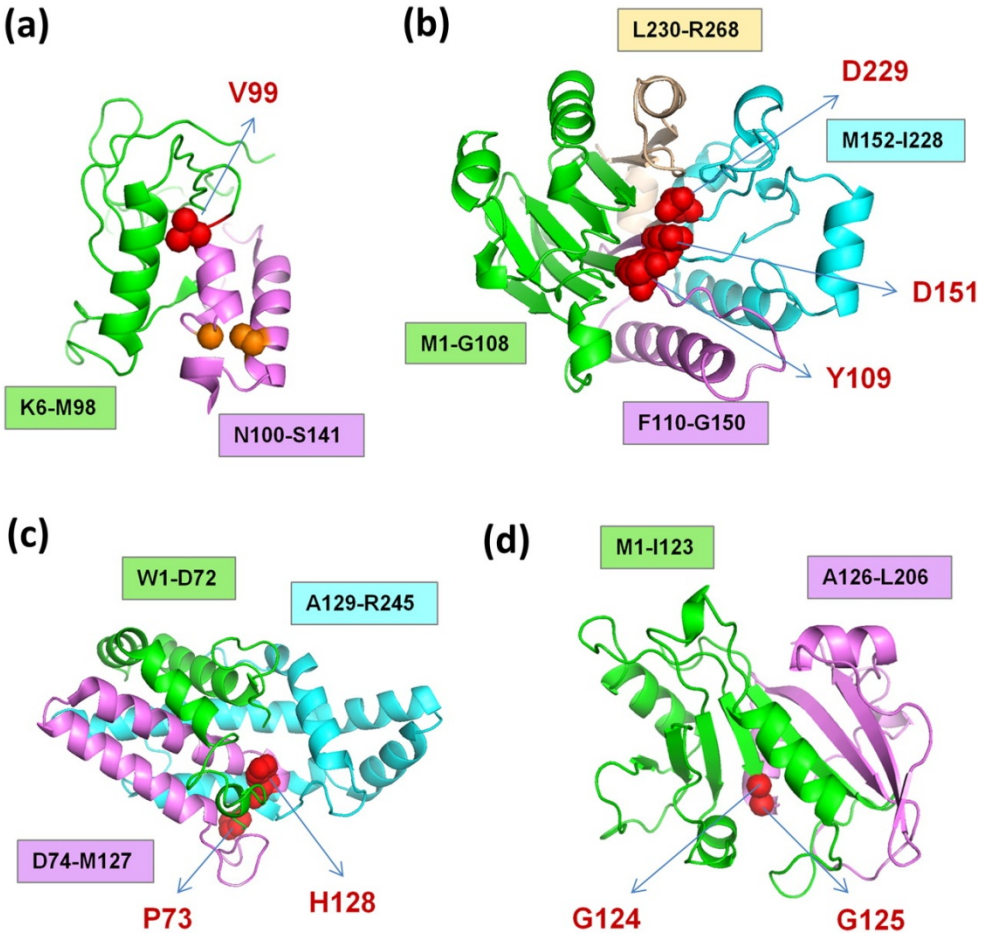


Liu & Bahar *Mol Biol Evol* (2012)

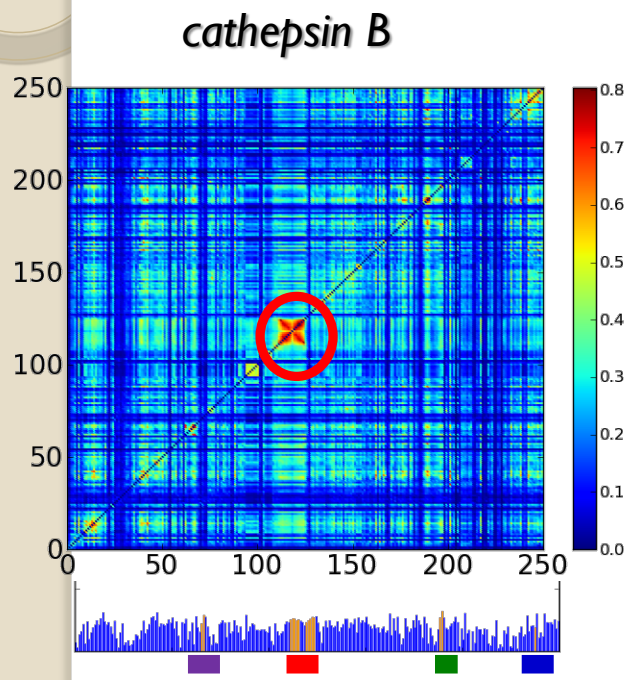
MBE MOLECULAR BIOLOGY AND EVOLUTION

Hinge sites are evolutionarily conserved

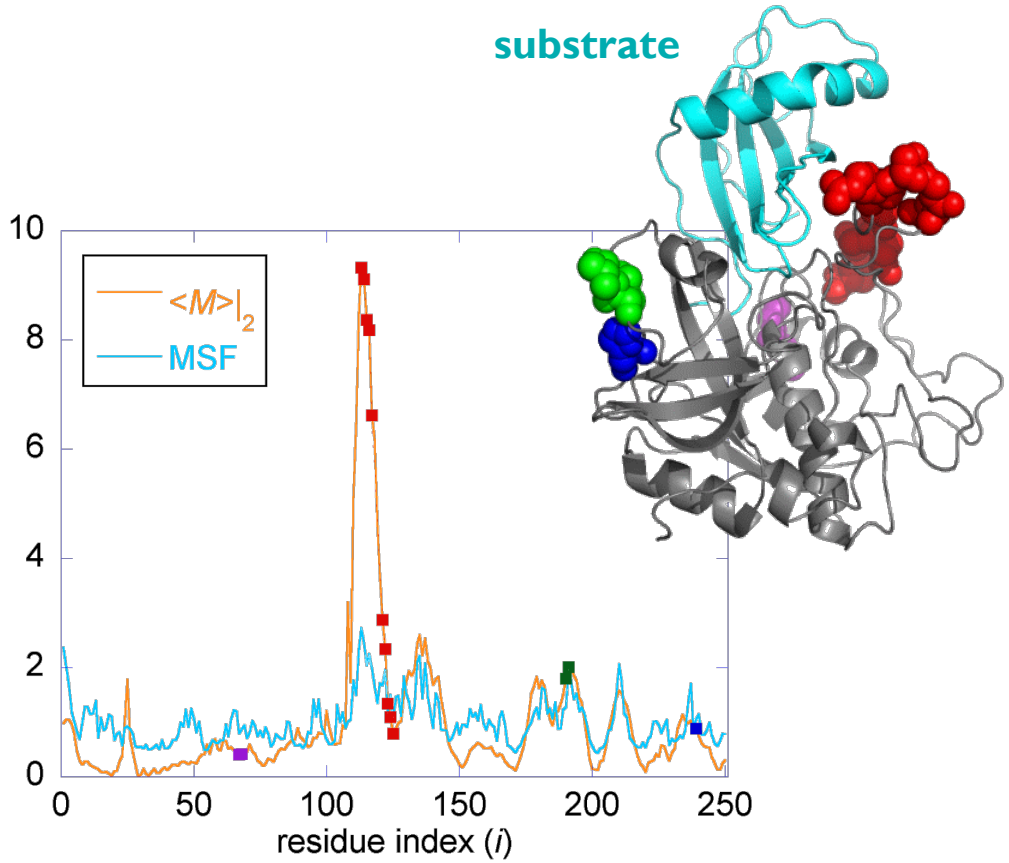
despite their moderate-to-high exposure to environment



Amino acids involved in intermolecular recognition exhibit **high global mobility and co-evolution**



residues involved in top 0.05% of $I(i,j)$ values



Liu Y, Bahar I (2012) "Sequence Evolution Correlates with Structural Dynamics" *Mol Biol Evol 9, 2253-63*

Summary

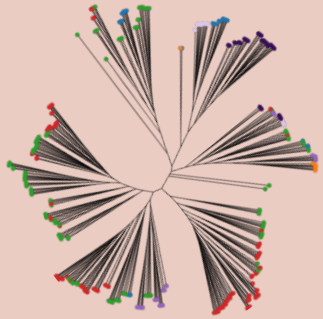
Four types of functional sites

Functional site	Mobility in global modes	Sequence evolution	Dominant Feature
Chemical (catalytic, ligand binding)	Minimal	Conserved	high fidelity, precision
Core	Minimal	Conserved	high stability
Hinge sites	Minimal	Conserved	rotational flexibility
Substrate recog-nition (specific)	High	High co-evolution propensity	adaptability

Liu & Bahar *Mol Biol Evol* (2012); Liu, Gierasch & Bahar, *PLoS Comp Bio* (2010)

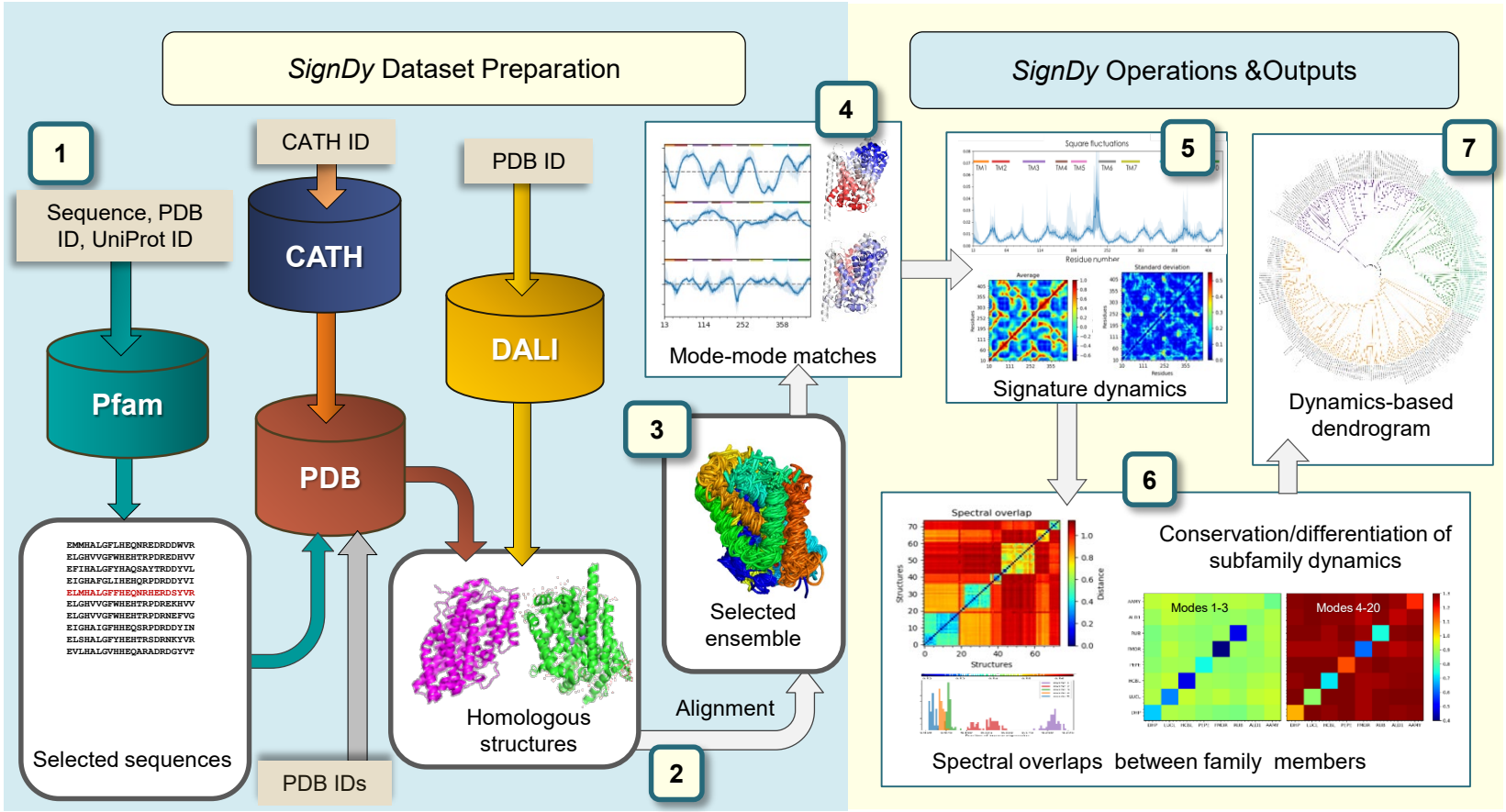
SignDy: Signature dynamics of families

- How does functional differentiation take place while maintaining the fold?
- What are the shared/differentiated dynamics of family members?
- Can we categorize family members based on dynamics?



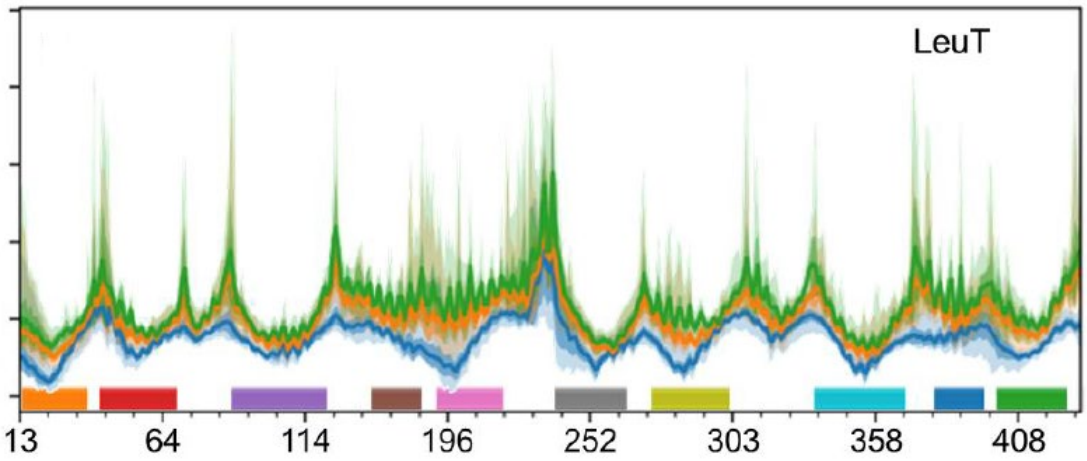
Zhang, S., Li, H., Krieger, J.M. and Bahar, I., 2019. Shared signature dynamics tempered by local fluctuations enables fold adaptability and specificity. *Mol. Biol. Evol.* (doi: 10.1093/molbev/msz102)

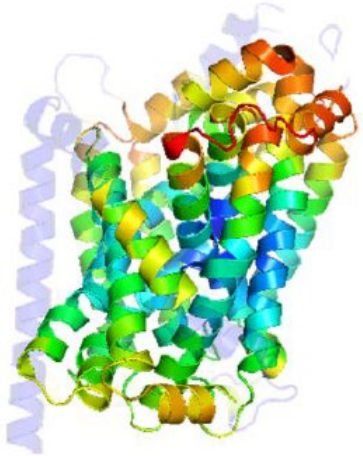
SignDy pipeline for evolution of dynamics



Zhang, S., Li, H., Krieger, J.M. and Bahar, I. (2019) *Mol. Biol. Evol.*

SignDy results for LeuT family

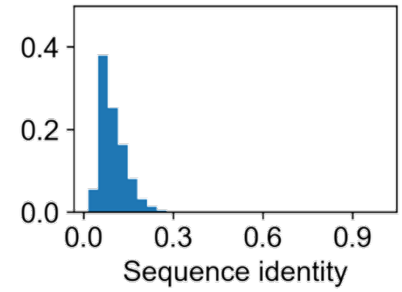


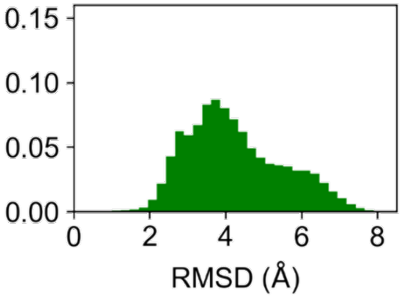


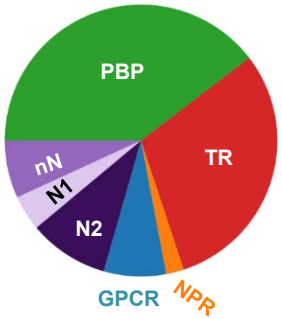
blue: first 3, orange: first 10, green: first 20 modes

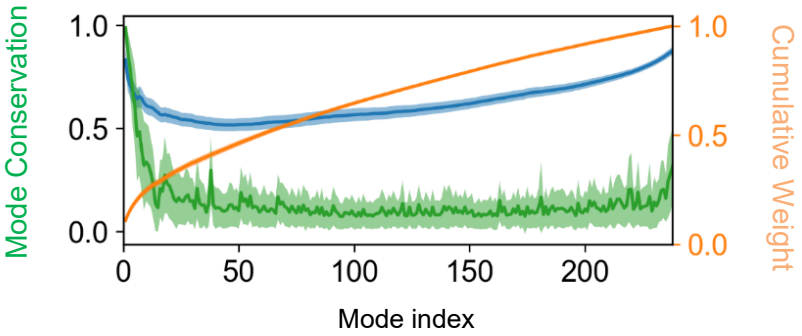
Signature-dynamics of each family is robustly defined by the global motions that are unique to the fold

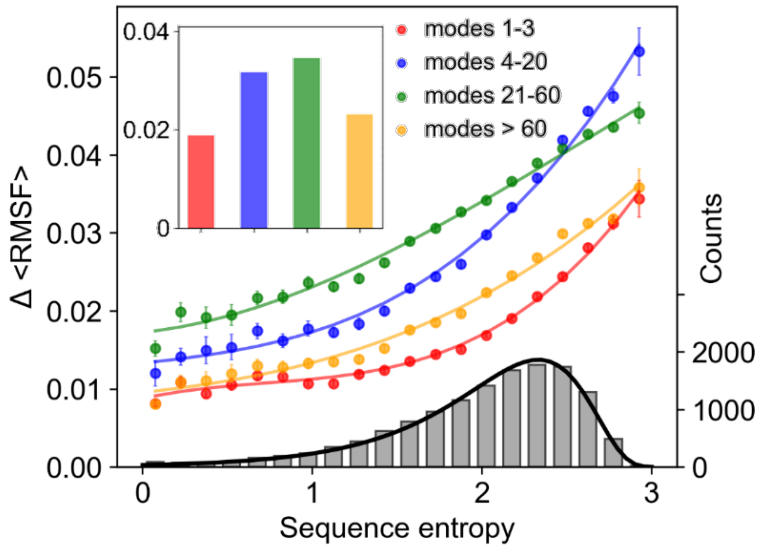
SignDy reveals shared and divergent motions of domains/folds





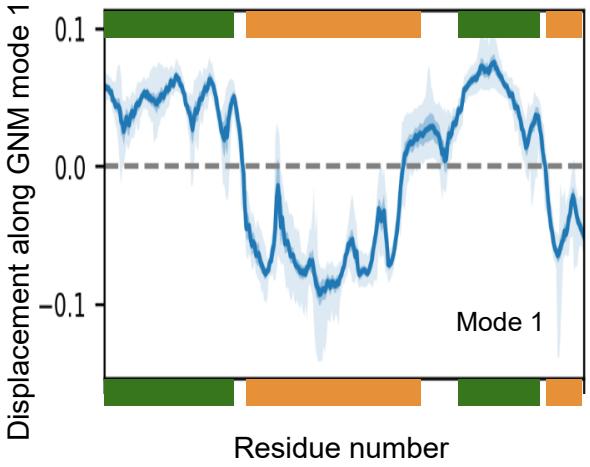


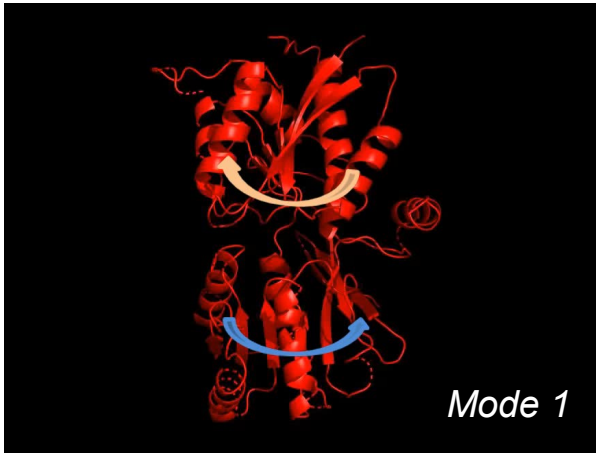


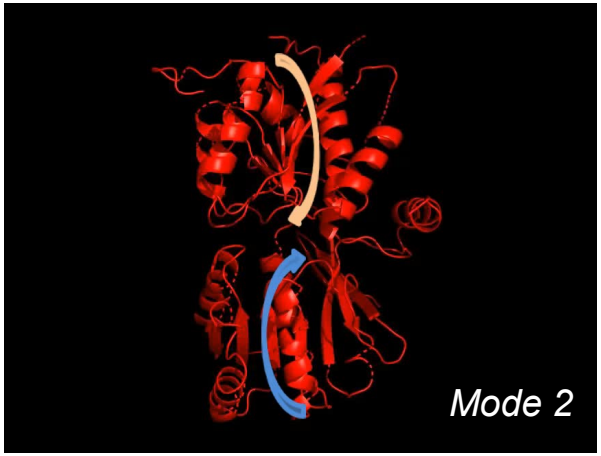


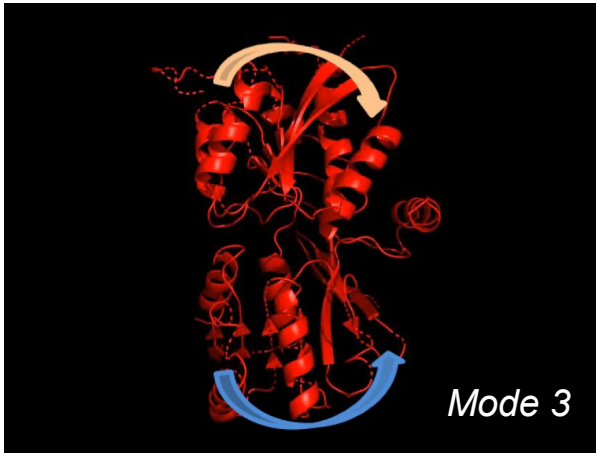
Zhang, S., Li, H., Krieger, J.M. and Bahar, I., 2019. *Mol. Biol. Evol.*

Signature modes match functions



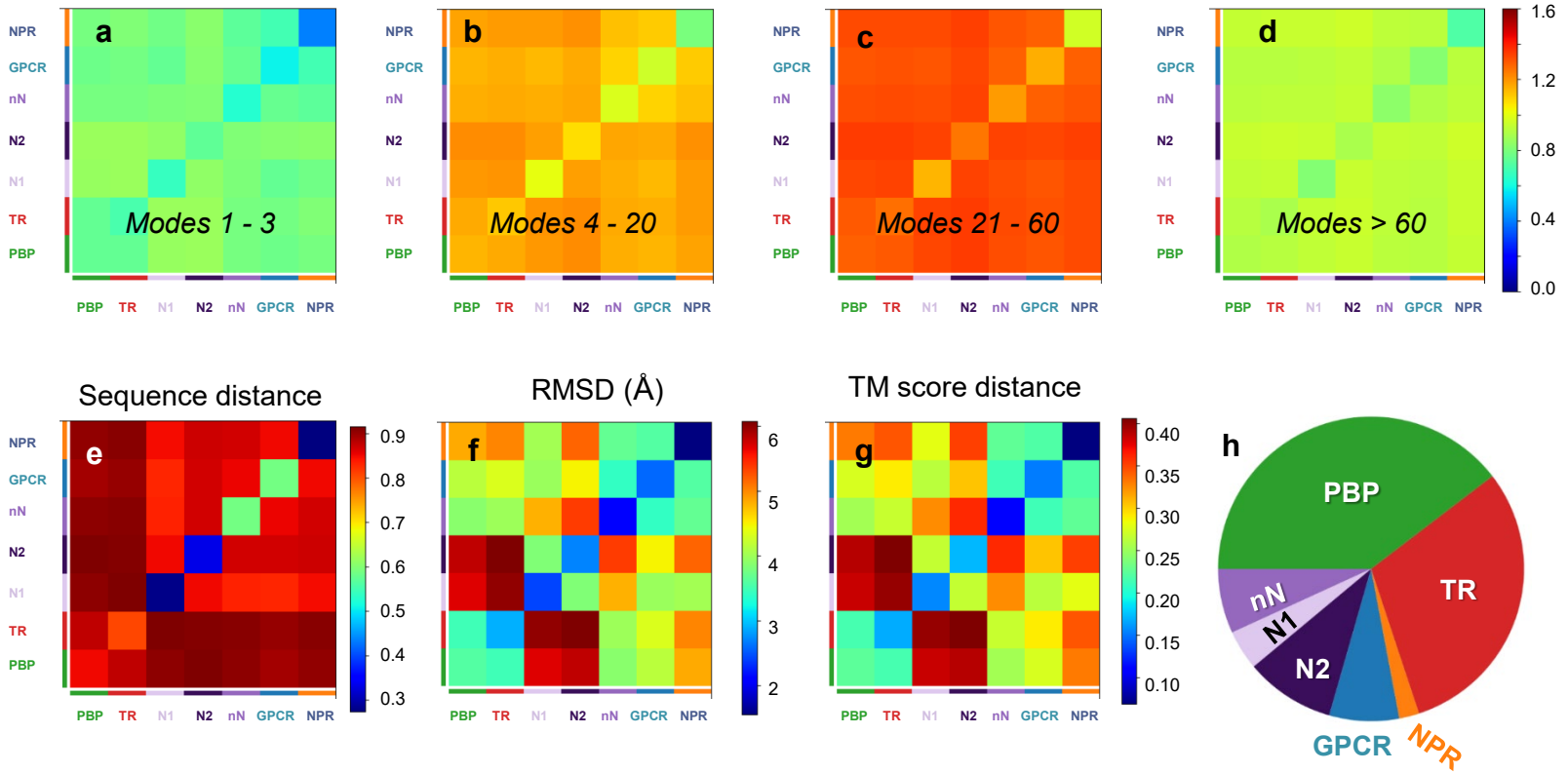






Low to intermediate frequency modes drive subfamily specificity

Frequency-dependent conservation/divergence of equilibrium dynamics across PBP-1 subfamilies

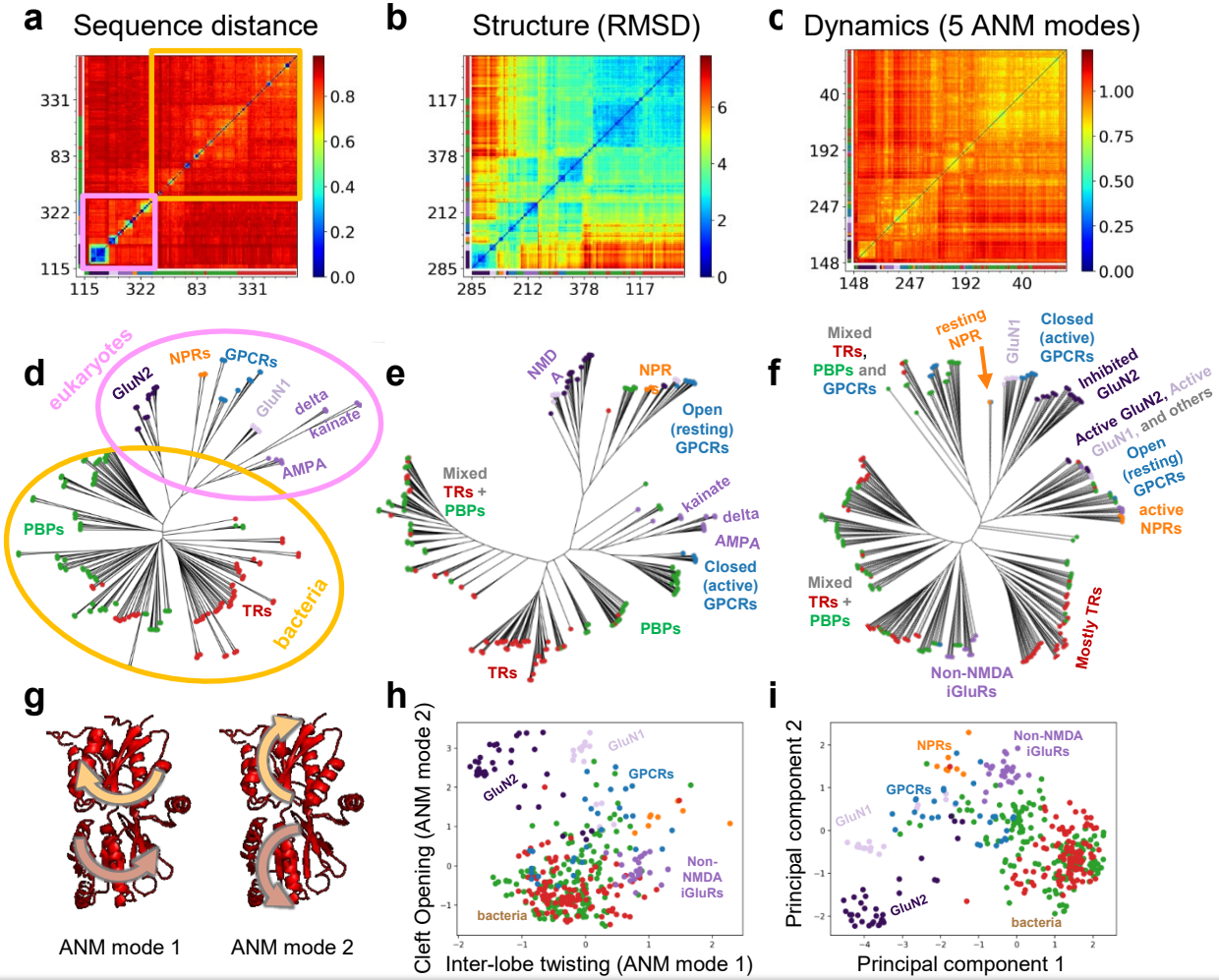


Sequence distance

Structural differences between subfamilies

Function distribution

Dynamics allows classification like sequence and structure



Zhang, S., Li, H., Krieger, J.M. and Bahar, I., 2019. *Mol. Biol. Evol.*

Summary

1. Theory
   a. Gaussian Network Model (GNM)
   b. Anisotropic Network Model (ANM)
   c. Resources/Servers/Databases (ProDy, DynOmics)

2. Bridging Sequence, Structure and Function
   a. Ensemble analysis using the ANM
   b. Combining sequence and structure analyses – signature dynamics
   c. **Allosteric communication – sensors and effectors**

3. Membrane proteins and druggability
   a. Modeling environmental effects using elastic network models
   b. Modeling & simulations of Membrane Proteins with ENMs for lipids
   c. Druggability simulations

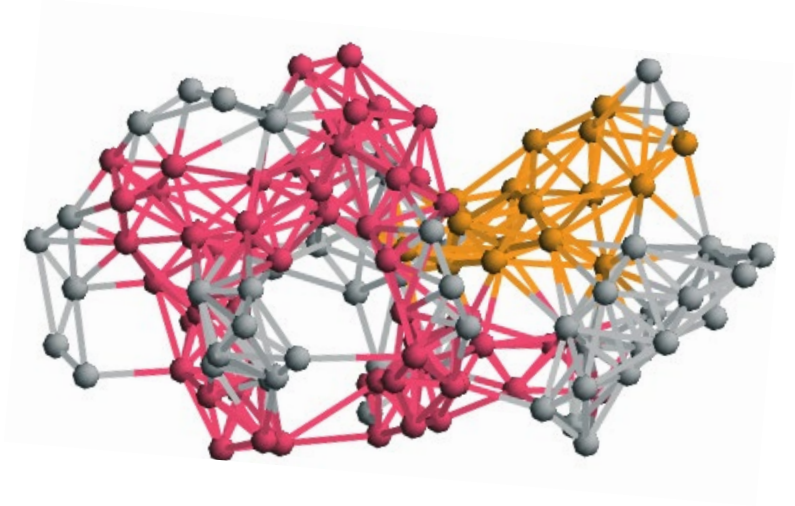
PRS

Perturbation-Response Scanning

Sensors and Effectors of allosteric signals

General, Liu, Blackburn, Mao, Gierasch & Bahar I (2014) ATPase subdomain IA is a mediator of interdomain allostery in Hsp70 molecular chaperones. *PLoS Comp Bio.* 10: e1003624.

GNM Basics - Linear theory



Single spring

$F = k \Delta x$

$E = \frac{1}{2} k (x - x_0)^2$

Network of springs (bead-and-spring model)

$\mathbf{F} = \gamma \Gamma \Delta \mathbf{R}$

$V = \frac{1}{2} \gamma \Delta \mathbf{R}^T \Gamma \Delta \mathbf{R}$

$\Delta \mathbf{R}^T = (\Delta R_1 \quad \Delta R_2 \quad \Delta R_3 \quad \ldots\ldots \quad \Delta R_N)$

Γ = Kirchhoff matrix

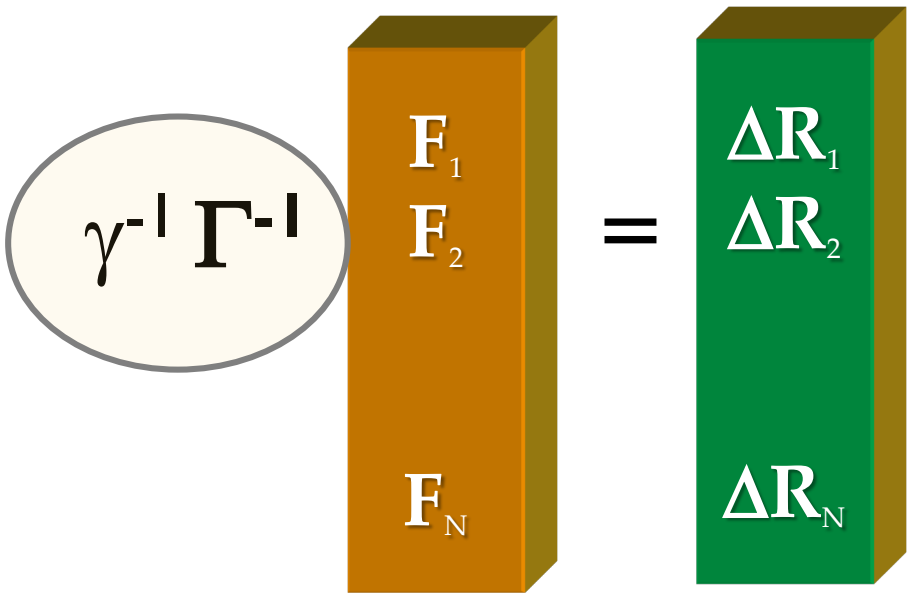
Perturbation-response scanning (PRS) theory

$$\mathbf{F} = \gamma \Gamma \Delta \mathbf{R}$$

perturbation

$$\gamma^{-1} \Gamma^{-1} \mathbf{F} = \Delta \mathbf{R}$$

response



You can evaluate the response of the structure to any external force

Atilgan & Atilgan (2009) *PLoS Comp Biol* 5(10):e1000544;
Atilgan, Gerek, Ozkan, Atilgan, (2010) *Biophys. J.* 99, 933-943

Covariance matrix

$\gamma^{-1}\,\Gamma^{-1}$

In NMA, the covariance matrix is given by

$C_{3N} = k_B T H^{-1}$

$C_N = (3k_B T/\gamma)\,\Gamma^{-1}$

where k_B is the Boltzmann constant, T is the absolute temperature and H is the (Hessian) matrix of the second derivatives of the potential.

In the GNM, H is replaced by the Kirchhoff matrix $\gamma\Gamma$.

Perturbation-response scanning (PRS) theory

We replace $\gamma^{-1}\,\Gamma^{-1}$ on the lefthand side by $(3k_B T)^{-1}$ **C:**

$(3k_B T)^{-1}$

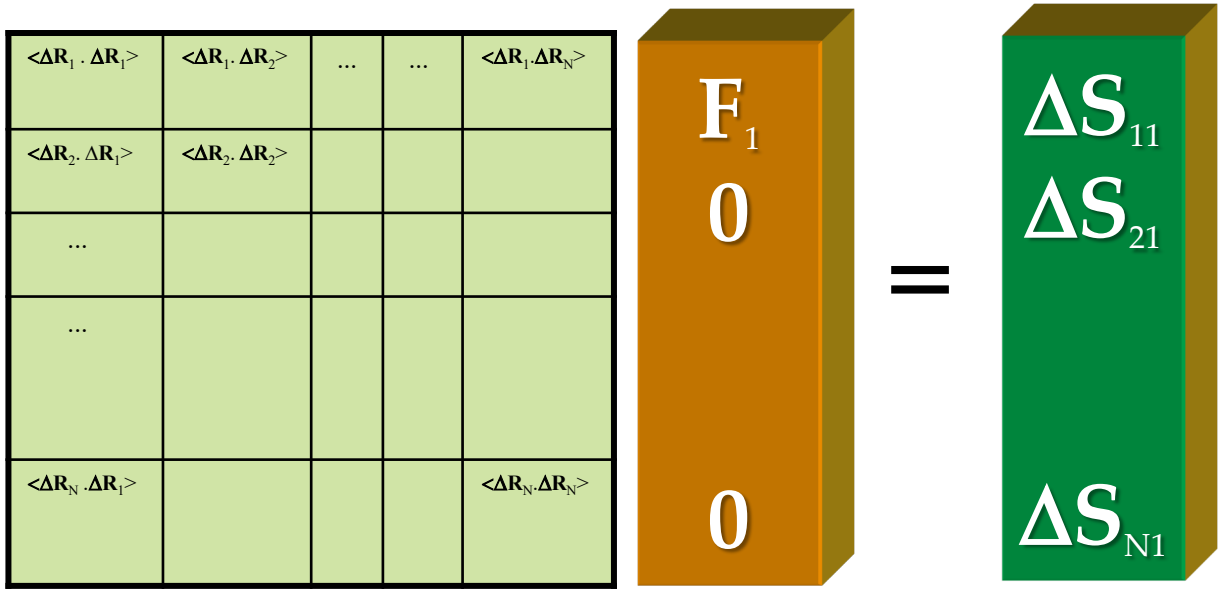
$\langle \Delta R_1 \,.\, \Delta R_1 \rangle$	$\langle \Delta R_1 .\, \Delta R_2 \rangle$	…	…	$\langle \Delta R_1 . \Delta R_N \rangle$
$\langle \Delta R_2 .\, \Delta R_1 \rangle$	$\langle \Delta R_2 .\, \Delta R_2 \rangle$			
…				
…				
$\langle \Delta R_N \,.\Delta R_1 \rangle$				$\langle \Delta R_N . \Delta R_N \rangle$

The response is defined by the covariance matrix

Perturbation-response scanning (PRS) theory

Start perturbation from residue 1, by applying a force F1 on node 1:

$(3k_B T)^{-1}$

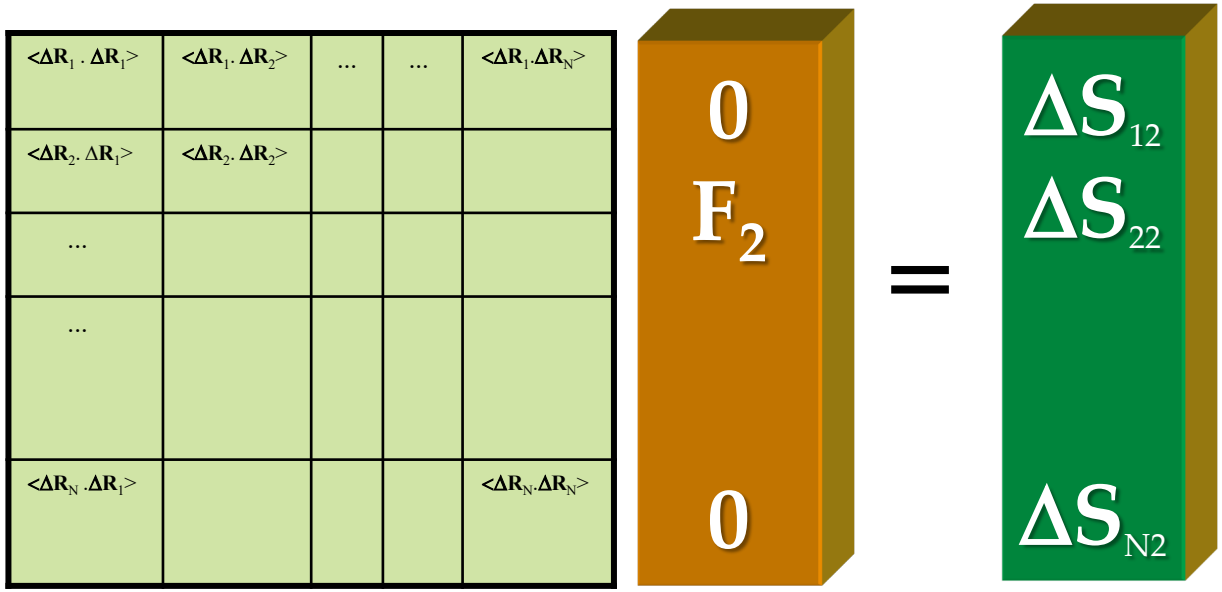


Due to perturbation of node 1

Perturbation-response scanning (PRS) theory

Continue with the perturbation of residue 2, by applying a force F2 on node 2:

$(3k_B T)^{-1}$

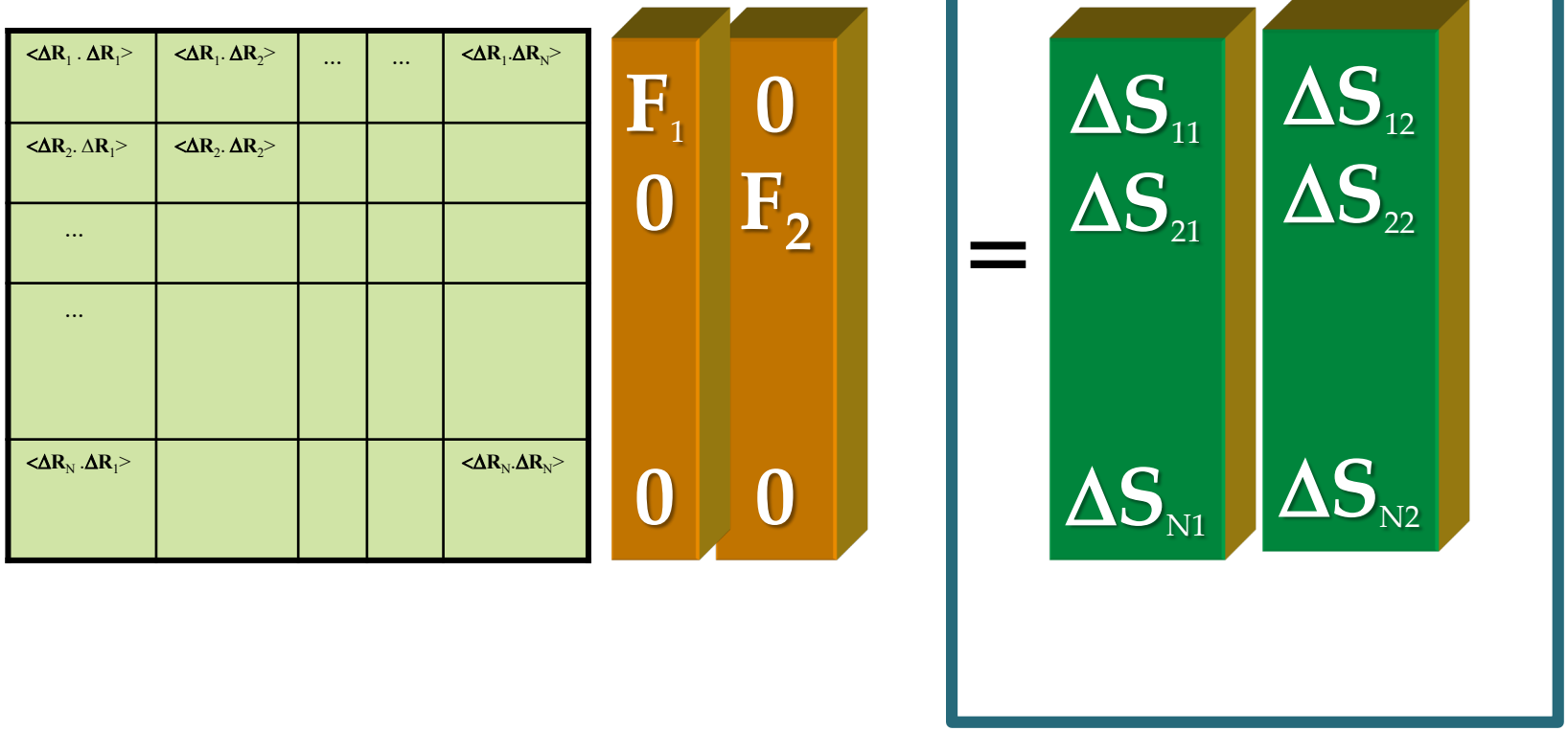


Due to perturbation of node 2

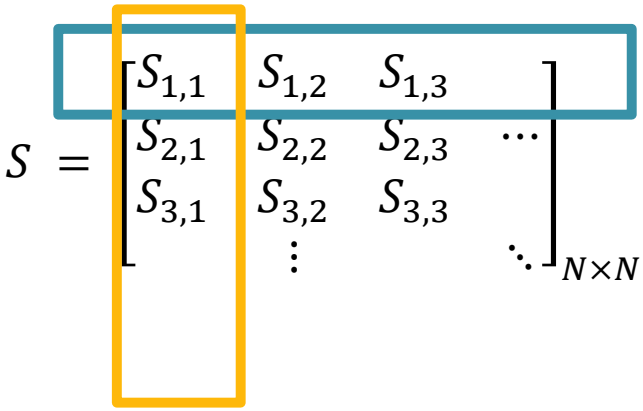
Perturbation-response scanning (PRS) theory

Repeat with all nodes and organize in a matrix

$(3k_B T)^{-1}$



Response matrix



Response of residue 1 to perturbation at all other residues

Strong response [illegible] esidue 1 communicates ef[illegible]er residues. The row average is the effector propensity of residue 1

Effectors

Division by diagonal element ensure the removal of the intrinsic effect of residue 1

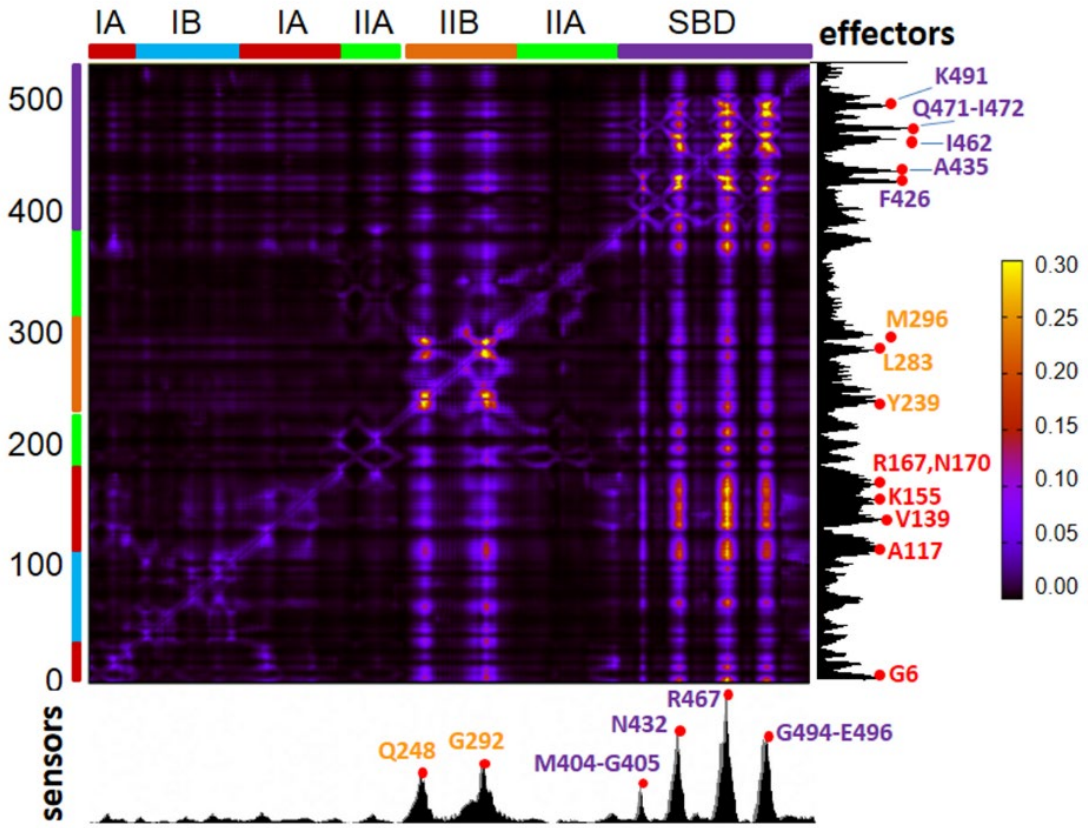
Response of all residues to perturbation at residue 1; shows the influence of residue 1 on all others.

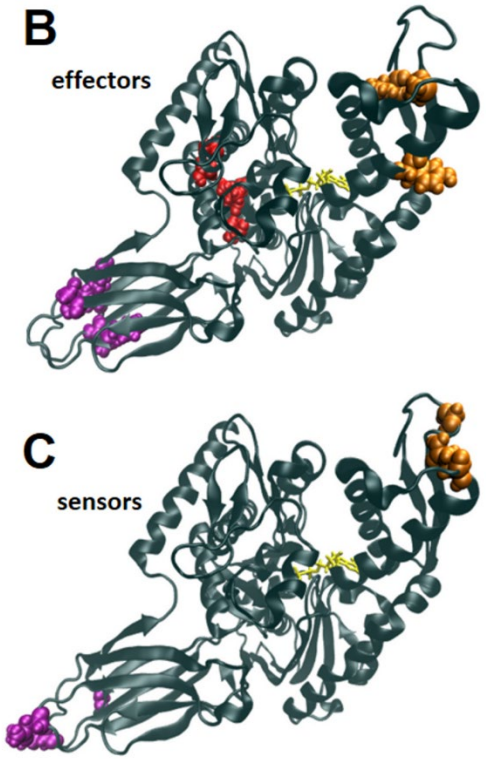
May be red[illegible]umber for each residue, by averaging out over the elements. The most influential residue serves as a sensor to efficiently send signals to all other residues

Sensors

$S_{i,j}$ = response of residue i to perturbation at residue j

Results from PRS analysis of HSP70





General, Liu, Blackburn, Mao, Gierasch & Bahar I (2014) ATPase subdomain IA is a mediator of interdomain allostery in Hsp70 molecular chaperones. *PLoS Comp Bio.* 10: e1003624.

DynOmics Portal 1.0 - Dy

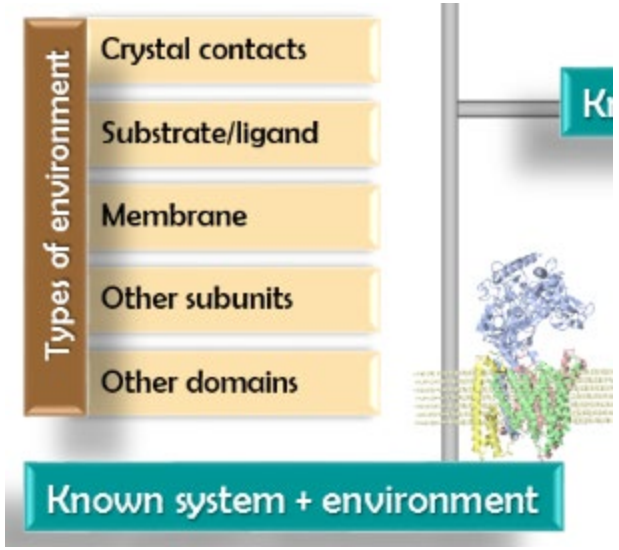
enm.pitt.edu

DynOmics using Elastic Network Models - ENM 1.0

Home | DynOmics 1.0 | Tutorials | Theory | References | iGNM 2.0 | ANM 2.0 | NTHU site

Features

- sensors and effectors (PRS)
- first passage times for signaling
- mechanically functional sites
- effect of oligomerization
- coupling to membrane



Dynamics of Structural Proteomics and Beyond

Li et al (2017) *Nucleic Acids Research*. 45, W374-W380

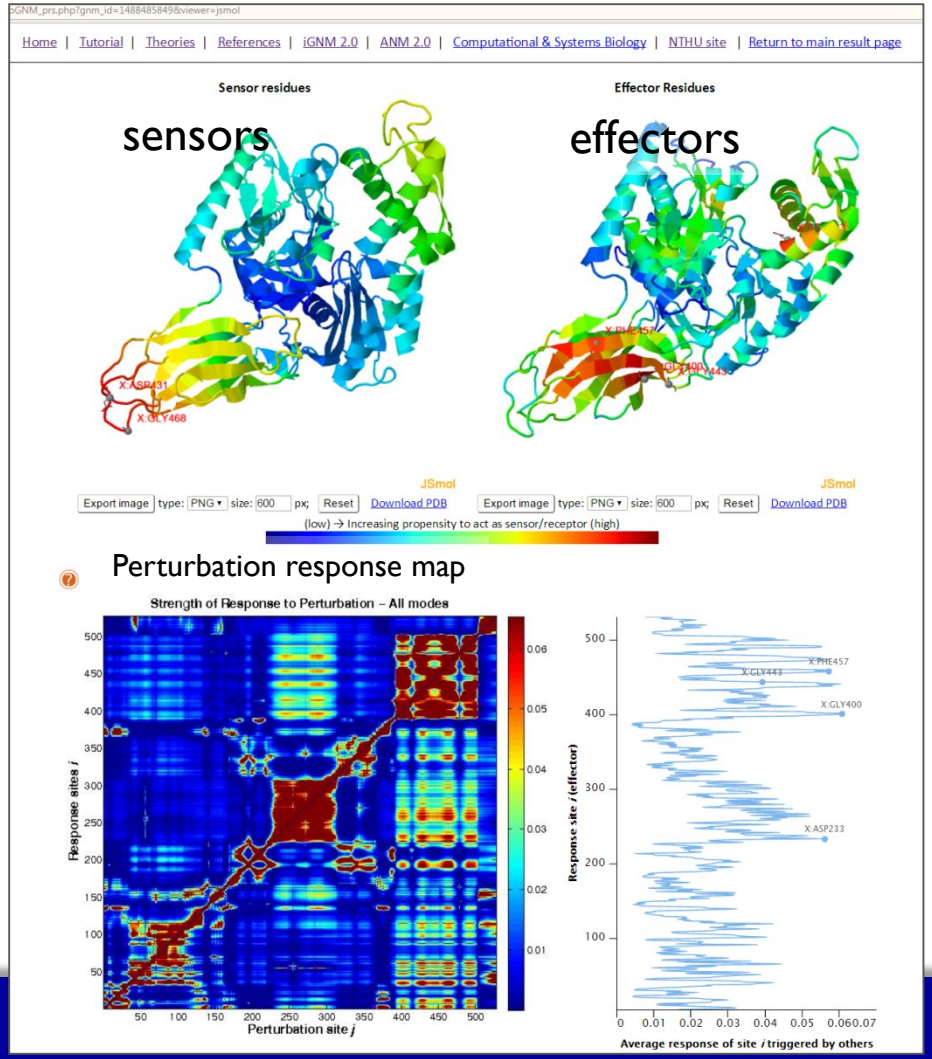
Ic

DynOmics Portal 1.0 - Dy

enm.pitt.edu

DynOmics using Elastic Network Models - ENM 1.0

Home | DynOmics 1.0 | Tutorials | Theory | References | iGNM 2.0 | ANM 2.0 | NTHU site



Thank you!