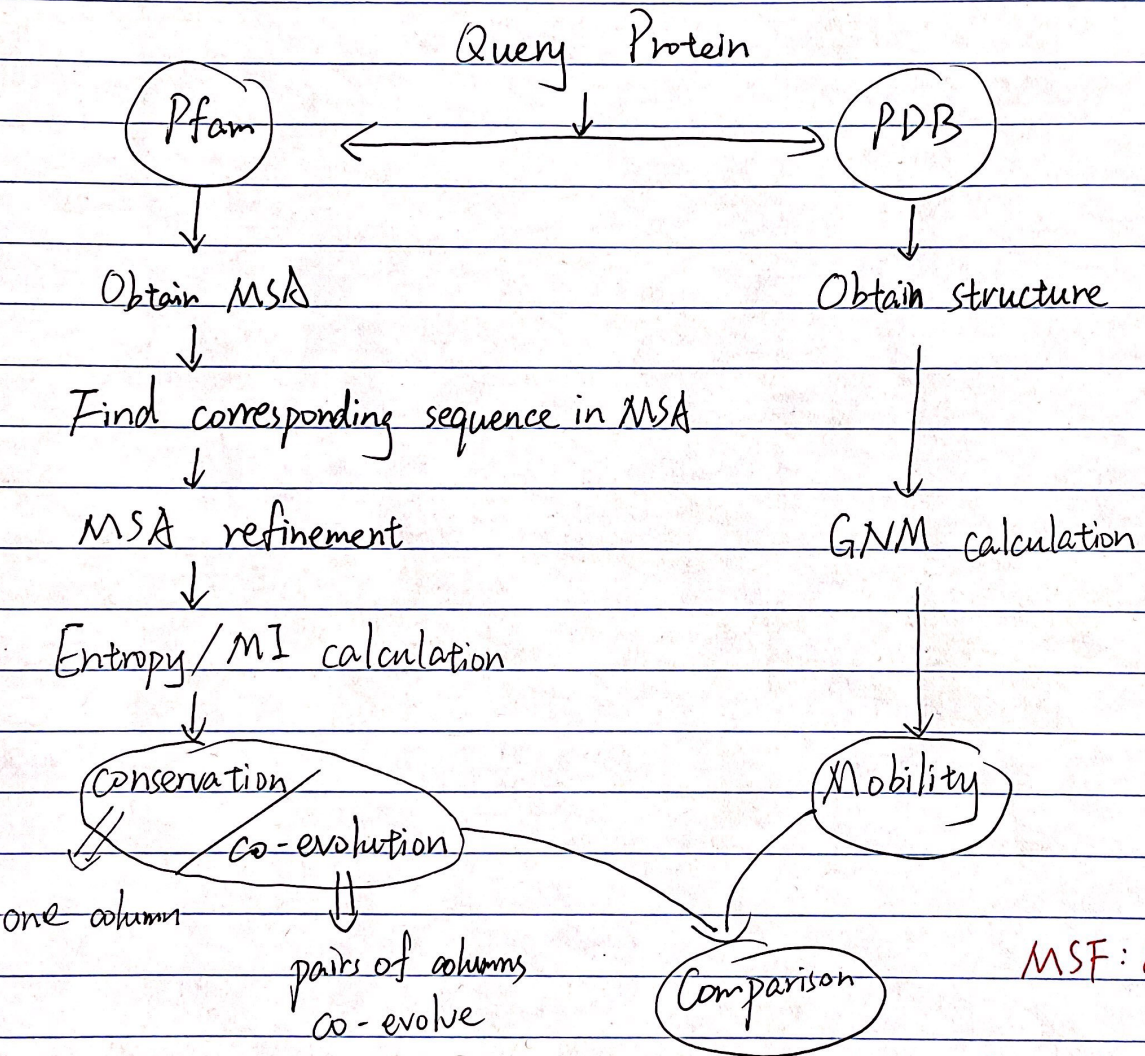


Bridging Sequence Evolution and Structural Dynamics - Evol

sequence \leftrightarrow structure \leftrightarrow dynamics \leftrightarrow function

- 1) Sequence encodes structure
- 2) Each structure has a unique dynamics
- 3) Dynamics is functional

? Did sequences evolve to enable functional dynamics



MSF: Mean Square Fluctuations

low frequency modes (soft modes/global modes) \Rightarrow dominant role in defining the most cooperative events

Less conserved \leftrightarrow more flexible

co-evolving residues : not conserved ; change in regulated way \Rightarrow maintain function

Sequence Entropy : less \leftrightarrow conserved residue

co-evolution patterns \rightarrow predict structures
why? \Rightarrow co-evolving residues are interacting \curvearrowright

Information entropy (Shannon, 1951)

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

for correlated mutations analysis (CMA)

Mutual Information (MI) \Leftarrow

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

Mobility increases with sequence entropy

Hinge sites are evolutionarily conserved
(despite their moderate-to-high exposure to environment)

AA involved in intermolecular recognition are distinguished by
co-evolution propensities
high global mobility

Types of functional sites $\times 4$

Functional site	Mobility in global modes	Sequence evolution	Dominant Feature
Chemical	Min	Conserved	high fidelity; precision
Core	Min	Conserved	high stability
Hinge sites	Min	Conserved	rotational flexibility
Substrate recognition	High	High co-evolution propensity	adaptability

\Rightarrow PPI