

Understanding biomolecular interactions and simulations
Frederic.Cazals@inria.fr

Biomolecular recognition

PART 1: Introduction to Protein Science

PART 2: Biomolecular recognition

Biomolecular recognition

Computational Structural Biology: what is a protein?

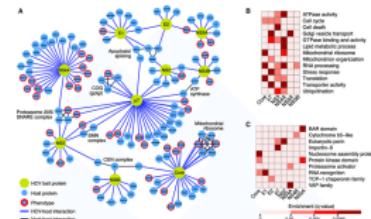
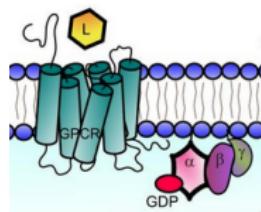
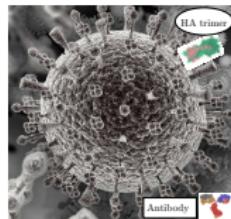
Protein Structure Resolution

The importance of dynamics

Protein functions: examples

Computational Structural Biology: challenges

Computational structural biology: perspective towards a new era in biology, medicine, material sciences



- ▶ **Biology:** help unveil all core mechanisms of life at the atomic level
 - ▶ metabolism, immune system, genetic information processing, cognition, ...
- ▶ **Medicine:** foster the design of novel therapeutics
 - ▶ optimizing specific molecules e.g. antibodies
 - ▶ discovering novel drug targets / transient conformations ¹
 - ▶ bridging the gap systems biology – structural biology
- ▶ **Material sciences at large:** atomic level design and engineering

¹(2017) 35% of FDA approved drugs: 108 GPCRs

Computational Structural Biology

- ▷ **Goals:** unveil the *structure-dynamics-function* conundrum for biomolecules (proteins and nucleic acids)
- ▷ **Methods:** biophysics (crystallography, NMR, cryo-microscopy) + modeling
- ▷ **Nobel prizes as of 01/2019**²: related to molecular/structural biology
 - ▶ Chemistry or Physiology-medicine for structures and mechanisms: 64
 - ▶ Chemistry or Physics for Methods : 11
 - ▶ Chemistry 2013: Levitt, Karplus, Warshel for *the development of multiscale models for complex chemical systems*
- ▷ **An extraordinary field**
 - ▶ Technology driven: novel biophysical experiments,
 - ▶ Reveals the molecular foundations of biology and medicine,
 - ▶ Raises open mathematical / computational questions.

²<https://pdb101.rcsb.org/learn/fliers-posters-and-other-resources/other-resource/structural-biology-and-nobel-prizes>

Methods: molecular simulation



The Nobel Prize in Chemistry 2013

Martin Karplus, Michael Levitt, Arieh Warshel

The Nobel Prize in Chemistry 2013



© Harvard University
Martin Karplus



Photo: © S. Fisch
Michael Levitt



Photo: Wikimedia Commons
Arieh Warshel

The Nobel Prize in Chemistry 2013 was awarded jointly to Martin Karplus, Michael Levitt and Arieh Warshel *"for the development of multiscale models for complex chemical systems"*.

What is a protein?

- ▷ Primary structure: sequence of amino acids

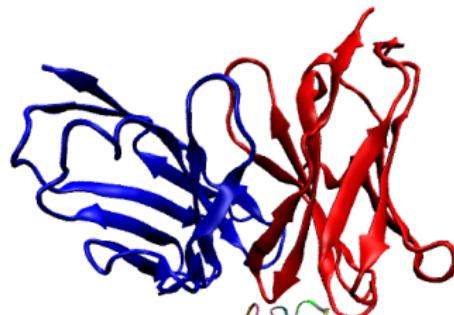
P69905 (HBB_HUMAN)	MV-LSPADKTNVKAAWGVGAHAGEYGAEEALERMFLSFPTTKTYFPHF-DLSH-----GS	53
P68871 (HBB_HUMAN)	MVHLTPEEKSAVTALWGKV--NVDEVGGGEALGRLLVVYPTQRFESFGDLSTPDAVMGN	58
P02144 (MYG_HUMAN)	-MGLSDGEWQLVLNVWGKVVEADIPGHGQEVILRLFKGHPETLEKFDFKHLKSEDEMKA	59

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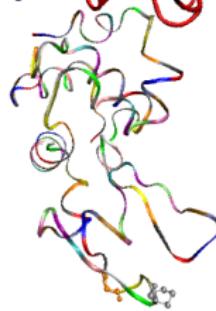
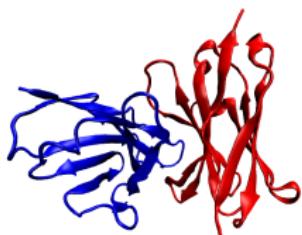
- ▷ Polypeptide chain



- ▷ Protein - protein complex



- ▷ Heterodimeric protein

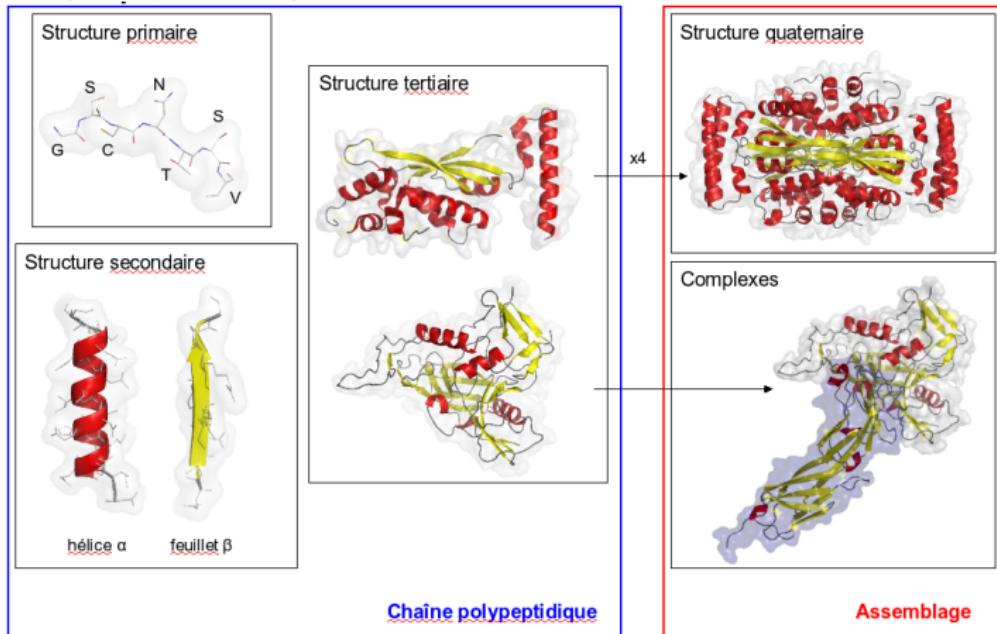


- ▷ Nb: median number of a.a. in a chain: ~ 400

What is a protein?

Importance of non-covalent interactions

► Primary to quaternary structure



► Grand Challenges: folding and docking ... related businesses!

The Folding Problem

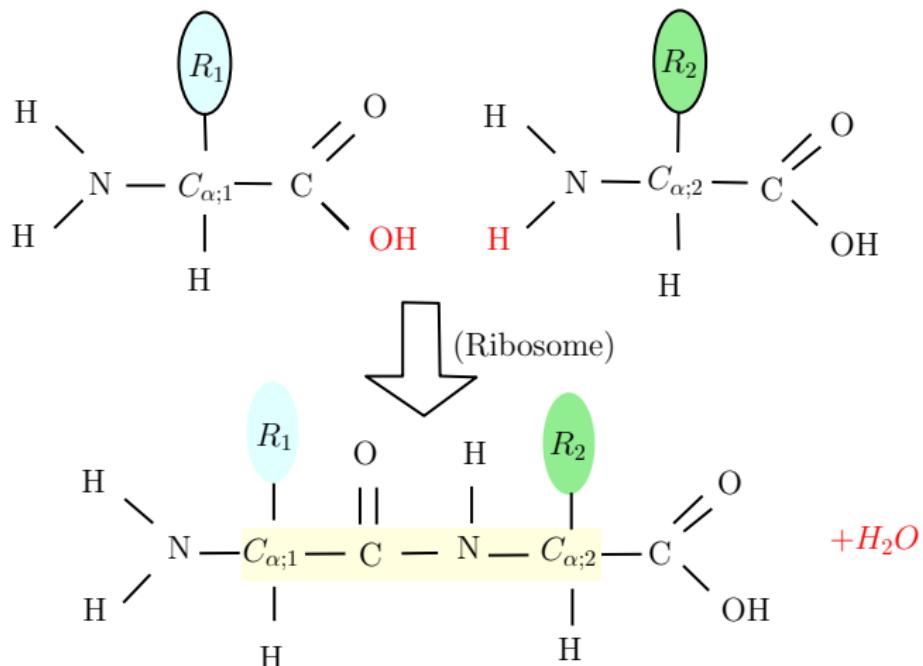
- ▷ C. Anfinsen's experiment (Nobel 1972), the sequence determines the structure:
 - ▶ Identification of the native state —minimum of free energy
 - ▶ Determination of the folding pathways
- ▷ Levinthal's paradox. n amino-acids with r conformations: r^n states.
 - Random searches would require astronomical time
 - Nature requires from milliseconds (helical prot.) to (tens) seconds (complex geom.)
- ▷ Other systems: clusters (water molecules, rare gases), crystallization etc

Amino acids and the peptide bond

▷ Natural amino acids and their side chains

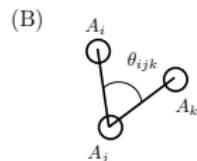
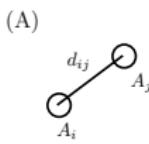
Nb: 0 to 10 heavy atoms per side chain

▷ Peptide bond synthesis:

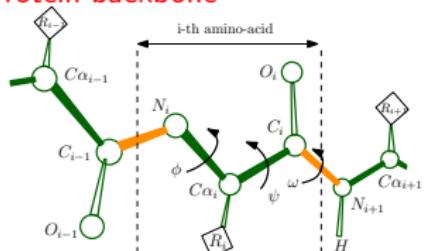


Geometric models: Cartesian and internal coordinates

- ▶ Cartesian versus internal coordinates: $\{x_i y_i z_i\}_i$ versus $\{d_{ij}, \theta_{ijk}, \sigma_{ijkl}\}$
- ▶ Bond length and valence angle



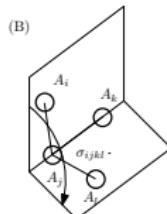
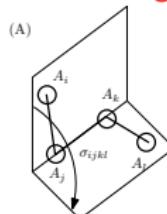
▶ Protein backbone



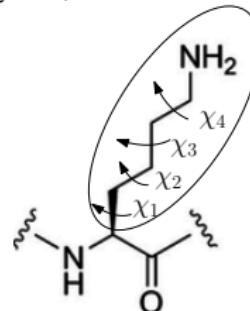
Ramachandran diagram, per a.a. type:

- ▶ bivariate distribution for (ϕ, ψ)

▶ Dihedral angles



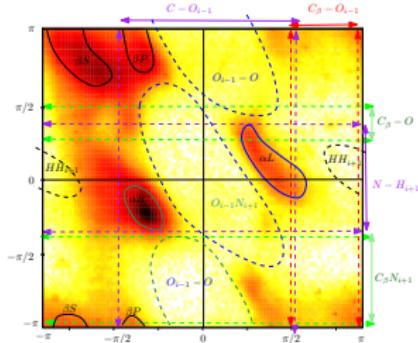
- ▶ Side chain: 20 natural amino acids
Exple: Lysine, 4 dihedral angles



LYS

The Ramachandran diagrams

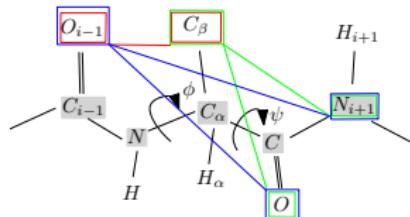
► Ramachandran diagrams and populated regions



- Main regions: $\alpha L, \alpha R, \beta S, \beta P$
- Three prototypical diagrams
 - Glycine
 - Proline
 - Others – e.g. Aspartic acid

► Distance constraints and the Ramachandran tetrahedron

$$\begin{aligned}C1 : C_\beta - O_{i-1} & \quad C2 : C_\beta - O + C_\beta N_{i+1} \\C3 : O_{i-1} - O + O_{i-1} N_{i+1}\end{aligned}$$



► Ref: Stereochemistry of polypeptide chain configurations, JMB, 1963;
Ramachandran et al

► Ref: Revisiting the Ramachandran plot, Protein Science, 2003; Ho et al

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The importance of dynamics

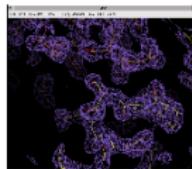
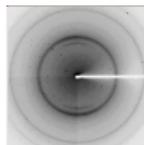
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Computational Structural Biology: challenges

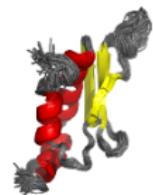
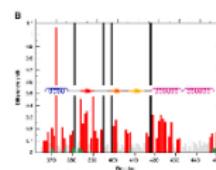
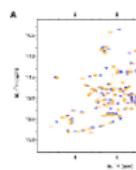
Structure resolution:

X ray crystallography, NMR, cryo-electron microscopy

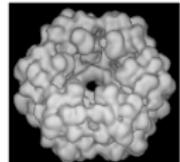
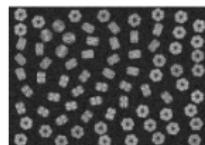
Crystallography



NMR



Cryo electron microscopy



Note: resolutions between 1 and 15 Å

X ray crystallography

▷ (Selenium) crystals



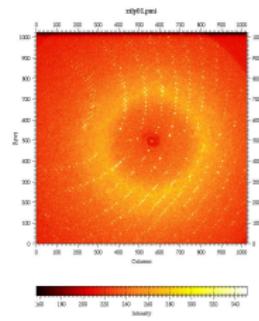
▷ X ray diffraction



▷ Protein crystals

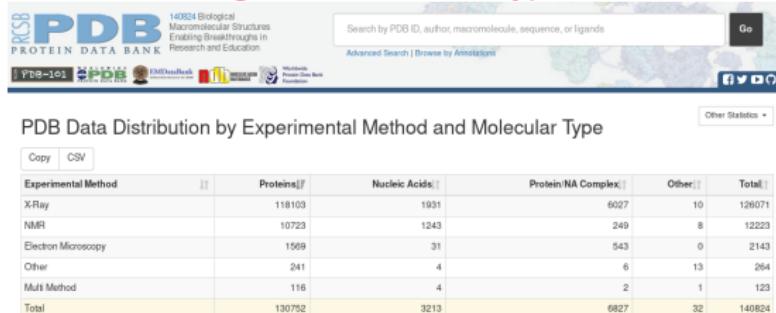


▷ Diffraction pattern



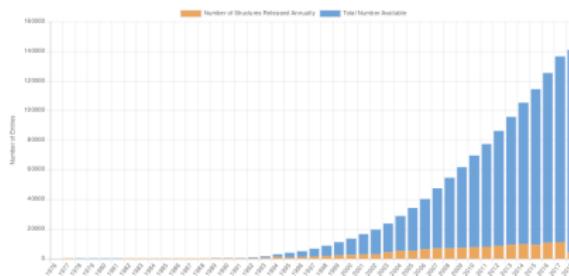
The Protein Data Bank

▷ Structures in the PDB: origin and molecular type



▷ Growth of the PDB

PDB Statistics: Overall Growth of Released Structures Per Year



▷ To learn more: <https://www.rcsb.org/stats>

A typical PDB file

- ▷ **Geometry information:** n atoms yield $3n$ Cartesian coordinates . . . and $3n - 6$ degrees of freedom

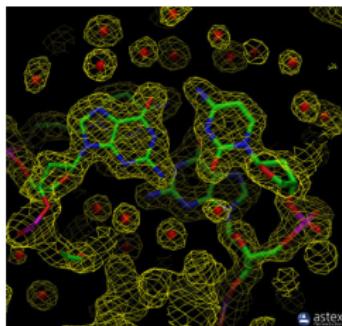
ATOM	1	N	ASP A	1	23.963	-0.947	-1.031	1.00	37.52	N
ATOM	2	CA	ASP A	1	25.119	-0.797	-1.881	1.00	32.56	C
ATOM	3	C	ASP A	1	25.715	0.493	-1.356	1.00	29.72	C
ATOM	4	O	ASP A	1	24.964	1.396	-0.971	1.00	28.87	O
ATOM	5	CB	ASP A	1	24.721	-0.606	-3.341	1.00	34.71	C
ATOM	6	CG	ASP A	1	24.061	-1.777	-4.067	1.00	35.11	C
ATOM	7	OD1	ASP A	1	23.841	-2.849	-3.496	1.00	35.99	O
ATOM	8	OD2	ASP A	1	23.798	-1.612	-5.255	1.00	38.08	O
ATOM	9	H1	ASP A	1	23.429	-0.061	-1.100	1.00	20.00	H
ATOM	10	H2	ASP A	1	23.417	-1.821	-1.194	1.00	20.00	H
ATOM	11	H3	ASP A	1	24.348	-0.968	-0.067	1.00	20.00	H
ATOM	12	N	ILE A	2	27.025	0.577	-1.277	1.00	26.56	N
ATOM	13	CA	ILE A	2	27.669	1.808	-0.873	1.00	25.29	C
ATOM	14	C	ILE A	2	27.740	2.665	-2.147	1.00	26.50	C
ATOM	15	O	ILE A	2	28.123	2.164	-3.216	1.00	26.25	O

- ▷ **Other pieces of information:** organism, molecules / sequences (and their engineering), crystal resolution and symmetry group, secondary structures, disulfide bonds.

PDB files: pitfalls

▷ Focus on files from X ray crystallography:

- ▶ Crystal structures: a confined environment
- ▶ Asymmetric unit versus biological unit
- ▶ Extra atoms/molecules: water, chemical, co-factors, etc
- ▶ Missing atoms: H systematically, heavy atoms . . . often
- ▶ Alternate locations – if several conformations
- ▶ Atoms retain dynamics encoded in B factors
- ▶ Resolution and precision on coordinates – a complex problem



▷ To learn more: <https://pdb101.rcsb.org/learn/guide-to-understanding-pdb-data/methods-for-determining-structure>

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Statics vs dynamics



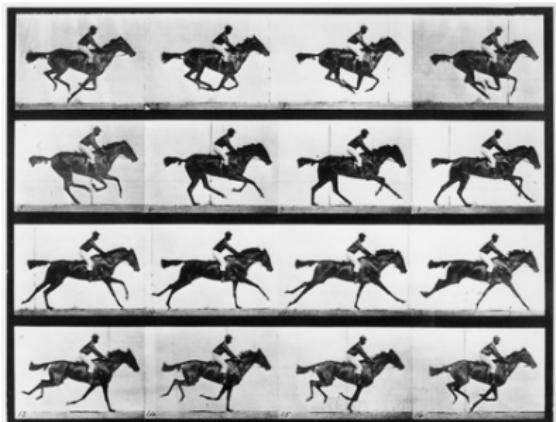
Two schools: static versus dynamic studies

- ▶ Balls and sticks



(Watson and Crick, DNA model)

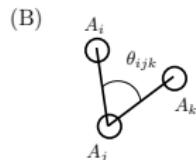
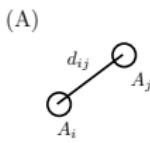
- ▶ The Ballet & time lapse



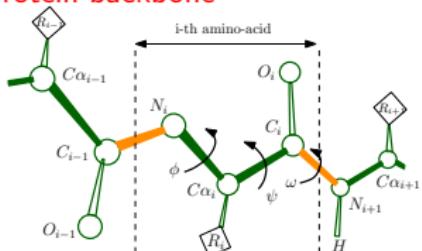
- ▶ Static analysis using crystal structure from the Protein Data Bank
<http://rcsb.org>
- ▶ Dynamical analysis using molecular mechanics

Geometric models: Cartesian and internal coordinates

- ▶ Cartesian versus internal coordinates: $\{x_i y_i z_i\}_i$ versus $\{d_{ij}, \theta_{ijk}, \sigma_{ijkl}\}$
- ▶ Bond length and valence angle



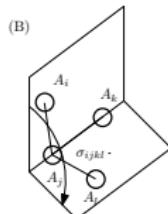
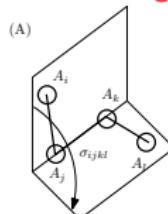
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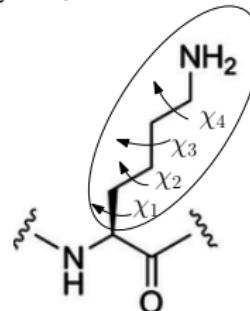
Ramachandran diagram, per a.a. type:

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▶ Dihedral angles



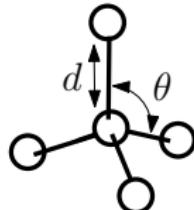
- ▶ Side chain: 20 natural amino acids
Exple: Lysine, 4 dihedral angles



LYS

The potential energy of (bio-)molecules: force fields

▷ The $3n - 6$ degrees of freedom of a molecule:



- types for atoms (element, bonds)
- covalent: bond lengths, angles
- non covalent: pairwise distances
- solvent model

▷ Potential energy: non linear function

$$V_{\text{total}} = V_{\text{bond}} + V_{\text{angle}} + (V_{\text{proper}} + V_{\text{improper}}) + (V_{\text{vdw}} + V_{\text{electro}}) \quad (1)$$

V_{bond} : bonds

V_{improper} : improper dihedrals

V_{angle} : covalent angles

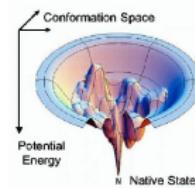
V_{vdw} : van der Walls

V_{proper} : proper dihedrals

V_{electro} : electrostatics

▷ Examples:

- ▶ AMBER: $S_u = (73, 133, 112, 3, 14, 758)$
1093 unique parameters
- ▶ CHARMM: $S_u = (85, 152, 209, 13, 33, 1)$
493 unique parameters
- ▶ MARTINI: $S_u = (16, 4, 0, 2, 21, 3)$
46 unique parameters



(Open problem) Complexity of Potential Energy Landscape

▷ Consider a force field of the following type:

$$\begin{aligned} V_{BLN} = & \frac{1}{2} \cdot K_r \sum_{i=1}^{N-1} (R_{i,i+1} - R_e)^2 + \frac{1}{2} K_0 \sum_{i=1}^{N-2} (\theta_i - \theta_e)^2 \\ & + \epsilon \cdot \sum_{i=1}^{N-3} [A_i(1 + \cos \phi_i) + B_i(1 + 3 \cos \phi_i)] \\ & + 4\epsilon \sum_{i=1}^{N-2} \sum_{j=i+2}^N \cdot C_{ij} \left[\left(\frac{\sigma}{R_{i,j}}\right)^{12} - D_{ij} \left(\frac{\sigma}{R_{i,j}}\right)^6 \right] \end{aligned}$$

▷ Open questions:

- ▶ Number of critical points (local minima, index one saddles)
- ▶ Geometry of the catchment basins (stable manifolds for $-\nabla V$)
- ▶ (Topological) Persistence of local minima

▷ Rationale:

- ▶ Separation bounds for polynomials
- ▶ Complexity results à-la Yomdin-Comte / Tame geometry

Thermodynamics

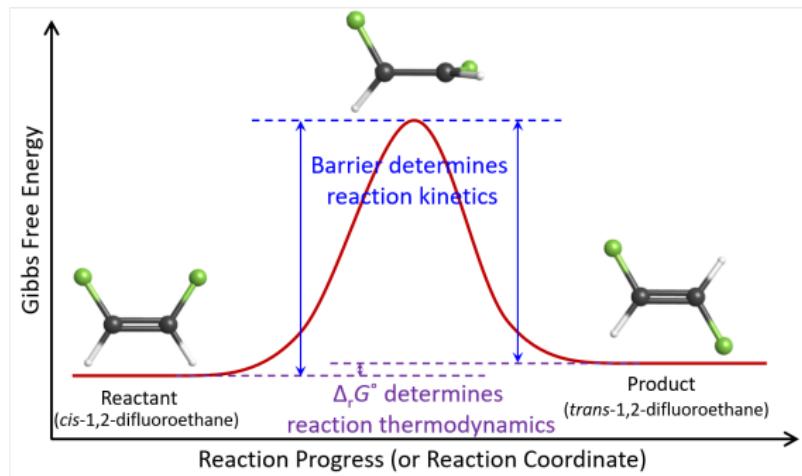
▷ Quantities defined for a conformation x :

- ▶ potential energy: $V(x)$
- ▶ kinetic energy: $K(x)$
- ▶ total energy: $E(x) = V(x) + K(x)$
- ▶ Boltzmann's distribution: $P^{\text{eq}}(x) = e^{-\beta E(x)} / Z, Z = \sum_{\text{Conformation}_x} P^{\text{eq}}(x)$

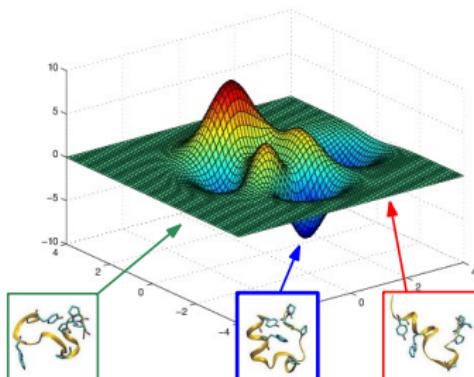
▷ Quantities defined for ensembles:

- ▶ Average of observable \mathcal{O} wrt an ensemble:
$$\langle \mathcal{O} \rangle \equiv \sum_{\text{Conformation}_x} \mathcal{O}(x) P^{\text{eq}}(x)$$
- ▶ Exple: average total energy $U = \langle E \rangle$
- ▶ NVT: Helmholtz free energy $A = U - TS = k_B T \ln Z$
- ▶ NPT: Gibbs free energy $G = U + PV - TS = H - TS$

Emergence of macromolecular function(s) from Structure – Thermodynamics – Kinetics

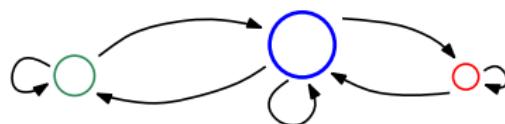


Emergence of macromolecular function(s) from Structure – Thermodynamics – Kinetics



Potential Energy Landscape

- large number of local minima
- enthalpic barriers
- entropic barriers

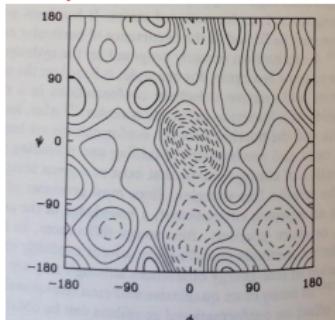
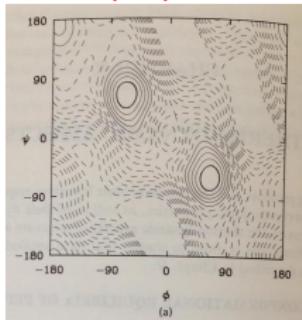
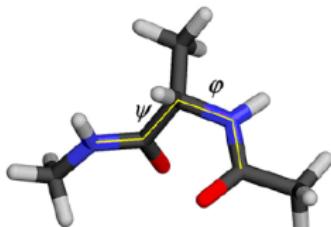


Thermodynamics: meta-stable conformations i.e. ensemble of conformations easily inter-convertible into one - another.

Kinetics: transitions between meta-stable conformations e.g. Markov state model

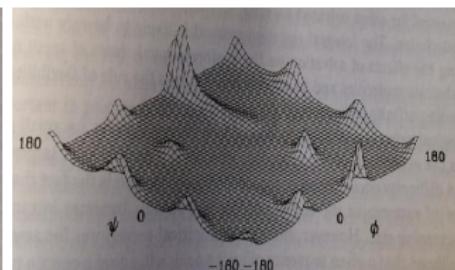
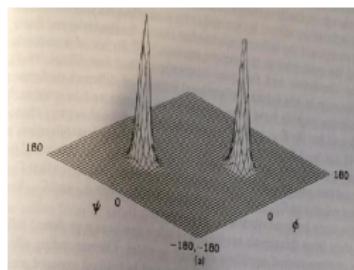
Potential energy landscapes: illustration

- ▷ Potential energy map: vacuum (PE) versus solvated (PMF):



- ▷ Corresponding Boltzmann-weighted probability maps:

Solvent stabilizes many more conformers—hydrogen bonding.



- ▷ Ref: Petitt, Karplus, Chem. Phys. Lett., 121, 1985

Dynamics of biomolecules: first molecular simulation of a protein

About the simulation duration, quoting M. Levitt “*Cannot remember, but likely less than 100 picoseconds.*
Nb: from the late eighties”

Challenge *Dynamics of proteins*: specification

Youtube

▷ **Input:** structure(s) of biomolecules + potential energy model

▷ **Output**

- ▶ Thermodynamics: meta-stable states and observables
- ▶ Kinetics: transition rates, Markov state models

▷ **Time-scales**

- ▶ Biological time-scale > millisecond
- ▶ Integration time step in molecular dynamics: $\Delta t \sim 10^{-15} s$

- ▶ 162 amino acids, > 2000 atoms
- ▶ 5.058ms of simulation time
- ▶ ~ 230 GPU years on NVIDIA GeForce GTX 980 processor

▷ Ref: Chodera et al, eLife, 2019

Protein motions: time scales

Table 1. Characteristic Time Scales for Protein Motions

event	spatial extent (nm)	amplitude (nm)	time (s)	appropriate simulations
bond-length vibration	0.2–0.5	0.001–0.01	10^{-14} – 10^{-13}	QM methods
elastic vibration of globular domain	1.0–2.0	0.005–0.05	10^{-12} – 10^{-11}	conventional MD
rotation of solvent-exposed side chains	0.5–1.0	0.5–1.0	10^{-11} – 10^{-10}	conventional MD
torsional libration of buried groups	0.5–1.0	0.05	10^{-11} – 10^{-9}	conventional MD
hinge bending (relative motion of globular domains)	1.0–2.0	0.1–0.5	10^{-11} – 10^{-7}	Langevin dynamics, enhanced sampling MD methods?
rotation of buried side chains	0.5	0.5	10^{-4} –1	enhanced sampling MD methods?
allosteric transitions	0.5–4.0	0.1–0.5	10^{-5} –1	enhanced sampling MD methods?
local denaturation	0.5–1.0	0.5–1.0	10^{-5} – 10^1	enhanced sampling MD methods?
loop motions	1.0–5.0	1.0–5.0	10^{-9} – 10^{-5}	Brownian dynamics?
rigid-body (helix) motions		1.0–5.0	10^{-9} – 10^{-6}	enhanced sampling MD methods?
helix–coil transitions		>5.0	10^{-7} – 10^4	enhanced sampling MD methods?
protein association	$\gg 1.0$			Brownian dynamics

►Ref: Adcock and McCammon, Chem. Rev., 2006

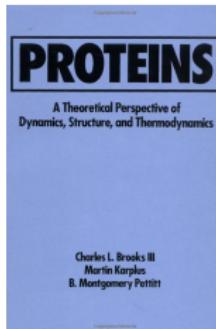
Potentials of Mean Force and free energies

- ▷ **Rationale:** decouple the slow and fast dof of a system. Example: solvated protein:
 - ▶ slow dof: protein
 - ▶ fast dof: solvent molecules
- ▷ **How to:** replace the overall potential energy by an average, computed over the fast dof
- ▷ **PMF definition:**

$$\exp(-\beta PMF(x_1, \dots, x_n)) \propto \frac{\int \exp(-\beta V(x_1, \dots, x_d)) dx^{n+1, \dots, d}}{\rho_{\text{unif.}}(x_1, \dots, x_n)} \quad (2)$$

Nb: in this equation, $\rho_{\text{unif.}}$ stand for the uniform distribution on the slow dof, which naturally depends on the nature of these parameters – cartesian or internal coordinates.

Dynamics: *alea jacta est* in the mid eighties



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at

►Ref: Brooks, Karplus, Montgomery Pettitt; Advances in Chemical Physics, Proteins; Wiley, 1988

Biomolecular recognition

Computational Structural Biology: what is a protein?

Protein Structure Resolution

The importance of dynamics

Protein functions: examples

Computational Structural Biology: challenges

Molecular dynamics and protein functions: movies

▷ Selected (great) movies:

- ▶ Protein synthesis by the ribosome:
https://www.youtube.com/watch?v=TfYf_rPWUdY
- ▶ Membrane fusion and infection by SARS-CoV-2:
<https://youtu.be/e2Qi-hAXdJo>
- ▶ Molecular motors: https://www.youtube.com/watch?v=X_tYrnv_o6A

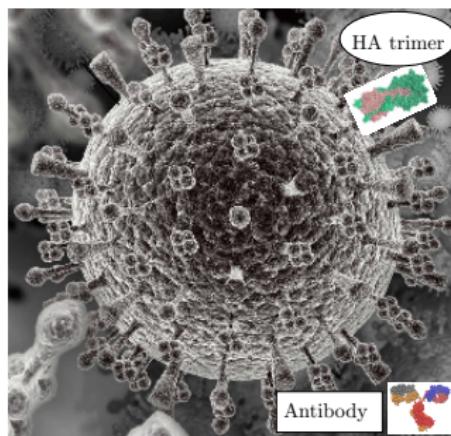
▷ Other videos of interest:

- ▶ Various phenomena in this movie:
<https://www.youtube.com/watch?v=wJyUtbn005Y>
- ▶ More X Vivo movies at
https://www.youtube.com/channel/UCAUL7Wl_lydKXI8q0oi4CUw

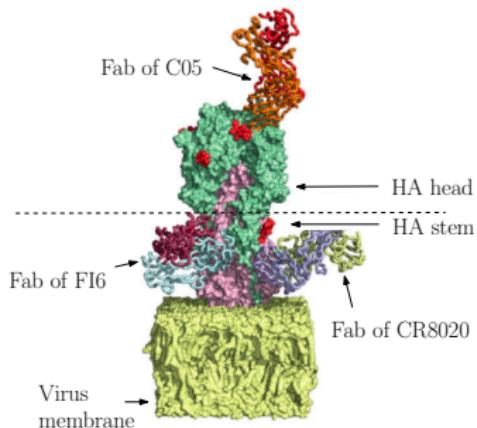
▷ **Rmk.** Remarkable illustration of the aforementioned mechanisms can be found in the book [?]; see also the gallery on the PDB portal, at <https://pdb101.rcsb.org/sci-art/goodsell-gallery>.

Structure - dynamics - function: illustration on antibody - antigen complexes

▷ Influenza



▷ (Broadly) neutralizing antibodies

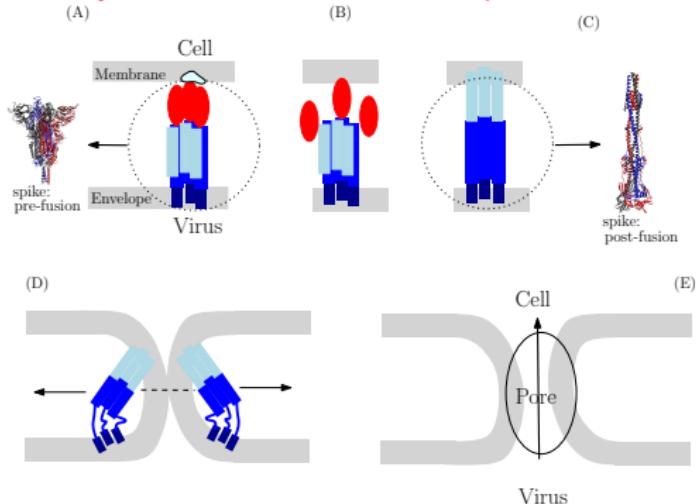


▷ Core questions – illustrated on on IG-Ag complexes

- Binding affinity: geometry (cf lock and key) + dynamics (entropy / free energy)
- Interaction specificity
- Multivalent binding: affinity - avidity - virus entry inhibition

SARS-CoV-2: cell entry mechanism

- ▷ SARS-CoV-2: cell entry mechanism via virus envelope - cell membrane fusion:



- ▷ Spike, the S1 and S2 domains: S1: the receptor binding domain (RBD, red ellipsis); S2: the fusion machinery (blue rectangles)

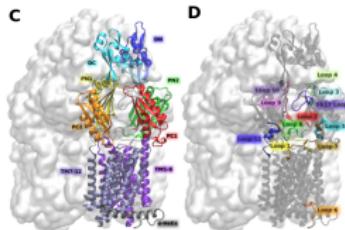
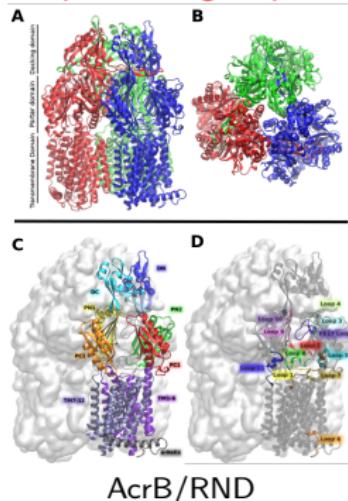
- ▶ (A) Attachment of the RBD to its receptor ACE2
- ▶ (B) Cleavage step removing the S1 subunit
- ▶ (C) Fusion machinery: refolding + membrane anchoring
- ▶ (D,E) Formation of the hemi-pore and pore

- ▷ Biophysics and biology of SARS-CoV-2/Omicron – Marc Gozlan:

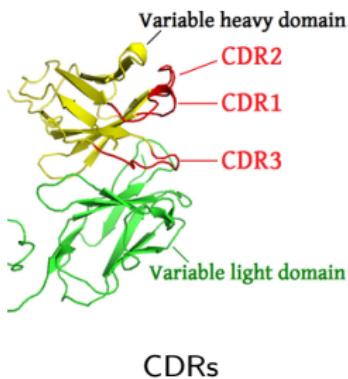
<https://www.lemonde.fr/blog/realitesbiomedicales/2022/02/09/omicron-une-biologie-et-une-dynamique-virale-differentes-de-celles-observees-288>

Loops: biological relevance and dynamics

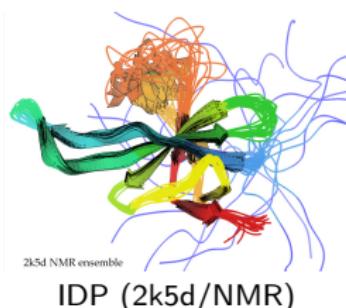
► Loops in biological processes



AcrB/RND



CDRs



IDP (2k5d/NMR)

► Action modes

- ▶ (Structure) Global dynamics: global motions of domains
- ▶ (Thermodynamics) Localized dynamics of CDR in antibodies (binding affinity)
- ▶ (Mix) IDP and more generally highly flexible regions

► Open problems: accurate predictions for structure / thermodynamics / kinetics



L'intelligence artificielle au défi du design de protéines : des prouesses et limites d'AlphaFold

Publié: 30 octobre 2022, 20:55 CET

Keywords: AI, deep learning, AlphaFold2, Covid19, protein design, flexibility, thermodynamics

Biomolecular recognition

Computational Structural Biology: what is a protein?

Protein Structure Resolution

The importance of dynamics

Protein functions: examples

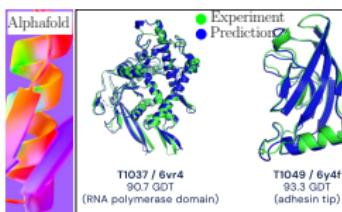
Computational Structural Biology: challenges

Challenge *Structure of proteins*: specification

- ▷ Input: sequences from genome sequencing projects

P69905 (HBB_HUMAN)	MV-LSPADKTNVKAAWGKVGAHAGEYGAEALERMFLSFPTTKTYFPHF-DLSH-----GS	53
P68871 (HBB_HUMAN)	MVHLTPEEKSAVTALWGKV--NVDEVGGEALGRLLVVYPWTQRFESFGDLSTPDAVMGN	58
P02144 (MYG_HUMAN)	-MGLSDGEWQLVLNVWGKVEADIPGHGQEVLIRLFKGHPETLEKFDFKHLKSEDEMKA	59
	: *: : * ***** * * *;: * * * *	

- ▷ Output: plausible structures i.e. atomic coordinates $\{(x_i, y_i, z_i)\}$



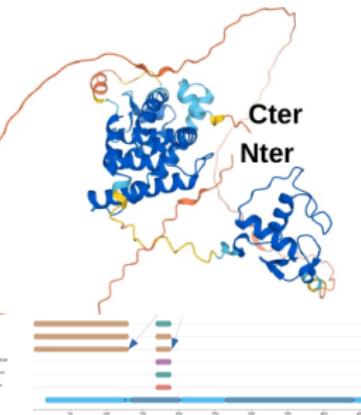
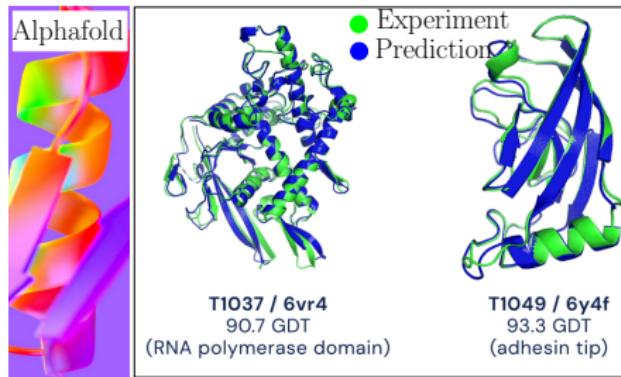
- ▷ Protein sequences versus structures: numbers
 - ▶ Num. sequences in UniProtKB: TrEMBL ($\sim 10^8$), Swiss-Prot ($\sim 10^5$)
 - ▶ Num. structures in the Protein Data Bank: $\sim 150,000$ structures
- ▷ Recent & notable: the Deepmind combined approach (DL, optimization)
 - ▶ Bias towards well folded structure – no disorder (IDP)
 - ▶ Structure only – neither thermodynamics nor kinetics
 - ▶ Predicting is not explaining

AlphaFold by Deepmind

AI: what is being learned?

▷ Successes

▷ ...and failures



▷ Recent & notable: the Deepmind combined approach (DL, optimization)

- Structure only – neither thermodynamics nor kinetics
- Bias towards well folded structure – no disorder (IDP)
- Predicting is not explaining
- Heavy engineering (team: 34 scientists/engineers)

▷ Ref: Jumper et al, Nature, 2021

Challenge *Dynamics of proteins*: specification

Youtube

▷ **Input:** structure(s) of biomolecules + potential energy model

▷ **Output**

- ▶ Thermodynamics: meta-stable states and observables
- ▶ Kinetics: transition rates, Markov state models

▷ **Time-scales**

- ▶ Biological time-scale > millisecond
- ▶ Integration time step in molecular dynamics: $\Delta t \sim 10^{-15} s$

- ▶ 162 amino acids, > 2000 atoms
- ▶ 5.058ms of simulation time
- ▶ ~ 230 GPU years on NVIDIA GeForce GTX 980 processor

▷ Ref: Chodera et al, eLife, 2019

Modeling dynamics: shear difficulties

▷ Three sources of difficulties

- ▶ System size: $3n - 6$ degrees of freedom: typically $> 10^4$
- ▶ Time scales: 15 orders of magnitude
- ▶ Spatial scales: 3 orders of magnitude

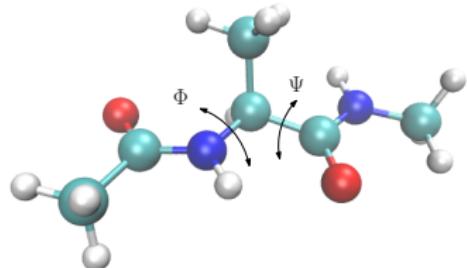
Table 1. Characteristic Time Scales for Protein Motions

event	spatial extent (nm)	amplitude (nm)	time (s)	appropriate simulations
bond-length vibration	0.2–0.5	0.001–0.01	10^{-14} – 10^{-13}	QM methods
elastic vibration of globular domain	1.0–2.0	0.005–0.05	10^{-12} – 10^{-11}	conventional MD
rotation of solvent-exposed side chains	0.5–1.0	0.5–1.0	10^{-11} – 10^{-10}	conventional MD
torsional libration of buried groups	0.5–1.0	0.05	10^{-11} – 10^{-9}	conventional MD
hinge bending (relative motion of globular domains)	1.0–2.0	0.1–0.5	10^{-11} – 10^{-7}	Langevin dynamics, enhanced sampling MD methods?
rotation of buried side chains	0.5	0.5	10^{-4} –1	enhanced sampling MD methods?
allosteric transitions	0.5–4.0	0.1–0.5	10^{-5} –1	enhanced sampling MD methods?
local denaturation	0.5–1.0	0.5–1.0	10^{-5} – 10^1	enhanced sampling MD methods?
loop motions	1.0–5.0	1.0–5.0	10^{-9} – 10^{-5}	Brownian dynamics?
rigid-body (helix) motions		1.0–5.0	10^{-9} – 10^{-6}	enhanced sampling MD methods?
helix–coil transitions		>5.0	10^{-7} – 10^4	enhanced sampling MD methods?
protein association	$\gg 1.0$			Brownian dynamics

▷ Ref: Adcock and McCammon, Chem. Rev., 2006

Density of states and partition functions

Dialanine

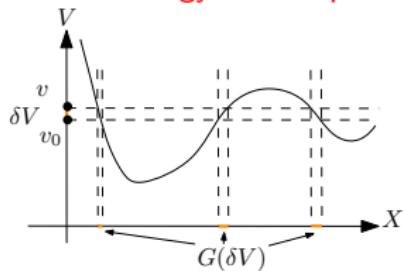


Molecule in water at temperature T

- ▶ q : vector of positions of atoms
- ▶ Potential energy:

$$V(q)$$

- ▶ Potential energy landscape:



- ▶ Density of states (DoS):

- ▶ Push forward of the Lebesgue measure by the potential energy V :
- ▶ For any $v_0 < v_1$:

$$g([v_0, v_1]) = \int_X 1_{[v_0, v_1]}(V(q)) dq$$

- ▶ Partition function for $A \subset X$: integrate Boltzmann's factor

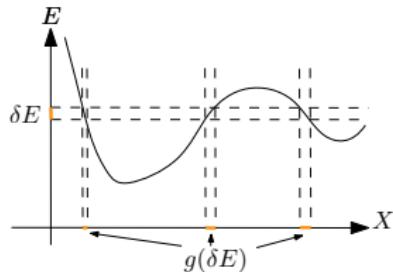
$$Z_A(T) = \int_A e^{-\beta u} dg(u)$$

- ▶ NB: n atom: $d = 3n$ Cartesian coordinates. Exple: antibody: $d \approx 42,000$

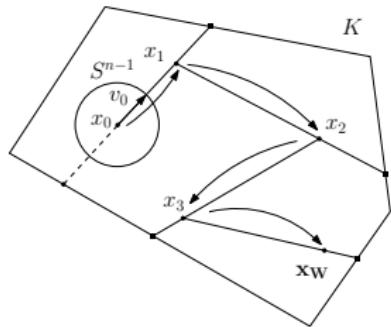
Free energy, Density of States, Volumes

- ▷ Partition function and density of states:

$$\begin{aligned} Z &= \sum_{x_i: \text{state}} e^{-\beta E(x_i)} \\ &= \sum_{j: \text{energy level}} g(E_j) e^{-\beta E_j} \end{aligned}$$



- ▷ Learning from simpler cases: polytopes in \mathbb{R}^d , $d \in [100 \dots 1000]$



- ▷ Unless P=NP: no polynomial time algorithm with approx factor $(cd/\log d)^d$
- ▷ But: probabilistic algorithms running in $O^*(d^{3.5})$

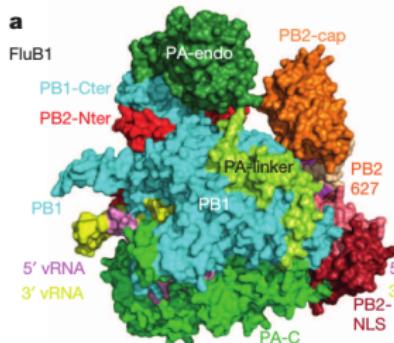
- ▷ Ref: Cousins and Vempala, Math. Prog. Comp., 2016
- ▷ Ref: Chalkis, Emiris, Fisikopoulos, arXiv:1905.05494, 2019
- ▷ Ref: Chevallier et al, AISTATS, 2022

Challenge Molecular machines—structure and dynamics: specification

- ▷ Molecular machines: assemblies with tens / hundreds of subunits
- ▷ Input
 - ▶ cryo-electron microscopy (cryo-EM) maps of whole assemblies
 - ▶ crystal structures of subunits
 - ▶ other data: native mass spectrometry data, ...
- ▷ Output: structure(s) + mechanism(s)

▷ Polymerase of E. coli:
structure+dynamics

▷ Polymerase of influenza:
structure



▷ Ref: Scheres et al, Elife, 2015; ▷ Ref: Cusak et al, Nature, 2015

Modeling dynamics: shear difficulties

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▷ Ref: Adcock and McCammon, Chem. Rev., 2006

Biomolecular recognition

PART 1: Introduction to Protein Science

PART 2: Biomolecular recognition

Main points

Main points:

- ▶ Proteins and binding affinity
- ▶ Enthalpy - entropy compensation
- ▶ The time dimension $1/K_{\text{off}}$
- ▶ Application: antibodies binding viruses

Biomolecular recognition

Biomolecular recognition: proteins and binding affinity

Association and dissociation constants K_a, K_d

Enthalpy - entropy compensation

The time dimension: K_d, K_{on}, K_{off} and $1/K_{off}$

Application: influenza - antibody complexes

Biological complexes: structural diversity

- ▷ Biology rests on interactions biomolecules make with one another. A remarkable variety of such complexes exist, both in size and time scales spanned [?].
- ▷ Size-wise, complexes span a range from $O(100\text{ kDa})$ up to 120 MDa (mammalian NPC). Note that the nuclear pore complex is the largest assembly known (to date) in eukaryotic cells, as it involves circa 500 polypeptide chains.

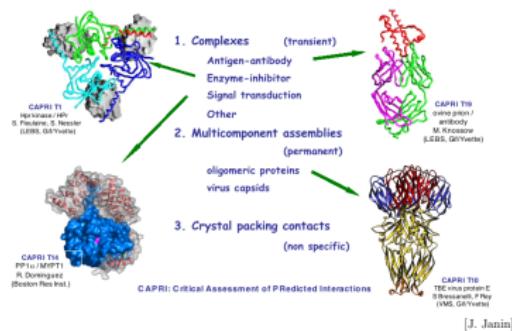
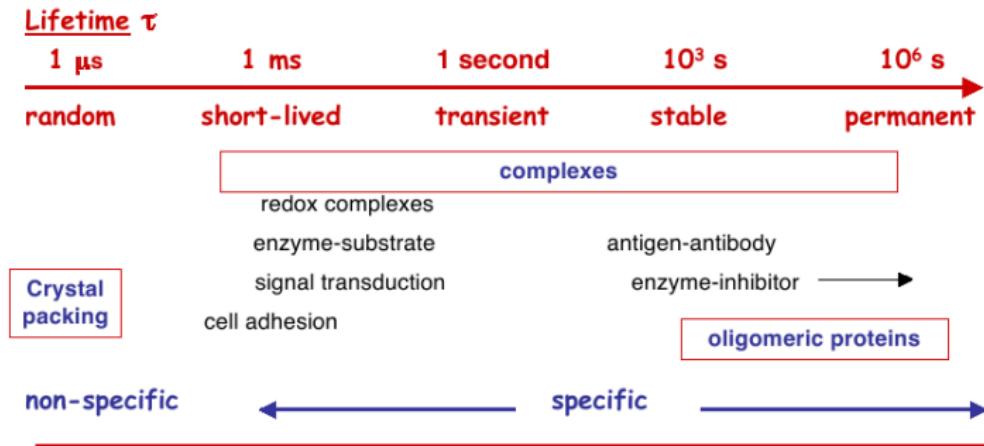


Figure: Biological complexes: diversity. From [?].

Biological complexes: time-wise

- Time-wise, biological complexes also span several orders of magnitude, say from the millisecond to years for permanent ones (Fig. 2).



Short-lived complexes ($\tau < 1$ second) are relevant to many important biologically processes.

Only a few examples of these are present in the PDB (Nooren & Thornton, 2003).

These systems may resemble **crystal packing** more than permanent assemblies.

[J. Janin]

Figure: **Biological complexes: time scales.** From [?].

Docking models

- ▷ Over the years, several docking models have been proposed (Fig. 4):
 - ▶ Lock-and-key Fisher, 1894. In this model, the two partners associate as rigid bodies.
 - ▶ Induced fit: Koshland, 1958. While getting close, the partners *shape* one-another, resulting in the conformations found in the complex.
 - ▶ Conformer selection, Monod-Wyman-Changeux, 1965. In solution or in the cell, each molecule exists in a variety of conformations. In the course of their diffusion, *compatible* conformations stumble onto one-another, and the complex gets formed.

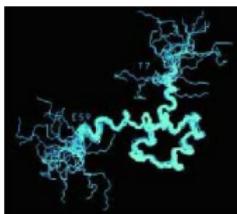


Figure: Flexibility of biomolecules: illustration.
From the Nobel lecture of K. Wütricht.

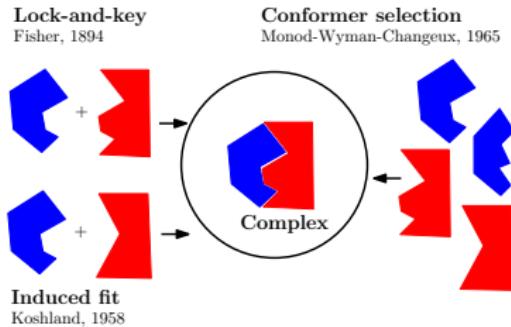
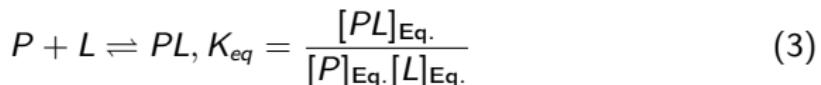


Figure: Docking models.

Chemical equilibrium

- ▷ Setup: we consider a protein P and a ligand L which interact in a non-covalent fashion. This means that no chemical bonds get created or removed. We further assume that these two species form a chemical equilibrium:



- ▷ The notion of *equilibrium* is central here, and owes to competing effects:
 - ▶ Due to attraction forces, P and L get closer to one another.
 - ▶ Due in particular to thermal fluctuations, they get away.
- ▷ In the medium considered (test tube, cell): three chemical species: P, L, and the complex PL.
- ▷ In the sequel, we consider the standard setup:
 - ▶ We start from std concentrations of the individual species, say 1 Molar
 - ▶ We consider the equilibrium concentrations

Binding affinity: spectrum

- Typical binding affinity values are presented in Table 5.

Type of Interaction	K_D (molar)	ΔG_{bind}^0 (at 300K) kJ mol ⁻¹
Enzyme:ATP	$\sim 1 \times 10^{-3}$ to $\sim 1 \times 10^{-6}$ (millimolar to micromolar)	-17 to -35
signaling protein binding to a target	$\sim 1 \times 10^{-6}$ (micromolar)	-35
Sequence-specific recognition of DNA by a transcription factor	$\sim 1 \times 10^{-9}$ (nanomolar)	-52
small molecule inhibitors of proteins (drugs)	$\sim 1 \times 10^{-9}$ to $\sim 1 \times 10^{-12}$ (nanomolar to picomolar)	-52 to -69
biotin binding to avidin protein (strongest known non-covalent interaction)	$\sim 1 \times 10^{-15}$ (femtomolar)	-86

Figure: **binding affinity: typical examples.** Table from [?, Chapter 12].

Binding affinity and specificity

- ▷ The two critical notions for protein interactions are
 - ▶ Binding affinity: the *strength* of the interactions.
 - ▶ Binding specificity: the variety of partners a molecules binds sufficiently strongly with.

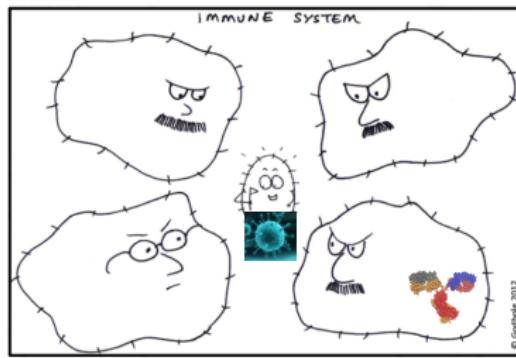


Figure: Binding affinity and specificity: how to for the immune system. The molecules secreted should bind strongly enough the pathogens; but they should also be quite specific.

Biomolecular recognition

Biomolecular recognition: proteins and binding affinity

Association and dissociation constants K_a, K_d

Enthalpy - entropy compensation

The time dimension: K_d, K_{on}, K_{off} and $1/K_{off}$

Application: influenza - antibody complexes

Equilibrium constants K_a , K_d

- ▷ Consider the non-covalent interaction $P + L \rightleftharpoons PL$
- ▷ The law of mass action yields the association and dissociation constants:

$$\left\{ \begin{array}{l} \text{Association constant : } K_a = \frac{[PL]_{\text{Eq.}}}{[P]_{\text{Eq.}} [L]_{\text{Eq.}}} \\ \text{Dissociation constant : } K_d = \frac{[P]_{\text{Eq.}} [L]_{\text{Eq.}}}{[PL]_{\text{Eq.}}} \end{array} \right. \quad (4)$$

Using std units, K_a is expressed in moles $^{-1}$, and K_d is in moles.

- ▷ Determine the concentration of the molecular species, here P, L, and PL, when the binding reaction reaches an equilibrium.
- ▷ The relationship between K_a and the variation of free energy satisfies:

$$\Delta G_a^0 = -RT \log c^0 K_a = RT \log \frac{K_d}{c^0}. \quad (5)$$

- ▷ **Rmk.** In Eq. 5, c^0 is meant to obtain a unit-less number: if K_a is expressed in moles $^{-1}$, then C^0 is equal to 1 molar.

Fractional saturation

- The fraction of proteins with bound ligand satisfies:

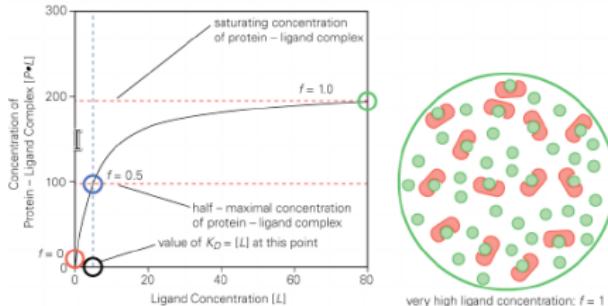
$$f = \frac{\text{\# num proteins with bound ligand}}{\text{total \# proteins}} \quad (6)$$

$$= \frac{[PL]_{\text{Eq.}}}{[P]_{\text{Eq.}} + [PL]_{\text{Eq.}}} \quad (7)$$

$$= \frac{[P]_{\text{Eq.}}[L]_{\text{Eq.}}}{K_d([P]_{\text{Eq.}} + \frac{[P]_{\text{Eq.}}[L]_{\text{Eq.}}}{K_d})} \quad (8)$$

$$= \frac{1}{K_d(\frac{1}{K_d} + \frac{1}{[L]_{\text{Eq.}}})} = \frac{[L]_{\text{Eq.}}}{[L]_{\text{Eq.}} + K_d} \quad (9)$$

- Varying the concentration of the ligand, one gets from Eq. 6:
 - Observation:** K_d is the concentration of the ligand such that the fraction of bound equals 1/2.



Biomolecular recognition

Biomolecular recognition: proteins and binding affinity

Association and dissociation constants K_a, K_d

Enthalpy - entropy compensation

The time dimension: K_d, K_{on}, K_{off} and $1/K_{off}$

Application: influenza - antibody complexes

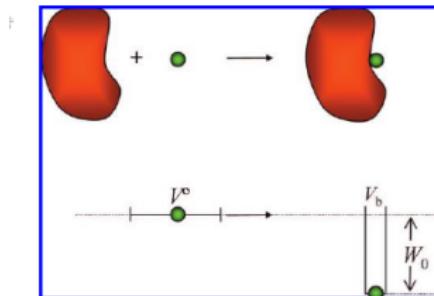
Enthalpy - entropy compensation - I

- To understand the components of binding, let us recall:

$$\Delta G_a^0 = -RT \log c^0 K_a = RT \log \frac{K_d}{c^0} = \Delta H - T\Delta S. \quad (10)$$

- To understand the relative variations of ΔH and $T\Delta S$, we need to discuss several components in turn:

- ▶ (1) System protein + ligand, enthalpy
- ▶ (2) Mixing: Two versus three species
- ▶ (3) Ligand and its translational / rotational entropy
- ▶ (4) System protein + ligand, conformational + vibrational entropy
- ▶ (5) Solvent and its entropy



Binding affinity: enthalpy-entropy competition illustrated along the binding process. The volume accessible to the ligand decreases, whence $T\Delta S < 0$ and $-T\Delta S > 0$. On the other hand, the interaction energy (enthalpy) decreases by W_0 . From [?].

Enthalpy - entropy compensation - II

1. System protein + ligand, enthalpy:
 - ▶ Energy minimization when P and L get closer. (Exple: strong electrostatic interactions.)
2. Mixing: Two versus three species:
 - ▶ Three species (P, L, PL) have more entropy than two.
3. Ligand and its translational / rotational entropy:
 - ▶ Assuming P fixed: 6 dof of the ligand get constrained.
Translation/rotational entropy decreases.
4. System protein + ligand, conformational + vibrational entropy:
 - ▶ In PL, conformational changes hindered + coupled harmonic oscillators: conformational and vibrational entropy decrease.
5. Solvent and its entropy:
 - ▶ Buried surface area at the interface \Rightarrow the solvent S increases.

Summary:

- ▶ During association, grossly speaking: ΔH is negative, and $-T\Delta S$ is positive.
- ▶ Variation of enthalpy and entropy are very subtle, and the balance depends in general on the temperature.
- ▶ For biological systems: this subtlety is key to **regulation**. By slightly changing the conditions (temperature, pH, ionic strength which alter the electrostatic interactions), the behavior changes.

Enthalpy-entropy competition: illustration on protein unfolding



Typical protein unfolding thermodynamics...

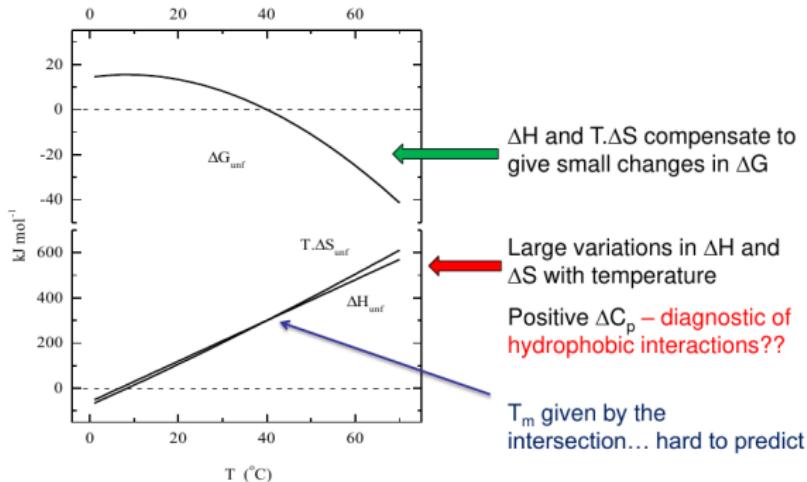


Figure: Protein unfolding: illustration of the enthalpy-entropy competition. Courtesy of Alan Cooper.

Binding affinity: ab initio calculations

▷ Model from molecular mechanics: potential energy / force field. With $X \in \{P, L, PL\}$:

- ▶ r_X internal coordinates of molecular species X
- ▶ $V(r_X)$ the potential energy, and $W(X)$ be the solvation energy.

▷ Dissociation free energy reads as – std concentration $c^\circ (= 1M)$:

$$\Delta G_d^\circ = -RT \ln \left(\frac{c^\circ}{8\pi^2} \frac{\left(\int e^{-(V(r_P) + W(r_P))/RT} dr_P \right) \left(\int e^{-(V(r_L) + W(r_L))/RT} dr_L \right)}{\int e^{-(V(r_{PL}) + W(r_{PL}))/RT} dr_{PL}} \right). \quad (11)$$

▷ Major difficulties:

- ▶ Very high dimensionality
- ▶ Complex energy functions

▷ Ref: Gilson, Zhou; Ann. Rev. Biomol. Struct., 2007

Biomolecular recognition

Biomolecular recognition: proteins and binding affinity

Association and dissociation constants K_a, K_d

Enthalpy - entropy compensation

The time dimension: K_d, K_{on}, K_{off} and $1/K_{off}$

Application: influenza - antibody complexes

Equilibrium constants and reaction rates

- ▷ To account for kinetics, one resorts to the reaction rates



Note that K_{on} is expressed $\text{mol}^{-1}\text{s}^{-1}$ while K_{off} is expressed in s^{-1} . These rates account for the fact that in order to assemble, the molecules must first meet/collide.

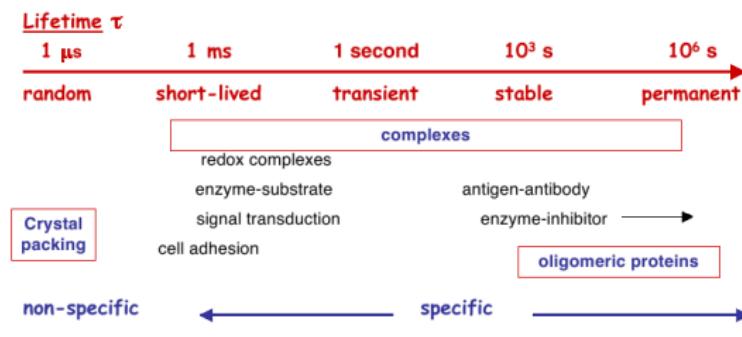
- ▷ The relationship with dissociation is as follows:

$$K_a = \frac{K_{\text{on}}}{K_{\text{off}}}. \quad (13)$$

Residence times

Binding affinity is a thermodynamic quantity. On the other hand, time is clearly involved in biomolecular interactions – Chapter ??.

- ▶ Mean life of the complex, $1/K_{\text{off}}$: average life span of the PL complex.
- ▶ Half-time of the complex, $\log 2/K_{\text{off}}$: the time required for half of a population of complexes to unbind.



Short-lived complexes ($\tau < 1$ second) are relevant to many important biologically processes.

Only a few examples of these are present in the PDB (Nooren & Thornton, 2003).

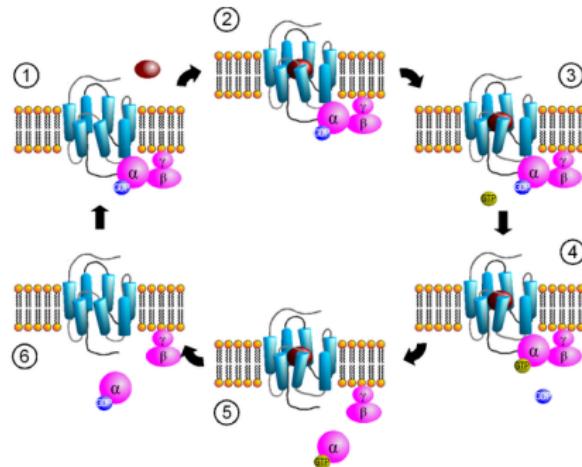
These systems may resemble **crystal packing** more than permanent assemblies.

[J. Janin]

Figure: Biological complexes: time scales. From [?].

Example: ligand binding for GPCR

- ▷ GPCR - protein G complexes: involved in signal transduction inside the cell. The structure of such complexes is as follows (Fig. 10):
 - ▶ GPCR are receptors involving 7 trans-membrane helices.
 - ▶ Heterotrimeric G proteins, made of three subunits denoted α , β , γ .
- ▷ Ligand binding on the extra-cellular side: N-ter region, within the helices.
- ▷ Triggers (Fig. 10): (1) conformational changes in the cytoplasmic side of the receptor (2) dissociation of the subunits G_α (+GDP) on the one hand, and the dimer $G_\beta\gamma$ on the other hand (3). These trigger signaling cascades
 - ▷ Time constraint: ligand must stay long enough for the conformational change to occur; if not, abortive complex.



Biomolecular recognition

Biomolecular recognition: proteins and binding affinity

Association and dissociation constants K_a, K_d

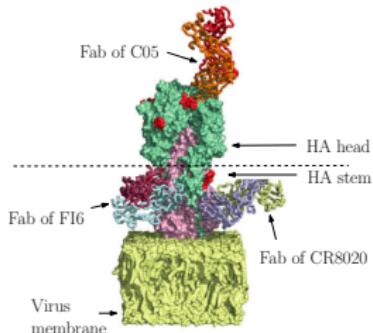
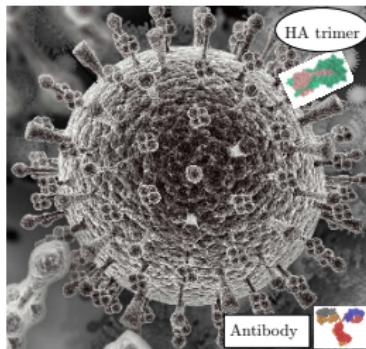
Enthalpy - entropy compensation

The time dimension: K_d, K_{on}, K_{off} and $1/K_{off}$

Application: influenza - antibody complexes

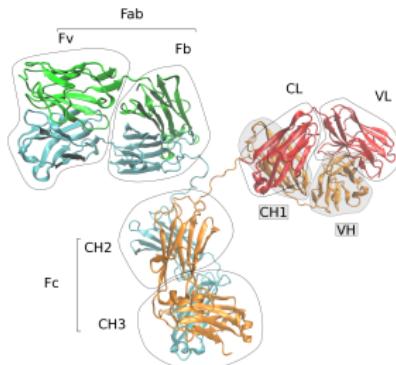
Virus neutralization by antibodies: the problem

- ▷ Enveloped viruses: the case of influenza
- ▷ Broadly neutralizing antibodies targeting the fusion protein of influenza:
 - ▶ Ig on top: prevent the virus attachment
 - ▶ Ig on stem: preventing the conformational changes required for envelope-membrane fusion
- ▷ **The influenza virus.** Drawn to scale a trimer of the fusion protein (HA)
- ▷ **Broadly neutralizing antibodies :** hemagglutinin (HA) of influenza is depicted in green



The structure of antibodies – IgG immunoglobulins

▷ Overall structure



▷ FABs and CDRs

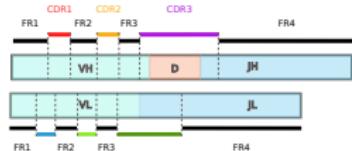
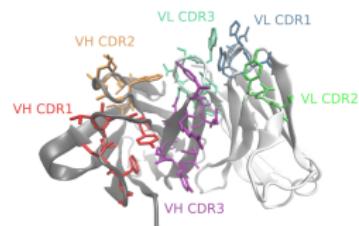


Figure: (A) Antigen-binding fragment (FAB) and Complementarity Determining Regions (CDRs) (B) Encoding of CDRs and Frs by the V, D and J genes

Affinity maturation: process

- ▷ Affinity maturation: secretion of more potent antibodies
- ▷ IgG lineage
- ▷ Evolution of the affinity

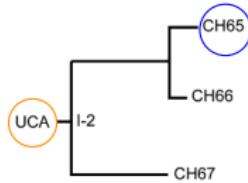


Figure: Lineage of IgG observed during an immune response against influenza.

Fab	$K_d(\mu M)$
UCA	118 ± 14
I-2	142 ± 15
CH65	$0.49 \pm .10$
CH67	0.36 ± 0.04

Table: Binding affinities: K_d analysis by SPR NB: CH65 ~ CH67; wrt UCA: $\Rightarrow \sim 200$ -fold improvement

Affinity enhancement: origin

- ▷ Ancestor and matured IgG have similar binding modes

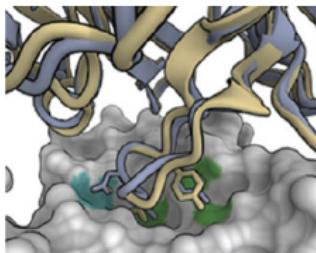


Figure: But UCA and CH65 have similar binding modes. Displayed: backbone traces of the CDR3. From [?].

- ▷ But matured IgG have a pre-formed binding site:

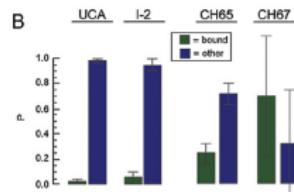


Figure: CDR3: time spent in bound and unbound conformations. Matured IgG (CH65, CH67): more time in the bound conformation. From [?].

- ▷ Origin of the affinity enhancement: lesser entropic penalty.
“In both branches (CH65, CH67), increased conformational restriction of CDR H3 has been the principle consequence of affinity maturation.”

Bibliography