MOLECULAR ALGORITHMS

- The most sophisticated organization of matter is biology, spanning 24 orders of magnitude (10^{-19} TO 10^{5} Grams)

Biological organization is information based. DNA sequences, refined by evolution, encode both the COMPONENTS and the PROCESS that guide the development into an organism. It is a world of molecular algorithms.

Molecular algorithms, energy, entropy are essential concepts to understand how physical processes create order.

A single group of atoms existing in one copy produces orderly events, marvelously tuned with each other and with the environment.
The "statistical mechanism" produces order from disorder and the "biological mechanism" order from order.

E.Schrodinger, What is life(1944)

A.TURING UNIVERSAL COMPUTATION

If you construct an automaton right, then any additional requirements about the automaton can be handled by sufficiently elaborated instructions. This is only true if A is sufficiently complicated, if it has reached a minimal level of complexity. A simpler thing will never perform certain operations, no matter what instructions you give it; but there is a definite finite point where an automaton of this complexity can, when given suitable instructions, do anything that can be done by automata at all.

The laws of physics"happen to" permit the existence of physical models for the operations of arithmetic. Thus , at least at the level of investigation of "reasonable' instances of computation, the theory of computation is part of physics.

D,Deutsch, on computation.

Towards a minimal cell
A vesicle bioreactor
V.NOIREAUX

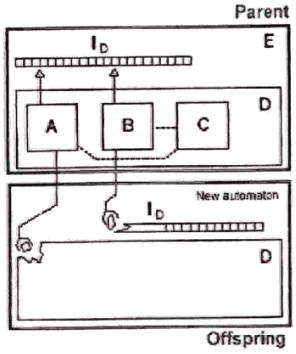
In his Theory of Automata,J.Von Neumann compared computing machines and living organisms.The self reproduction of automata was discussed and linked to a Turing like principle. In parallel the biological sciences have raised the question of how to engineer a minimal self-reproducing living cell. Any attempt would give clues to how self-replication emerges and also lead to insights on replicators based on inorganic materials.

Von Neumann self reproducing automaton

The Hixon Symposium 1951

Wiley.

von Neumann's construction is as follows. Define automaton A, which, given instructions I (the analog of Turing's tape) describing the functions another automaton can carry out, will construct that automaton. Define automaton B, which makes a copy of any instructions I given to it. Combine automata A and B into automaton C, which serves as a "control mechanism." C functions in such a way that if its A component is supplied with instructions I, C will cause A to construct the automaton A(I) described by the instructions I, and C will have its B component copy instructions I, insert I into the new automaton A(I), and release this automaton. Define automaton D as the combination of automata A, B, and C, and let J be the instructions that describe D. Place instructions J into component A of D and define the resulting automaton as E. Von Neumann shows that E is self-reproductive.



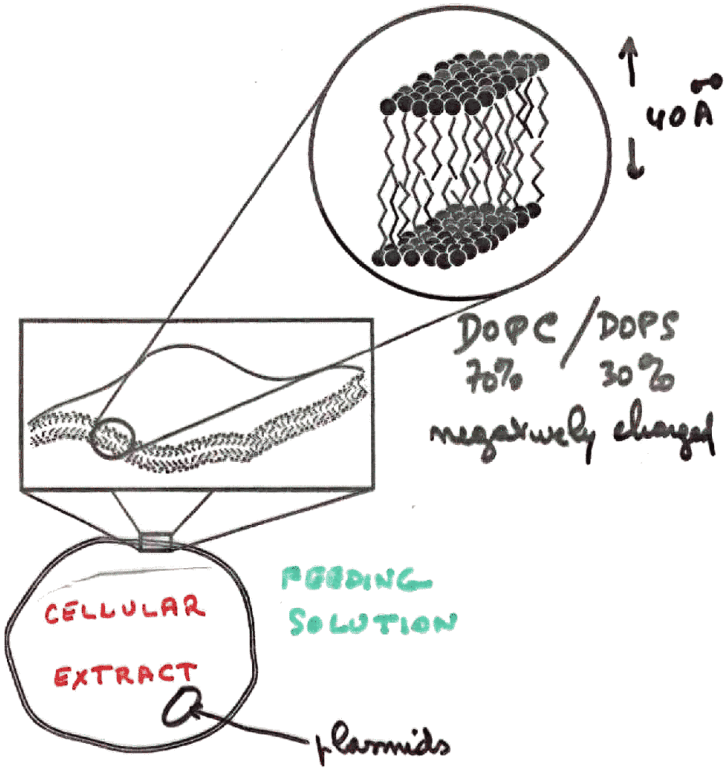
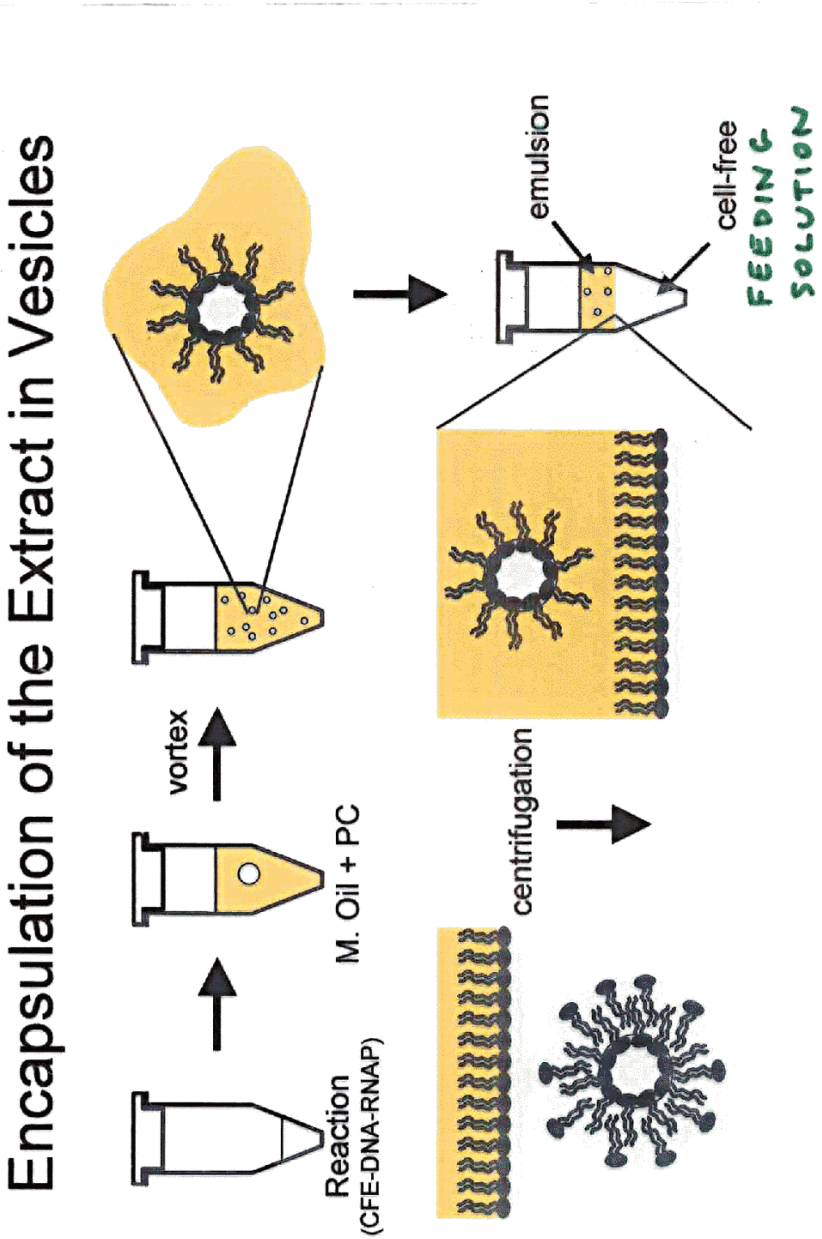


Fig. 5.1. Schematic of the structure of a lipid bilayer membrane. On a scale hundreds or thousands of times larger than its thickness (40Å), the bilayer curves to enclose a finite volume. Within the bilayer itself, the lipid molecules are aligned perpendicular to the plane of the membrane and are disordered (liquid-like) in the plane.

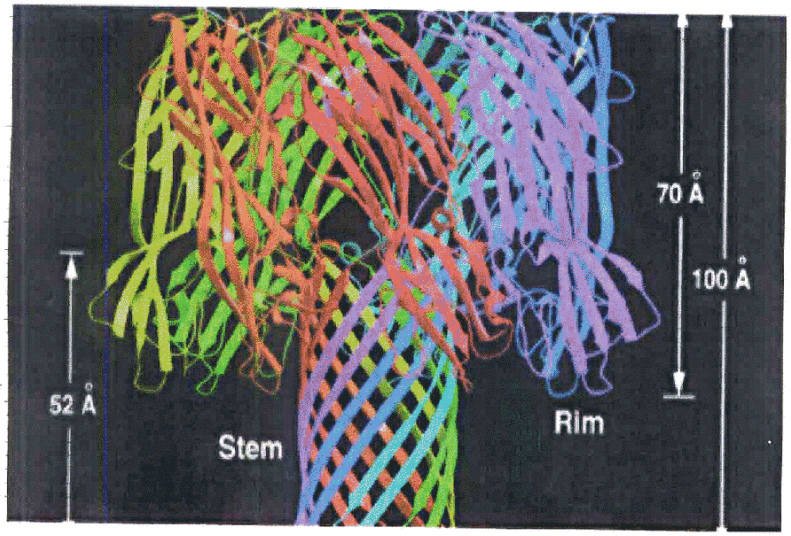


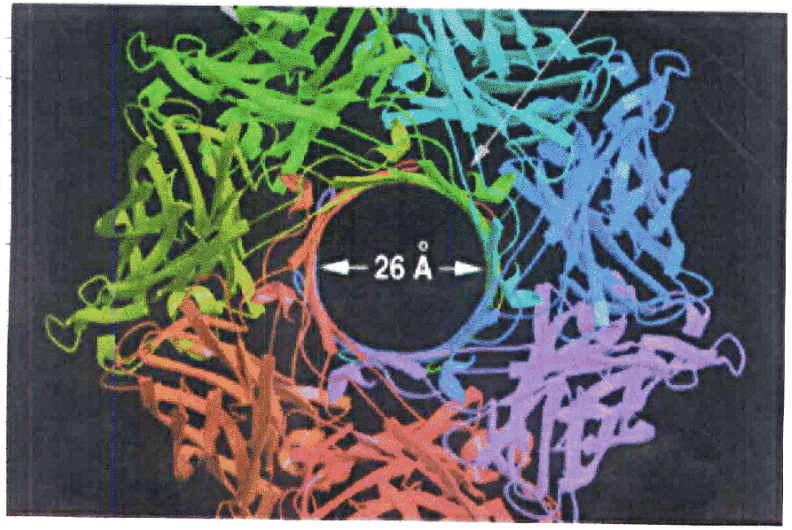
Gene Expression Inside Vesicle

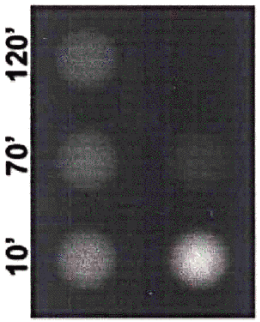
Taupin C. et al, Osmotic pressure induced pores in phospholipid vesicles, Biochem., 1975

α HEMOLYSIN

STAPHYLOCOCCUS AUREUS

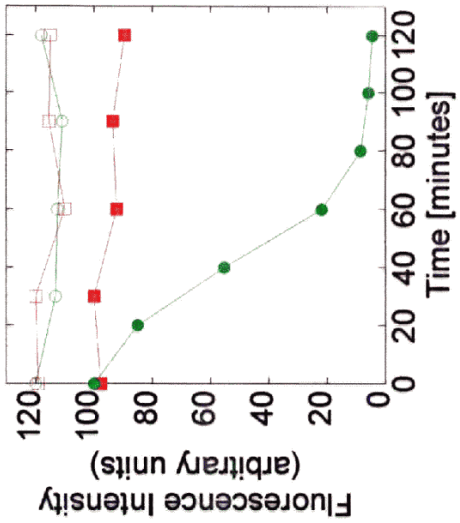


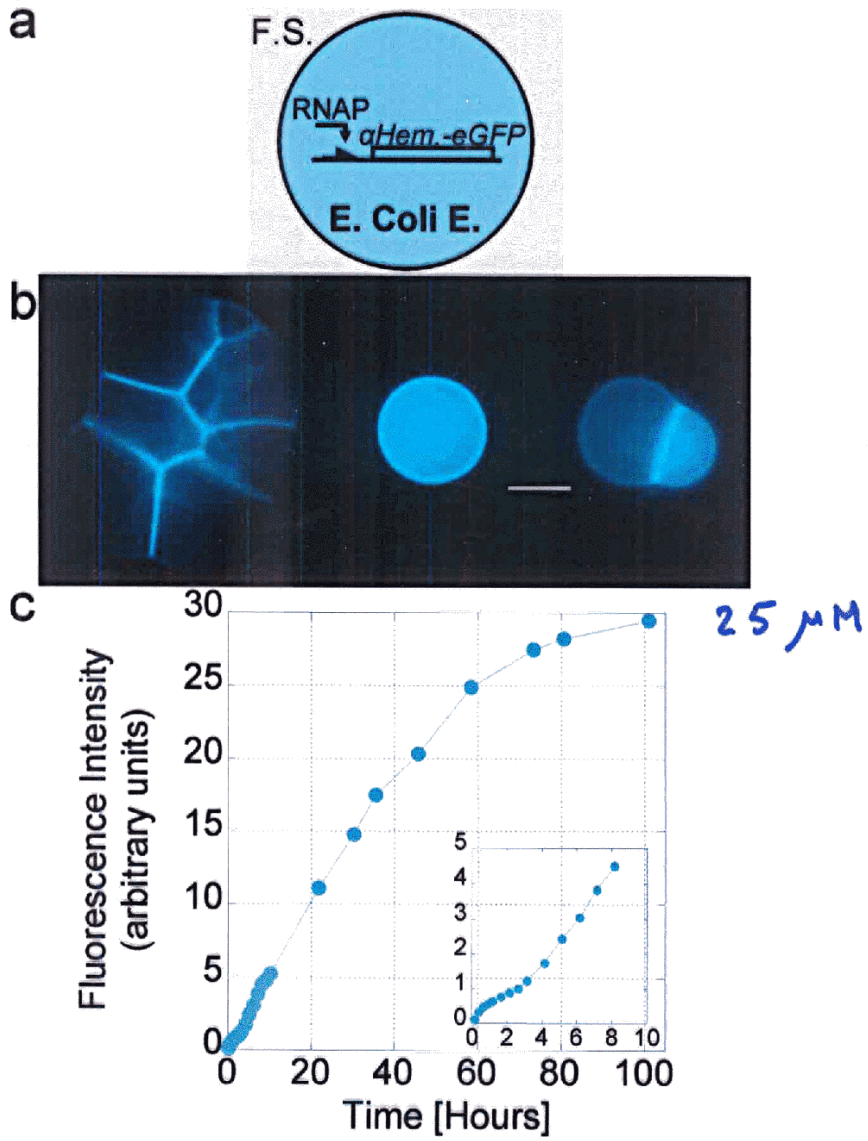




BSA-RITC

Fluorescein-UTP





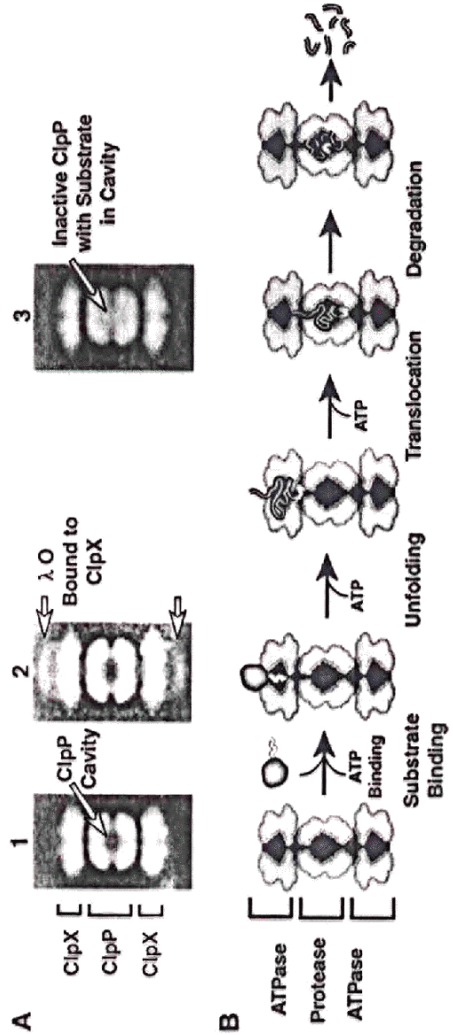


Figure 1 (*A*) Proteolytic cycle: EM images of ClpXP degrading lambda O protein. *Left-most panel*: ClpXP. Complexes with ClpX ATPase on either or both sides of ClpP are active for proteolysis. *Second panel*: Density associated with binding of a substrate (lambda O protein) can be seen at the surface of the ATPase. *Third panel*: After treatment with ATP, in an inactive ClpP derivative, lambda O disappears from the surface and density can be seen inside of ClpP, consistent with translocation. EM photos courtesy of M. Maurizi (Ortega et al. 2000). (*B*) Schematic of Clp protease function. The substrate tags (*yellow*) are recognized by ATPase, leading to substrate binding in the presence of nucleotides. ATP hydrolysis is accompanied by substrate unfolding in the ATPase, followed by translocation to the proteolytic core. Degradation yields short peptides; it is not known how these peptides escape the proteolytic chamber.

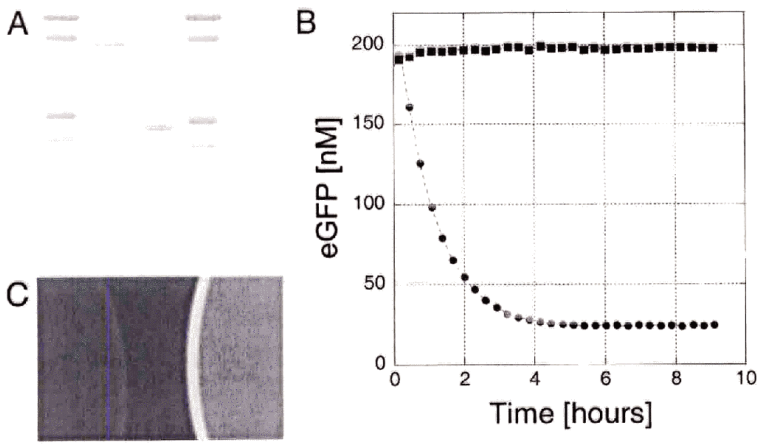
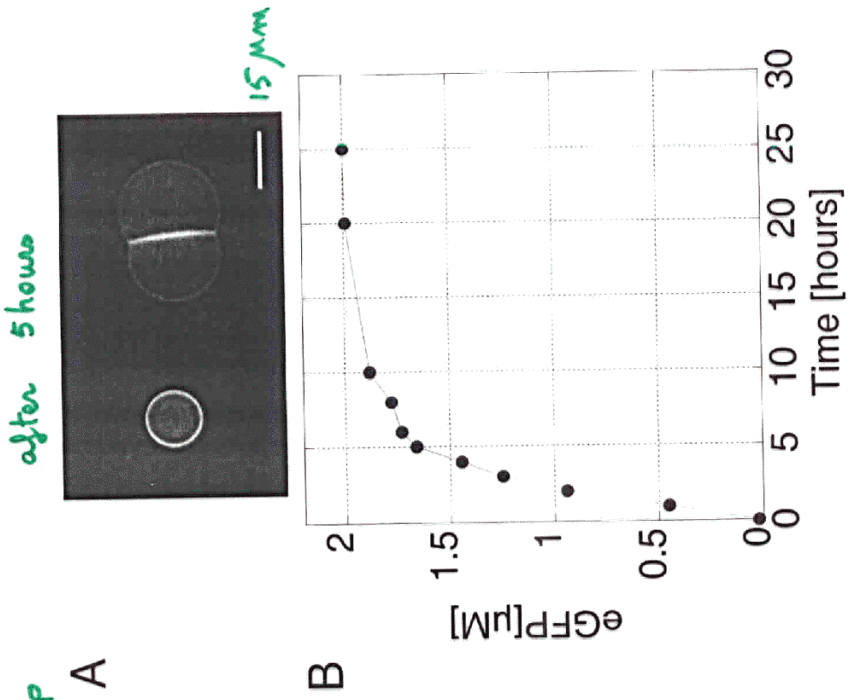


Fig. 5. Specific protein degradation with the ClpXP complex of E. coli. (A) SDS PAGE 15% showing the protein purified. Lane 1 and 4, marker (75, 50, 37, 25, 15 kDa); lane 2, His-ClpX; lane 3, ClpP-His; lane 5, eGFP-ssrA. (B) kinetics of degradation in a buffer of His-eGFP-ssrA (closed circles) and His-eGFP-ssrA/DD (closed squares), with 1.5μM ClpP and 2μM ClpP. (C) Fluorescence images of two droplets on a cover glass after a few hour incubation, left with His-eGFP-ssrA and right with His-eGFP-ssrA/DD.



18L polypeptide - eGFP
& shelly incubating
with the liposomes
A