IS BASIC SCIENCE ESSENTIAL FOR SIGNIFICANT AND FUNDAMENTAL DISCOVERIES?

Lindau NLM 27 June 2018

Michael Levitt

Robert W. & Vivian K. Cahill Professor in Cancer Research, Stanford School of Medicine Structural Biology & Computer Science



- 1. A Biophysical Revolution in Biology.
- 2. Computational Structural Biology.
- 3. Applied Computational Structural Biology
- 4. Young Basic Scientists in the USA.
- 5. Is Basic Science Important?
- 6. How to Win Many Nobel Prizes?

AREVOLUTION IN BIOLOGY

BETWEEN 1950 AND 1960 SCIENTISTS DEFINED MODERN **BIOLOGY AS** PHYSICS

1953: FRANCIS CRICK AND DNA

737

No. 4356 April 25, 1953 NATURE

equipment, and to Dr. G. E. R. Deacon and the captain and officers of R.R.S. Discovery II for their part in making the observations.

Young, F. B., Gerrard, H., and Jerums, W., Poil, Mag., 40, 149 ¹ Longuet Higgins, M. S., Mon. Nol. Roy. Astro. Soc., Geophys. Supp., 5, 285 (1949).

Von Arz, W. S., Wools Hole Papers in Phys. Occaroc. Meteor., 11 (3) (1960).

*Ekman, V. W., Arkin, Mat. Astron. Pyells (Stockholm), 2 (11) (1900).

MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic /

WE wish to suggest a structure for the of deoxyribose nucleic acid (D.N.A.), structure has novel features which are of consider biological interest.

A structure for nucleic acid has already proposed by Pauling and Corey¹. They kindly r their manuscript available to us in advance publication. Their model consists of three twined chains, with the phosphates near the axis, and the bases on the outside. In our opi this structure is unsatisfactory for two reas (1) We believe that the material which gives X-ray diagrams is the salt, not the free acid. Wit the acidic hydrogen atoms it is not clear what f would hold the structure together, especially a regel such other. (2) Some of the van der V distances appear to be too small.

Another three-chain structure has also been gested by Fraser (in the press). In hig mode phosphates are on the outside and the bases or inside, linked together by hydrogen bonds. structure as described is rather ill-defined, and

on it.

We wish to put forwa radically different structur the salt of deoxyribose m seid. This structure has helical chains each coiled r the same axis (soo diagram). have made the usual chemical assumptions, namely, that each chain consists of phosphate diester groups joining β n-deoxy-ribofurences residues with 3',5' linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow righthanded heliece, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions. Each chain toosely resembles Fur-berg's' model No. 1; that is, the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furberg's 'standard configuration'

is a residue on each chain every 3-4 A, in the z-direction. We have assumed an angle of 36° between adjacent residues in the same chain, so that the structure repeats after 10 residues on each chain, that is, after 34 A. The distance of a phosphorus atom from the fibre axis is 10 A. As the phosphates are on the outside, cations have easy access to them.

The structure is an open one, and its water content is rather high. At lower water contents we would expect the bases to tilt so that the structure could become more compact.

The novel feature of the structure is the manner in which the two chains are held together by the 738

King's College, London. One of ns (J. D. W.) has been aided by a fellowship from the National Foundation for Infantile Paralysis. J. D. WATSON

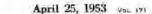
F. H. C. Cater

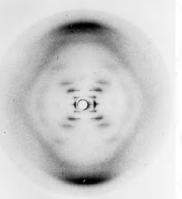
NATURE

Medical Research Council Unit for the Study of the Molecular Structure of Biological Systems.

Cavandish Laboratory, Cambridge. April 2.

¹ Paullag, L., and Corry, R. B., Salars, 171, 346 (1963); Prov. U.S. Net. Acid. 36, 38, 81 (1953). * Furbarg, S., Acta Chem. Scand. 6, 634 (1052).





Plat 1. Place diagram of deoxypentose outleis sold from S. solt. Films axis vertical

innermost maxima of each Bessel function and origin. The angle this line makes with the equator roughly equal to the angle between an element of e helix and the helix axis. If a unit repeats a times ing the helix there will be a meridional reflexion ") on the ath layer line. The holical configuration ochices side bands on this fundamental frequency, o effect' being to reproduce the intensity distribution out the origin around the new origin, on the atla ver line, corresponding to C in Fig. 2. We will now briefly analyse in physical torus some

the effects of the shape and size of the repeat unit nucleotide on the diffraction pattern. First, if the elsotide consists of a unit having circular symmetry out an axis parallel to the helix axis, the whole Bruction pattern is modified by the form factor of e aucleotide. Second, if the nucleotide consists of extine of points on a radius at right-angles to the lix axis, the phases of radiation scattered by the lices of different diameter passing through each int are the same. Summation of the corresponding ead functions gives minforcement for the inne-

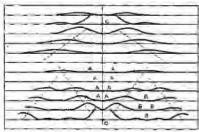


Fig. 3. Diffraction painters of systems of helices corresponding to sorticitize of decaypointoirs nucleicit acid. The squares of Borel immitions size helicit disbut () on the quildes and mn has first, and 20 Å. diamonies and remainder distributed along 5 radius, first many at a size radius tring proportional in the mains. About C on the seath layer line immits functions are global for an outse distributed of the seath second second second second second distributed and the second second second second second second consistent of the second second second second second second distributed second second second second second second distributed second second second second second second second second second distributed second second second second second second second second distributed second secon

structure with axis perallel to fibre longth.

the intensity distribution in the diffraction pattern of a series of points equally speced along a helix is given by the squares of Bessel functions. A uniform continuous helix gives a series of layer lines of spacing corresponding to the helix pitch, the intensity diswibution along the ath layer line being proportional

DNA Model and Experiment

5

©Michael Levitt 18

es a fibre diagram as shown astbury suggested that the corresponded to the interie fibro axis. The ~ 34 A. not due to a repeat of a

on, but to the chain consauses strong diffraction as ve higher density than the interstitial water. The absence of reflexions on or near the meridian immediately suggests a helical

Diffraction by Helices

It may be shown (elso Stokes, unpublished) that

1916-2004

be regarded as unproved against more exact result in the following commun of the details of the rest devised our structure, wh

entirely on published experimental data and storeochemical arguments.

It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material. Full details of the structure, moluding the conditions assumed in building it, together with a set of co-ordinates for the atoms, will be published alsowhere.

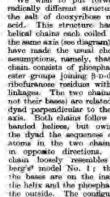
We are much indebted to Dr. Jerry Donohue for constant advice and criticism, especially on interatomic distances. We have also been stimulated by

vibose nucleic acid are in

of our structure. So far

compatible with the exp

this reason we shall not com



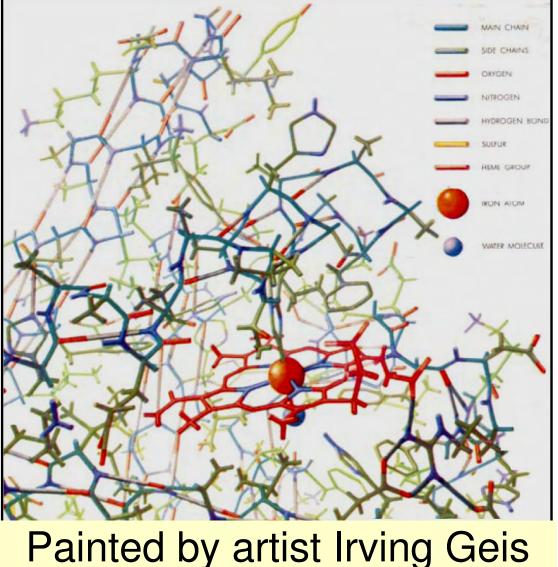
This figure is figure is purely rammatic. The two two phosphate sugar chains, and the bori mutal rods the pairs of bases holding the chains together. The vertical line marks the thre axis sugar being roughly perp cube to the attached base. I

1959: KENDREW AND MYOGLOBIN



First protein X-ray structure.

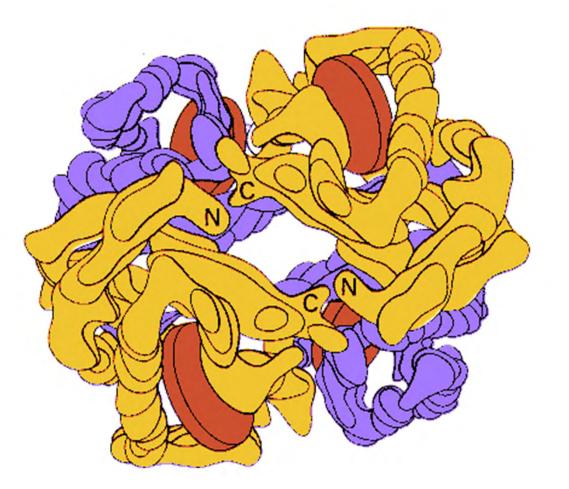
Scientific American 1961



1962: PERUTZ AND HEMOGLOBIN

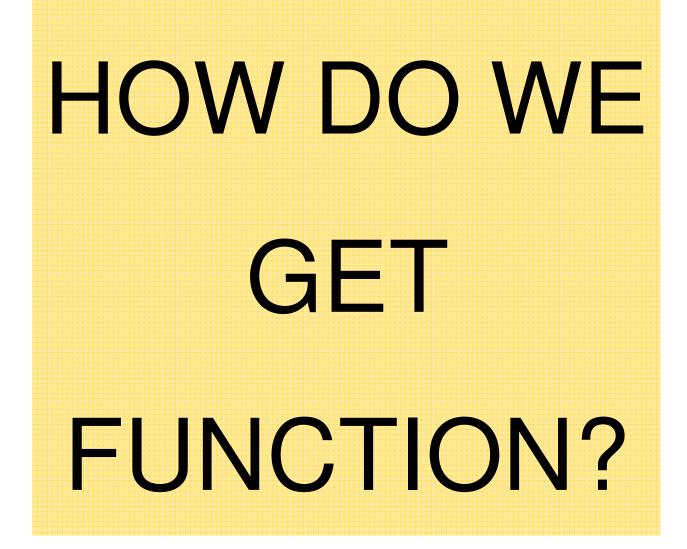


1914-2002



The REAL HERO of structural biology.

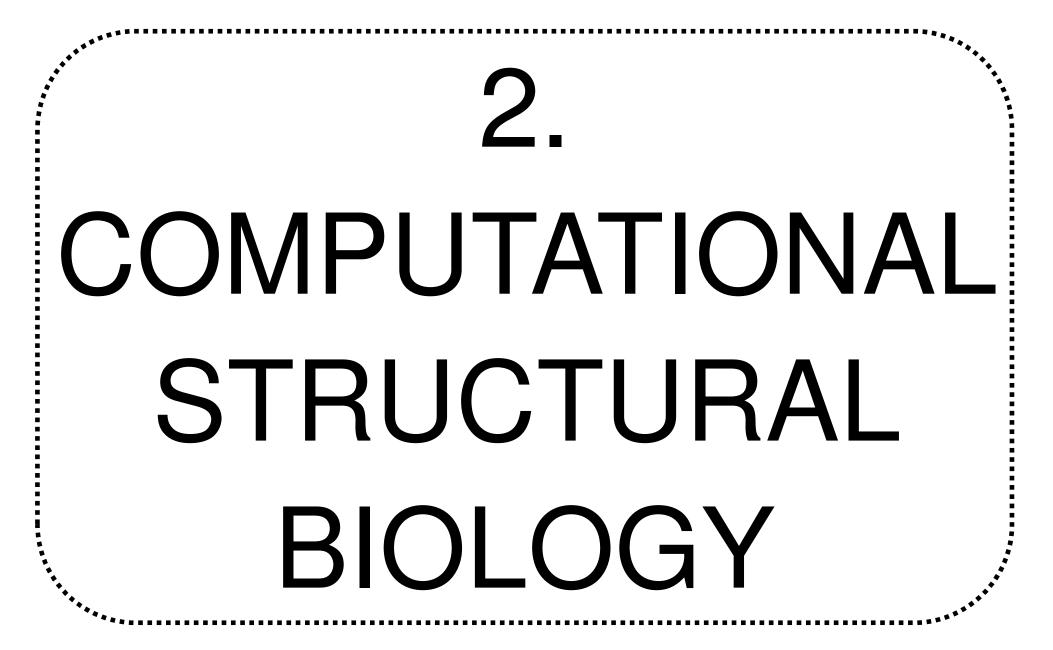
CRYSTALLOGRAPHY GIVES STRUCTURE





\checkmark 1. A Biophysical Revolution in Biology.

- 2. Computational Structural Biology.
- 3. Applied Computational Structural Biology
- 4. Young Basic Scientists in the USA.
- 5. Is Basic Science Important?
- 6. How to Win Many Nobel Prizes?



KENDREW. ME & ISRAEL

See all 41

amazon.com Michael's Books **Product Categories** Amazon.com Drime The Thread of Life: an introduction to

molecular biology. Based on the series of B.B.C. Television Lectures of the same title (Hardcover)

by John C. Kendrew (Author), b/w photos. Illustrated by Diagrams

The Thread of Life: An INTRODUCTION TO **MOLECULAR BIOLOGY**

Episodes (BBC TV Winter 1964)

The REVOLUTION IN BIOLOGY (04/01/1964)

INSIDE THE CELL (11/01/1964)

PROTEINS IN ONE DIMENSION (18/01/1964)

PROTEINS IN THREE DIMENSIONS (25/01/1964)

REPRODUCTION AND GENETICS (01/02/1964)

NUCLEIC ACID The INFORMATION CARRIER (08/02/1964)

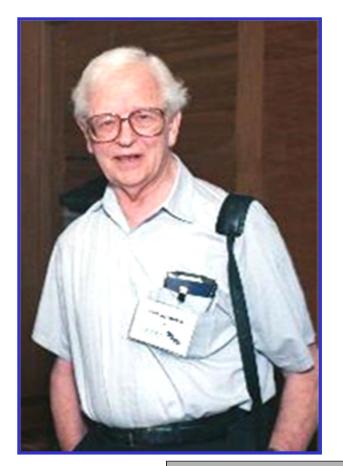
The MESSENGER OF THE GENES (15/02/1964)

SOLVING THE CODE (22/02/1964)

LIVING ARCHITECTURE The VIRUSES (29/02/1964)

The WAY AHEAD (07/03/1964)

Nobel Prize in 1962 Gave BBC Series in 1964 Sent me to Israel in 1967



CONSISTENT FORCE-FIELD 1968Small molecules,



Hydrocarbons, Saturated, -CH₂-



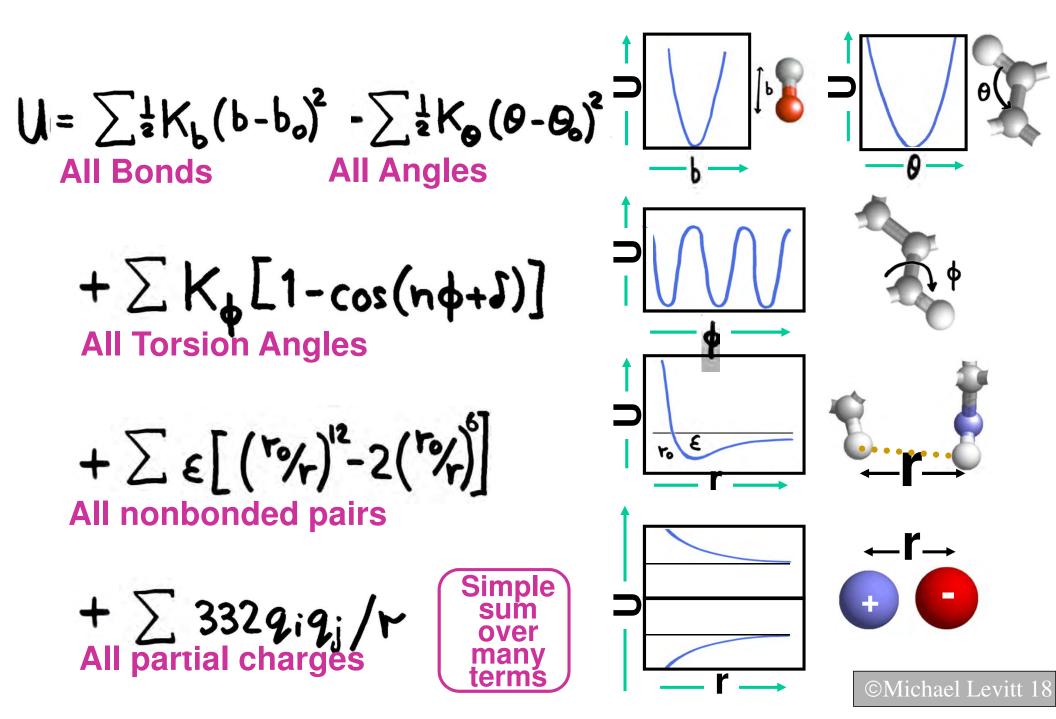
THE JOURNAL OF CHEMICAL PHYSICS VOLUME 49, NUMBER 11 1 DECEMBER 1968

Consistent Force Field for Calculations of Conformations, Vibrational Spectra, and Enthalpies of Cycloalkane and n-Alkane Molecules

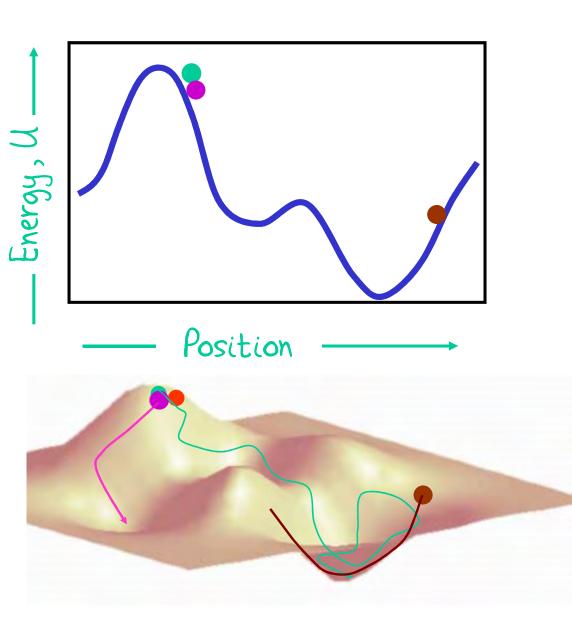
S. LIFSON AND A. WARSHEL

Department of Chemical Physics, Weizmann Institute of Science, Rehovot, Israel (Received 13 May 1968)

MOLECULAR POTENTIAL ENERGY



MOVING OVER ENERGY SURFACE



- EM: Energy Minimization drops into local minimum.
- NMD: Normal Mode Dynamics vibrates about minimum.
- MD: Molecular Dynamics uses thermal energy to move smoothly over surface.



MULTISCALE MODELING OF MACROMOLECULES



EINSTEIN* ON SIMPLIFICATION

"Everything Should Be Made As Simple As It Can Be, But Not Simpler"

*Einstein may have crafted this aphorism, but there is no direct evidence in his writings. He did express a similar idea in a lecture but not concisely. Roger Sessions was a key figure in the propagation of the saying. In fact, he may have crafted it when he attempted to paraphrase an idea imparted by Einstein.

http://quoteinvestigator.com/2011/05/13/einstein-simple/

PROTEIN ENERGY MINIMIZATION

1969



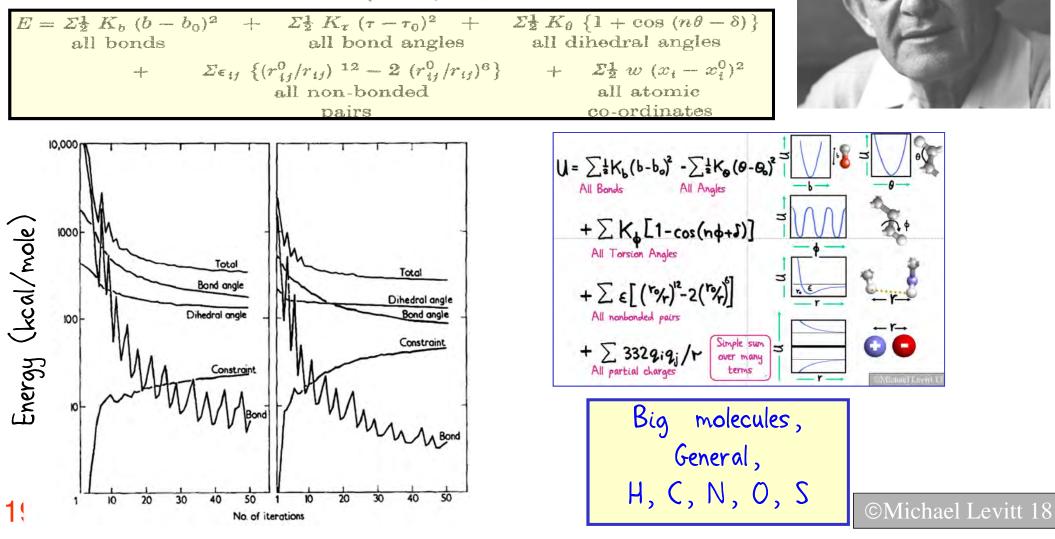
MACROMOLECULAR ENERGY MINIMIZATION

Refinement of Protein Conformations using a Macromolecular Energy Minimization Procedure

MICHAEL LEVITT AND SHNELOR LIFSON

Weizmann Institute of Science

J. Mol. Biol. (1969) 46, 269-279

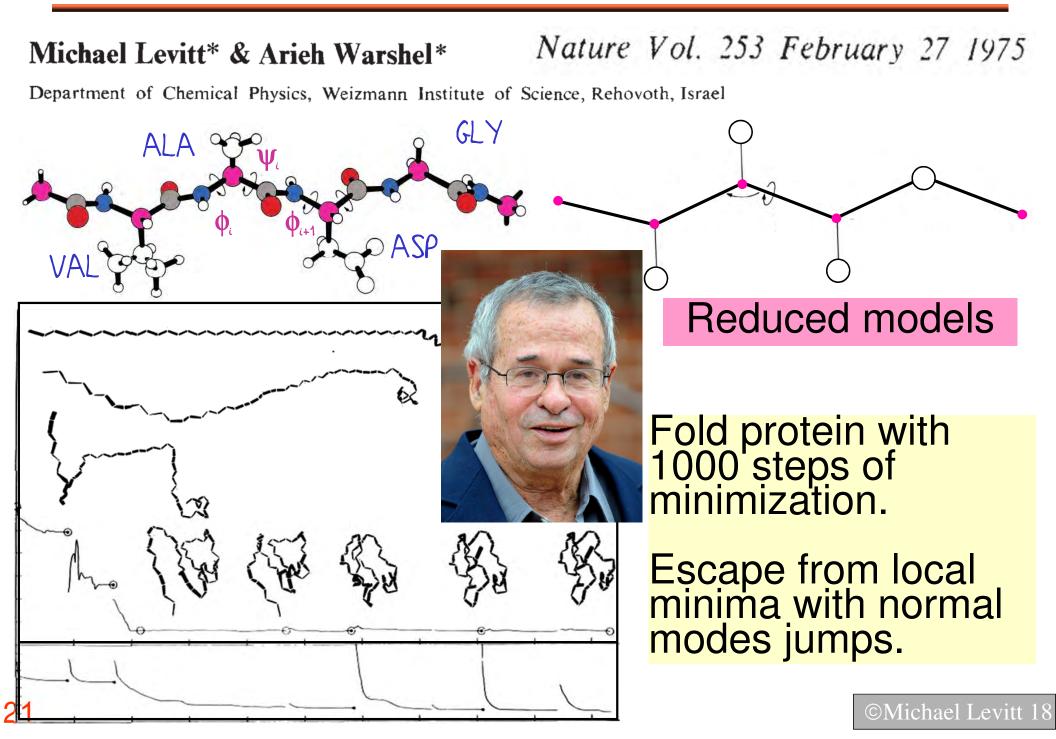


COARSE-GRAINED MODELS

1975



COMPUTER SIMULATION OF PROTEIN FOLDING



QM/MMMODELS FOR CATALYSIS 1976



THEORETICAL STUDIES OF ENZYMIC REACTIONS

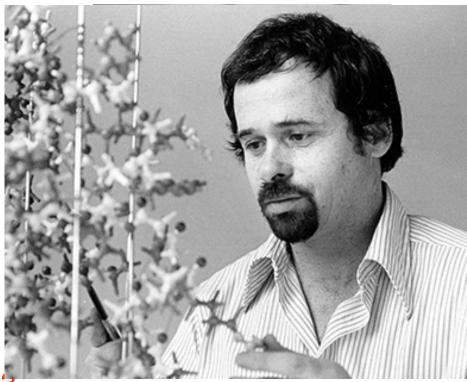
J. Mol. Biol. (1976) 103, 227-249

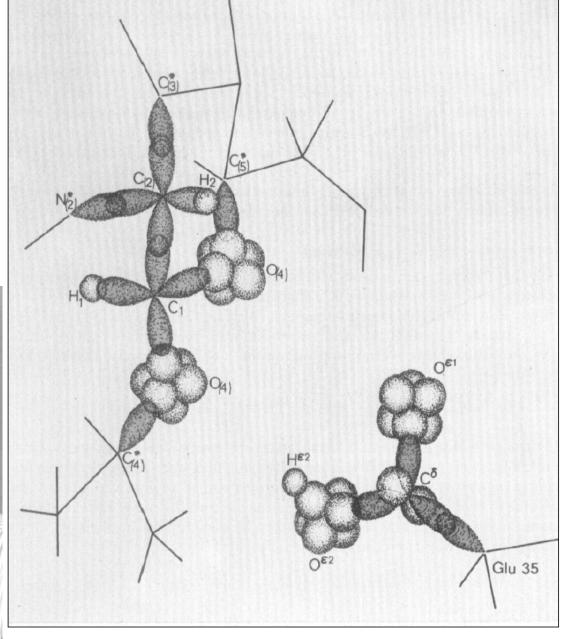
A. WARSHEL AND M. LEVITT

Medical Research Council Laboratory of Molecular Biology Hills Road, Cambridge CB2 2QH, England

and

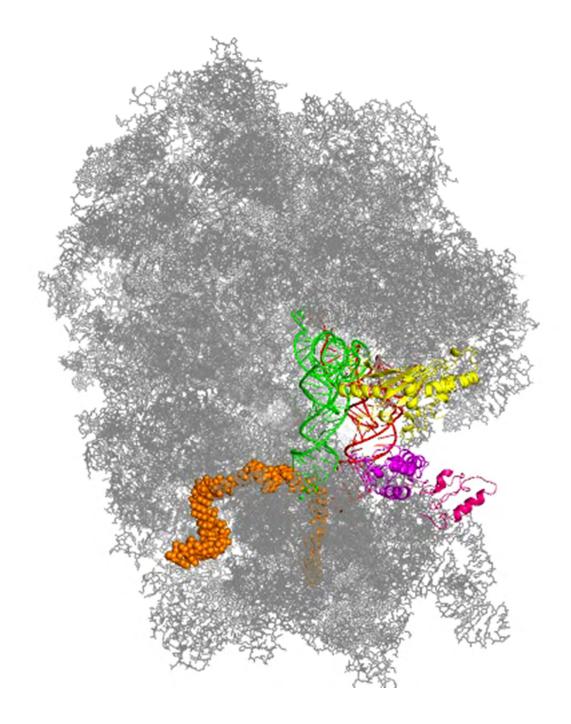
Department of Chemical Physics The Weizmann Institute of Science Rehovot, Israel



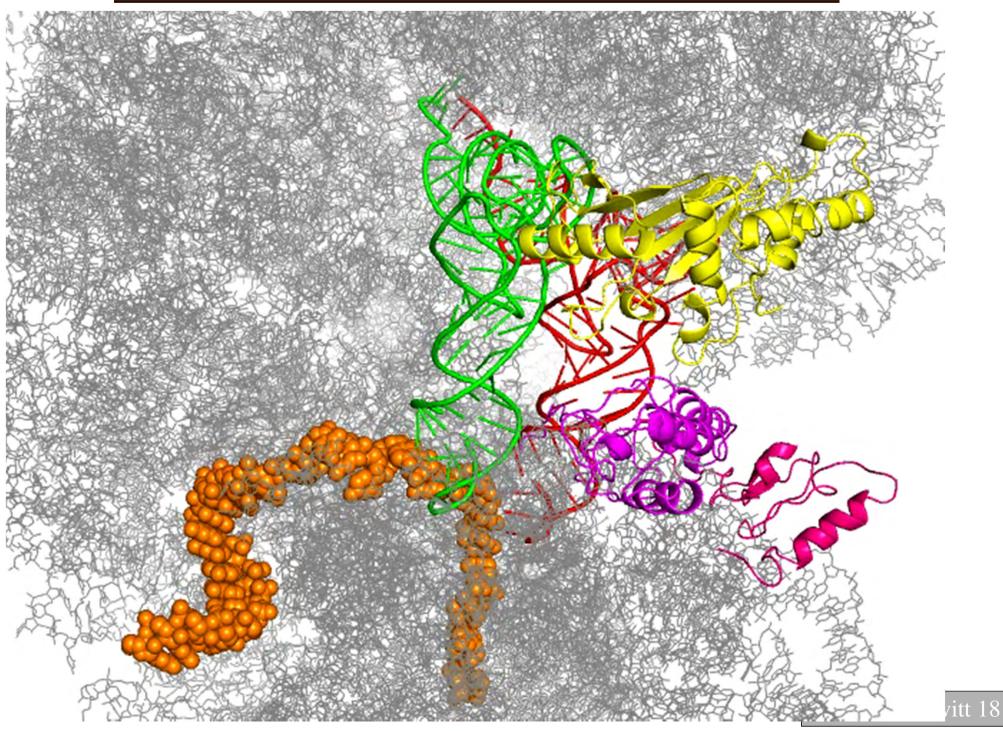


SIMULATING FUNCTIONAL MOTION

RIBOSOME TRANSLOCATION



RIGID BODY MORPHING



MY WORK IS ALL BASIC SCIENCE

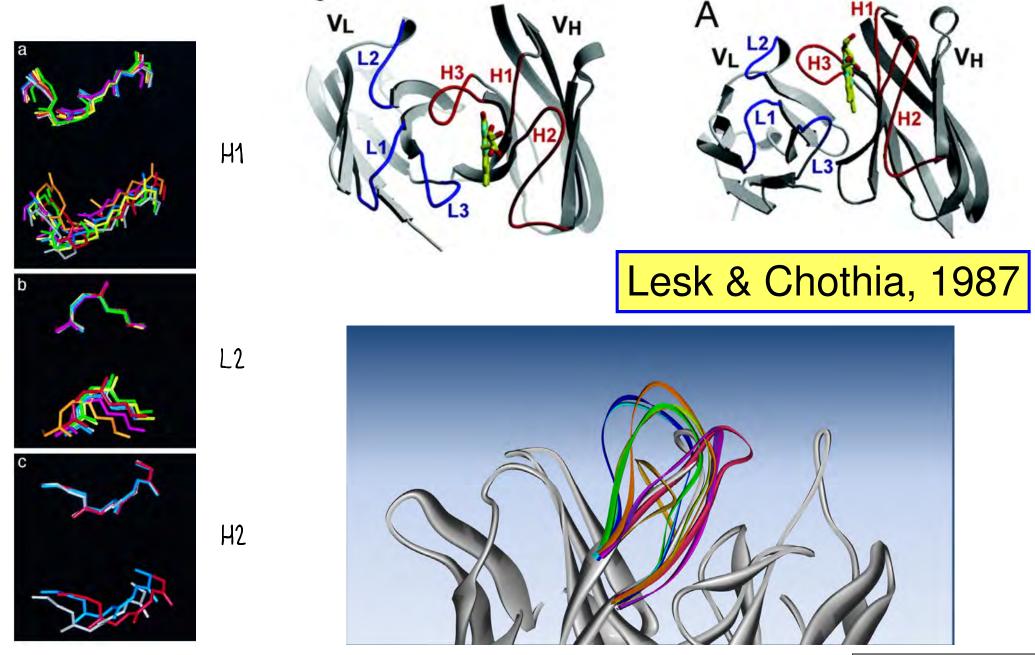
BUTSIT **OF ANY** USE OR VALUE?



- \checkmark 1. A Biophysical Revolution in Biology.
- 2. Computational Structural Biology.
 - 3. Applied Computational Structural Biology
 - 4. Young Basic Scientists in the USA.
 - 5. Is Basic Science Important?
 - 6. How to Win Many Nobel Prizes?

3. APPLIED COMPUTATIONAL STRUCTURAL BIOLOGY

CANONICAL HYPER-VARIABLE REGIONS



<u>QUEEN ET AL 1989</u>

Proc. Natl. Acad. Sci. USA Vol. 86, pp. 10029–10033, December 1989 Immunology

A humanized antibody that binds to the interleukin 2 receptor

(chimeric antibody/antibody affinity/autoimmune disease)

Cary Queen*, William P. Schneider*, Harold E. Selick*[†], Philip W. Payne*, Nicholas F. Landolfi*, James F. Duncan*[‡], Nevenka M. Avdalovic*, Michael Levitt[§], Richard P. Junghans[¶], and Thomas A. Waldmann[¶]

*Protein Design Labs, 3181 Porter Drive, Palo Alto, CA 94304; [§]Department of Cell Biology, Stanford University, Stanford, CA 94305; and [¶]Metabolism Branch, National Cancer Institute, National Institutes of Health, Bethesda, MD 20892

Contributed by Thomas A. Waldmann, August 30, 1989

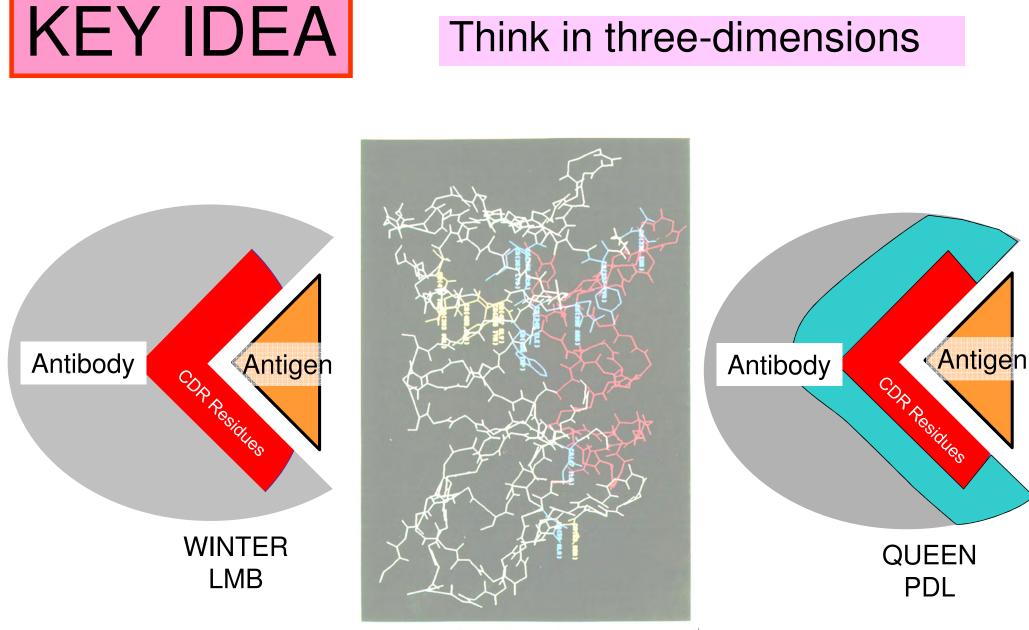
The anti-Tac monoclonal antibody is known ABSTRACT to bind to the p55 chain of the human interleukin 2 receptor and to inhibit proliferation of T cells by blocking interleukin 2 binding. However, use of anti-Tac as an immunosuppressant drug would be impaired by the human immune response against this murine antibody. We have therefore constructed a "humanized" antibody by combining the complementaritydetermining regions (CDRs) of the anti-Tac antibody with human framework and constant regions. The human framework regions were chosen to maximize homology with the anti-Tac antibody sequence. In addition, a computer model of murine anti-Tac was used to identify several amino acids which, while outside the CDRs, are likely to interact with the CDRs or antigen. These mouse amino acids were also retained in the humanized antibody. The humanized anti-Tac antibody has an affinity for p55 of 3×10^9 M⁻¹, about 1/3 that of murine anti-Tac.

partial or complete remission in three of nine patients with Tac-expressing adult T-cell leukemia (14). However, as a murine monoclonal antibody, anti-Tac elicits a strong human antibody response against itself, as does OKT3 (15). This response would prevent its long-term use in treating autoimmune conditions or suppressing organ transplant rejection.

The immune response against a murine monoclonal antibody may potentially be reduced by transforming it into a chimeric antibody. Such antibodies, produced by methods of genetic engineering, combine the variable (V) region binding domain of a mouse (or rat) antibody with human antibody

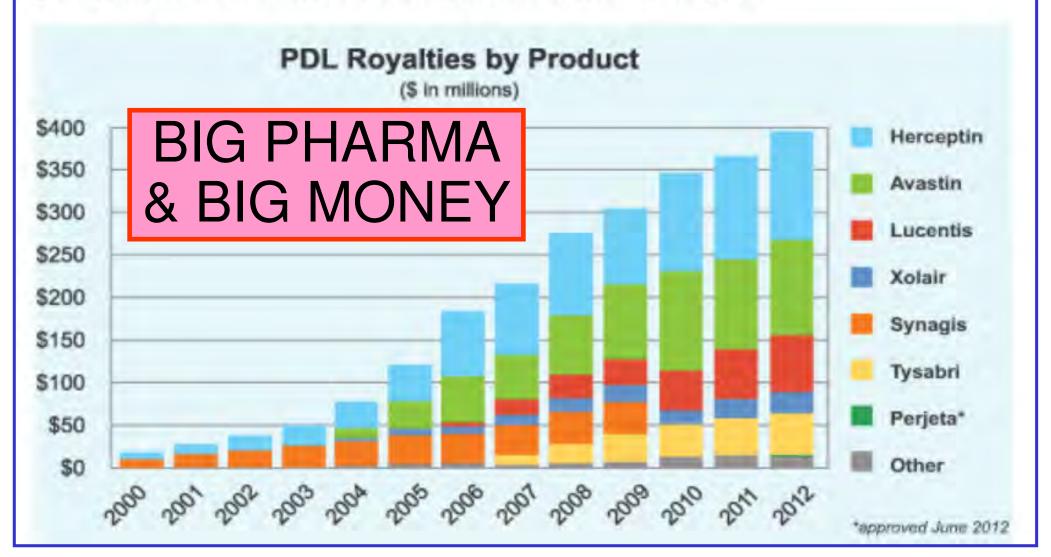


BETTER SCIENCE LED TO BETTER PATENTS



BETTER PATENTS LED TO BETTER DRUGS

Our royalty revenues have grown significantly over the last several years and we expect continued growth before the expiration of our Queen et al patents in December 2014.



I ENJOYED A WONDERFUL LIFE IN BASIC SCIENCE

WHAT ABOUT TODAY'S YOUNG SCIENTIST?

SUMMARY

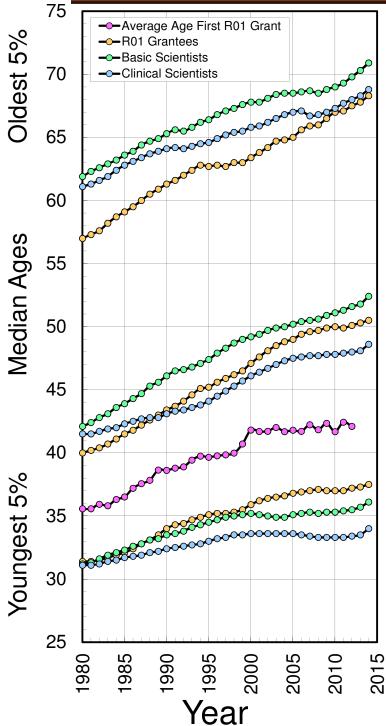
\checkmark 1. A Biophysical Revolution in Biology.

- 2. Computational Structural Biology.
- 3. Applied Computational Structural Biology
 - 4. Young Basic Scientists in the USA.
 - 5. Is Basic Science Important?
 - 6. How to Win Many Nobel Prizes?

4. YOUNG BASIC SCIENTISTS IN THE USA

Levitt, M. and J.M. Levitt. Future of fundamental discovery in US biomedical research. *Proceedings of the National Academy of Sciences*, **114** (25) 6498-6503 (2017).

AGING OF R01 GRANTEES & PIs



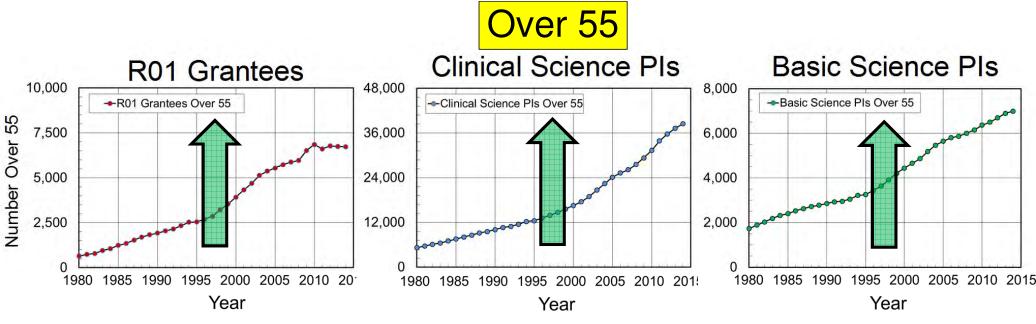
The First-Time PIs are not young;
5 years older than youngest 5%.

All R01 Grantees are aging.

Young Clinical Science PIs age least.Young Basic Science PIs age most.

 Clinical Science PIs aging less than Basic PIs for Median and Oldest 5%.

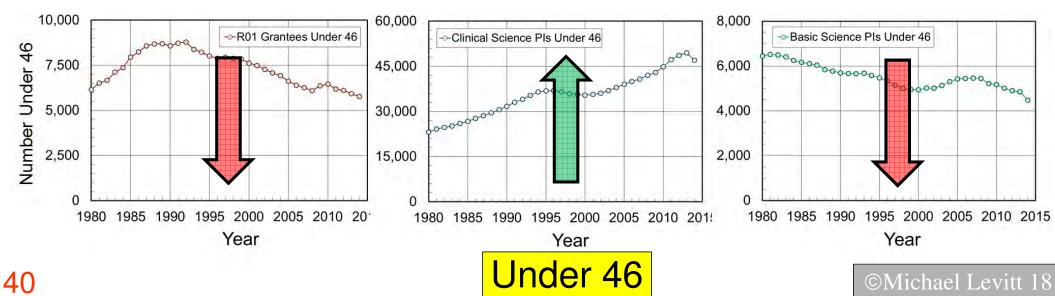
CHANGING NUMBERS IN AGE RANGES



Older Increase Younger Decrease

Older Increase Younger Increase

Older Increase Younger Decrease

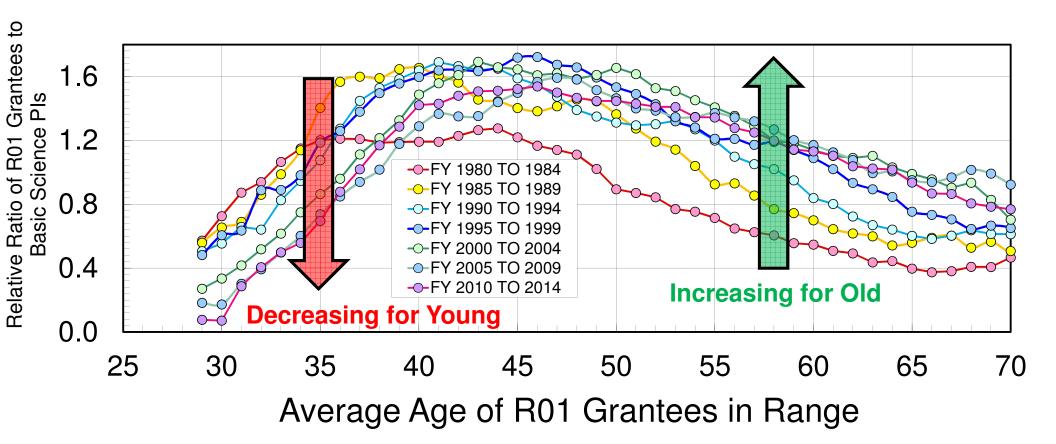


HOW RELATIVE PI SUCCESS RATIO HAS CHANGED

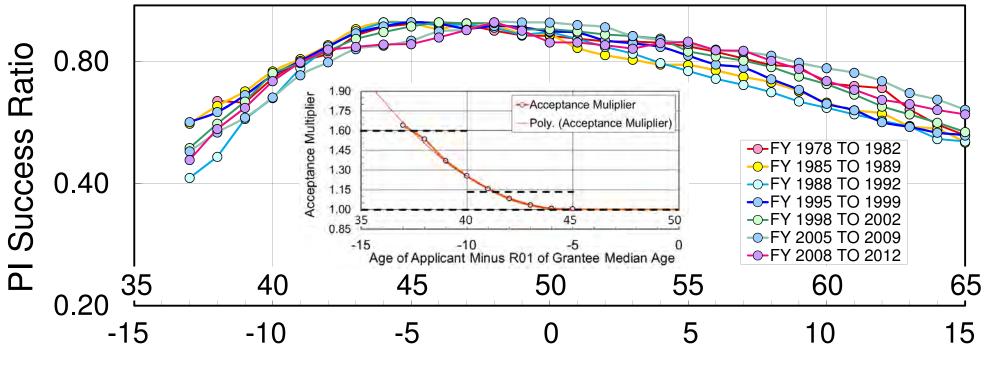
PI Success Ratio = Number of R01 Grantees of Age in Year

Number of Basic Science PIs of Same Age in Same Year

Grantees/Basic Science Pls



PI SUCCESS RATIO DRIVES NUMBER OF PIs



Grantees Age Minus Median R01 Age (40 in 1980, 50 in 2014)

- When a smaller and smaller fraction of PIs under 40 are getting grants, department will hire fewer young PIs.
- When more and more PIs between 50 and 70 are getting grants, departments will keep them on.

THE US BIOMEDICAL ENTERPRISE IS ELIMINATING YOUNG BASIC SCIENTISTS

DOES THIS **REALLY MATTER?** WE CAN APPLY THE IDEAS WE HAVE

SUMMARY

\checkmark 1. A Biophysical Revolution in Biology.

- 2. Computational Structural Biology.
- 3. Applied Computational Structural Biology
- \checkmark 4. Young Basic Scientists in the USA.
 - 5. Is Basic Science Important?
 - 6. How to Win Many Nobel Prizes?

(5) IS BASIC SCIENCE IMPORTANT NATIONALLY?

SERENDIPITY OF BASIC SCIENCE

 Story: "The Three Princes of Serendip" Michele Tramezzino Venice 1557 They were lucky and smart.

Geography: Where is Serendip?



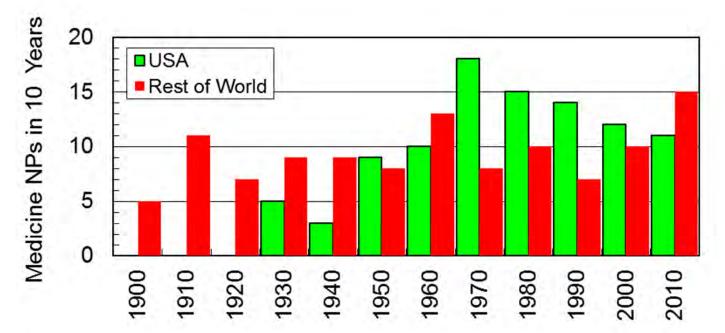


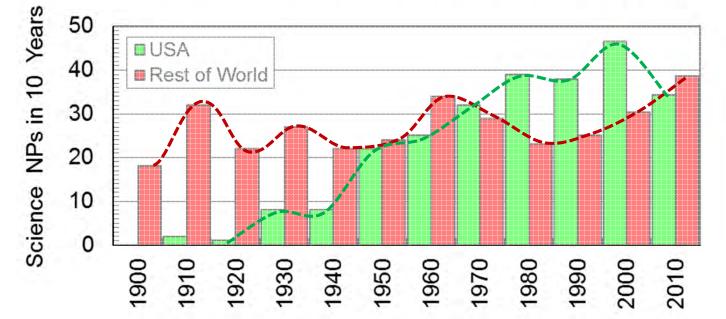
 A scientific discovery is like winning a lottery. Cannot really be planned or predicted. You have to have a ticket. Having more ticket than one ticket helps.

IS BASIC SCIENCE IMPORTANT?

- Very hard to tell who did what in science? Priority is a subject of intense argument and needs to be disentangled with great care. Ambitious scientists often bury the work of others.
- •Not easy to estimate the value of Basic Science without intimate knowledge of the scientific field.
- Take the easy way out and rely on the Nobel Committee.
- They take more care than all other prize committees taken together and have done so for 121 years.

THE USA VS. THE REST OF THE WORLD?





In four of the past five decades, the USA has won more Nobel Prizes than the rest of the world.

In the USA loosing is advantage?

Center of Ten-Year Interval

SCIENTIFIC AMERICAN SEPTEMBER 2015

HOW BIG Manhattan Project \$23,000 million \$27000 million **IS SCIENCE?** (\$2,200 million in 1945) Total cost 1942-1945 THE BOMB MAMMOTH INSTRUMENTS OF SCIENCE SUCH AS CERN'S The Manhattan Project, which developed the first atomic Large Hadron Collider are often held up as symbombs, cost more than \$23 billion bols of the human commitment to decoding the and employed 130,000 people. For better or worse, it became world. But how highly does humanity as a whole a model of what "Big Science" actually regard science? How big is science-all could achieve. of it? This is not an easy question to answer, but by gathering what credible data exist, we can approximate an answer. -The Editors **BRAIN Initiative** 453,544 M\$ US \$300 million+ Federal investment through 2015 Launched in 2013 BRAIN STUDIES Human Brain Project One of the greatest remaining *All country R&D values expressed in \$1,630 million scientific mysteries is how the purchasing parity dollars, a currency conversion Estimated total project costs designed to reflect the varying cost three-pound lumps of meat in 2012-2023 our heads produce consciousof living in different countries ness. Several large, well-funded CN initiatives, including the Human Human Genome

Project

\$4,730 million

Total project costs

1990-2003

100,000

\$471 million

2012-2017

* All project values

converted to

2015 U.S. dollars.

Large Hadron

Collider -

\$5,370 million

Personnel, materials

R&D, tests and preoperation costs

Operational in 2008

JP.

Japan \$148.389 million

148,389 M\$.

GLOBAL SCIENCE

No single data set captures every

dollar spent on scientific research

worldwide, but by looking at R&D

spending by the world's biggest

economies, we can get a sense of

the scale of global research.

243,293 M\$

China

\$243,293 million

2012

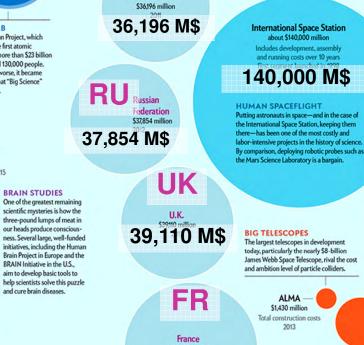
SPENDING

THE GENOME The \$4.7-billion, 13-year Human Genome Project, which in April 2003 finished sequencing the entire human genetic code, was arguably the first true Big Science project in the realm of biology and

medicine. New efforts include the 100,000 Genomes Project, which aims to sequence the full **Genomes Project** genomes of 100,000 U.K. National Health Service patients to search for genetic links to disease. Current investments **Proposed Collider**

> in China They are expensive, enormous \$3,020 million and, for physicists, essential: Estimated construction costs there is no way to test certain Approvals pending theories without replicating the conditions immediately following the big bang. The 27-kilometer Large Hadron European

Collider near Geneva is the world's largest, but China has proposed a collider that, if built, will be almost twice the size. Spallation Source \$2,260 million Projected construction costs Broke ground in 2014 DE



IN

India

27,430 M\$

Brazil \$27,430 million

2011

26,321 M\$

Italy \$26.321 million

2012

24,801 M\$

Canada

\$24,801 million

2012

53,680 M\$

South KR

58,380 M\$

Korea

\$58,380 million

\$19660 million Estimated construction costs Target completion date: 2027

ITER

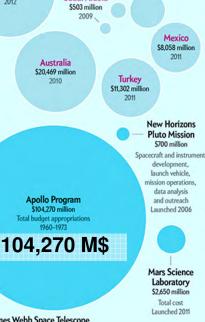
\$2,788 million Worldwide box-office gross Released 2009

Alcoholic bever \$174,314 million

Money spent on alcohol in the U.S. 2013

Graphic by Jen Christiansen, Research by Amanda Hobbi

SUBJECT SUBJECT SUBJECT Specification on result and development by source). THE MARKET NUMBECT THE ARCHITE NOTE CONTROL HERE TO DEVELOP AND PROCEED AN EPARTMENT OF DEFENSE SELECTED ACQUINTION REPORTS (SARS) (AS OF DECEMBER 20. 2040," BY U.S. DEPARTMENT OF DEFENSE, MARCH 19. 2015 (F.



STATE OF THE WORLD'S SCIENCE

South Africa

\$3,986 million

2010

BIG SCIENCE, BIG CHALLENGES

Indonesia

\$795 million

2009

Saudi Arabia

Australia

\$20,469 million

2010

\$104,270 million

1960-1973

James Webb Space Telescope \$7,998 million NASA's cost to build, launch and commission

Target launch date: 2018

BIG ENERGY

Humanity's greatest problem-powering civilization without destroying the planet-is urgent enough to justify massive undertakings such as ITER, a collaboration among China, the European Union, India, Japan, South Korea, Russia and the U.S. Once completed, ITER will be the biggest fusion reactor ever built.

F-35 (fighter jet)

\$391,100 million Program cost for a total of 2,457 planes as of December 31, 2014

USEFUL PERSPECTIVE Even at the highest levels. spending on science is dwarfed

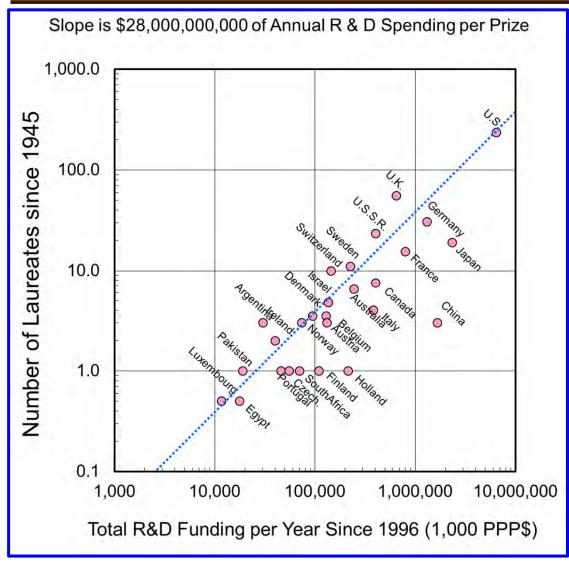
by consumer expenditures and military budgets. For example \$2.65 billion for the Mars Science Laboratory sounds like a lot of money-and it is-but it is still less than the worldwide box-office gross for the film Avatar. The F-35 Lightning II provides perhaps the ultimate point of reference; the stealthy fifth-generation fighter cost some \$391 billion to develop

Germany \$100,248 million 100,248 M\$

PARTICLE COLLIDERS

510

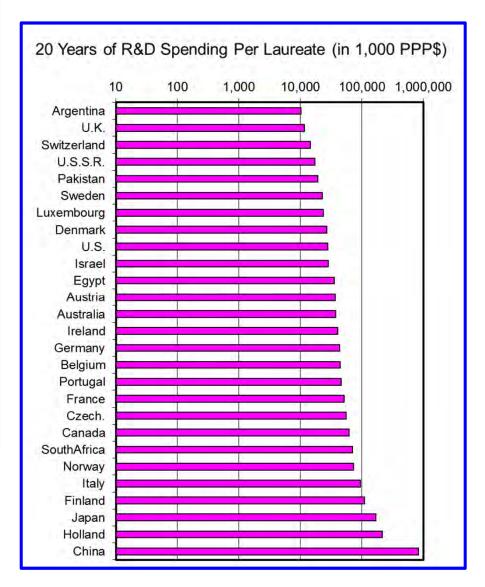
MORE R&D SPENDING GIVES MORE NOBEL PRIZES



Cost per laureate in PPP\$ Billions:

US:	28 B\$	UK:	13 B\$
Germany:	66 B\$	Holland:	214 B\$
Japan:	168 B\$	China:	840 B\$

Linear dependence on R&D spending over range of 10,000×



SUMMARY

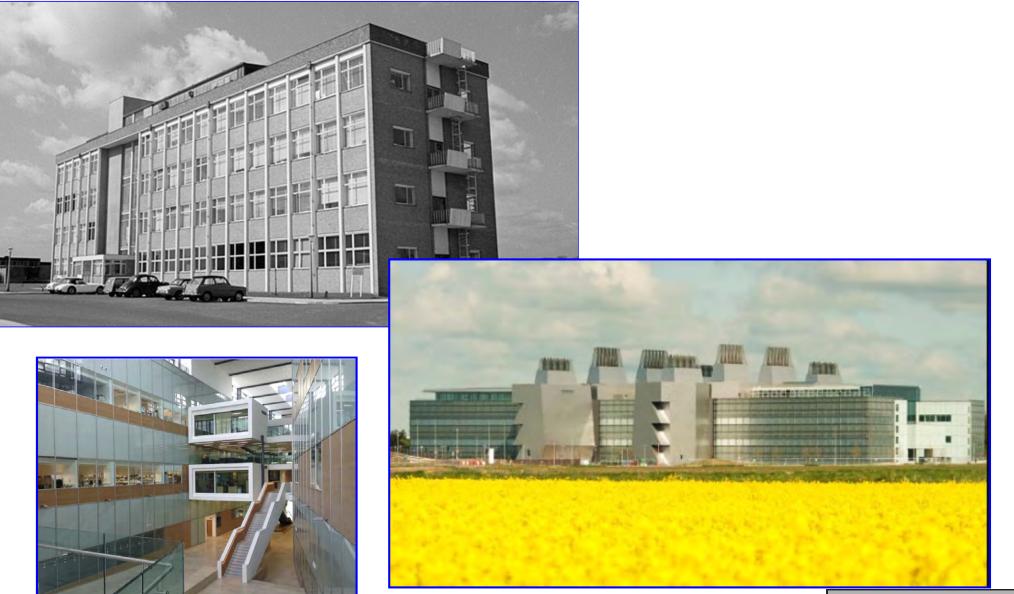
\checkmark 1. A Biophysical Revolution in Biology.

- 2. Computational Structural Biology.
- 3. Applied Computational Structural Biology
- \checkmark 4. Young Basic Scientists in the USA.
- √5. Is Basic Science Important?
 - 6. How to Win Many Nobel Prizes?

QUALITY BASIC SCIENTIFIC **RESEARCH NEEDS MONEY AND FULL-**TIME RESEARCH COMMITMENT

(6) HOW TO WIN MANY NOBEL PRIZES

MEDICAL RESEARCH COUNCIL LABORATORY OF MOLECULAR BIOLOGY (LMB) IN CAMBRIDGE



27 LMB NOBEL PRIZES

1958	Fred Sanger	Chemistry	Determination of the Structure of the Insulin Molecule	
1962	Francis Crick	Medicine	Discoveries Concerning the Molecular Structure of DNA	
1962	Jim Watson	Medicine	Discoveries Concerning the Molecular Structure of DNA	
1962	John Kendrew	Chemistry	Determination of the Structure of Hemoproteins	
1962	Max Perutz	Chemistry	Determination of the Structure of Hemoproteins	
1980	Fred Sanger	Chemistry	Development of Chemical and Biological Analyses of DNA Structure	
1982	Aaron Klug	Chemistry	Determination of the Structure of Biological Substances	
1984	César Milstein	Medicine	Theory and Development of a Technique for Producing Monoclonal Antibodies	
1984	Georges Köhler	Medicine	Theory and Development of a Technique for Producing Monoclonal Antibodies	
1989	Sidney Altman	Chemistry	Discovery of Certain Basic Properties of RNA	
1993	Michael Smith	Chemistry	Invention of Techniques for Gene Study and Manipulation	
1993	Richard Roberts	Medicine	Discovery of Split, or Interrupted, Genetic Structure	
1997	John Walker	Chemistry	Explanation of the Enzymatic Conversion of Adenosine Triphosphate	
2002	Bob Horvitz	Medicine	Discoveries Concerning Genetic Regulation of Organ Development and Programmed Cell Death	
2002	John Sulston	Medicine	Discoveries Concerning Genetic Regulation of Organ Development and Programmed Cell Death	
2002	Sydney Brenner	Medicine	Discoveries Concerning Genetic Regulation of Organ Development and Programmed Cell Death	
2006	Andrew Fire	Medicine	Discovery of RNA Interference—Gene Silencing by Double-Stranded RNA	
2006	Roger Kornberg	Chemistry	Work Concerning the Molecular Basis of Eukaryotic Transcription	
2008	Martin Chalfie	Chemistry	Discovery and Development of the Green Fluorescent Protein, GFP	
2009	Elizabeth Blackburn	Medicine	Discovery of How Chromosomes Are Protected by Telomeres and the Enzyme Telomerase	
2009	Tom Steitz	Chemistry	Studies of the Structure and Function of the Ribosome	
2009	Venki Ramakrishnan	Chemistry	Studies of the Structure and Function of the Ribosome	
2012	John Gurdon	Medicine	Discovery that Mature Cells Can be Reprogrammed to Become Pluripotent	
2013	Arieh Warshel	Chemistry	Development of Multiscale Models for Complex Chemical Systems	
2013	Martin Karplus	Chemistry	Development of Multiscale Models for Complex Chemical Systems	
2013	Michael Levitt	Chemistry	Development of Multiscale Models for Complex Chemical Systems	
2017	Richard Henderson	Chemistry	Developing cryo-electron microscopy for the high-resolution structure determination of biomolecules	
(1) Green from Southern Hemisphere				
57				

Light Yellow from USA

A RECIPE FOR NOBEL PRIZES

(1) Ample research support.

- (2) No visible bureaucracy (hidden from us by leader):
 - Free supplies, advanced equipment, computing.
- (3) Small groups (average three, often one).
- (4) Collaborate with peers
- (5) Intense peer pressure:

You are only as good as your next paper.

(6) No hierarchy: Students are as good as Nobel Laureates.

<u>QUESTIONS</u>

- 1. Does my life path generalize?
- 2. What does it take to be a scientist? **PPOK** Passion Persistence Originality Kindness
- 3. How are young scientists best encouraged? Independence or Collaboration? Teams or Stars?
- 4. Is universal fundamental research needed?
- 5. Should scientists be entrepreneurs?
- 6. Are Nobel Prizes important?

