



# Chemische Aspekte der Evolution

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Gesellschaft der Freunde der ÖAW

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Web-Page für weitere Informationen:

<http://www.tbi.univie.ac.at/~pks>

„Nothing in biology makes sense except in  
the light of Evolution.“



Theodosius Dobzhansky, 1900-1975

„Alles Leben ist Chemie“



Hermann F. Mark, 1895-1992



1. Historischer Weg zur Evolutionstheorie
2. Molekülstruktur in Chemie und Biologie
3. Autokatalyse und Vermehrung von Molekülen
4. Reaktionskinetik und Evolution von Molekülen
5. Molekulare Information als eine Domäne der Biologie
6. Sequenzanalyse und Darwins "Baum des Lebens"
7. Evolutionäres Basteln und die Komplexität der Biologie
8. Molekularbiologie im 21. Jahrhundert

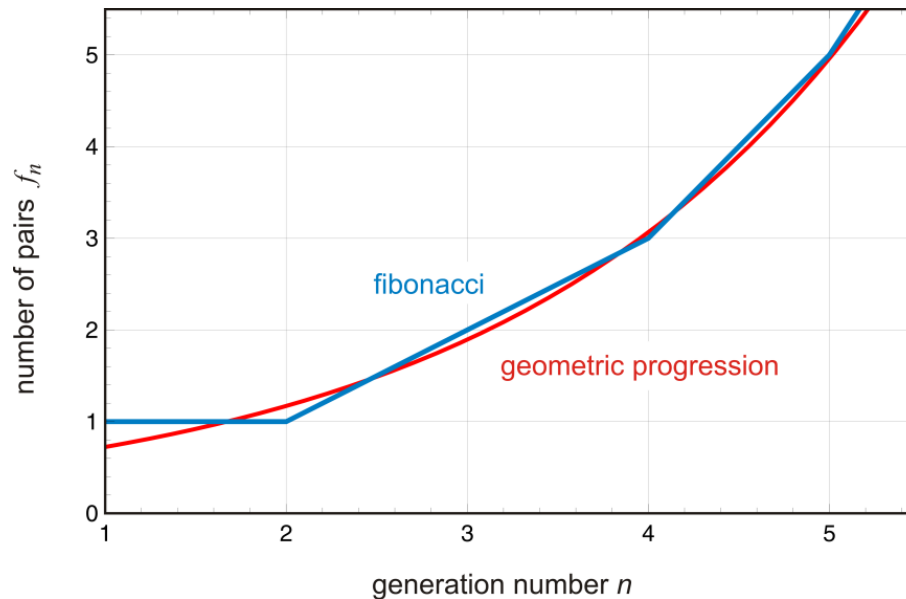
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Thomas Robert Malthus,  
1766 – 1834

2 → 4 → 8 → 16 → 32 → 64 → 128 → 256 → 512 → 1024 →

**geometric progression**



Leonardo da Pisa  
„Fibonacci“  
~1180 – ~1240



Thomas Robert Malthus,  
1766 – 1834

Population, when unchecked, increases in a **geometrical** ratio. Subsistence increases only in an **arithmetical** ratio. A slight acquaintance with numbers will shew the immensity of the first power in comparison of the second.

T.R. Malthus. Essay on the Principle of Populations.  
John Murray: London, 1798.

Das Vermögen des Bevölkerungswachstums ist viel größer als die Fähigkeiten der Erde, Nahrungsmittel für die Menschen zu produzieren. Das ungehinderte Bevölkerungswachstum nimmt in **geometrischer**, die Nahrungsmittelproduktion in **arithmetischer** Rate zu ...

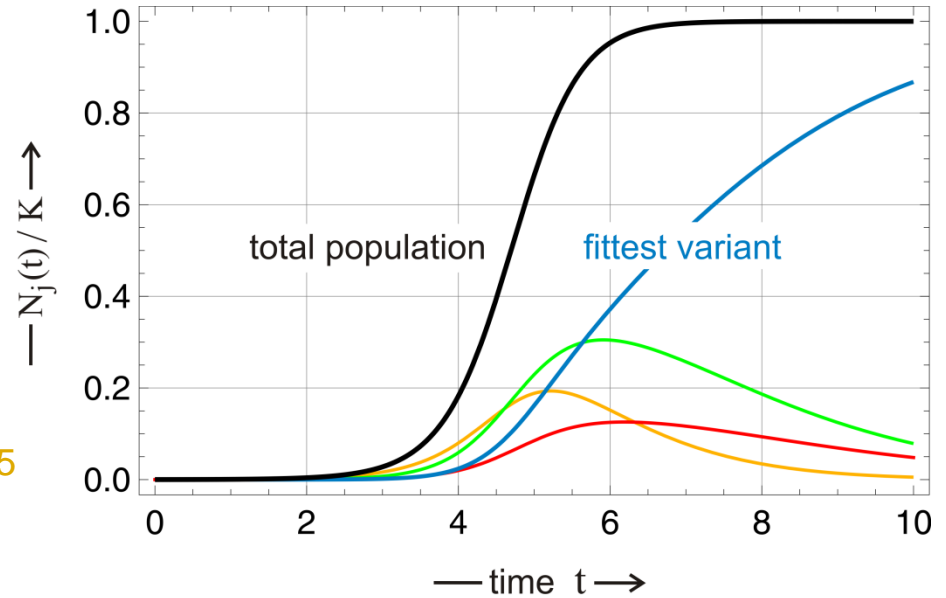
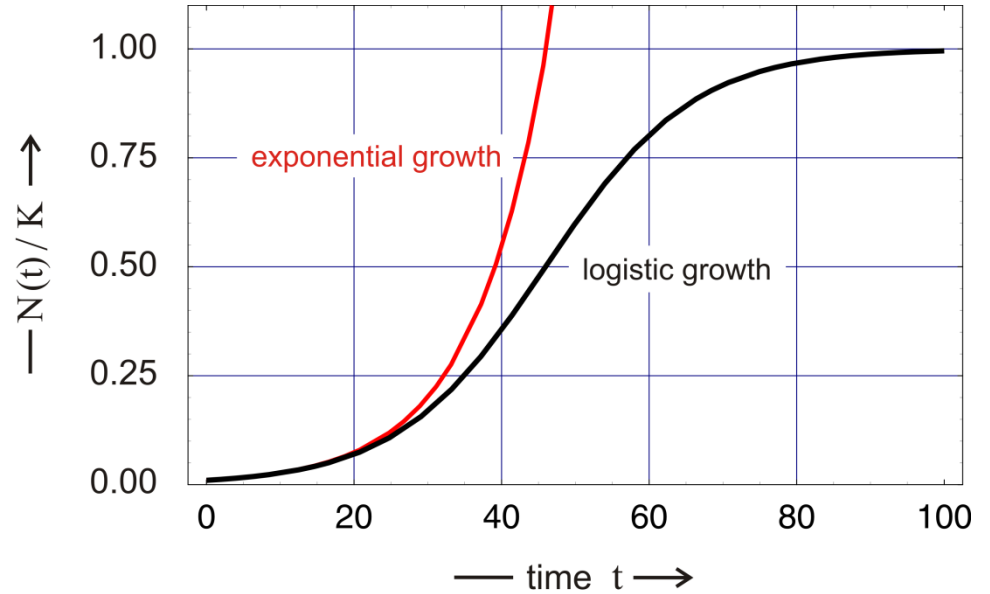


Pierre-François Verhulst,  
1804-1849

the consequence of finite resources

fitness values:

$$f_1 = 2.80, f_2 = 2.35, f_3 = 2.25, \text{ and } f_4 = 1.75$$



The logistic equation, 1828

P. Schuster. Theory Biosciences 130:71-89, 2011

## Die fünf Darwinschen Thesen:

1. **Evolution** verstanden als Abstammung mit Modifikation ist ein realhistorischer Prozess der stattgefunden hat und andauert.
2. **Gemeinsame Abstammung** aller Organismen auf der Erde.
3. **Gradualismus**, das Konzept des sich in kleinen Schritten vollziehenden Artenwandels.
4. **Diversifizierung der Lebensformen** im Verlaufe von Generationen.
5. **Natürliche Selektion**. Zuchtwahl der freien Natur.

Nach Ulrich Kutschera. 2009. Tatsache Evolution.  
Was Darwin nicht wissen konnte.  
DTV: München.

Natürliche Selektion

Darwin und Wallace, 1859

Sexuelle Vermehrung,  
Keimbahn und Soma

Weismann, 1892

Vererbungslehre  
(Genetik)

Mendel, 1866

Sexuelle Vermehrung,  
Keimbahn und Soma

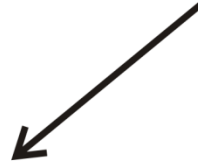
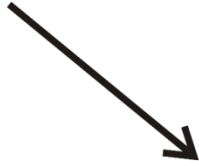
Vererbungslehre  
(Genetik)

Weismann, 1892

Mendel, 1866

Natürliche Selektion

Darwin und Wallace, 1859



Neo-Darwinsche Evolutionstheorie



Sexuelle Vermehrung,  
Keimbahn und Soma

Vererbungslehre  
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Natürliche Selektion

Weismann, 1892

Mendel, 1866

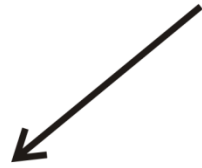
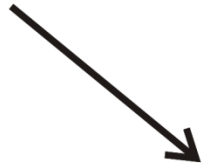
Darwin und Wallace, 1859

Neo-Darwinsche Evolutionstheorie

Biometrie

X

Genetik



Sexuelle Vermehrung,  
Keimbahn und Soma

Vererbungslehre  
(Genetik)

Natürliche Selektion

Weismann, 1892

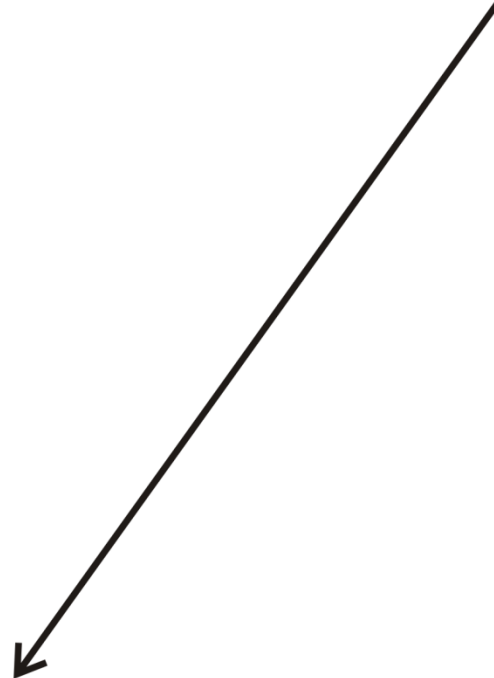
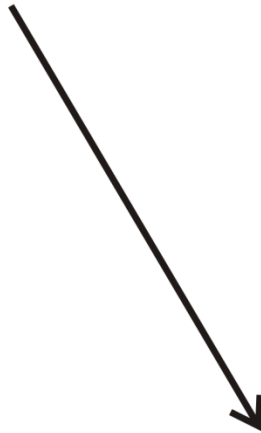
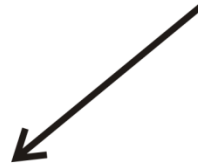
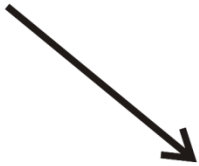
Mendel, 1866

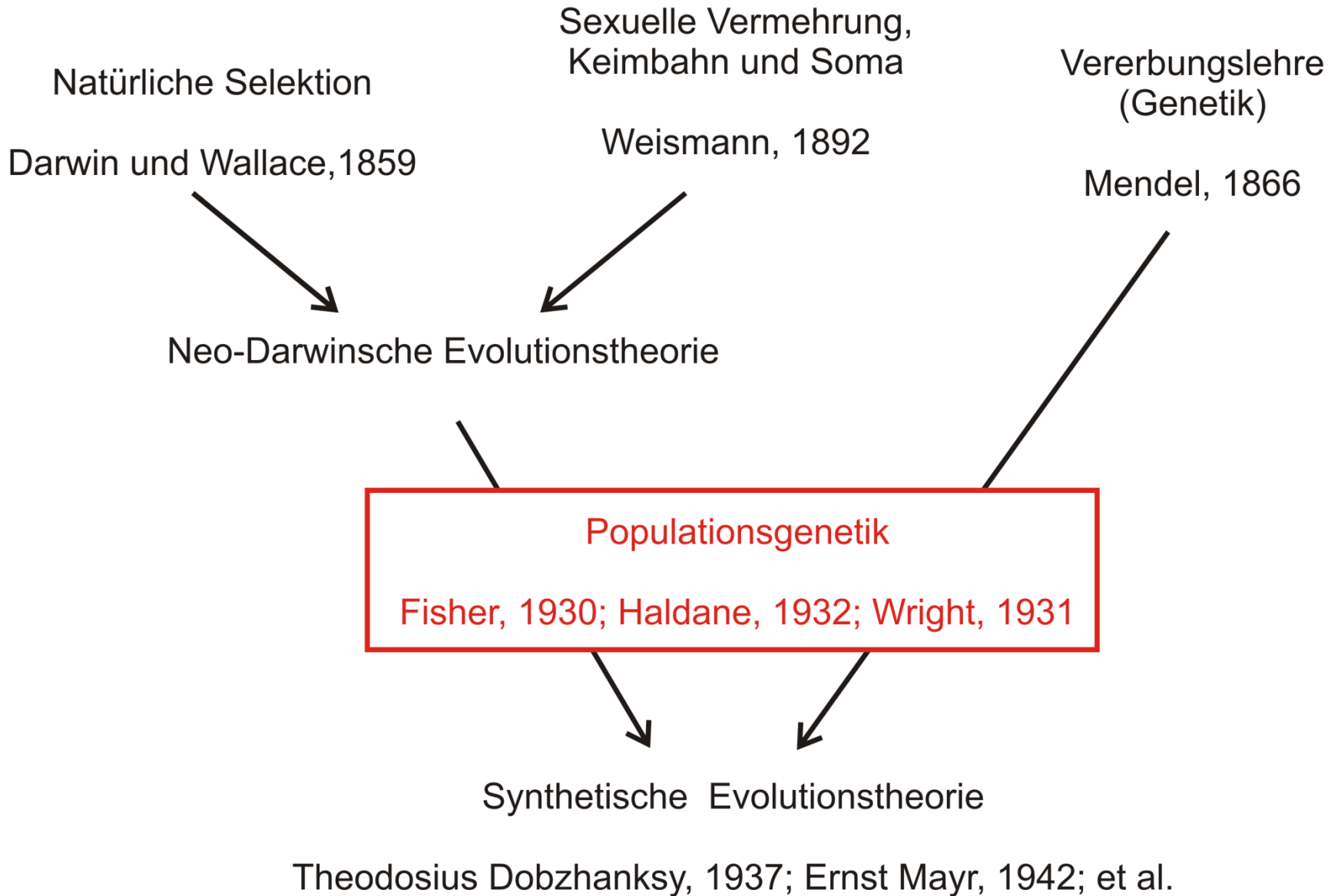
Darwin und Wallace, 1859

Neo-Darwinsche Evolutionstheorie

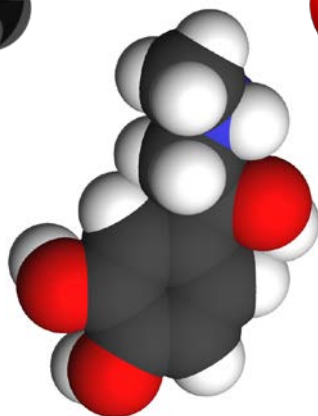
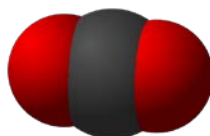
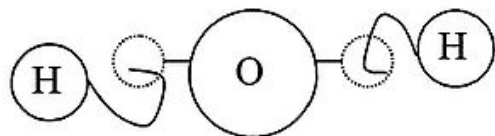
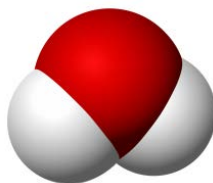
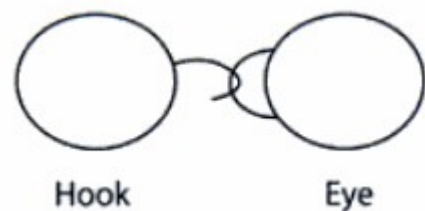
Synthetische Evolutionstheorie

Theodosius Dobzhansky, 1937; Ernst Mayr, 1942; et al.





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THE NATURE OF THE CHEMICAL BOND.  
APPLICATION OF RESULTS OBTAINED FROM THE  
QUANTUM MECHANICS AND FROM A THEORY OF  
PARAMAGNETIC SUSCEPTIBILITY TO THE STRUCTURE  
OF MOLECULES

BY LINUS PAULING

RECEIVED FEBRUARY 17, 1931

PUBLISHED APRIL 6, 1931

During the last four years the problem of the nature of the chemical bond has been attacked by theoretical physicists, especially Heitler and London, by the application of the quantum mechanics. This work has led to an approximate theoretical calculation of the energy of formation and of other properties of very simple molecules, such as  $H_2$ , and has also provided a formal justification of the rules set up in 1916 by G. N. Lewis for his electron-pair bond. In the following paper it will be shown that many more results of chemical significance can be obtained from the quantum mechanical equations, permitting the formulation of an extensive and powerful set of rules for the electron-pair bond supplementing those of Lewis. These rules provide information regarding the relative strengths of bonds formed by different atoms, the angles between bonds, free rotation or lack of free rotation about bond axes, the relation between the quantum numbers of bonding electrons and the number and spatial arrangement of the bonds, etc. A complete theory of the magnetic moments of molecules and complex ions is also developed, and it is shown that for many compounds involving elements of the transition groups this theory together with the rules for electron-pair bonds leads to a unique assignment of electron structures as well as a definite determination of the type of bonds involved.<sup>1</sup>

## I. The Electron-Pair Bond

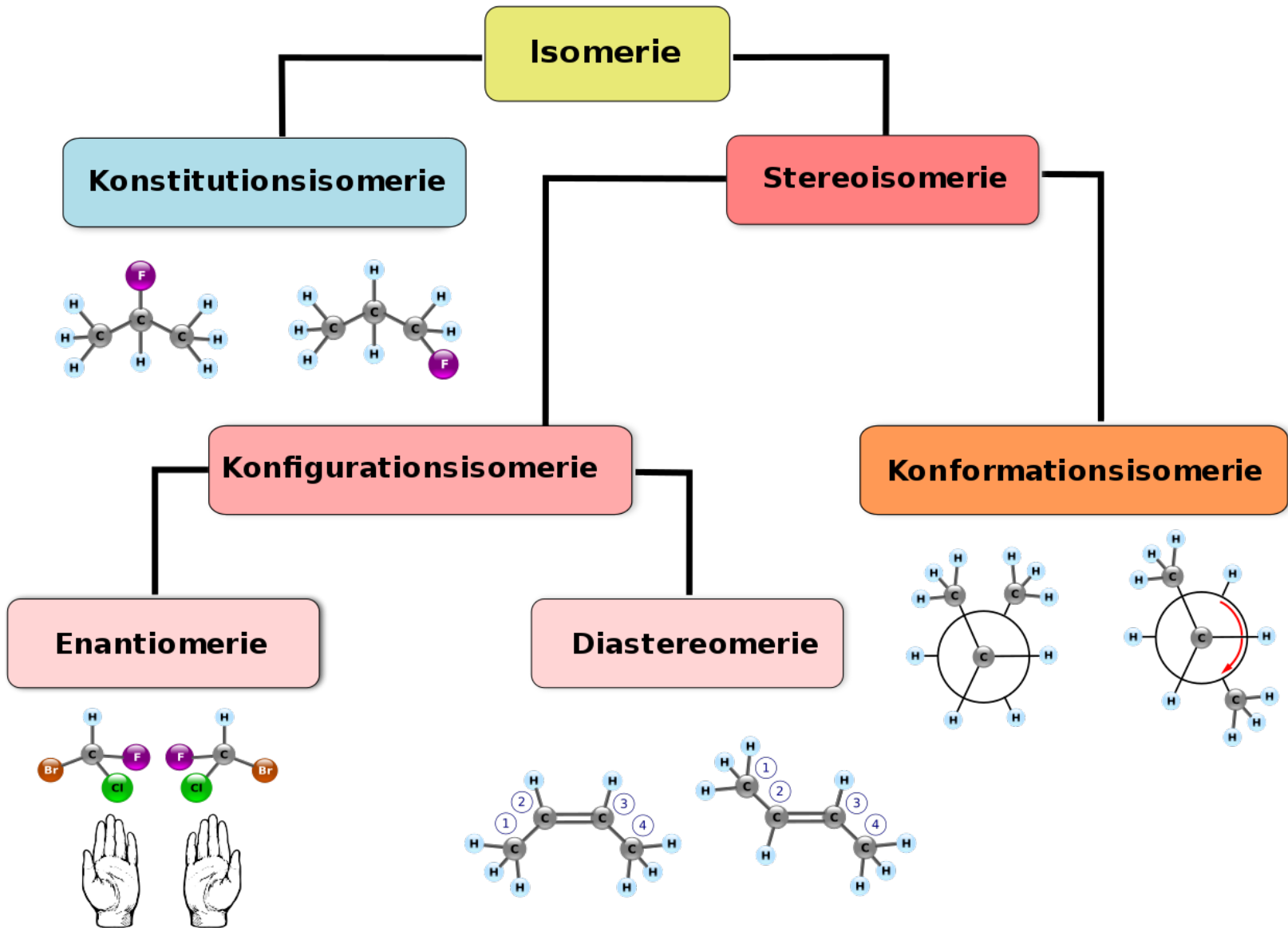
The Interaction of Simple Atoms.—The discussion of the wave equation for the hydrogen molecule by Heitler and London,<sup>2</sup> Sugiura,<sup>3</sup> and Wang<sup>4</sup> showed that two normal hydrogen atoms can interact in either of two ways, one of which gives rise to repulsion with no molecule formation, the other

<sup>1</sup> A preliminary announcement of some of these results was made three years ago [Linus Pauling, *Proc. Nat. Acad. Sci.*, 14, 359 (1928)]. Two of the results ( $90^\circ$  bond angles for  $p$  eigenfunctions, and the existence, but not the stability, of tetrahedral eigenfunctions) have been independently discovered by Professor J. C. Slater and announced at meetings of the National Academy of Sciences (Washington, April, 1930) and the American Physical Society (Cleveland, December, 1930).

<sup>2</sup> W. Heitler and F. London, *Z. Physik*, 44, 455 (1927).

<sup>3</sup> Y. Sugiura, *ibid.*, 45, 484 (1927).

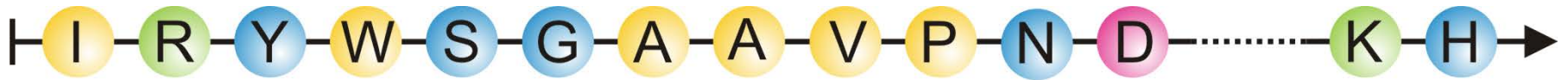
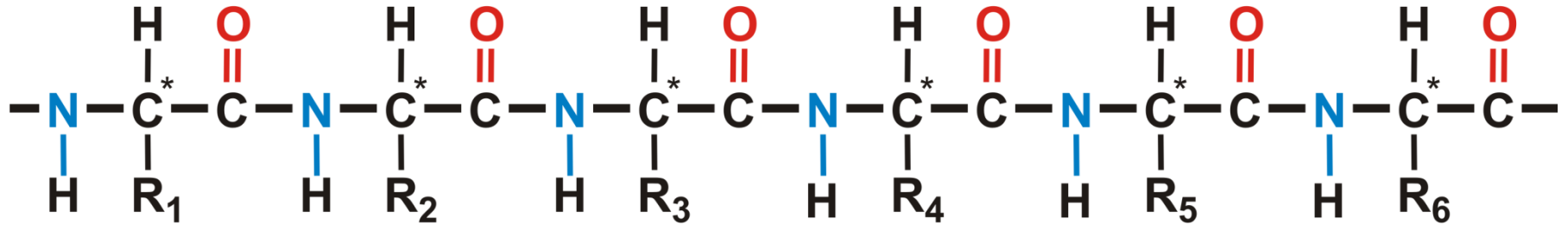
<sup>4</sup> S. C. Wang, *Phys. Rev.*, 31, 579 (1928).



Von Isomerism-ball.svg: GYassineMrabetTalk ☒ Diese W3C-unbestimmte Vektorgrafik wurde mit Inkscape erstellt.

Isomerism-ball-de.svg: \*Isomerism-ball.svg: YassineMrabet.derivative work: Matt (talk)derivative work:

Roland.chem (talk) - Isomerism-ball.svgIsomerism-ball-de.svg, CC BY-SA 3.0, <https://commons.wikimedia.org/w/index.php?curid=11812815>



**A** ≡ **alanine**

**G** ≡ **glycine**

**M** ≡ **methionine**

**S** ≡ **serine**

**C** ≡ **cysteine**

**H** ≡ **histidine**

**N** ≡ **asparagine**

**T** ≡ **threonine**

**D** ≡ **aspartic acid**

**I** ≡ **isoleucine**

**P** ≡ **proline**

**V** ≡ **valine**

**E** ≡ **glutamic acid**

**K** ≡ **lysine**

**Q** ≡ **glutamine**

**W** ≡ **tryptophane**

**F** ≡ **phenyl alanine**

**L** ≡ **leucine**

**R** ≡ **arginine**

**Y** ≡ **tyrosine**

Primärstruktur oder Sequenz von Proteinen



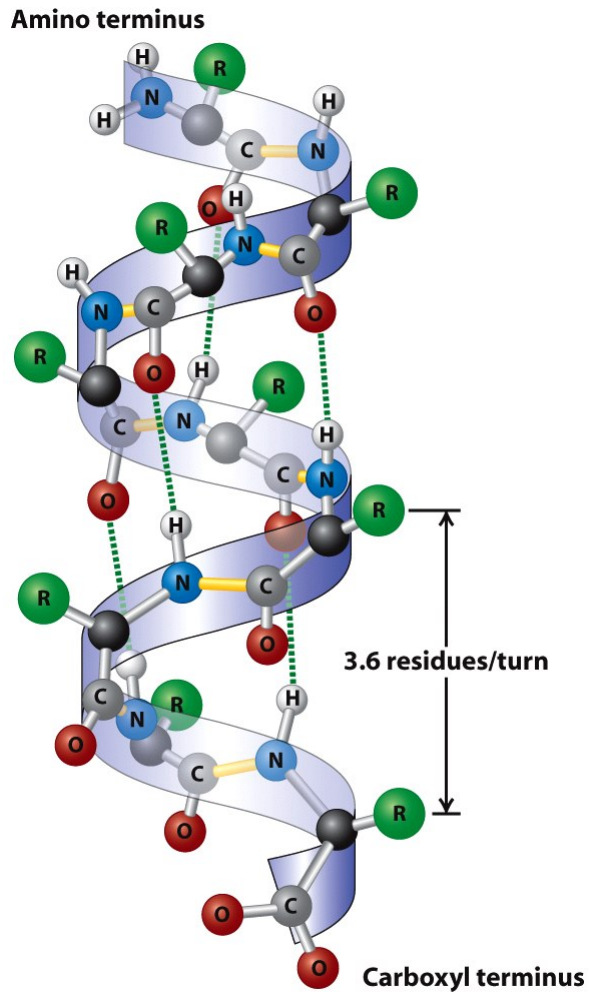


Figure 3-4  
*Molecular Cell Biology, Sixth Edition*  
 © 2008 W.H. Freeman and Company

$\alpha$ -helix

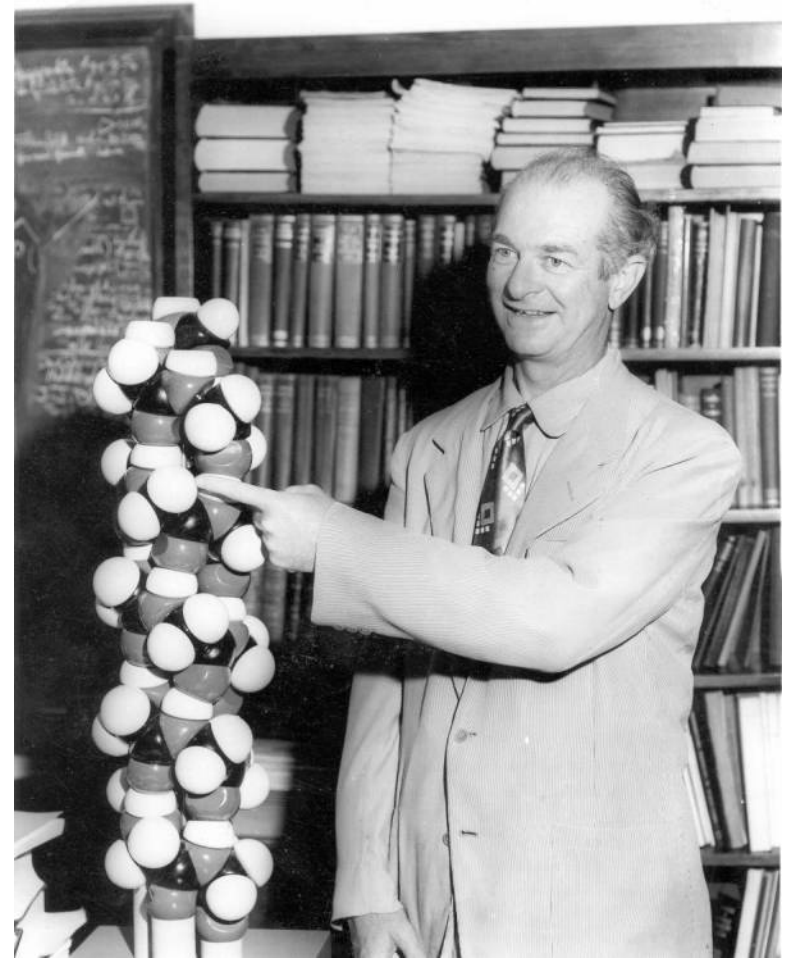
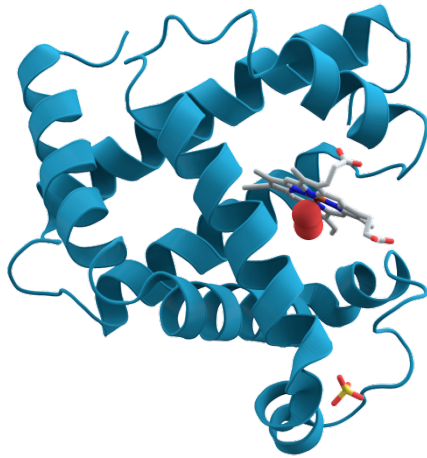


Photo by CalTech News Bureau

Linus Pauling, 1901-1994

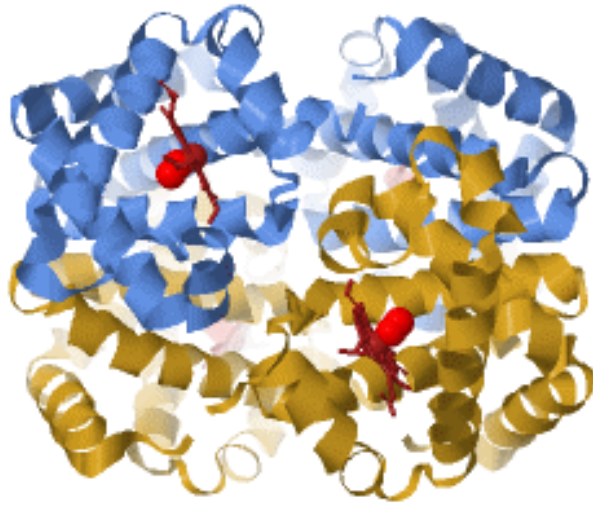
L. Pauling, R.B. Corey, H.R. Branson. The structure of proteins: Two hydrogen-bonded helical configurations of the polypeptide chain. *Proc.Natl.Acad.Sci.USA* 37(4):205-211. 1951.





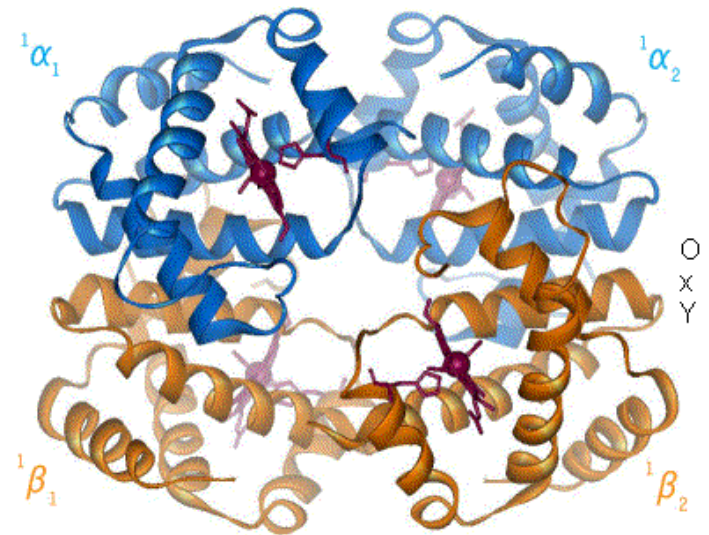
myoglobin structure

J.C. Kendrew et al. Nature 181:662-666, 1958



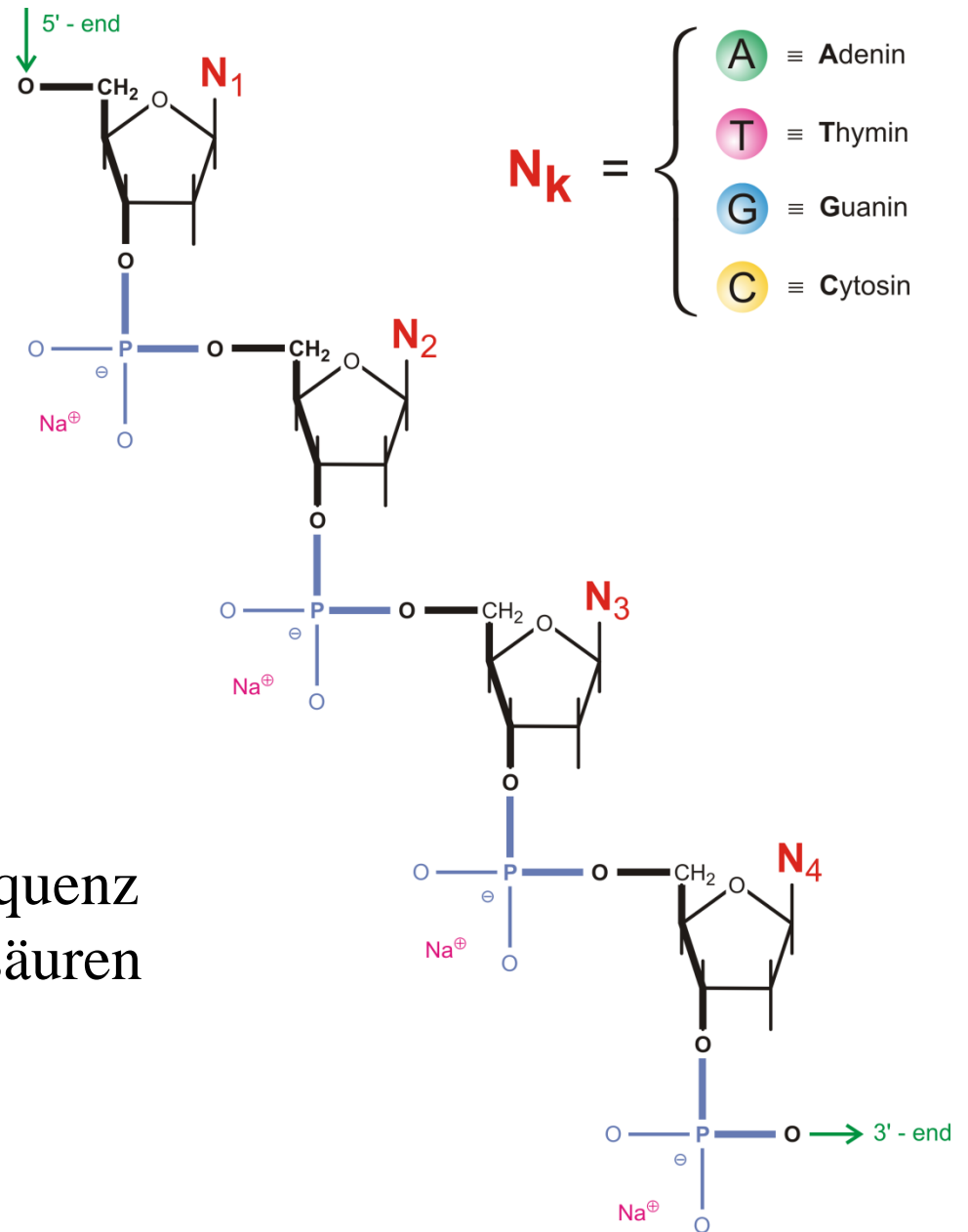
hemoglobin structure

M.F. Perutz et al. Nature 185:416-422, 1960

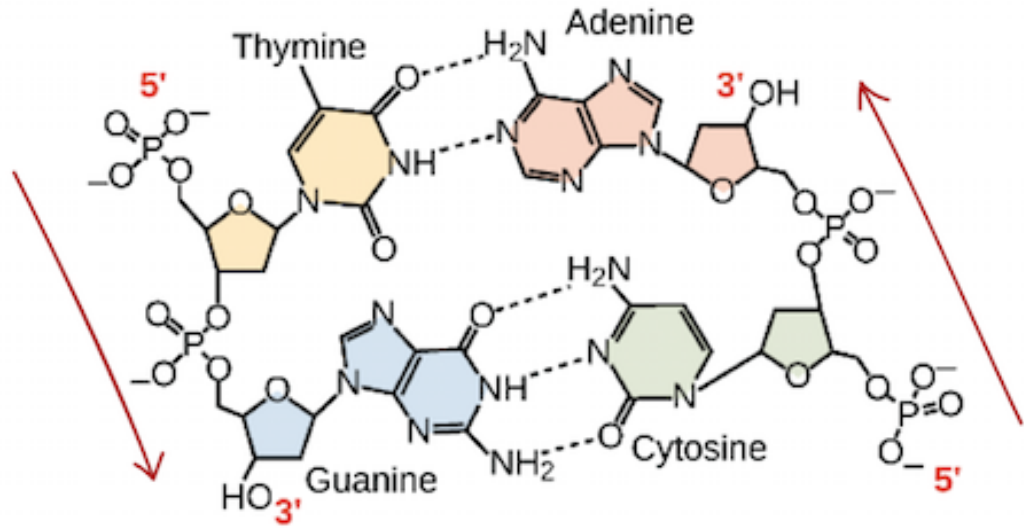


conformational change  $R \leftrightarrow T$

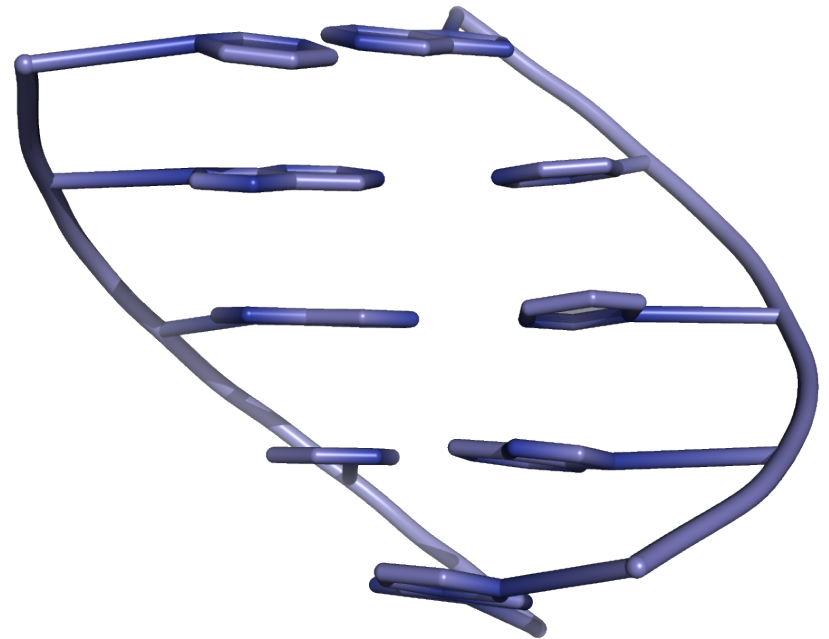
# Primärstruktur oder Sequenz der Desoxyribonukleinsäuren DNA



DNA base pairing

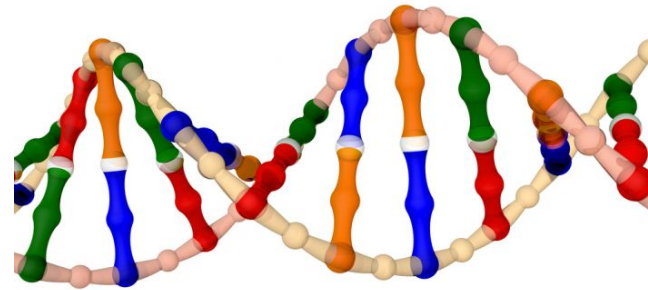
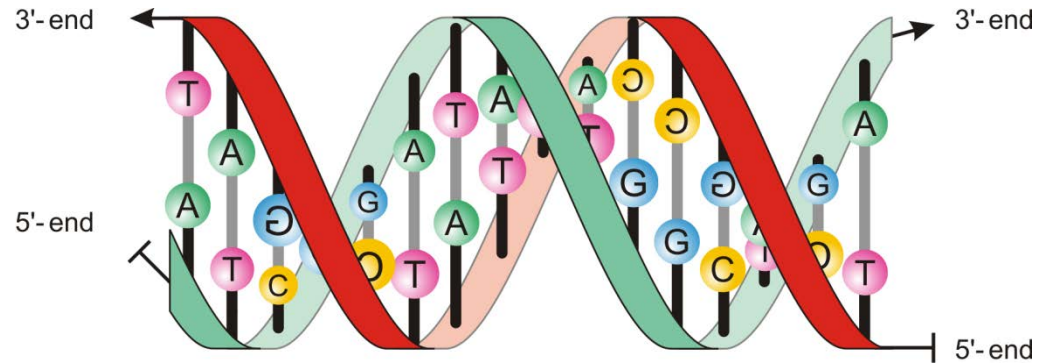


DNA base stacking



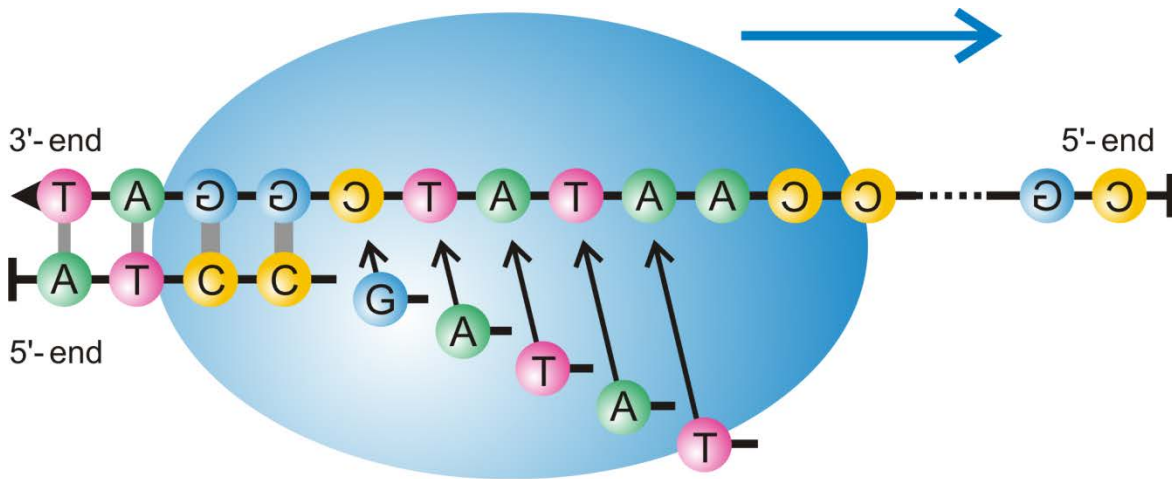


This figure is purely diagrammatic. The two ribbons symbolize the two phosphate—sugar chains, and the horizontal rods the pairs of bases holding the chains together. The vertical line marks the fibre axis

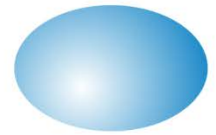


"It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material."

J.D. Watson, F. H.C. Crick. A structure for deoxyribose nucleic acid.  
Nature 171(4356):737-738, 1953.



correct replication



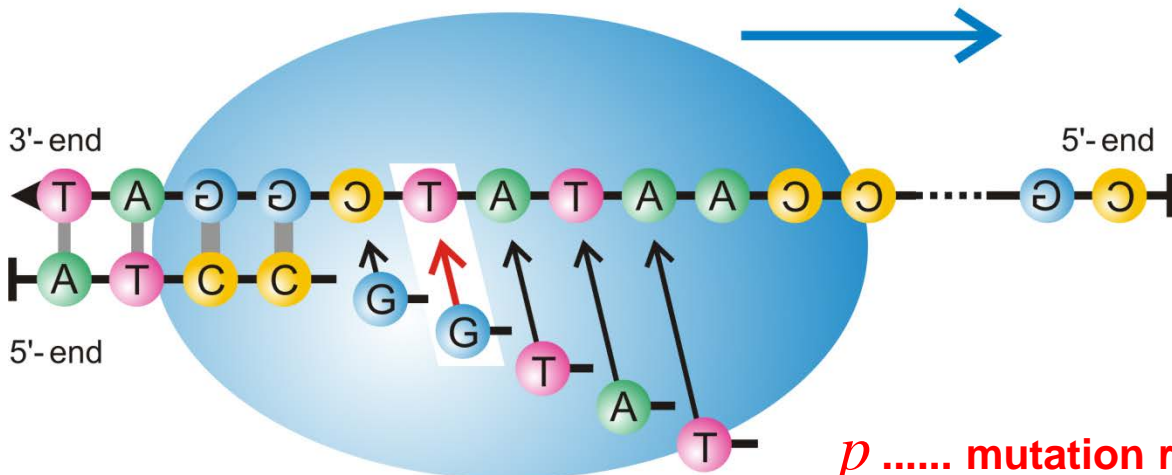
Taq-polymerase

adenine 

thymine 

guanine 

cytosine 

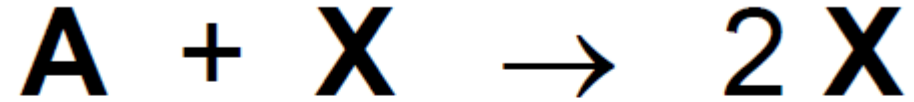


mutation

$p$  ..... mutation rate per site  
and replication

### DNA replication and mutation

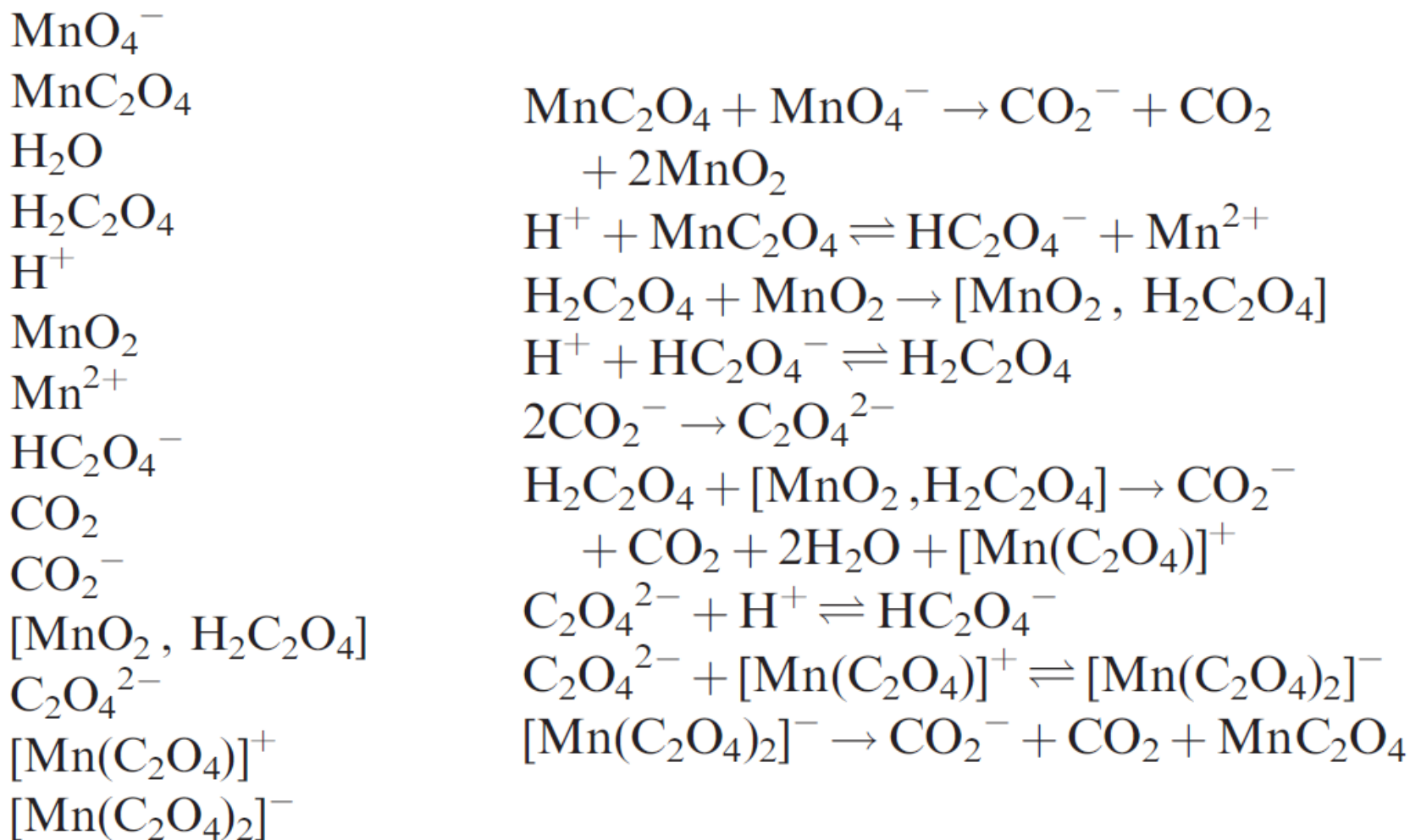
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Autokatalyse erster Ordnung



Autokatalyse zweiter Ordnung

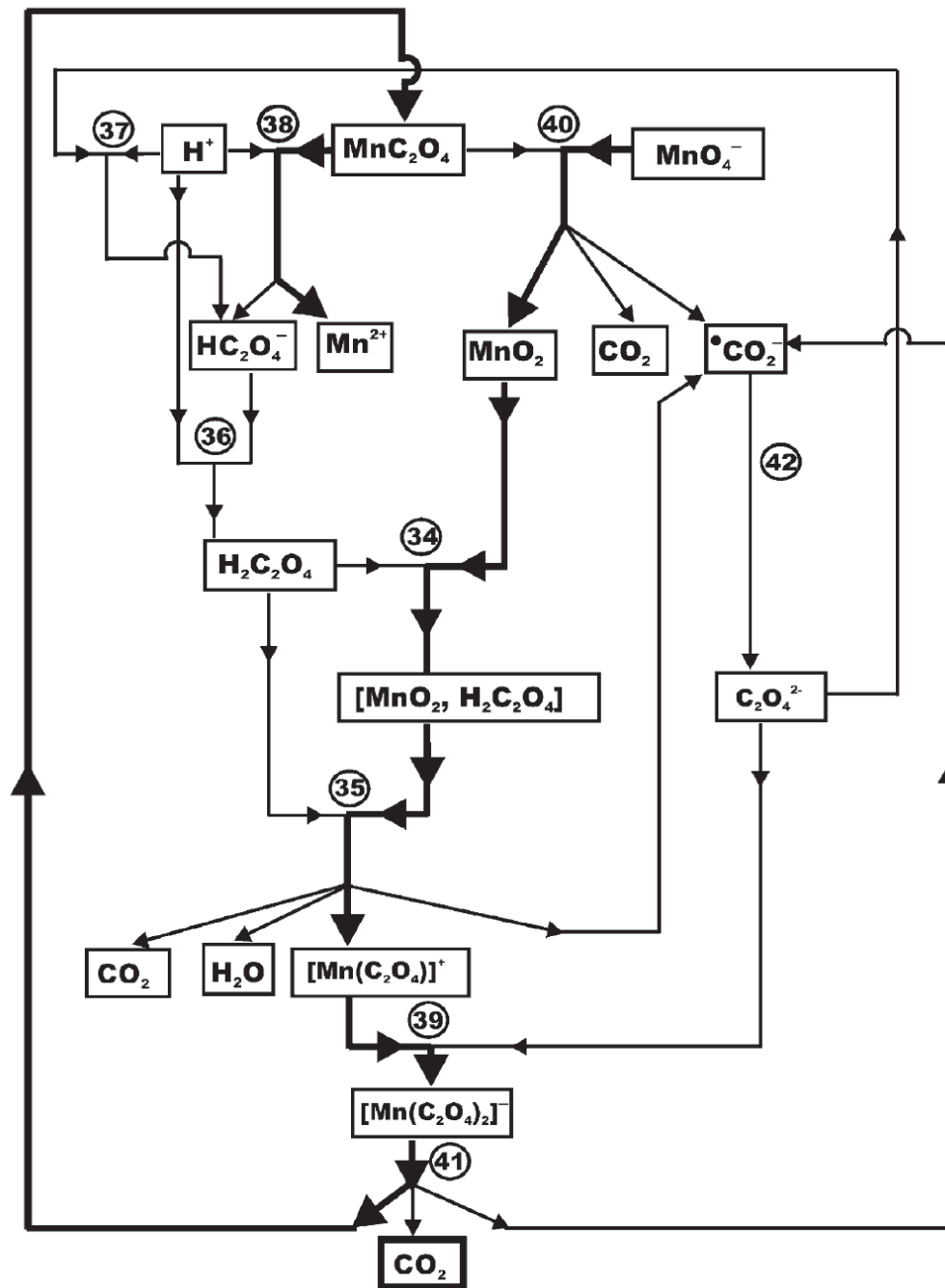


K. Kovács, B. Vizvári, M. Riedel, J. Tóth. 2004. Decomposition of the permanganate/oxalic acid overall reaction to elementary steps based on integer programming theory.

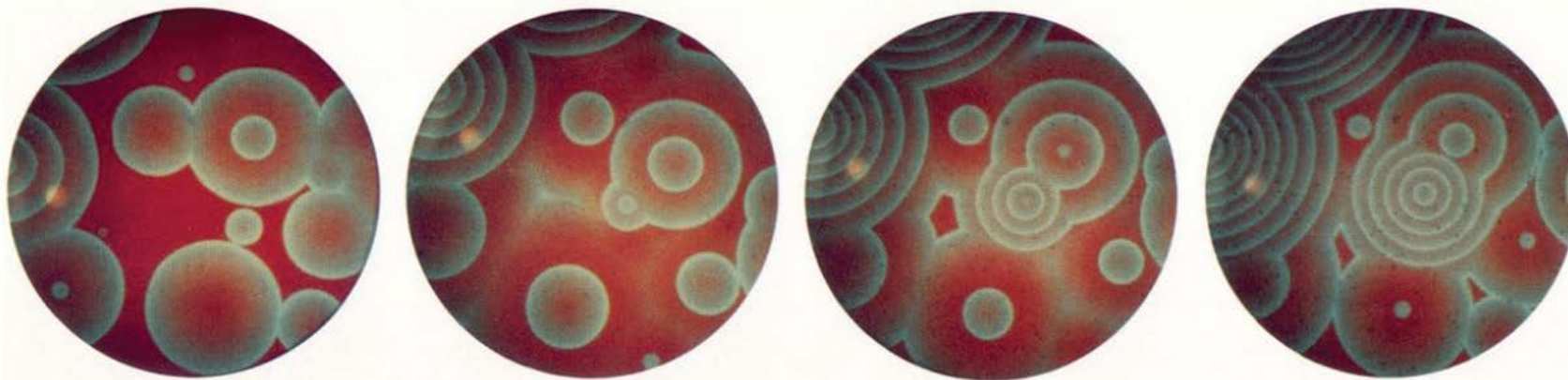
Phys.Chem.Chem.Phys. 6:1236-1242



K. Kovács, B. Vizvári, M. Riedel,  
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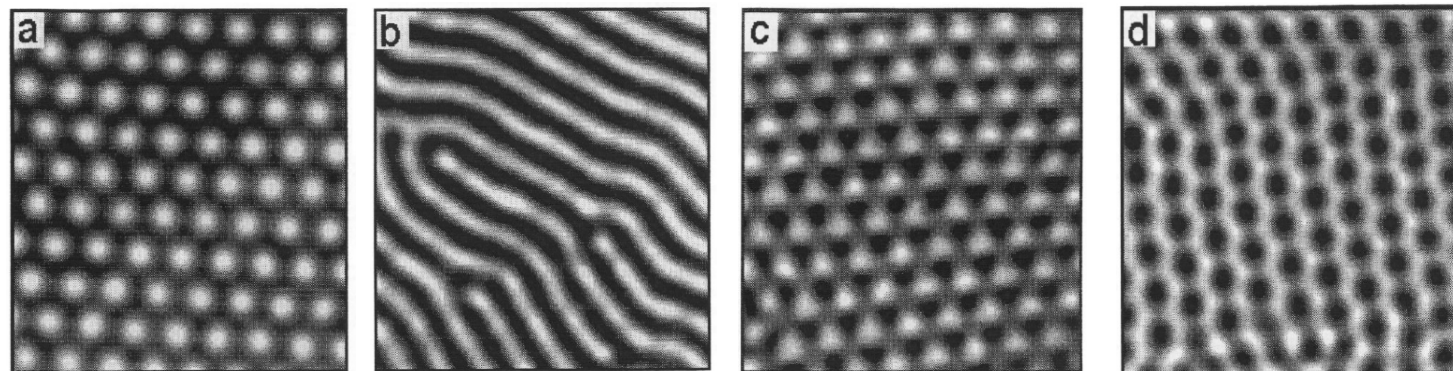


Reaction	Rate Constant	Ref.
1. $\text{Br}^- + 2\text{H}^+ + \text{BrO}_3^- \rightleftharpoons \text{HOBr} + \text{HBrO}_2$	$k_1 = 2.1 \text{ M}^{-2}\text{sec}^{-1}$	6
2. $\text{Br}^- + \text{HBrO}_2 + \text{H}^+ \rightleftharpoons 2\text{HOBr}$	$k_{-1} = 1.0 \times 10^4 \text{ M}^{-1}\text{sec}^{-1}$	6
3. $\text{Br}^- + \text{HOBr} + \text{H}^+ \rightleftharpoons \text{Br}_2 + \text{H}_2\text{O}$	$k_2 = 2.0 \times 10^9 \text{ M}^{-2}\text{sec}^{-1}$	6
4. $\text{H}^+ + \text{CH}_2(\text{COOH})_2 \rightleftharpoons (\text{OH})_2\text{C}=\text{CHCOOH} + \text{H}^+$	$k_{-2} = 5.0 \times 10^{-5} \text{ M}^{-1}\text{sec}^{-1}$	6
5. $\text{Br}_2 + (\text{OH})_2\text{C}=\text{CHCOOH} \rightleftharpoons \text{H}^+ + \text{Br}^- + \text{BrCH}(\text{COOH})_2$	$k_3 = 8.0 \times 10^9 \text{ M}^{-2}\text{sec}^{-1}$	6
6. $\text{HOBr} + (\text{OH})_2\text{C}=\text{CHCOOH} \rightleftharpoons \text{H}_2\text{O} + \text{BrCH}(\text{COOH})_2$	$k_{-3} = 110. \text{ sec}^{-1} (a)$	6
7. $\text{HBrO}_2 + \text{BrO}_3^- + \text{H}^+ \rightleftharpoons 2\text{BrO}_2 \cdot + \text{H}_2\text{O}$	$k_4 = 1.3 \times 10^{-2} \text{ M}^{-1}\text{sec}^{-1}$	6
8. $\text{BrO}_2 \cdot + \text{Ce}(\text{III}) + \text{H}^+ \rightleftharpoons \text{Ce}(\text{IV}) + \text{HBrO}_2$	$k_{-4} = 1.3 \times 10^4 \text{ M}^{-1}\text{sec}^{-1}$	19
9. $\text{Ce}(\text{IV}) + \text{BrO}_2 \cdot + \text{H}_2\text{O} \rightleftharpoons \text{BrO}_3^- + 2\text{H}^+ + \text{Ce}(\text{III})$	$k_5 = 6.0 \times 10^6 \text{ M}^{-1}\text{sec}^{-1}$	19
10. $2\text{HBrO}_2 \rightleftharpoons \text{HOBr} + \text{BrO}_3^- + \text{H}^+$	$k_{-5} = 0.$	22
11. $\text{Ce}(\text{IV}) + \text{CH}_2(\text{COOH})_2 \rightarrow \cdot\text{CH}(\text{COOH})_2 + \text{Ce}(\text{III}) + \text{H}^+$	$k_6 = 0.$	This work
12. $\cdot\text{CH}(\text{COOH})_2 + \text{Ce}(\text{IV}) + \text{H}_2\text{O} \rightarrow \text{HOCH}(\text{COOH})_2 + \text{Ce}(\text{III}) + \text{H}^+$	$k_{-6} = 0.$	22
13. $\text{Ce}(\text{IV}) + \text{BrCH}(\text{COOH})_2 + \text{H}_2\text{O} \rightarrow \text{Br}^- + \text{HO}\dot{\text{C}}(\text{COOH})_2 + \text{Ce}(\text{III}) + \text{H}^+$	$k_7 = 1.0 \times 10^4 \text{ M}^{-2}\text{sec}^{-1}$	6
14. $\cdot\text{CH}(\text{COOH})_2 + \text{BrCH}(\text{COOH})_2 + \text{H}_2\text{O} \rightarrow \text{HO}\dot{\text{C}}(\text{COOH})_2 + \text{CH}_2(\text{COOH})_2 + \text{Br}^- + \text{H}^+$	$k_{-7} = 2.0 \times 10^7 \text{ M}^{-1}\text{sec}^{-1} (a)$	6
15. $\text{HO}\dot{\text{C}}(\text{COOH})_2 + \text{Ce}(\text{IV}) \rightarrow \text{O}=\text{C}(\text{COOH})_2 + \text{Ce}(\text{III}) + \text{H}^+$	$k_8 = 6.5 \times 10^5 \text{ M}^{-2}\text{sec}^{-1}$	This work
16. $\text{HO}\dot{\text{C}}(\text{COOH})_2 + \text{BrCH}(\text{COOH})_2 + \text{H}_2\text{O} \rightarrow \text{HOCH}(\text{COOH})_2 + \text{Br}^- + \text{HO}\dot{\text{C}}(\text{COOH})_2 + \text{H}^+$	$k_{-8} = 2.4 \times 10^7 \text{ M}^{-1}\text{sec}^{-1}$	This work
17. $\text{Ce}(\text{IV}) + \text{HOCH}(\text{COOH})_2 \rightarrow \text{HO}\dot{\text{C}}(\text{COOH})_2 + \text{Ce}(\text{III}) + \text{H}^+$	$k_9 = 9.6 \times 10^4 \text{ M}^{-1}\text{sec}^{-1} (a,b)$	This work
18. $\text{Ce}(\text{IV}) + \text{O}=\text{C}(\text{COO}\cdot)(\text{COOH}) \rightarrow \text{O}=\text{C}(\text{COO}\cdot)(\text{COOH}) + \text{Ce}(\text{III}) + \text{H}^+$	$k_{-9} = 0.$	6
19. $\text{O}=\text{C}(\text{COO}\cdot)(\text{COOH}) + \text{Ce}(\text{IV}) + \text{H}_2\text{O} \rightarrow \text{HCOOH} + \text{Ce}(\text{III}) + \text{H}^+ + 2\text{CO}_2$	$k_{10} = 4.0 \times 10^7 \text{ M}^{-1}\text{sec}^{-1}$	6
20. $\text{O}=\text{C}(\text{COO}\cdot)(\text{COOH}) + \text{BrCH}(\text{COOH}) + \text{H}_2\text{O} \rightarrow$ $\text{HO}\dot{\text{C}}(\text{COOH})_2 + \text{O}=\text{C}(\text{COOH})_2 + \text{Br}^- + \text{H}^+$	$k_{-10} = 2.0 \times 10^{-10} \text{ M}^{-2}\text{sec}^{-1}$	6
	$k_{11} = 1.7 \times 10^{-1} \text{ M}^{-1}\text{sec}^{-1}$ ( $[\text{MA}] \ll 0.5 \text{ M}$ )	6,22,25
	$k_{12} = 1.0 \times 10^5 \text{ M}^{-1}\text{sec}^{-1} (a)$	This work
	$k_{13} = 8.5 \times 10^{-2} \text{ M}^{-1}\text{sec}^{-1} (a)$ ( $[\text{BrMA}] \ll 0.1 \text{ M}$ )	6,22,25
	$k_{14} = 1.0 \times 10^5 \text{ M}^{-1}\text{sec}^{-1} (a,b)$	This work
	$k_{15} = 1.0 \times 10^5 \text{ M}^{-1}\text{sec}^{-1} (b)$	This work
	$k_{16} = 1.0 \times 10^5 \text{ M}^{-1}\text{sec}^{-1} (a,b)$	This work
	$k_{17} = 1.0 \times 10^5 \text{ M}^{-1}\text{sec}^{-1} (b)$	This work
	$k_{18} = 1.0 \times 10^5 \text{ M}^{-1}\text{sec}^{-1} (b)$	This work
	$k_{19} = 1.0 \times 10^5 \text{ M}^{-1}\text{sec}^{-1} (b)$	This work
	$k_{20} = 1.0 \times 10^5 \text{ M}^{-1}\text{sec}^{-1} (a,b)$	This work



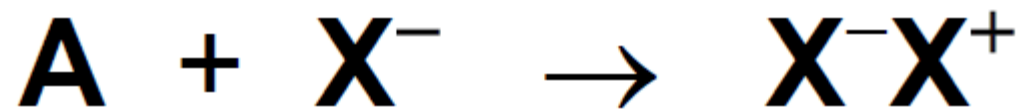
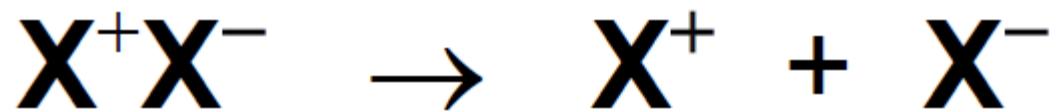
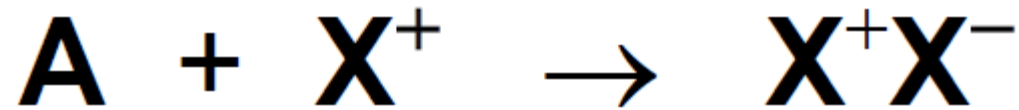
**Fig. 1. Sequence of snapshots of target patterns in the aqueous Belousov-Zhabotinsky (BZ) reaction.** Patterns emerge from an initially homogeneous red solution. Catalyst/indicator is ferroin. Red areas are more reduced; blue areas are more oxidized.

V. K. Vanag, I. R. Epstein. *Internat.J.Developmental Biology* 53, 673-681

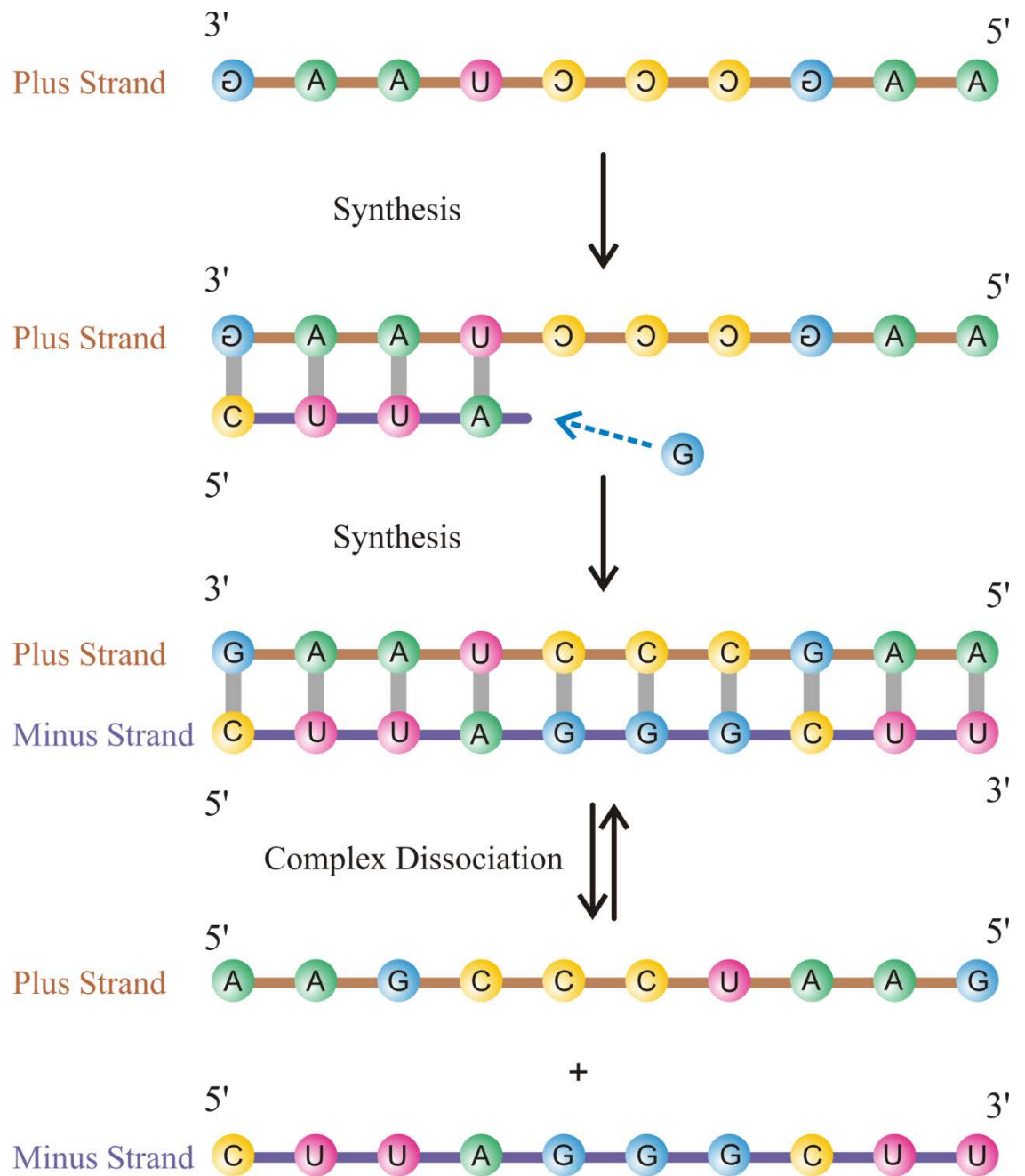


**Fig. 3. Stationary planforms observed in the disc reactor.** Standard patterns: (a) hexagonal array of "clear" spots from region IIa ( $[KI]_B = 2.0 \times 10^{-3} M$ ;  $[CH_2(COOH)_2]_B = 2.25 \times 10^{-3} M$ ); (b) array of parallel stripes (bands) from region IIb ( $[KI]_B = 2.0 \times 10^{-3} M$ ,  $[CH_2(COOH)_2]_B = 2.5 \times 10^{-3} M$ ). Non-standard patterns: (c) array of symmetric triangles from region IIc ( $[KI]_B = 3.0 \times 10^{-3} M$ ,  $[CH_2(COOH)_2]_B = 3.2 \times 10^{-3} M$ ); (d) array of "dark" hexabands from region II d ( $[KI]_B = 2.5 \times 10^{-3} M$ ,  $[CH_2(COOH)_2]_B = 3.1 \times 10^{-3} M$ ). All patterns are at the same scale: view size  $1.7 \times 1.7$  mm.

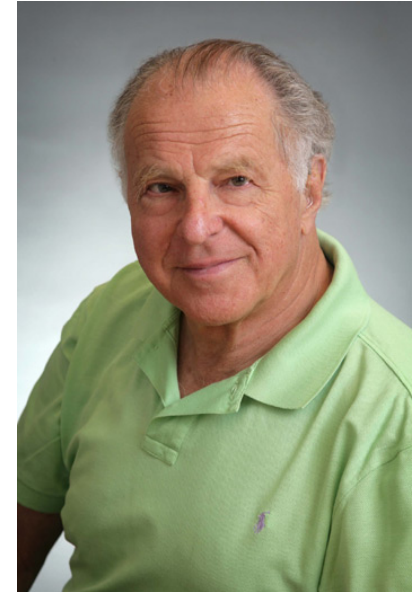
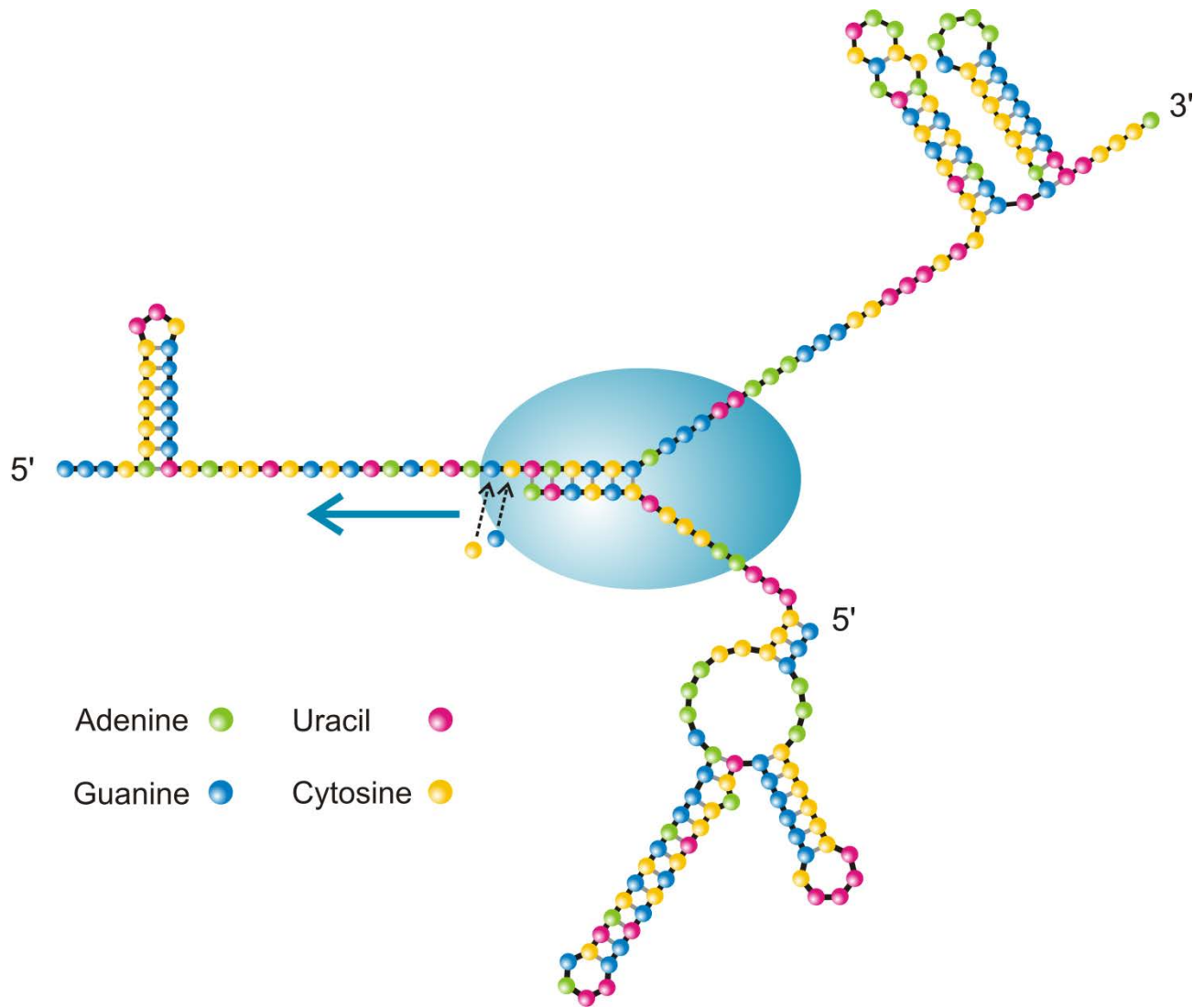
B. Rudovics, E. Dulos, P. De Kepper. *Physica Scripta T67*, 43-50, 1996



Komplementäre Replikation



Complementary replication  
of RNA by virus specific  
replicase



Charles Weissmann  
1931-

RNA replication by Q $\beta$ -replicase

C. Weissmann, The making of a phage. FEBS Letters **40** (1974), S10-S18

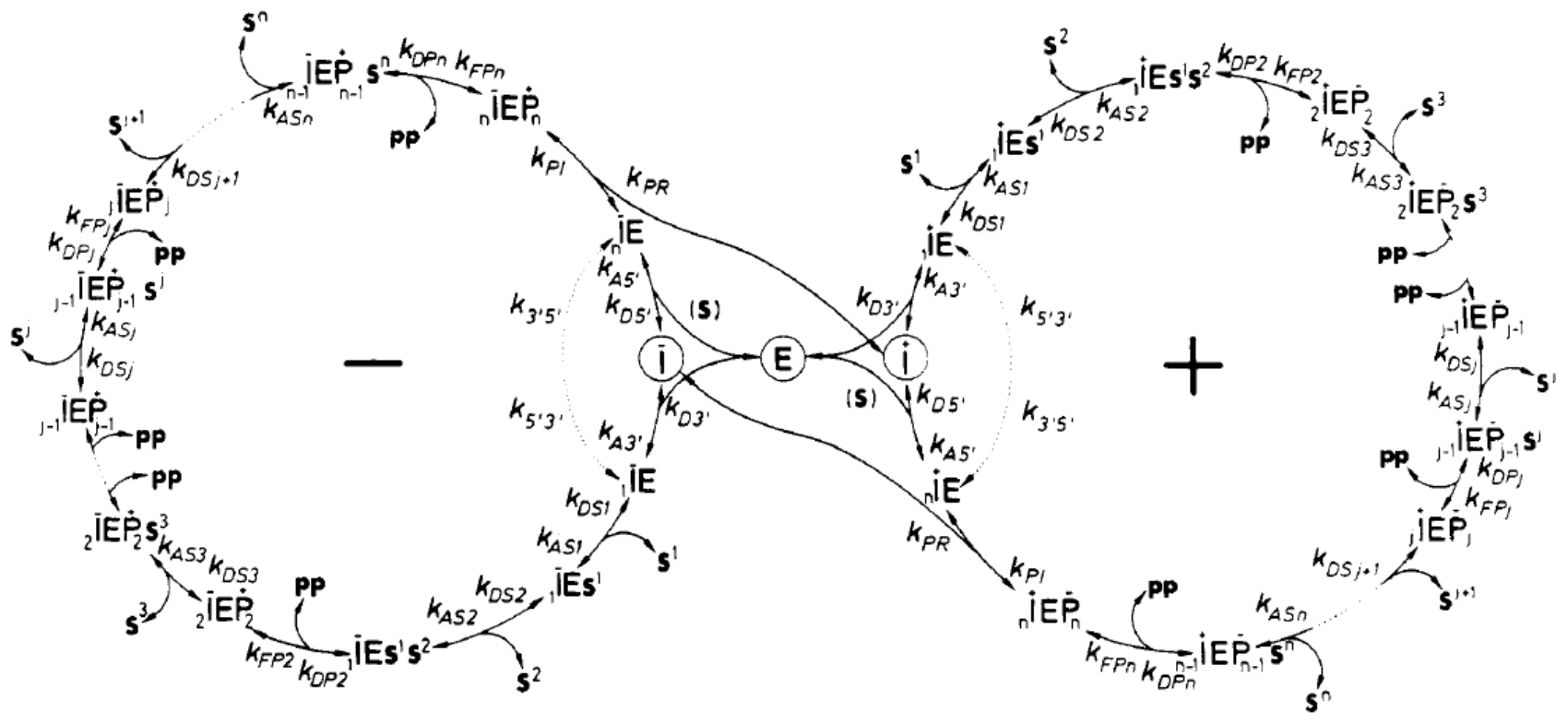
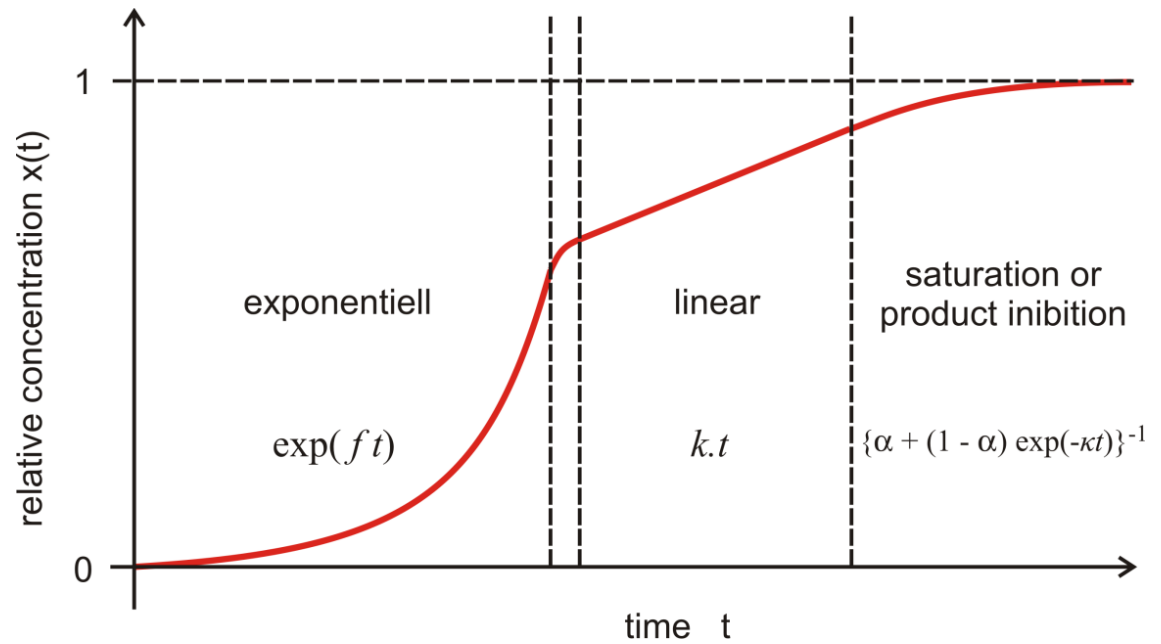


FIGURE 4: Complete replication mechanism, combining the initiation, elongation, and termination steps of both cross-catalytic cycles (cf. Figures 1-3). The indices + and - of the rate constants for the two cycles have been omitted for clarity, but corresponding steps of the two cycles may have different rates. The species and rate constant symbols are explained in Table I.



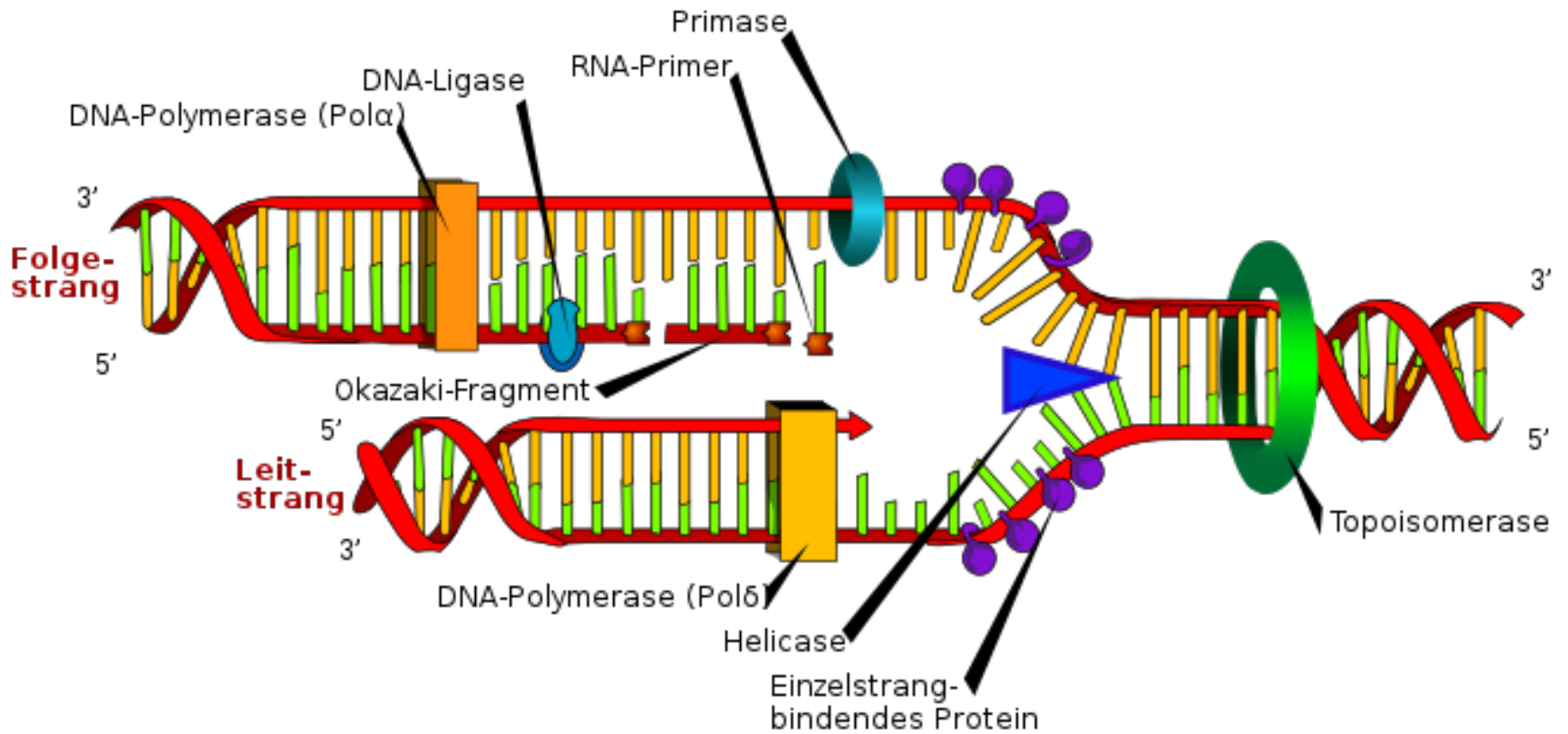


Christof K. Biebricher,  
1941-2009



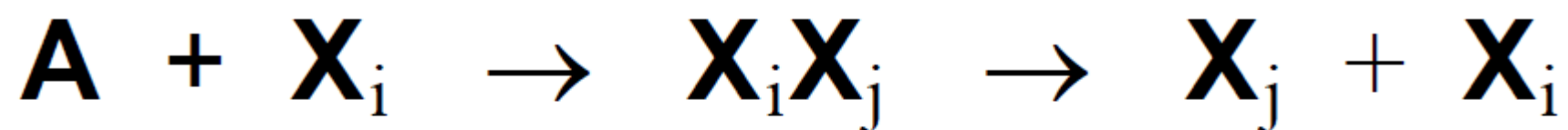
C.K. Biebricher, M. Eigen, W.C. Gardiner, Jr. 1983. Kinetics of RNA Replication.  
Biochemistry **22**(10):2544-2559.



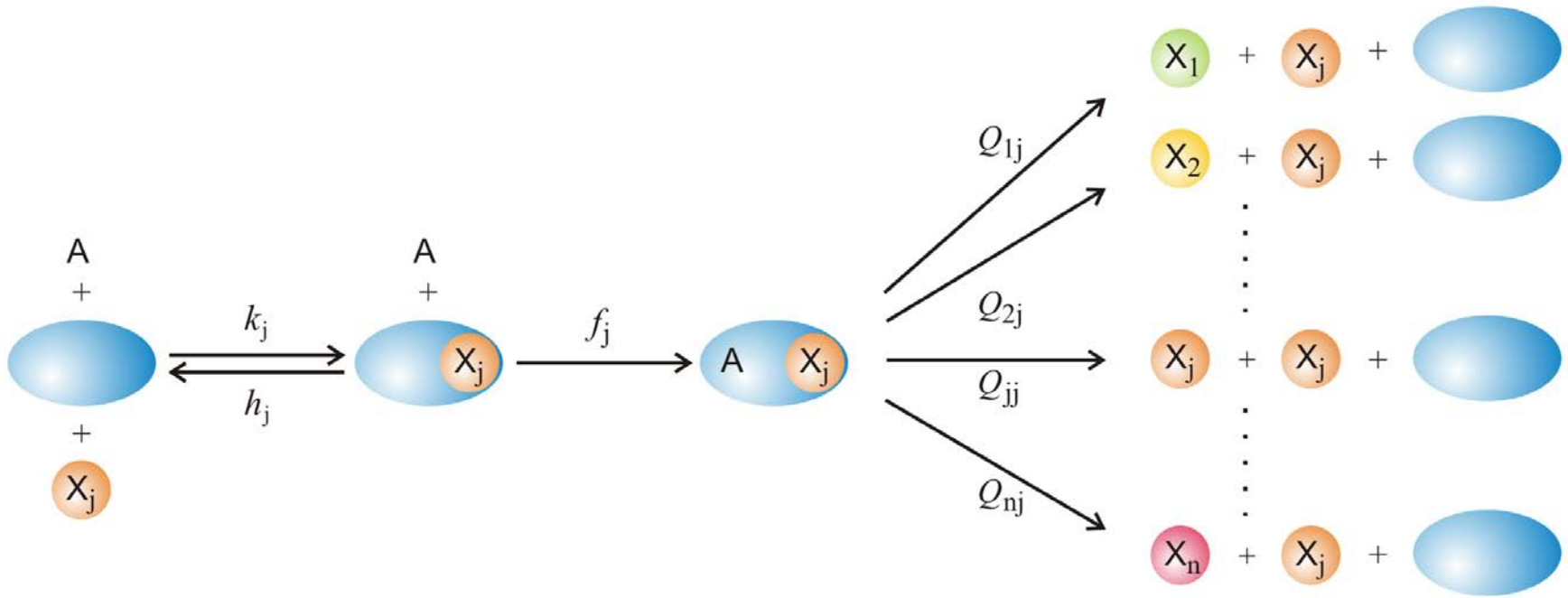


## DNA Replikationsmaschinerie

1. Historischer Weg zur Evolutionstheorie
2. Molekülstruktur in Chemie und Biologie
3. Autokatalyse und Vermehrung von Molekülen
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5. Molekulare Information als eine Domäne der Biologie
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Mutation



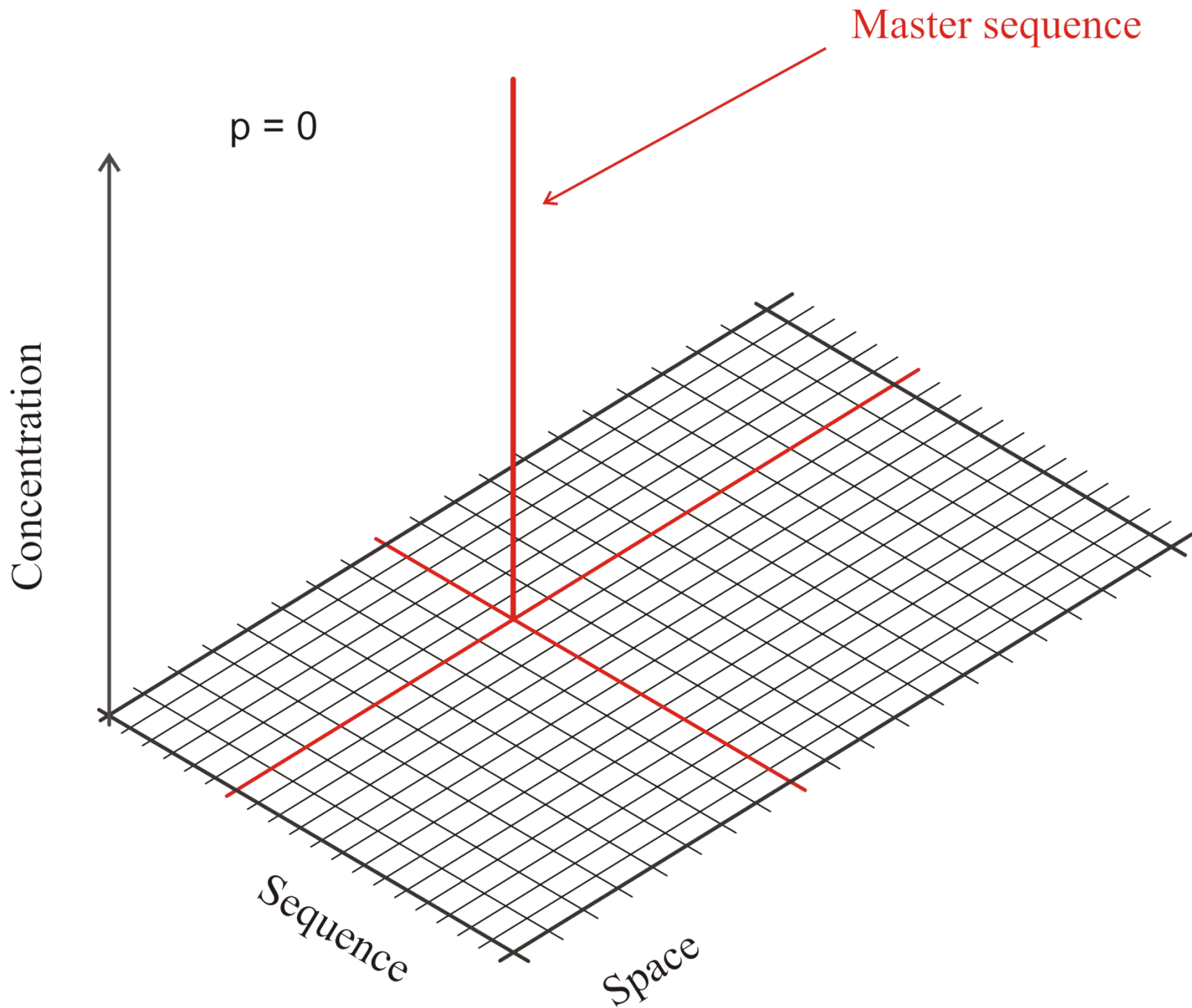
Manfred Eigen. 1971. Self-Organization of Matter and the Evolution of Biological Macromolecules. *Naturwissenschaften* 58(10):465-523

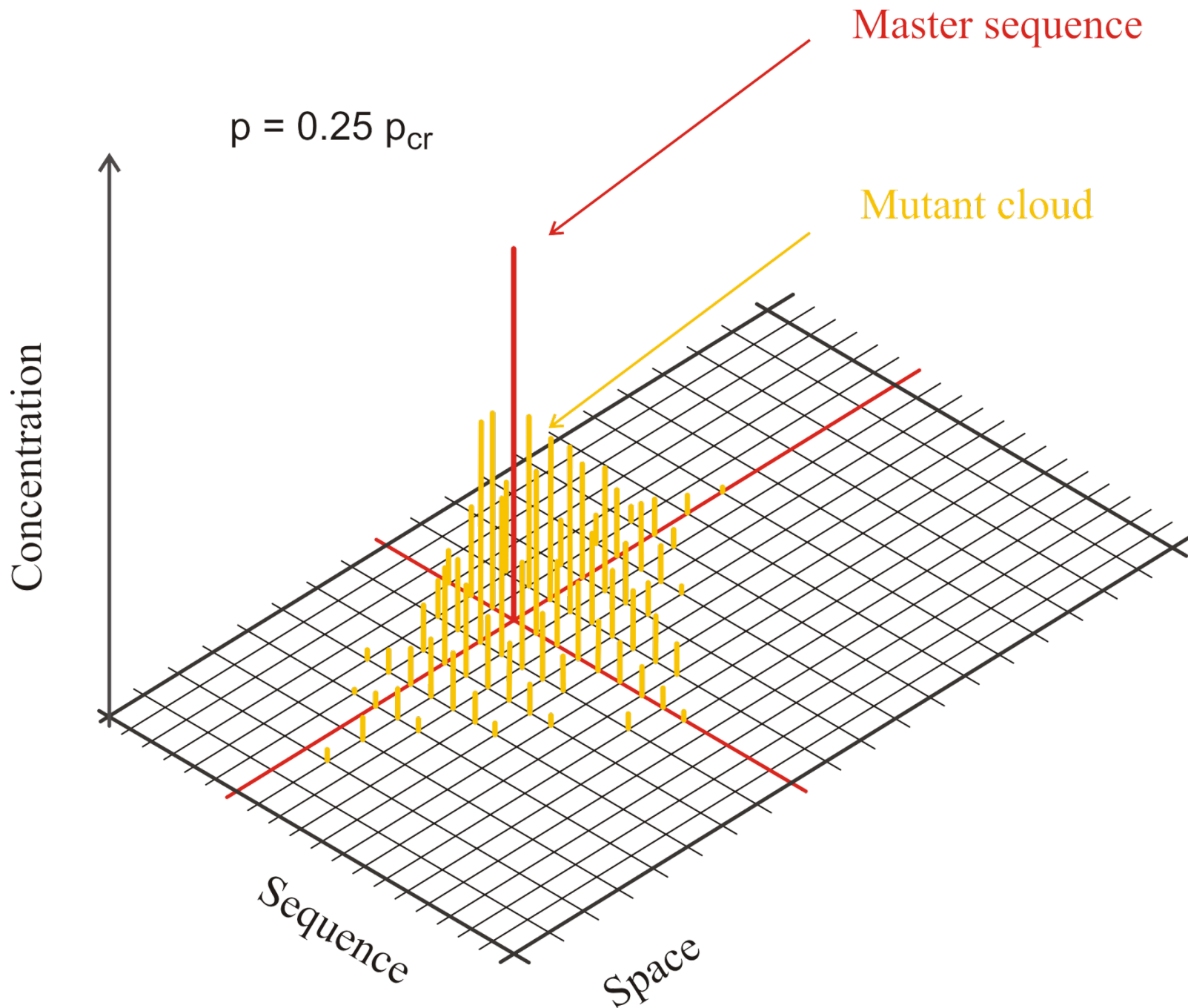
$$p \times l \leq \ln \sigma \approx 1$$

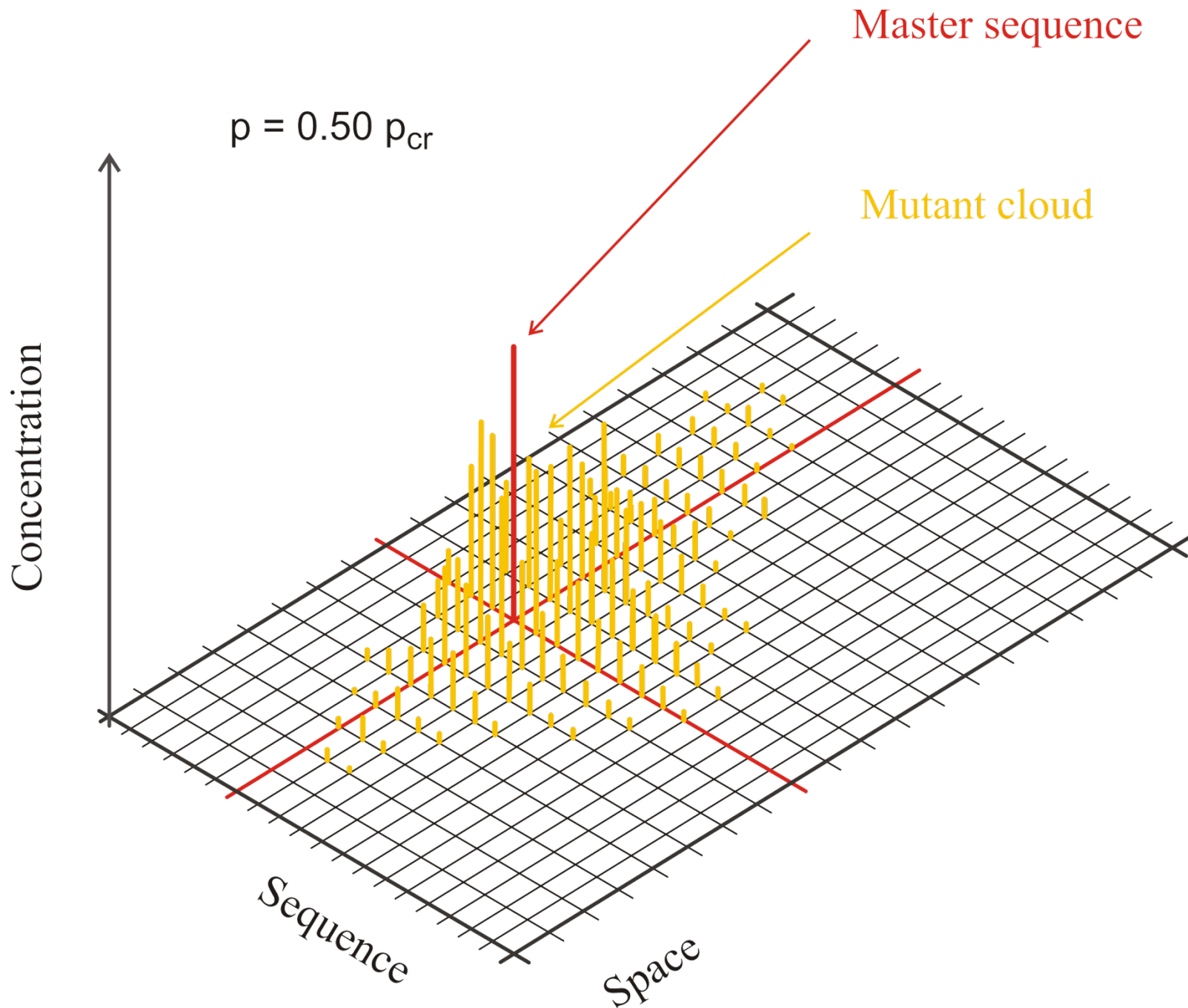
$$p_{\text{crit}} = 1 / l_0$$

Quasispecies, error threshold and maximal genome lengths

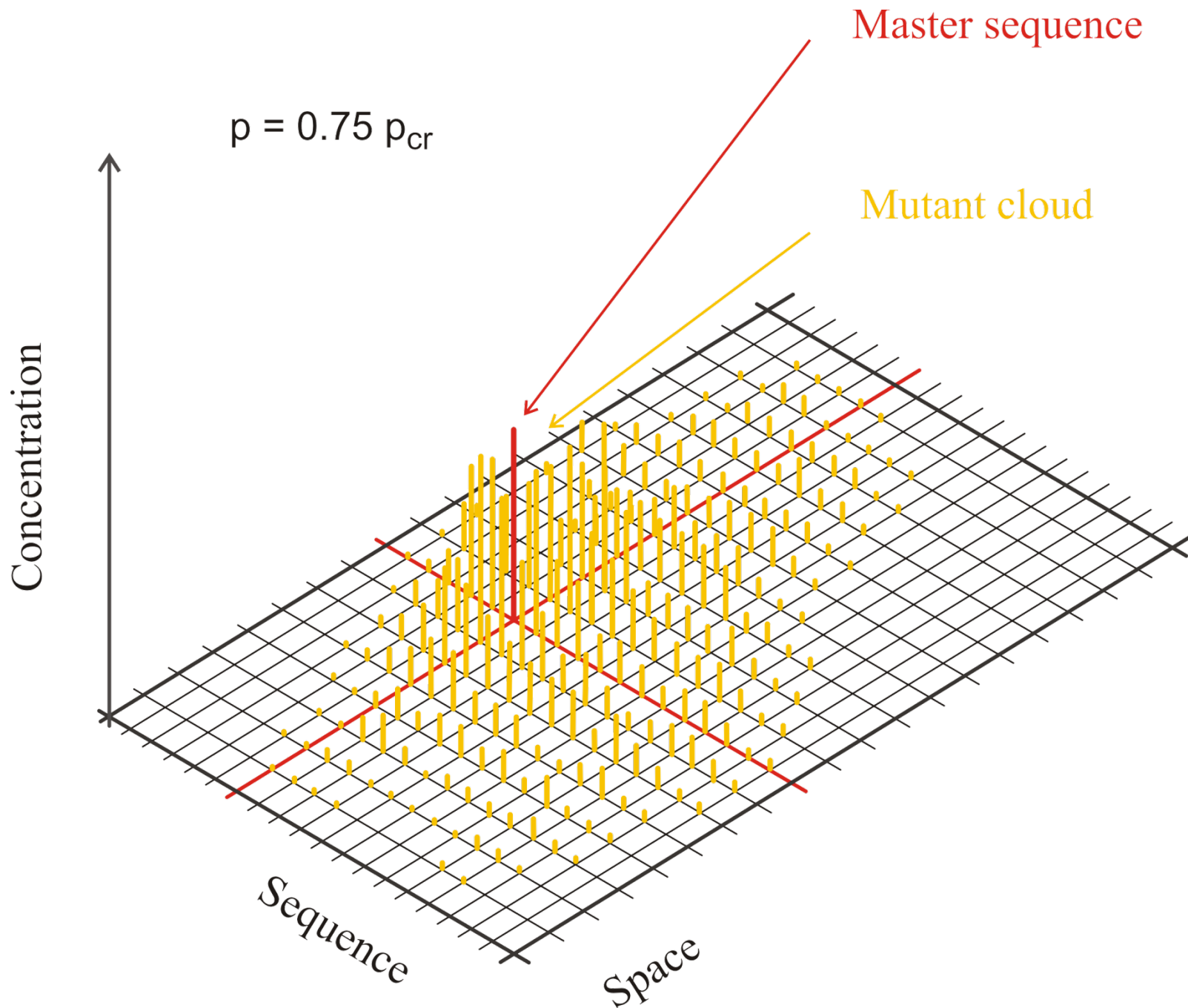
Manfred Eigen, Peter Schuster. 1977. The Hypercycle: A Principle of Natural Self-Organisation.  
Part A: Emergence of the Hypercycle. *Naturwissenschaften* 64(11):541-565

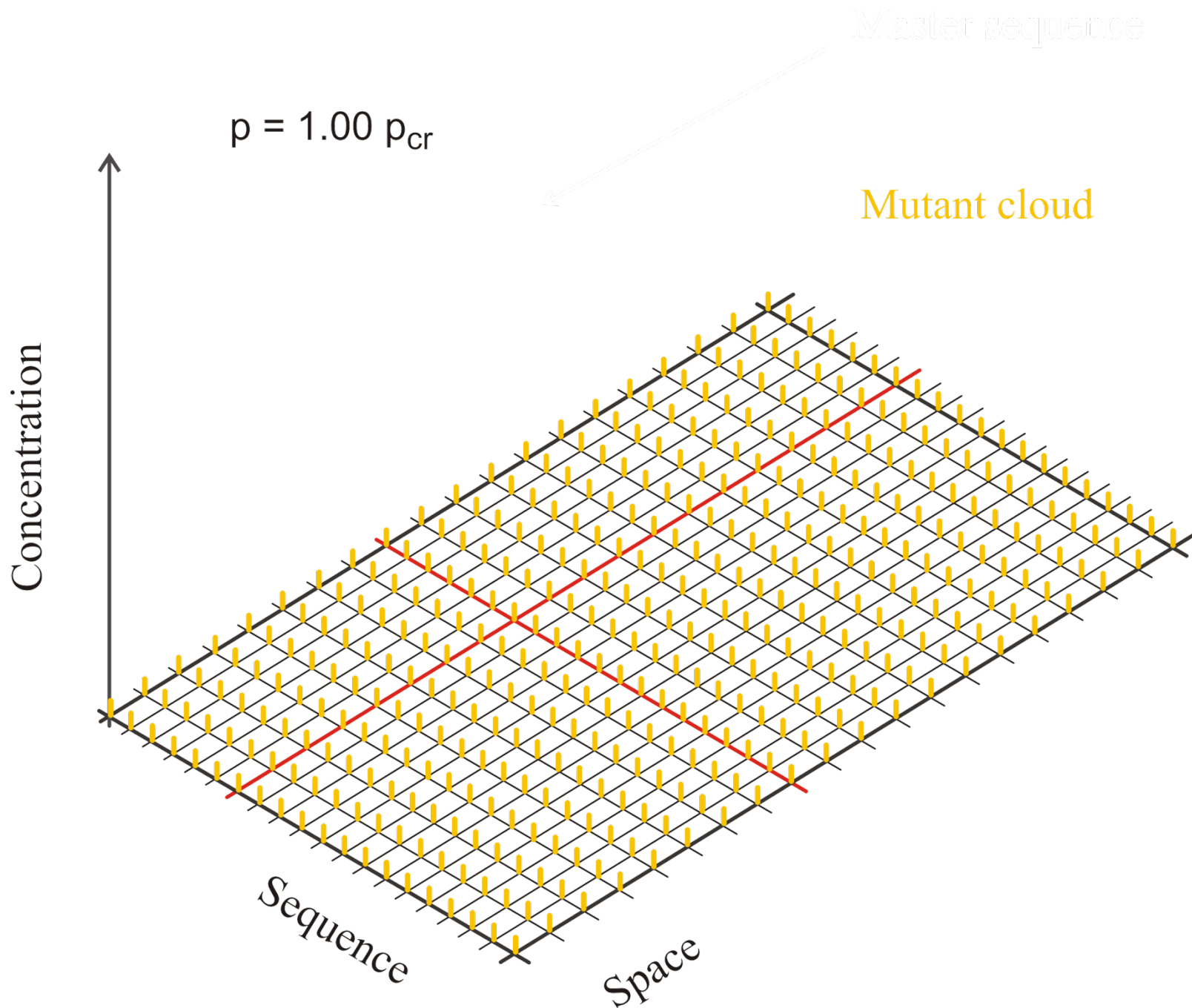


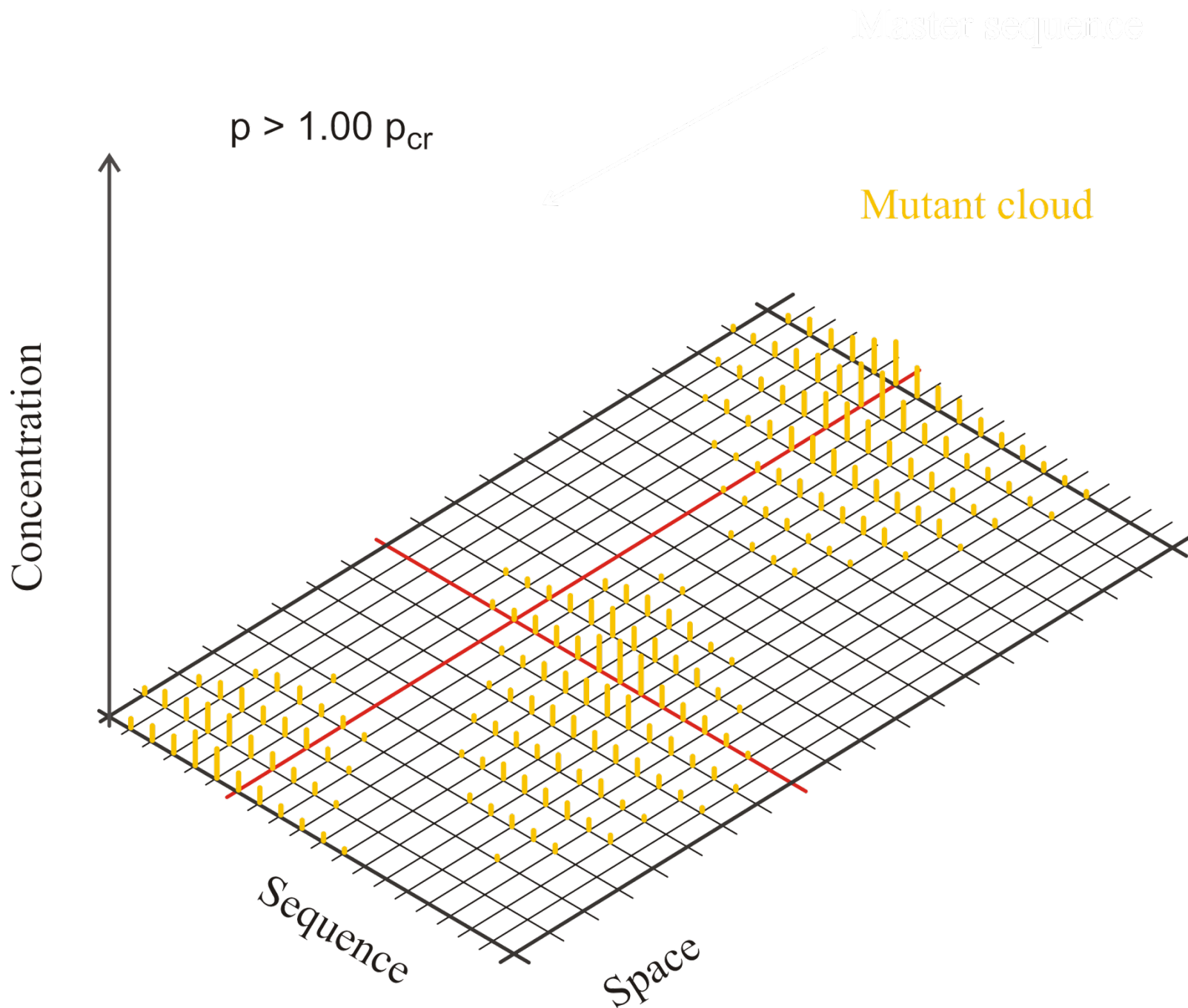










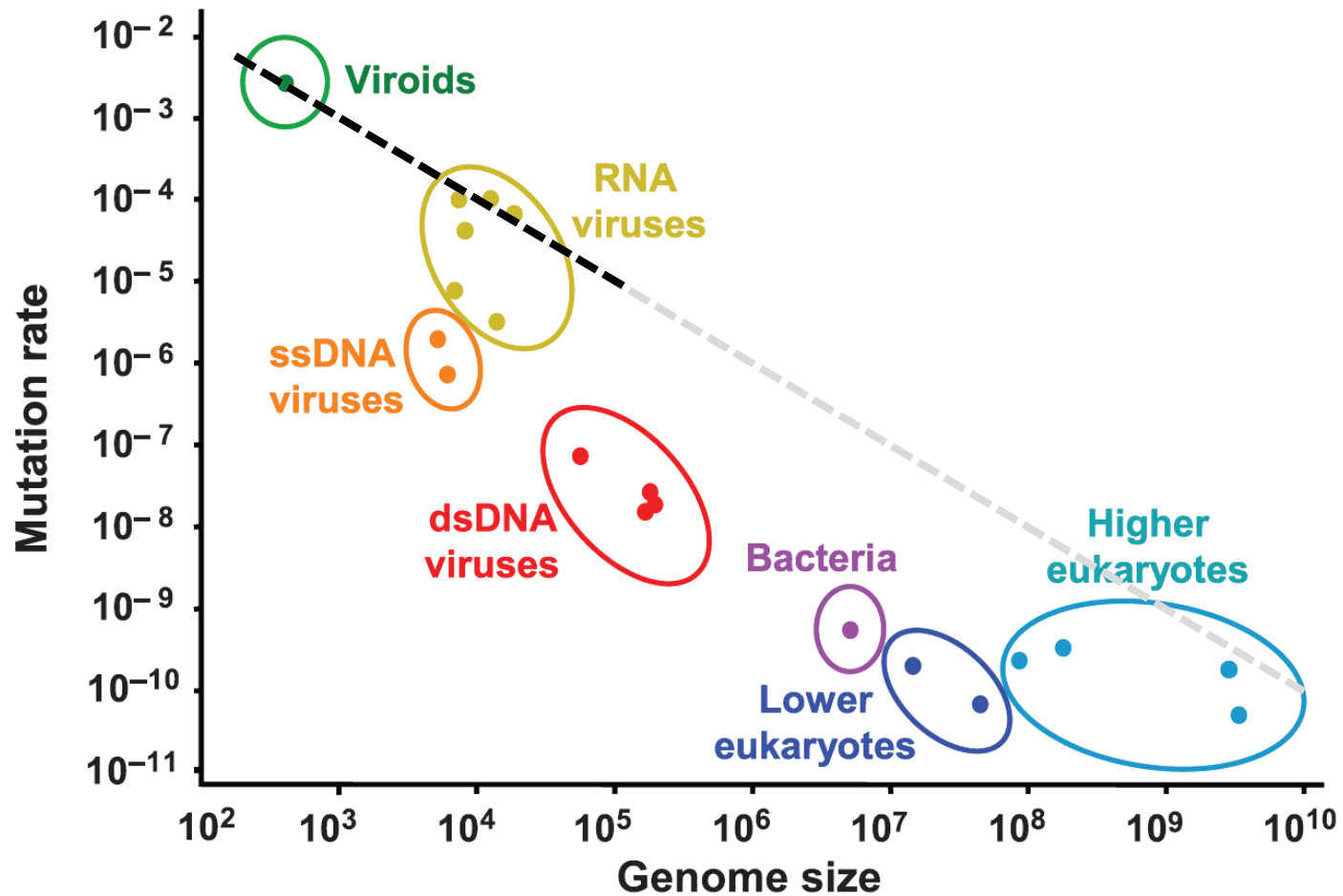


$$p \times l \leq \ln \sigma \approx 1$$

$$l_{\text{crit}} = 1 / p_0$$

Quasispecies, error threshold and maximal genome lengths

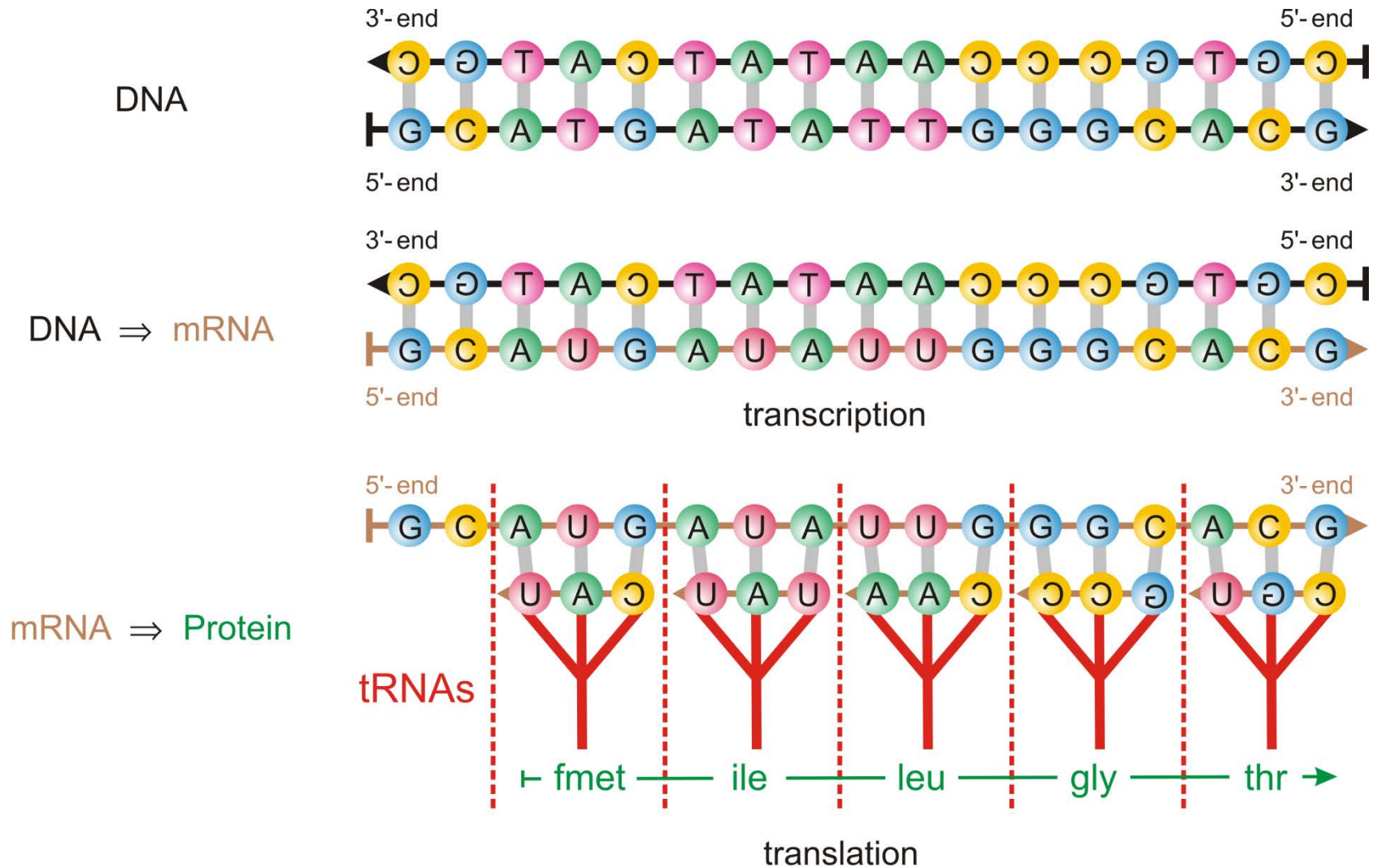
Manfred Eigen, Peter Schuster. 1977. The Hypercycle: A Principle of Natural Self-Organisation.  
Part A: Emergence of the Hypercycle. *Naturwissenschaften* 64(11):541-565



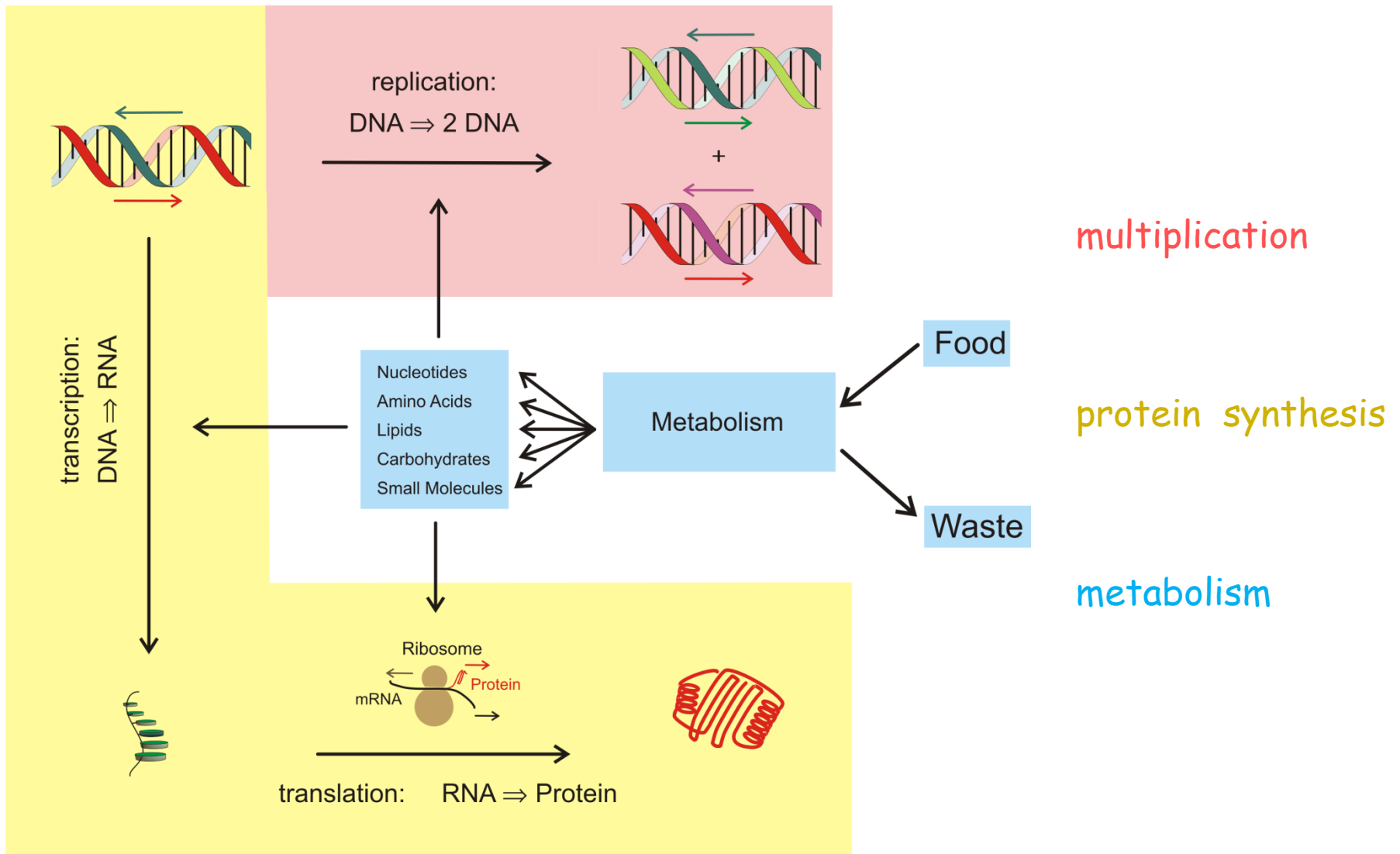
Selma Gago, Santiago F. Elena, Ricardo Flores, Rafael Sanjuán. Extremely high mutation rate of a hammerhead viroid. *Science* 323(5919):1308, 2009.

mutation rate and genome size

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transcription and translation

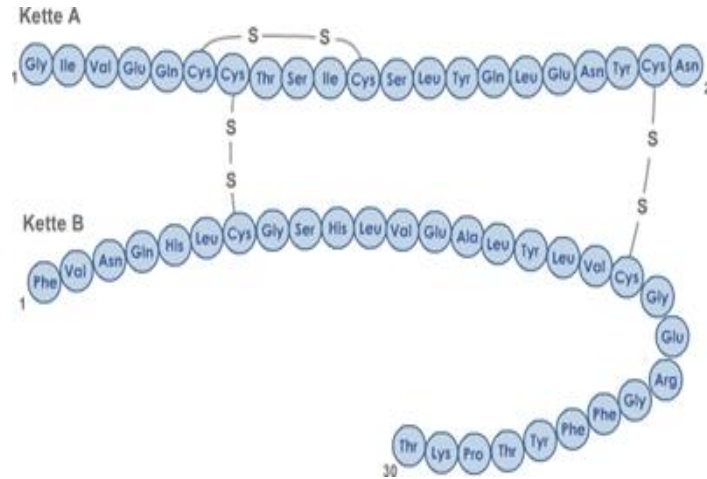


sketch of the cellular metabolism after deciphering the genetic code



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## human insulin



Frederick Sanger, Hans Tuppy. 1951. Amino Acid Sequence of the Phenylalanyl Chain of Insulin. II. The Investigation of Peptides from Enzymic Hydrolysates. *Biochem.J.* 49(4):481-490.

012...

50

**MGDVEKGGKKIFVQKCAQCHTVEKGGKHKKTGPNLHGLFGRKTGQAPGFTYTD**

**ANKNKGITWKEETLMEYLENPKKYIPGTKMIFAGIKKKTEREDLIAYLKKATNE**

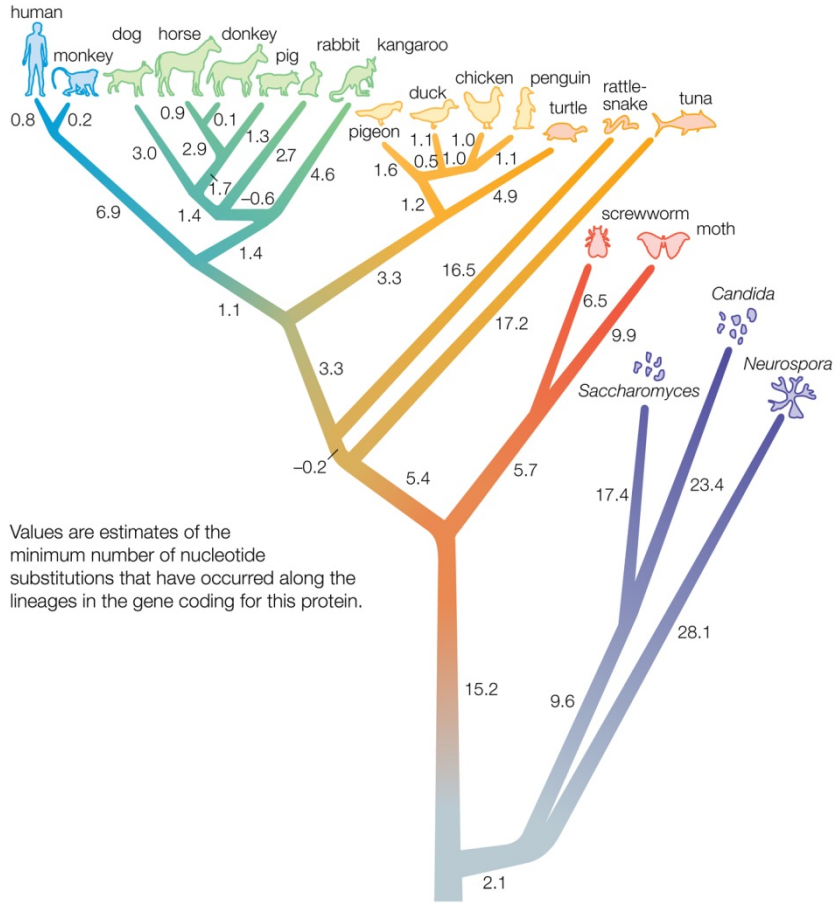
51.....

104

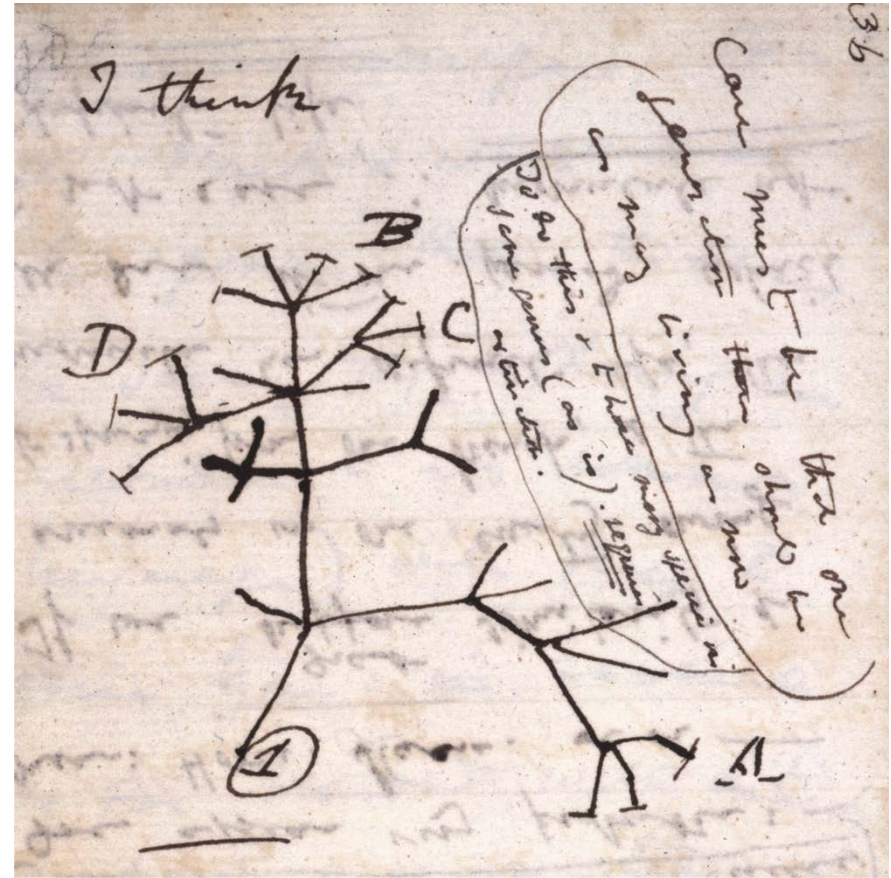
## cytochrome c

E. Margoliash, Emil L. Smith, Günther Kreil, Hans Tuppy. 1961. The Complete Amino Acid Sequence. *Nature* 192(4808):1125-1127.

Phylogeny based on nucleotide differences in the gene for cytochrome c



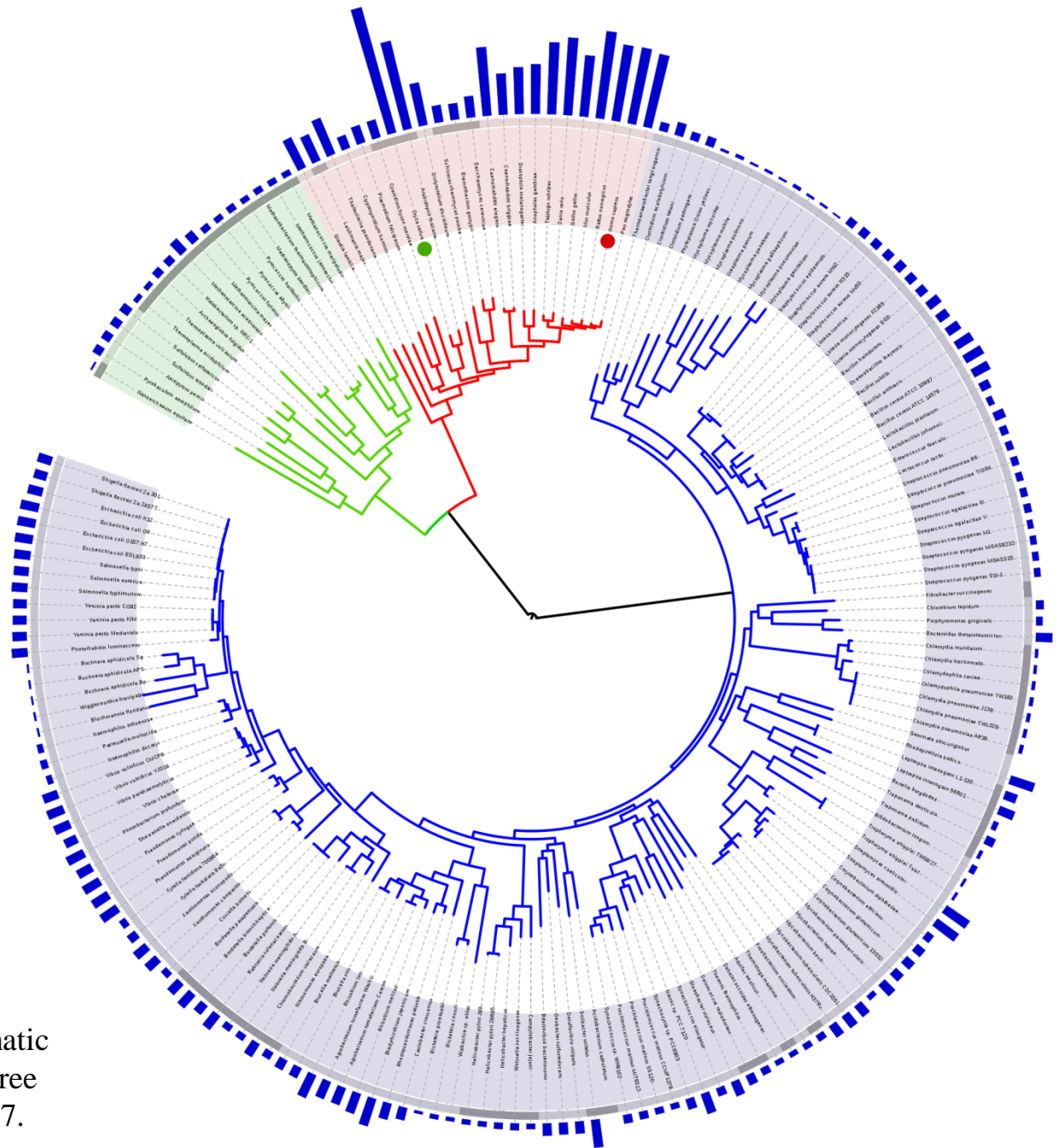
Encyclopedia Britannica, retrieved 27.02.2020



An evolutionary tree by Charles Darwin.

First Notebook on Transmutation of Species, 1837.  
 Courtesy of Cambridge University Library, 2014.

Darwins „Tree of Life“



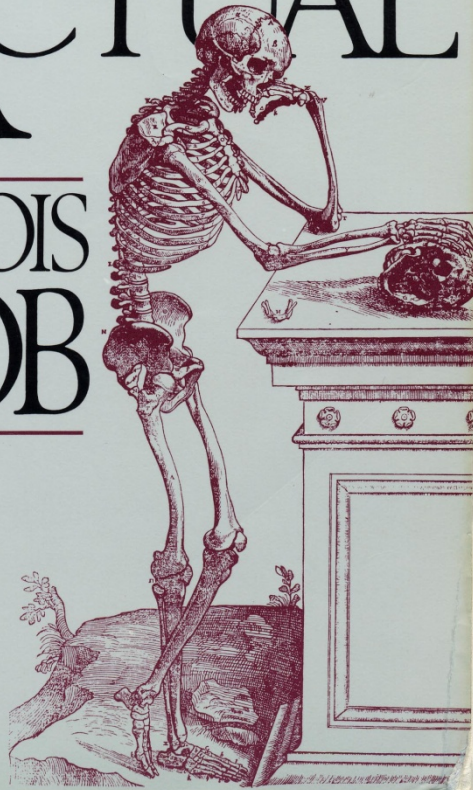
F.D. Ciccarelli. 2006. Toward automatic reconstruction of a highly resolved tree of life. *Science* 311(5765):1283-1287.

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# THE POSSIBLE & THE ACTUAL

FRANÇOIS  
JACOB



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## EVOLUTIONARY TINKERING

*Blood . . . is the best possible thing to have coursing  
through one's veins.*

—Woody Allen, *Getting Even*

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Evolution does not design with  
the eyes of an engineer,  
**evolution works like a tinkerer.**

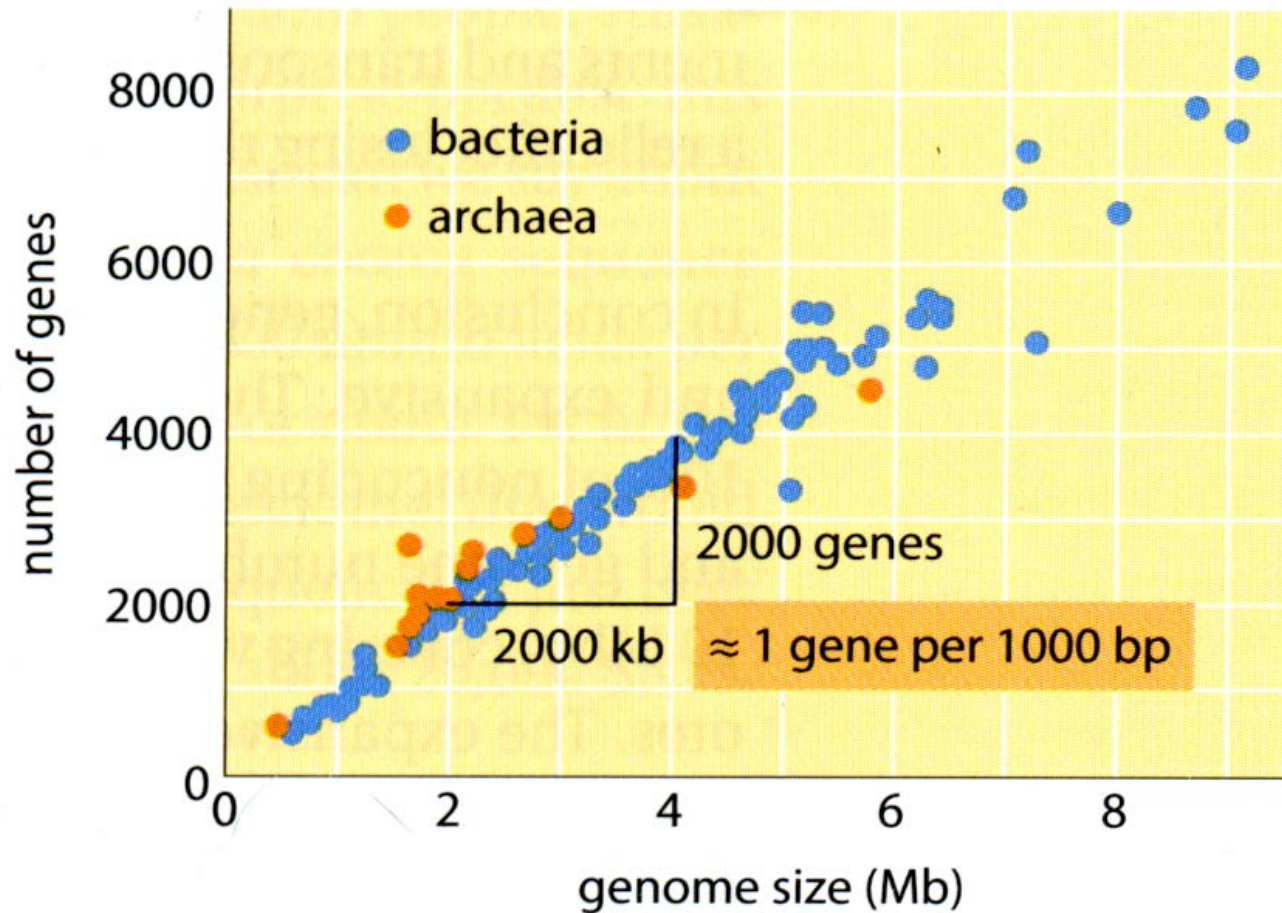
Francois Jacob, Pantheon Books,  
New York 1982

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Organismus	Protein kodierende Gene	Protein kodierbare Gene	Quotient
HIV	9	10	0.9
Bakteriophage $\lambda$	66	49	1.4
Epstein-Barr-Virus	80	170	0.47
<i>Thermotoga maritima</i>	1 900	1 900	<b>1.0</b>
<i>Staphylococcus aureus</i>	2 700	2 900	<b>0.93</b>
<i>Vibrio cholerae</i>	3 900	4 000	<b>0.98</b>
<i>Escherichia coli</i>	4 300	4 600	<b>0.93</b>
<i>Saccharomyces cerevisiae</i>	6600	12 000	0.55
<i>Caenorhabditis elegans</i>	20 000	100 000	0.5
<i>Arabidopsis thaliana</i>	27 000	140 000	0.19
<i>Zea mays</i>	33 000	2 300 000	0.014
<i>Mus musculus</i>	20 000	2 800 000	0.0075
<i>Homo sapiens</i>	21 000	3 200 000	0.0065

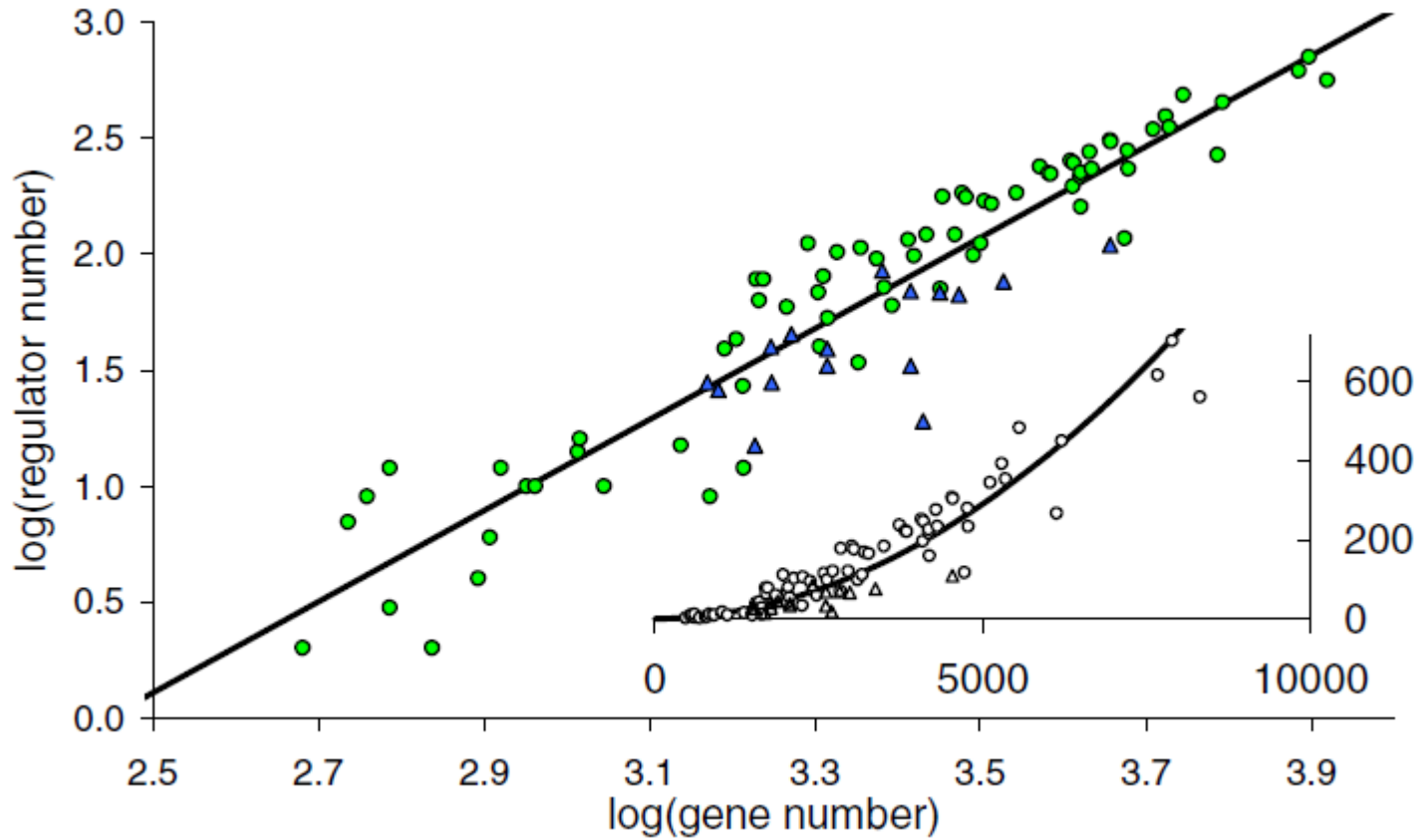
Zahl der kodierenden Proteine verglichen mit der Maximalzahl der kodierbaren Proteine.





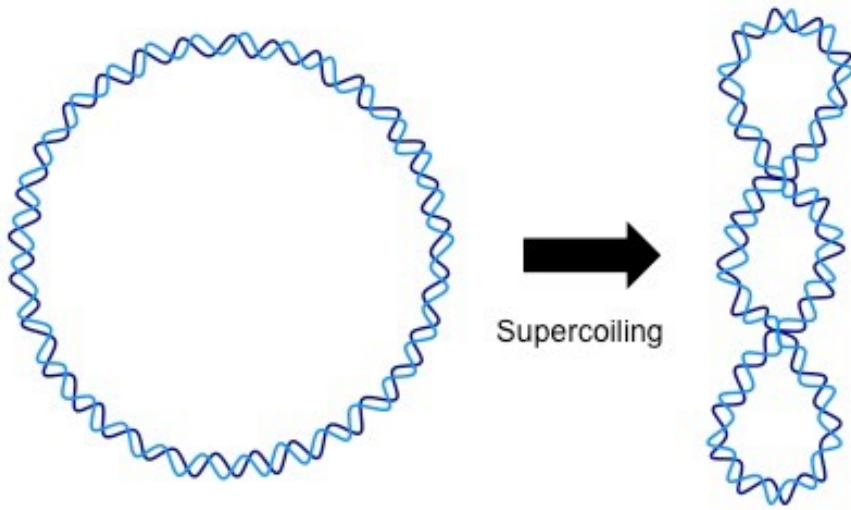
Number of genes as a function of genome size.

Ron Milo, Rob Phillips. Cell biology by the numbers. Garland Science, Tylor & Francis: New York, 2016, p.293.  
Adapted from Michael Lynch. The origins of genome architecture. Sinauer Associates, Oxford University Press: New York, 2007.

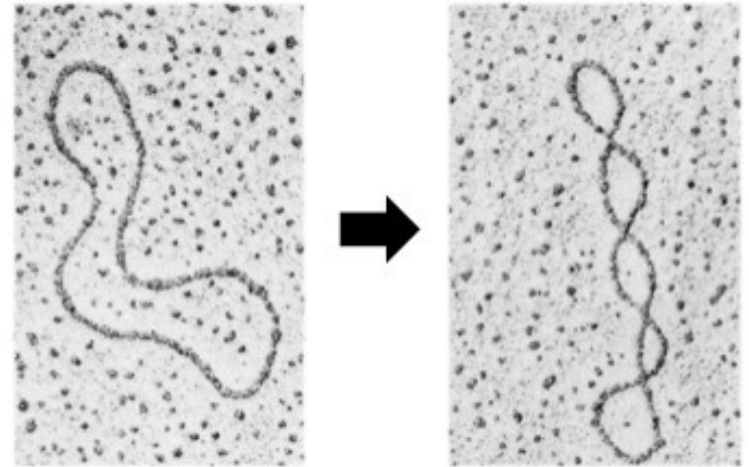


Double-logarithmic plot of transcriptional regulator number against total gene number for bacteria (green circles) and archaea (blue triangles).

Larry J. Croft, Martin J. Lercher, Michael J. Gagen, John S. Mattick. 2003. Is prokaryotic complexity limited by accelerated growth in regulatory overhead? *Genome Biology* 5:P2.



schematisch



Relaxed State

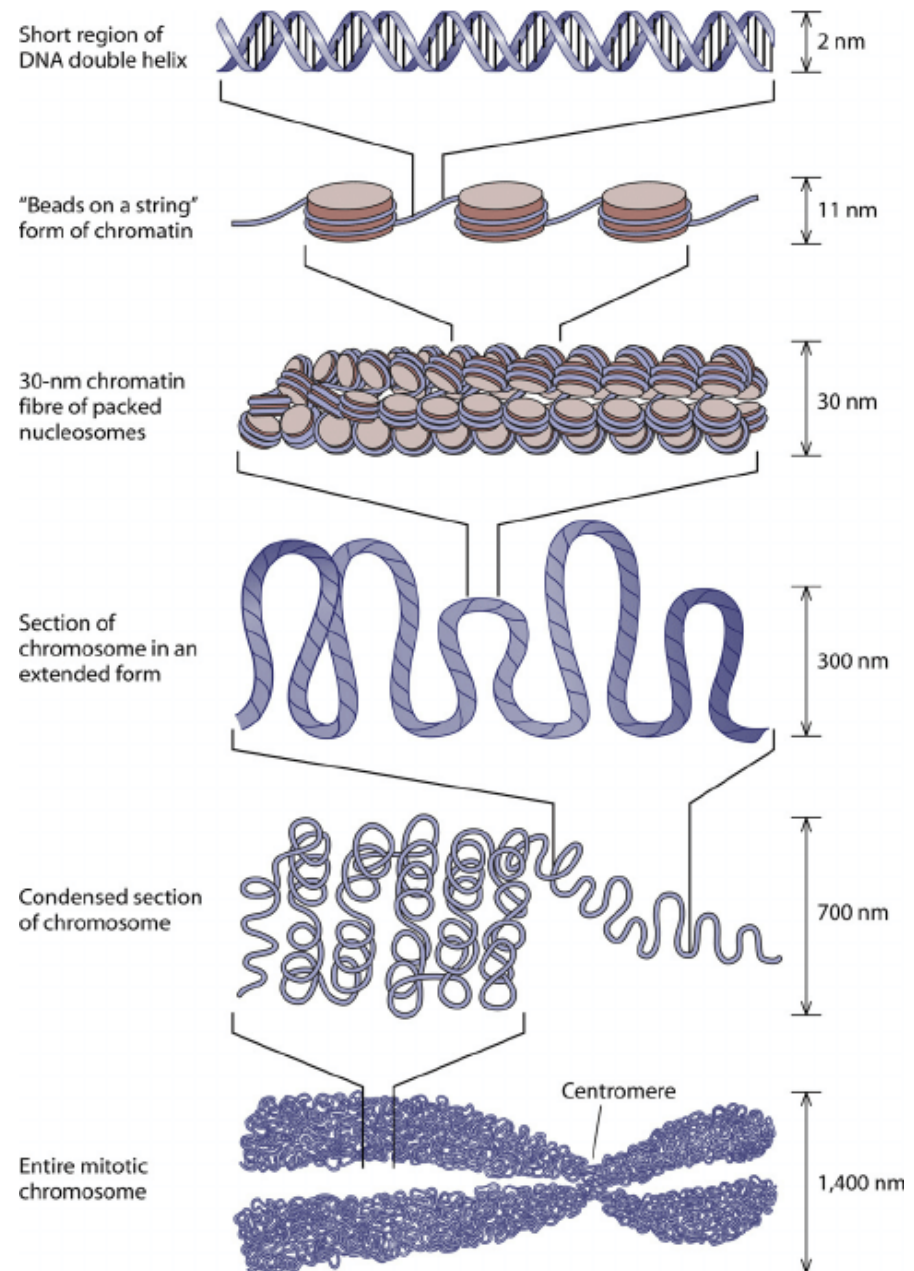
Supercoiled

elektronenmikroskopische Aufnahme

## DNA-Supercoil

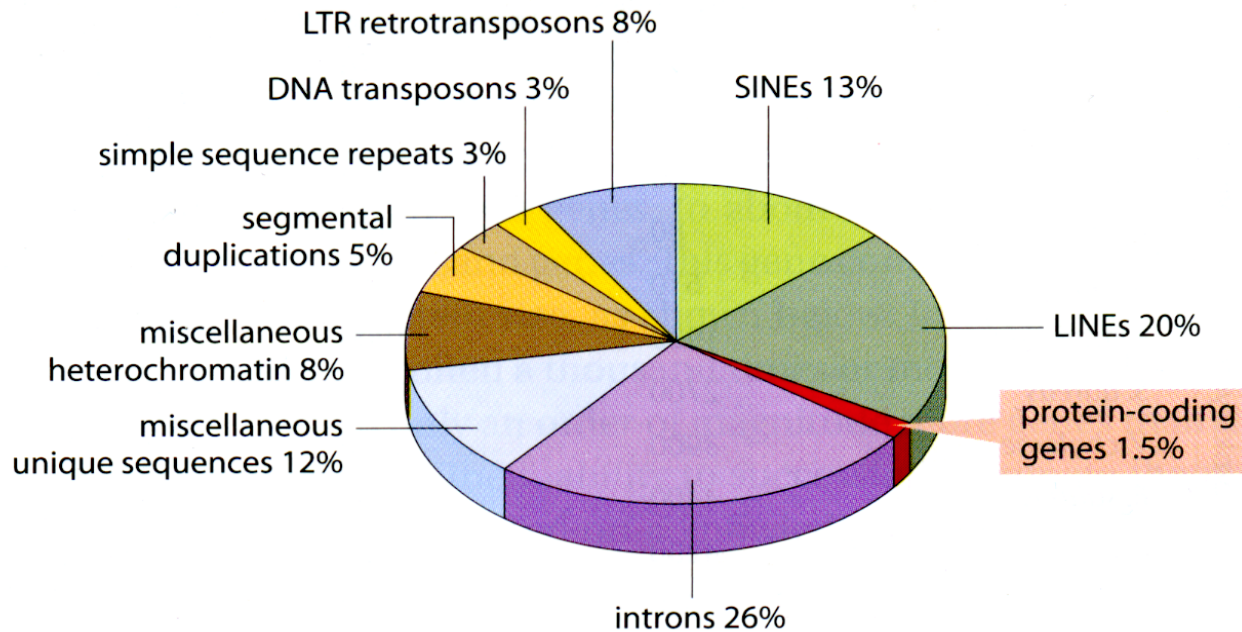
**Chromatin structure.** DNA is wrapped around a histone octamer to form nucleosomes. Nucleosomes are connected by stretches of linker DNA. This basic nucleosome structure is folded into a fiber-like structure of about 30 nm in diameter. These 30-nm fibers are further compacted into higher-order structures, which have not been characterized in detail.

An Jansen, Kevin J. Verstrepen. 2011. Nucleosome Positioning in *Saccharomyces cerevisiae*. *Microbiology and Molecular Biology Reviews* 75(2):301-320.





## main components of the human genome



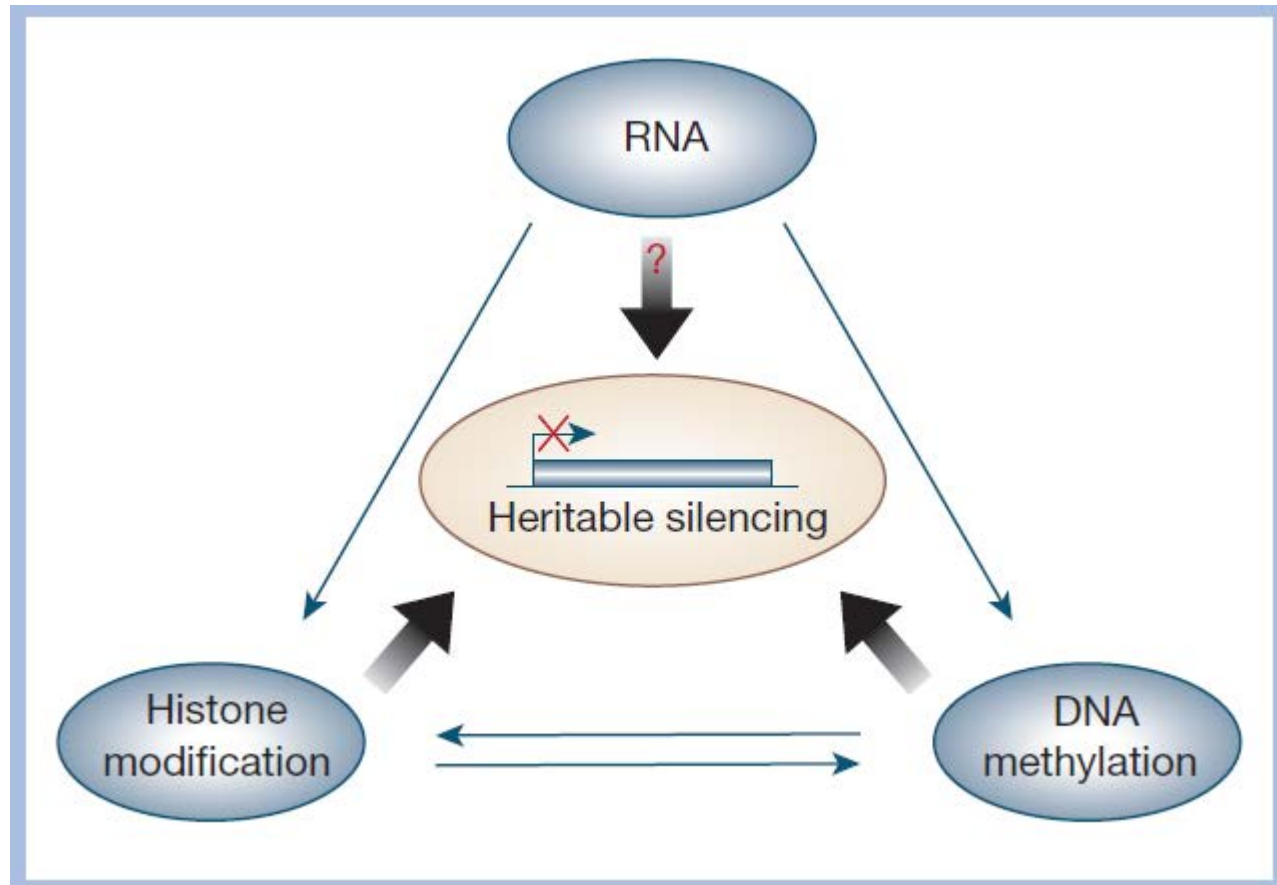
**Figure 5-7** The different sequence components making up the human genome. About 1.5% of the genome consists of the  $\approx 20,000$  protein-coding sequences, which are interspersed by the noncoding introns, making up about 26%. Transposable elements are the largest fraction (40–50%), including, for example, long interspersed nuclear elements (LINEs) and short interspersed nuclear elements (SINEs). Most transposable elements are genomic remnants, which are currently defunct. (BNID 110283) (Adapted from Gregory TR [2005] *Nat Rev Genet* 9:699-708.)

„Der Begriff Epigenetik definiert alle meiotisch und mitotisch vererbaren Veränderungen der Genexpression, die nicht in der DNA-Sequenz selbst codiert sind.“

Übersetzt aus dem englischen Originaltext:

„The term *epigenetic* defines all meiotically and mitotically heritable changes in gene expression that are not coded in the DNA sequence itself.“

Gerda Egger, Gangning Liang, Ana Aparicio, Peter A. Lones. 2004. Epigenetics in Human Disease and Prospects for Epigenetic Therapy. Nature 429(6990):457-463.



Interaction between RNA, histone modification and DNA methylation in heritable silencing

Gerda Egger, Gangning Liang, Ana Aparicio, Peter A. Jones. 2004. Epigenetics in human disease and prospects for epigenetic therapy. Nature 429(6990):457-463.



Leading Edge  
Review

Cell

# The Noncoding RNA Revolution— Trashing Old Rules to Forge New Ones

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<sup>1</sup>Howard Hughes Medical Institute

<sup>2</sup>Department of Chemistry & Biochemistry, BioFrontiers Institute, University of Colorado Boulder, Boulder, CO 80309, USA

<sup>3</sup>Department of Molecular Biophysics and Biochemistry, Boyer Center for Molecular Medicine, Yale University School of Medicine, New Haven, CT 06536, USA

\*Correspondence: [thomas.cech@colorado.edu](mailto:thomas.cech@colorado.edu)  
<http://dx.doi.org/10.1016/j.cell.2014.03.008>

Noncoding RNAs (ncRNAs) accomplish a remarkable variety of biological functions. They regulate gene expression at the levels of transcription, RNA processing, and translation. They protect genomes from foreign nucleic acids. They can guide DNA synthesis or genome rearrangement. For ribozymes and riboswitches, the RNA structure itself provides the biological function, but most ncRNAs operate as RNA-protein complexes, including ribosomes, snRNPs, snoRNPs, telomerase, microRNAs, and long ncRNAs. Many, though not all, ncRNAs exploit the power of base pairing to selectively bind and act on other nucleic acids. Here, we describe the pathway of ncRNA research, where every established “rule” seems destined to be overturned.



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**Ivo L. Hofacker**, **Christoph Flamm**, Theoretische Chemie, Universität Wien, AT

Danke für die Aufmerksamkeit!

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<http://www.tbi.univie.ac.at/~pks>

