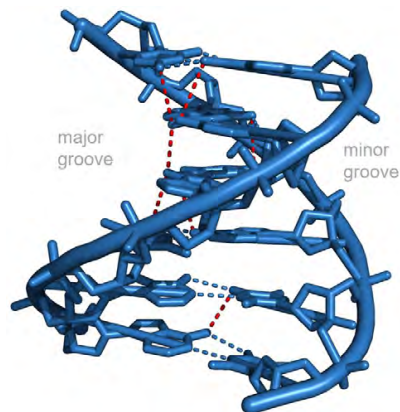




"МИС-РТ"-2022 Сборник №79-2 <http://ikar.udm.ru/mis-rt.htm>



Modeling of charge oscillations in DNA. A search for resonance structures in the genome.

Max Myakishev-Rempel, max@dnaresonance.org

I. Savelev¹, A. Samchenko¹, A. Klimov¹, L. Shishkin¹, L. Yulmetova¹, O. Polesskaya², V. Bashinskaya¹, A. Voronka¹, A. Vetcher^{1,3,4}, R. Miller⁵, E. Naumova⁶, M. Myakishev-Rempel¹

1 - DNA Resonance Research Foundation, San Diego, CA, USA

2 - University of California, San Diego, USA

3 - Nanotechnology Scientific and Educational Center, Institute of Biochemical Technology

and Nanotechnology, Peoples Friendship University of Russia, Moscow, Russia

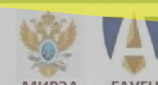
4 - Shishonin Complementary and Integrative Health Clinic, Moscow, Russia

5 - OAK, Inc., Grants Pass, OR, USA

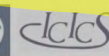
6 - Rzhzanov Institute of Semiconductor Physics, Siberian Branch of RAS, Novosibirsk, Russia

Jan 18, 2022

Международный междисциплинарный семинар
"АЛГЕБРАИЧЕСКАЯ БИОЛОГИЯ И ТЕОРИЯ СИСТЕМ"



при участии
учредителей

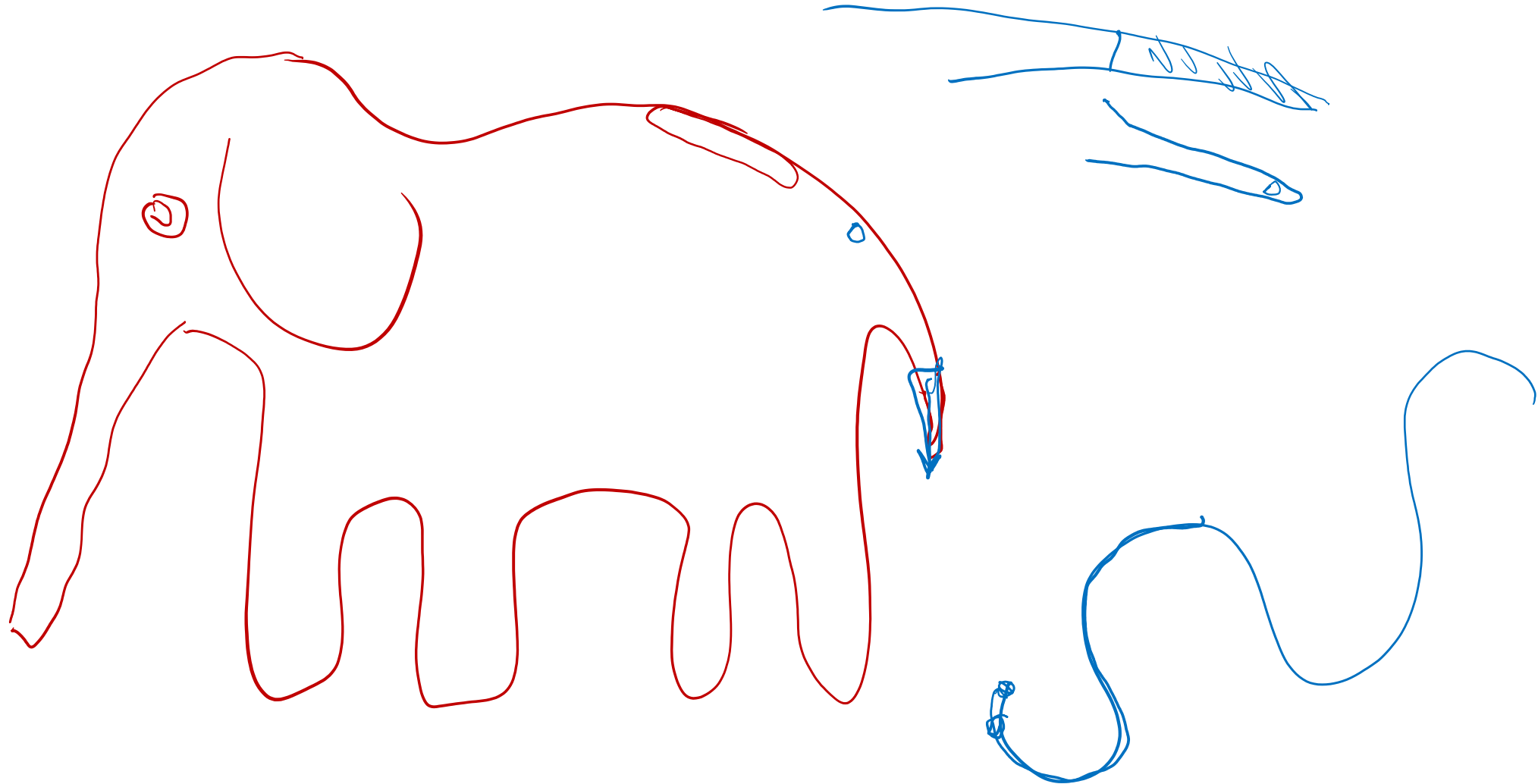


Linnaeus
University,
Hörsalen
Linnéhuset ...

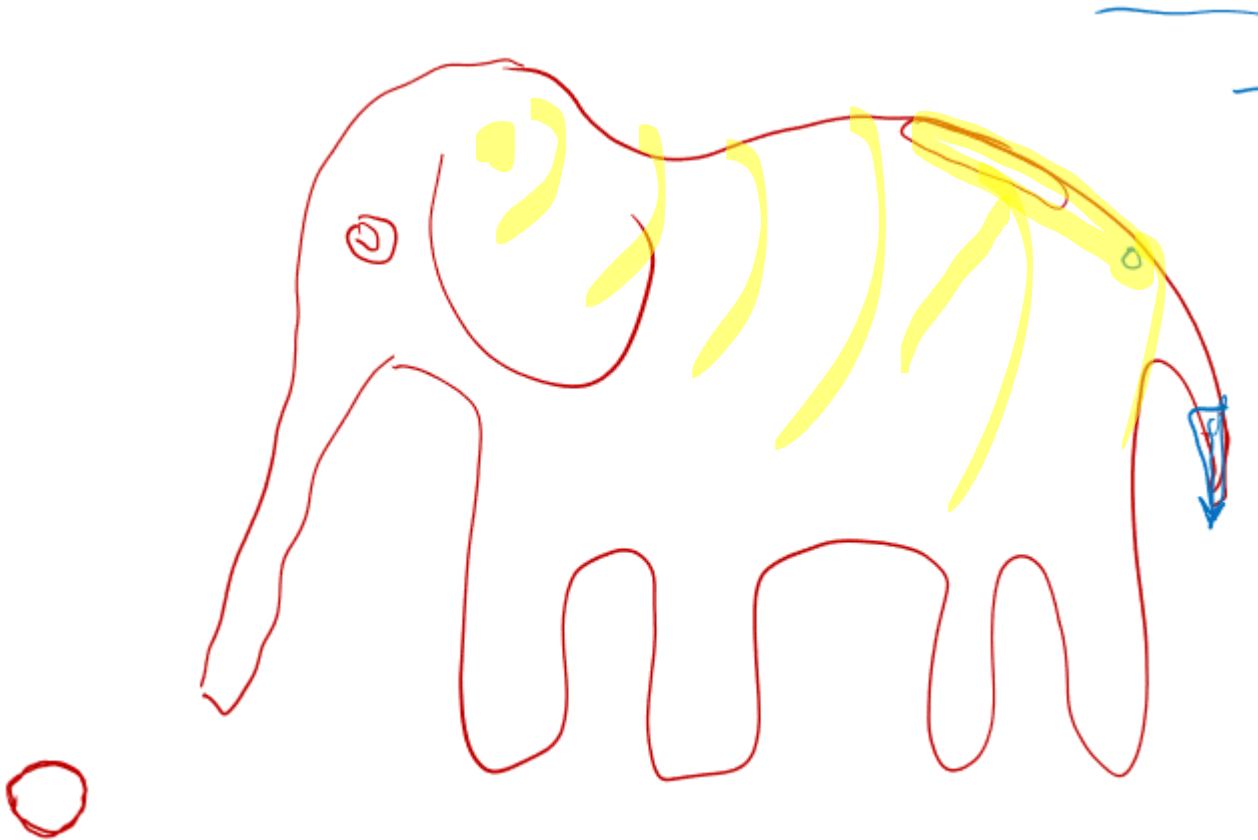
Morphogenetic field



Morphogenetic field



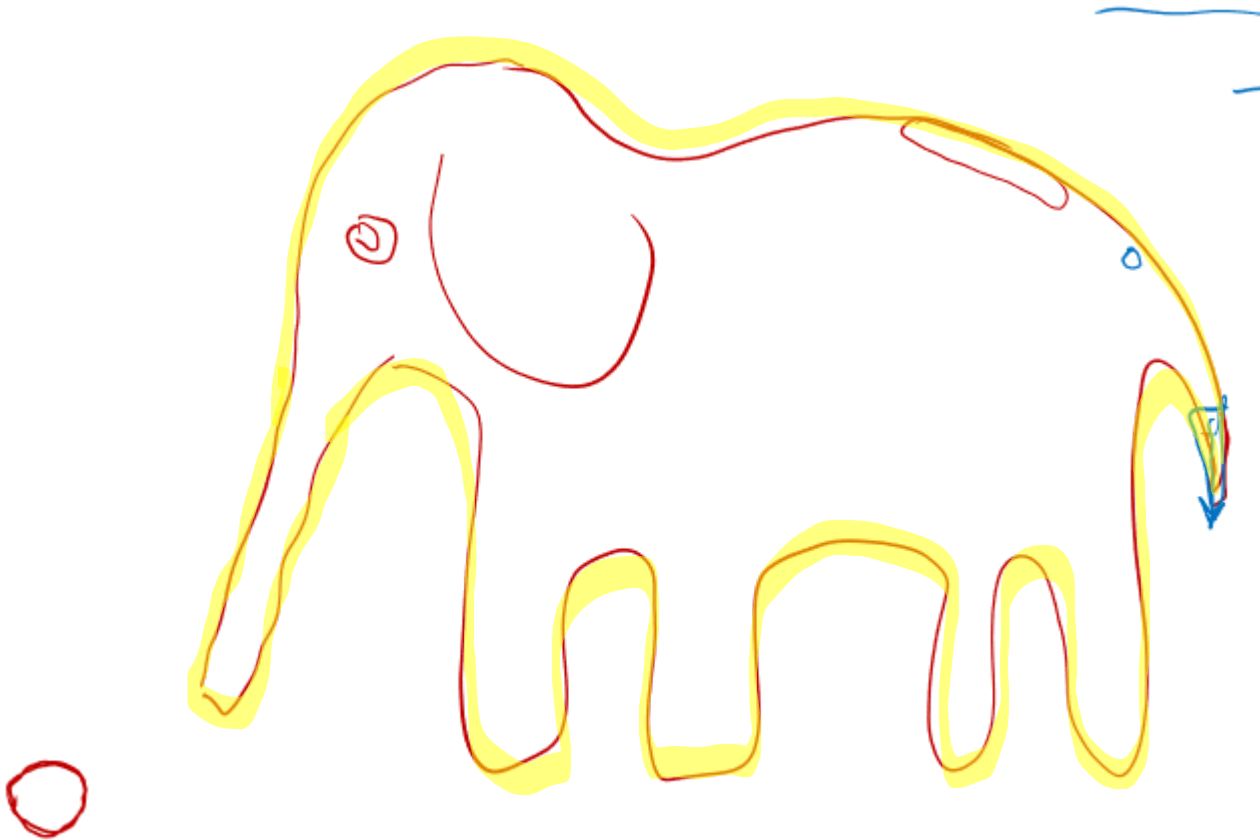
Morphogenetic field



- Gradients of morphogenic proteins and other signaling molecules
- Neuronal signaling
- Mechanoception
- Electrostatic fields
- [Electromagnetic, acoustic and other fields are rejected]

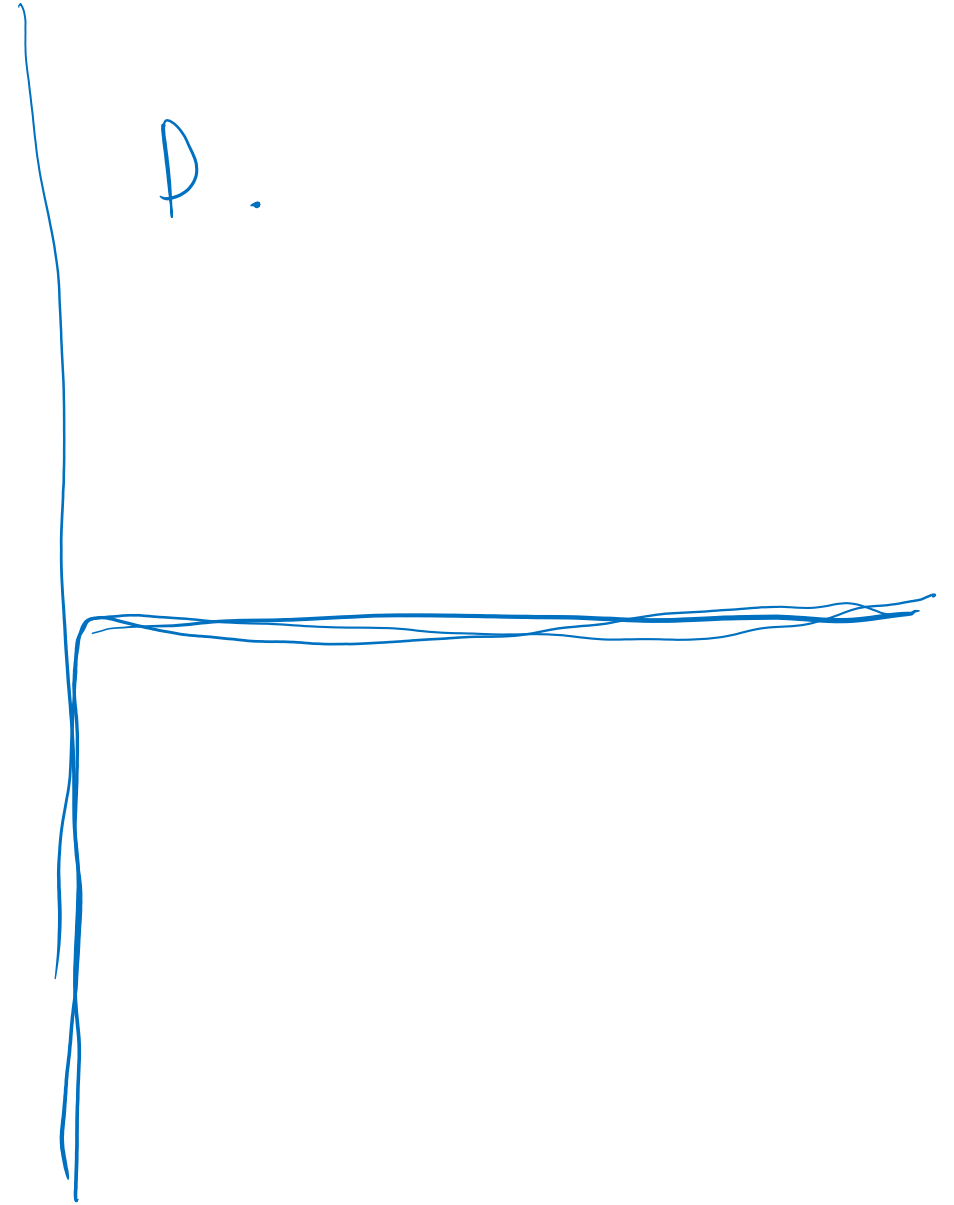
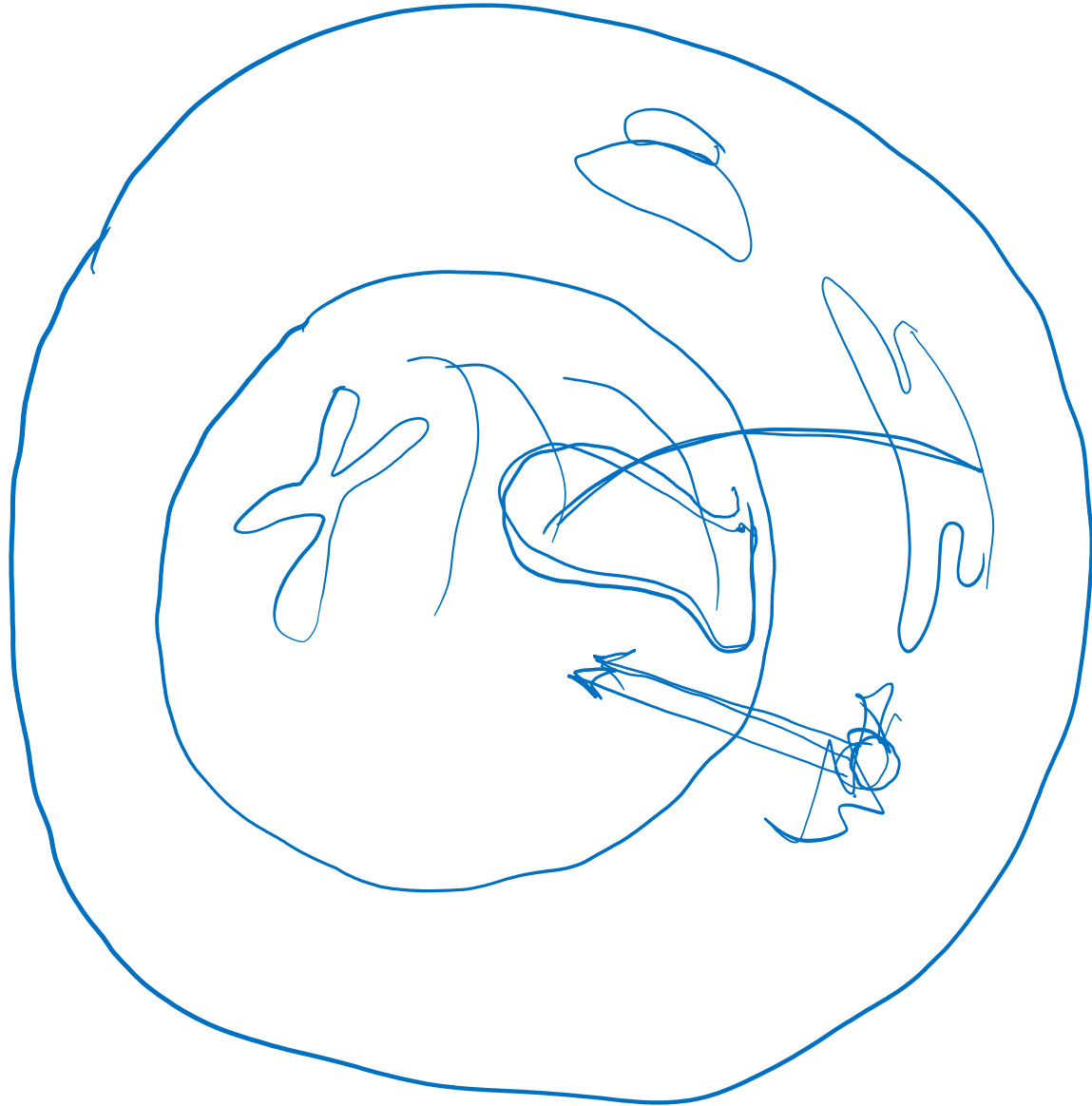


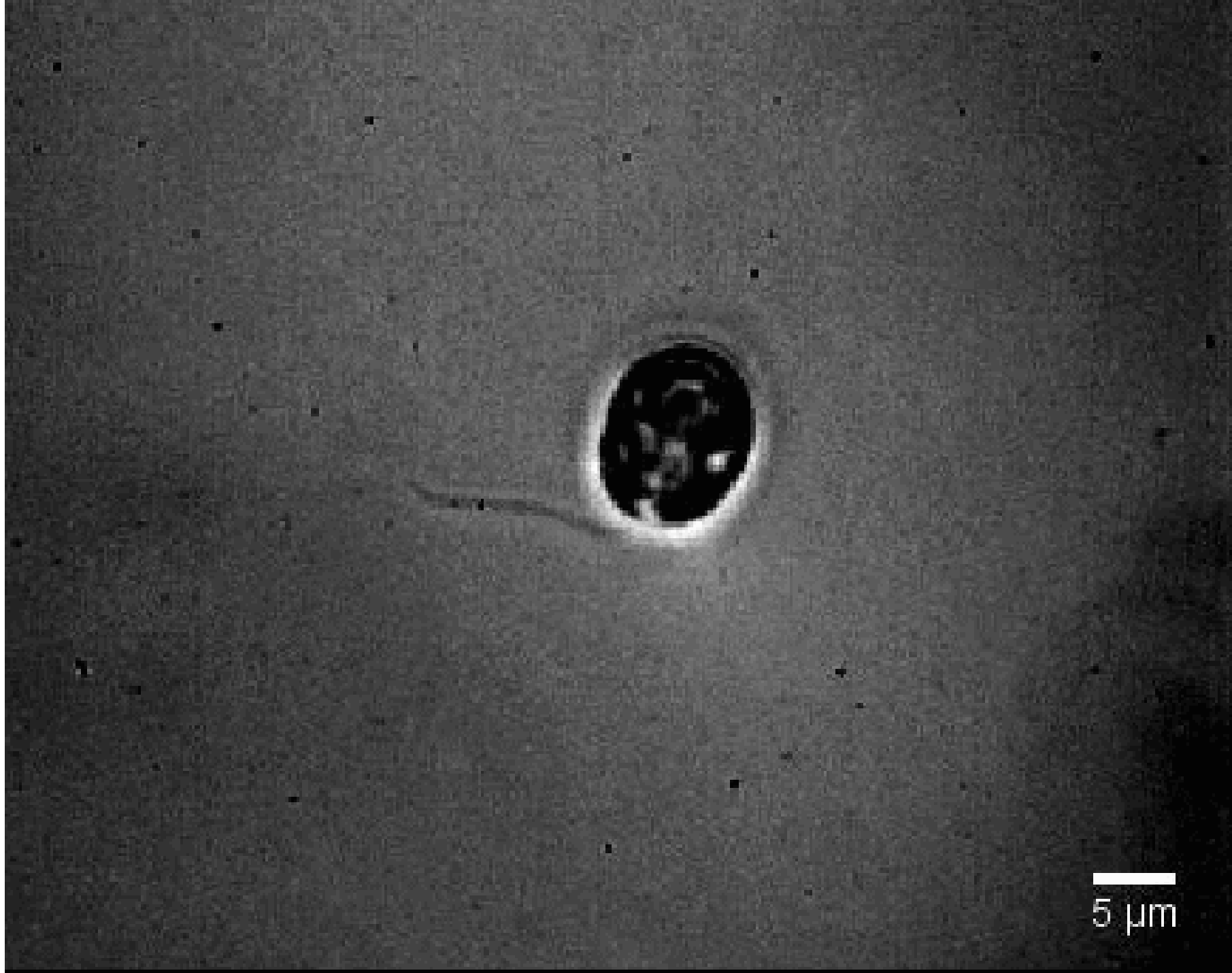
Morphogenetic field



- Gradients of morphogenic proteins and other signaling molecules
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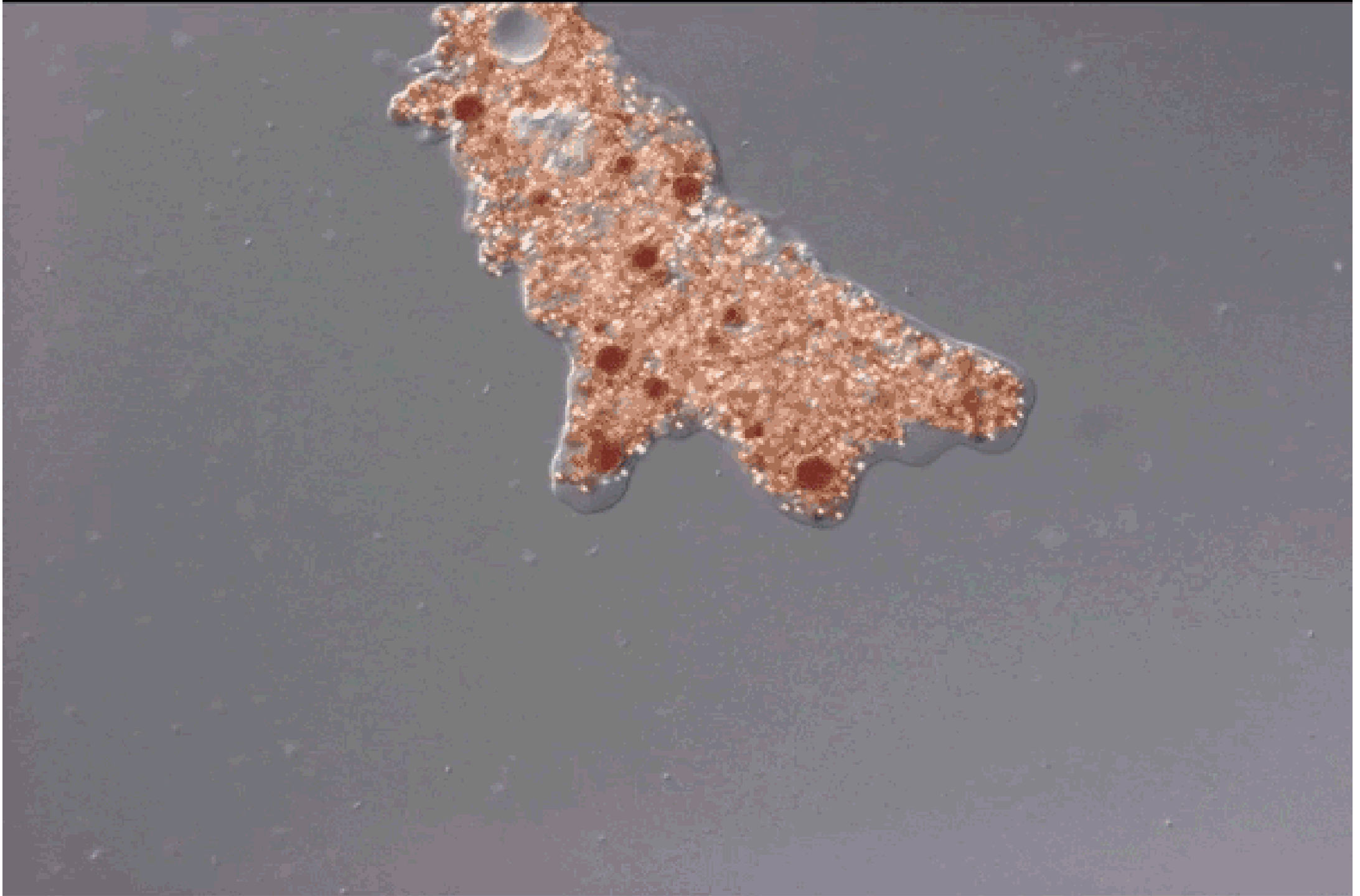


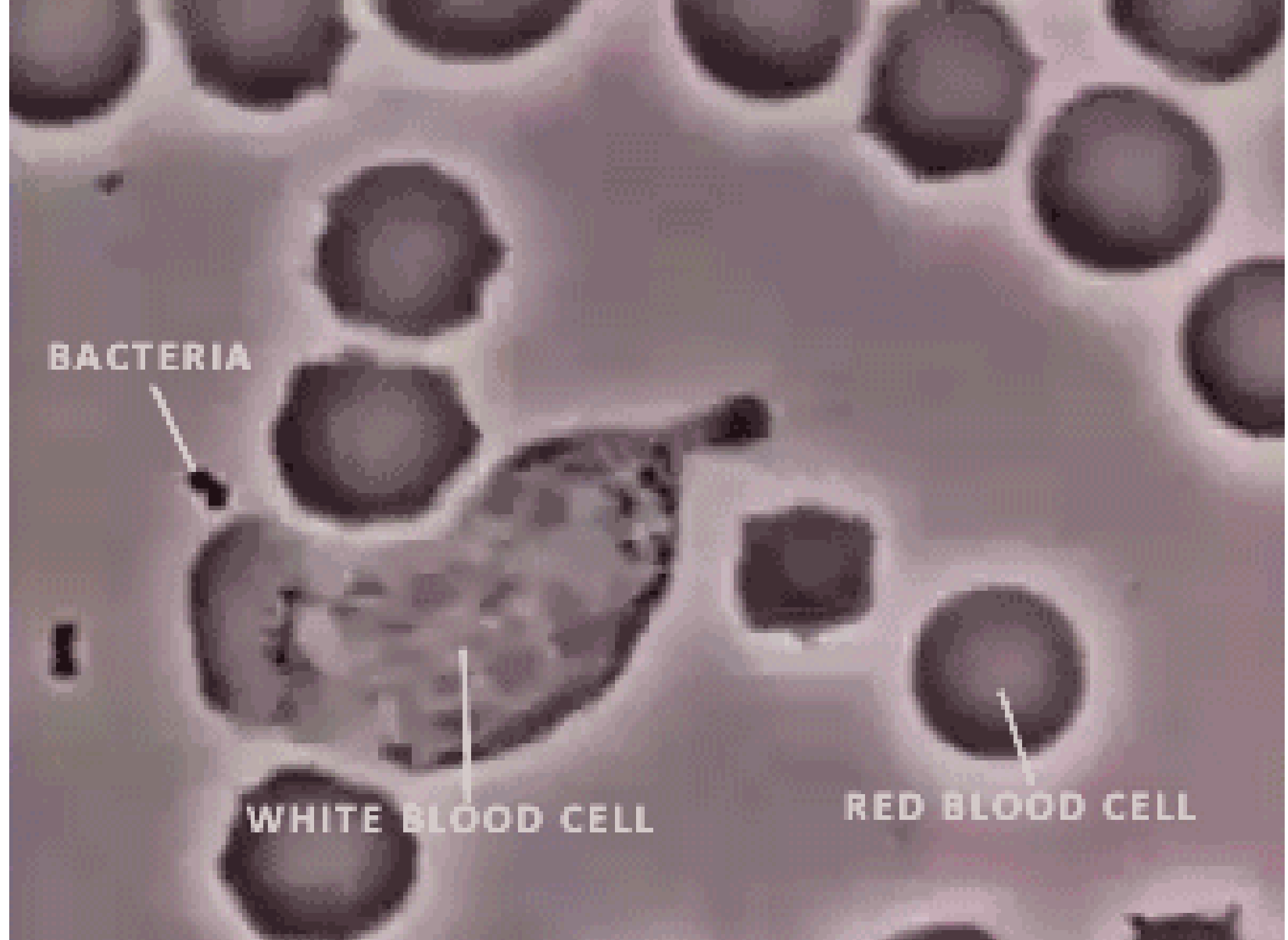












1774

Animal magnetism

Franz Mesmer



1810

vitalism: life is driven by a vital force.



Berzelius

1840



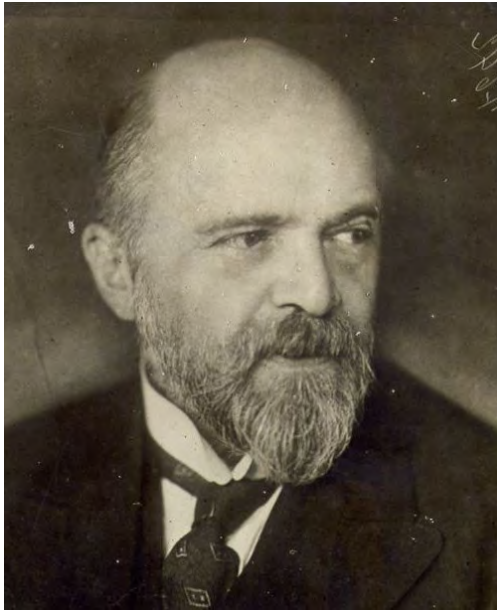
Johannes Peter Müller

- the presence of a soul makes each organism an indivisible whole and
- light and sound waves show that living organisms possess a life-energy unexplainable by physical laws.



1892

Based on experiments with fertilized sea urchin eggs
proposed **biofield**



THE
HISTORY & THEORY
OF VITALISM

BY
HANS DRIESCH

PROFESSOR OF PHILOSOPHY IN THE UNIVERSITY OF HEIDELBERG
AUTHOR OF 'THE SCIENCE AND PHILOSOPHY OF THE ORGANISM'
'THE PROBLEM OF INDIVIDUALITY,' ETC.



Experimental biologist and metaphysicist Hans Driesch.



early
1920s

Alexander Gurwitsch, Hans Spemann, and Paul Weiss
independently proposed **morphogenetic fields**



Alexander Gurwitsch



Hans Spemann



Paul Alfred Weiss



1953

Double helix



Crick, Watson, Franklin, Wilkins



1963

Per-Olov Löwdin

- Quantum genetics
 - proton tunneling in DNA
 - delocalized pi electrons in DNA
- (didn't expand to biofield, only discussed nano-scale quantum events).

Löwdin, Per-Olov. "Proton tunneling in DNA and its biological implications." *Reviews of Modern Physics* 35.3 (1963): 724.

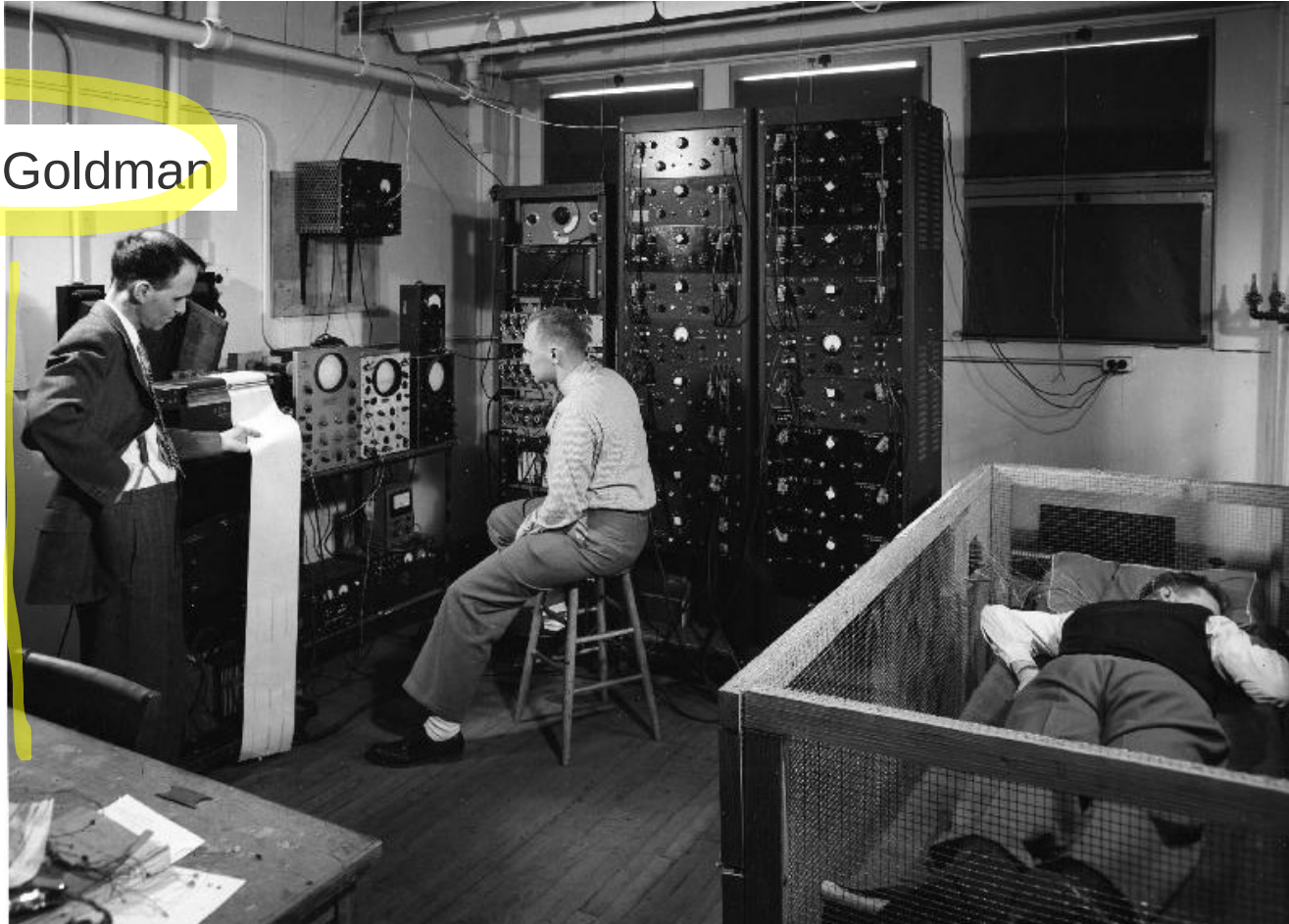
Löwdin, Per-Olov. "Quantum genetics and the aperiodic solid: Some aspects on the biological problems of heredity, mutations, aging, and tumors in view of the quantum theory of the DNA molecule." *Advances in quantum chemistry*. Vol. 2. Academic Press, 1966. 213-360.



1969

Biological Quantum Mechanics and DNA hologram - an electrical engineering view.

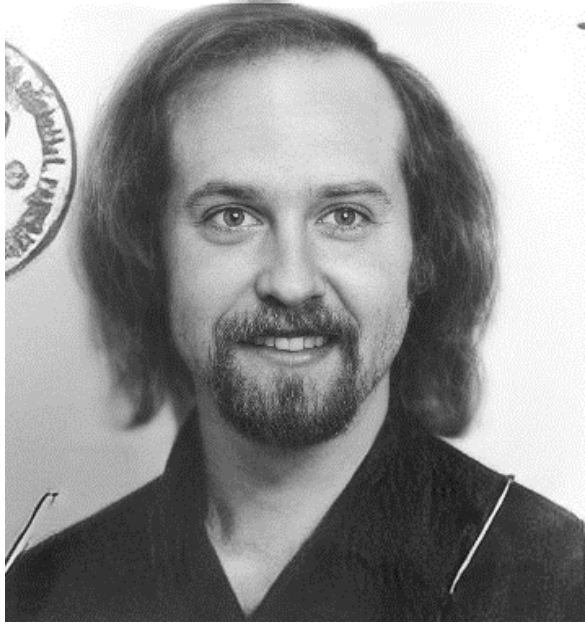
Stanford Goldman



Goldman, Stanford. *INTRODUCTION TO BIOLOGICAL QUANTUM MECHANICS*. SYRACUSE UNIV NY DEPT OF ELECTRICAL ENGINEERING, 1969.

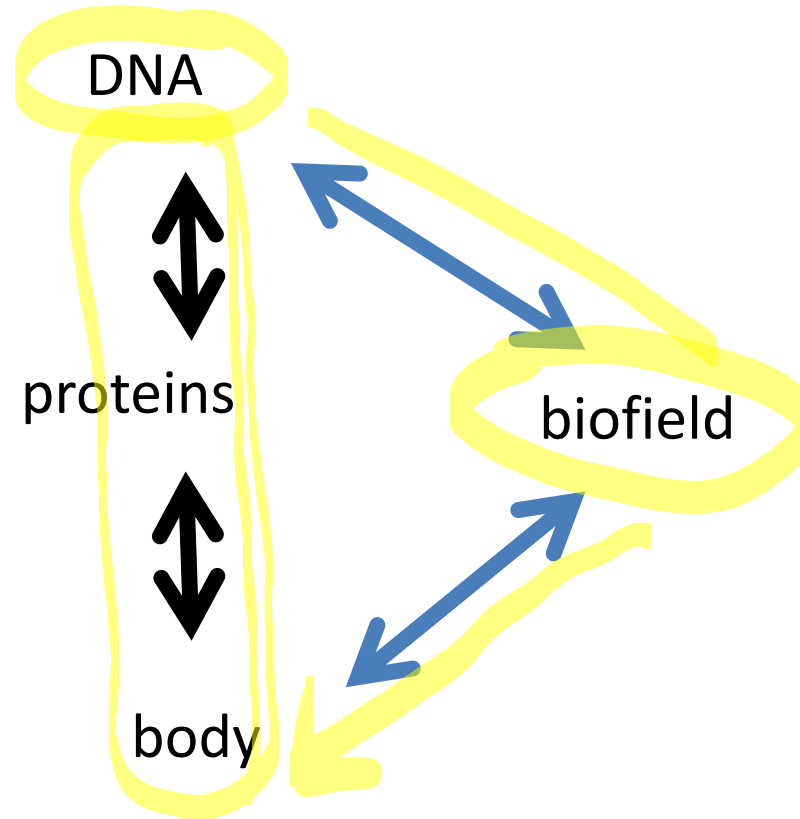


1972



Dr. Richard Alan Miller,
the coauthor,
proposed that DNA
creates biofield in
1972.

DNA hologram is the biofield

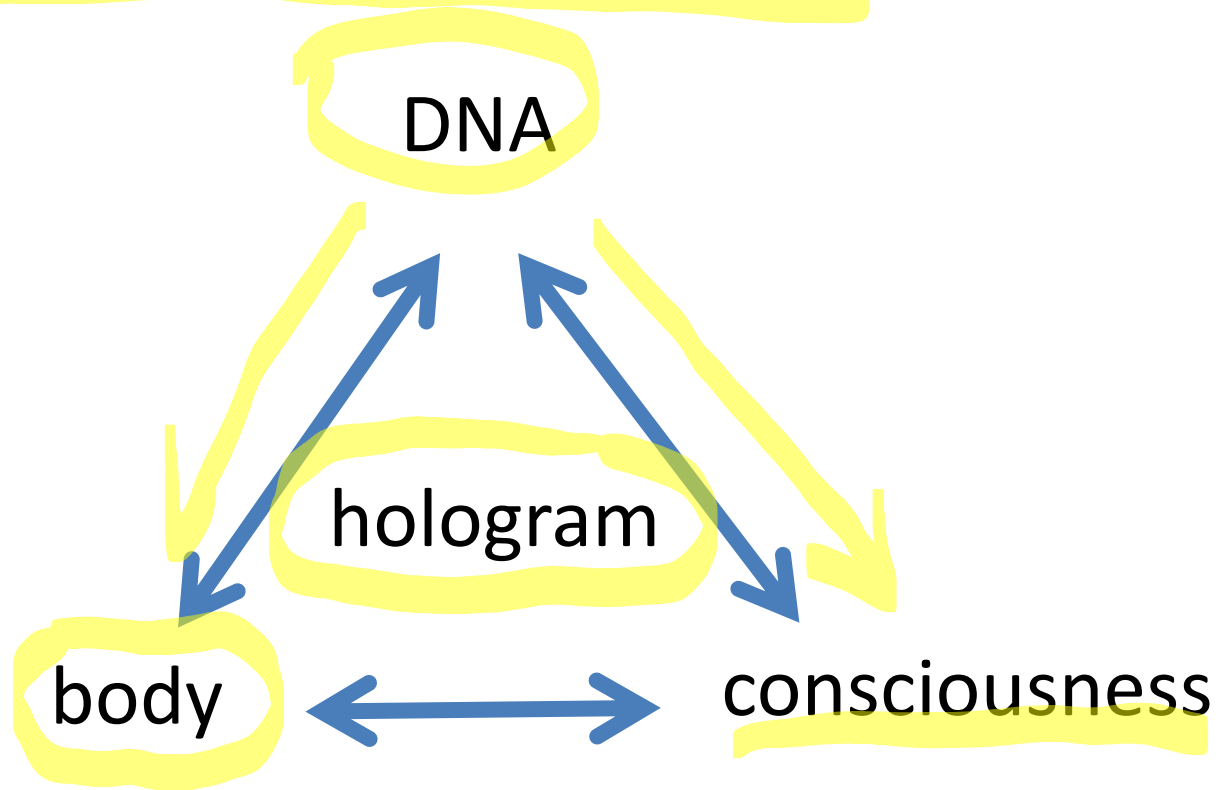


Richard Alan Miller, Burt Webb - conference presentation, 1972.
Richard Alan Miller, Burt Webb, and Darden Dickson. "A holographic concept of reality." *Psychoenergetic Systems* 1 (1975): 55-62.

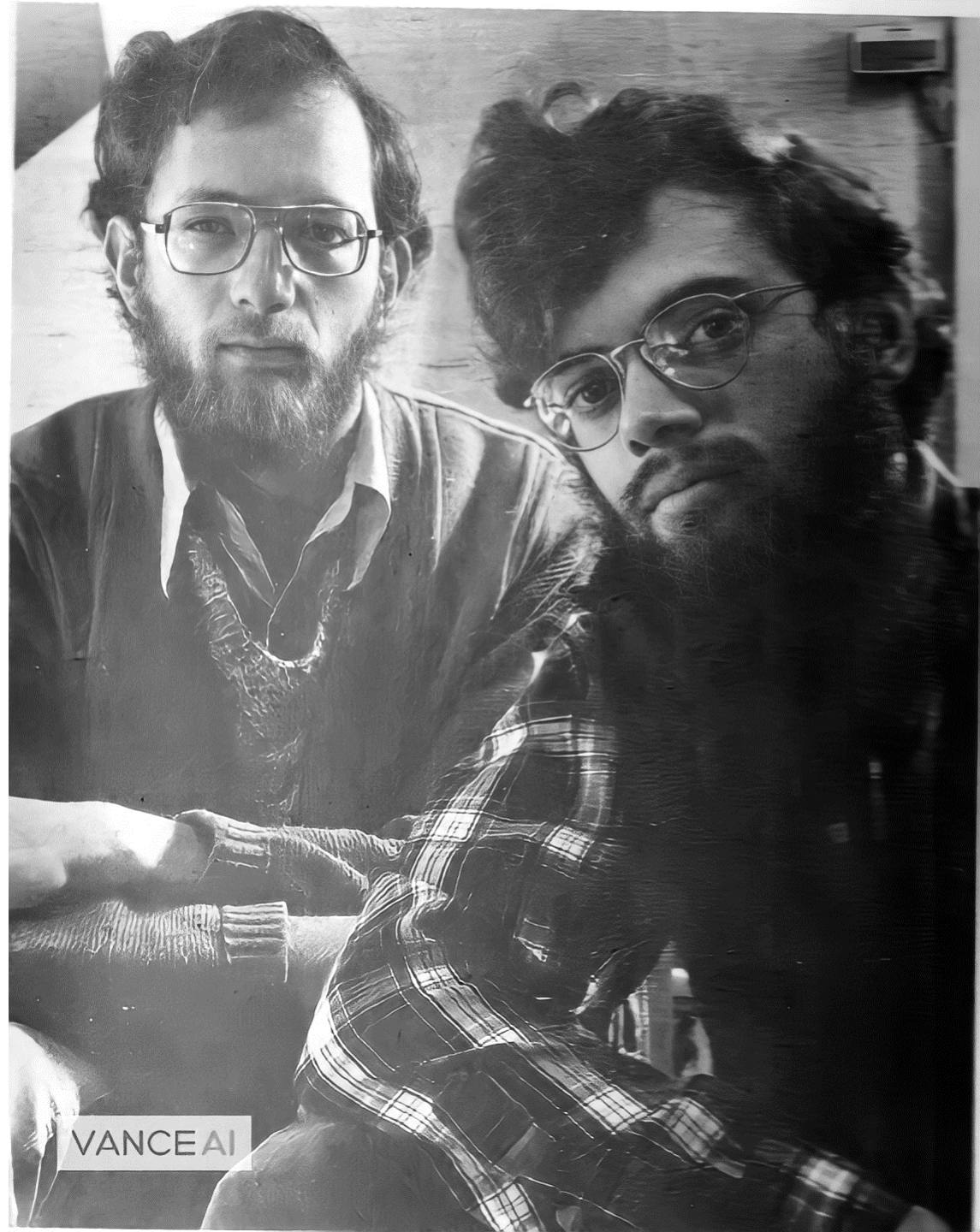


1976

Terence and Dennis McKenna



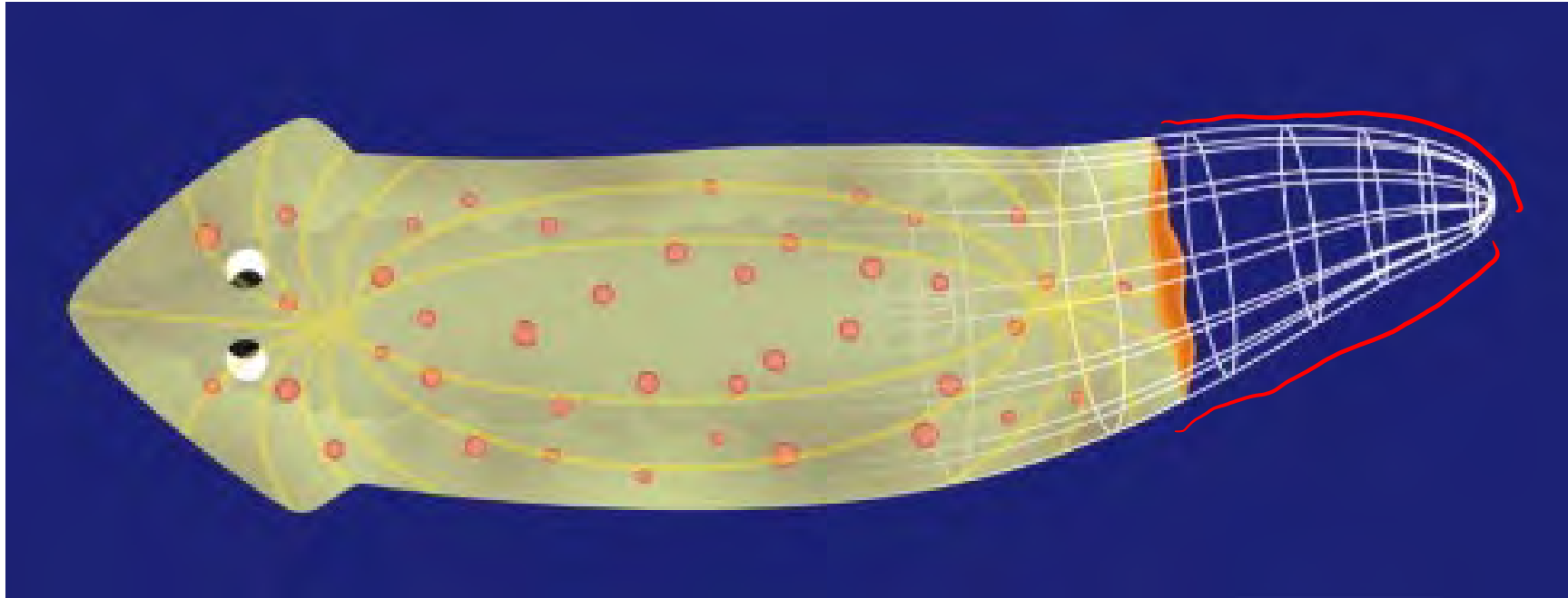
McKenna, Terence K., and Dennis J. McKenna. *The invisible landscape: Mind, hallucinogens, and the I Ching*. Harper San Francisco, 1993.



Experimental evidence is scarce



Objective: To verify the existence of the biofield

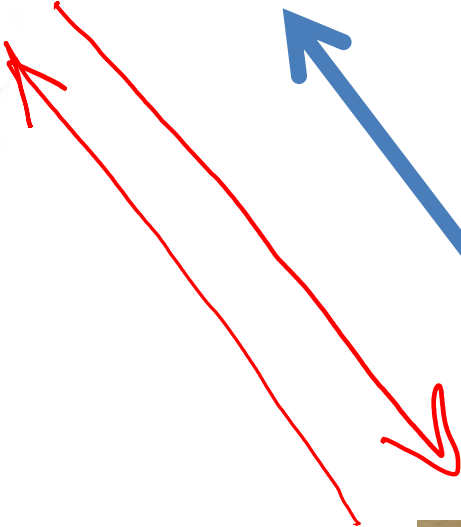
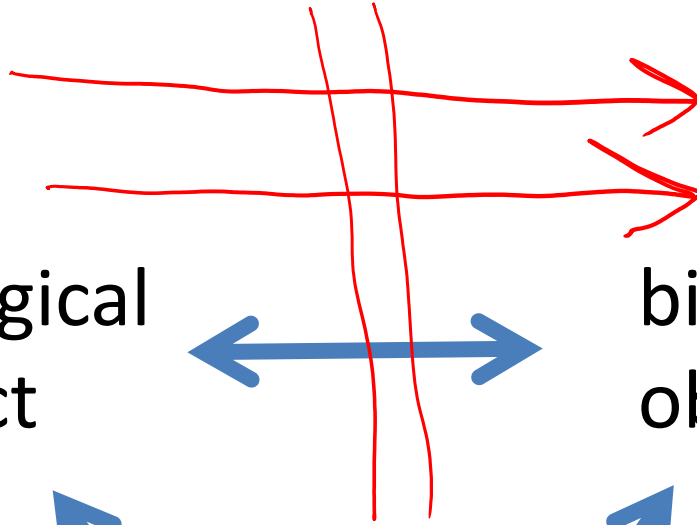




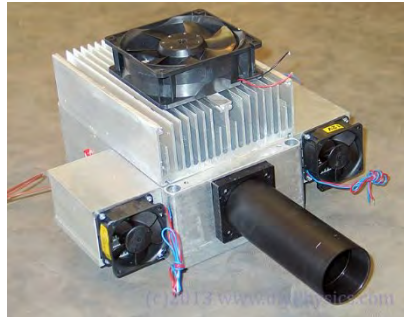
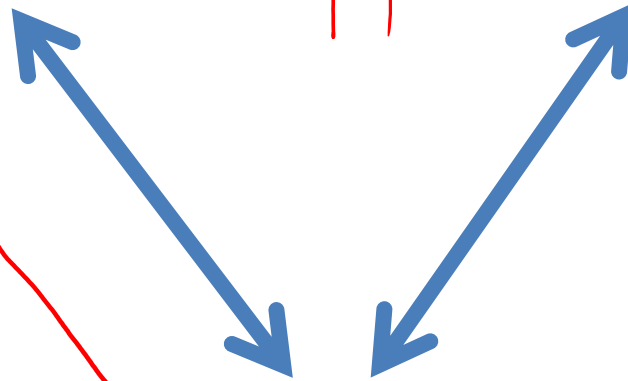
biological
object

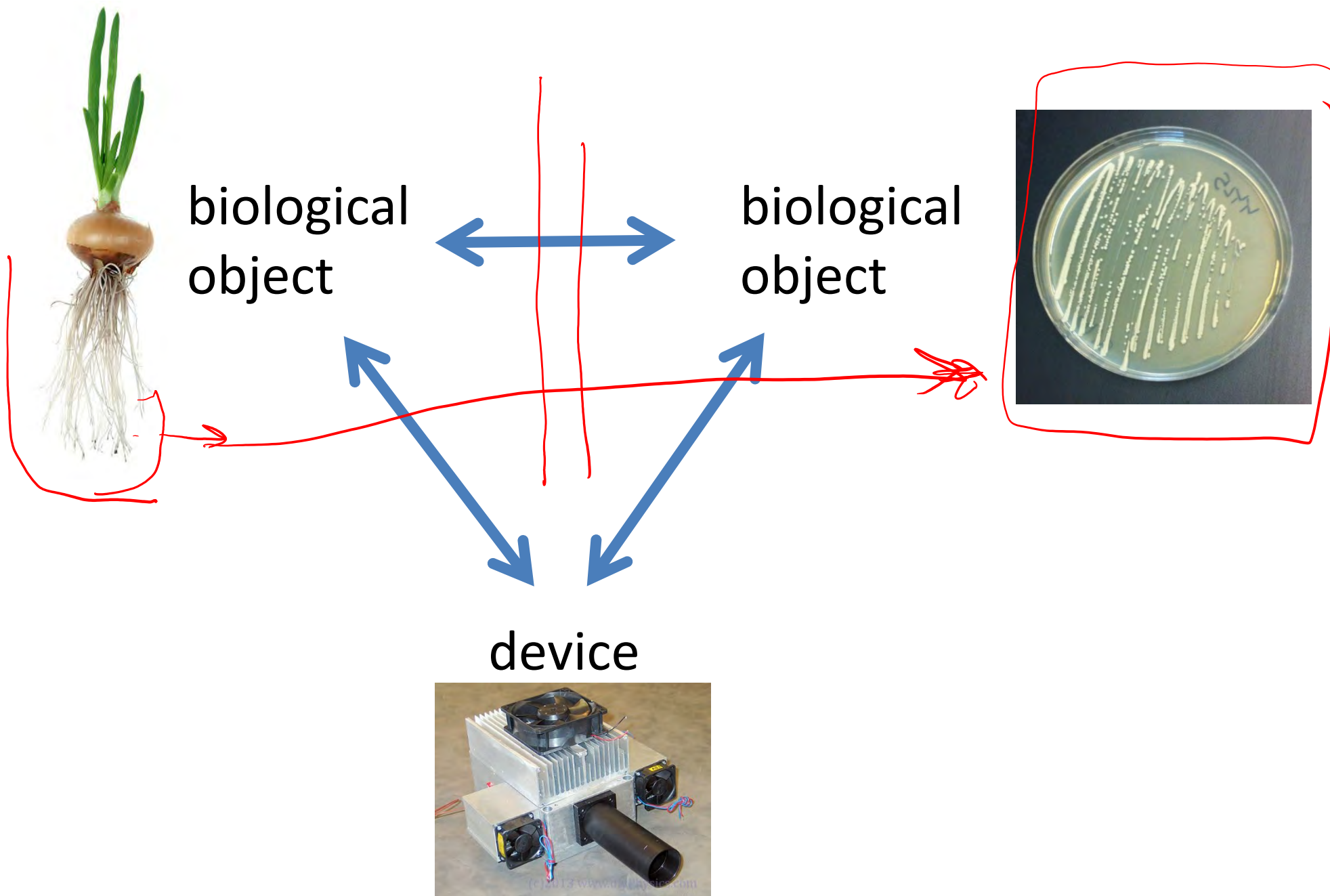


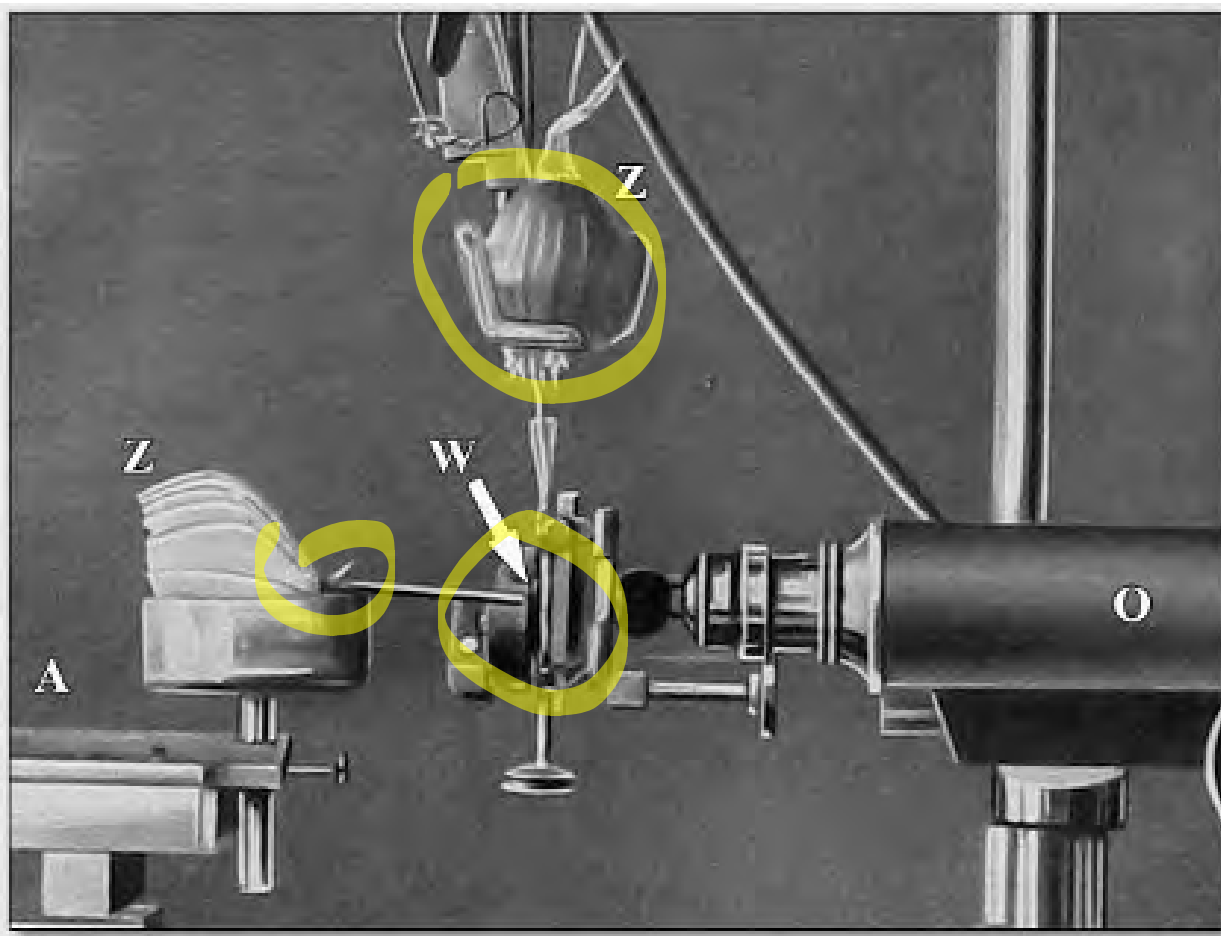
biological
object



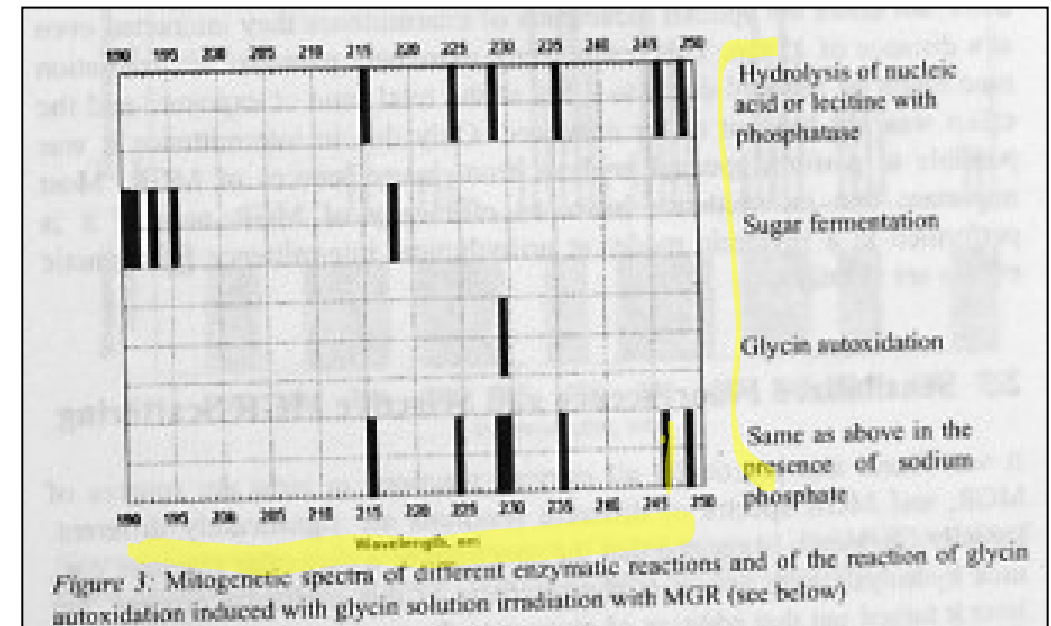
device



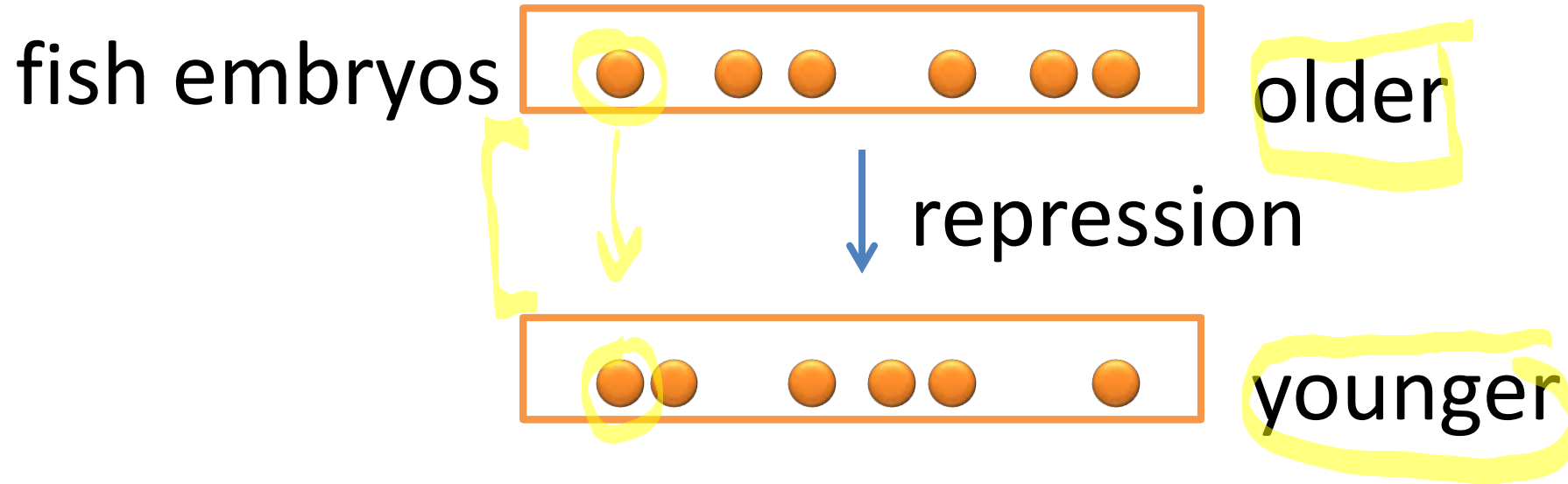


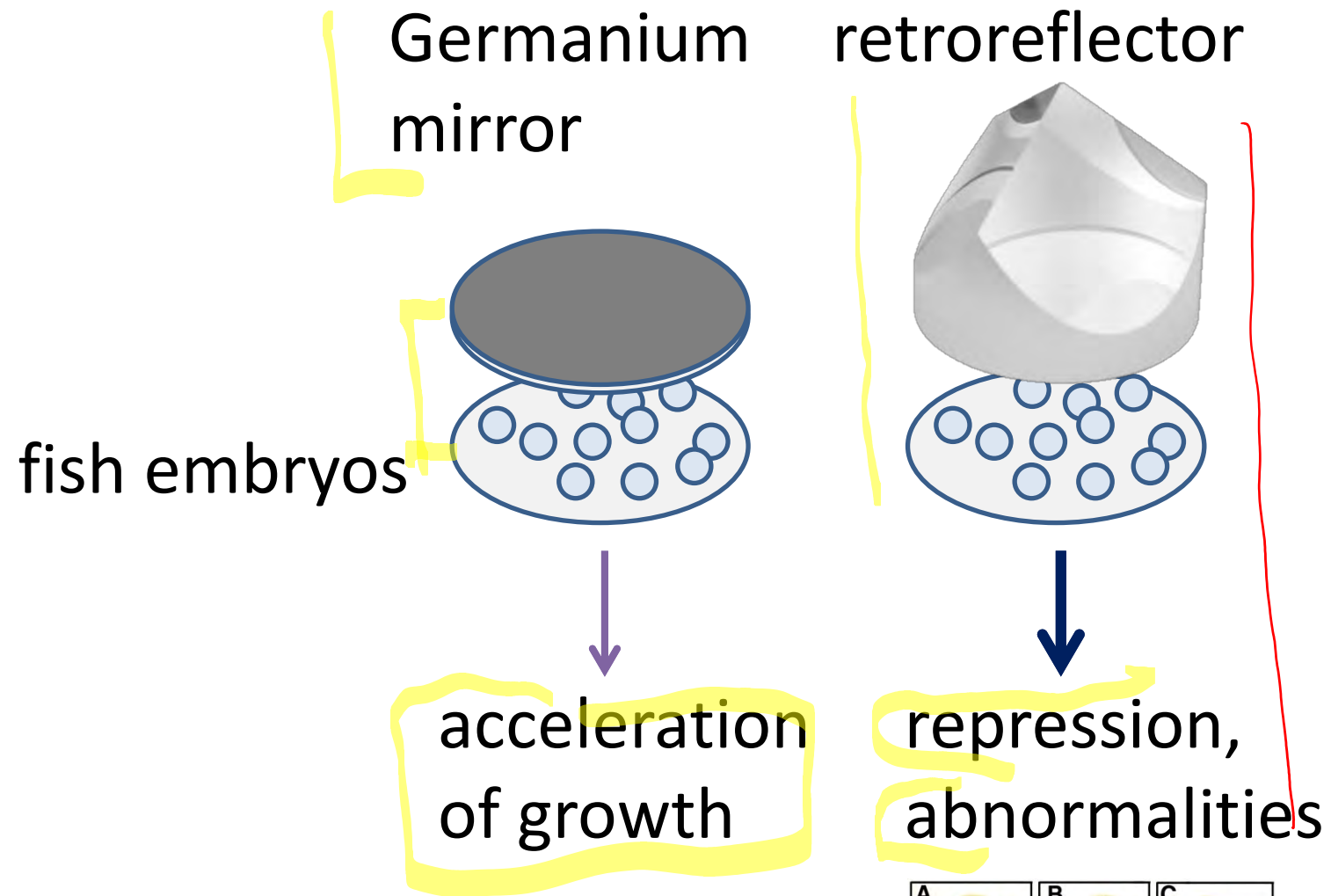


Gurwitsch, A. G., Über den Begriff des embryonalen Feldes. 1922
 "Die Mitogenetische Strahlung",
 Berlin, 1932



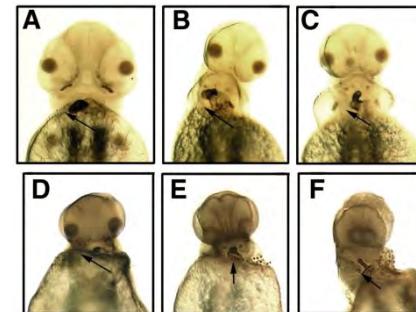
Non-chemical signaling





Burlakov 2013

bit.ly/burlakov



What needs to be proven or verified:

- The existence of biofield
- Its morphogenic function
- That DNA produces the biofield
- That DNA produces the biofield in a sequence-specific manner.



Гурвич, 1920е
годы

гипотеза морфогенного поля:
поле влияет на форму
организма

Гурвич 1923 г.
Частичное эксп.
подтверждение:
митогенетическое
излучение в УФ спектре
влияет на скорость роста

Бурлаков 1990е, эксп.
нарушение поля влияет на
форму организма

механизм?

Миллер 1973 г.
гипотеза о механизме:
ДНК создает морфогенное поле
посылает и принимает сигналы.

до сих пор нет
подтверждения

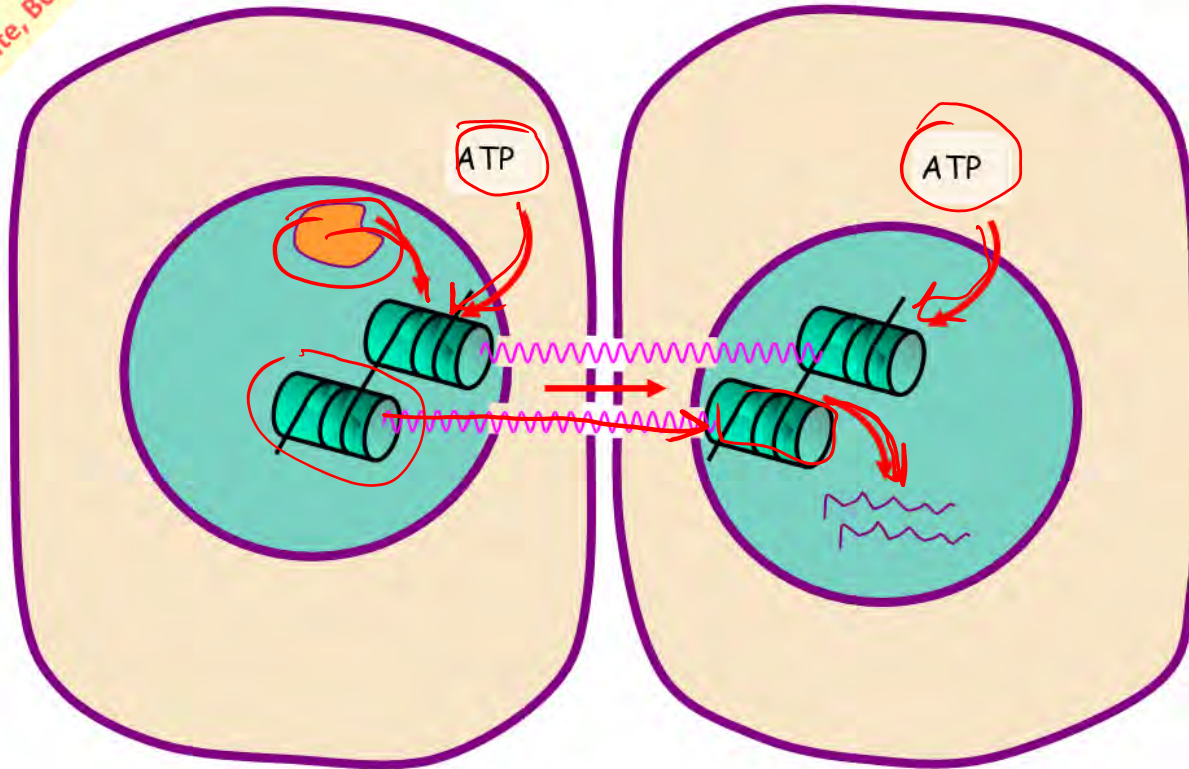
Наши исследования
1. Гипотеза о молекулярном
механизме
2. Косвенное подтверждение участия
ДНК в резонансной передаче
сигнала.



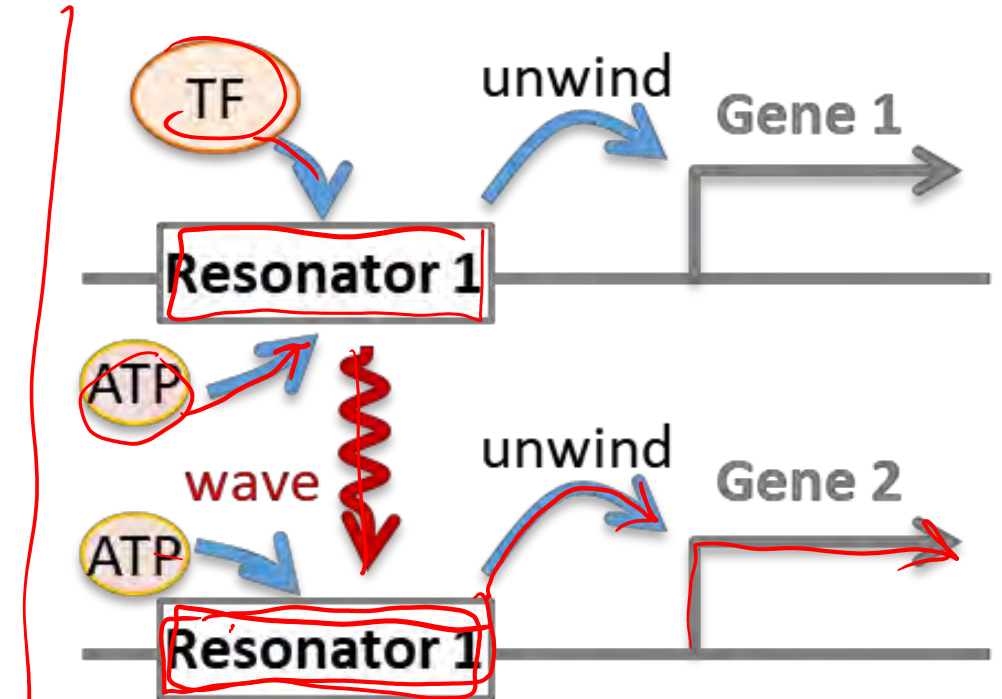
Max Rempel 2003

chromatin structures may transmit
and receive electric signals

A slide from 2003
talk in Forsyth
Institute, Boston



DNA RESONANCE



Electron wire patterns in the genome

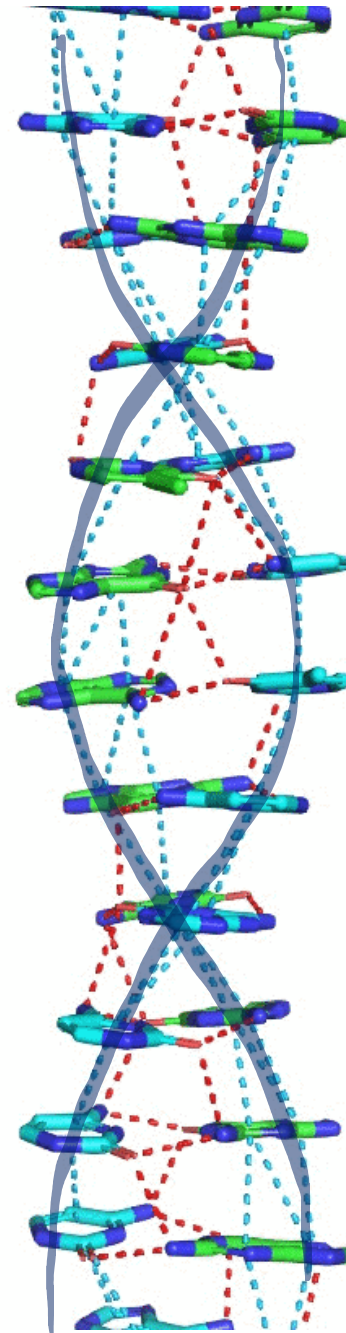
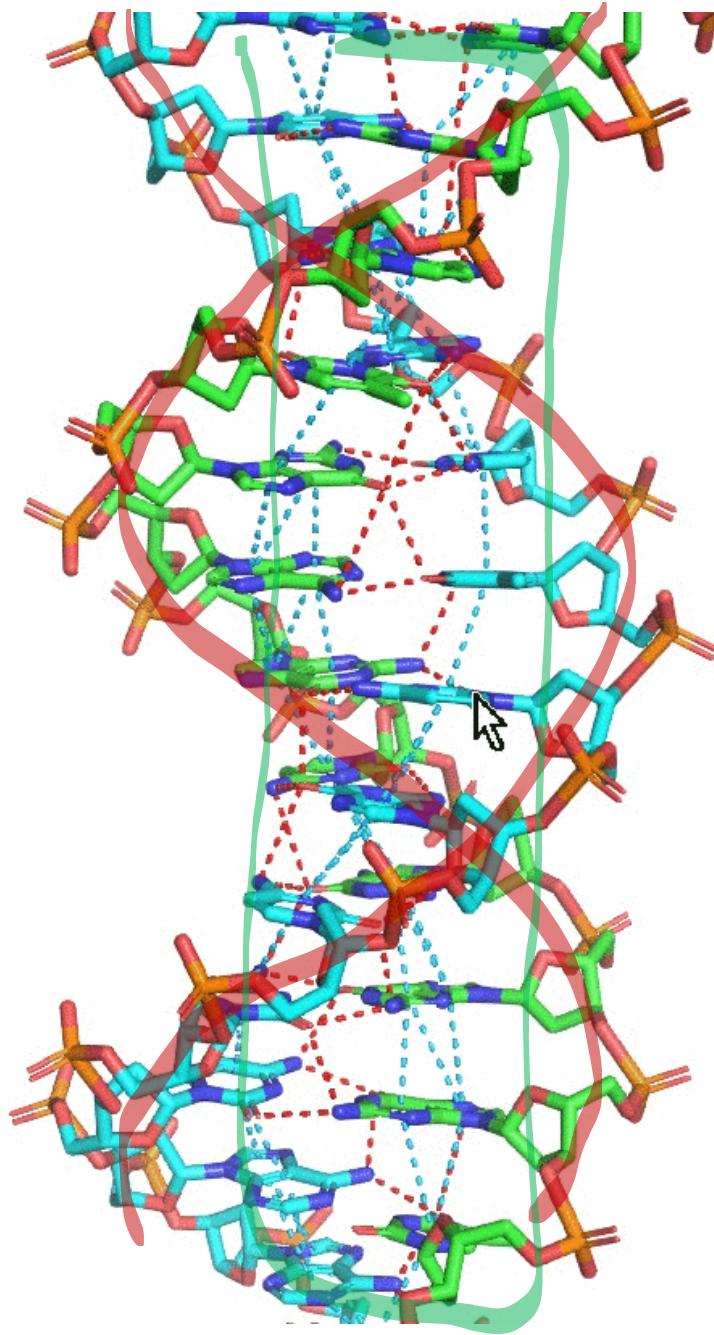


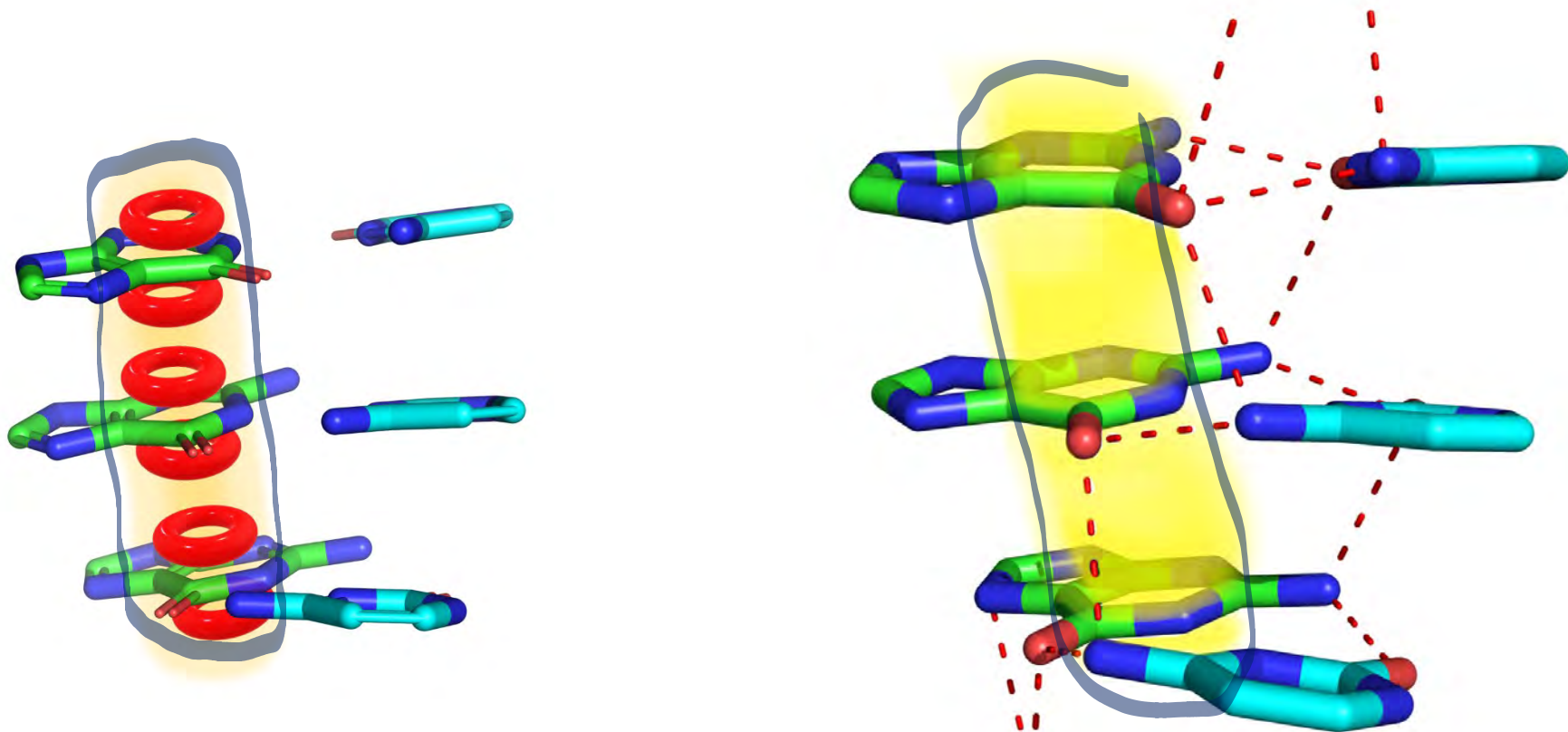
3.7Å cutoff
for h-bonds

electron wires

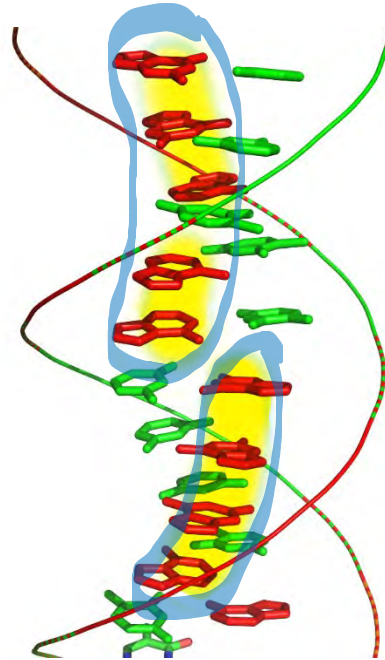


proton wires





Natural oscillation criteria

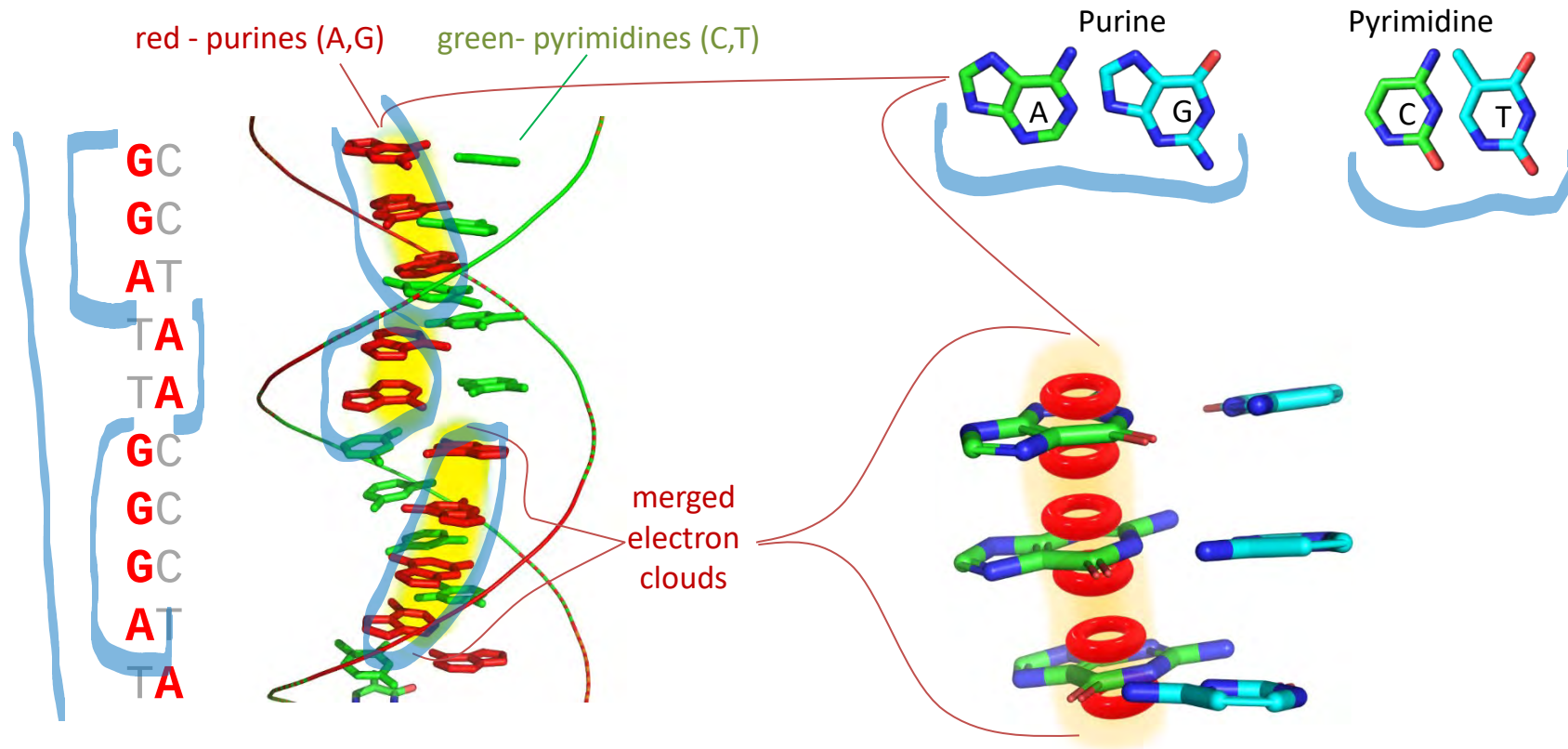


1. Not damped by viscosity
2. DNA sequence dependent

Electron clouds in
purine stretches
meet the requirements



Molecular modeling - merged electron clouds of purines as oscillators



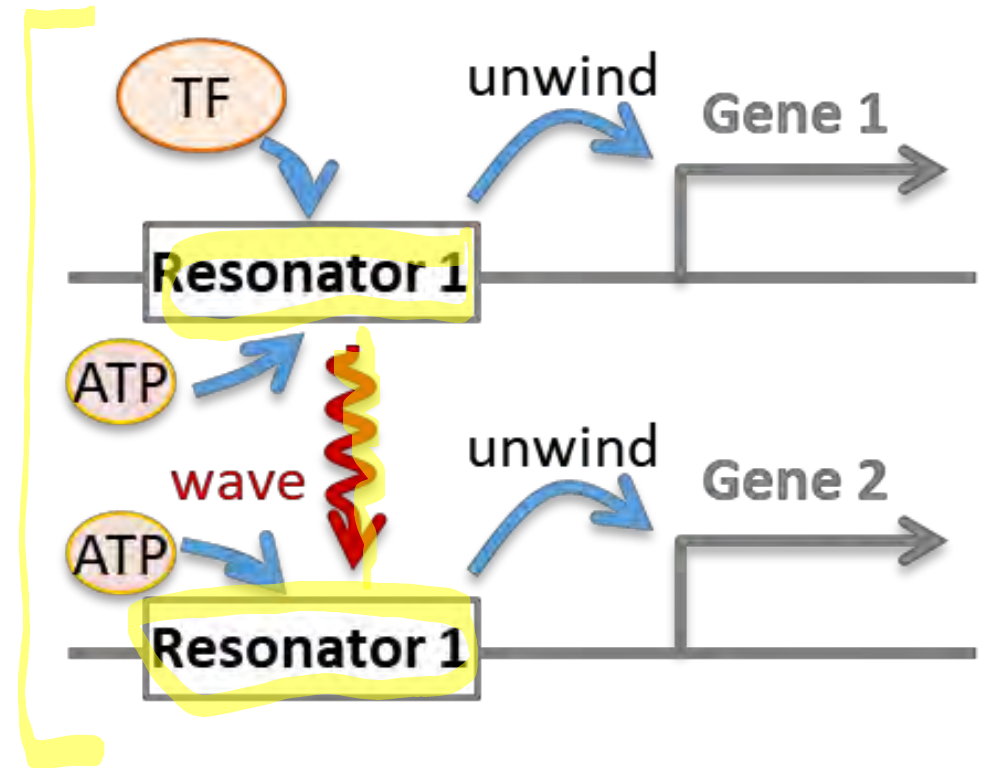
Rempel 2017 PMID: 29294317



Alu LINE



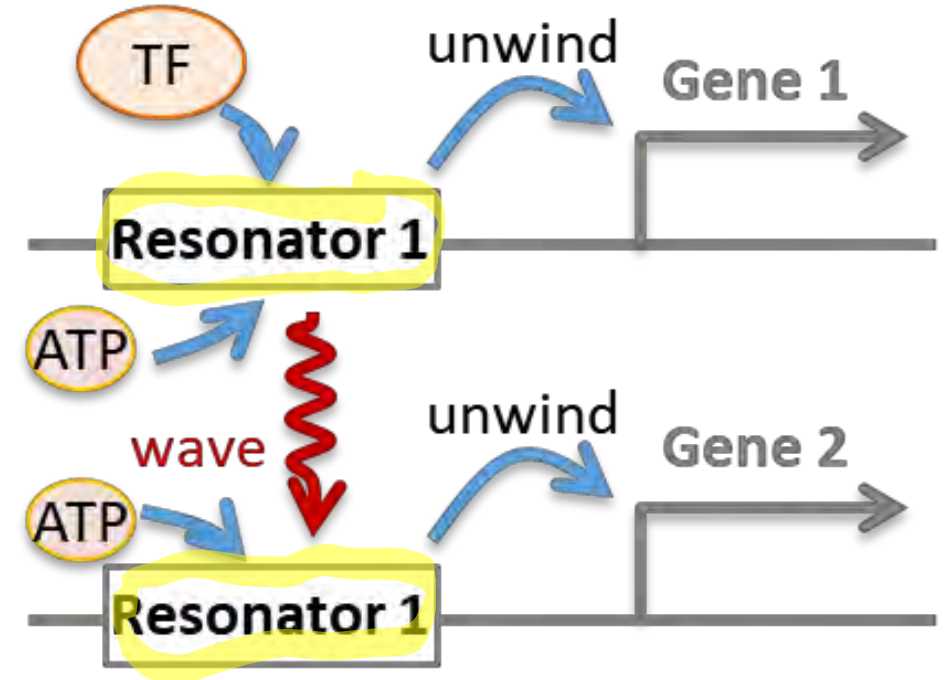
- Similar patterns resonate
- Our genome is 3 Gbps
- 50% of the genome is repetitive
- Alu repeat - 11% of our genome
- Line repeat - 6% of our genome.
- 50% of the genome is made of unique sequences

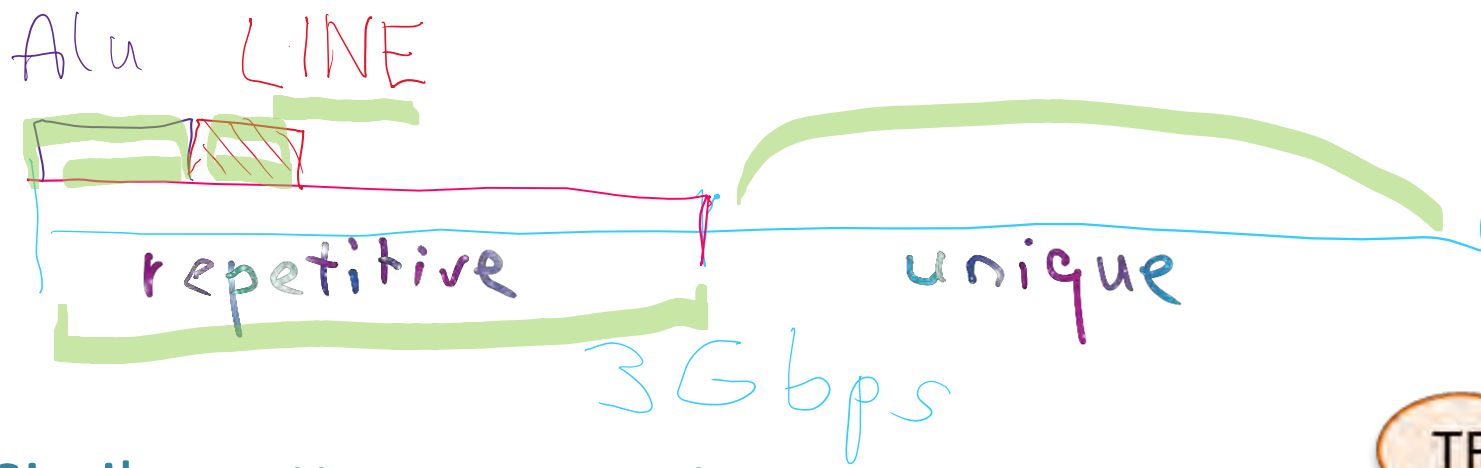


Alu LINE

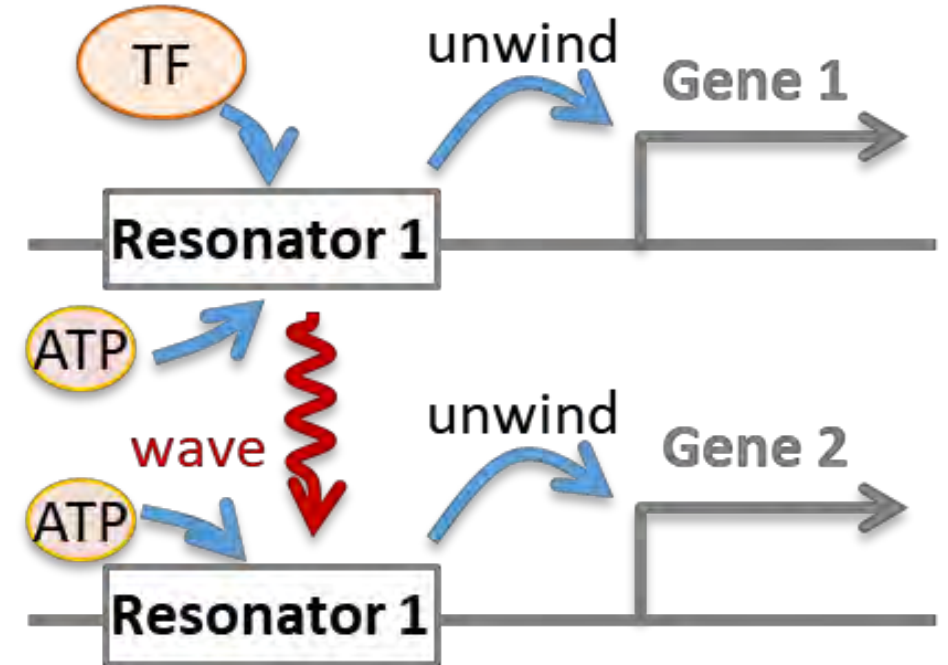


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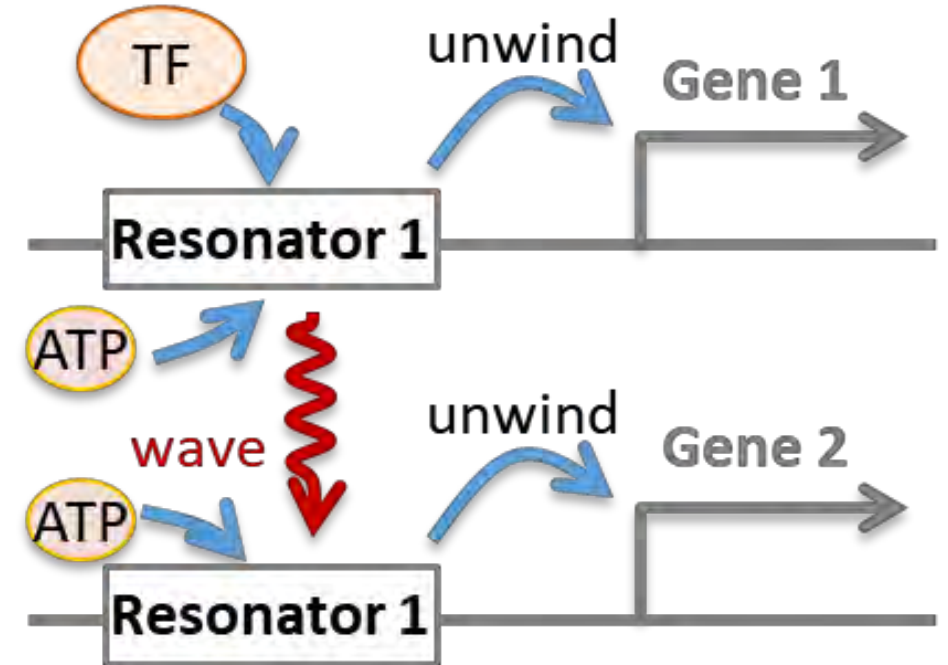


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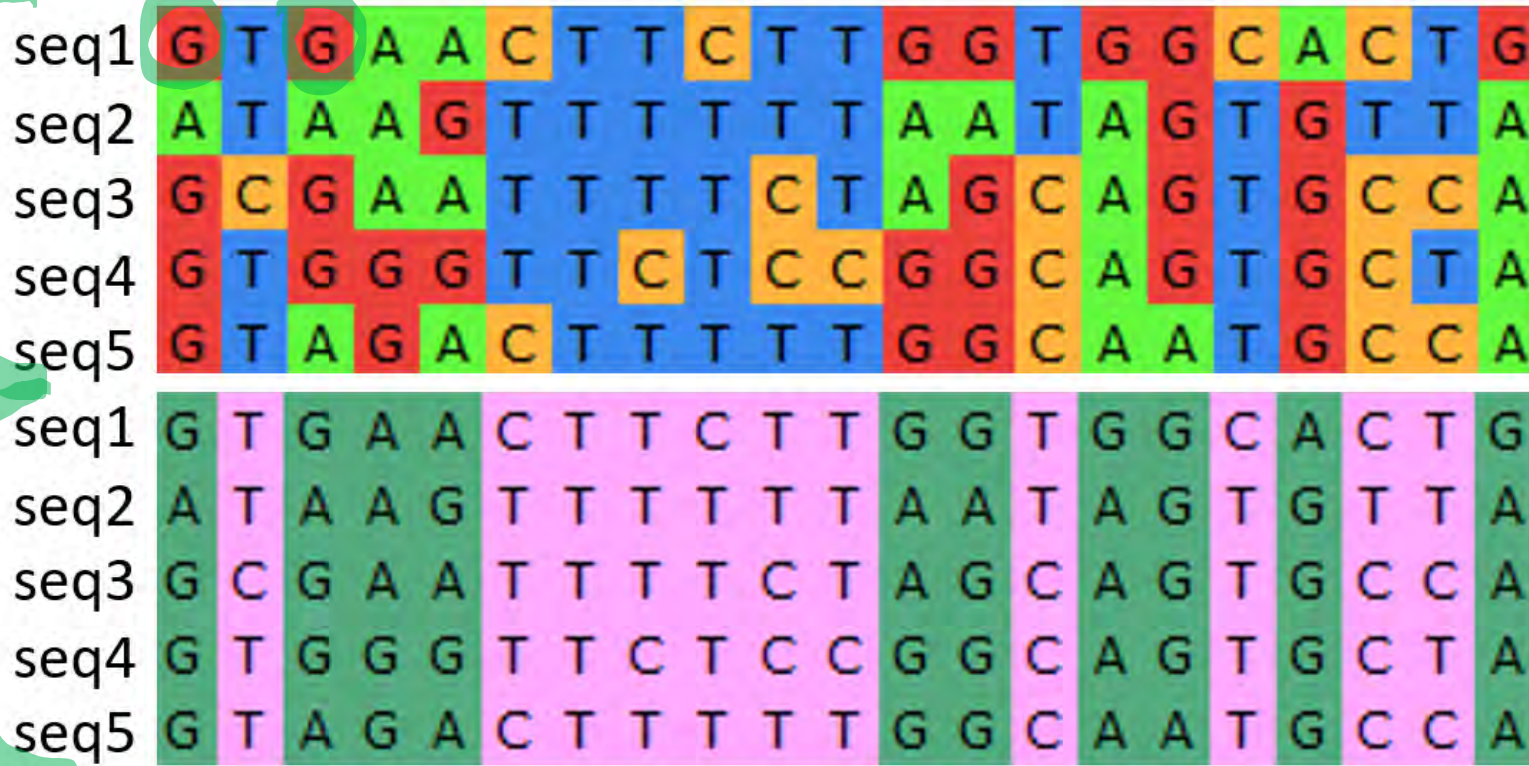




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- Line repeat - 6% of our genome.
- 50% of the genome is made of unique sequences



Purine HIDERs



A

Colored by nucleotide



B

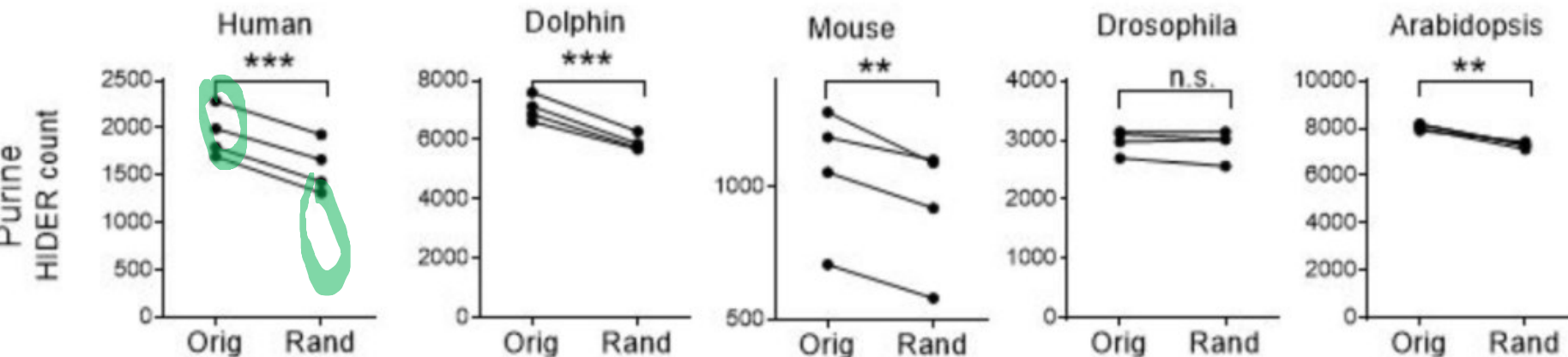
Colored by purine code

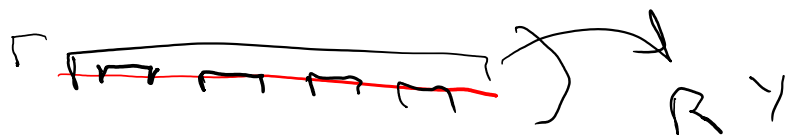


purines



pyrimidines



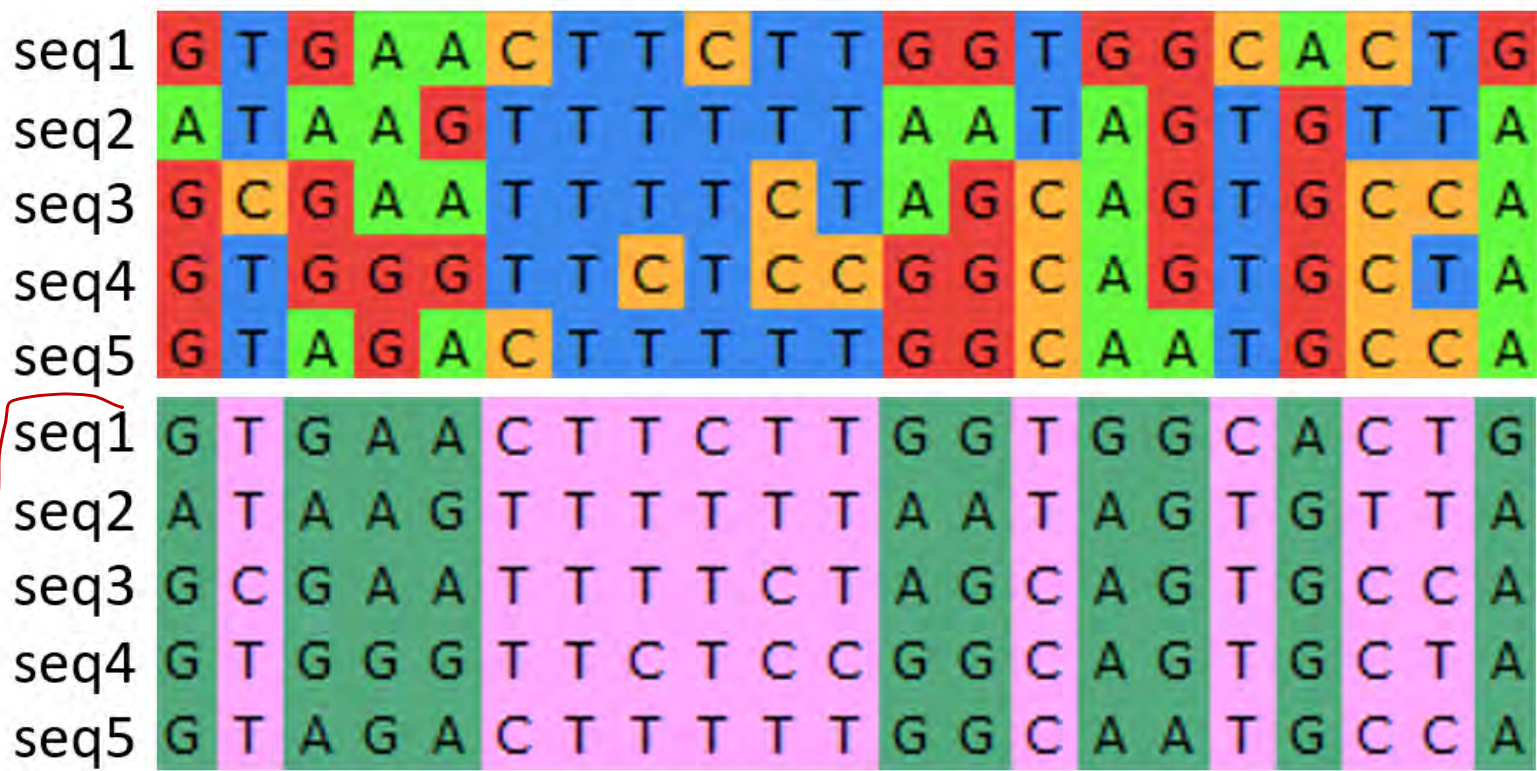




;



Purine HIDERs



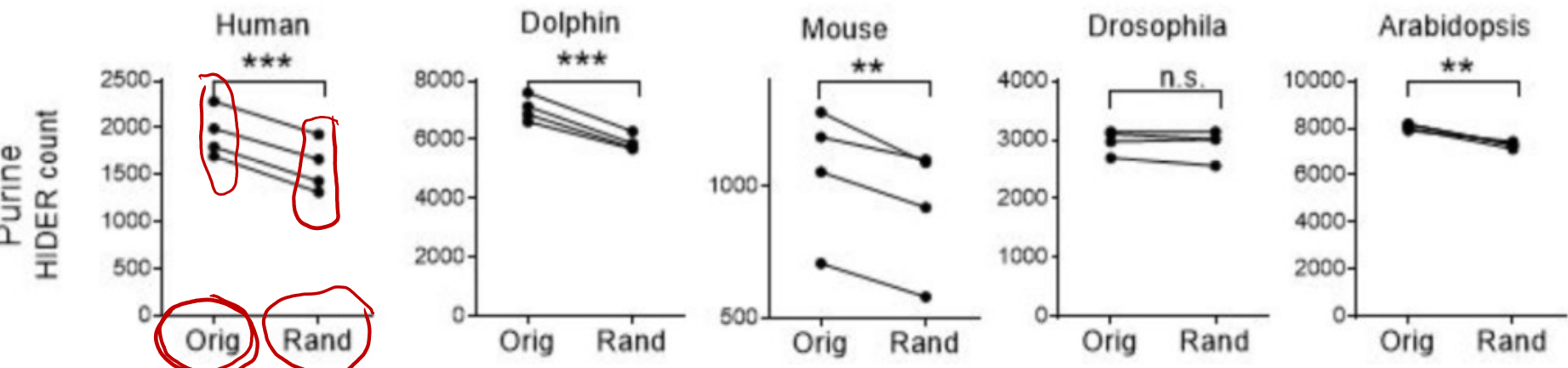
A

Colored by nucleotide



B

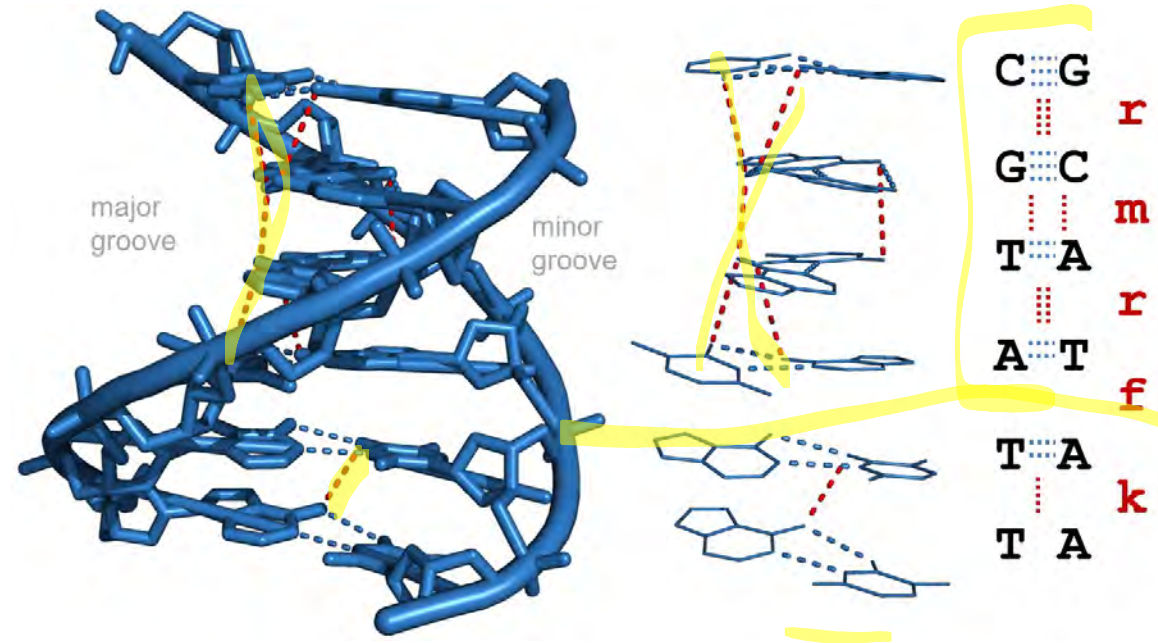
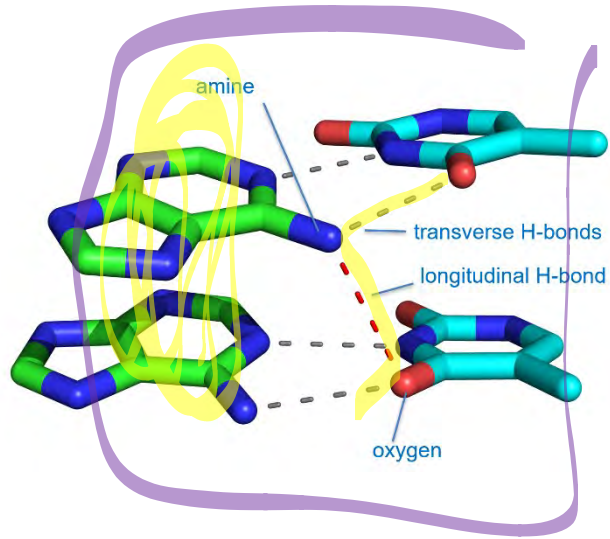
Colored by purine code



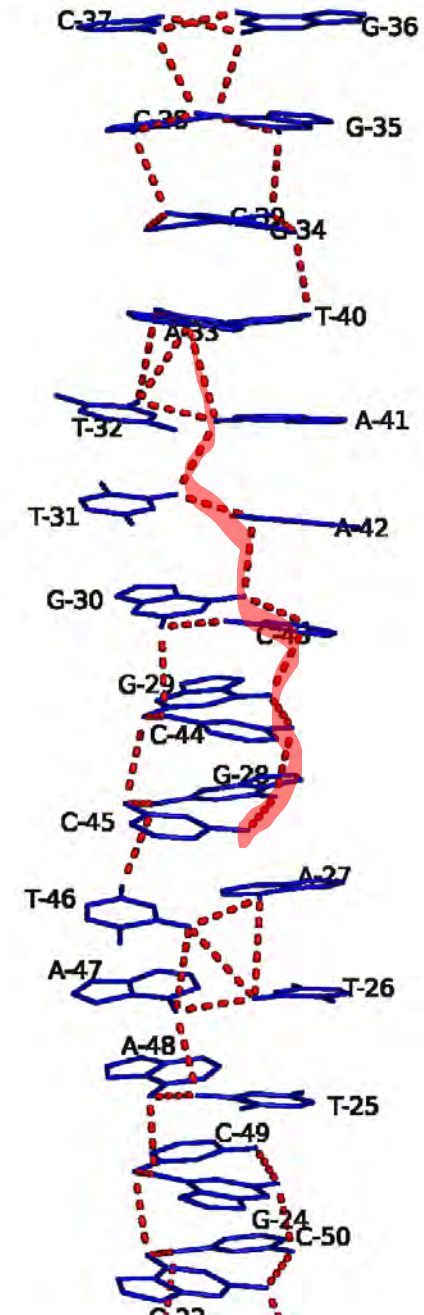
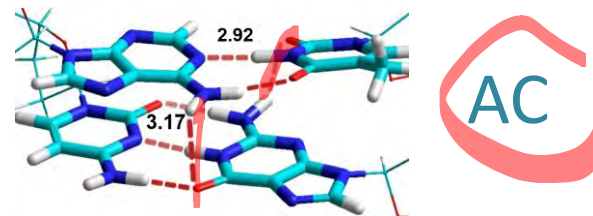
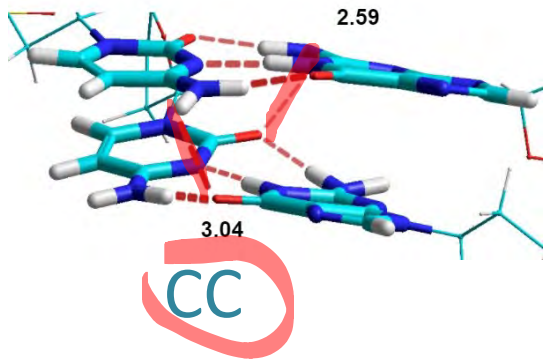
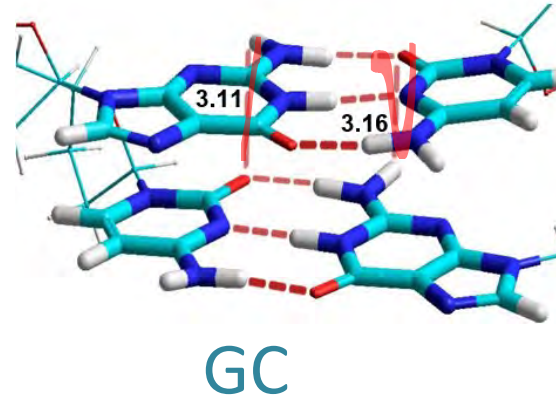
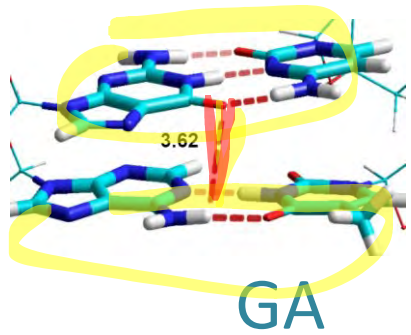
Proton wires



Longitudinal hydrogen bonds



Dinucleotides have different longitudinal hydrogen bonds



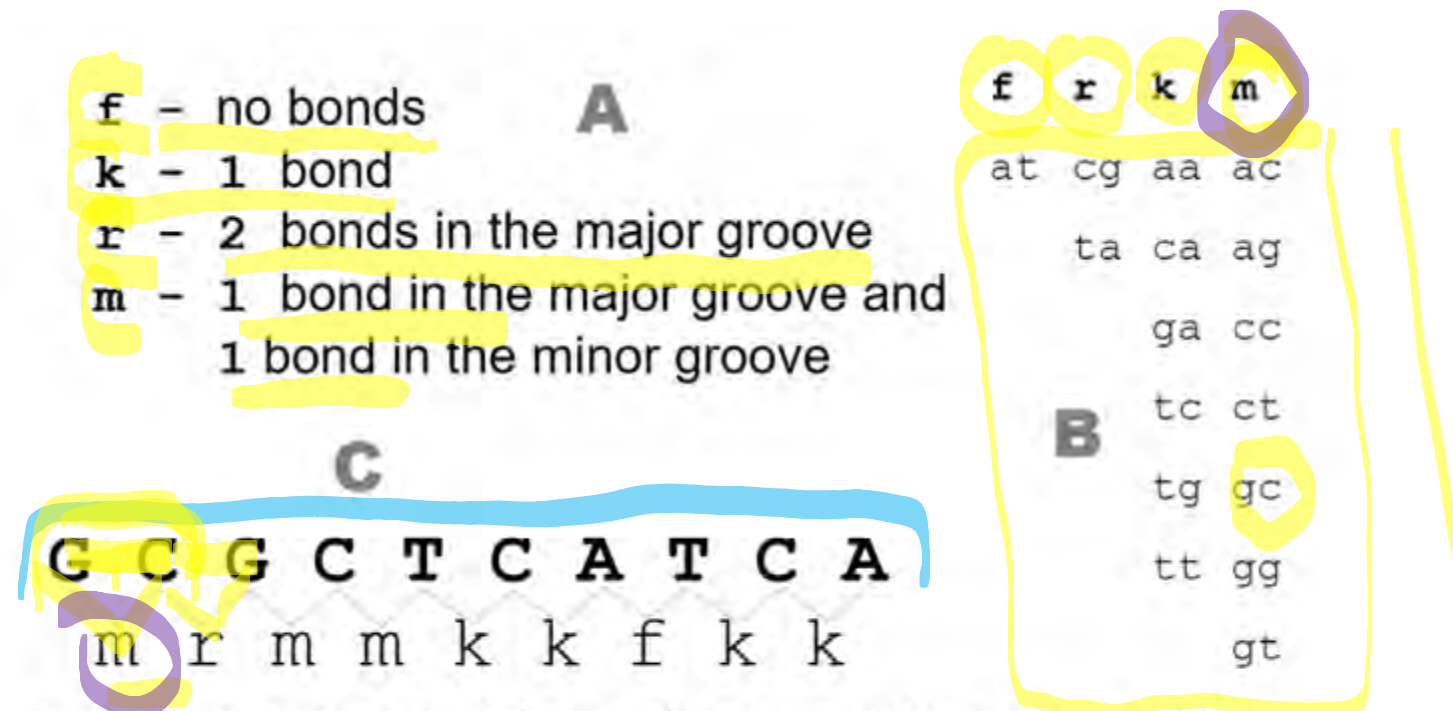
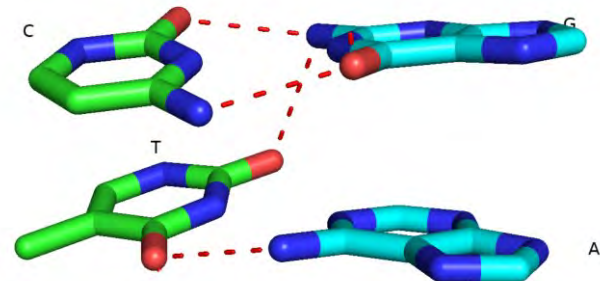
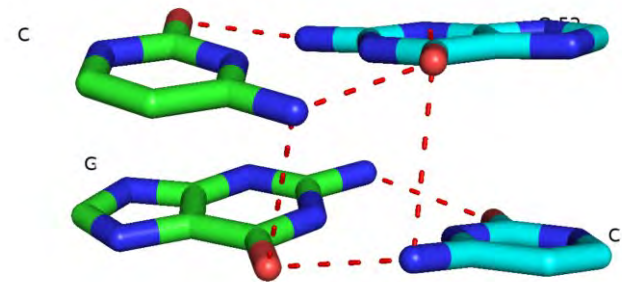
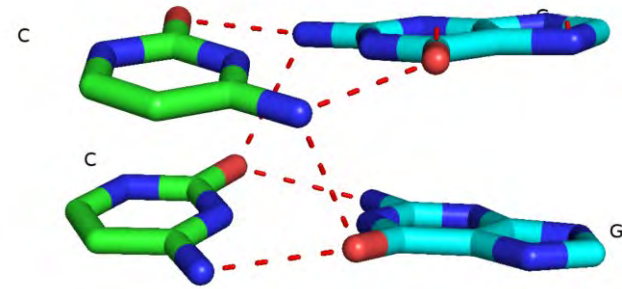
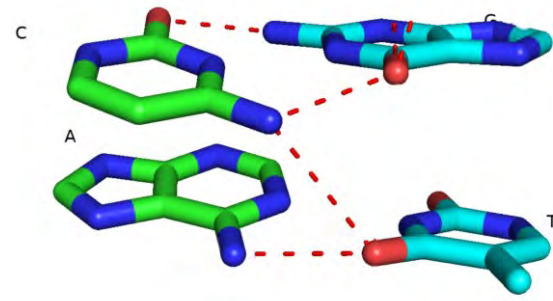
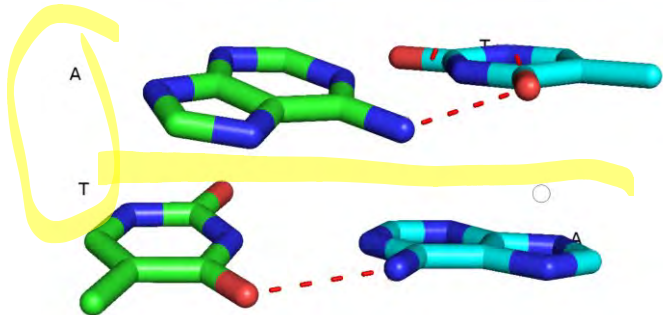
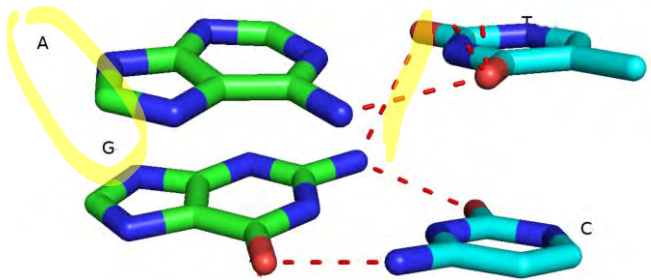
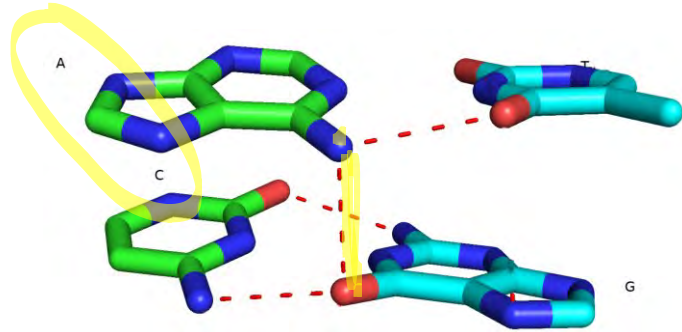
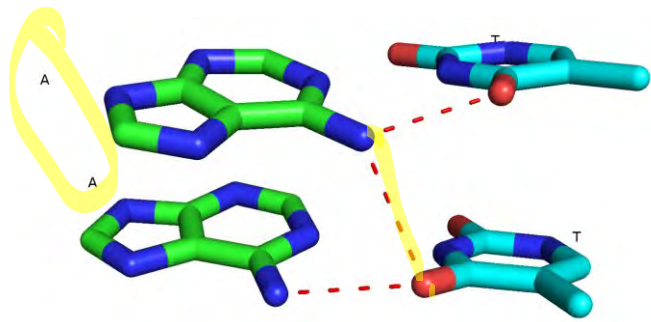


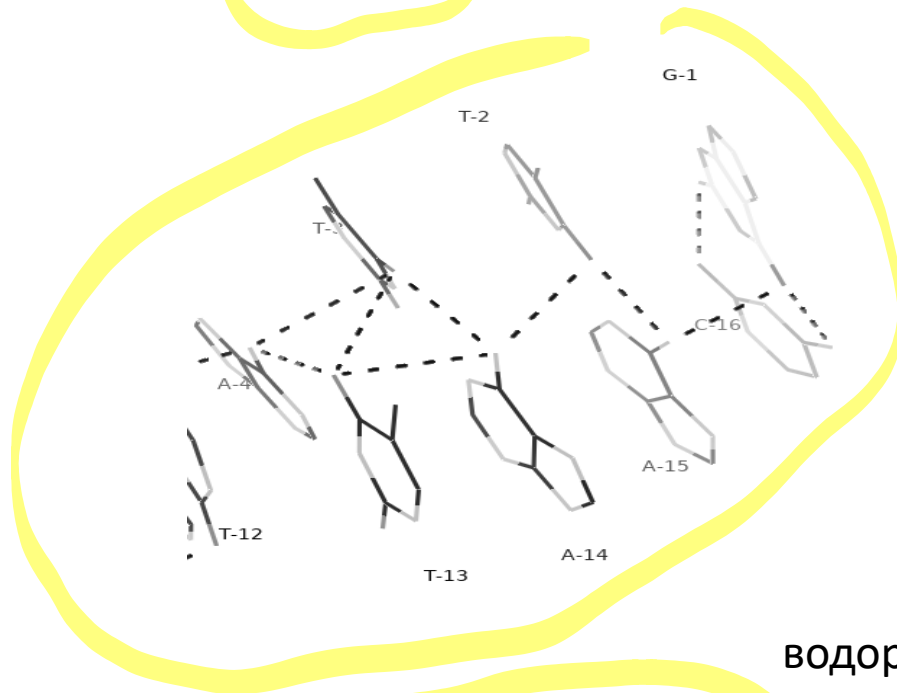
Fig. 3. Recoding scheme. (A) Definitions of longitudinal H-bond bond types. (B) Conversion table of dinucleotides to longitudinal H-bond types. (C) Algorithm of recoding a nucleotide sequence into protocol code.



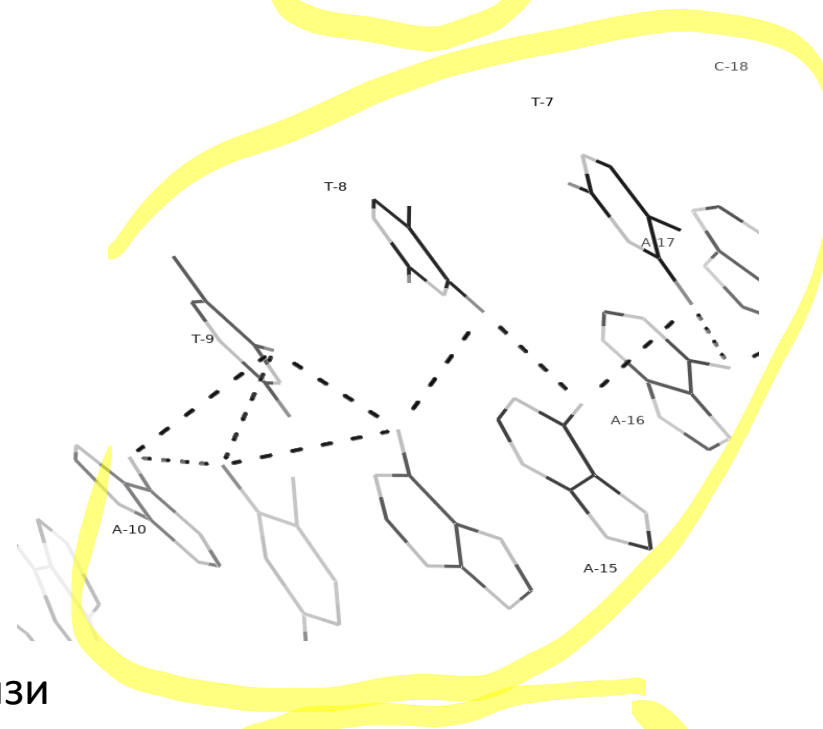


Хайдеры

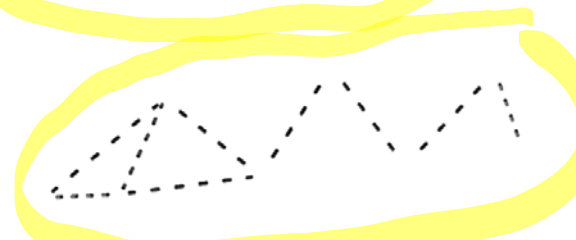
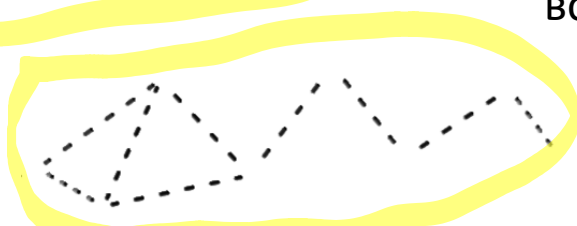
ATTG



ATTT



водородные связи



Мы предположили что даже различающиеся последовательности могут резонировать, если в них похожие структуры водородных связей.

Хайдеры = фрагменты ДНК, имеющие различные первичные последовательности, но совпадающие по структуре продольных водородных связей)



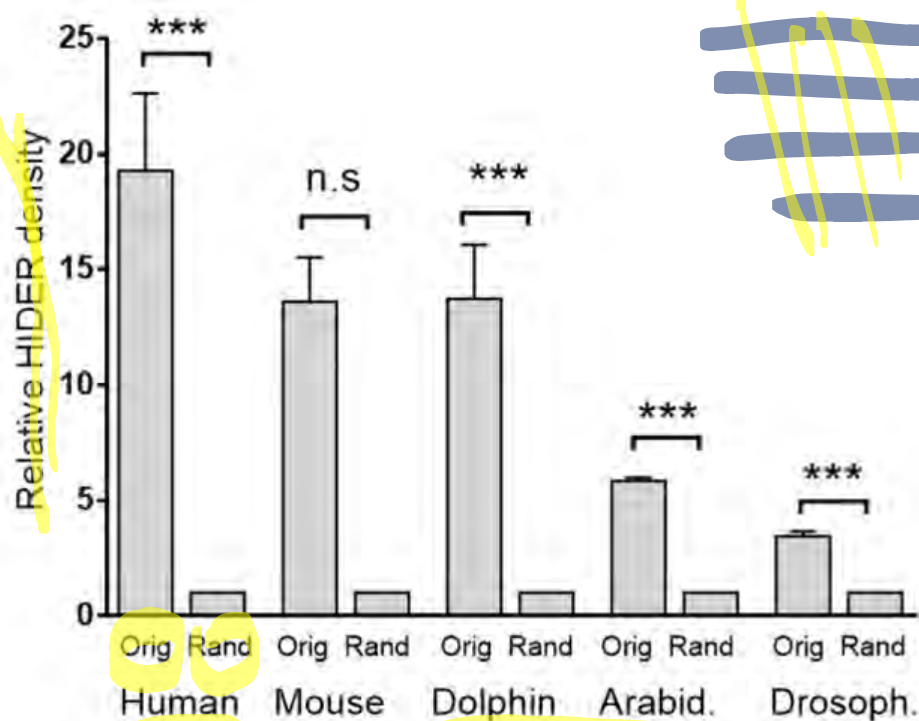


Fig. 5. HIDER density is enriched in the original over the randomized sequence.

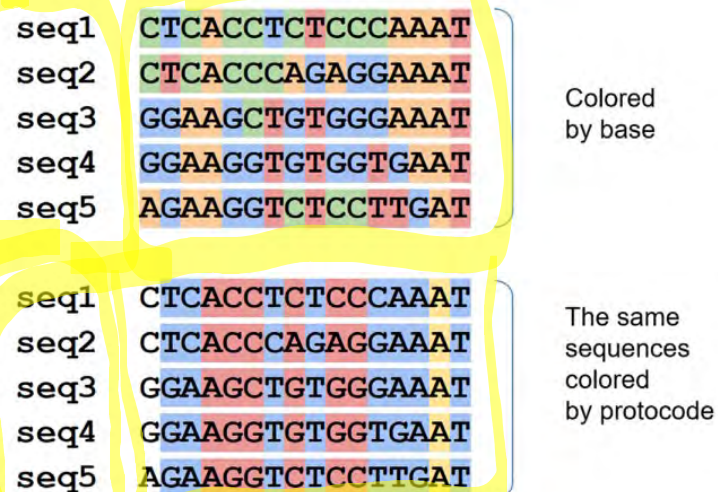


Fig. 4. Example of protocode HIDER sequences.

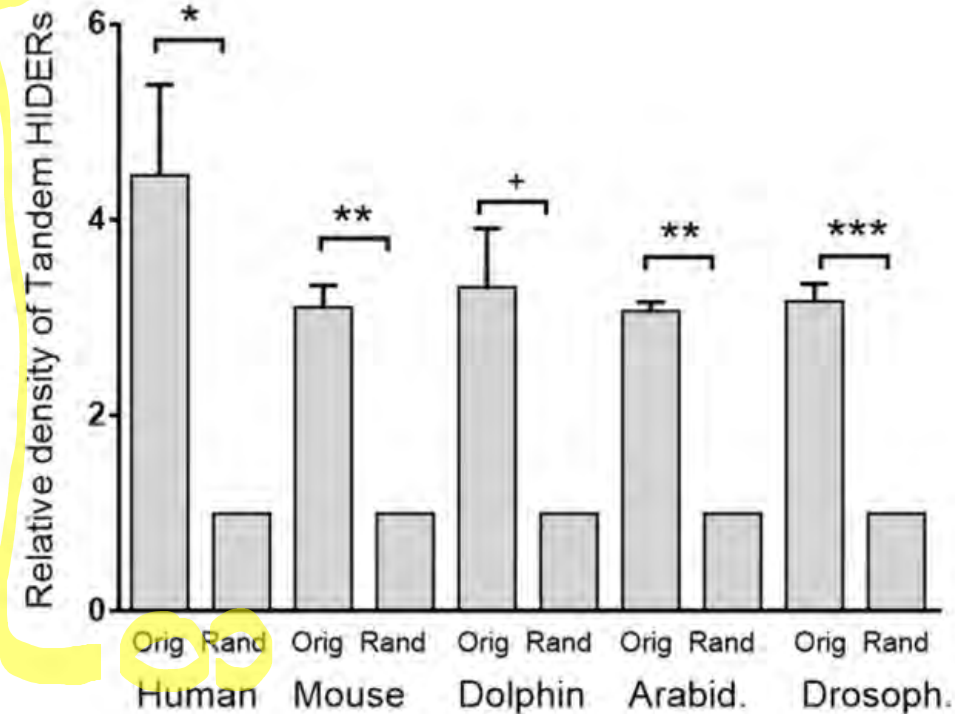
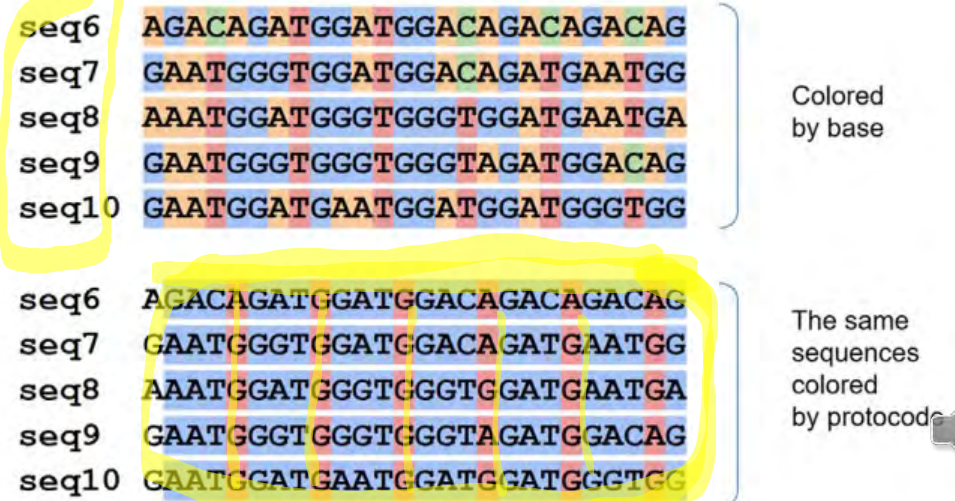


Fig. 7. The density of Tandem HIDERs is enriched in the original over the randomized sequence.

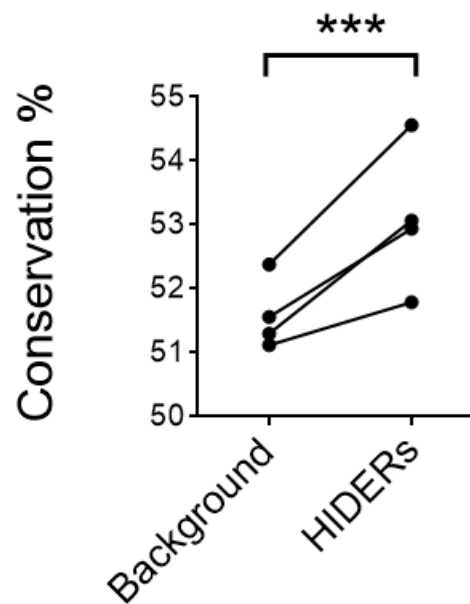
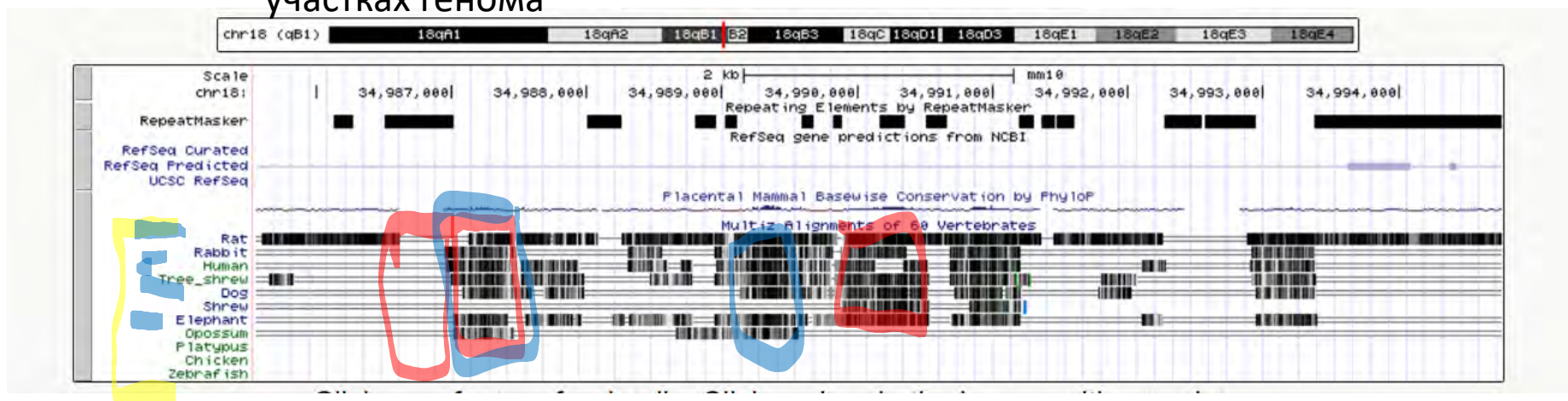


Логика

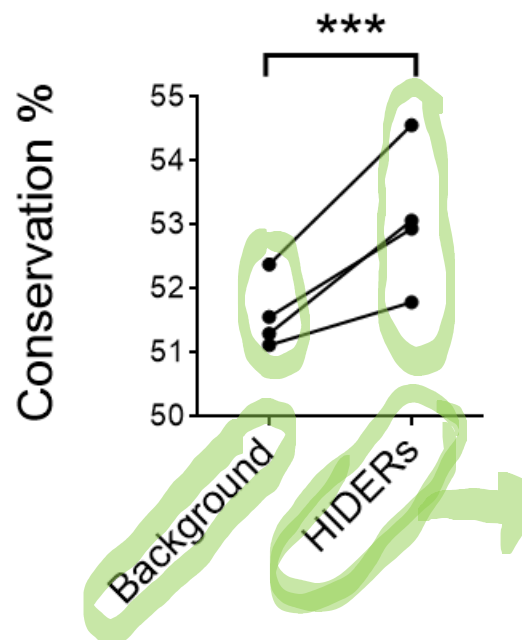
- Морфогенное поле должно создаваться ДНК (Гурвич - Миллер)
- Для добротности колебаний, ДНКовые резонаторы должны быть высококопийными повторами.
- Внутри резонатора должно быть изолированное облако делокализованных электронов или протонов, так чтобы форма облака зависела от последовательности.
- Облако делокализованных протонов (протонный провод) получается из продольных водородных связей
- Должны существовать Хайдеры. Повторы и хайдеры должны участвовать в передаче сигнала и регуляции генома.
- Хайдеры должны быть обогащены в процессе эволюции
- Проверили - обнаружено сильное и статистически значимое обогащение. Это косвенно подтверждает всю логическую цепочку.



Хайдеры обогащены в консервативных участках генома



Хайдеры обогащены в консервативных участках генома



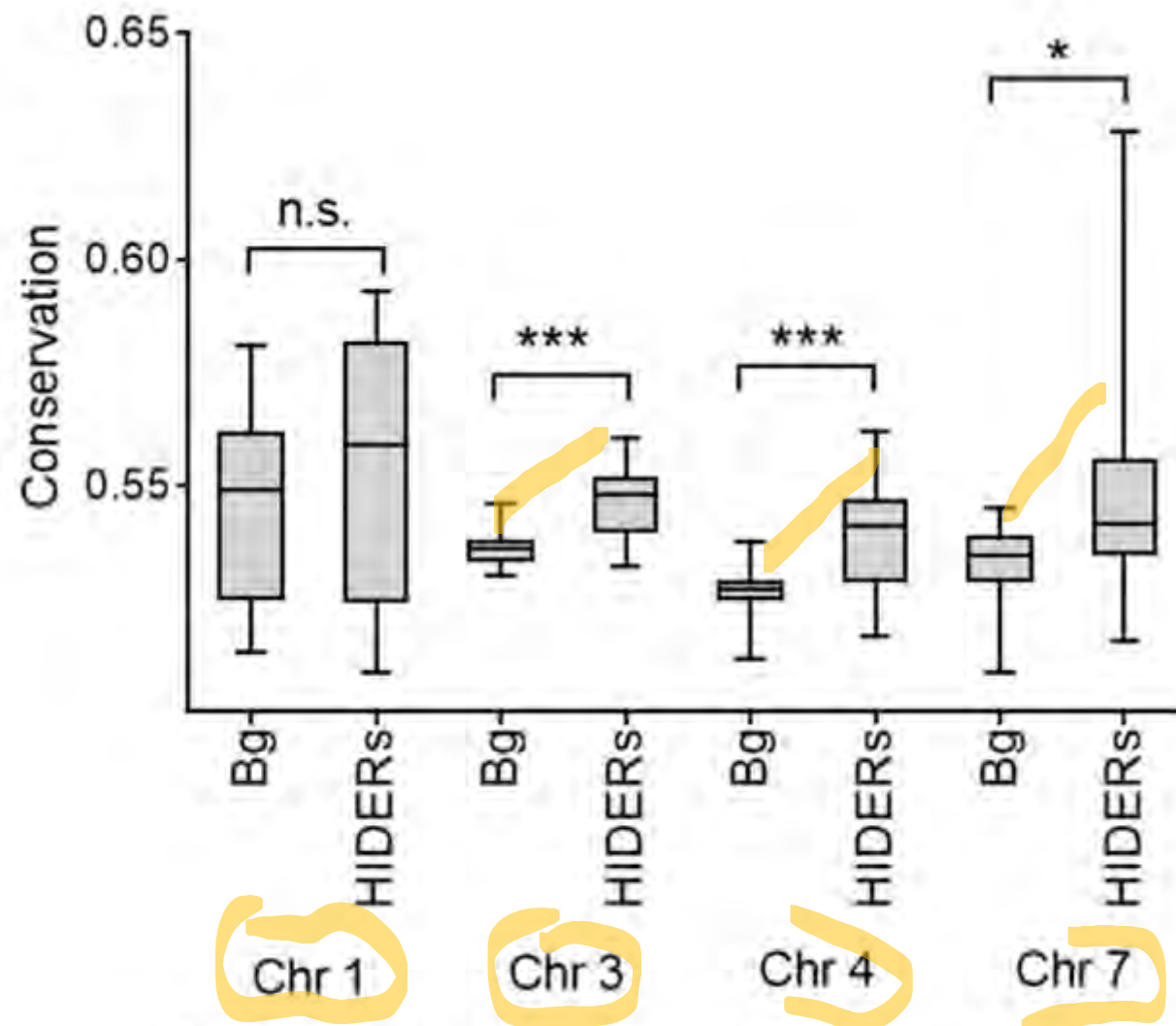
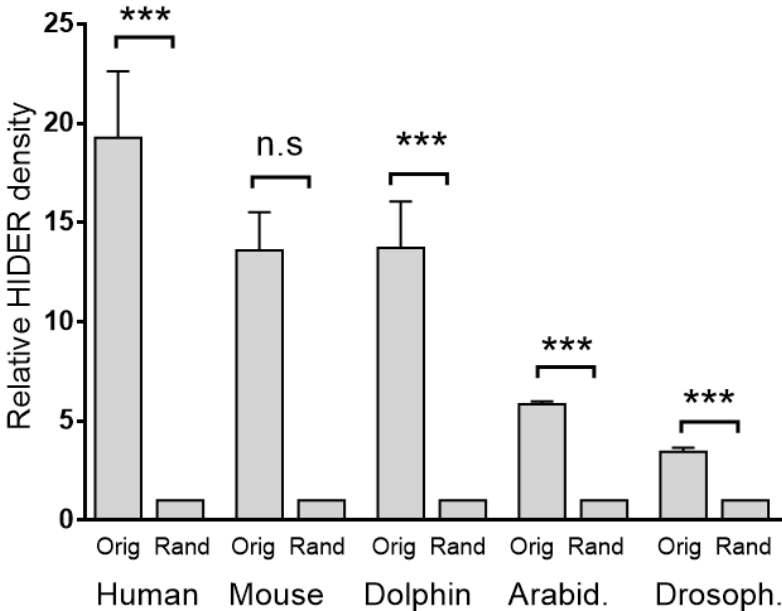
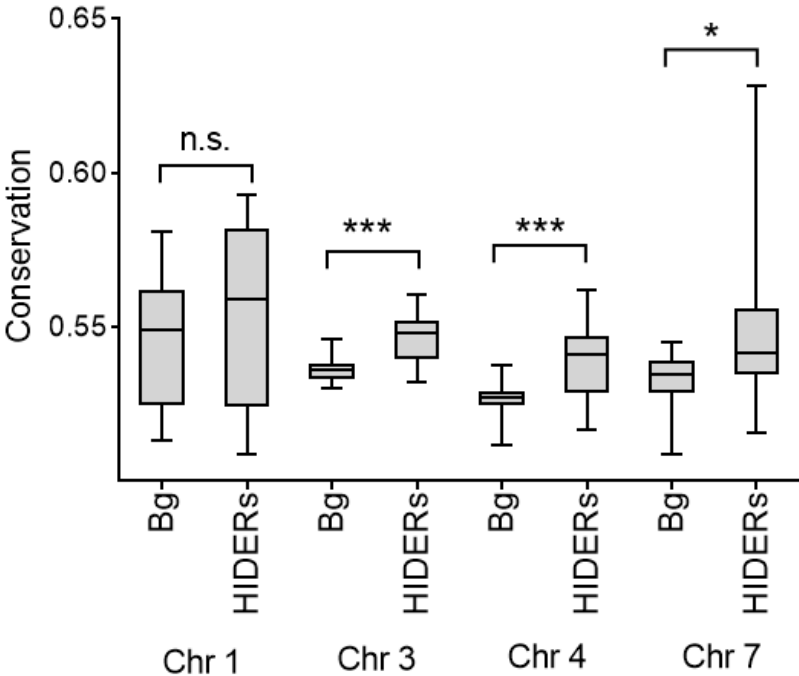


Fig. 8. Conservation of HIDERS compared to background (Bg).



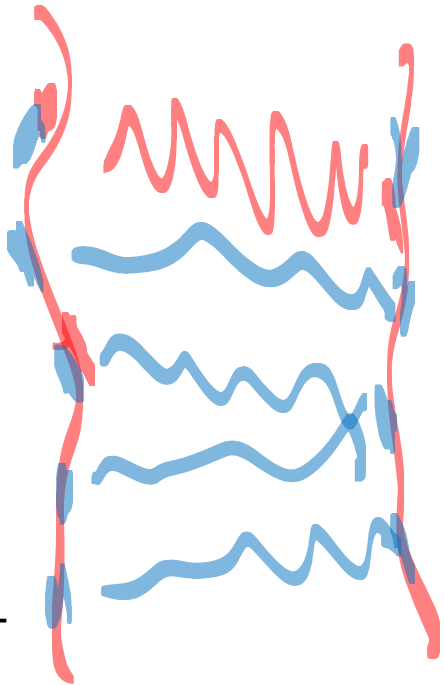
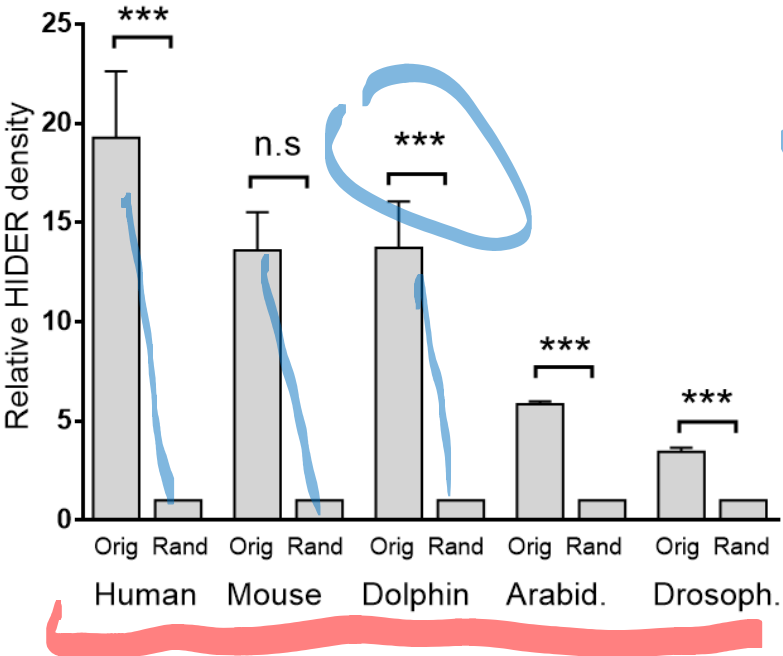
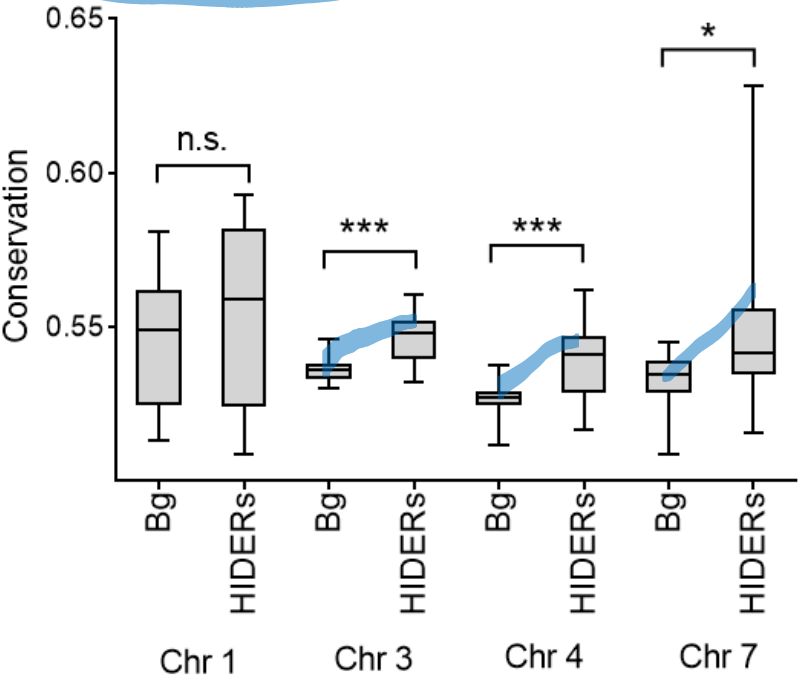
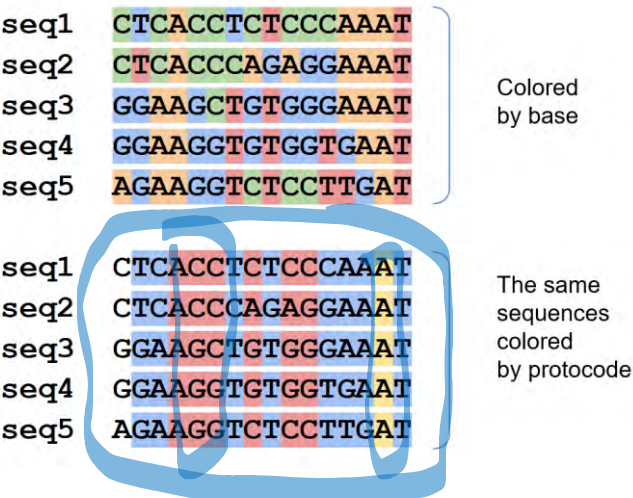
Repetitive patterns of proton wires are enriched by evolution in all tested species



Repetitive patterns of proton wires are enriched in conserved regions



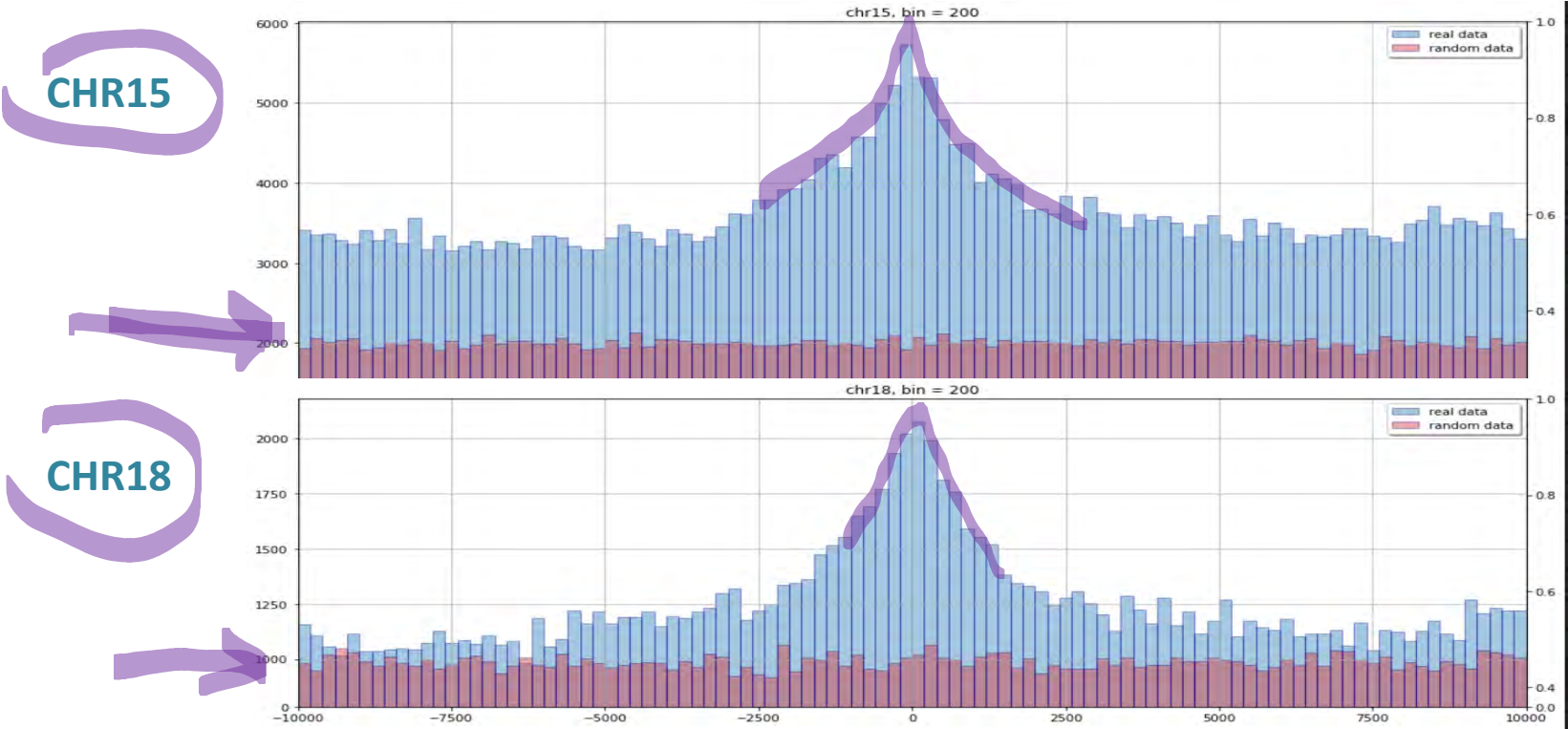
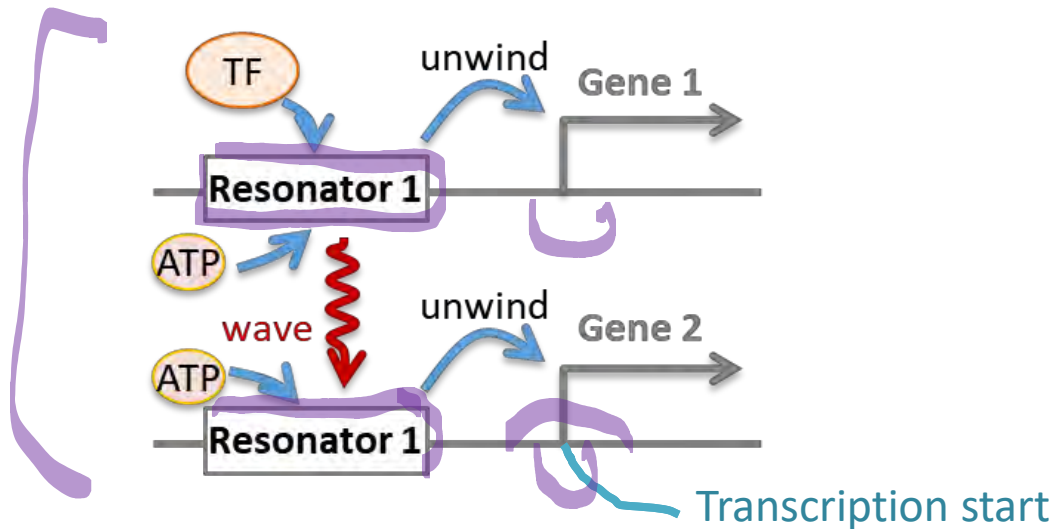
Repetitive patterns of proton wires are enriched by evolution in all tested species



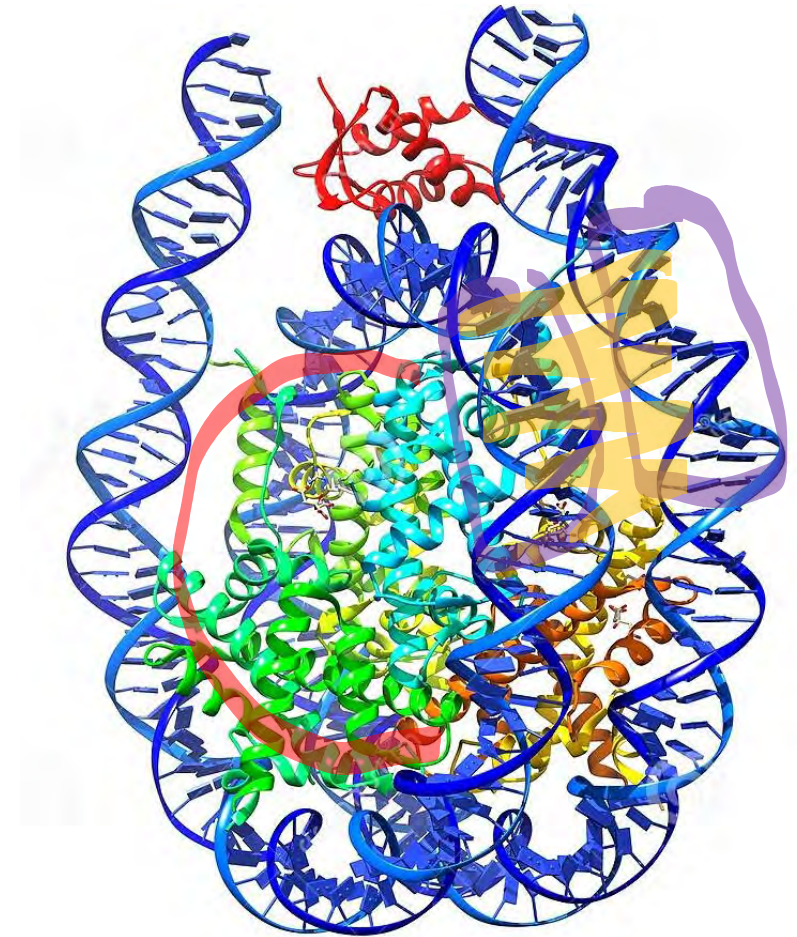
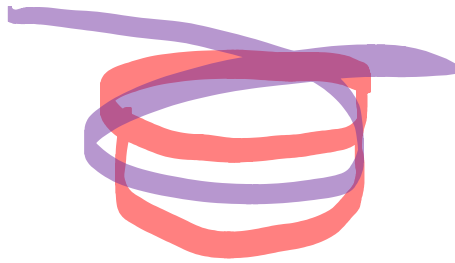
Repetitive patterns of proton wires are enriched in conserved regions



Repetitive patterns of proton wires (HIDERS) colocalize with gene transcription starts.



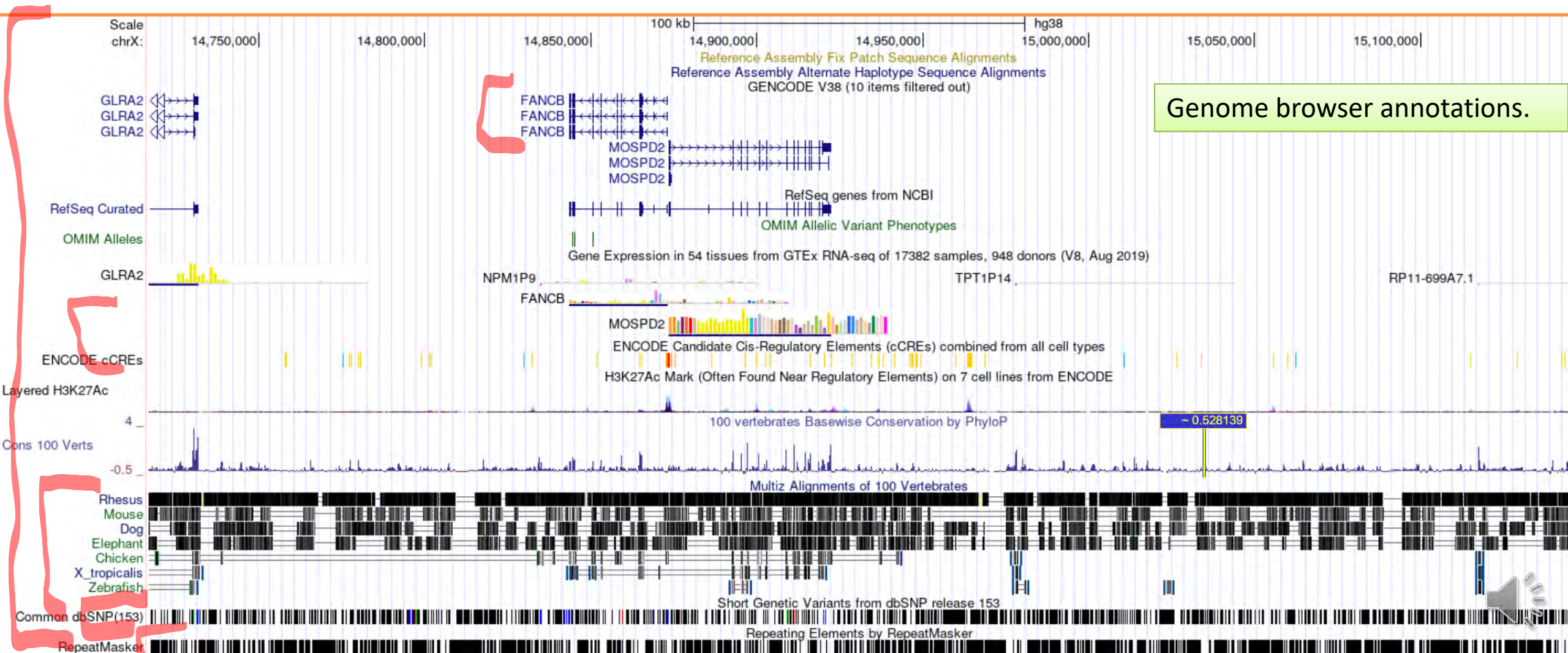
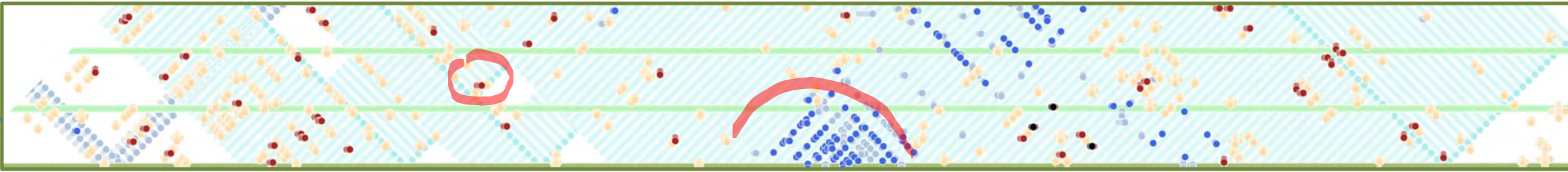
Does the nucleosome read DNA as a VCR head?



A Dotplot map of proton and electron wires.

How the future analysis may look like

Not yet
combined



Genome browser annotations.

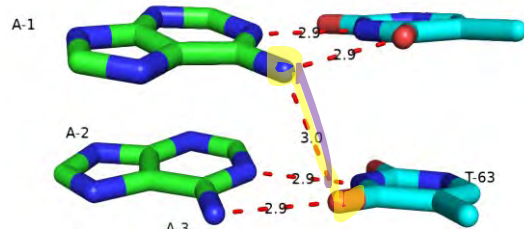
Quantum chemical modeling of proton wires



Comparison of different methods of prediction

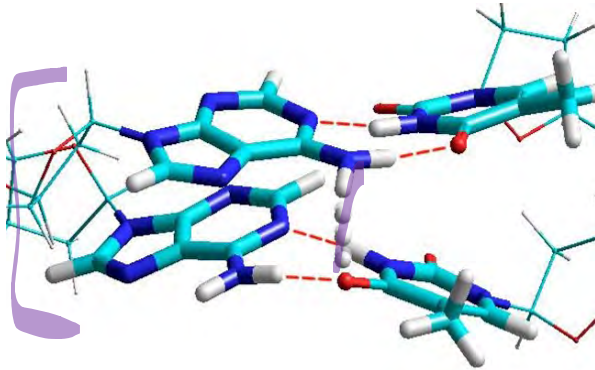
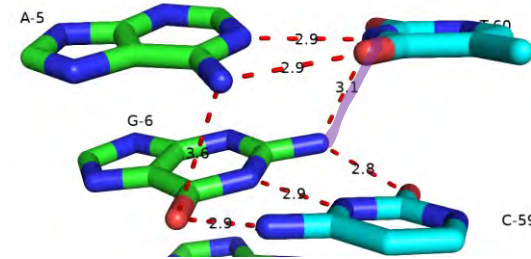
How flexible is B-form?

AA

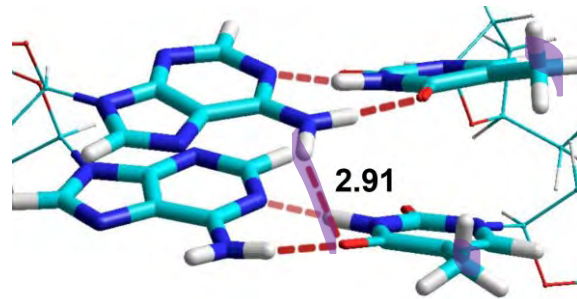
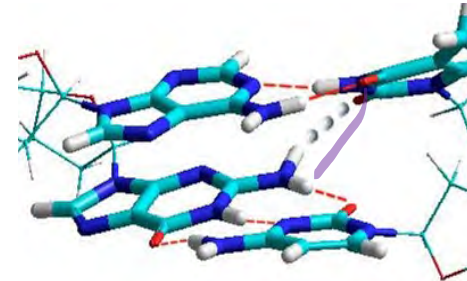


stereometric
by distance

AG

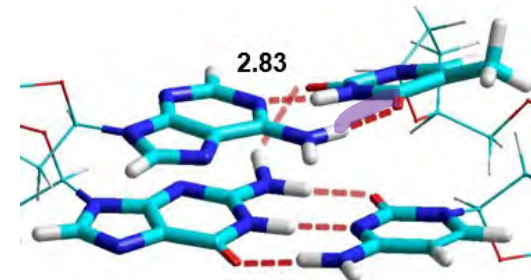


quantum
chemical
flexible model



complete agreement

quantum
chemical
B form



partial agreement



Quantum chemical modeling methods

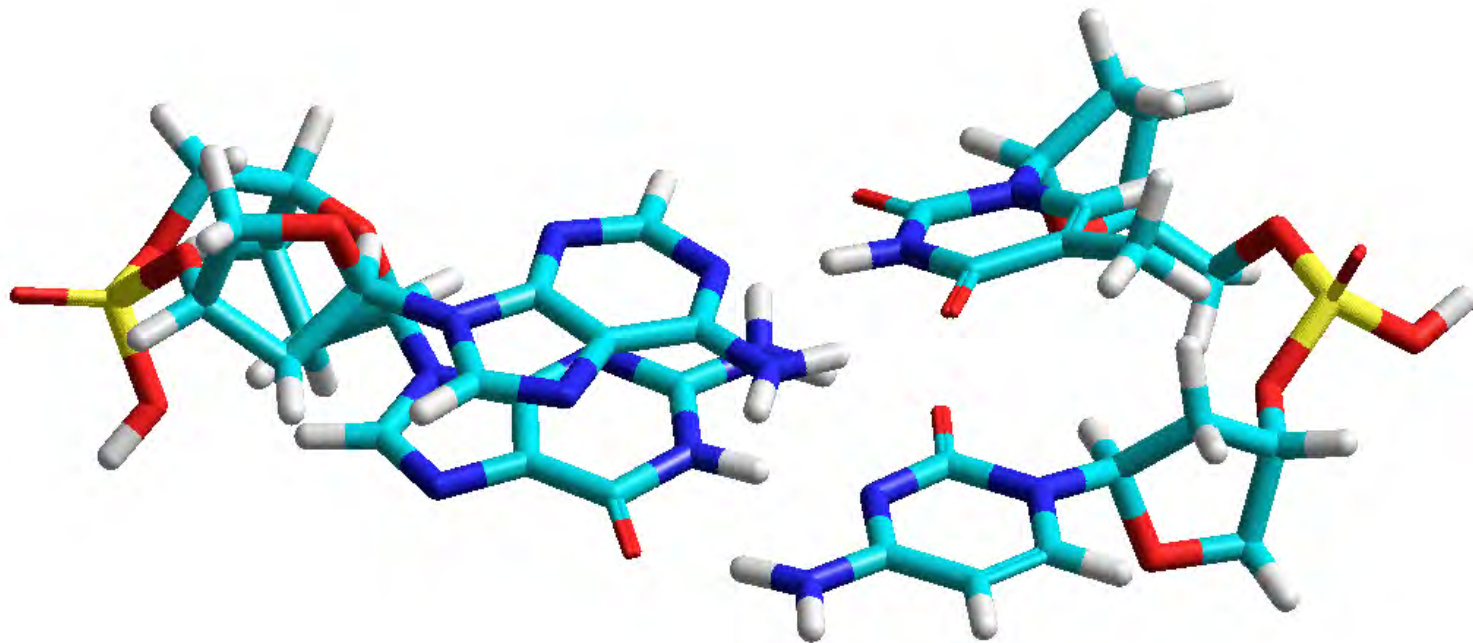
Designed B-DNA using Winmopac 7.21

MOPAC – molecular orbital modeling program

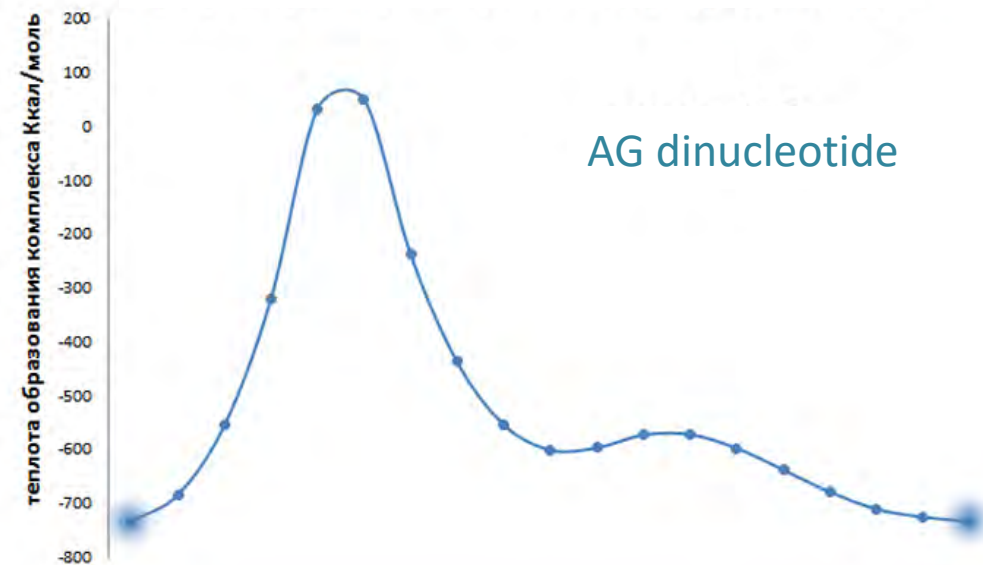
- Method UHF PM6-DH2X
 - is widely used for modeling macromolecules
 - good agreement with spectrometry and crystallography
 - does half-empirical computation = Ab initio + emprirical
 - does Schrödinger equation computation
- we computed transition energies for tautomeric transitions



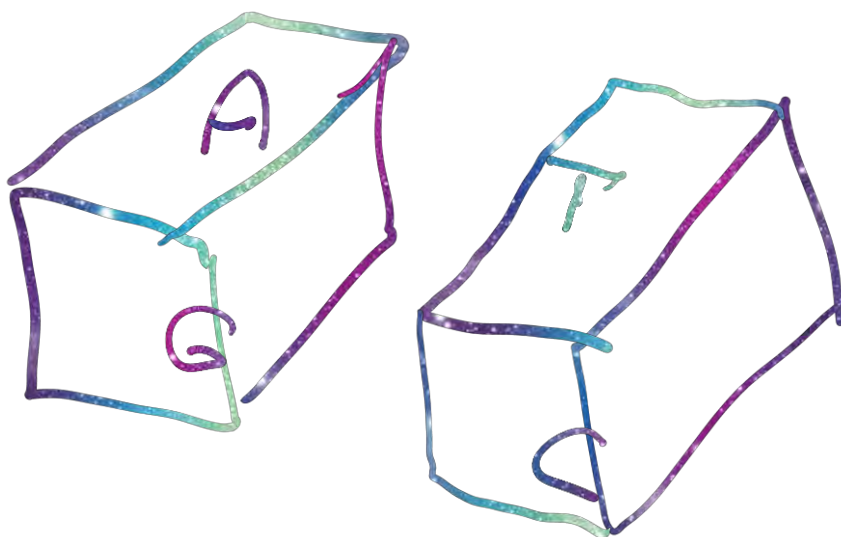
Closed-loop proton jumps obey neutrality requirement



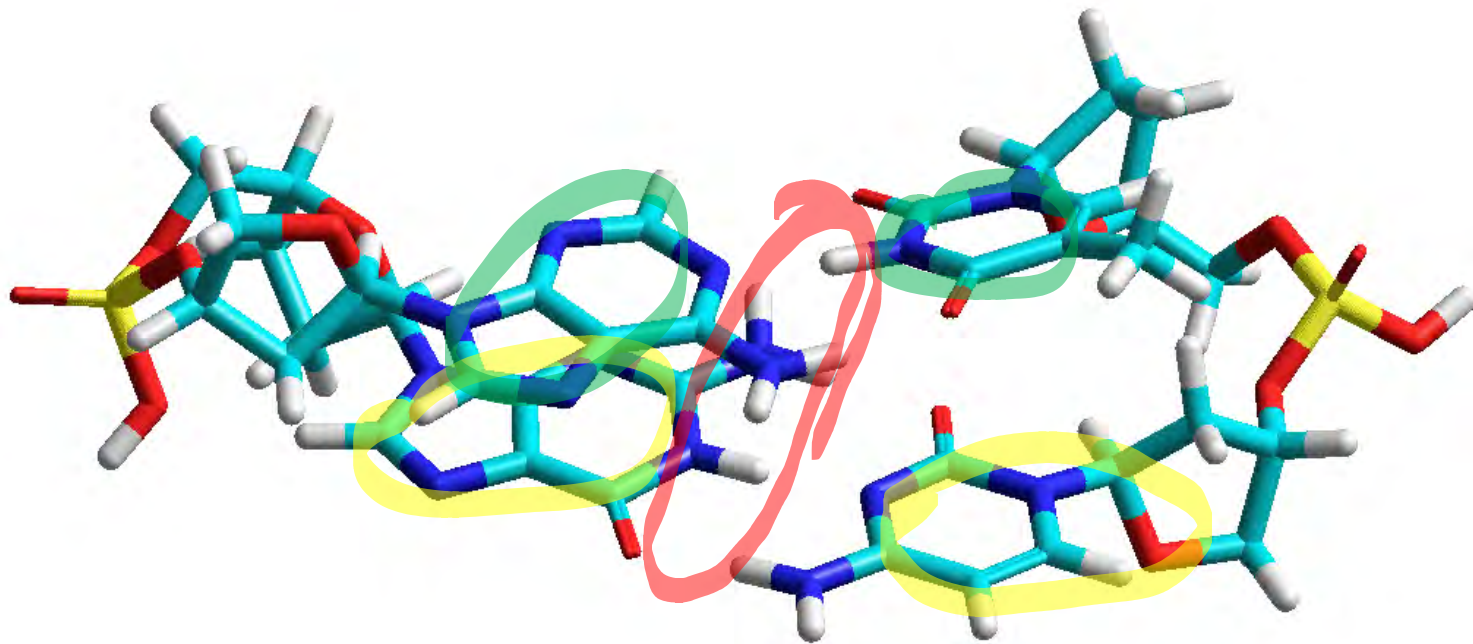
Tautomer transition energy



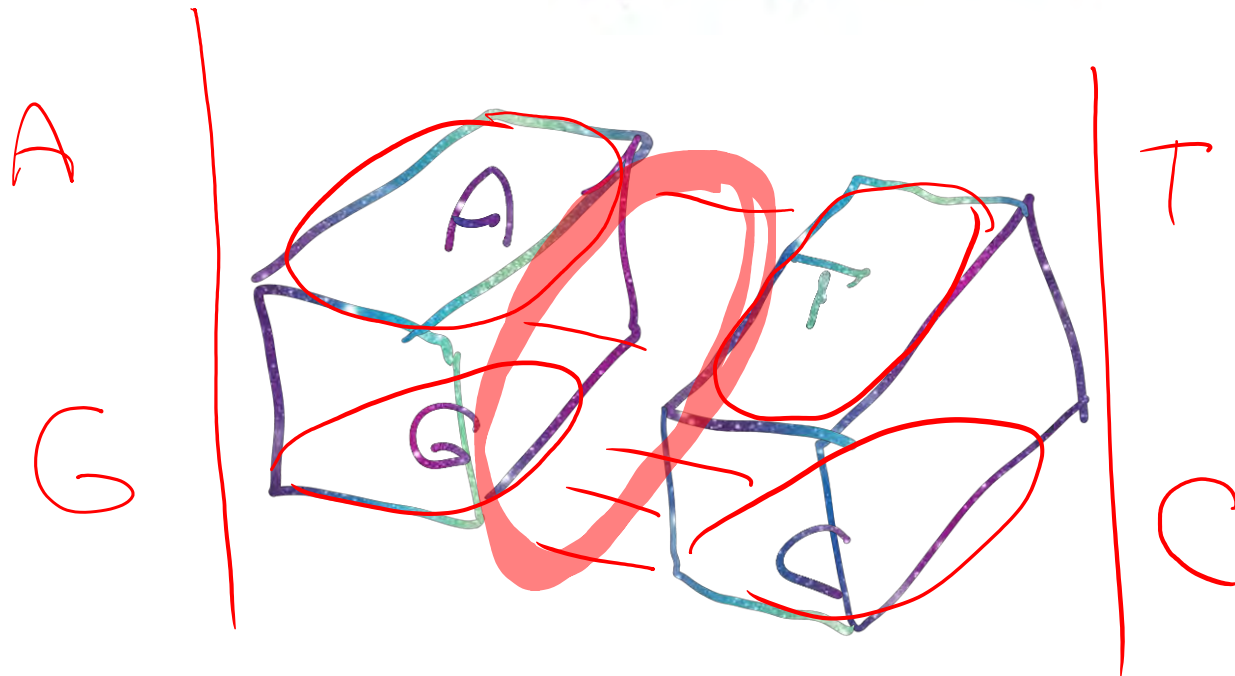
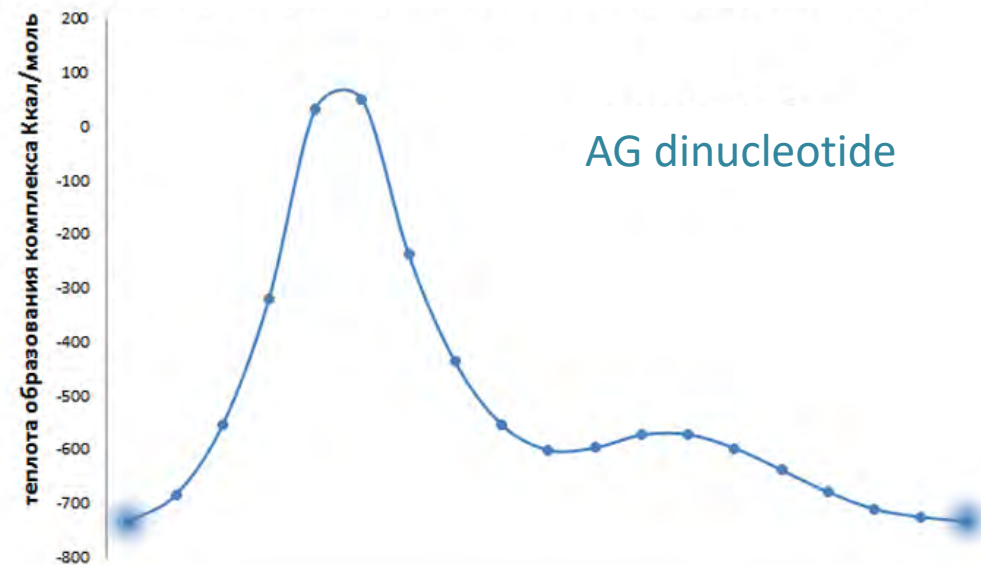
AG dinucleotide



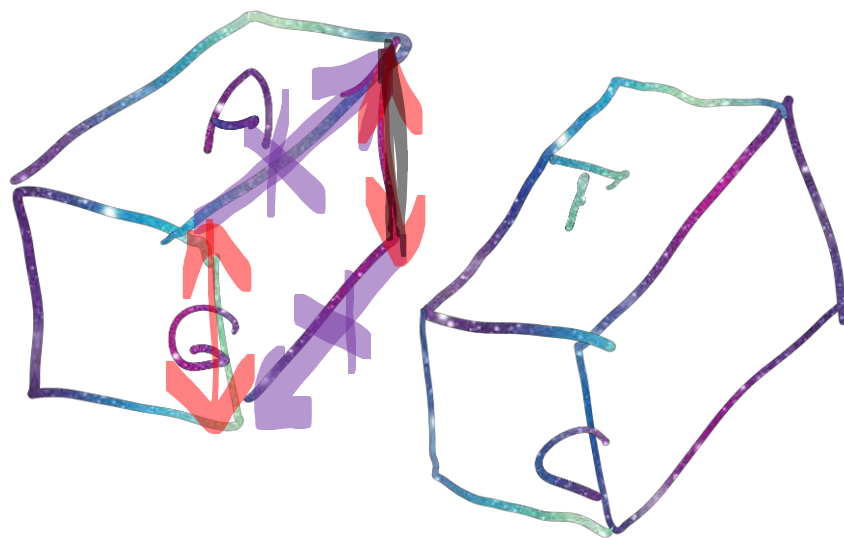
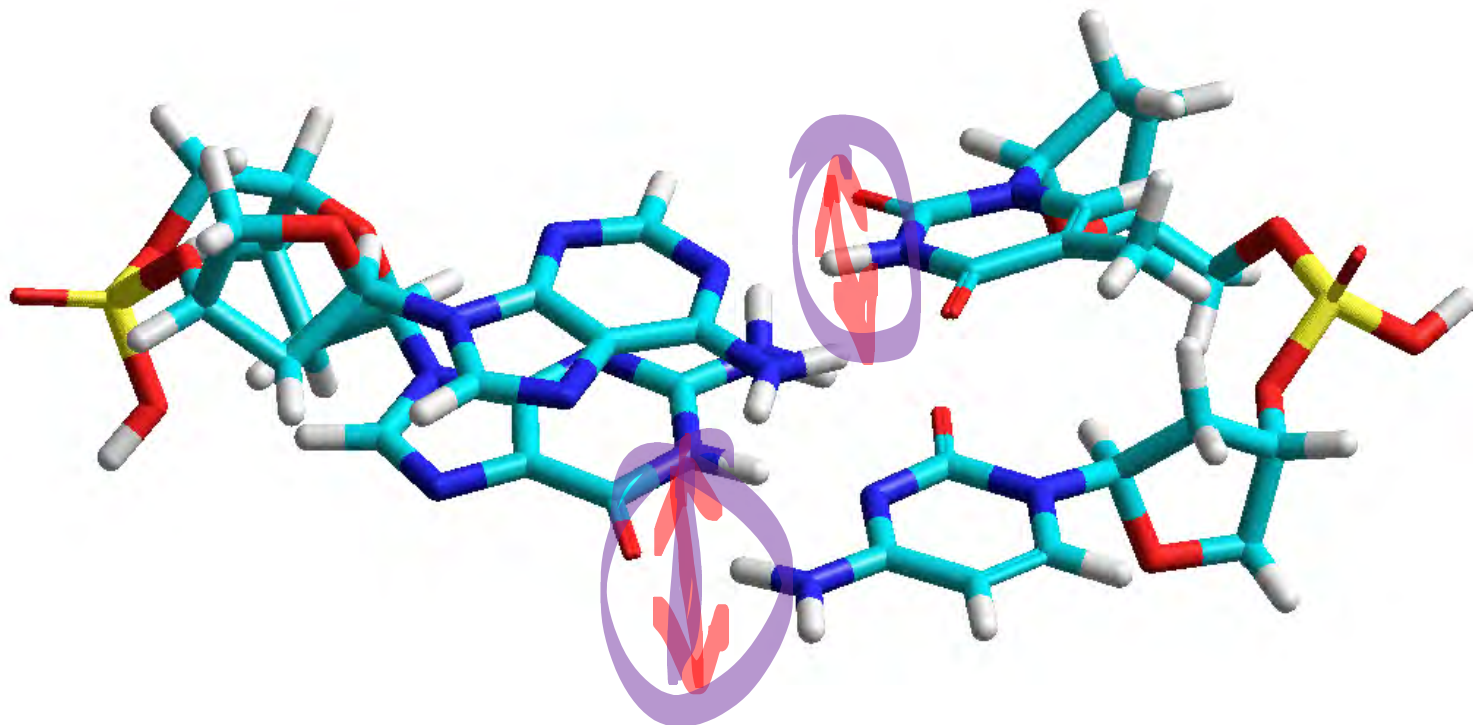
Closed-loop proton jumps obey neutrality requirement



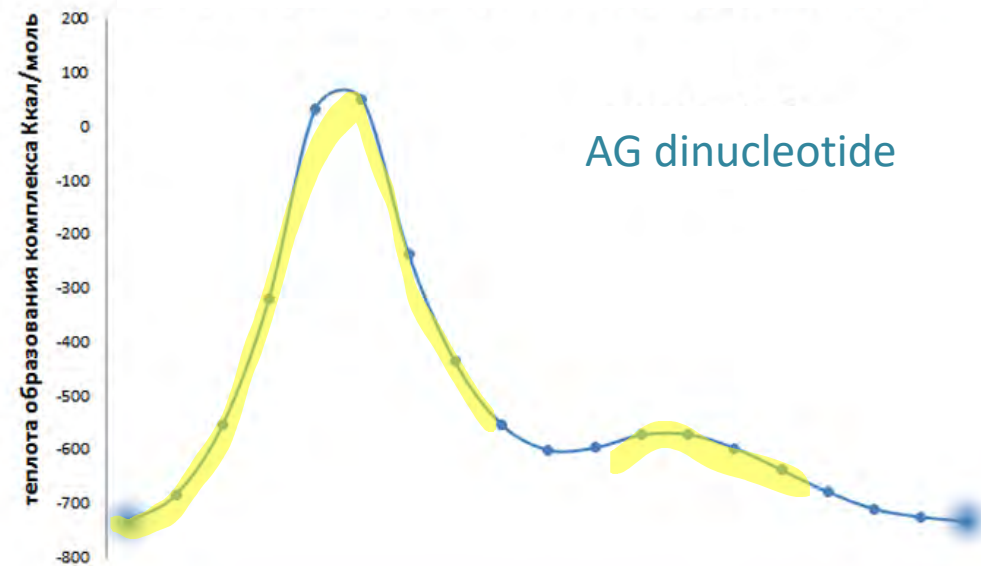
Tautomer transition energy



Closed-loop proton jumps obey neutrality requirement



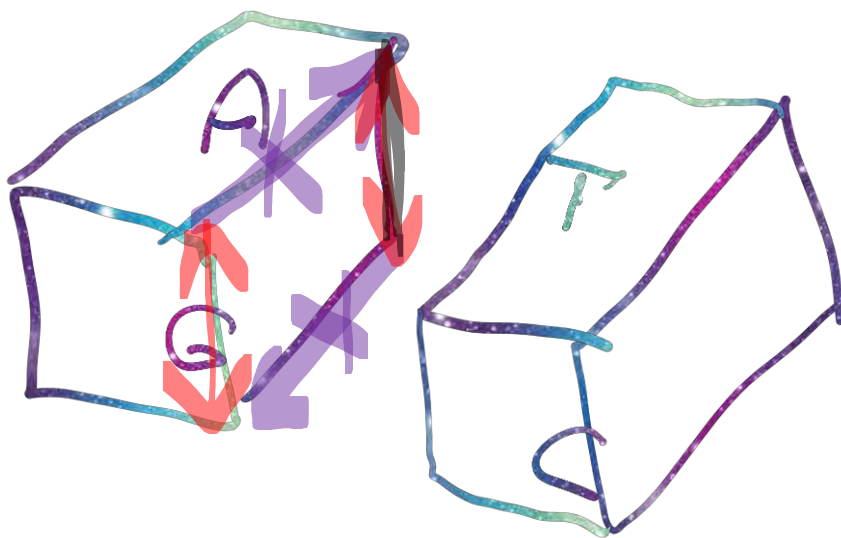
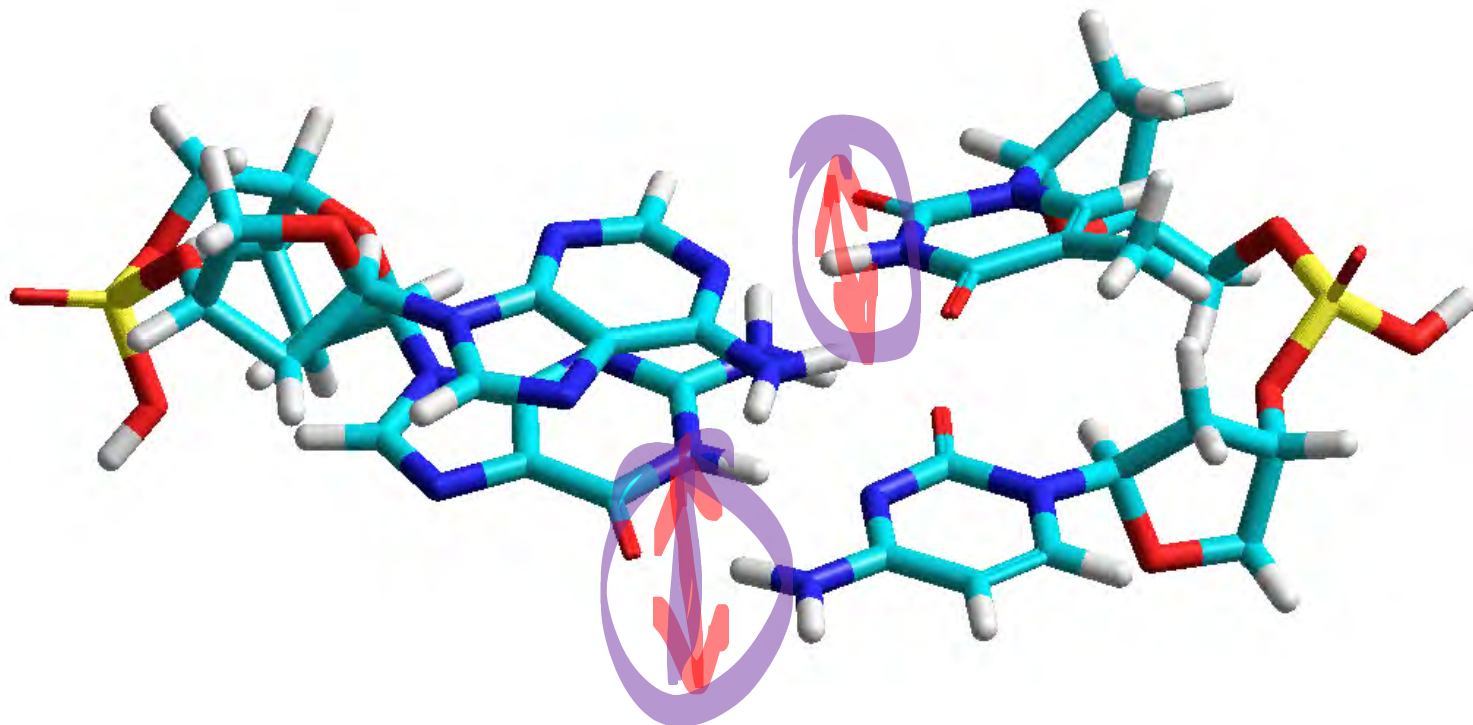
Tautomer transition energy



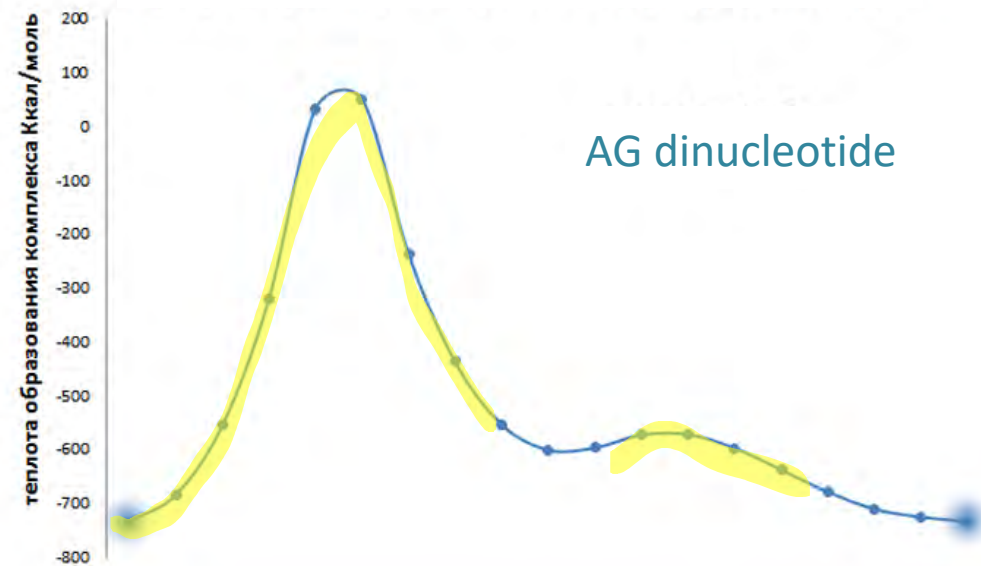
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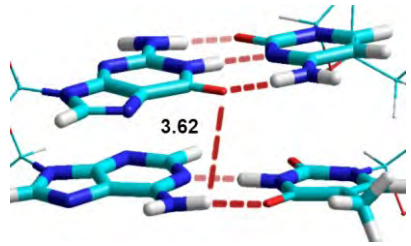
Tautomer transition energy



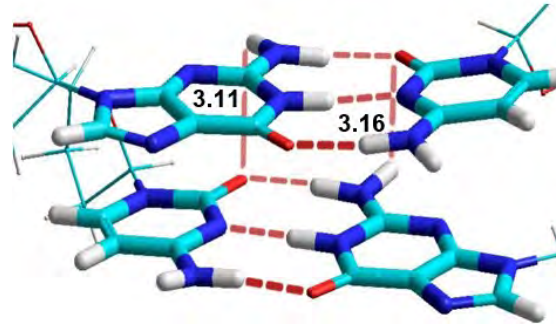
AG dinucleotide



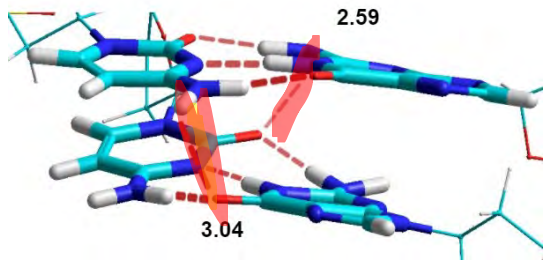
Dinucleotides have different longitudinal hydrogen bonds



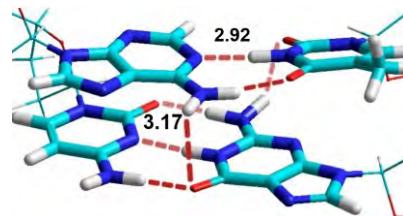
GA



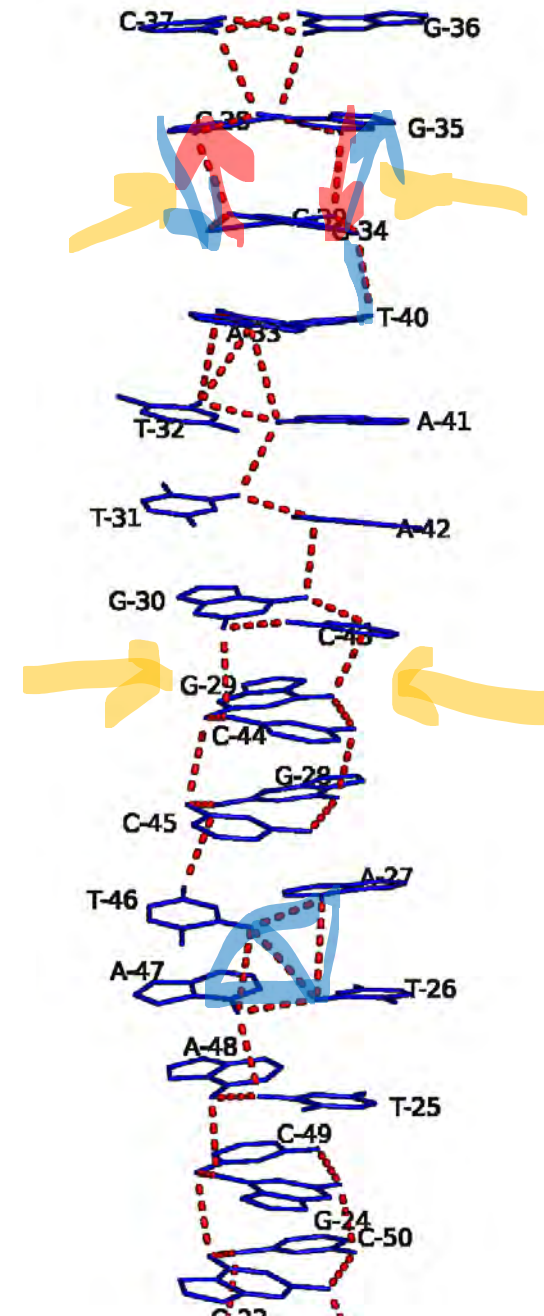
GC



CC



AC



Nonrandomness of mutations



Evolution favors longer purine chains

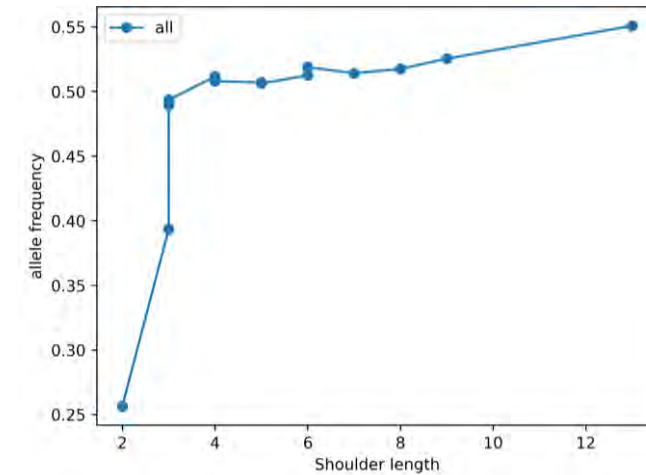
GWAS genome-wide SNP data.

GWAS – genome wide association studies

SNP – single nucleotide polymorphism

1000 volunteers

11M SNPs – Allele frequencies



SNP1

C G G G A G G A G G A A **G** A A G G A G T - 83%

↑ evolution

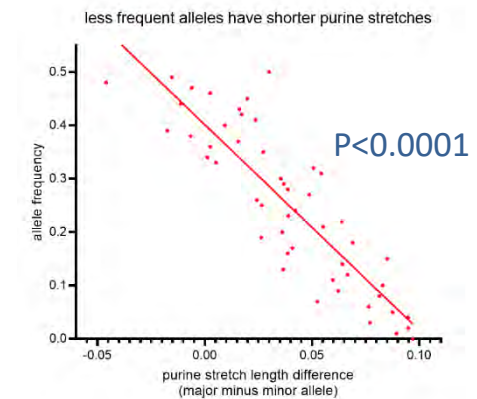
C G G G A G G A G G A A **C** A A G G A G T - 17%

SNP2

C A G A G G T - 28%

↓

C A G T G G T - 72%



Longer purine stretches evolve longer and shorter stretches evolve shorter

Suggesting biological function of longer stretches – oscillators



Evolution favors longer purine chains

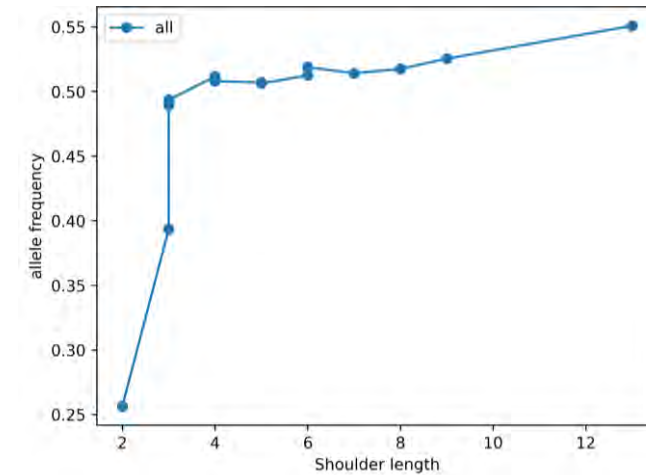
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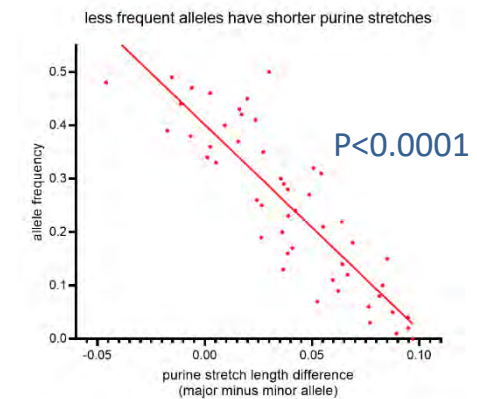
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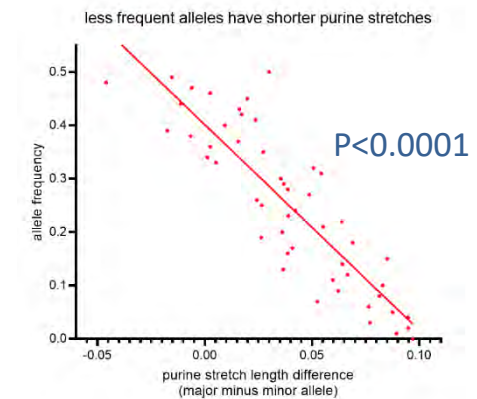
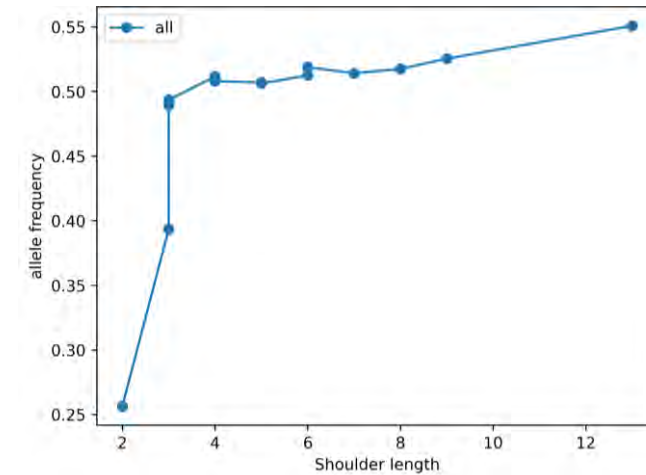
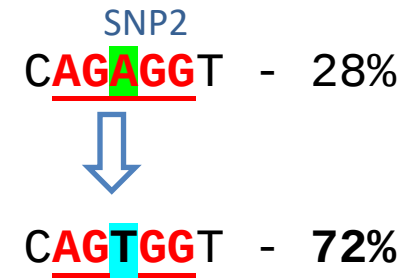
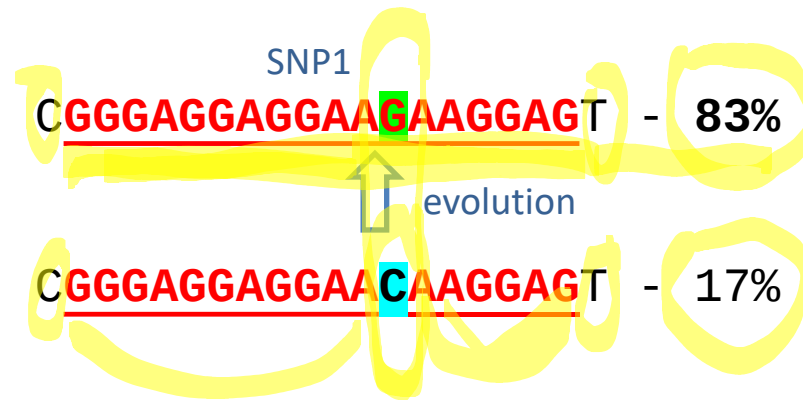
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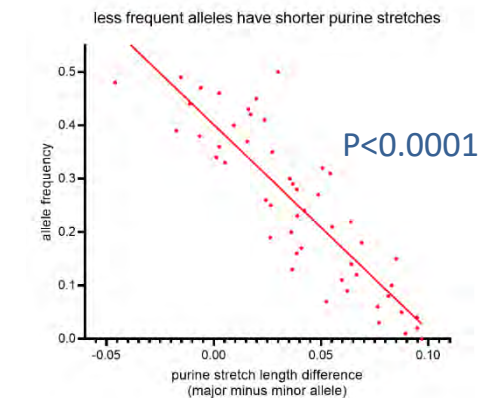
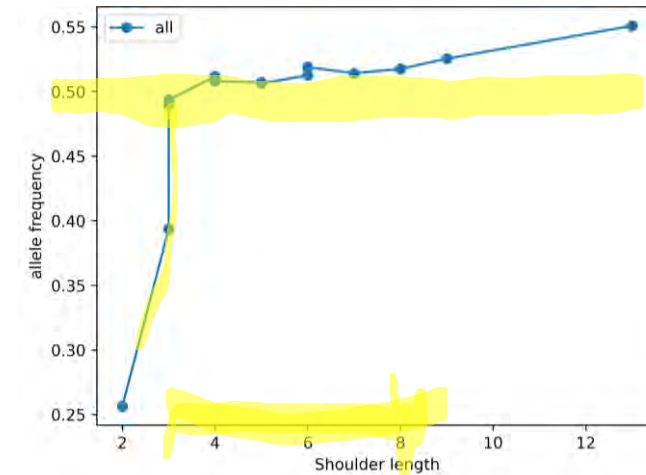
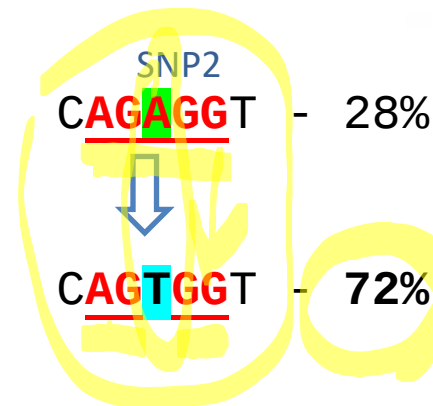
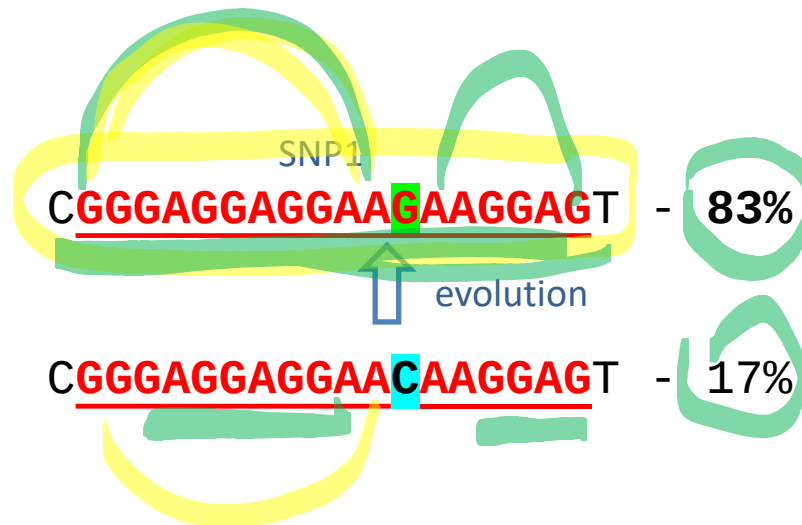
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Suggesting biological function of longer stretches – oscillators



Evolution favors longer purine chains

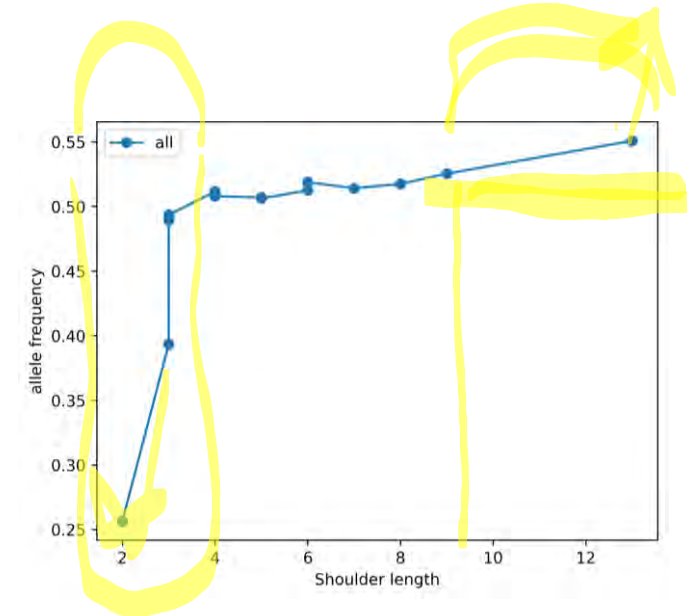
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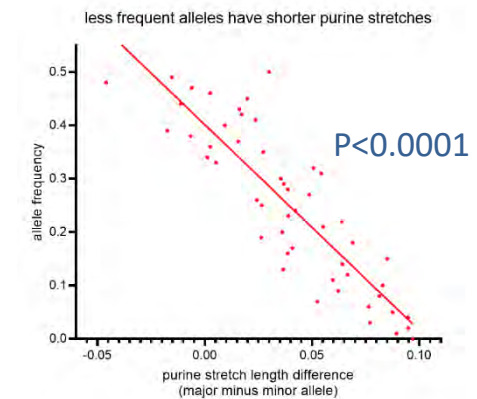
C G G G A G G A G G A A C A A G G A G T - 17%

SNP2

C A G A G G T - 28%

↓

C A G T G G T - 72%



Longer purine stretches evolve longer and shorter stretches evolve shorter

Suggesting biological function of longer stretches – oscillators

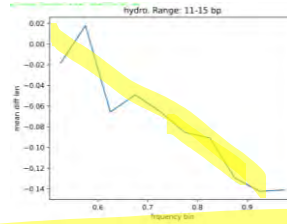
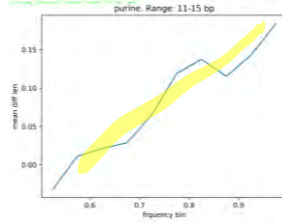


Purine stretches in other biological species plus proton chains

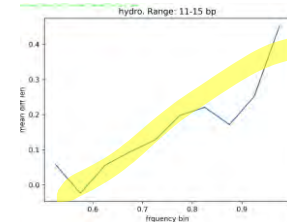
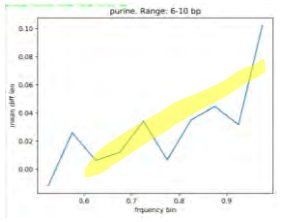
Electron chains
(purines)

Proton
chains

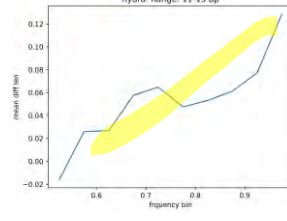
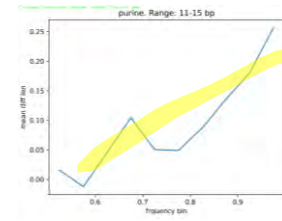
Human



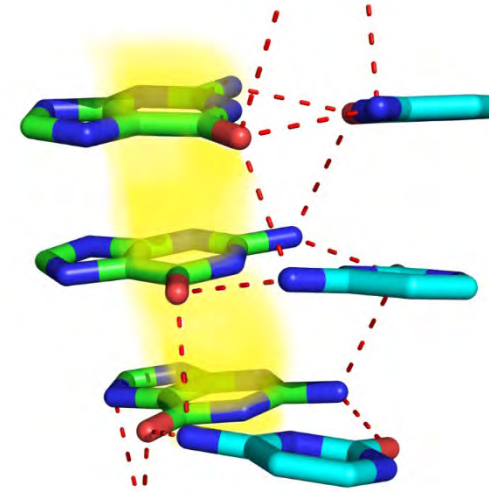
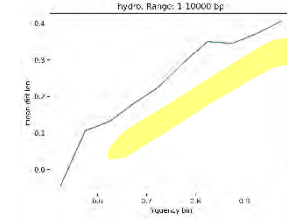
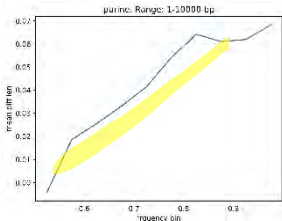
Bird



Fish



Plant

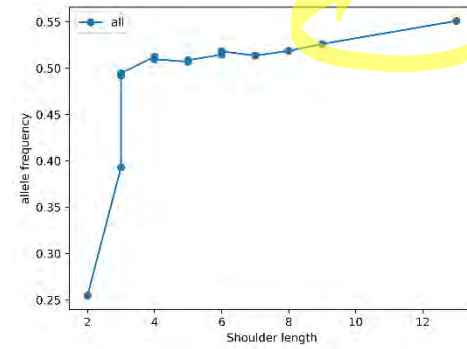


Rempel 2020 PMID: 32712047

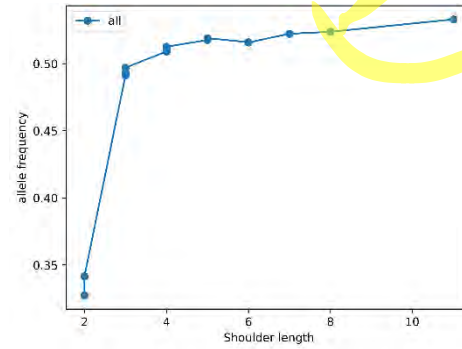


Evolutionary pressure to elongate purine chains

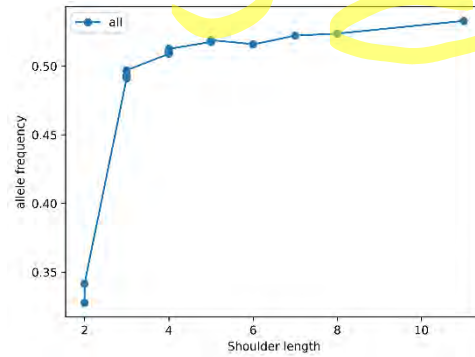
Human



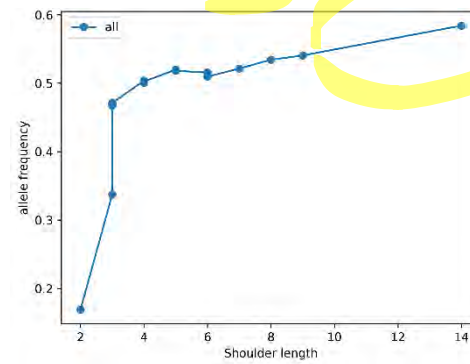
Fish (salmon)



Bird (Great Tit)



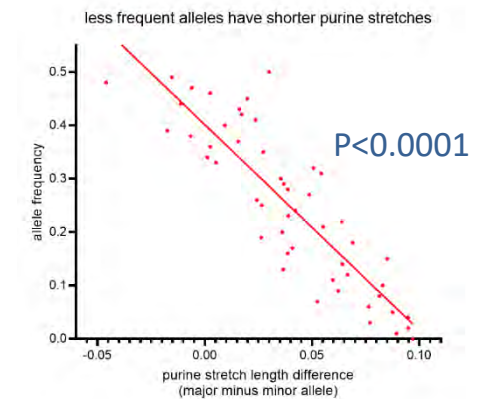
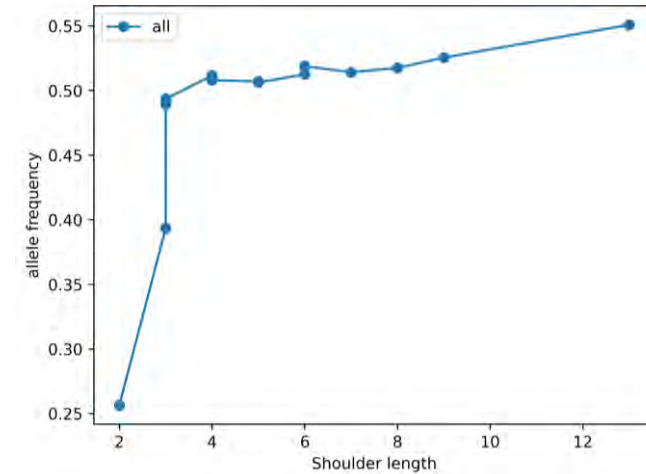
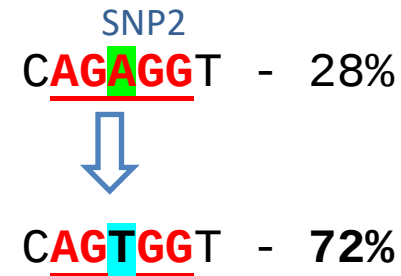
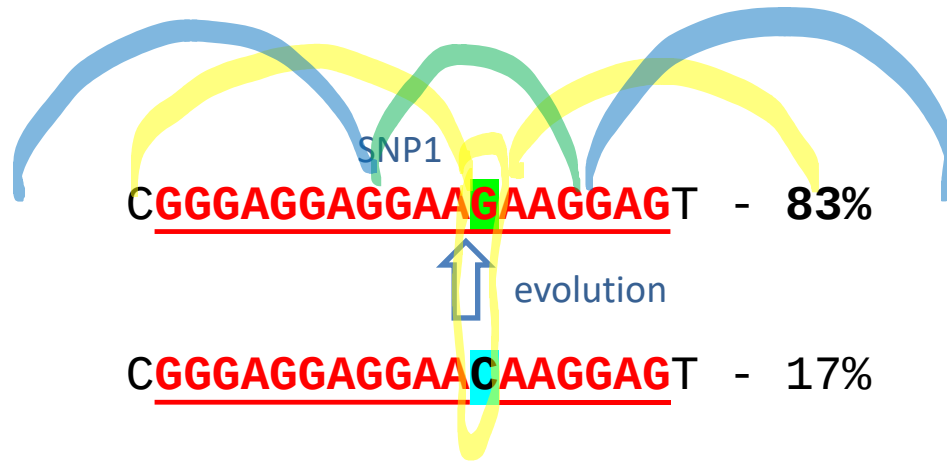
Plant (cocoa)



Evolution favors longer purine chains

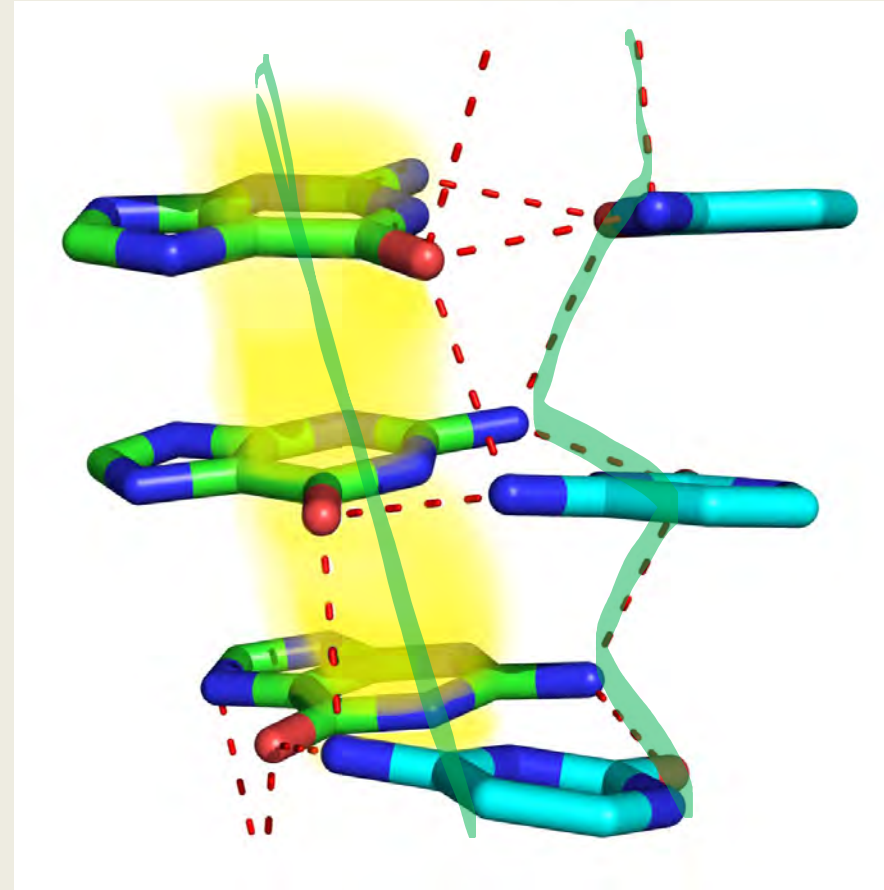
GWAS genome-wide SNP data.
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Longer purine stretches evolve longer and shorter stretches evolve shorter
Suggesting biological function of longer stretches – oscillators

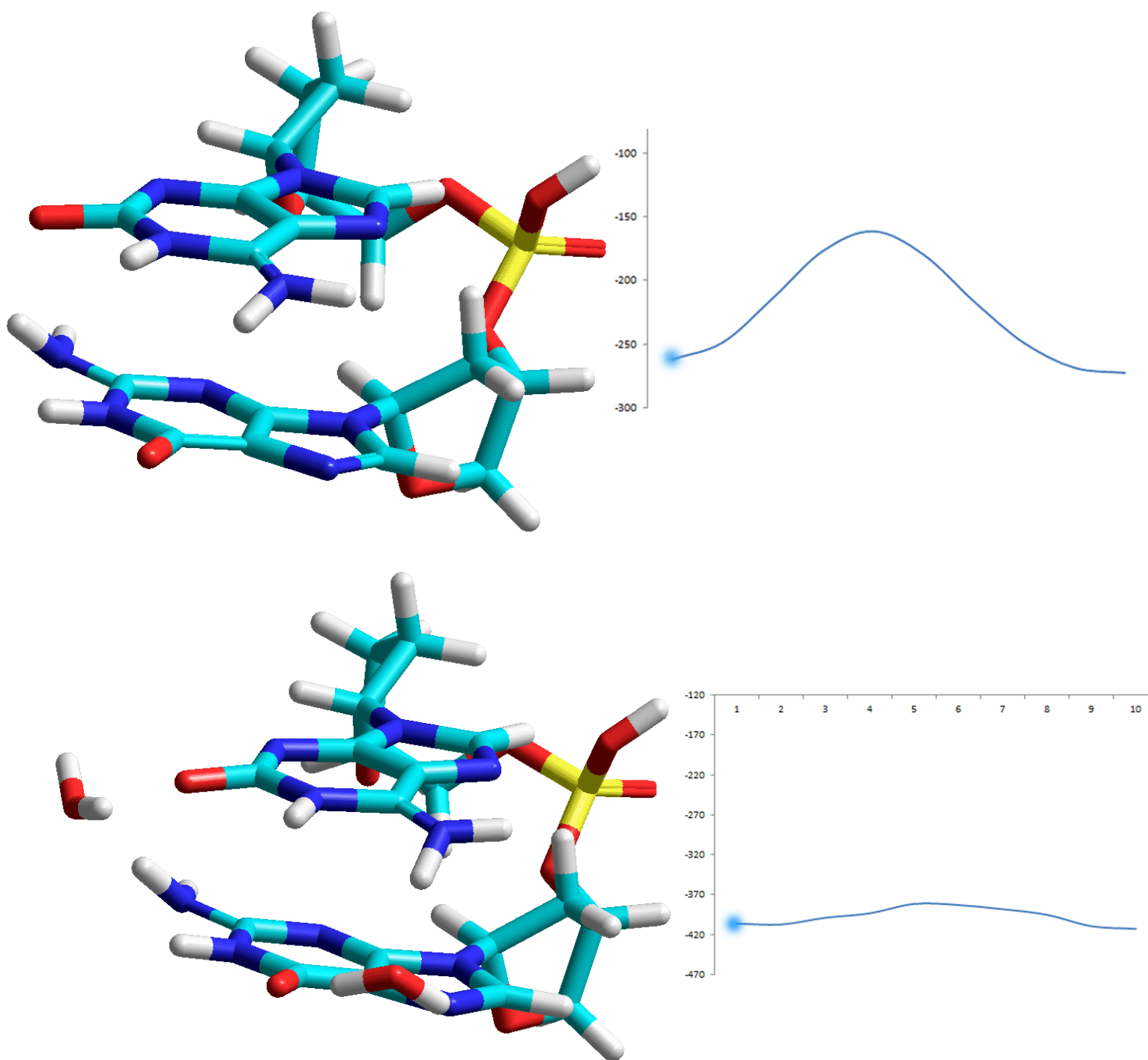




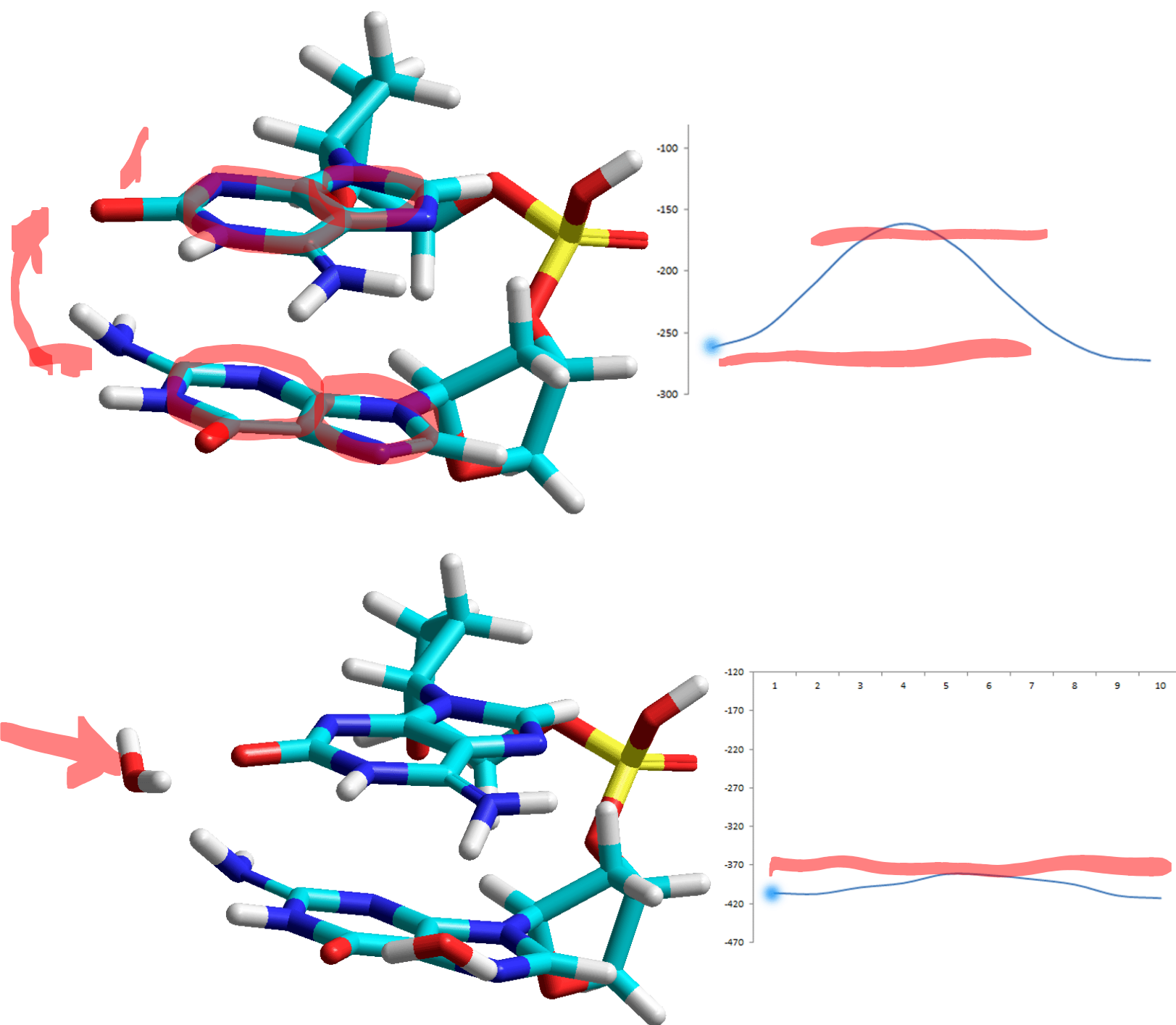
Water structures in DNA grooves



Does water mediate
longitudinal proton
jumping in DNA?



Does water mediate longitudinal proton jumping in DNA?

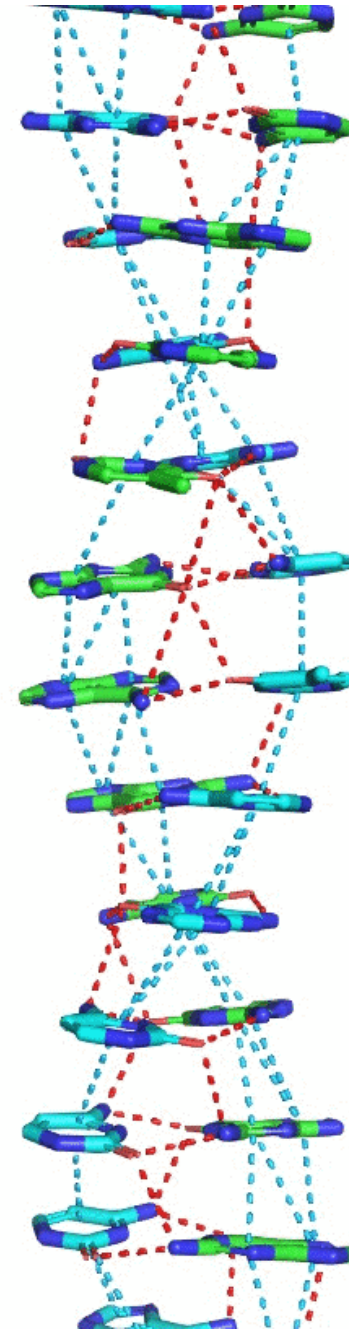
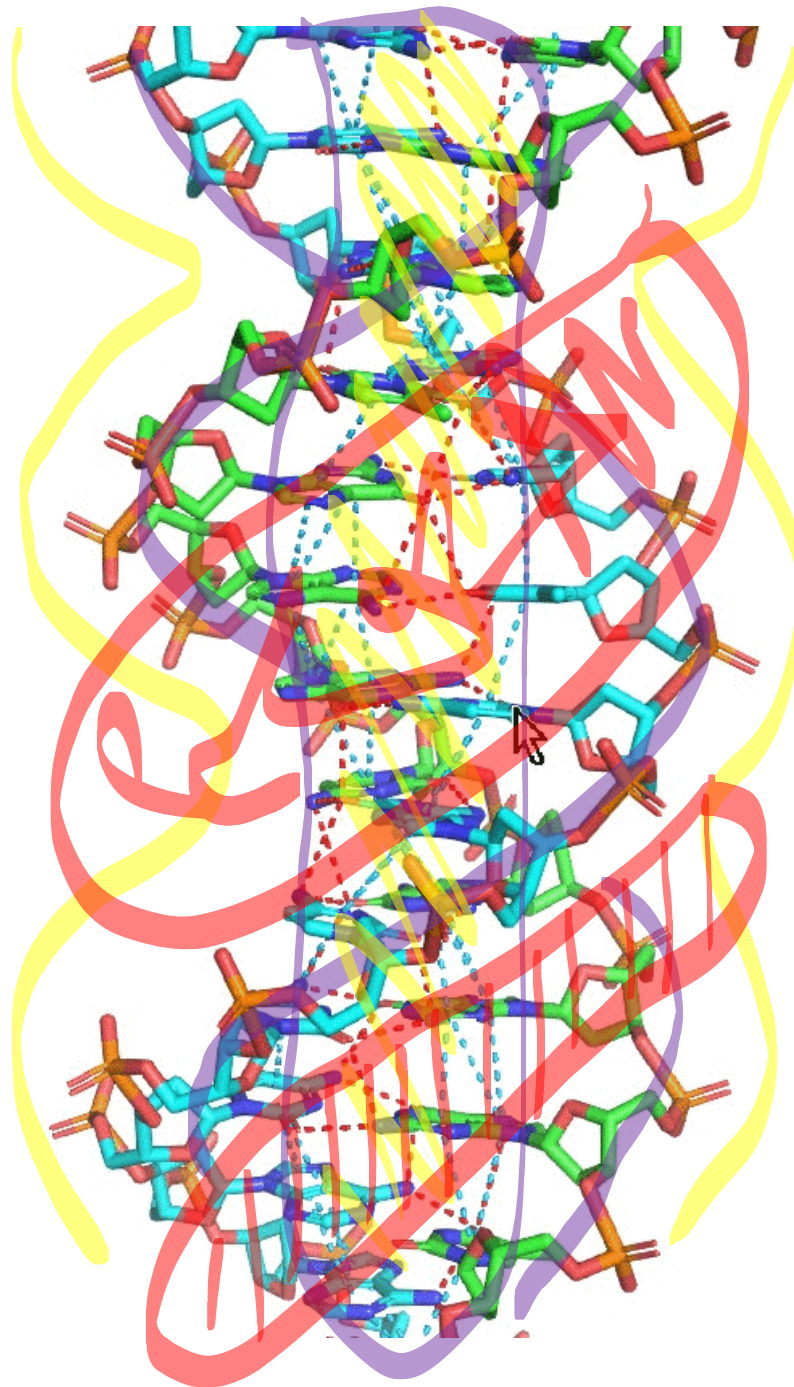


3.7Å cutoff
for h-bonds

electron wires



proton wires

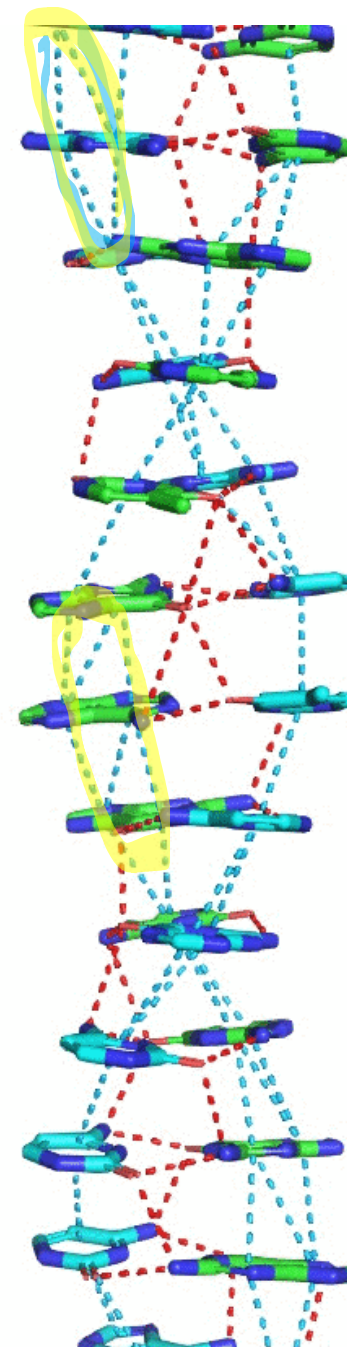
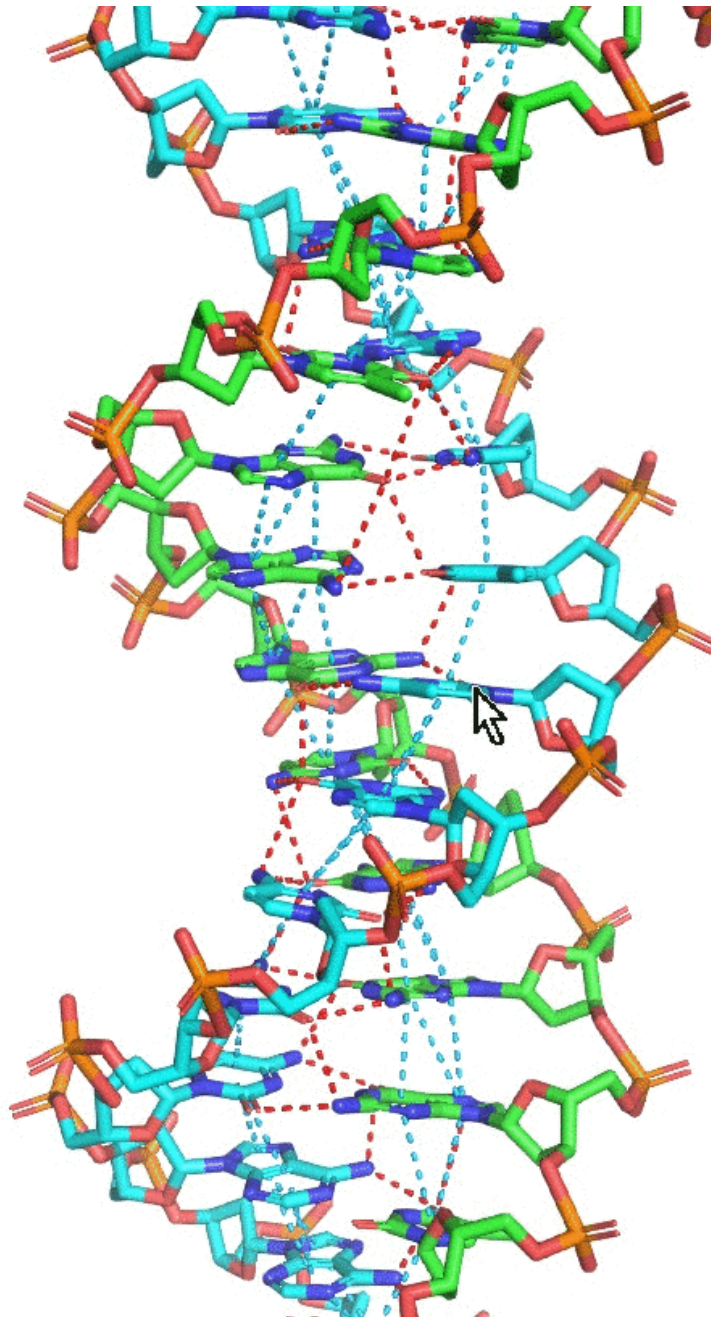


3.7Å cutoff
for h-bonds

electron wires



proton wires

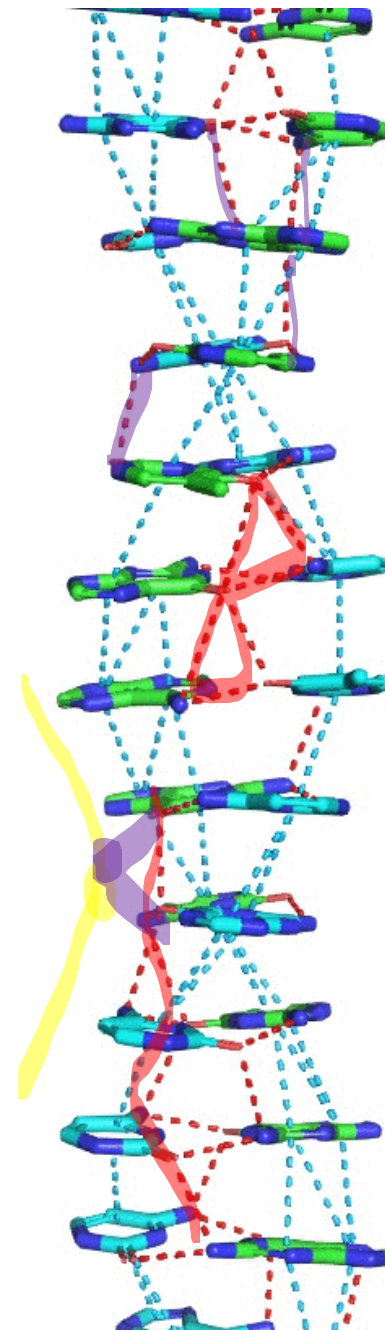
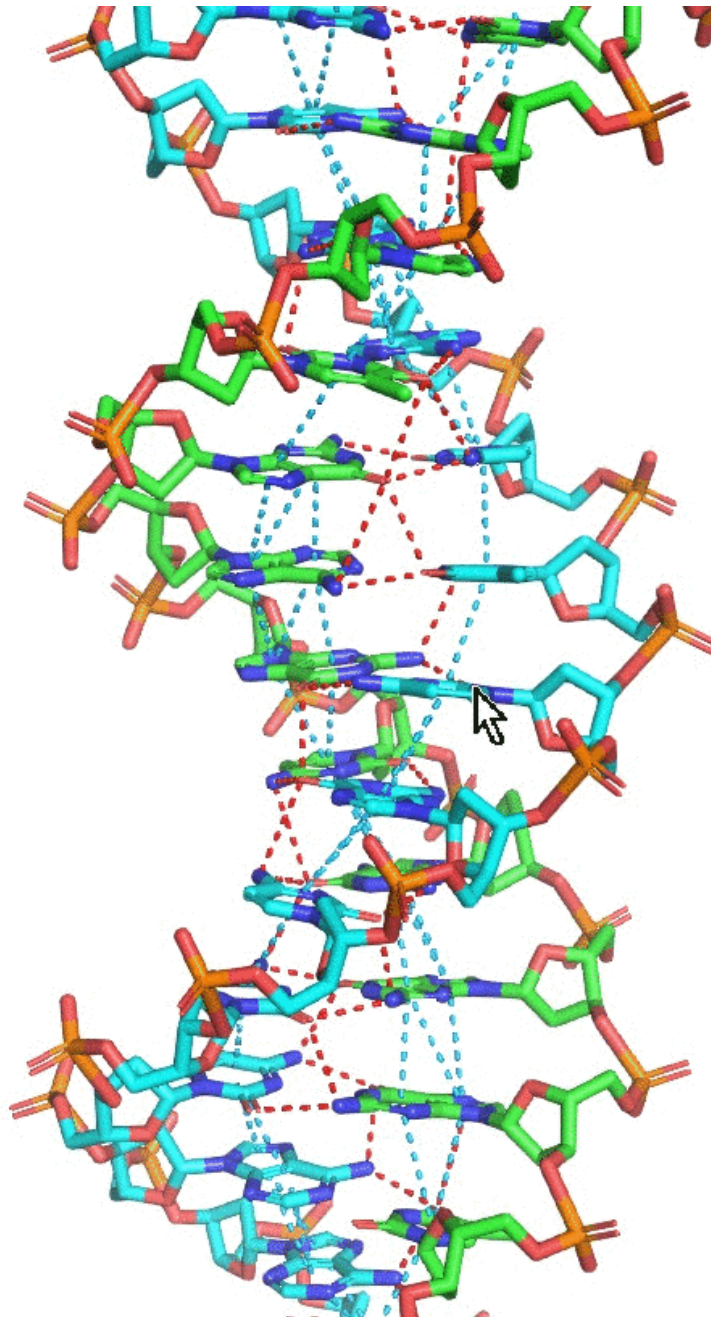


3.7Å cutoff
for h-bonds

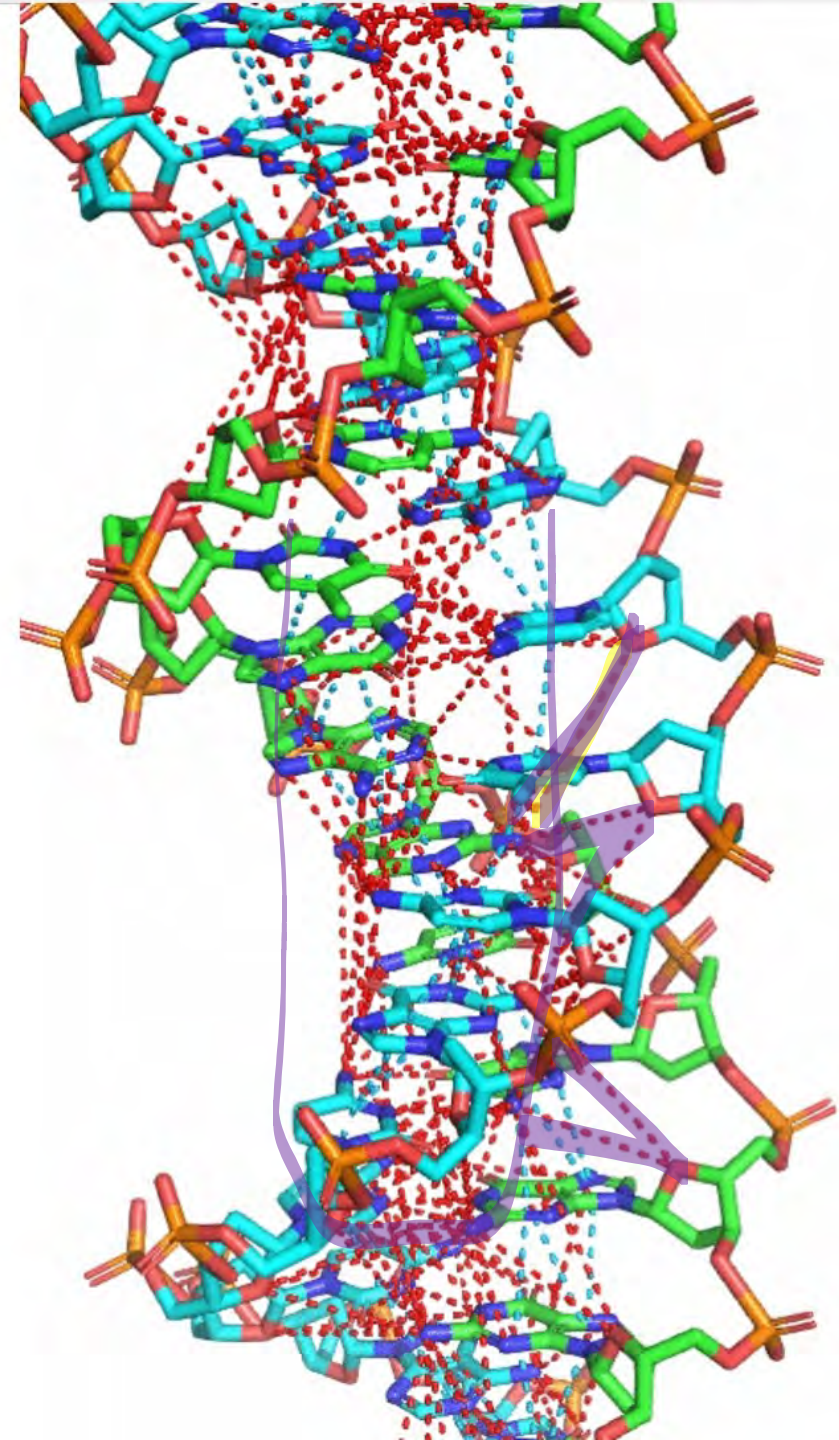
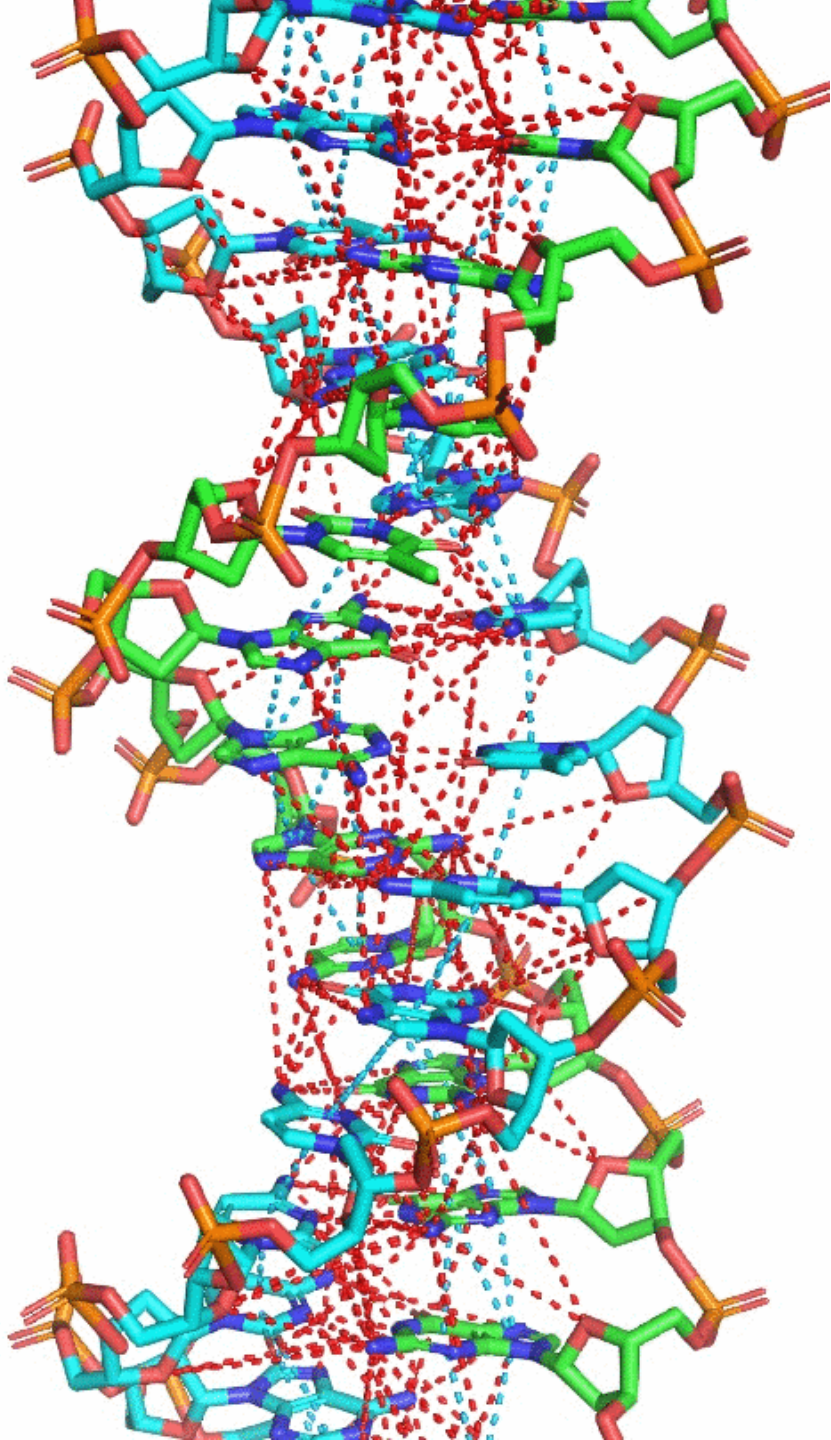
electron wires



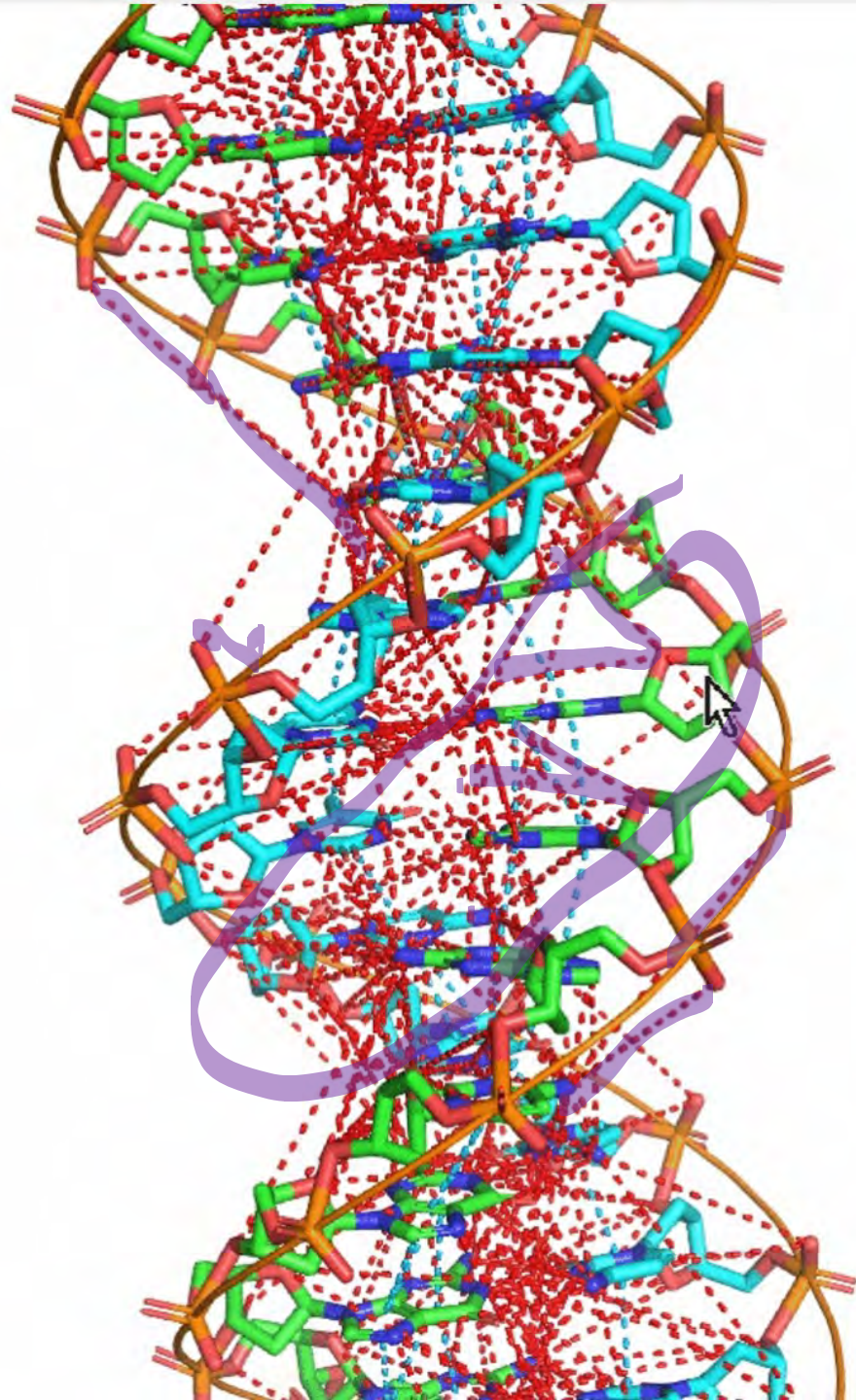
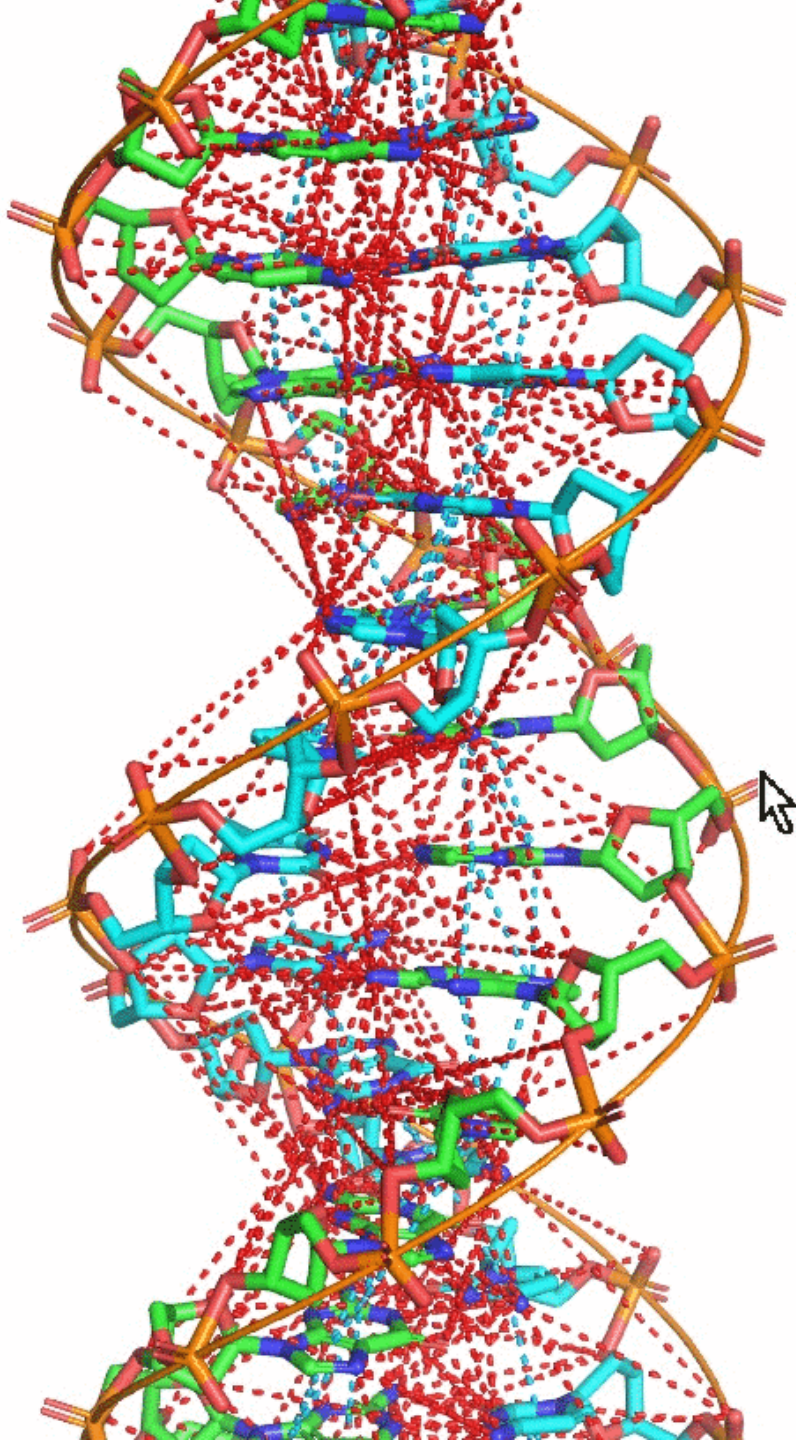
proton wires



7.5Å cutoff
for h-bonds



10Å cutoff
for h-bonds

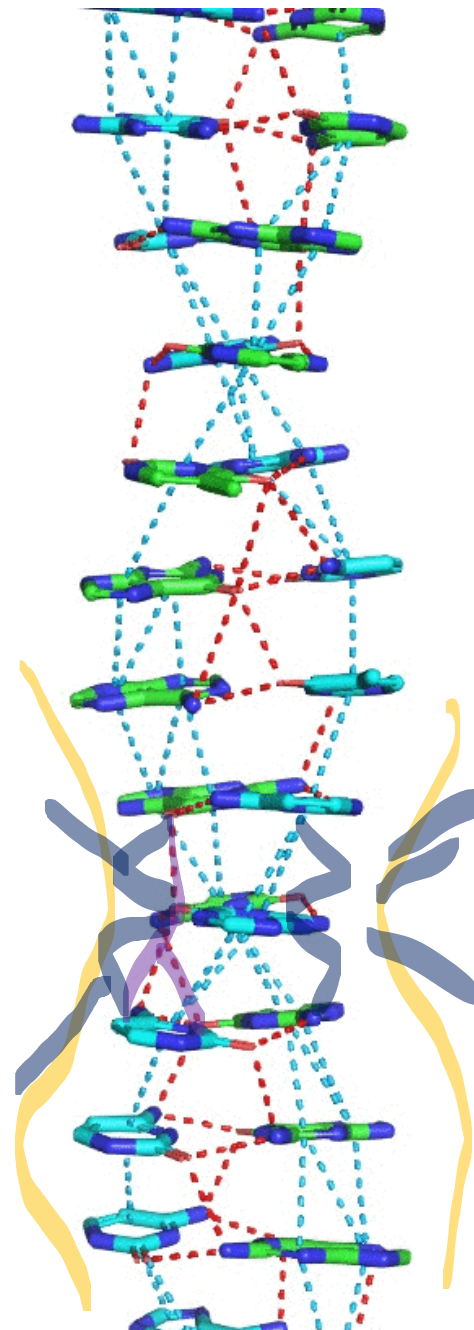
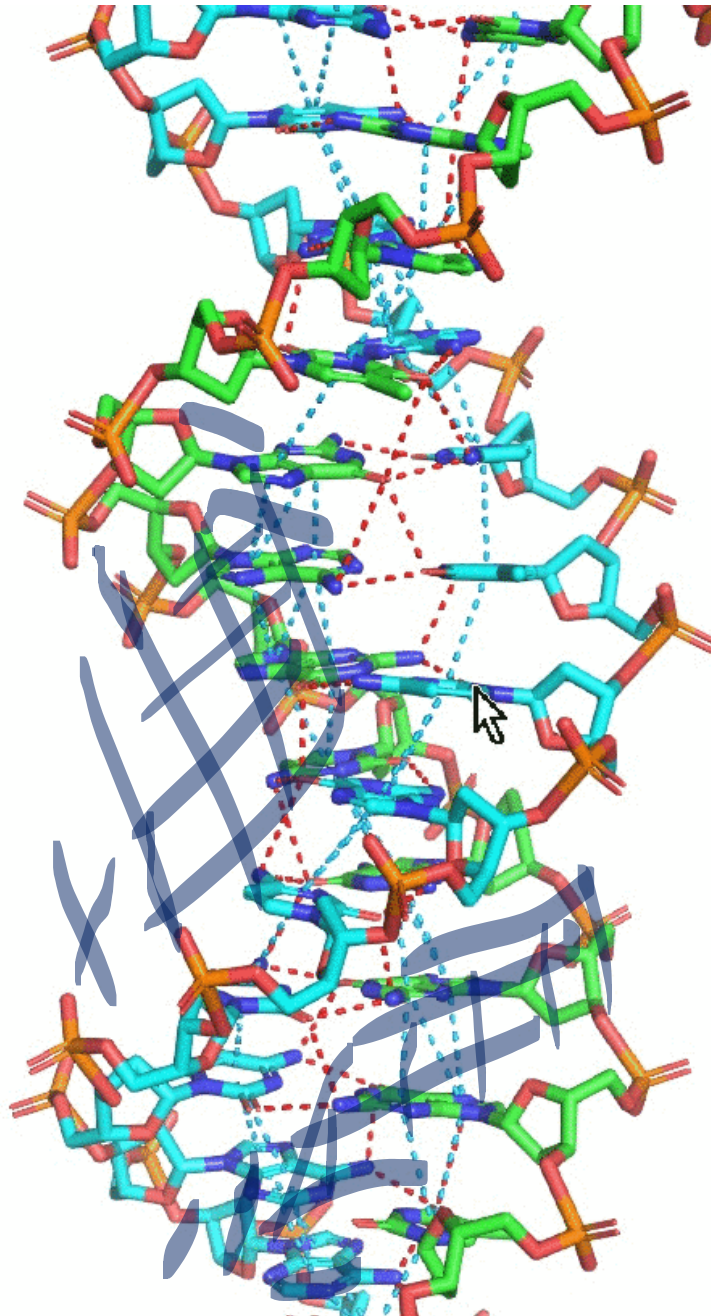


3.7Å cutoff
for h-bonds

electron wires

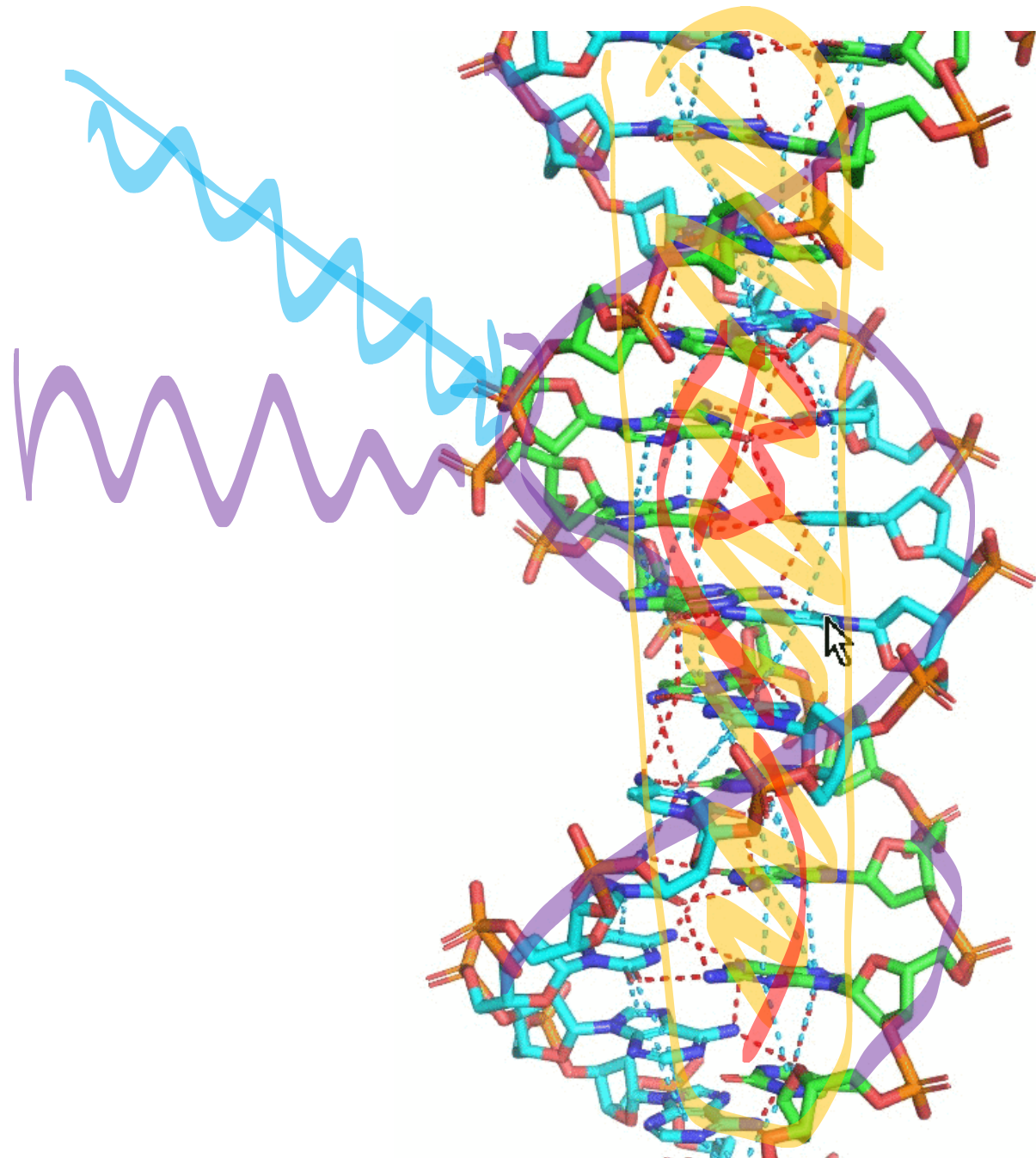


proton wires

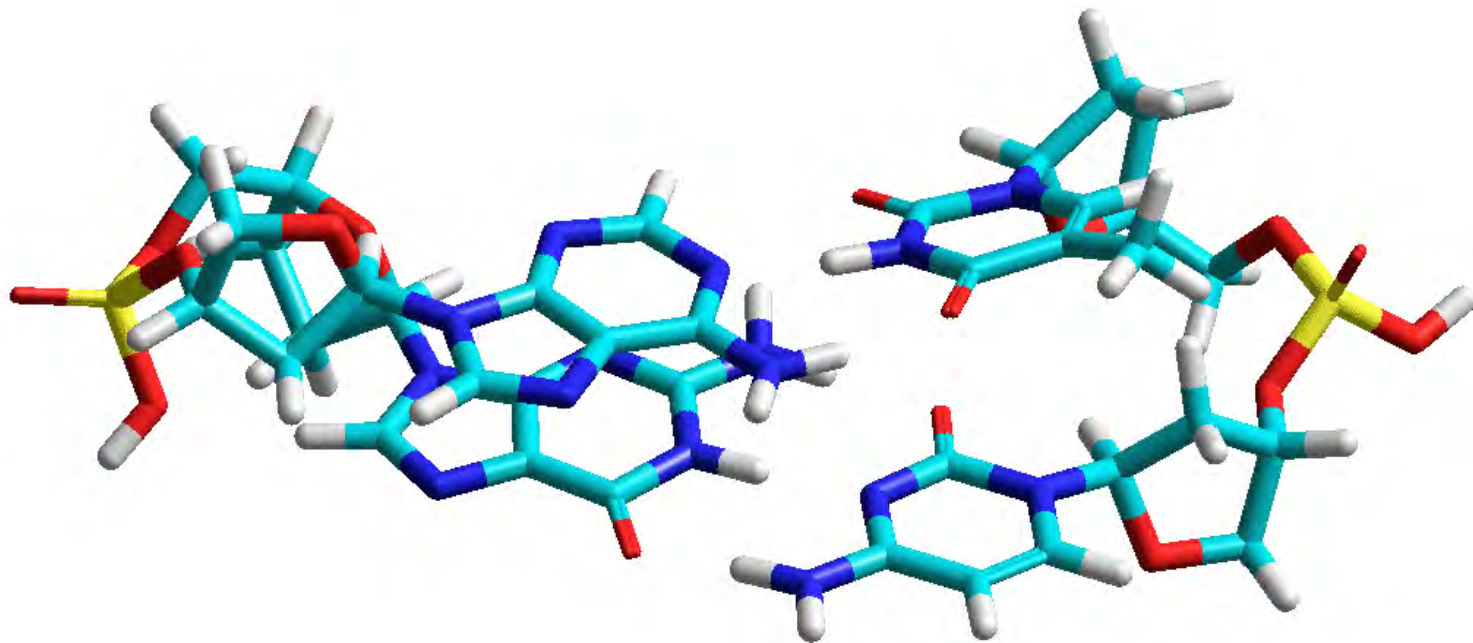


What is the physical nature of DNA resonance?

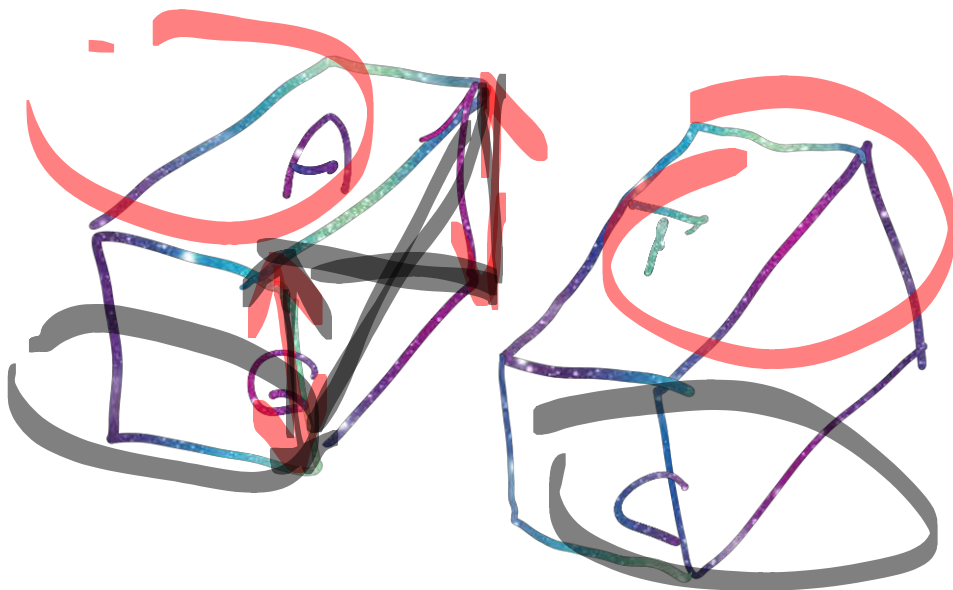
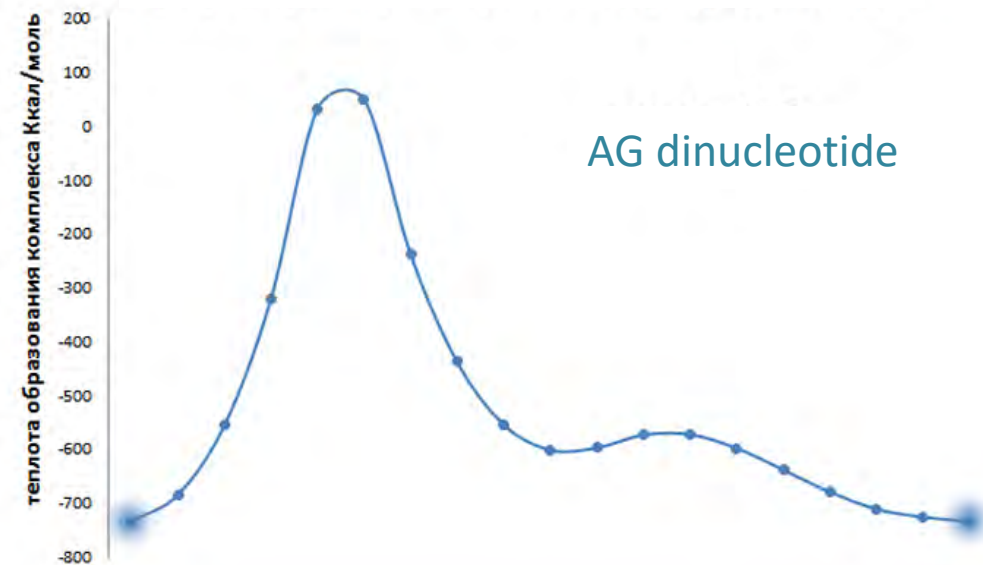


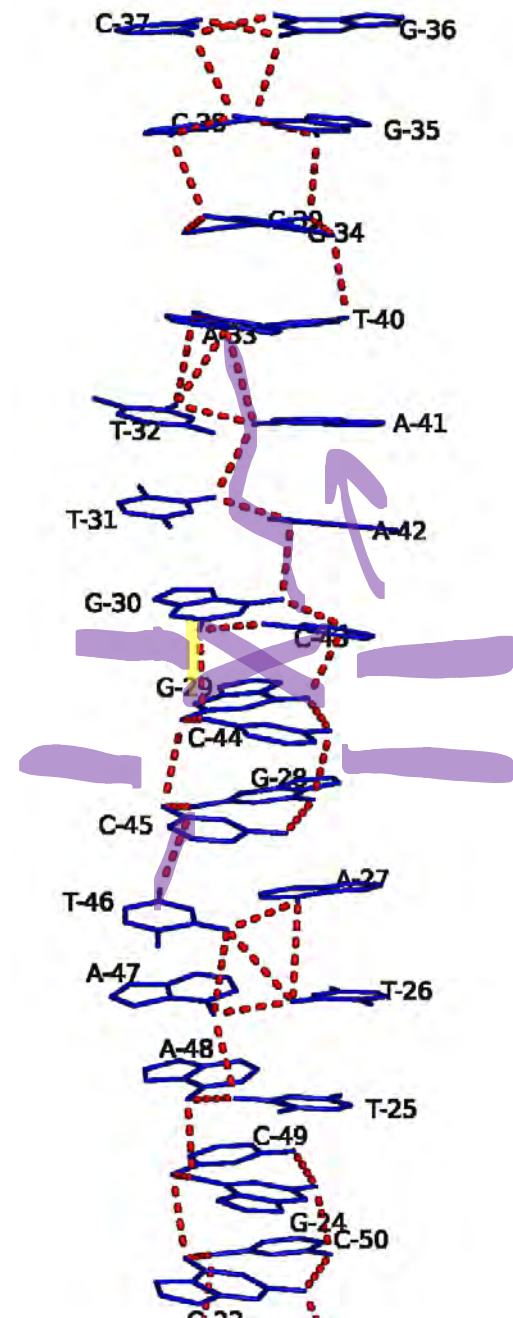


Closed-loop proton jumps obey neutrality requirement

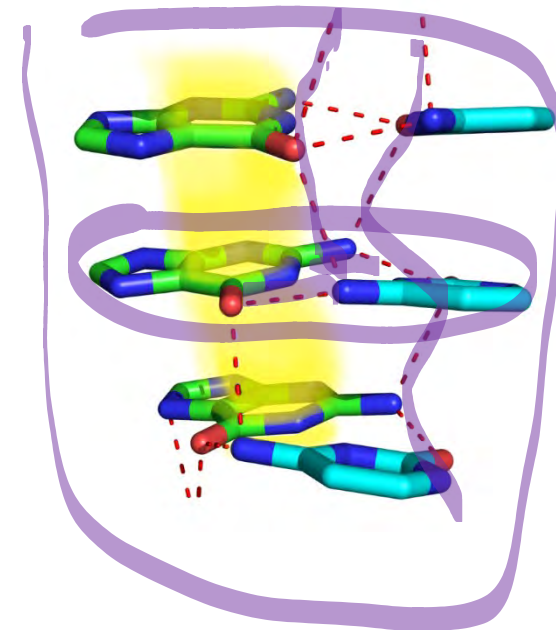
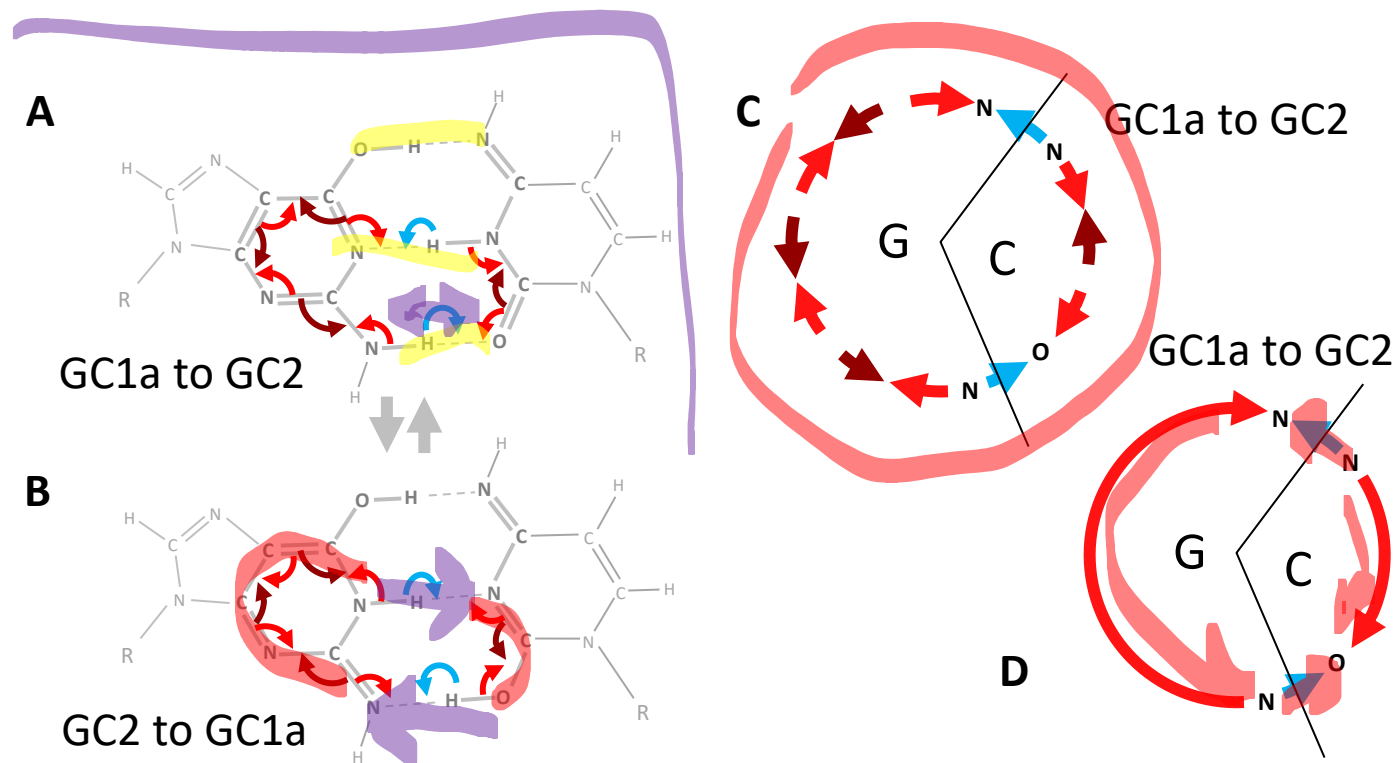


Tautomer transition energy



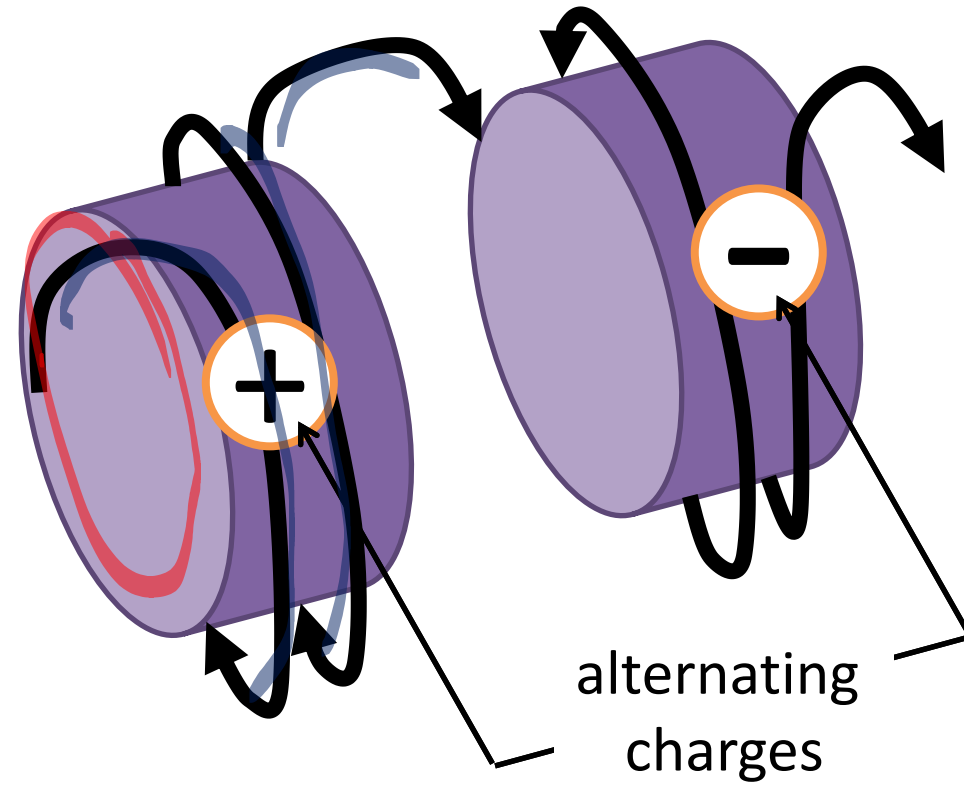
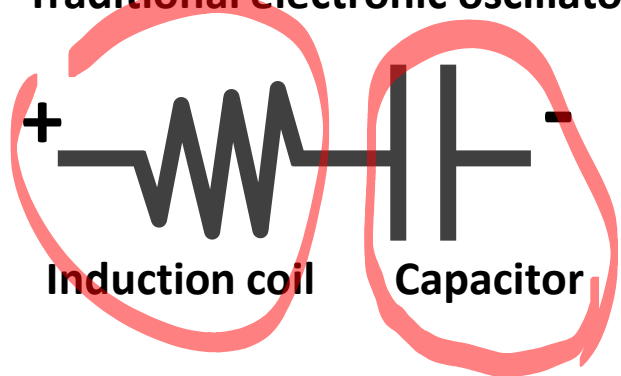


Oscillations of protons in tautomers and the requirement of neutrality



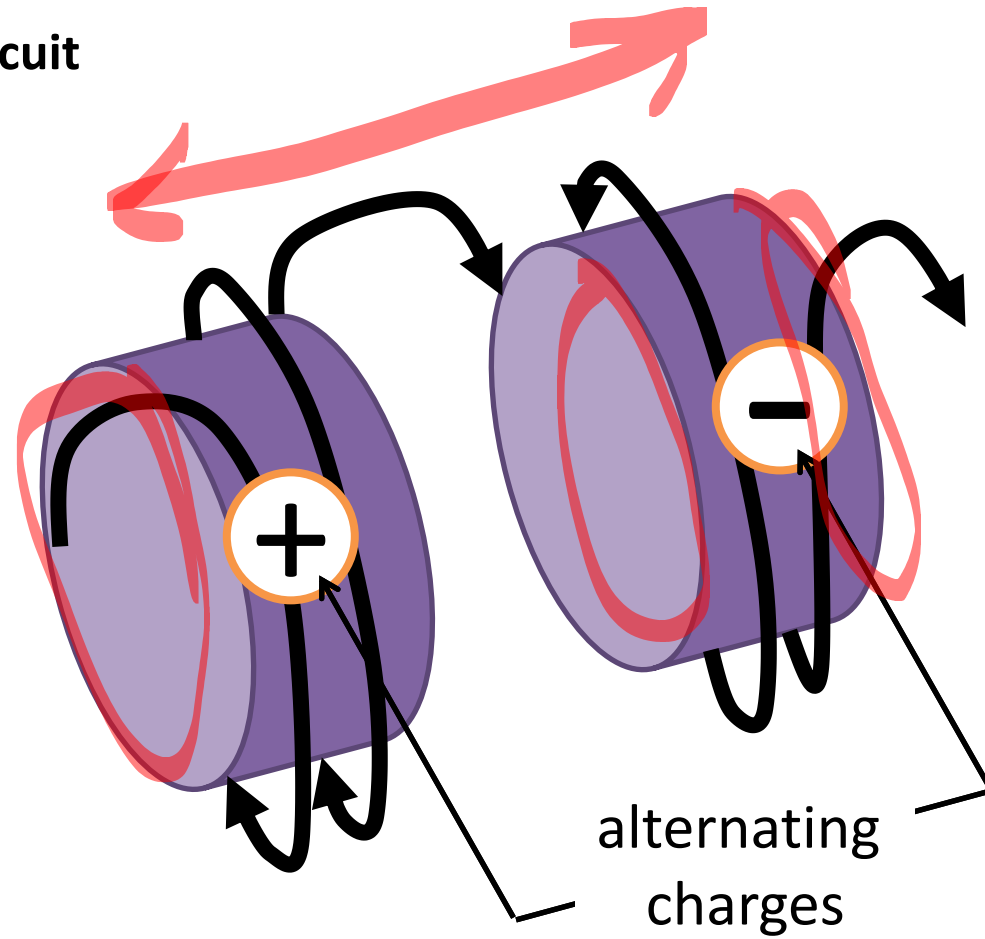
The dinucleosome as an LC circuit

Traditional electronic oscillator

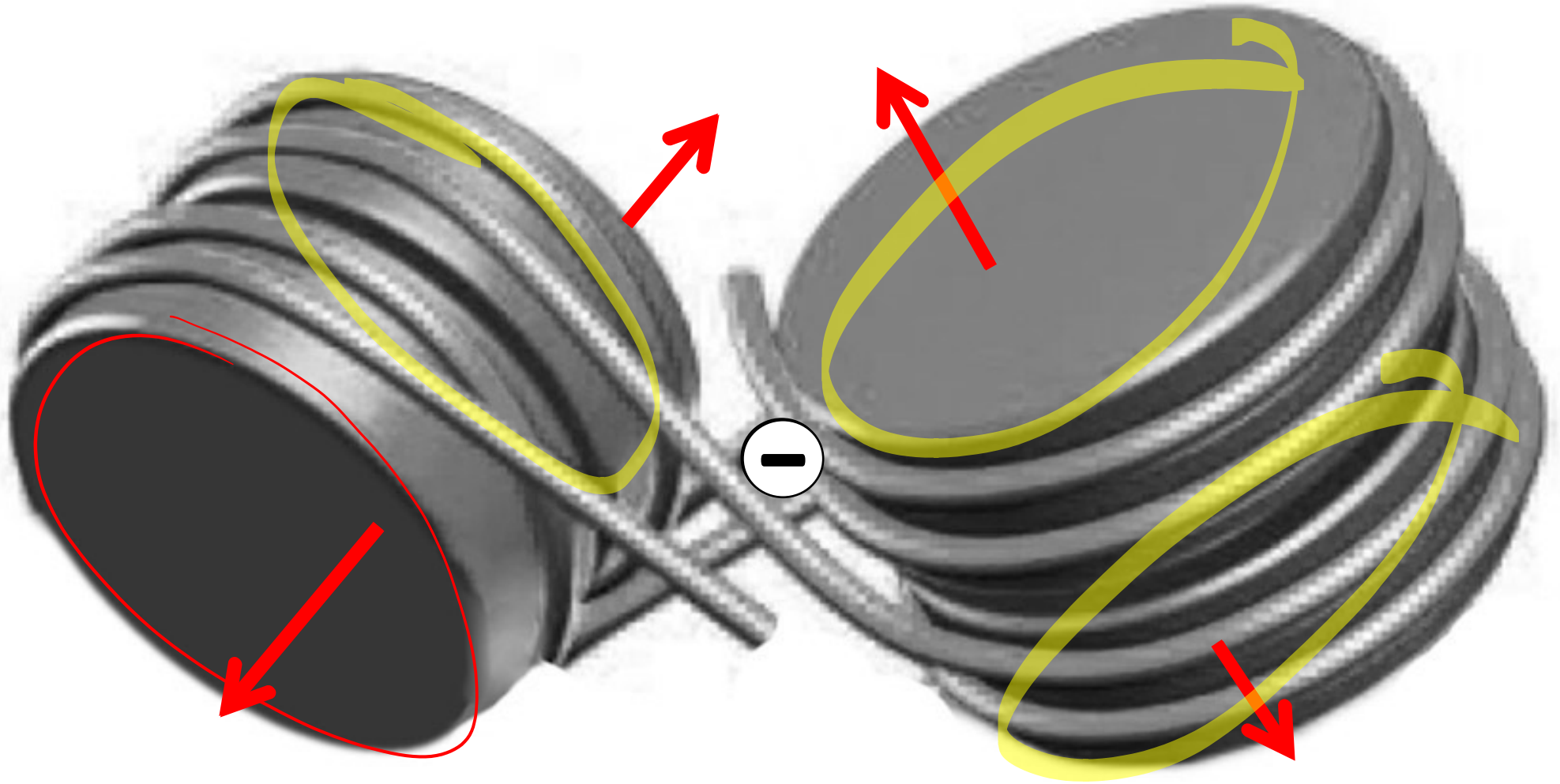


The dinucleosome as an LC circuit

Traditional electronic oscillator



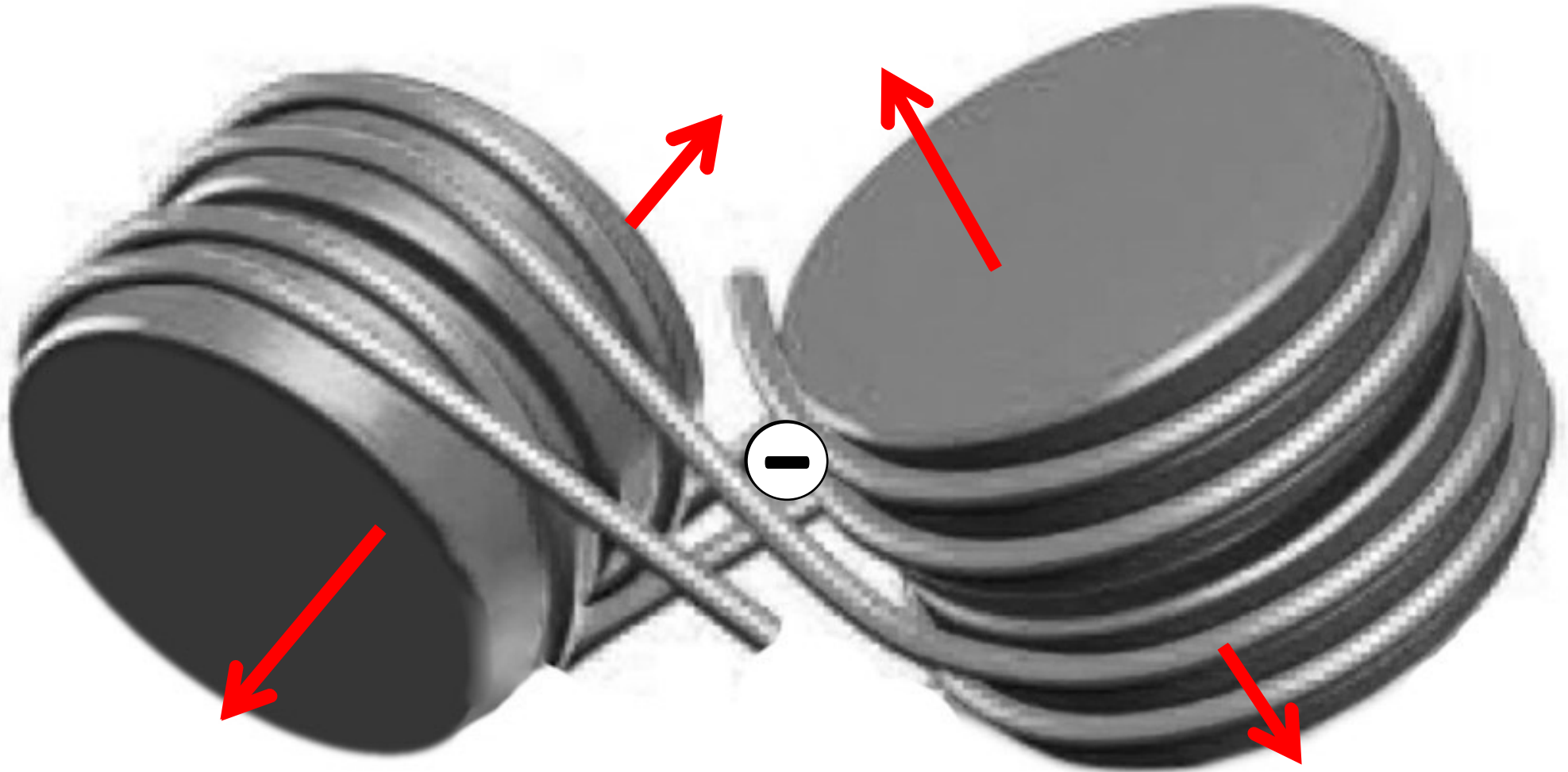
A model of charge oscillations in tetranucleosomes



Rempel 2017
PMID: 29294317

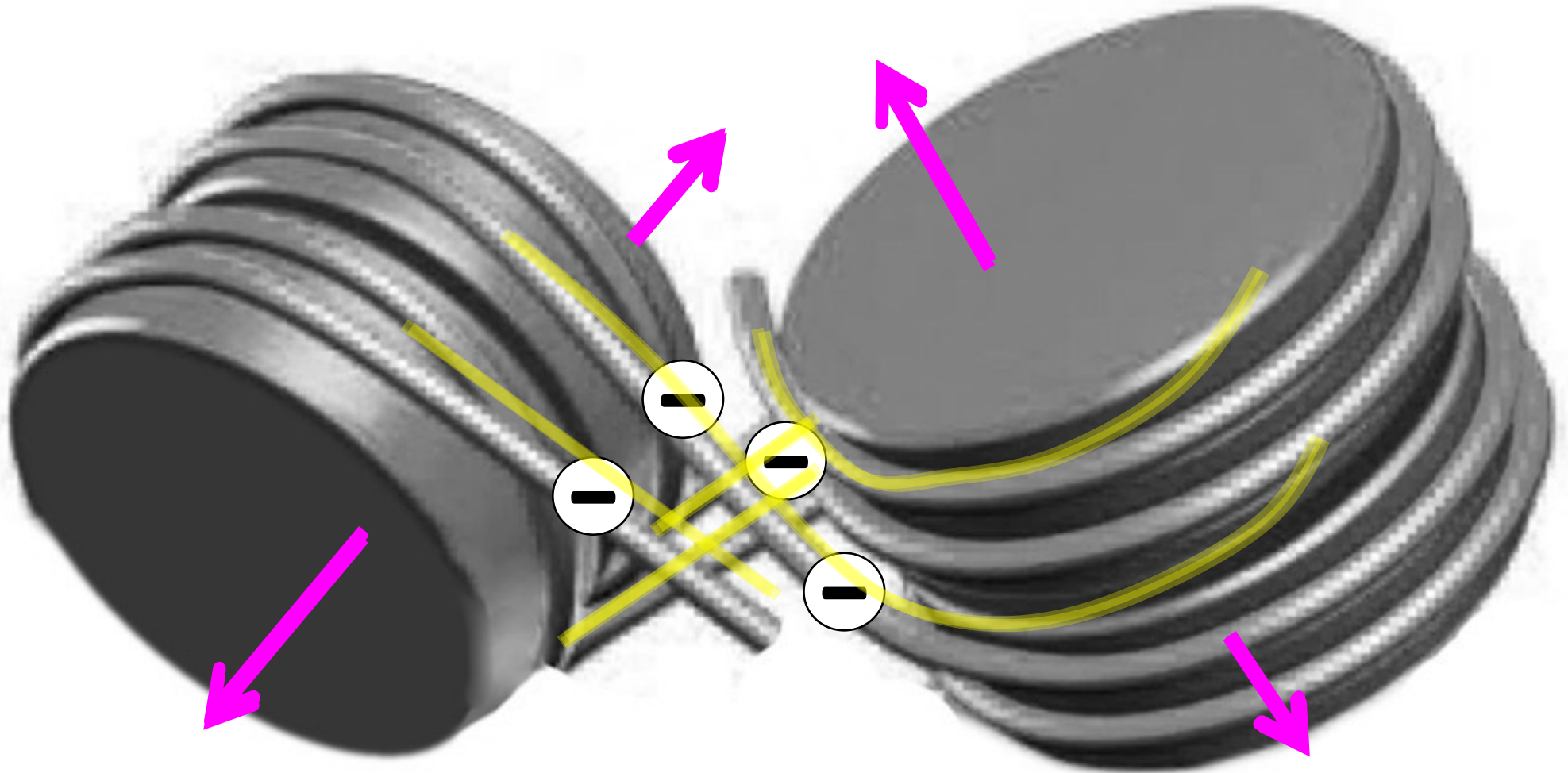


A model of charge oscillations in tetranucleosomes



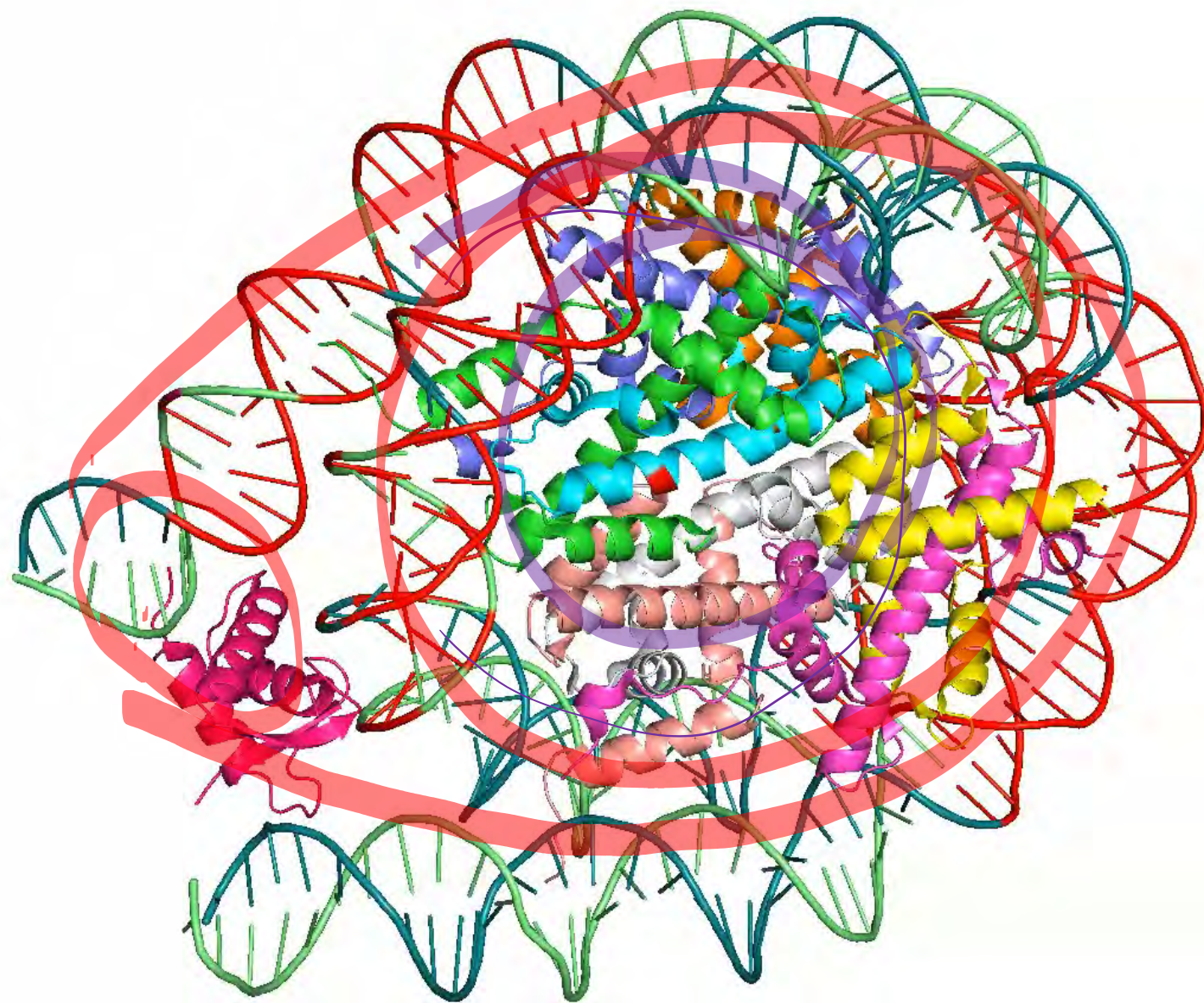
Rempel 2017
PMID: 29294317





Rempel 2017
PMID: 29294317



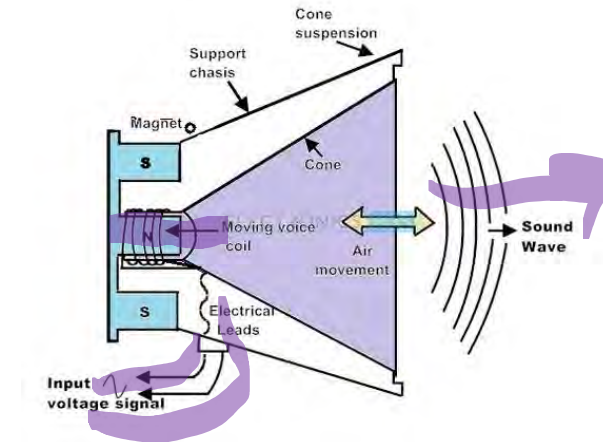


1.6

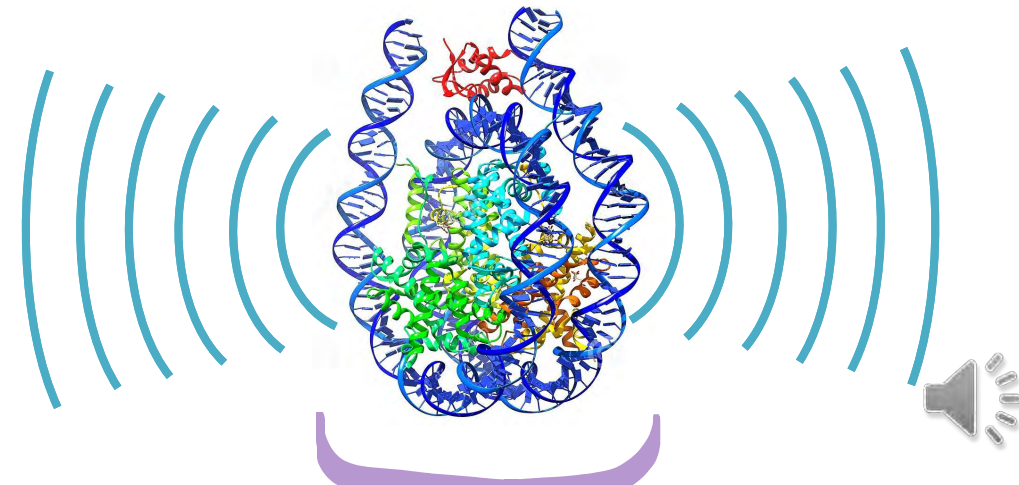


light		sound	
wavelength	frequency	wavelength	
1.5 mm	150 GHz	10 nm	nucleosome diameter
3.6 mm	63 GHz	24 nm	tetranucleosome width
3.7 mm	60 GHz	25 nm	millimeter wave therapy frequency
4.2 mm	53 GHz	28 nm	mm wave therapy, chromatin fiber diam.
5.3 mm	42 GHz	36 nm	millimeter wave therapy frequency
7.5 mm	30 GHz	50 nm	millimeter wave therapy frequency
1.5 cm	15 GHz	100 nm	Alu repetitive element, 300 bp
3.74 cm	6 GHz	250 nm	millimeter wave therapy frequency
15 cm	1.5 GHz	1.0 um	mitochondrion length
30 cm	753 MHz	2.0 um	Line repetitive element, 6 kbp
1.0 m	214 MHz	7 um	mammalian nucleus
3.0 m	75 MHz	20 um	mamallian cell
75 m	3 MHz	500 um	ultrasound imaging frequency
224 m	1 MHz	1.5 mm	ultrasound imaging frequency
2.2 km	100 kHz	1.5 cm	many biological objects
22 km	10 kHz	15 cm	chromosome length
224 km	1 kHz	1.5 m	human height
299 km	750 Hz	2 m	human height and genome length
12742 km	18 Hz	85 m	Earth diameter
28637 km	7.83 Hz	192 m	Schumann resonance frequency

Electroacoustic conversion of wavelengths. Currently, the shortest described wavelength for ultrasound is 250 nm, so the shorter wavelengths are shown in grey as tentative

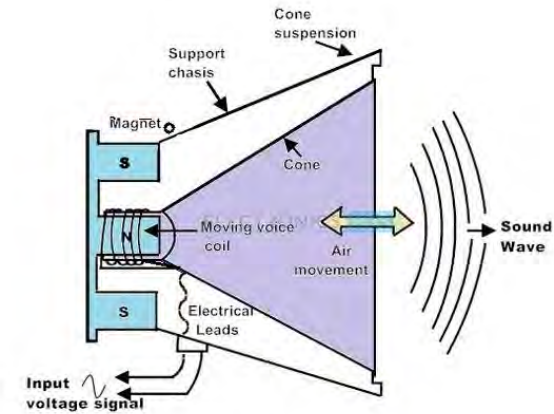


nucleosome as a speaker

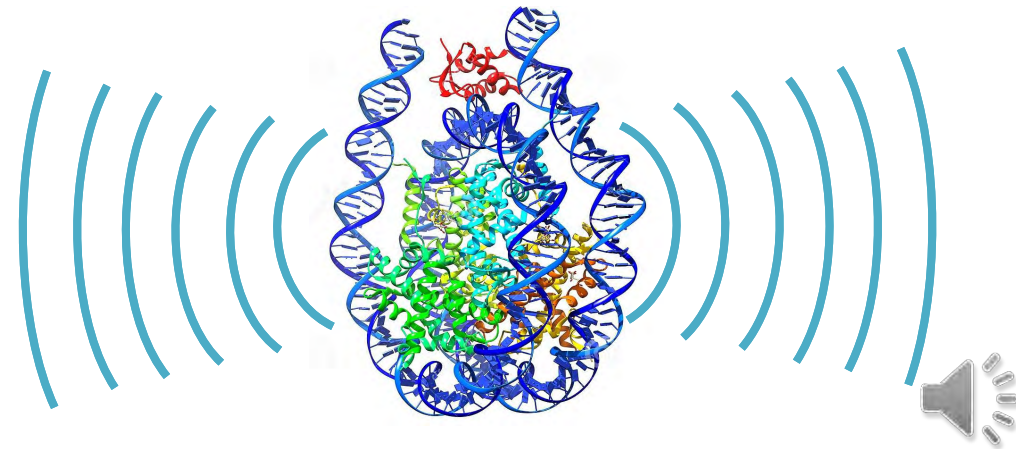


light	sound
wavelength	frequency wavelength
1.5 mm	150 GHz 10 nm nucleosome diameter
3.6 mm	63 GHz 24 nm tetranucleosome width
3.7 mm	60 GHz 25 nm millimeter wave therapy frequency
4.2 mm	53 GHz 28 nm mm wave therapy, chromatin fiber diam.
5.3 mm	42 GHz 36 nm millimeter wave therapy frequency
7.5 mm	30 GHz 50 nm millimeter wave therapy frequency
1.5 cm	15 GHz 100 nm Alu repetitive element, 300 bp
3.74 cm	6 GHz 250 nm millimeter wave therapy frequency
15 cm	1.5 GHz 1.0 μ m mitochondrion length
30 cm	753 MHz 2.0 μ m Line repetitive element, 6 kbp
1.0 m	214 MHz 7 μ m mammalian nucleus
3.0 m	75 MHz 20 μ m mammalian cell
75 m	3 MHz 500 μ m ultrasound imaging frequency
224 m	1 MHz 1.5 mm ultrasound imaging frequency
2.2 km	100 kHz 1.5 cm many biological objects
22 km	10 kHz 15 cm chromosome length
224 km	1 kHz 1.5 m human height
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Electroacoustic conversion of wavelengths. Currently, the shortest described wavelength for ultrasound is 250 nm, so the shorter wavelengths are shown in grey as tentative



nucleosome as a speaker



Nucleosome as a speaker

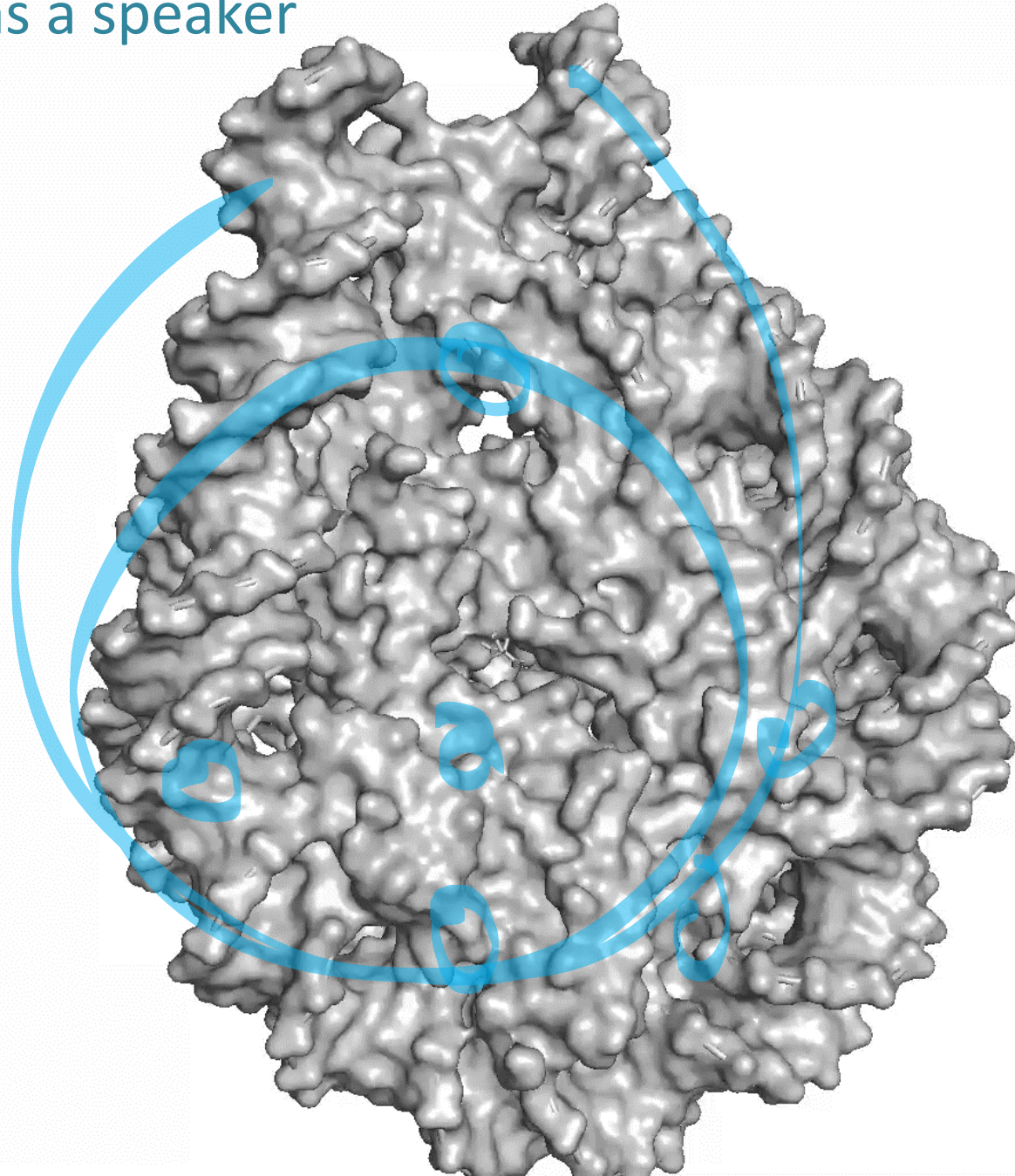
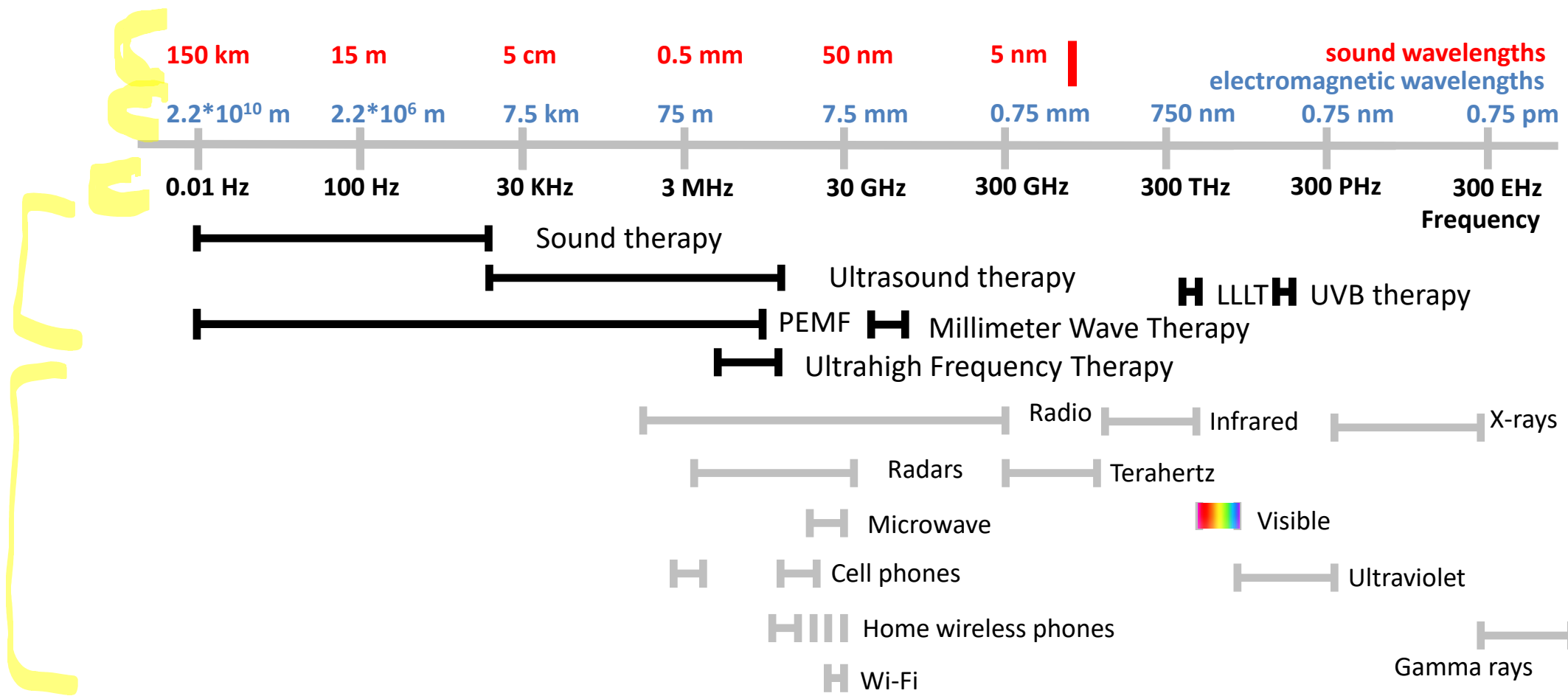


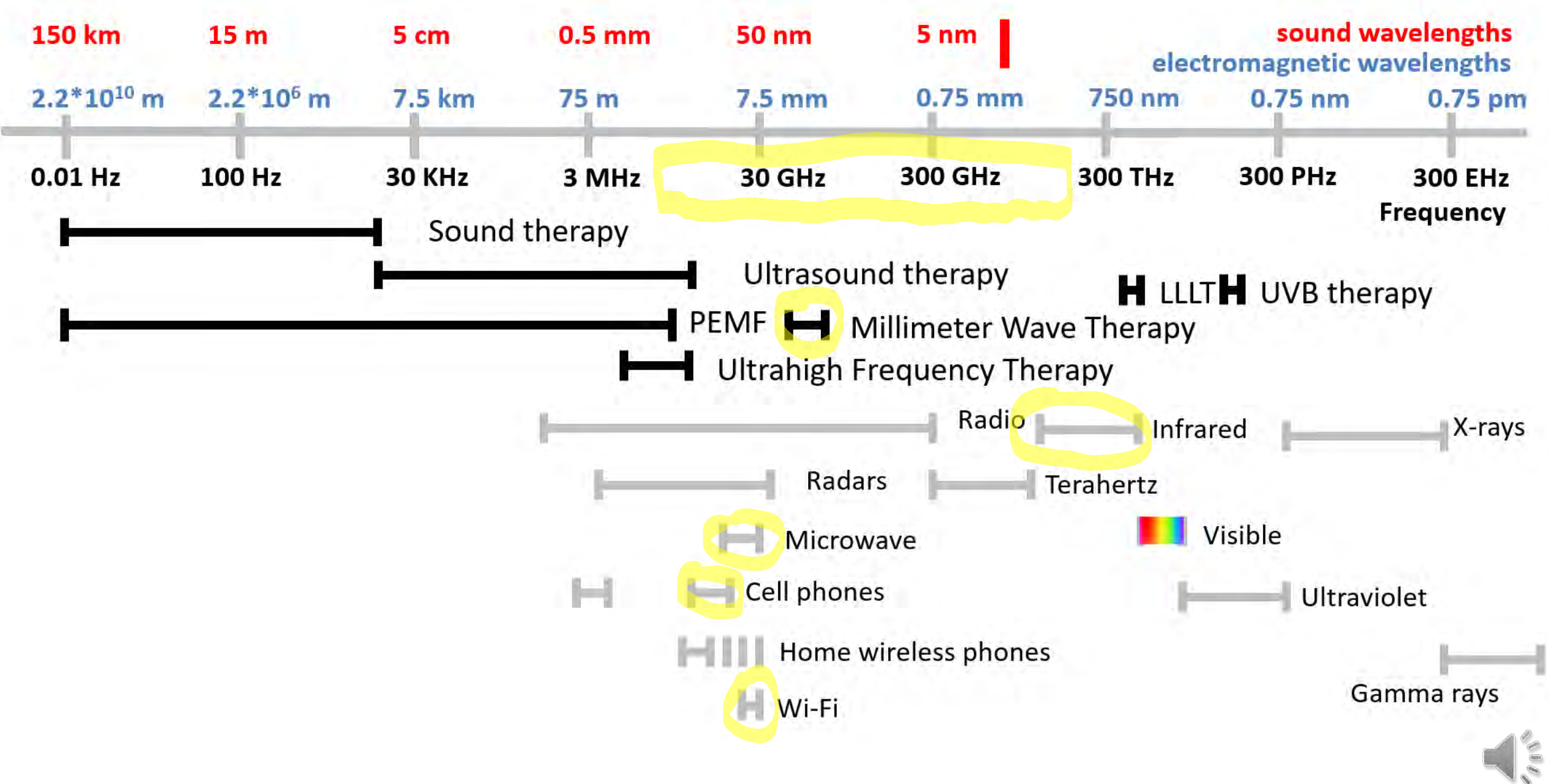
Table [Wavelengths]: A very approximate prediction of resonance wavelengths of genomic repeats

Repeat unit length	Periodic	Type	wavelength light sound	PEMF 37km 186m	UHF 0.3m 1.5um	MWT 7mm 30nm	LLLT 800nm 4nm	UVB 300nm 1.5nm
1 bp	0.3 nm	y	simple					
2 bp	0.7 nm	y	simple					
3 bp	1.0 nm	y	simple					
4 bp	1.3 nm	y	simple					
6 bp	2.0 nm	y	telomeric					
171 bp	57 nm	y	centromeric					
260 bp	86 nm	n	MIR					
300 bp	100 nm	n	Alu					
1000 bp	332 nm	n	Mariner					
6000 bp	1992 nm	n	LINE1					

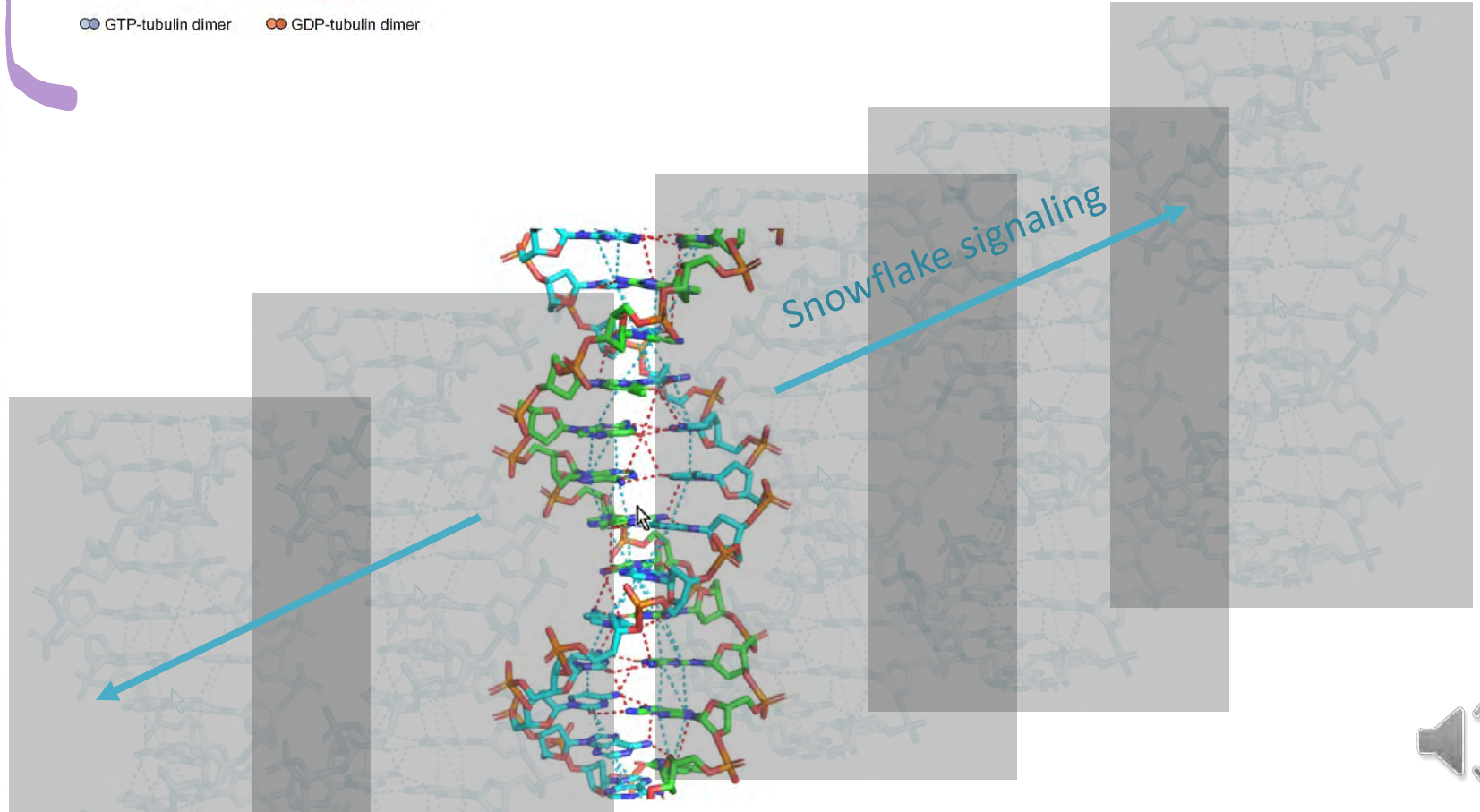
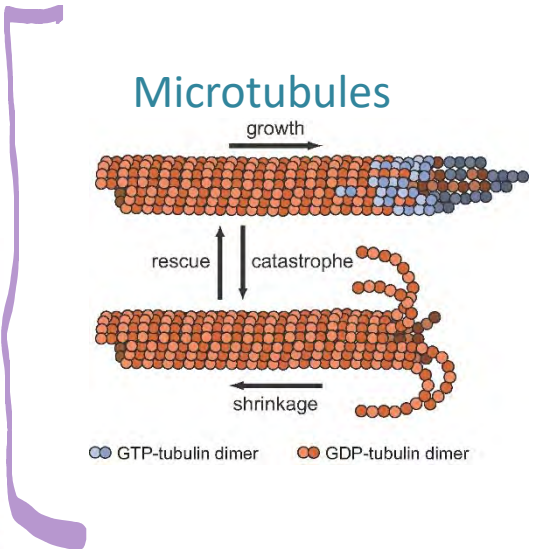
(UHF - ultra high frequency, MWT - millimeter wave therapy)



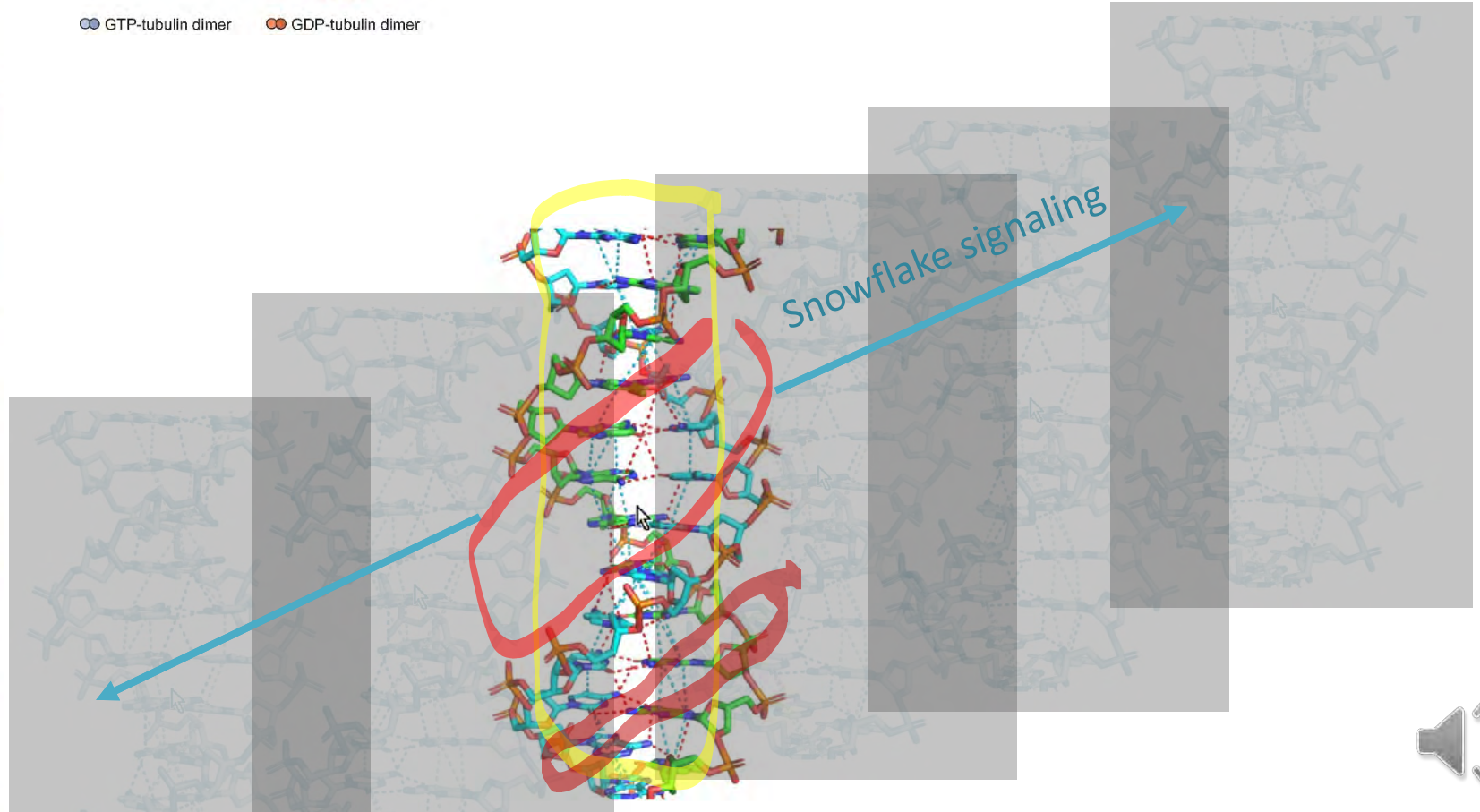
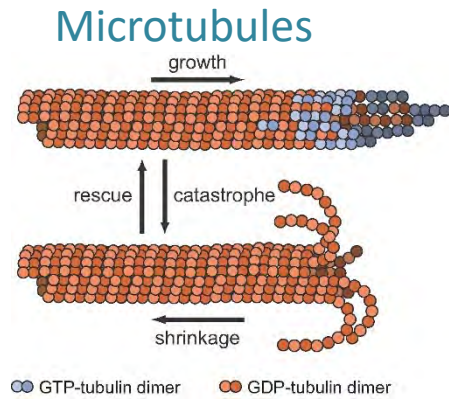




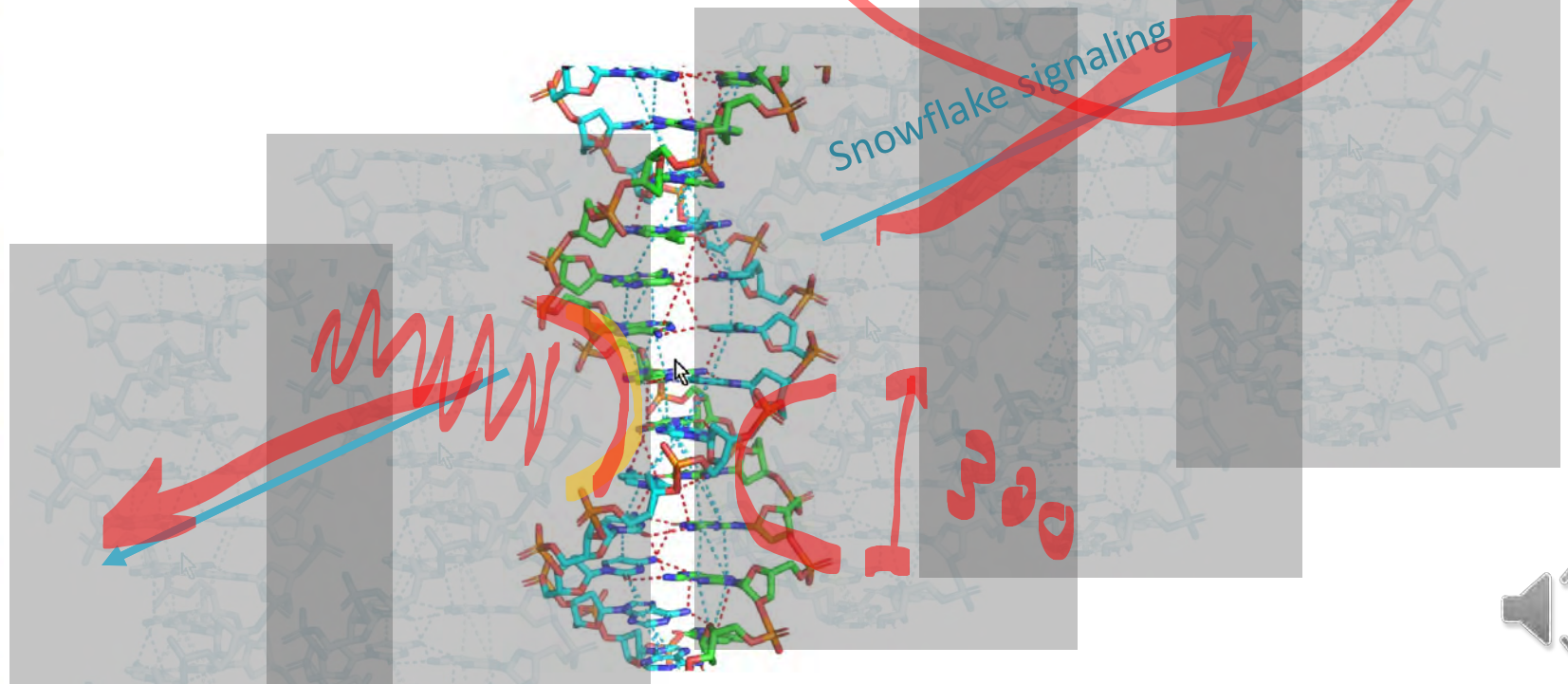
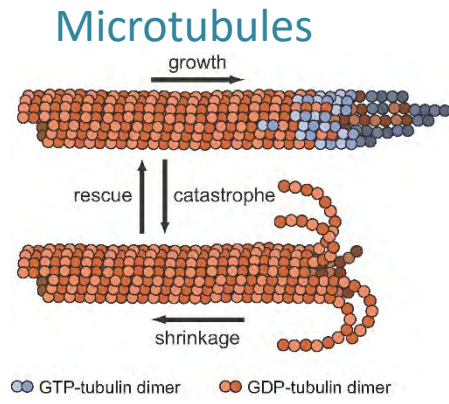
Snowflake type of signaling (crystal pattern propagation)



Snowflake type of signaling (crystal pattern propagation)



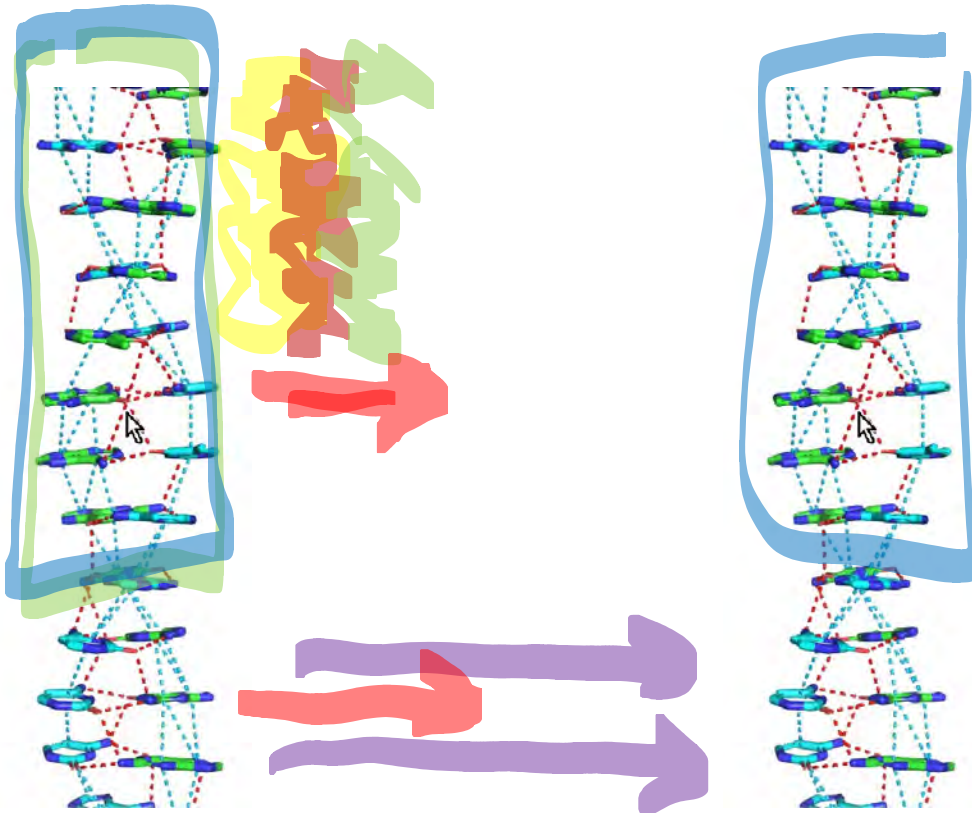
Snowflake type of signaling (crystal pattern propagation)



Heat signaling -

Hypothetical resonance signaling via radiant and conductive heat

Coherence transfer - quantum entanglement - spintronics



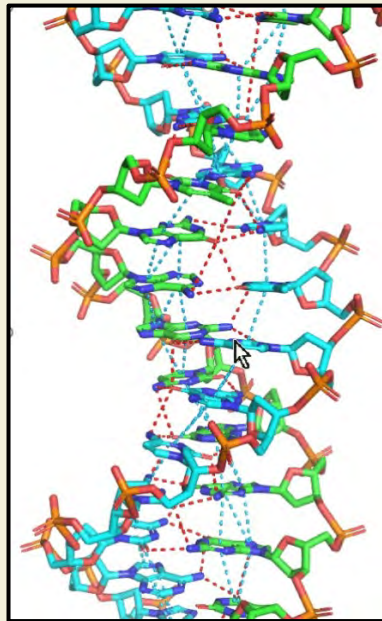
- Sauna
- Moxibustion
- Acupuncture with moxibustion
- Tanning with sunscreen



What is the nature of DNA resonance signaling?

physical in the traditional sense

nonphysical in the traditional sense



can be studied with live sensor models

the experimental study
is challenging

can be studied experimentally with traditional devices

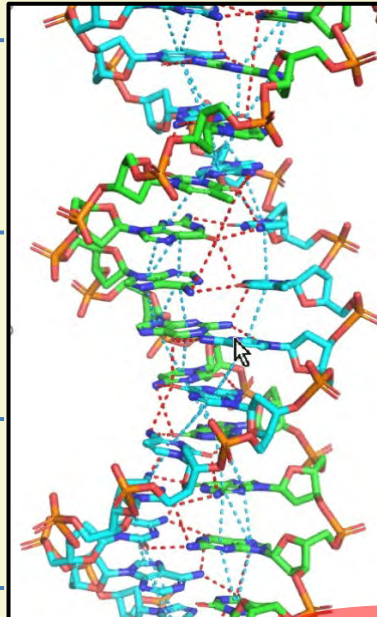
physical in the traditional sense

1. electromagnetic
signaling

2. electroacoustic signaling

3. snowflake (crystal pattern
propagation) signaling

4. Brownian and radiant heat
- quantum entanglement -
mediated signaling



nonphysical in the traditional sense

local
signaling

detected by
living things
but not
devices

nonlocal
signaling

5. Subtle signaling (local, sequence-specific
based on resonance, agnostic to the nature
of the carrier wave)



We are heading towards spectroscopic experiments

We synthesized a series of DNA samples with varied predicted proton chains.

Same composition – varied chain lengths.



>F01w 1 wire 141 bp ea

GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG
TTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG
TTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG
TTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG

>F05w 24 wires, 6 bp ea

GGGATTGGGATTGGGATTGGGATTGGGATTGGG
ATT GGGATTGGGATTGGGATTGGGATTGGGATTGGG
ATT GGGATTGGGATTGGGATTGGGATTGGGATTGGG
ATT GGGATTGGGATTGGGATTGGGATTGGGATTGGG

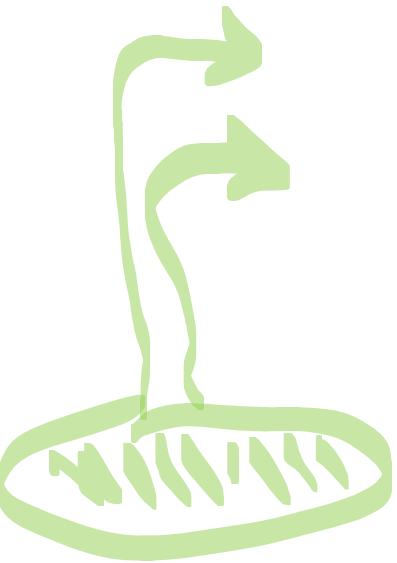


Spectroscopic measurements

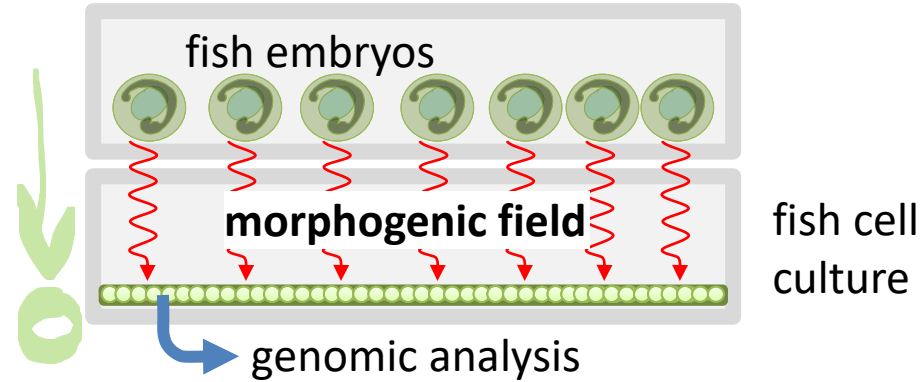
Will the spectrum changes reflect predicted proton chain lengths?

Looking for collaborators

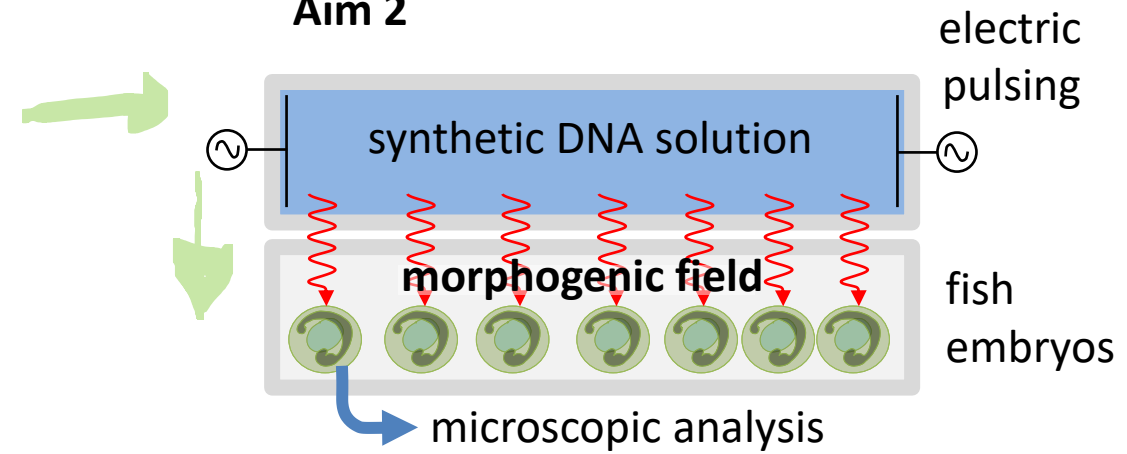




Aim 1



Aim 2

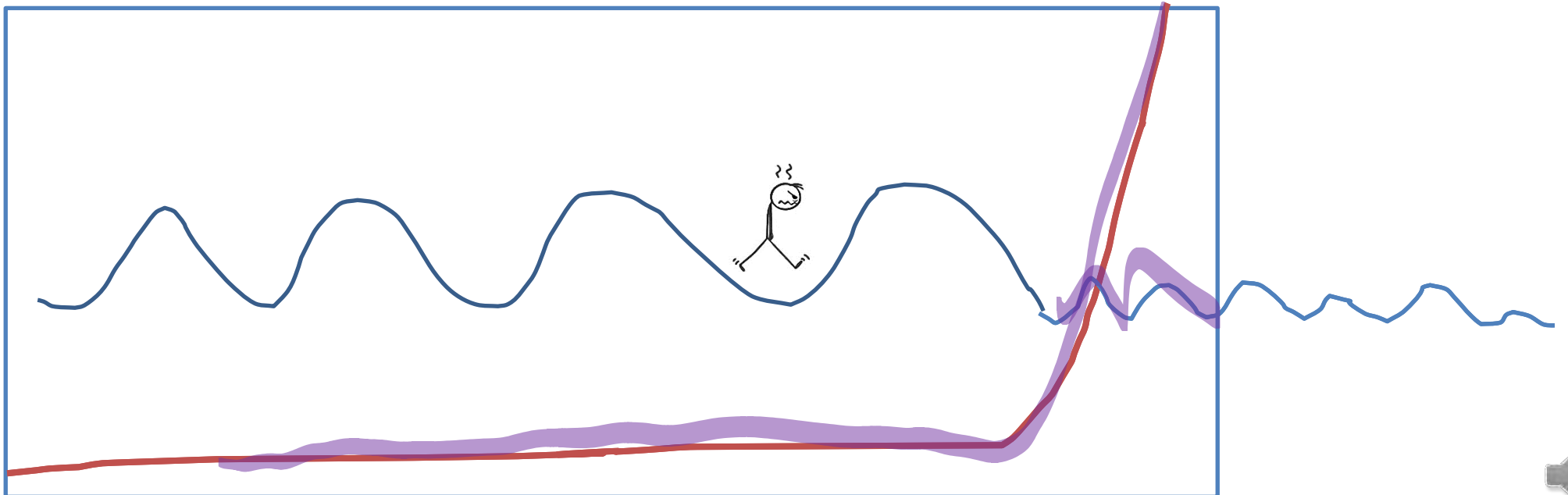


Future directions



What can serve as a breakthrough point?

- A model that explains much of the existing genomics data, or
- Independently reproduced evidence of sequence-specific DNA resonance signaling
- A practically useful method



Challenges and future directions of DNA resonance research (wave genetics)

Theory

- To find order in the genome
- To discover agreement between
- DNA resonance models and genomic data
- Incorporate water into models
- Integrate positive and negative charge oscillations
- Integrate chaos theory
- Integrate quantum entanglement

Experiments

- Demonstrate DNA resonance
- Develop easy to reproduce assays
- Have it independently reproduced
- Demonstrate the role of DNA resonance in morphogenesis
- Demonstrate the role of DNA resonance in the work of mind

Applications

- Therapeutic
- Diagnostic
- Brain-computer interface
- Mood, entertainment, meditation
- drug abuse monitoring
- Biotechnological
- Animals, plants, food.



Acknowledgements

Current:

Ivan Savelev
Elena Naumova
Anton Klimov
Alex Samchenko
Alex Voronka
Elena Erdyneyeva

Past:

Nellie Zyryanova
Nikolai Kondratyev
Eugenia Kananykhina
[Vadim Guschin]
Konstantin Kupriyanov
Irina Garanina
Ancha Baranova
Evgenia Kananykhina
Alexei Tovmash
Lev Shishkin
Liliya Yulmetova

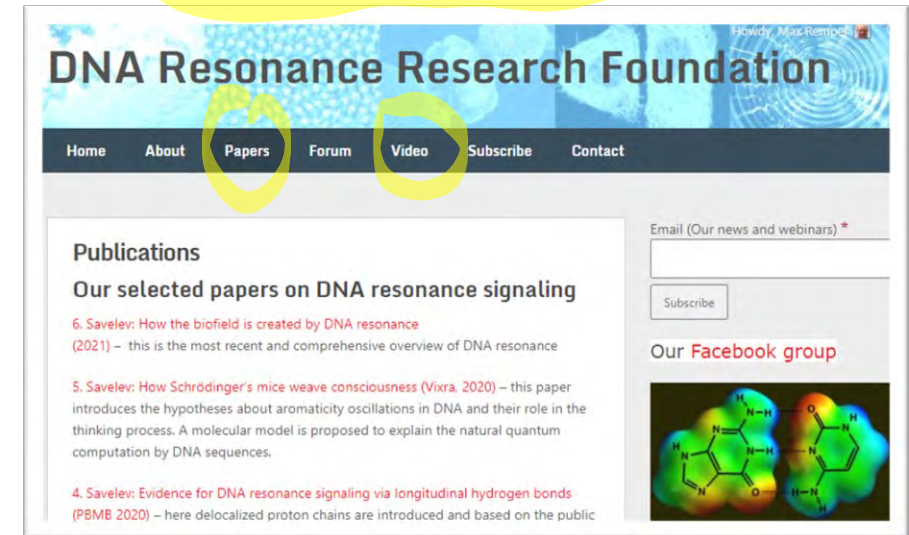
Collaborators:

Richard Alan Miller
Glen Rein
Anna Byalik
Alexandre Vetcher
[Irina Konstantinova]

Collaborations invited:

1. Spectroscopy
2. Electrodynamic modeling of oscillations
3. Quantum chemical modeling of oscillations

dnaresonance.org

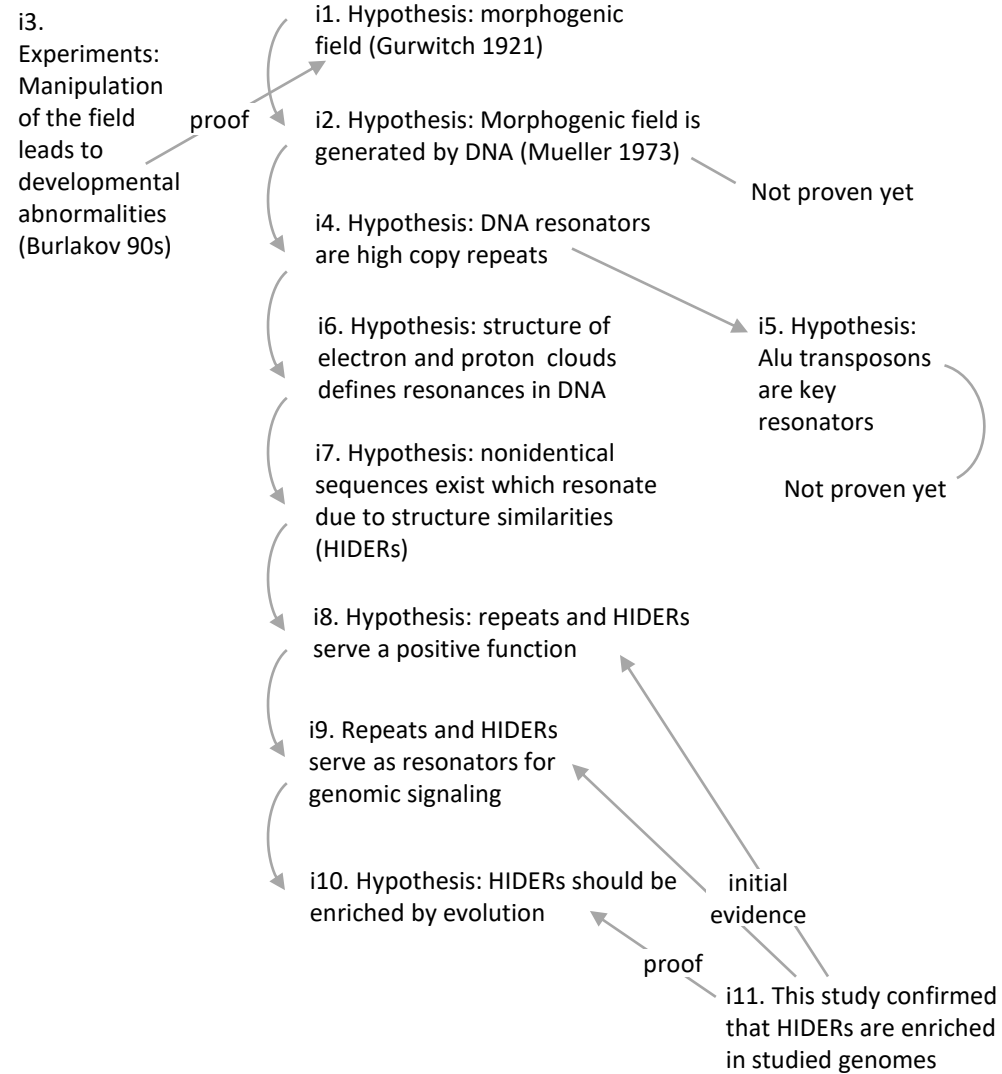


Contact:

Max Myakishev-Rempel, San Diego, CA, USA max@dnaresonance.org



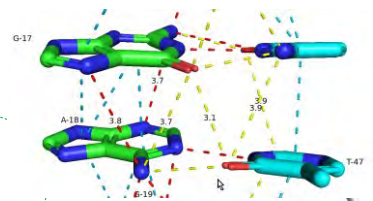
Overall logic



AA

how come good single RR to good single RR gives a 12% fall?
Just because of A to G?
maybe a result of PolyAdenilase? Maybe not

Alle	Alle	box	AlFrDif	tangent	Sho	Low	whi
AA	GA	AA	-12%	-0.30%	39.70	1	
AA	AC	AA	-9%	-0.24%	38.61	2	
AA	AG	AA	-6%	-0.15%	40.93	2	
AA	CA	AA	-6%	-0.16%	36.15	1	
AA	TA	AA	-5%	-0.15%	31.36	1	
AA	AT	AA	-4%	-0.12%	37.05	2	

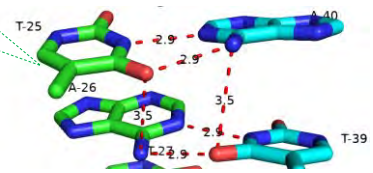
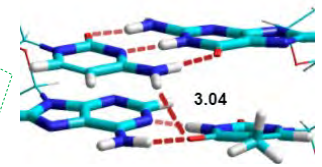


-12% fall
GA likely a stop
RR

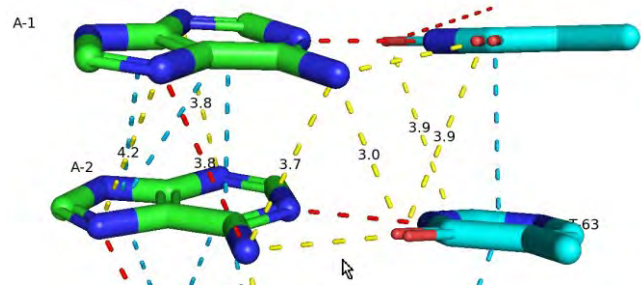
F - Maybe not a good single OO 3.1A maj
weak NNOON W maj

NN 3.7A min
OO 3.9A min

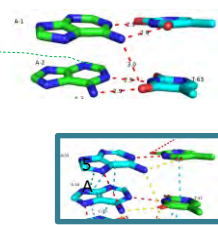
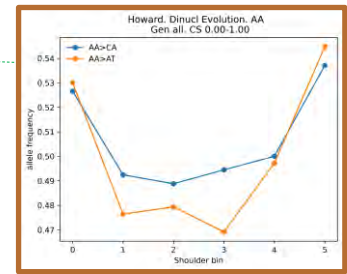
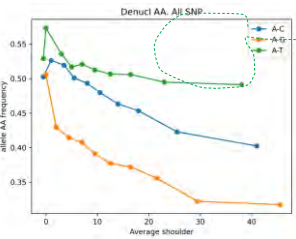
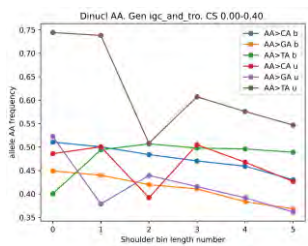
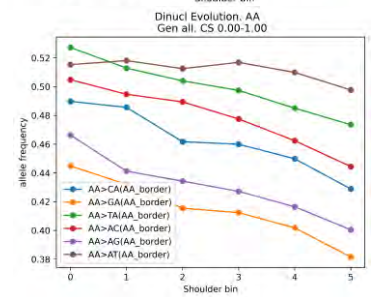
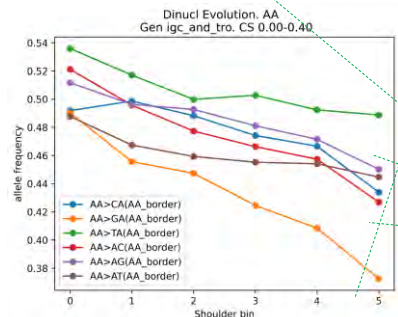
-6% fall
CA good Single



-4% fall
TA medium diamond



RR
K good single
NN - maj
NO 3.0A - maj
Nothing in min



AA Good single

