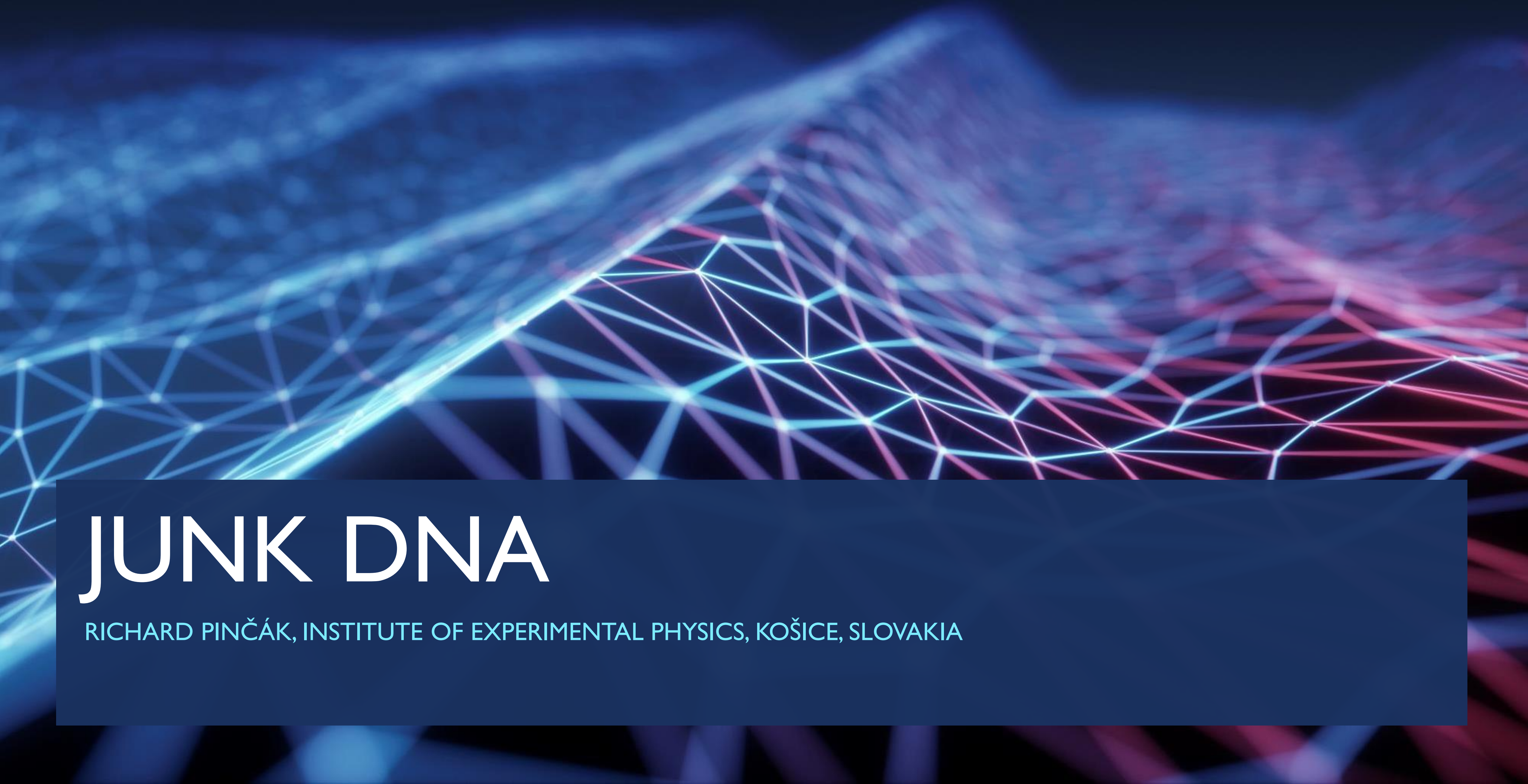


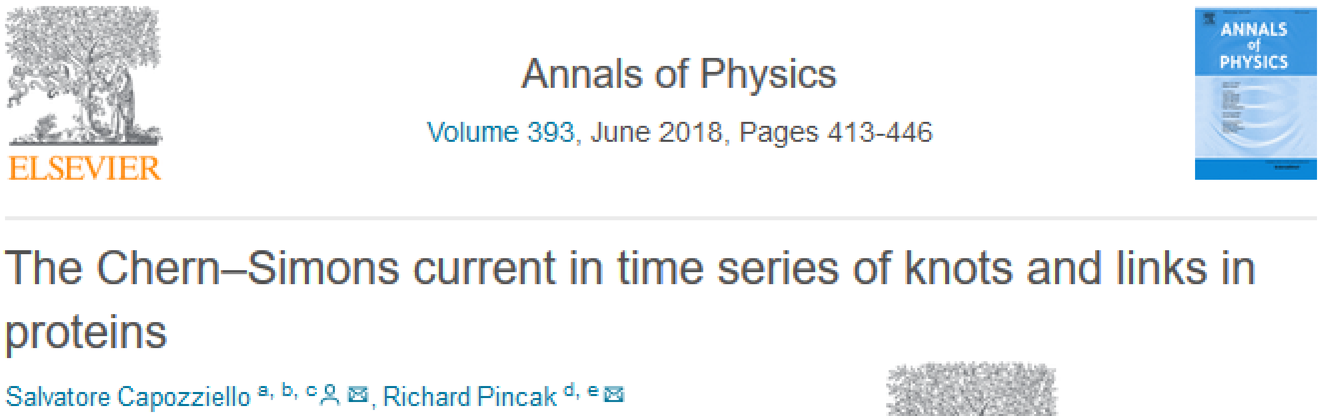
JUNK DNA

RICHARD PINČÁK, INSTITUTE OF EXPERIMENTAL PHYSICS, KOŠICE, SLOVAKIA

PUBLISHED SCIENTIFIC WORKS & RESULT FORMULATION NOMINÁCIA : MEDZINÁRODNÉ VEDECKÉ PROJEKTY

- The Chern-Simons current in systems of DNA-RNA transcriptions,
  S. Capozziello, R. Pincak, K. Kanjamapornkul, E. N. Saridakis: **Annalen der Physik** 530 (4), 1700271 (2018)
- The Chern–Simons current in time series of knots and links in proteins,
  S. Capozziello, R. Pincak: **Annals of Physics** 393, 413–446 (2018)
- Constructing superconductors by graphene Chern–Simons wormholes,
  S. Capozziello, R. Pincak, E. N. Saridakis: **Annals of Physics** 390, 303-333 (2018)

- **Result Formulation:** Nodal algebraic structures have been found to model the attachment to dissociate the protein-protein states involved in the interaction between hidden DNA states.
- **Formulácia výsledku:** Boli nájdene uzlové algebraické štruktúry na modelovanie pripojenia až po odpojenie stavov pôsobenia proteín-proteín, na ktorom sa podieľa interakcia medzi skrytými stavmi v DNA.

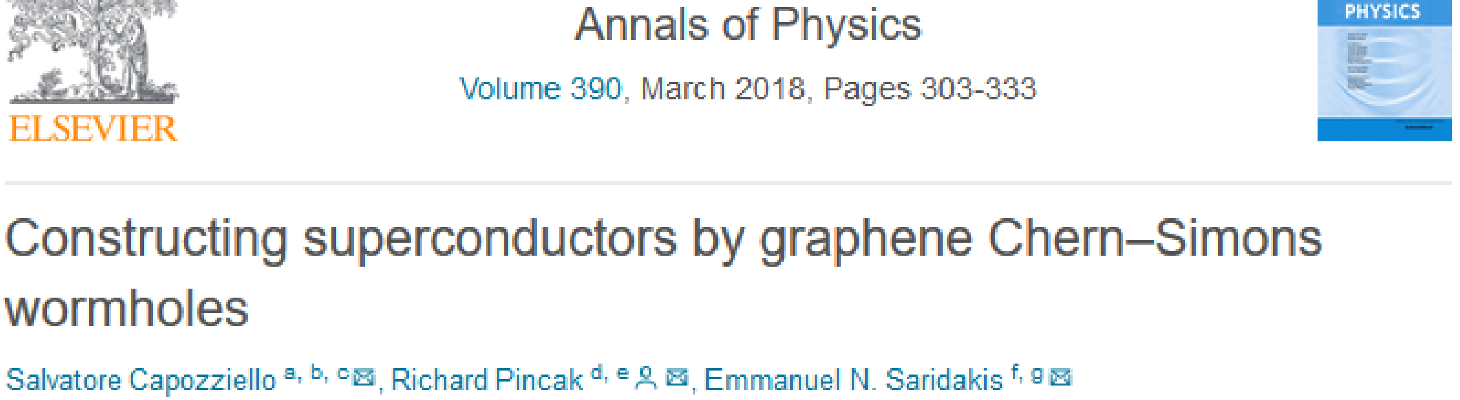


Annals of Physics

Volume 393, June 2018, Pages 413-446

The Chern–Simons current in time series of knots and links in proteins

Salvatore Capozziello [a, b, c] ✉, Richard Pincak [d, e] ✉

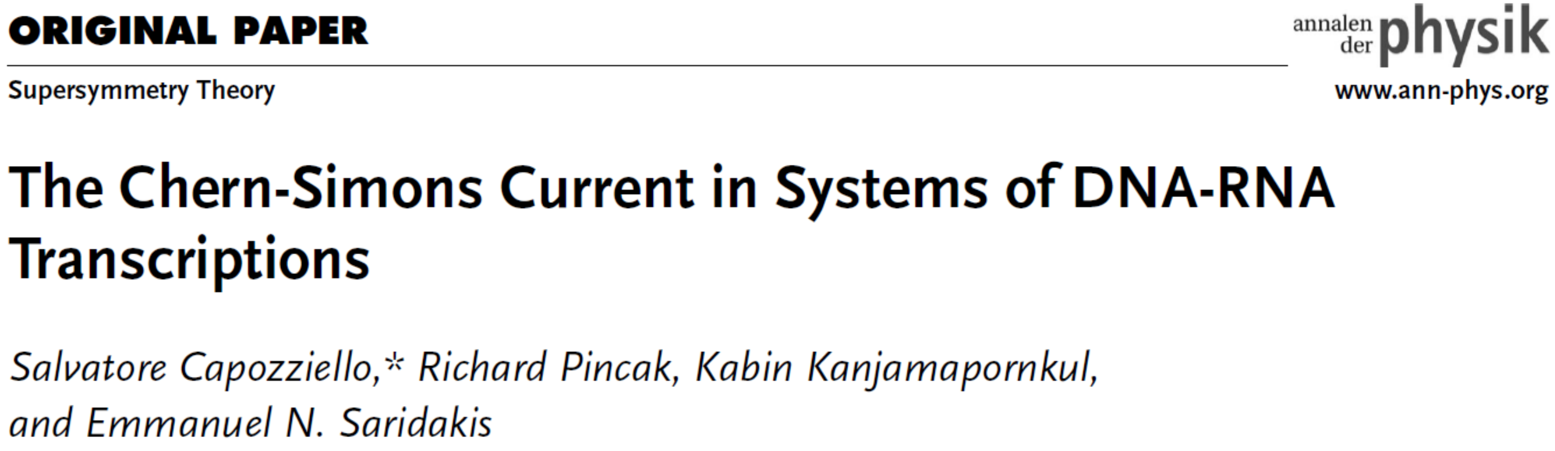


Annals of Physics

Volume 390, March 2018, Pages 303-333

Constructing superconductors by graphene Chern–Simons wormholes

Salvatore Capozziello [a, b, c] ✉, Richard Pincak [d, e] ✉, Emmanuel N. Saridakis [f, g] ✉



ORIGINAL PAPER

Supersymmetry Theory

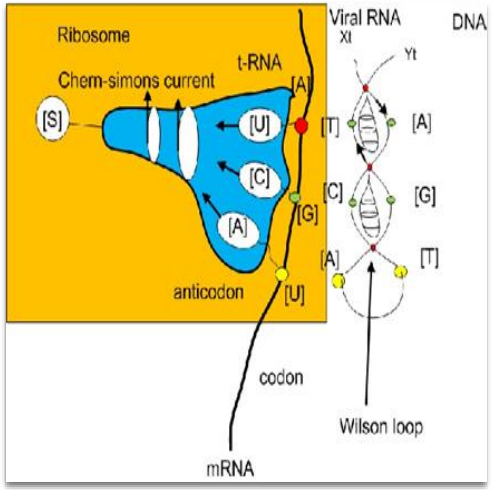
annalen der physik
www.ann-phys.org

The Chern-Simons Current in Systems of DNA-RNA Transcriptions

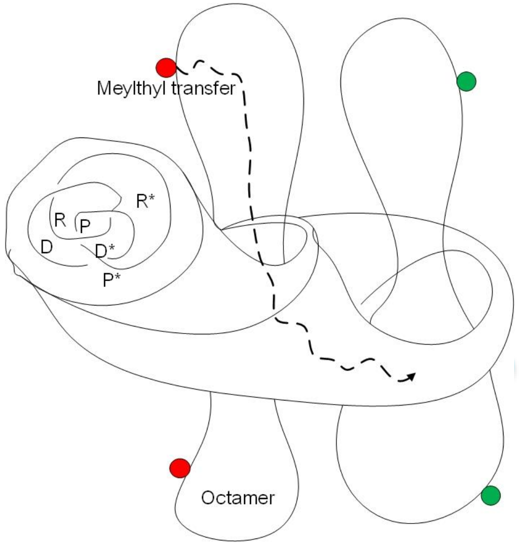
Salvatore Capozziello, Richard Pincak, Kabin Kanjamapornkul, and Emmanuel N. Saridakis*

COOPERATION & INSTITUTES

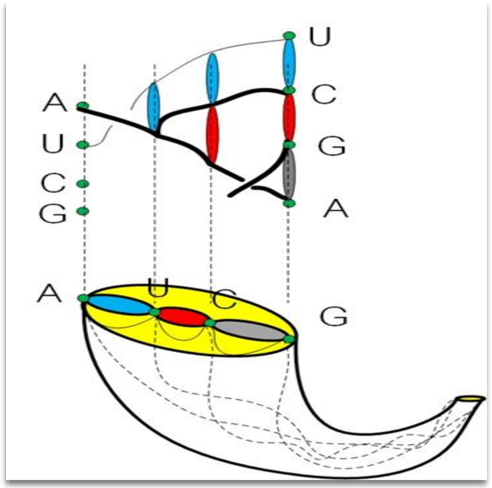
- **Salvatore Capozziello -** Universita di Napoli “Federico II”, Napoli, Italy & INFN, Napoli, **Italy**
- **Kabin Kanjamapornkul -** Faculty of Information Technology, Asia-Pacific International University, **Thailand**
- **Emmanuel N. Saridakis -** National Technical University of Athens, Greece & Baylor University, TX, **USA**
- **Richard Pinčák -** BLTP, Joint Institute for Nuclear Research, Dubna, **Russia**
- **Erik Bartoš -** Institute of Physics, SAS, Bratislava, **Slovakia**



retrotranspons



junkDNA



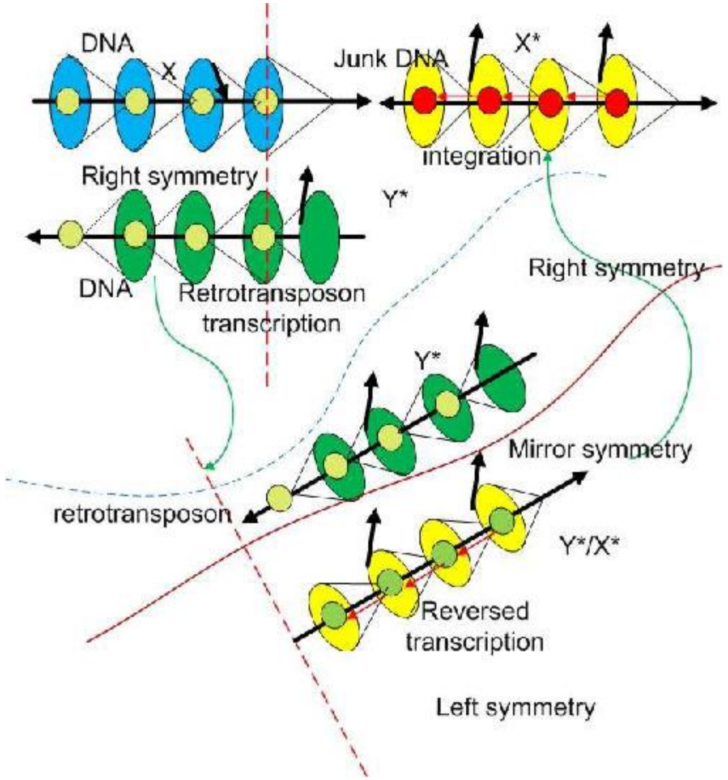
supercodon

CONTENTS

WHAT IS THE REAL FUNCTION OF JUNK DNA

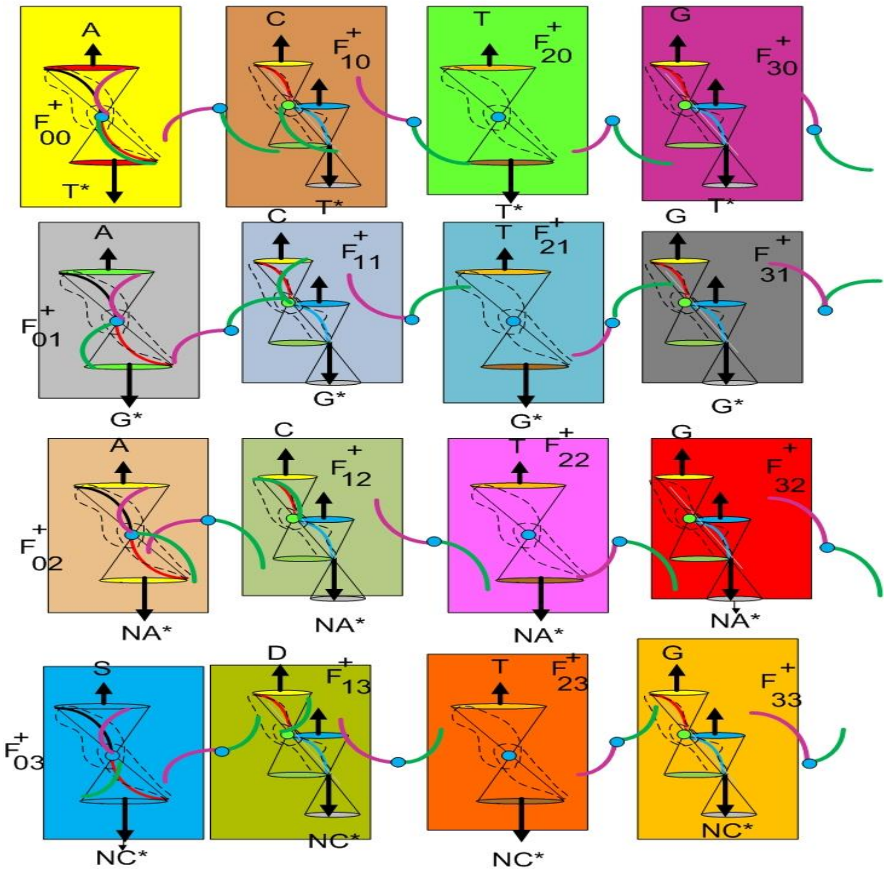
- **Why** gene expression exists only 2% and DNA contain 98% of junkDNA?
- **The answer** is a new definition of supercodon with mirror symmetry in alphabet code as pairs of state (A,NA)
- Is adenovirus live in junkDNA of our human genome? What is retrotransposon?
- The answer is an existence of jumping gene so called transposon element and retrotranposon element in junkRNA over Telomerase enzyme. If it is wrong function telomerase, cell will divide without stop and get cancer.

RESET STATE OF RETROTRANSPOSON AS MOVEMENT OF GENETIC CODE WITH ENERGY AND MOMENTUM IN JUNK DNA



- Retrotransposons comprise a significant fraction of mammalian genome with unclear functions. Increasing evidence shows that they are not just remnants of ancient retroviruses but play important roles in multiple biological processes.
- In addition, retrotransposons may mediate epigenetic memory, regulate gene expression posttranscriptionally, defend virus infection, and so on.

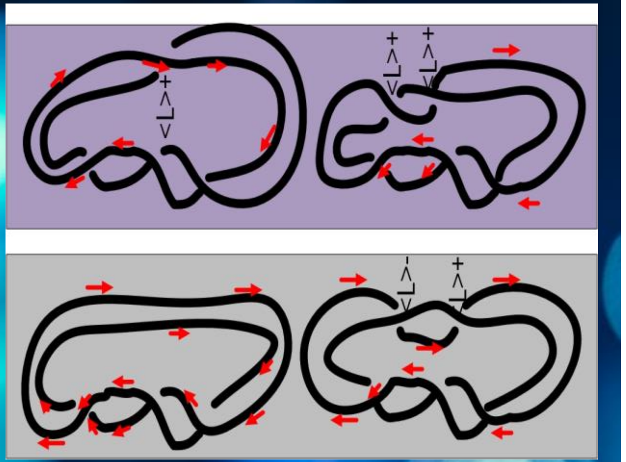
THE SOURCE OF CURVATURE IN PROTEIN DOCKING STATE

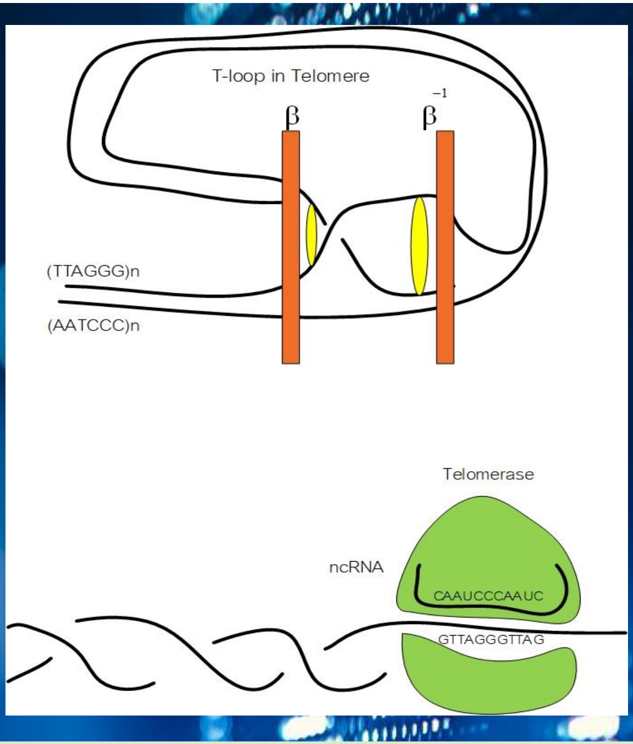


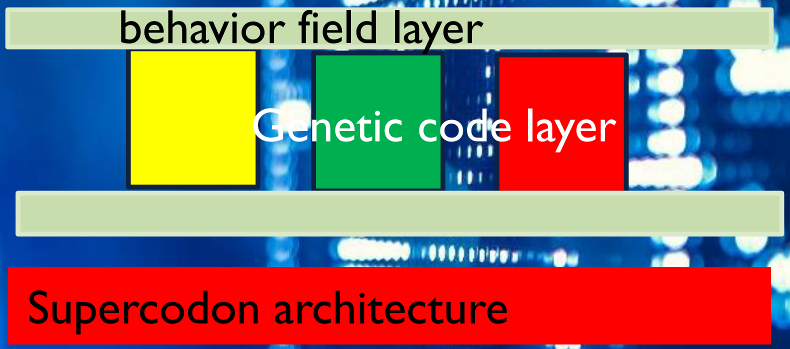
- Approximately 40% of the mammalian genome is comprised of retrotransposons, implying their important role in organizing genomic architecture, orchestrating biological processes, and contributing to species diversity and evolution.

TELOMERE

- Active DNA is 2%
- Trash DNA is 98%
- Telomere also belongs to trash DNA







- Chern-Simons current in genetic code is 3 differential form

  $$J^{(\mu=k)}=2/\sqrt{(k+2)}\int\llbracket \mathrm{Tr}(A\wedge A+2/3\,A\wedge A\,\llbracket\wedge A\rrbracket)\rrbracket$$

  It is an interaction between dbrane and anti-dbrane to produce a source of adaptive behavior field in genetic code.
- The supercodon is in junkDNA. It is a hidden behavior field in genetic code for control of changing the curvature.
- The 32 states is a partition function of hidden state in central dogma. The 64 states come from 8 states of spinor field in genetic code. But 32 states are all classifying all types of smallest subunit of curvature in the 3 forms of genetic code. Totally we have 96 states of supercodon.

SUPERCODON

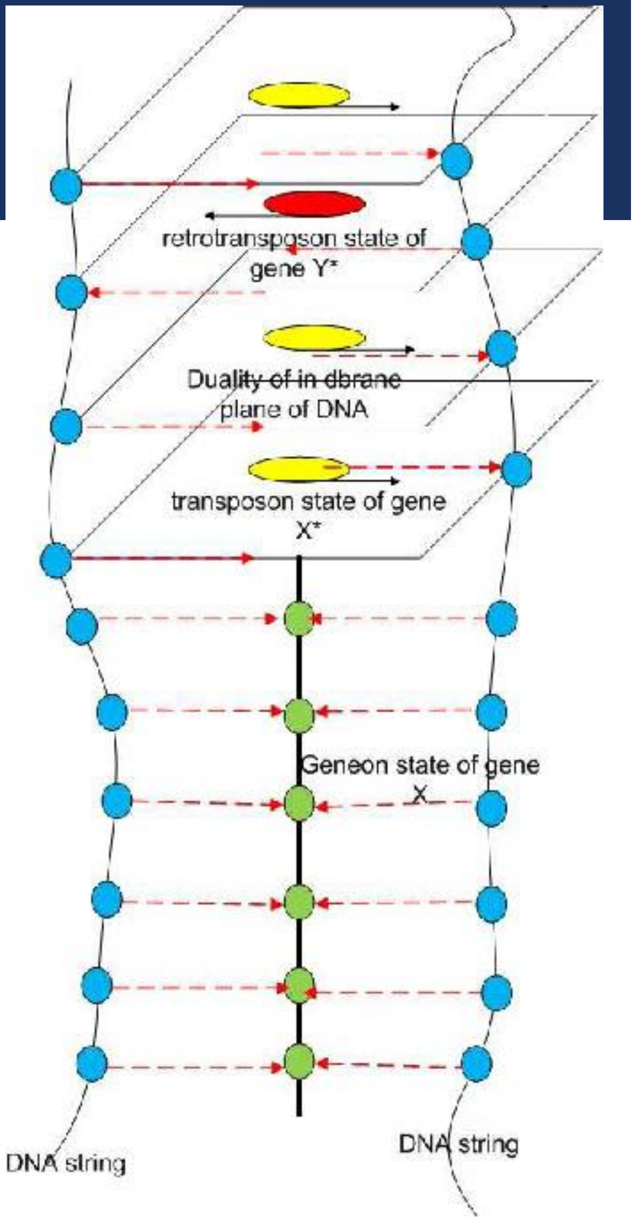
It is 96 states.

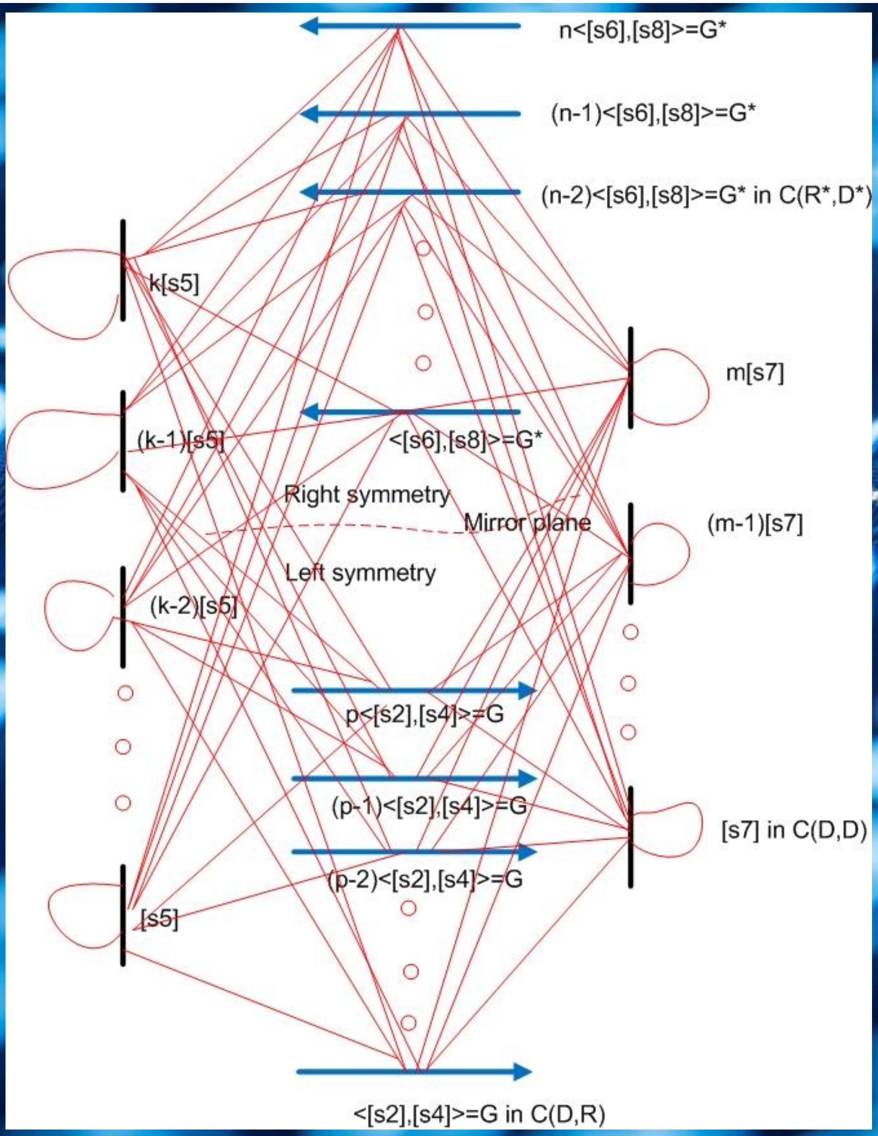
Come from 64 states of codon and 32 states

of chain of inflexion of classifications of curvature in junkDNA.

FUNCTIONAL ROLES OF RETROTRANSPOSONS

- Dynamic Balancing of Genomic Stability and Genetic Innovation
- Modulating Transcriptional and Posttranscriptional Regulatory Network
- Organizing High-Order Chromatin Structure
- Epigenetic Memory of Acquired Characteristics of Inheritance
- Inhibition of Virus Infection



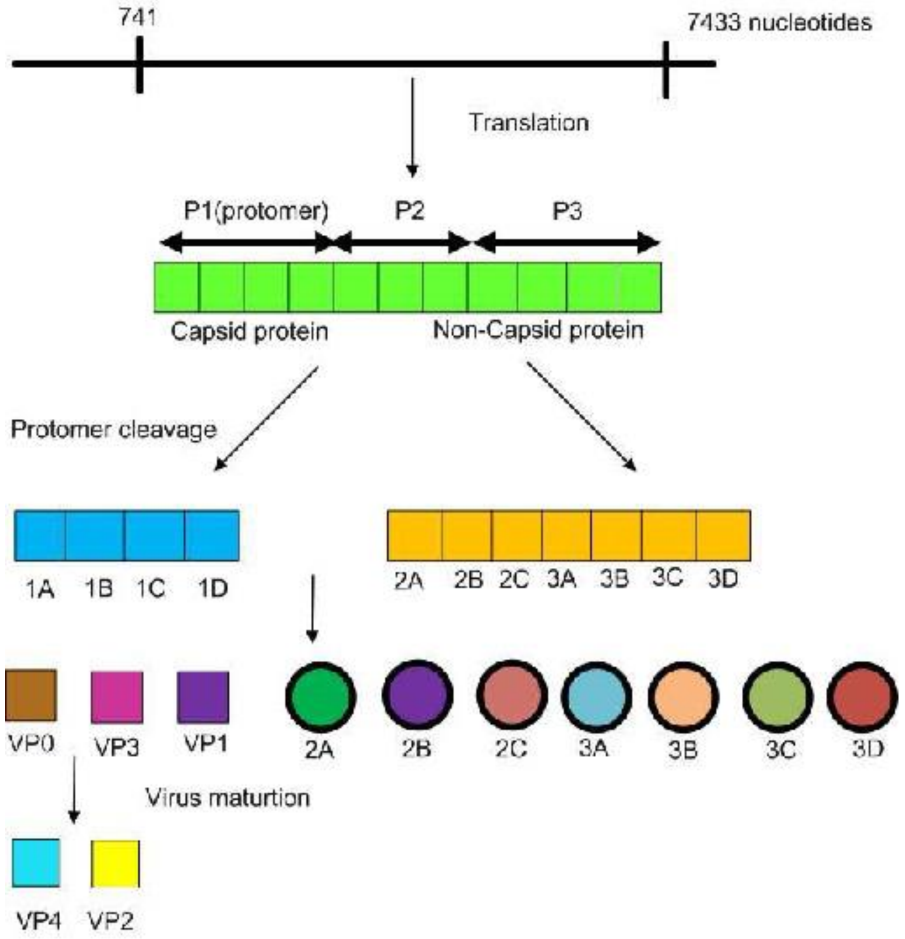


VIERBEIN MODEL OF JUNK DNA

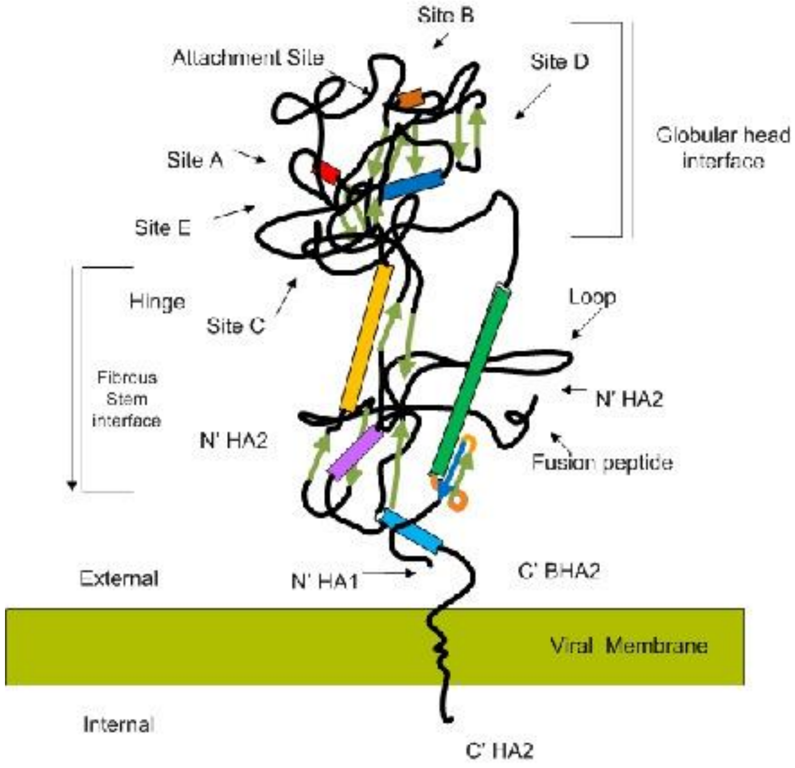
THE PASSIVE BEHAVIOR FIELD IN GENETIC CODE AS A VERBEIN MODEL OF TRANSITION STATES ARE THE REAL SOURCE OF SUPERCODON STATE.

RESULT OF DATA ANALYSIS

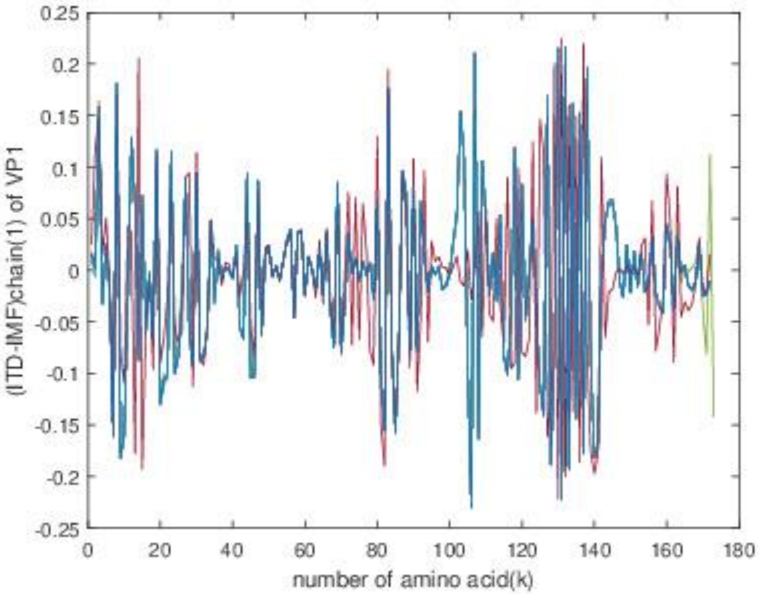
- We plot Chern-Simons current in junk area of RNA in icosahedral virus with the Chern-Simons current for biology.
- The genetic code of virus contains junkRNA and RNA reversed transcription part equivalent to retrotransposon transition state in junkDNA.
- It might be parasitism state with co-state of ncRNA with Telomerase enzyme at the end of human chromosome to be pairing with retrotransposon transition state.



RESULT OF PLOT OF VP1 IN ICOSAHEDRAL VIRUS

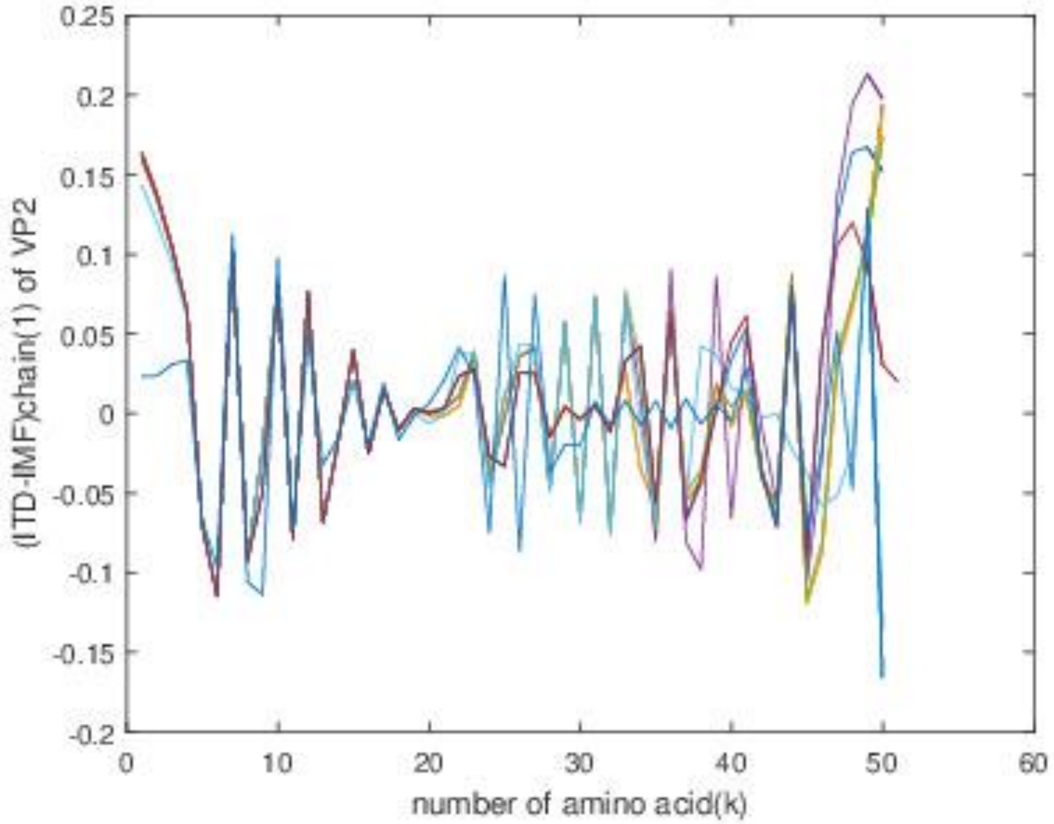


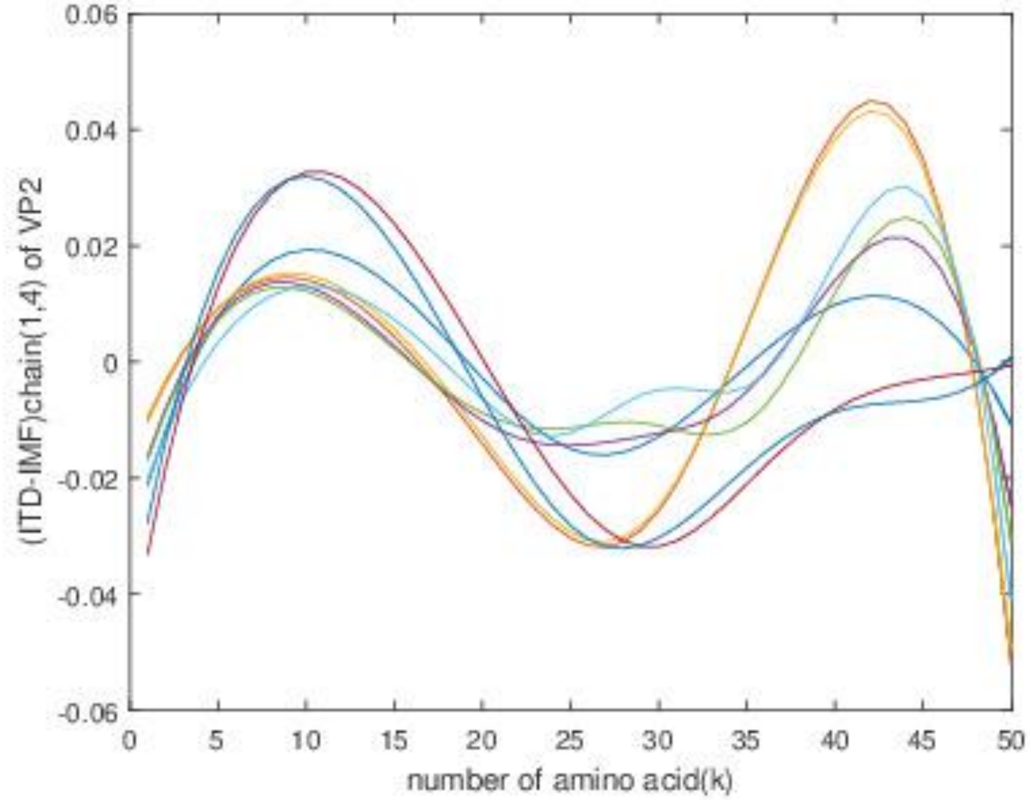
Picture drawing of vp1 viral capsid glycoprotein.



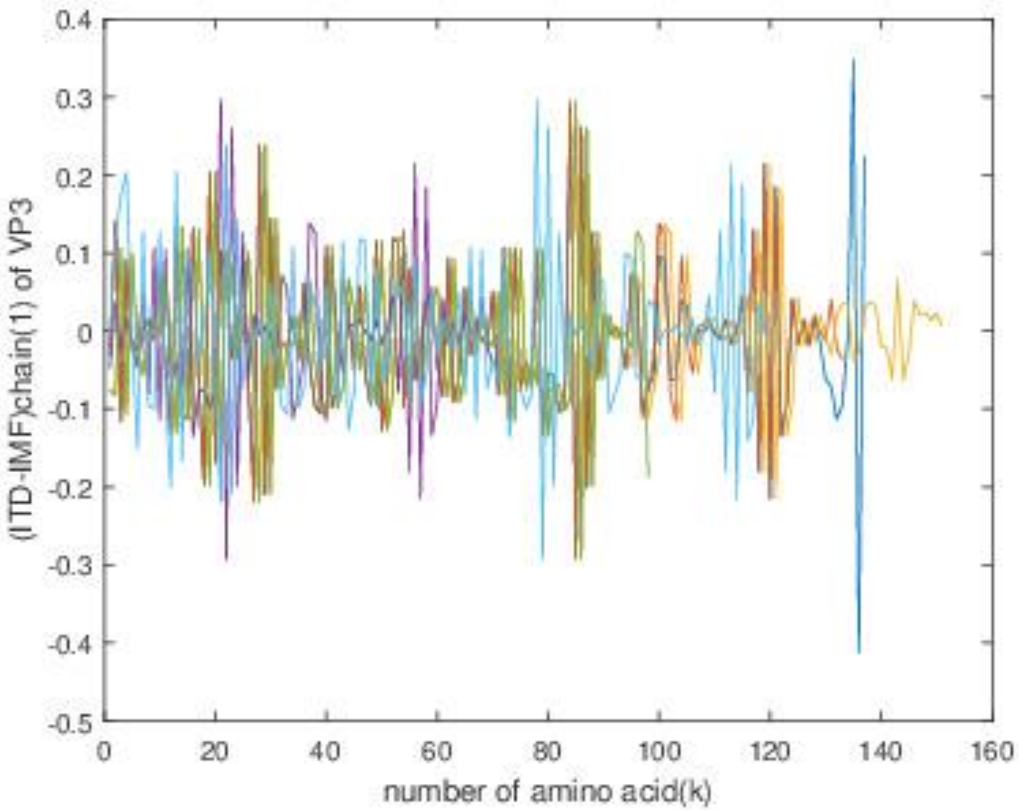
The plot of Chern-Simons current of 6 samples of vp1.This plot is an example of retrotranposon in viral RNA that use the area in junkDNA for reversed transcription.

RESULT OF VP2





RESULT OF VP3



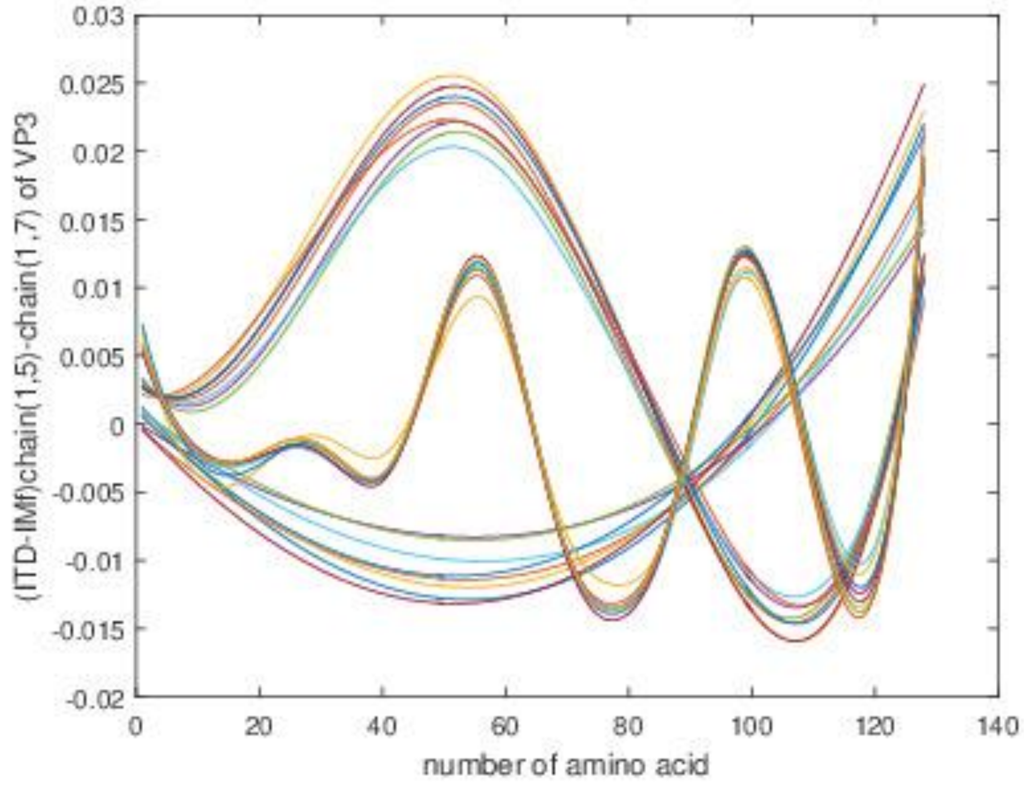
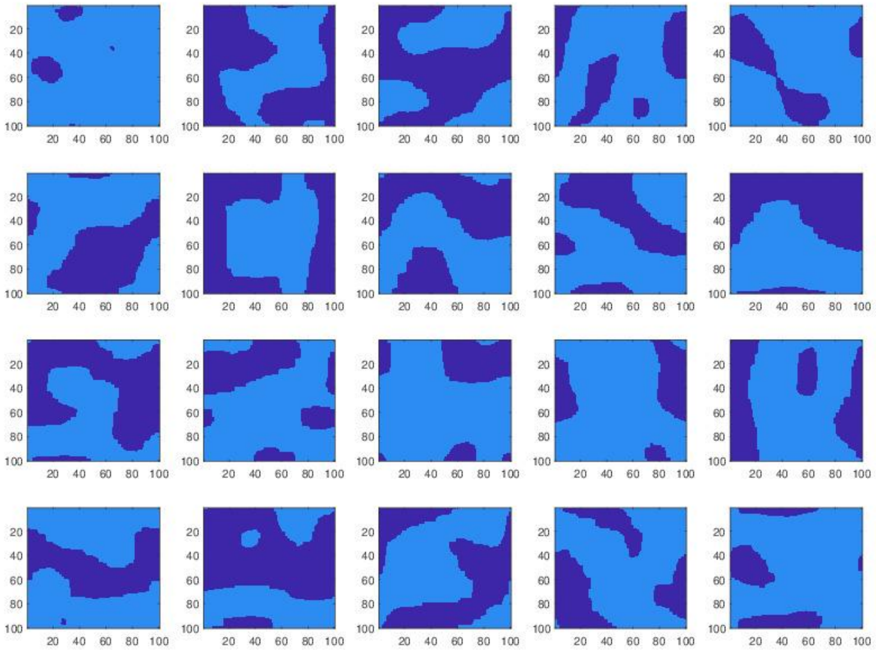


IMAGE OF GENEON TRANSITION STATE OF VP1



- Image of geneon represent the genetic variation in vp1. It is generated from Ising algorithm.

CONCLUSION AND DISCUSSION

- JunkDNA is not junk but important for cell functionallity.
- JunkDNA is a source of cancer and a source of how to find a way to treatment of cancer.
- Supercodon has more alphabet code to accepted more noncoding RNA as with 20 amino acids.