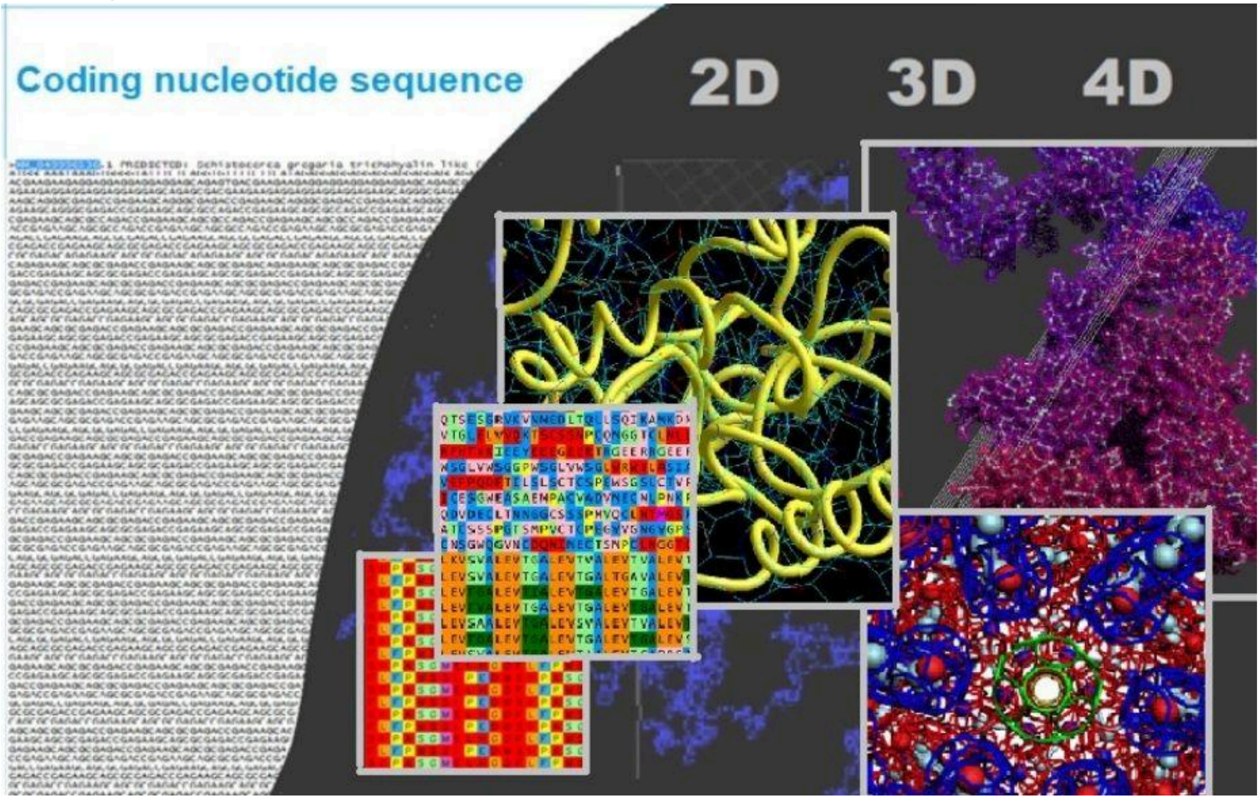
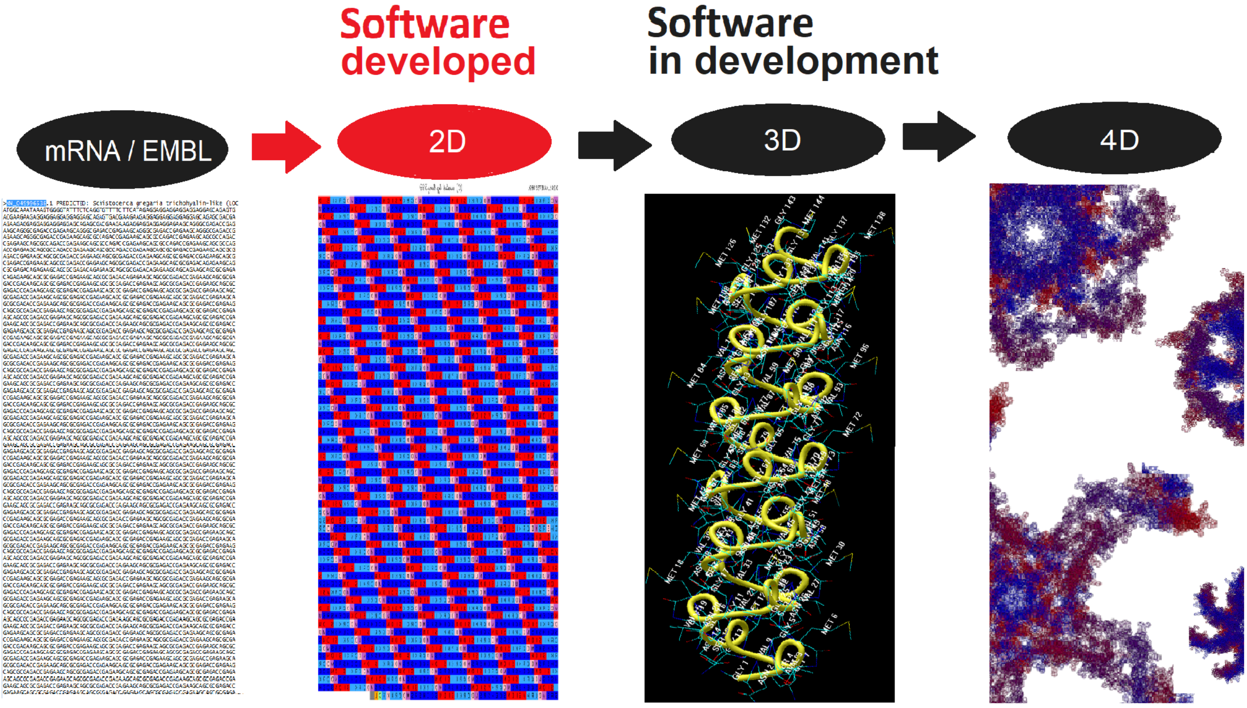
NANOWORLD LABORATORY

nanoworld_laboratory@mail.ru [3D Genetic Code]

Innovative method of converting nucleotide sequences into 2D, 3D and 4D structures

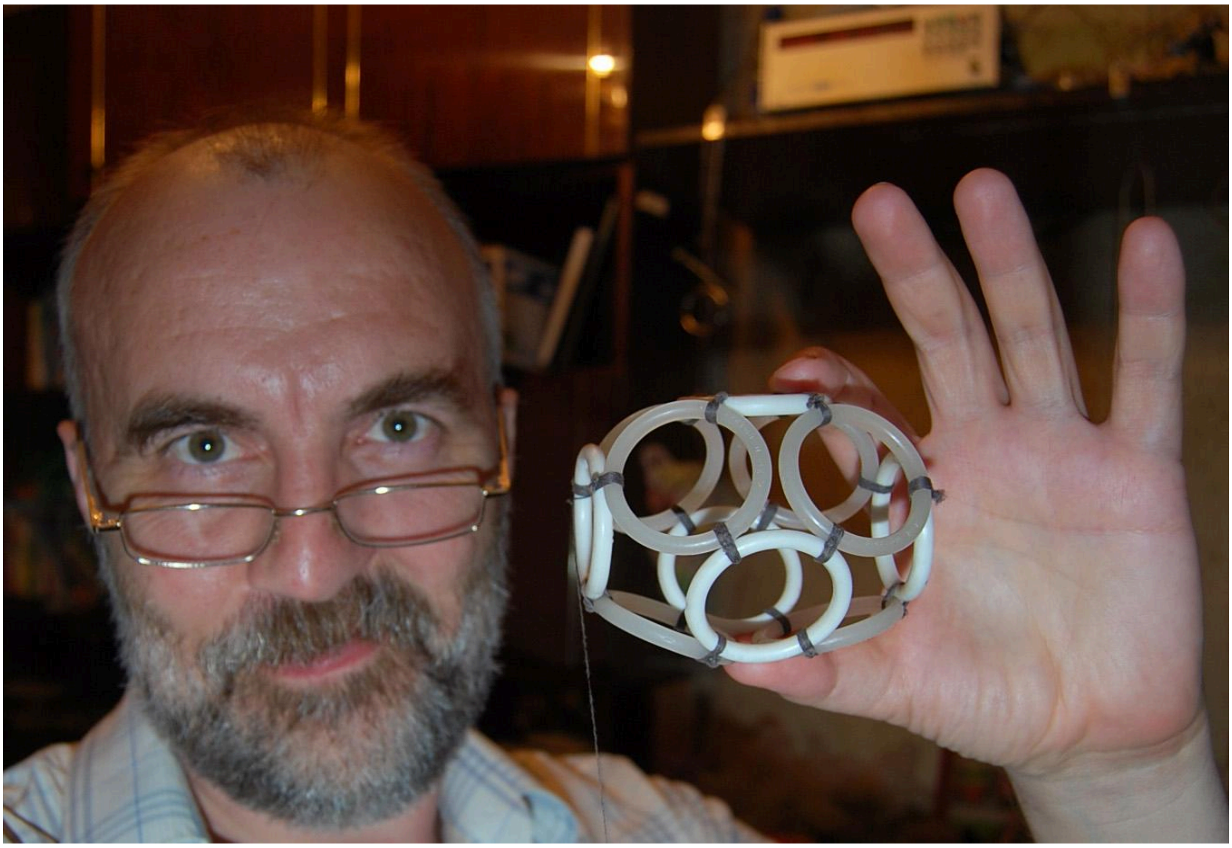




Software developed

Software in development

mRNA / EMBL → 2D → 3D → 4D



Dear Researchers !

Let us introduce to your attention our development – ***Picotechnology of proteins*** (3D Genetic code), a method of constructing accurate 2D structures, where the initial data is only the nucleotide sequence. Visualization of some part of the 3D and 4D structures is available. This approach was made possible by modeling electrons as tori (rings) of standing waves, and atomic shells as polyhedrons assembled from rings.

In this approach all amino acid residues have the same structural template, and the third letter of the triplet controls the angle of rotation of the next amino acid residue relative to the previous one. Each of the angles is marked on the 2D diagram with its own color and corresponds to the algorithm for forming alpha, beta, pi, 310, methionine and proline helices.

On the 2D color diagram we clearly see the helical sections, individual turns and individual amino acid residues.

We can directly convert the 2D colour diagram to 3D and 4D structure for some structural problems (3D and 4D modeling takes into account other adjustments). Software for 2D structures has been developed. Software for 3D and 4D structures is under development.

Our 2D diagrams reveal super-secondary structures (fractal helices, software helices), a coincidence confirmed by published data. The closure of disulfide bridges obtained on 2D and 3D models coincided with experimental data.

We hope that our algorithms will increase the accuracy of data processing both in the field of computational biology and in the field of X-ray structure prediction, CD and NMR methods. We would appreciate your comments and cooperation, see PICOTECHNOLOGY 2D, 3D, 4D SOLUTIONS AND ARTICLES .

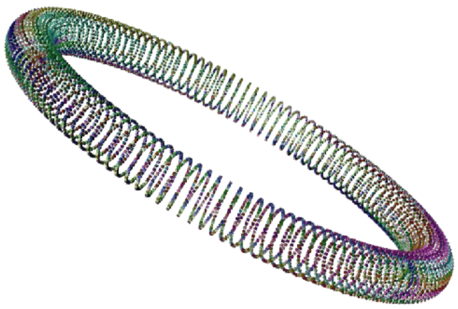
With best wishes,

Alexander Kushelev, Head of Nanoworld Laboratory

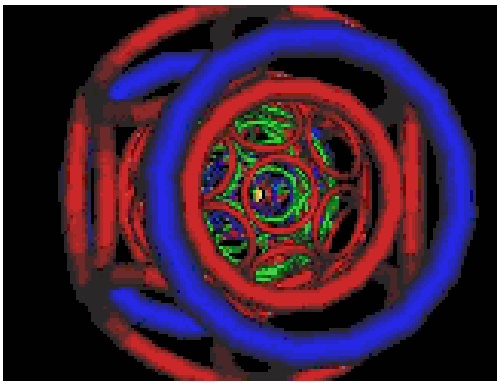
Tatyana Ryasina, Referent of Nanoworld Laboratory

Logic and Propaedeutics of the Protein Picotechnology Method

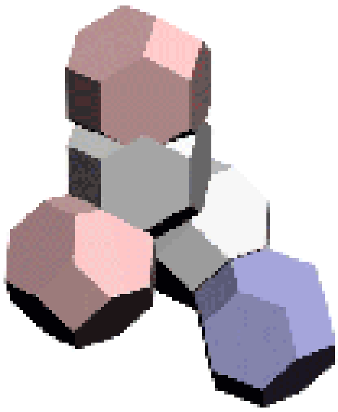
Toroidal (ring) models of particles as packets of standing waves



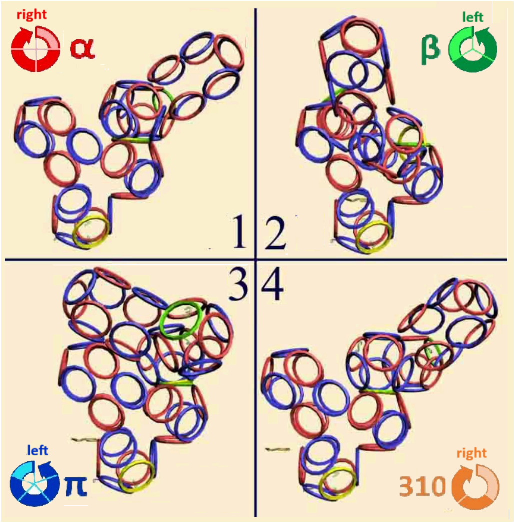
Ring-polihedron models of atoms



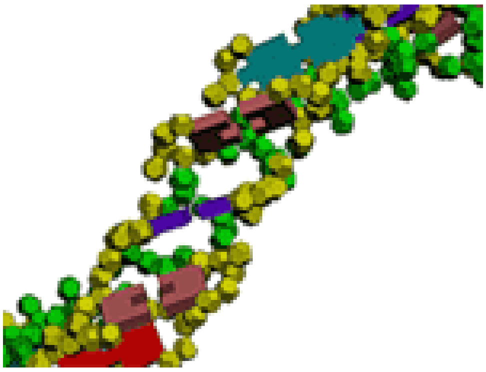
Peptide group included in the structure of all amino acid residues



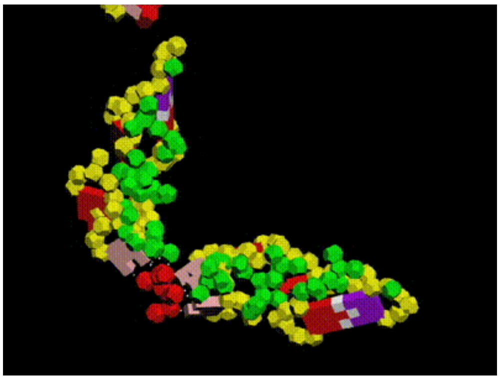
3D genetic code - algorithms for the rotation of amino acid residues relative to each other, according to their triplet letter codes



Stereometric structure of DNA

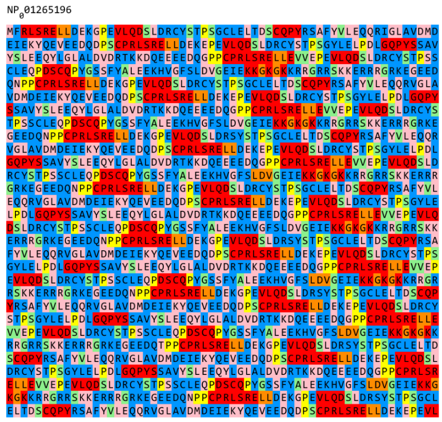
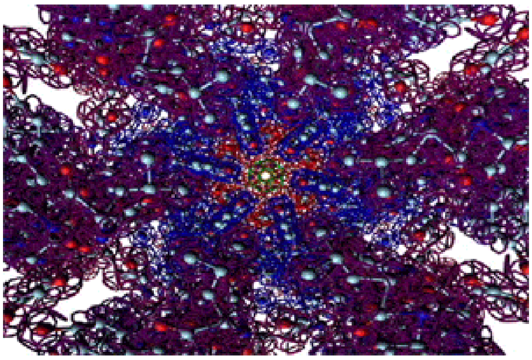


Stereometric mechanism of translation

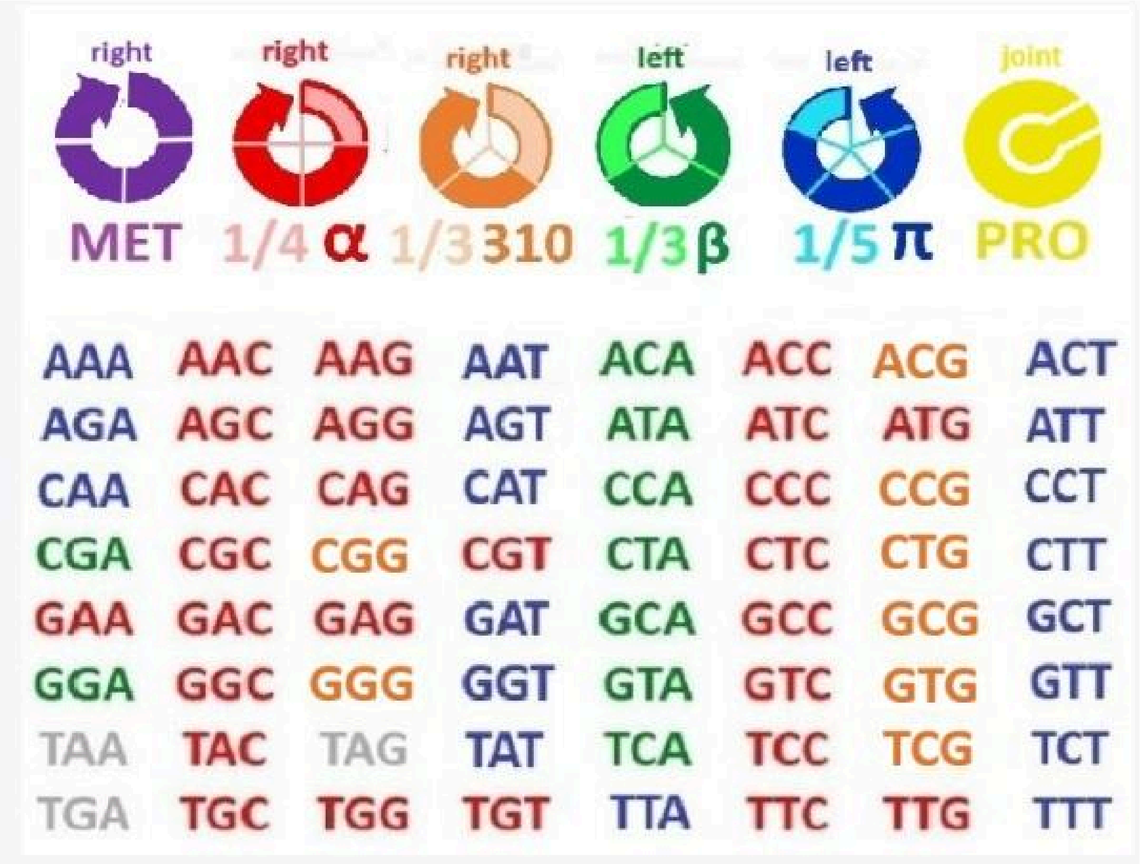


Accurate 2D Structures

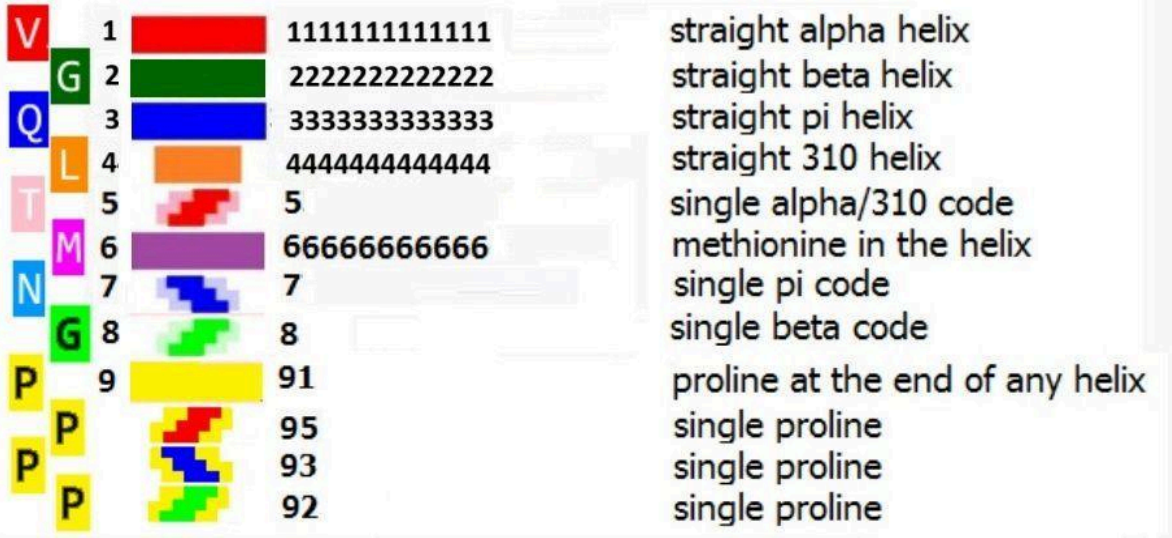
Accurate 3D and 4D Structures

 NP$_0$01265196 MFRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYVLEQQRIGLAVDMD EIEKYQEVEEDQDPSCPRLSRELLDEKEPEVLQDSLDRCYSTPSGYLELPDLGQPYSSAV YSLEEQYLGLALDVDRTKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQDSLDRCYSTPSS CLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEED QNPPCPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYVLEQQRVGLA VDMDEIEKYQEVEEDQDPSCPRLSRELLDEKEPEVLQDSLDRCYSTPSGYLELPDLGQPY SSAVYSLEEQYLGLALDVDRTKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQDSLDRCYS TPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKE GEEDQNPPCPRLSRELLDEKGPEVLQDSLDRSYSTPSGCLELTDSCQPYRSAFYVLEQQR VGLAVDMDEIEKYQEVEEDQDPSCPRLSRELLDEKEPEVLQDSLDRCYSTPSGYLELPDL GQPYSSAVYSLEEQYLGLALDVDRTKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQDSLD RCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIEKKGKGKKRRGRRSKKERRR GRKEGEEDQNPPCPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYVL EQQRVGLAVDMDEIEKYQEVEEDQDPSCPRLSRELLDEKEPEVLQDSLDRCYSTPSGYLE LPDLGQPYSSAVYSLEEQYLGLALDVDRTKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQ DSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIEKKGKGKKRRGRRSKK ERRRGRKEGEEDQNPPCPRLSRELLDEKGPEVLQDSLDRSYSTPSGCLELTDSCQPYRSA FYVLEQQRVGLAVDMDEIEKYQEVEEDQDPSCPRLSRELLDEKEPEVLQDSLDRCYSTPS GYLELPDLGQPYSSAVYSLEEQYLGLALDVDRTKKDQEEEEDQGPPCPRLSRELLEVVEP EVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIEKKGKGKKRRGR RSKKERRRGRKEGEEDQNPPCPRLSRELLDEKGPEVLQDSLDRSYSTPSGCLELTDSCQP YRSAFYVLEQQRVGLAVDMDEIEKYQEVEEDQDPSCPRLSRELLDEKEPEVLQDSLDRCY STPSGYLELPDLGQPYSSAVYSLEEQYLGLALDVDRTKKDQEEEEDQGPPCPRLSRELLE VVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIEKKGKGKK RRGRRSKKERRRGRKEGEEDQTPPCPRLSRELLDEKGPEVLQDSLDRSYSTPSGCLELTD SCQPYRSAFYVLEQQRVGLAVDMDEIEKYQEVEEDQDPSCPRLSRELLDEKEPEVLQDSL DRCYSTPSGYLELPDLGQPYSSAVYSLEEQYLGLALDVDRTKKDQEEEEDQGPPCPRLSR ELLEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIEKKG KGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKGPEVLQDSLDRSYSTPSGCL ELTDSCQPYRSAFYVLEQQRVGLAVDMDEIEKYQEVEEDQDPSCPRLSRELLDEKEPEVL			
Identification of functions arising from the designs of protein picomachines, reactors and other biomolecular devices (5D)			
			

An accurate 2D highly periodic Picotech structures

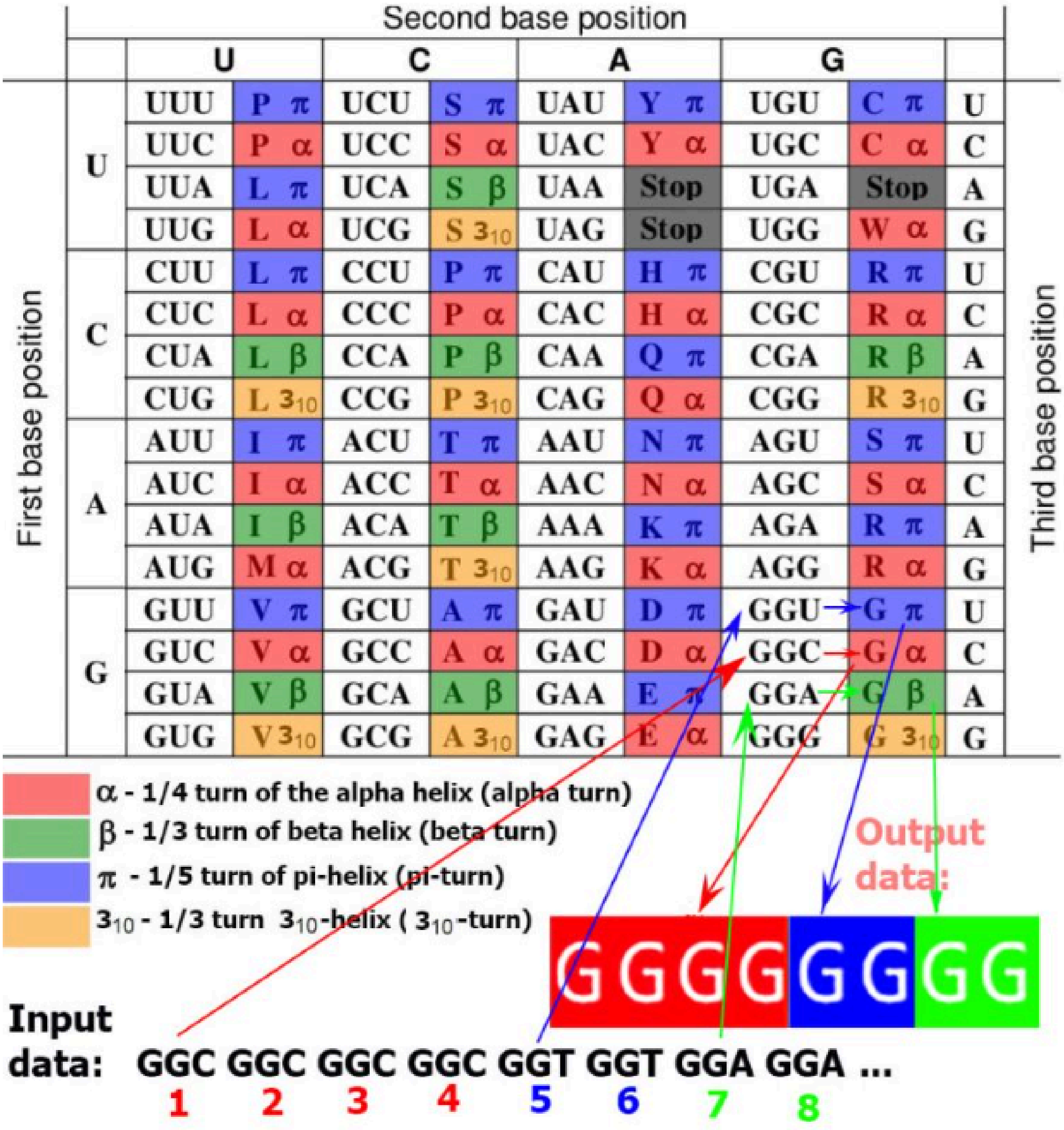


AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACT
AGA	AGC	AGG	AGT	ATA	ATC	ATG	ATT
CAA	CAC	CAG	CAT	CCA	CCC	CCG	CCT
CGA	CGC	CGG	CGT	CTA	CTC	CTG	CTT
GAA	GAC	GAG	GAT	GCA	GCC	GCG	GCT
GGA	GGC	GGG	GGT	GTA	GTC	GTG	GTT
TAA	TAC	TAG	TAT	TCA	TCC	TCG	TCT
TGA	TGC	TGG	TGT	TTA	TTC	TTG	TTT



V	1	1111111111111	straight alpha helix
G	2	2222222222222	straight beta helix
Q	3	3333333333333	straight pi helix
L	4	4444444444444	straight 310 helix
T	5	5	single alpha/310 code
M	6	66666666666	methionine in the helix
N	7	7	single pi code
G	8	8	single beta code
P	9	91	proline at the end of any helix
P		95	single proline
P		93	single proline
P		92	single proline

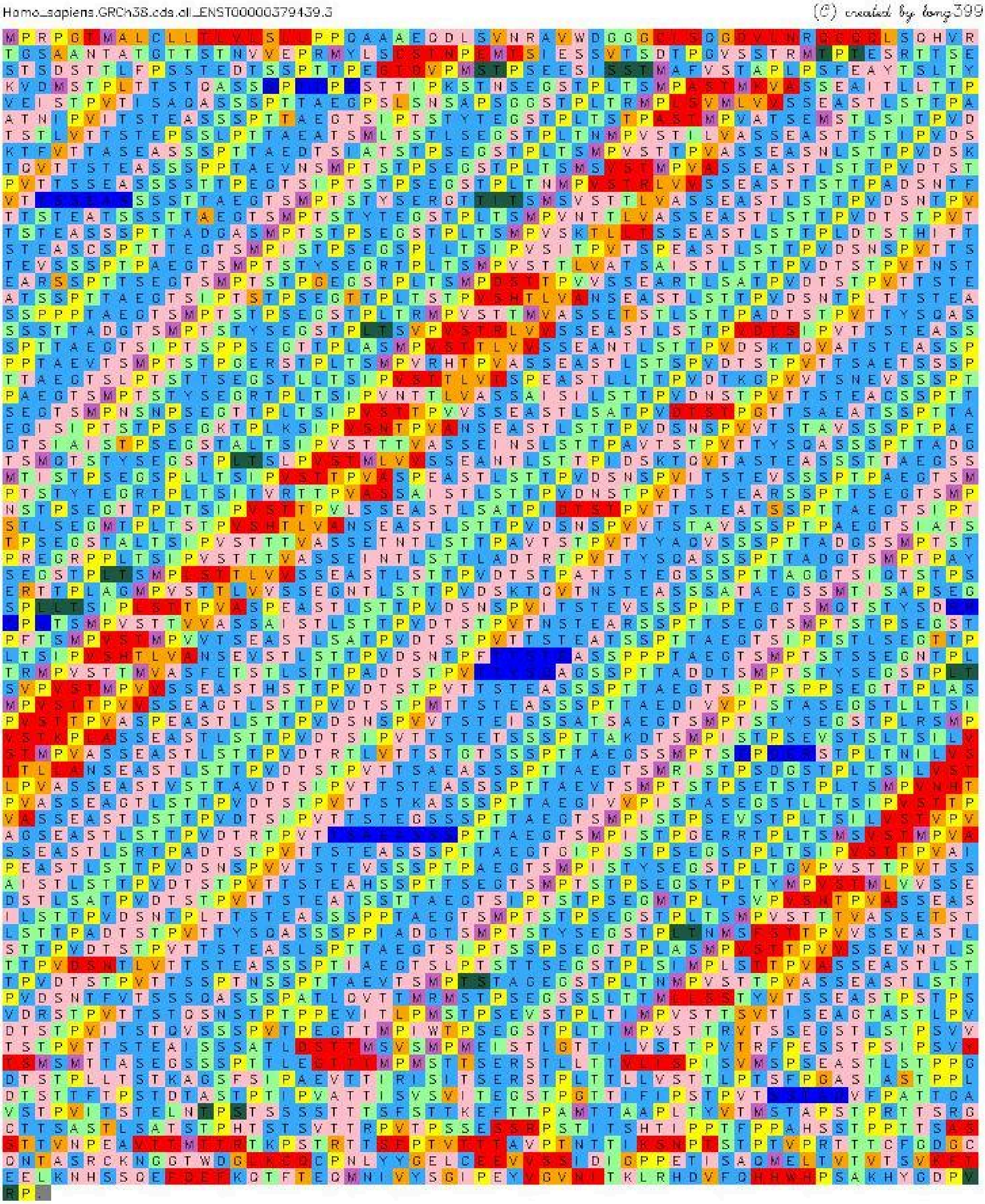
How does the 3D Genetic code table work?



	Second base position								
First base position	U		C		A		G		Third base position
U	UUU	P π	UCU	S π	UAU	Y π	UGU	C π	U
	UUC	P α	UCC	S α	UAC	Y α	UGC	C α	C
	UUA	L π	UCA	S β	UAA	Stop	UGA	Stop	A
	UUG	L α	UCG	S 3_{10}	UAG	Stop	UGG	W α	G
C	CUU	L π	CCU	P π	CAU	H π	CGU	R π	U
	CUC	L α	CCC	P α	CAC	H α	CGC	R α	C
	CUA	L β	CCA	P β	CAA	Q π	CGA	R β	A
	CUG	L 3_{10}	CCG	P 3_{10}	CAG	Q α	CGG	R 3_{10}	G
A	AUU	I π	ACU	T π	AAU	N π	AGU	S π	U
	AUC	I α	ACC	T α	AAC	N α	AGC	S α	C
	AUA	I β	ACA	T β	AAA	K π	AGA	R π	A
	AUG	M α	ACG	T 3_{10}	AAG	K α	AGG	R α	G
G	GUU	V π	GCU	A π	GAU	D π	GGU	G π	U
	GUC	V α	GCC	A α	GAC	D α	GGC	G α	C
	GUA	V β	GCA	A β	GAA	E π	GGA	G β	A
	GUG	V 3_{10}	GCG	A 3_{10}	GAG	E α	GGG	G 3_{10}	G

🟥 **α - 1/4 turn of the alpha helix (alpha turn)**
🟩 **β - 1/3 turn of beta helix (beta turn)**
🟦 **π - 1/5 turn of pi-helix (pi-turn)**
🟧 **3_{10} - 1/3 turn 3_{10}-helix (3_{10}-turn)**

Input data: GGC GGC GGC GGC GGT GGT GGA GGA ...
1 2 3 4 5 6 7 8



PRESENTATION OF THE METHOD '2025 & CONVENTIONAL DESIGNATIONS

A.Yu. Kushelev. Picotech Experiment: Detection of Cross-Diester Links in DNA Structure. MEDICINE, SOCIOLOGY, PHILOSOPHY. Applied research, No.3 2025 (MSF), pp.156-163

Kushelev A.Y., Kozhevnikov D.N. Modeling of shapes of electronic surfaces of chemical compounds with different covalent bonds in the form of polyhedra from rings (ring hedra). MEDICINE, SOCIOLOGY, PHILOSOPHY. Applied research, No.2 2025 (MSF), pp.151-156

A.Yu. Kushelev. Determination of protein secondary structure using a 3D genetic code table. MEDICINE, SOCIOLOGY, PHILOSOPHY. Applied research, N1 2025 (MSF), pp.70-78

MONOGRAPH IN RUSSIAN READ BUY PREFACE IN ENGLISH
V.V. Sokolik, A.Yu. Kushelev. Geometry of the living nanoworld. Picotechnology of proteins - Lambert Academic Publishing, 2016-08-04, ISBN 978-3-659-92862-8 - 292 p.

3D Genetic code. Music of proteins. Why is protein structure prediction possible based on only one nucleotide sequence?

"Careless Whisper by George Michael" Protein

4AG8/ VEGFR2

A.Yu. Kushelev, D.N. Kozhevnikov, V.V. Yakim, S.S. Markovskiy, V.V. Belyaev CONSTRUCTION OF A SCALE MODEL OF THE SPATIAL STRUCTURE OF A PROTEIN BASED ON ITS NUCLEOTIDE SEQUENCE PREPRINT

Calculation of coordinates of atoms common to all amino acids

One-to-one correspondence between the sequences and 2D and 3D Picotech diagrams

Intermediate 2.5D PicoTech diagrams How to see 3D structures on 2D Picotech diagram

Clarification of transposition angles using a joint-rod constructor '2024

Model experiments on a 3D printer to determine the values of transition angles between helices '2019

Composition, transposition and proline angles Methionine helix

Picotechnology of translation Proteins corresponding in shape and size to DNA

DNA is built on orthogonal geometric elements with fivefold symmetry

Highly periodic protein structures as a result of applying the toroidal polyhedral approach to modeling molecules

Will it be possible to assemble connexon from 6 connexins '2012 ?

Fractal Helices "Wet" experiments showed... fractal helices (helices of helices)

Masterpieces of protein architecture Q - Helicies Antihomologues

Picotechnology of proteins helps visually detect protein active sites

Picotech 3D model of interleukin-34

Picotechnological Anisotropic Ultra-High Pressure Reactors

The nuances of the functioning of the insulin hexamer picomachine

D.N.Kozhevnikov, Models of Molecules with Ring-Shaped Faces, Russian Journal of Physical Chemistry, Vol. 70, No. 6, 1996, pp. 1057-1059.

RING ELECTRONS AND RING-POLYHEDRAL MODELS OF ATOMS

X-ray structural analysis and Picotechnology 2D diagrams. What do we see?

Comparison of Picotechnology 3D diagram and data obtained by circular dichroism

1.5D PDB Schemes and Picotechnology

Structural features in genomes “Sapphire” genome 2D Picotech structure of 12 coronavirus proteins

Examples of two highly ordered hypothetical proteins

Irregular structures in the protein molecule

Refinement of 2D structures of some G-proteins, taken from the NCBI database, using the Picotechnology method

Terminating codons Incredible molecules

Proline Joint Pro and Proline tuning

Human Genome Protein 2D Picotechnology Structures Base

Picotechnology of Proteins - presentation by the author A.Kushelev

A.Yu.Kushelev. 3D GENETIC CODE. Abstracts for the conference "DNA-2020" PREPRINT

A.Yu.Kushelev 3D Genetic Code PREPRINT

V.Yakim, T.Riassina Picotechnology of proteins as an approach to modeling the spatial structure of the protein, complementing the possibilities of X-ray structural analysis PREPRINT

V Sokolik A Kushelev PIKOTECHNOLOGY - A NEW APPROACH TO MODELING THE SPATIAL STRUCTURE OF PROTEIN

V.V. Sokolik Implementation of the 3D genetic code of proteins by isoacceptor tRNAs

V.V.Sokolik Isoacceptor tRNAs in the mechanism for the implementation of the 3D genetic code of proteins

V.V.Sokolik THE MOLECULAR CONSTRUCTOR PROGRAM BUILDS STRUCTURAL TEMPLATES OF PROTEINS ACCORDING TO THEIR DETERMINING NUCLEOTIDE SEQUENCES

V V Sokolik Protein is Coded in Genome and Sythesized in Ribosomes as a Structural Template of a Rotameric Version Sequence of Peptide Bond Configuration

V V Sokolik MODELLING OF THE INDIVIDUAL STRUCTURAL TEMPLATE OF PROTEIN ON DETERMINING IT NUCLEOTIDE SEQUENCES

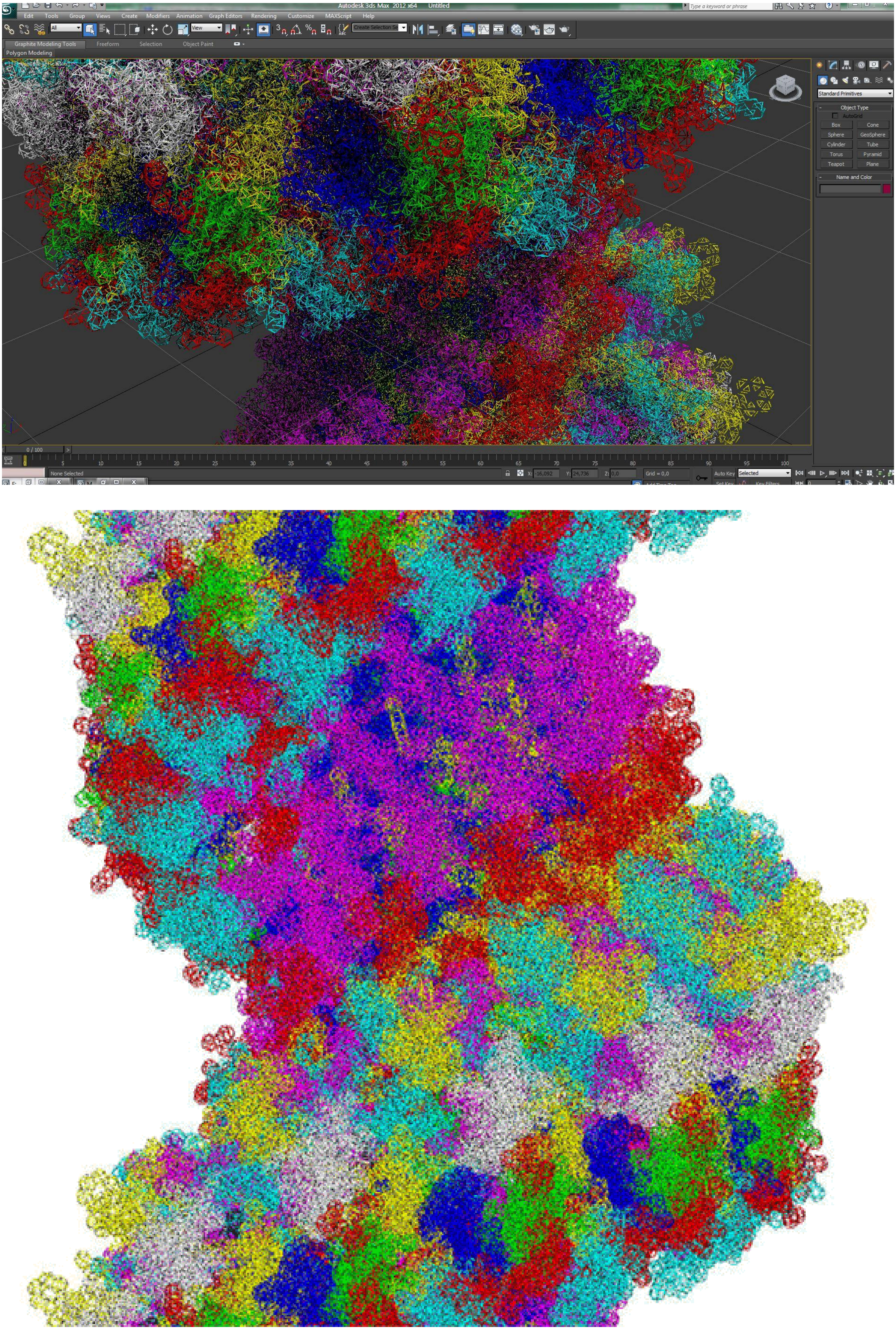
V.V. Sokolik Conundrum of Isoaceptor RNA

V.V. Sokolik "No additional information greater than that contained in DNA for protein folding is required"

V.Sokolik. ALGORITHM OF PROTEIN STRUCTURAL TEMPLATE DECODING ACCORDING TO ITS DETERMINED NUCLEOTIDE SEQUENCE

V. Sokolik. Modeling of the 3D structure of apoliprotezin E3 under its determining nucleotide sequence

V.V.Sokolik. Predicting the in silico spatial structure of a protein based on genome information and a geometric algorithm as an alternative to the quantum mechanical approach



3D Picotech collagen structure