NANOWORLD LABORATORY

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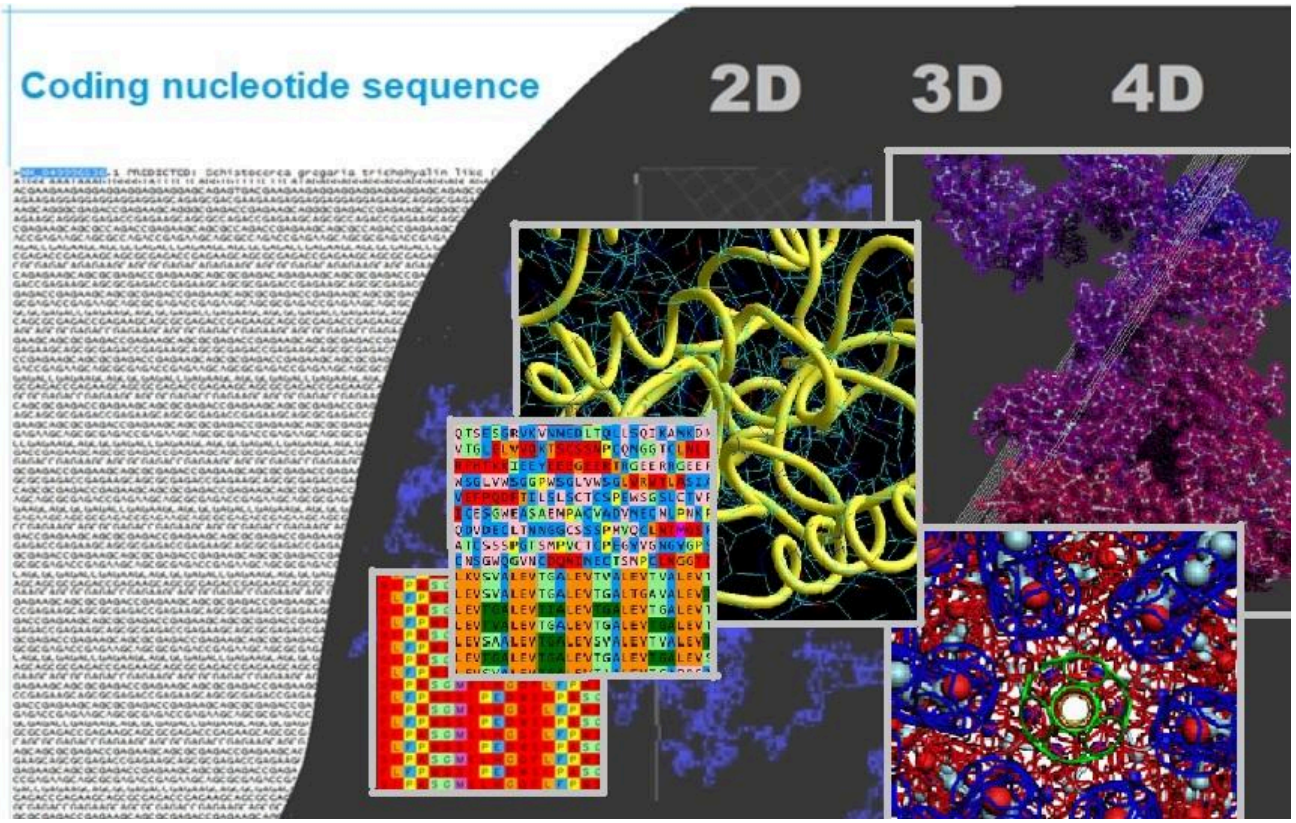
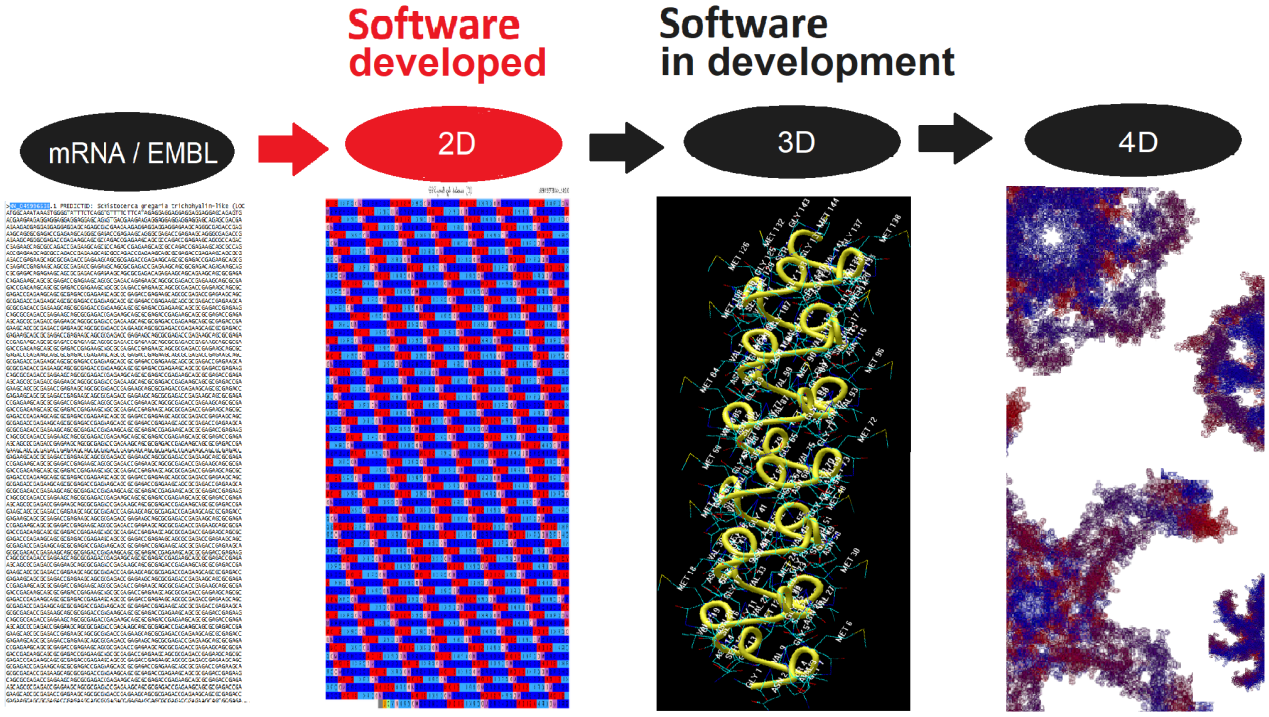
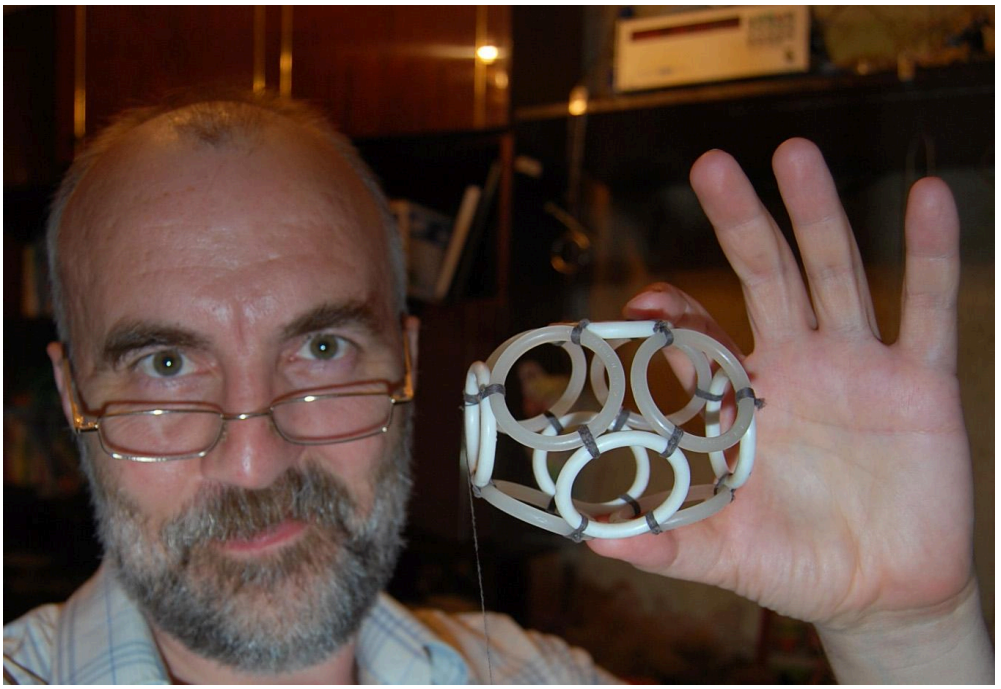
Innovative method of converting nucleotide sequences into 2D, 3D and 4D structures







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 **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.

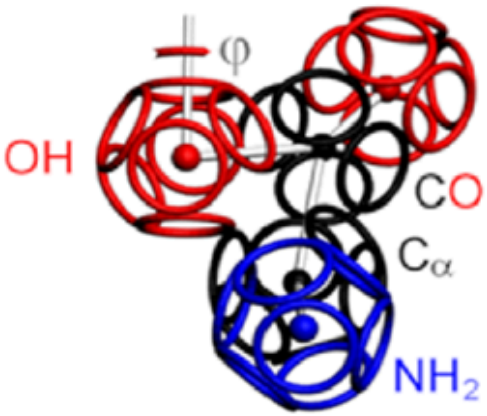
Our 2D diagrams reveal super-secondary structures (**fractal helices**, **software helices**), a coincidence confirmed by published data. The closure of disulfide bridges obtained on 2D and 3D models coincided with experimental data.

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 **DEMO PICOTECH 2D, 3D, 4D, AND ARTICLES** .

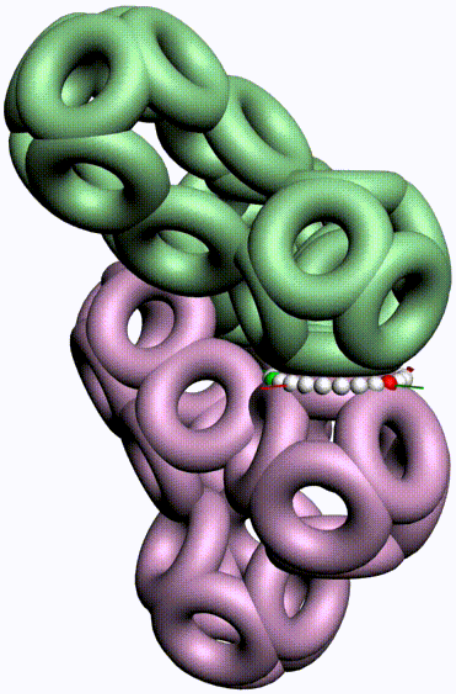
With best wishes,
Alexander Kushelev, Head of Nanoworld Laboratory
Tatyana Ryasina, Referent of Nanoworld Laboratory

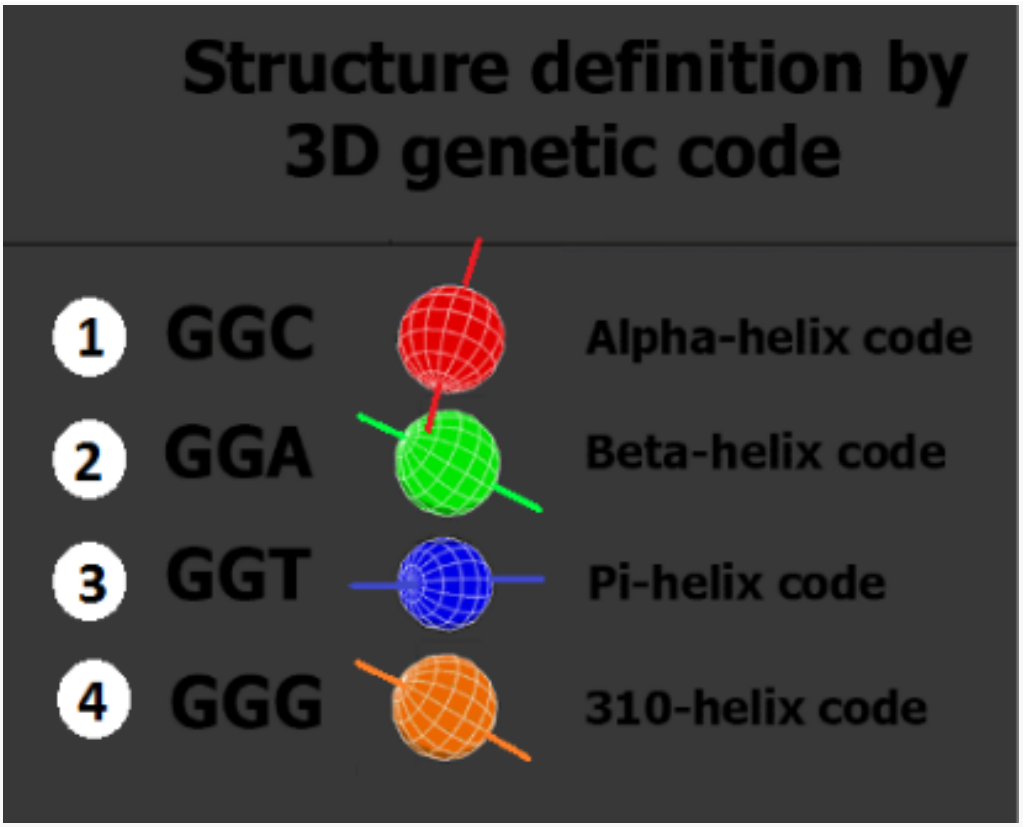
The Legend

HOW TO READ 2D DIAGRAMS OF 3D GENETIC CODE



Structural template of amino acid residue



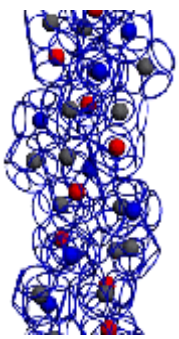


3D STRUCTURES OF AMINO ACID RESIDUES

Ala: *gcc, gca, gct, gcg*	**Val:** *gtc, gta, gtt, gtg*	**Gly:** *ggc, gga, ggt, ggg*
Ser^{L}: *tcc, tca, tct, tcg*	**Ser^{θ}:** *agc, agt*	**Thr:** *acc, aca, act, acg*
Glu: *gaa, gag*	**Gln:***caa, cag*	**Ile:** *atc, ata, att*
Asp: *gac, gat*	**Asn:** *aac, aat*	**Cys:** *tgc, tgt*

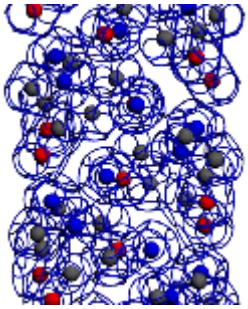
Leu^{L}: *ctc, cta, ctt, ctg*	**Leu^{θ}:** *tta, ttg*	**Lys:** *aaa, aag*
Met: *atg*	**Arg^{t}:** *cgc, cga, cgt, cgg*	**Arg^{b}:** *aga, agg*
Phe: *ttc, ttt*	**Tyr:** *tac, tat*	**Pro:** *ccc, cca, cct, ccg*
His: *cac, cat*	**Trp:** *tgg*	**Stop-кодон:** *taa, tag, tga*

Примечание. Ядра атомов кислорода показаны красным цветом, углерода – голубым, азота - - синим, серы – желтым. Электроны внешних электронных оболочек атомов, формирующие молекулярную электронную оболочку аминокислот, обозначены синими кольцами.
Для Arg, Leu и Ser представлены по две модели изомеров по положению радикала, которые кодируются по разному.

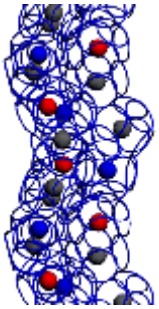


Alpha-helix

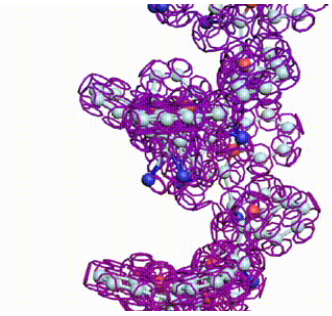
Beta-helix



Pi-helix



310-helix

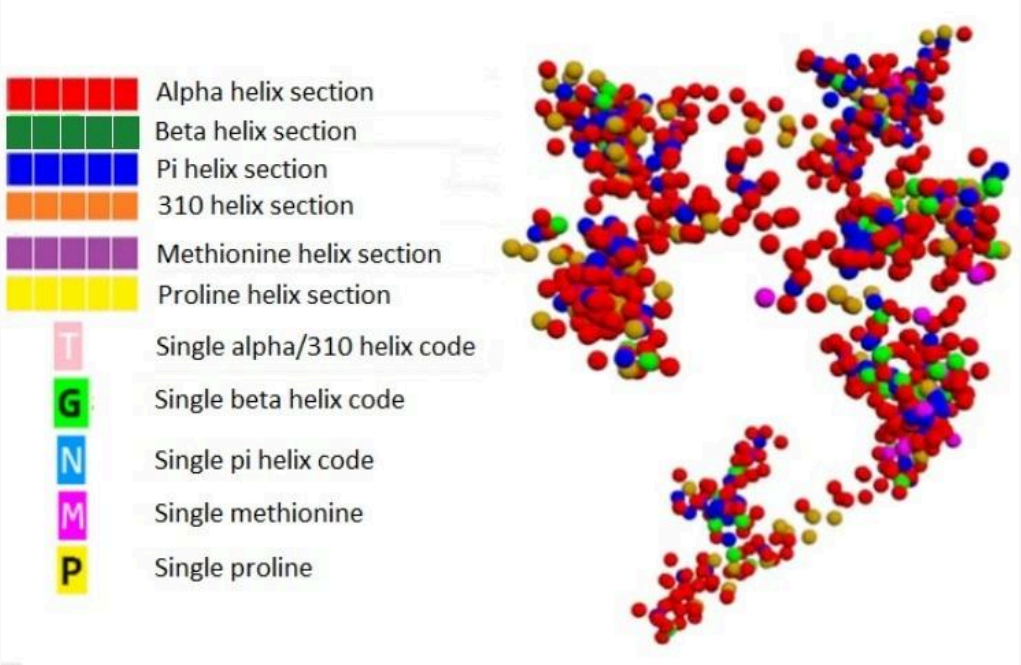


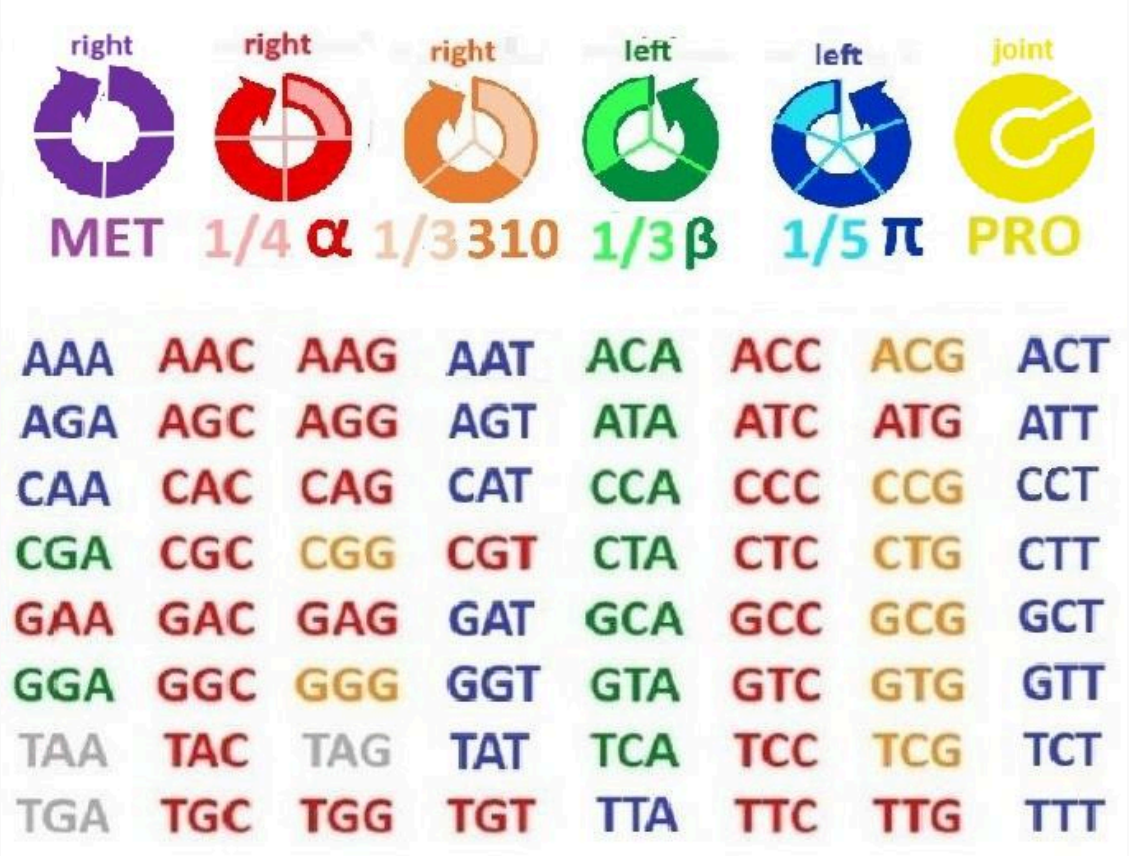
Methionine in a helix

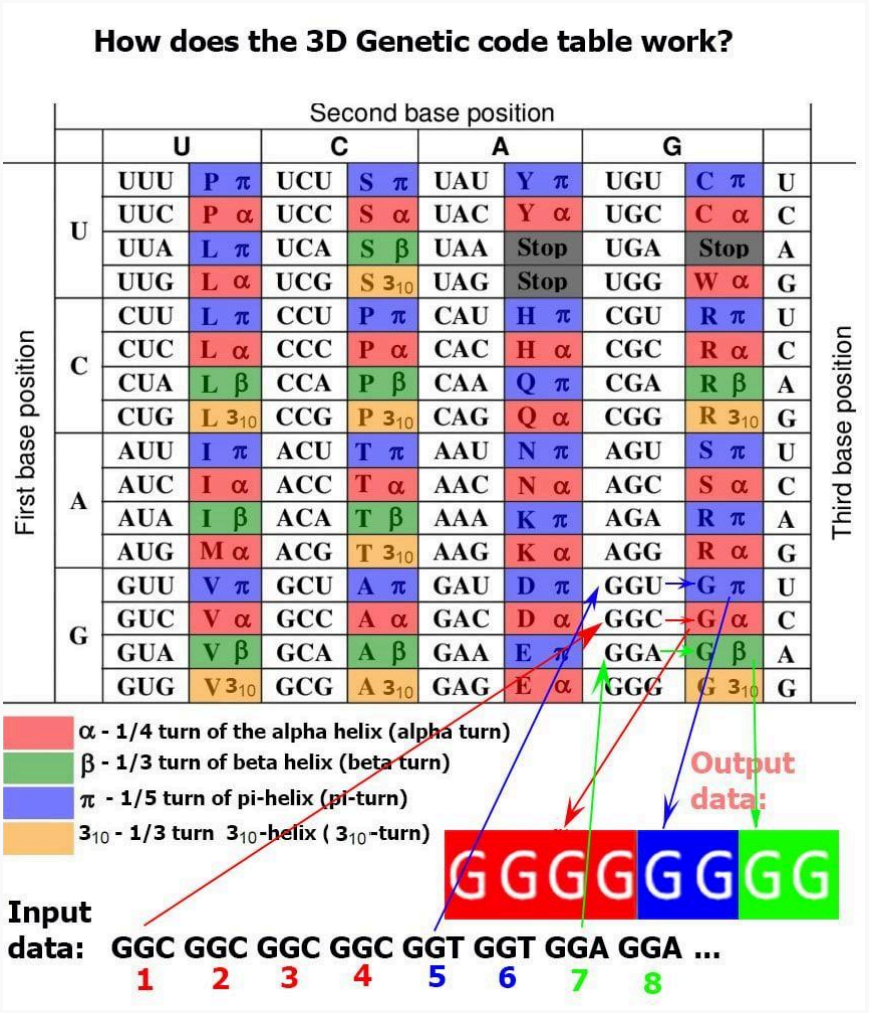
COMPACT 2D PICOTECHNOLOGY DIAGRAM

Red is an alpha helix.
The orange is a 310-helix.
Pink is a single alpha / 310 helix code.
Blue is a py-helix.
Green is a beta helix.
Lilac - methionine helix. It has a larger pitch of "thread" than the usual alpha-helix.
Black in abbreviated form and white in unfold means either an unknown code or the end of the translation.
Cyclic repetition of colors - software helix.

Alpha helix - right,
Pi helix - left,
Beta helix - left,
310 helix - right.





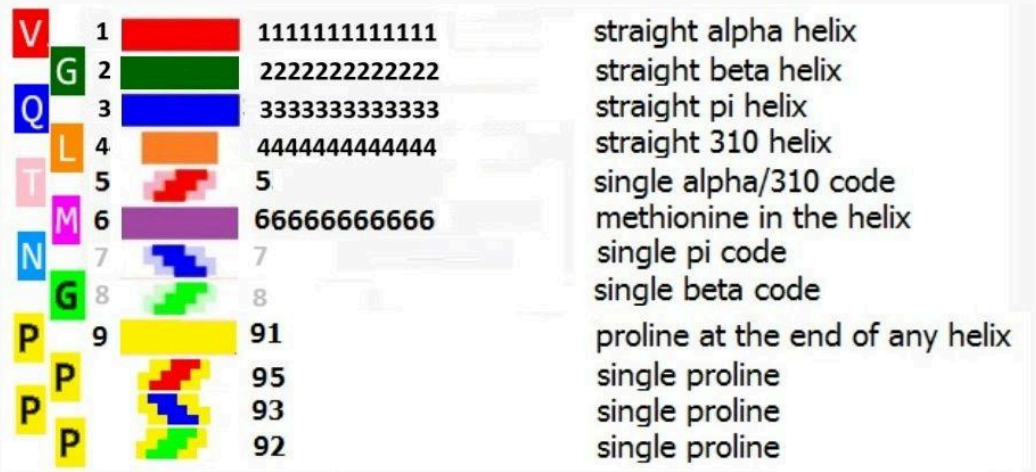


First base position	Second base position U		Second base position C		Second base position A		Second base position G		Third base position
U	UUU	P π	UCU	S π	UAU	Y π	UGU	C π	U
	UUC	P α	UCC	S α	UAC	Y α	UGC	C α	C
	UUA	L π	UCA	S β	UAA	Stop	UGA	Stop	A
	UUG	L α	UCG	S 3₁₀	UAG	Stop	UGG	W α	G
C	CUU	L π	CCU	P π	CAU	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 3₁₀	CCG	P 3₁₀	CAG	Q α	CGG	R 3₁₀	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 3₁₀	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 3₁₀	GCG	A 3₁₀	GAG	E α	GGG	G 3₁₀	G

FULL (EXPANDED) DIAGRAM

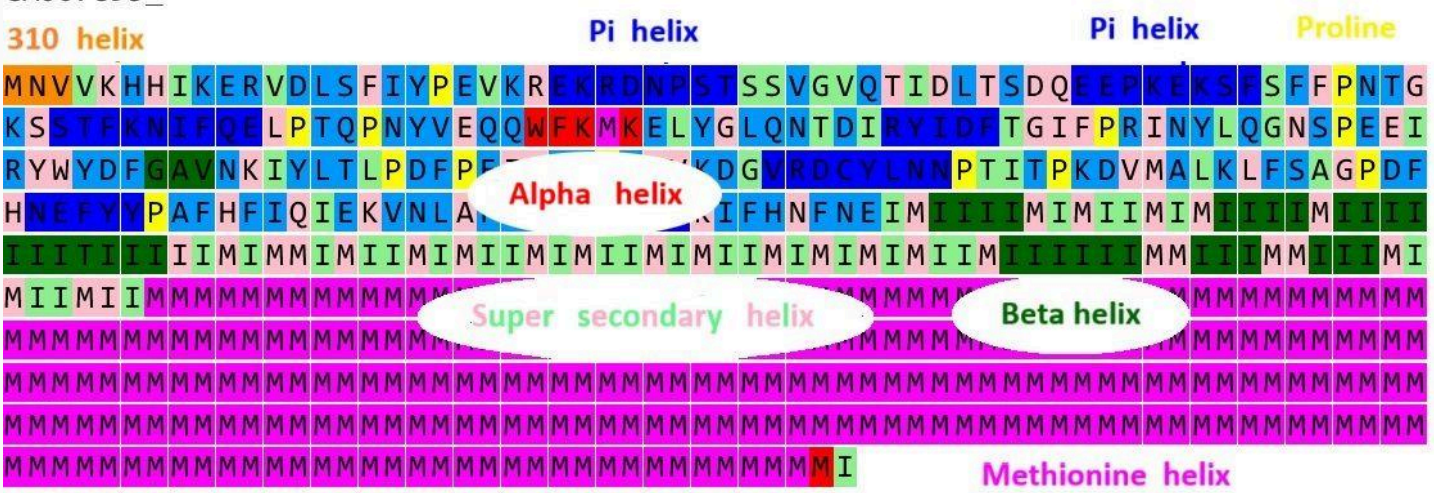
1 - ordinal number of the amino acid residue in the protein molecule
2 - triplet code
3 - one-letter code of amino acid residue
4 - three-letter designation of amino acid residue
5 - simplified composition code
6 - graphical interpretation of a simplified composition code
7 - composition code
8 - graphic interpretation of the composition code
9 - a note that sounds when you install this amino acid in a growing protein chain
10 - graphic representation of a note (or percussion instrument)
(Version Composition code 7)

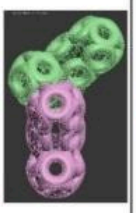
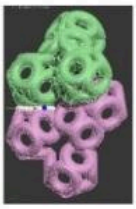
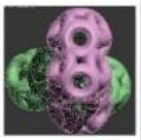
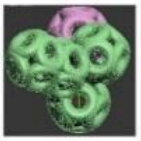
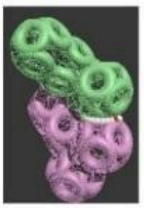
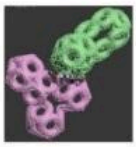
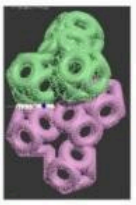
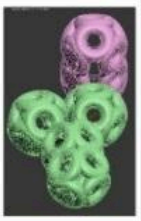
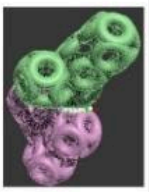
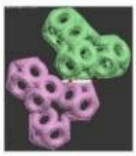
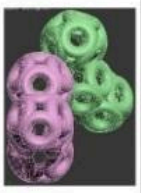
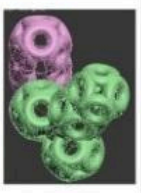
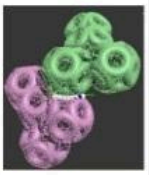
3D Genetic code code Version 9



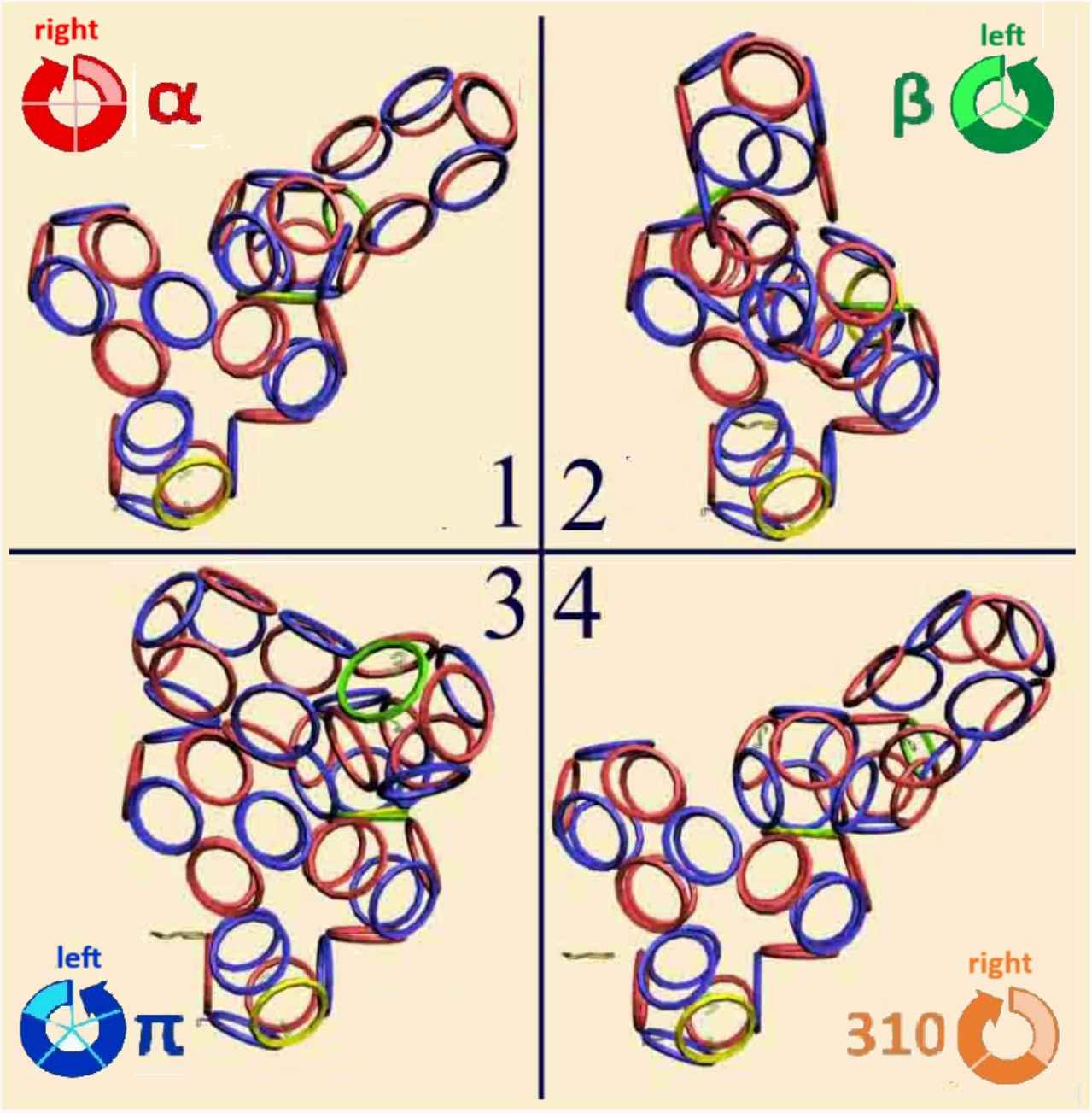
- coil of alpha helix (red)- 4 amino acid residues with the code "1",
- coil of beta-helix (green) - 3 amino acid residues with the code "2", -
310-helix coil (orange) - 3 amino acid residues with the code "4",
- coil of pi-helix (blue) - 5 amino acid residues with the code "3"
- light gray - stop codon

Program helices are a repetition of a sequence of compositions. For example, one alpha-helix code, then one pi-helix code. n (35) specifies a program spiral, and n3 or n5 are simple spirals (a pi-helix and an alpha-310 helix).
11111111111111111111 - straight alpha helix
4444444444444444444 - straight 310-helix
3333333333333333333 - straight pi-helix
22222222222222222222 - direct beta helix
232323 - software 23-helix
141414 - software 14-helix

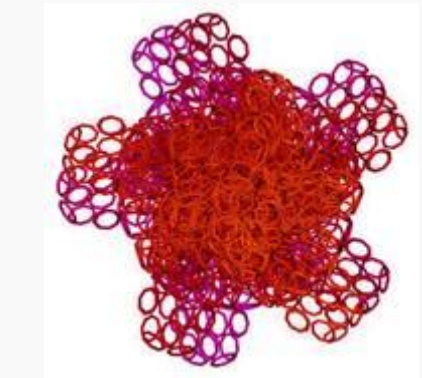


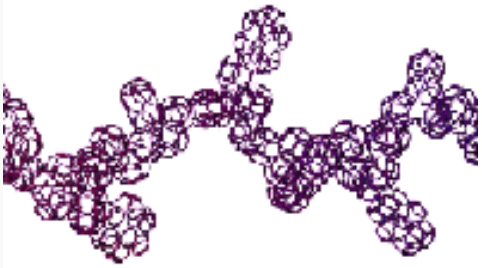
Front view	Back view	Left view	Right view	Bottom view	Top view	Perspective	Funda-mental helix
							α
							β
							π

X \ Y	C	a.o.	A	a.o.	T	a.o.	G	a.o.	Z	РВПС	ω
C	CCC	P	CAC	H	CTC	L	CGC	R	C	R	35°
	CCA		CAA	Q	CTA		CGA		A	0	155°
	CCT		CAT	H	CTT		CGT		T	L	275°
	CCG		CAG	Q	CTG		CGG		G	R	35°
A	ACC	T	AAC	N	ATC	I	AGC	S	C	R	35°
	ACA		AAA	K	ATA		AGA	R	A	0	155°
	ACT		AAT	N	ATT		AGT	S	T	L	275°
	ACG		AAG	K	ATG	M	AGG	R	G	R	35°
T	TCC	S	TAC	Y	TTC	F	TGC	C	C	R	35°
	TCA		TAA	Stop	TTA	L	TGA	Stop	A	0	155°
	TCT		TAT	Y	TTT	F	TGT	C	T	L	275°
	TCG		TAG	Stop	TTG	L	TGG	W	G	R	35°
G	GCC	A	GAC	D	GTC	V	GGC	G	C	R	35°
	GCA		GAA	E	GTA		GGA		A	0	155°
	GCT		GAT	D	GTT		GGT		T	L	275°
	GCG		GAG	E	GTG		GGG		G	R	35°

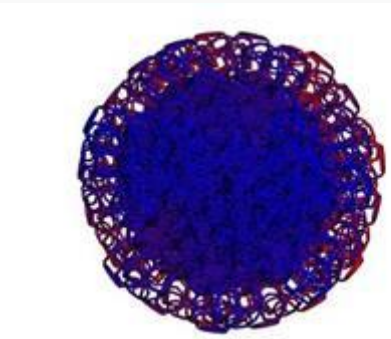


n 3212-helix

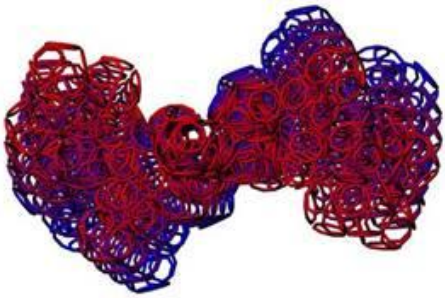


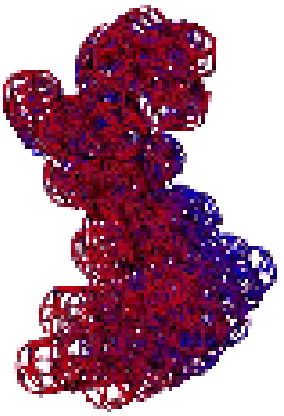


n 233 helix

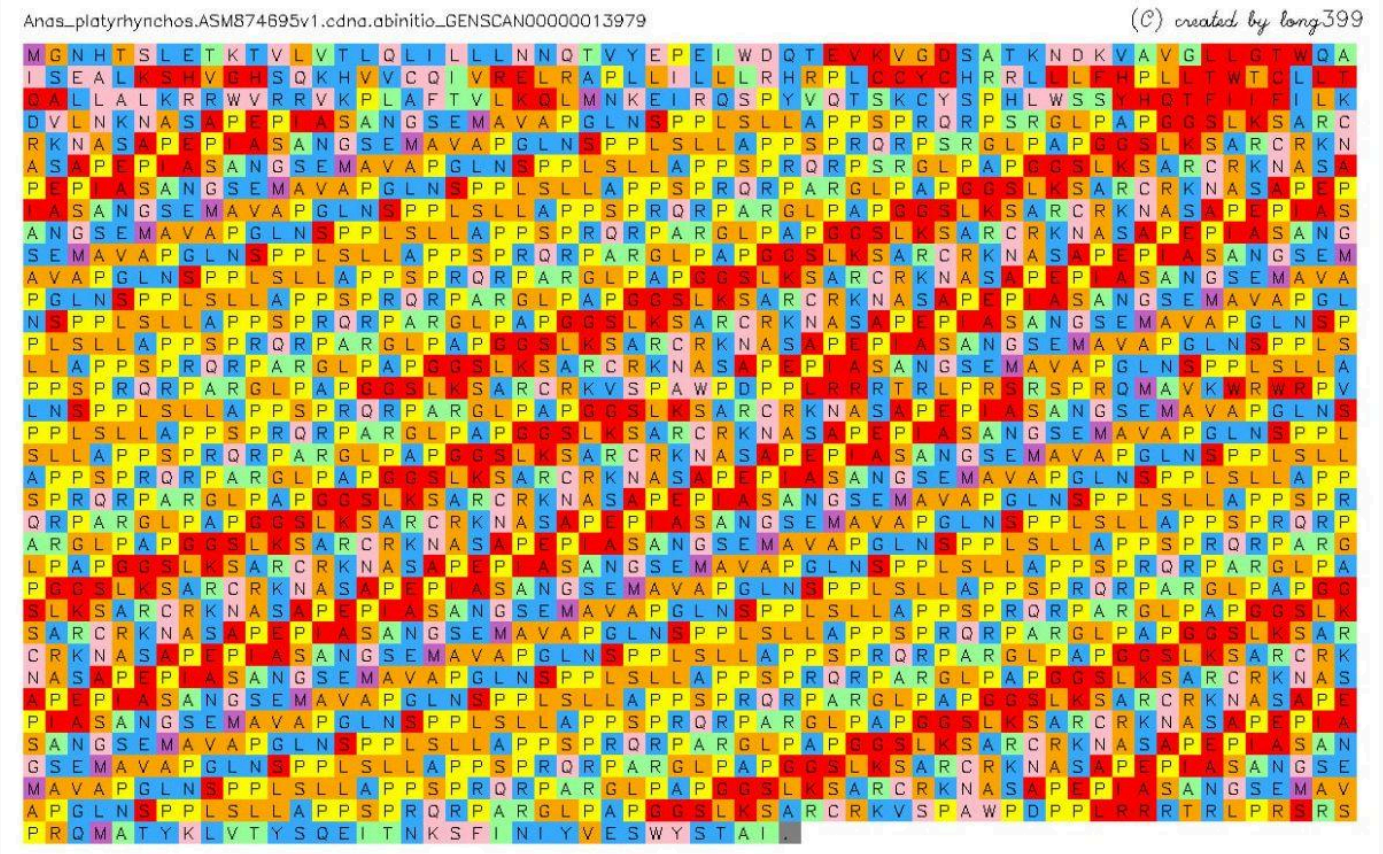


n 13323 helix





An example of a highly periodic structure



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

>ENA|KBQ88923|complement 2319 nucleotides

ttggccgccgttgccagcggtgccgttagcgccgccacccgcgccgccagccccggccgc
cccaccggcaccaccgctgccgccttgacctccttgcccgccgttgccgccgggactggt
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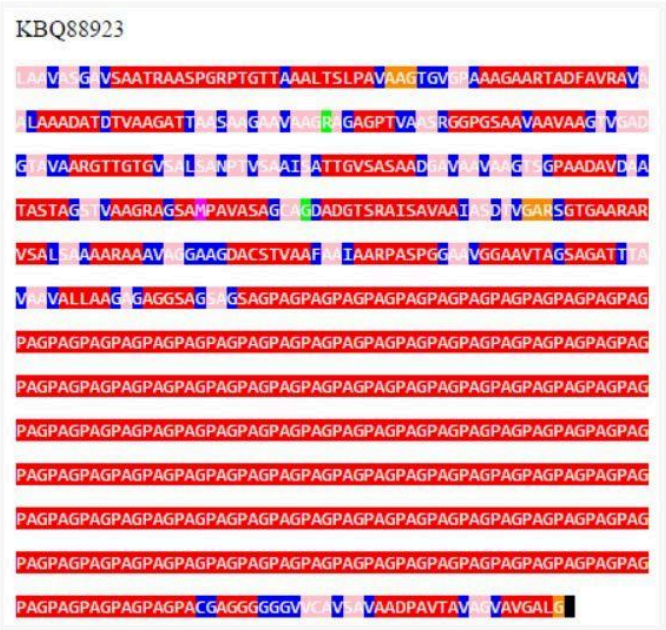
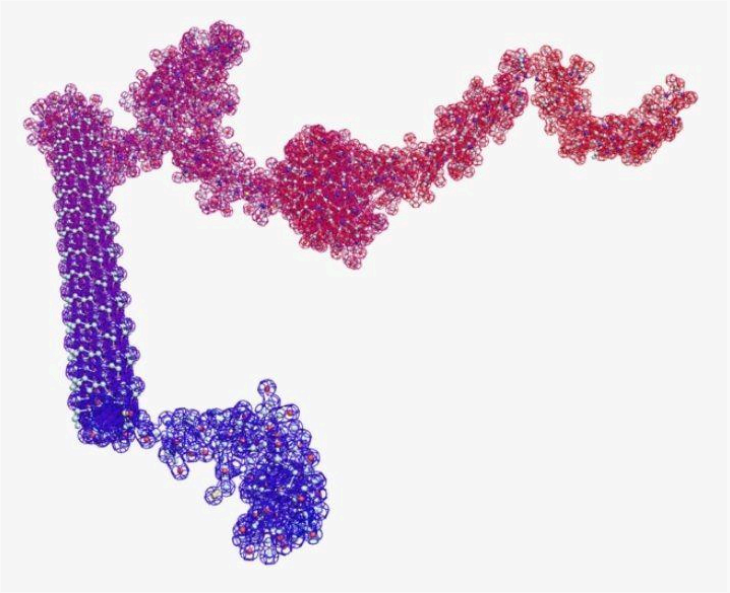
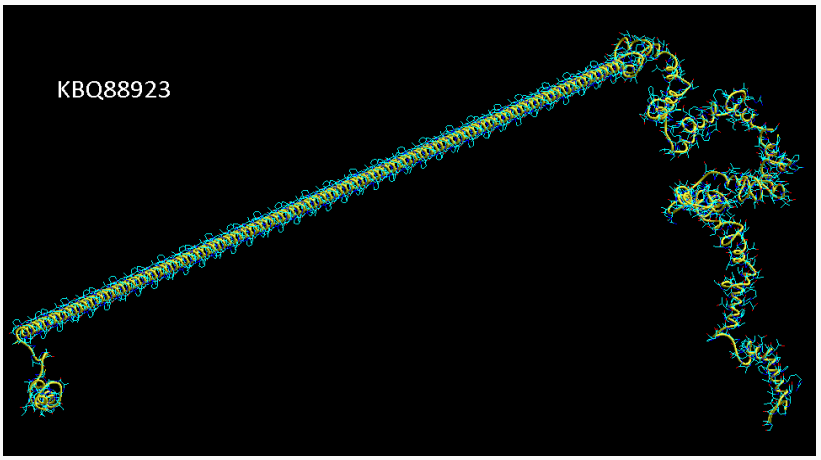
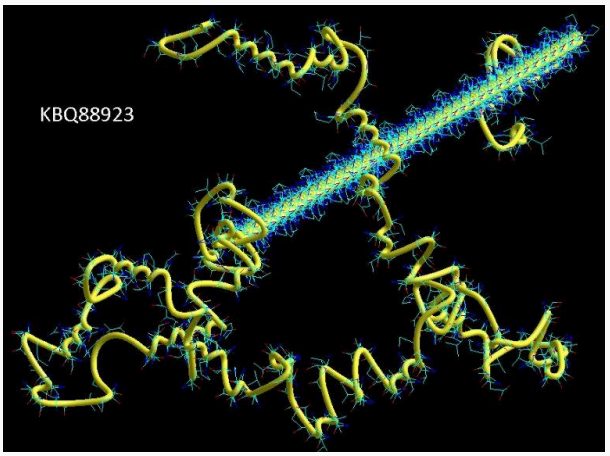
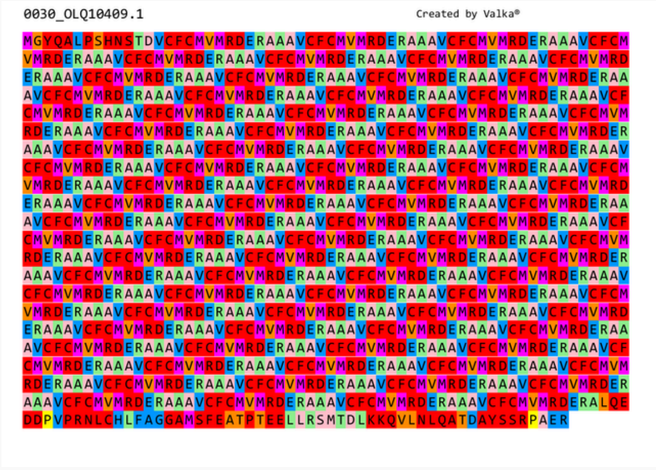








While the 3D picotech program is in development, we can model proteins manually and then digitize them to deliver the result as a 3D images and .pdb files.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Created by Valka®
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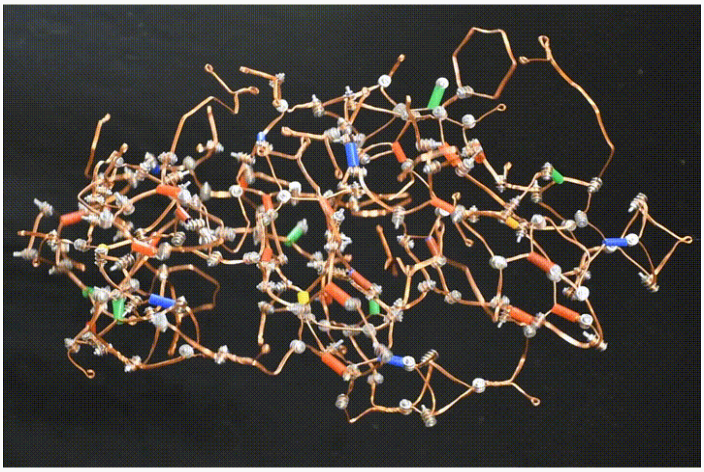

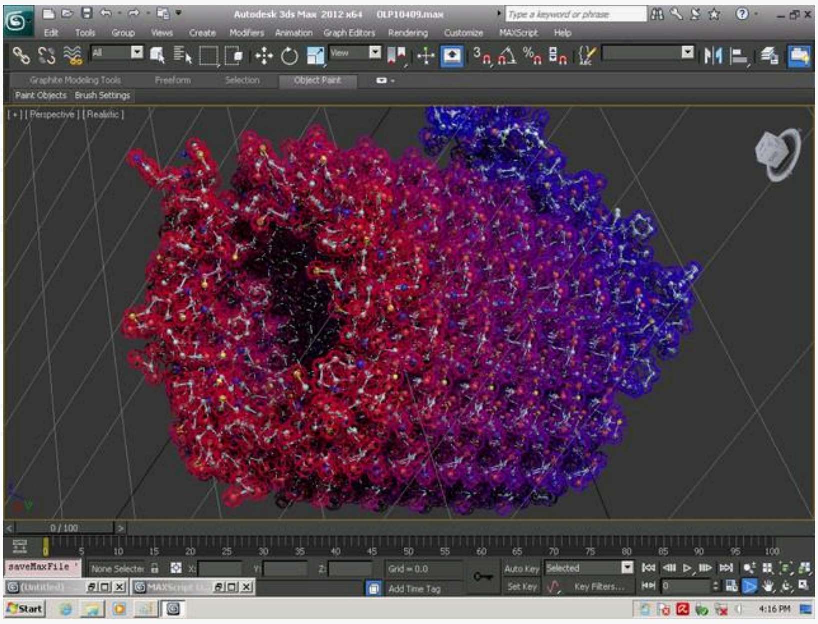
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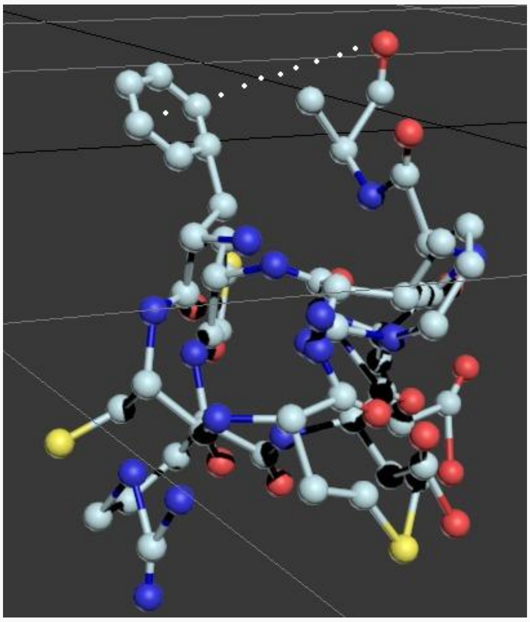

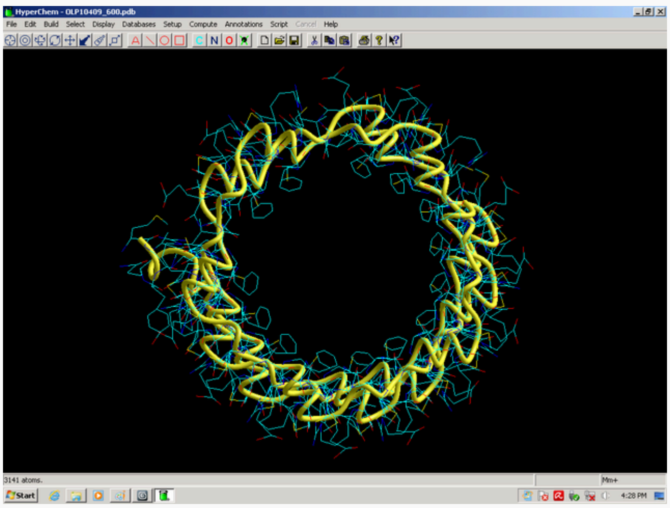
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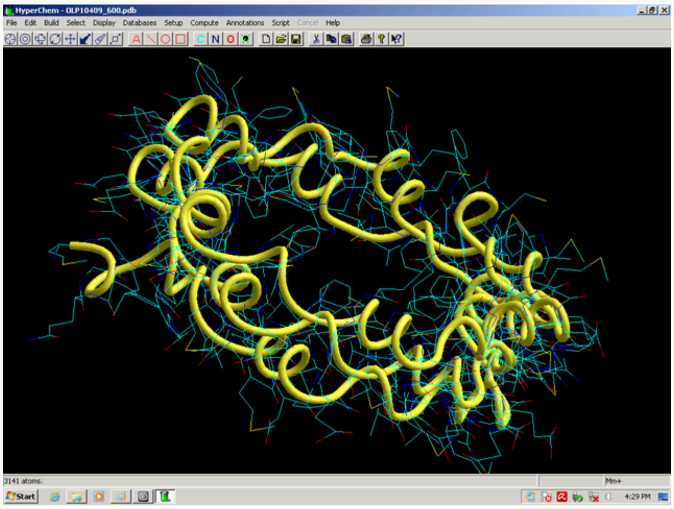
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3D-Genetic code

1992

Код	Остаток	Вариант
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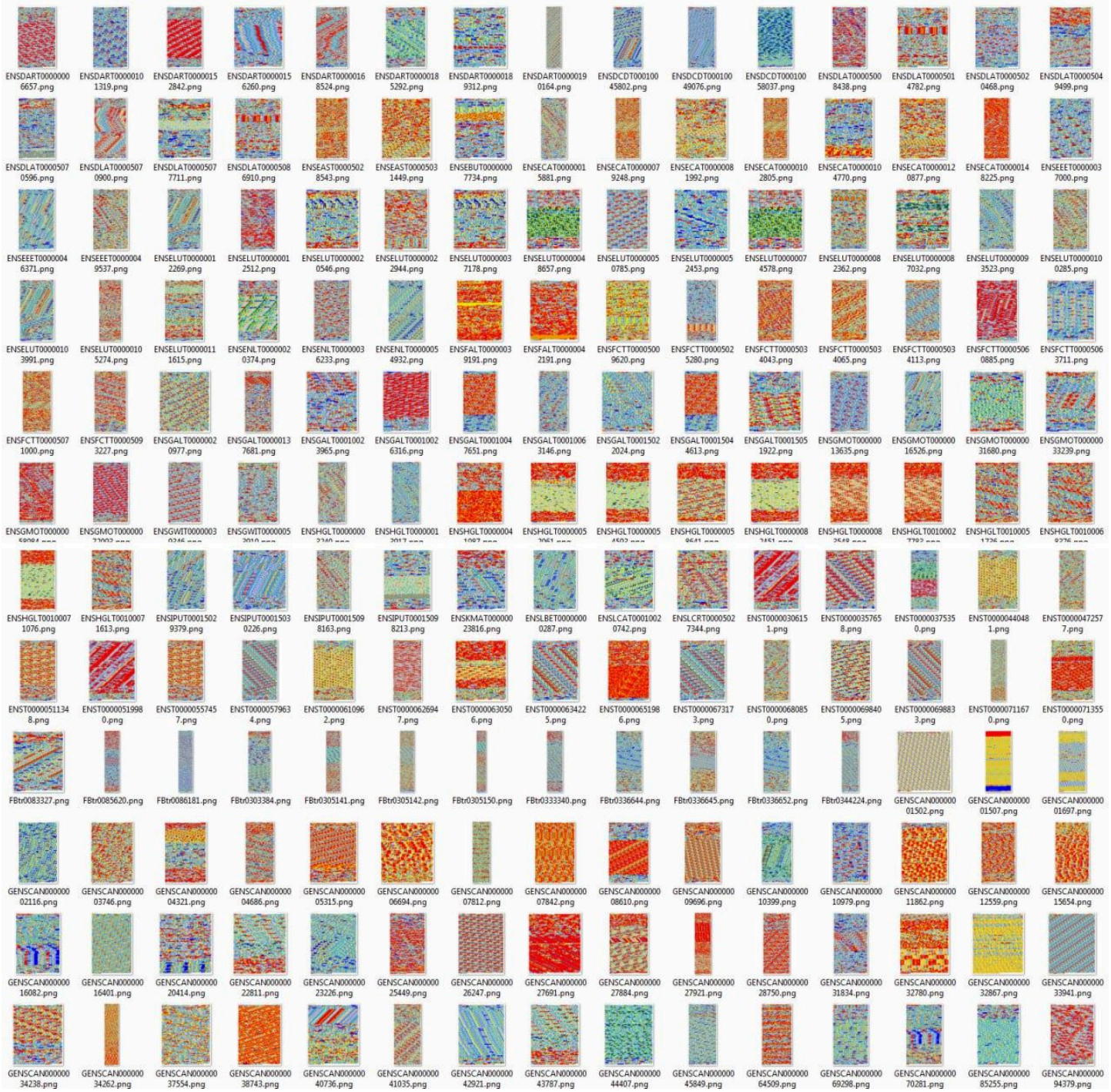
AAC	Asn	1
AAG	Lys	1
AAT	Asn	3
ACA	Thr	2
ACC	Thr	1
ACG	Thr	4
ACT	Thr	3
AGA	Arg	3
AGC	Ser	1
AGG	Arg	1
AGT	Ser	3
ATA	Ile	2
ATC	Ile	1
ATG	Met	1
ATT	Ile	3
CAA	Gln	3
CAC	His	1
CAG	Gln	1
CAT	His	3
CCA	Pro	2
CCC	Pro	1
CCG	Pro	4
CCT	Pro	3
CGA	Arg	2
CGC	Arg	1
CGG	Arg	4
CGT	Arg	3
CTA	Leu	2
CTC	Leu	1
CTG	Leu	4
CTT	Leu	3
GAA	Glu	3
GAC	Asp	1
GAG	Glu	1
GAT	Asp	3
GCA	Ala	2
GCC	Ala	1
GCG	Ala	4
GCT	Ala	3
GGA	Gly	2
GGC	Gly	1
GGG	Gly	4
GGT	Gly	3
GTA	Val	2
GTC	Val	1
GTG	Val	4
GTT	Val	3
TAA	TKD	-
TAC	Tyr	1
TAG	TKD	-
TAT	Tyr	3
TCA	Ser	2
TCC	Ser	1
TCG	Ser	4
TCT	Ser	3
TGA	TKD	-
TGC	Cys	1
TGG	Trp	1
TGT	Cys	3
TTA	Leu	3
TTC	Phe	1
TTG	Leu	1
TTT	Phe	3

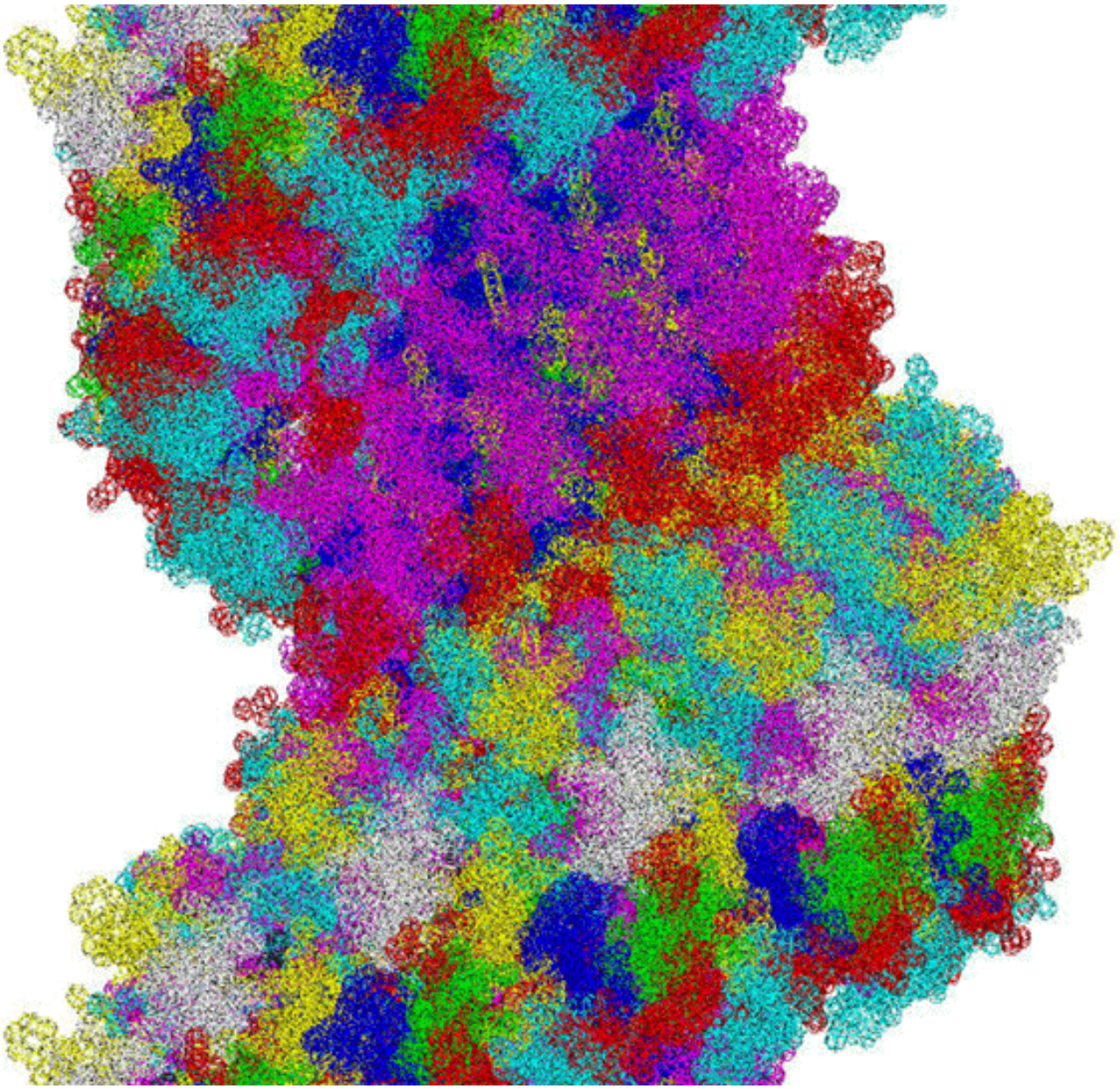
2019

№	DNA	ami	AMI	9var	Score
1	AAA	K	LYS	3	F#1
2	AAC	N	ASN	5	H1
3	AAG	K	LYS	5	F#1
4	AAT	N	ASN	3	H1
5	ACA	T	THR	2	E2
6	ACC	T	THR	5	E2
7	ACG	T	THR	5	E2
8	ACT	T	THR	3	E2
9	AGA	R	ARG	3	D1
10	AGC	S	SER	5	A2
11	AGG	R	ARG	5	D1
12	AGT	S	SER	3	A2
13	ATA	I	ILE	2	C2
14	ATC	I	ILE	5	C2
15	ATG	M	MET	6	G1
16	ATT	I	ILE	3	C2
17	CAA	Q	GLN	3	G1
18	CAC	H	HIS	5	A1
19	CAG	Q	GLN	5	G1
20	CAT	H	HIS	3	A1
21	CCA	P	PRO	92	A3
22	CCC	P	PRO	91	A3
23	CCG	P	PRO	95	A3
24	CCT	P	PRO	93	A3
25	CGA	R	ARG	2	D1
26	CGC	R	ARG	5	D1
27	CGG	R	ARG	5	D1
28	CGT	R	ARG	3	D1
29	CTA	L	LEU	2	H1
30	CTC	L	LEU	5	H1
31	CTG	L	LEU	5	H1
32	CTT	L	LEU	3	H1
33	GAA	E	GLU	3	G1
34	GAC	D	ASP	5	H1
35	GAG	E	GLU	5	G1
36	GAT	D	ASP	3	H1
37	GCA	A	ALA	2	A3
38	GCC	A	ALA	5	A3
39	GCG	A	ALA	5	A3
40	GCT	A	ALA	3	A3
41	GGA	G	GLY	2	G0
42	GGC	G	GLY	5	G0
43	GGG	G	GLY	5	G0
44	GGT	G	GLY	3	G0
45	GTA	V	VAL	2	G2
46	GTC	V	VAL	5	G2
47	GTG	V	VAL	5	G2
48	GTT	V	VAL	3	G2
49	TAA		TKD	0	
50	TAC	Y	TYR	5	D1
51	TAG		TKD	0	
52	TAT	Y	TYR	3	D1
53	TCA	S	SER	2	A2
54	TCC	S	SER	5	A2
55	TCG	S	SER	5	A2
56	TCT	S	SER	3	A2
57	TGA		TKD	0	
58	TGC	C	CYS	5	E2
59	TGG	W	TRP	5	D1
60	TGT	C	CYS	3	E2
61	TTA	L	LEU	3	H1
62	TTC	F	PHE	5	G1
63	TTG	L	LEU	5	H1
64	TTT	F	PHE	3	G1

The result of processing 62 genomes (approximately 6 million proteins) was obtained in an hour ‘2025



3D MODEL OF COLLAGEN



Software helices

Fractal helices

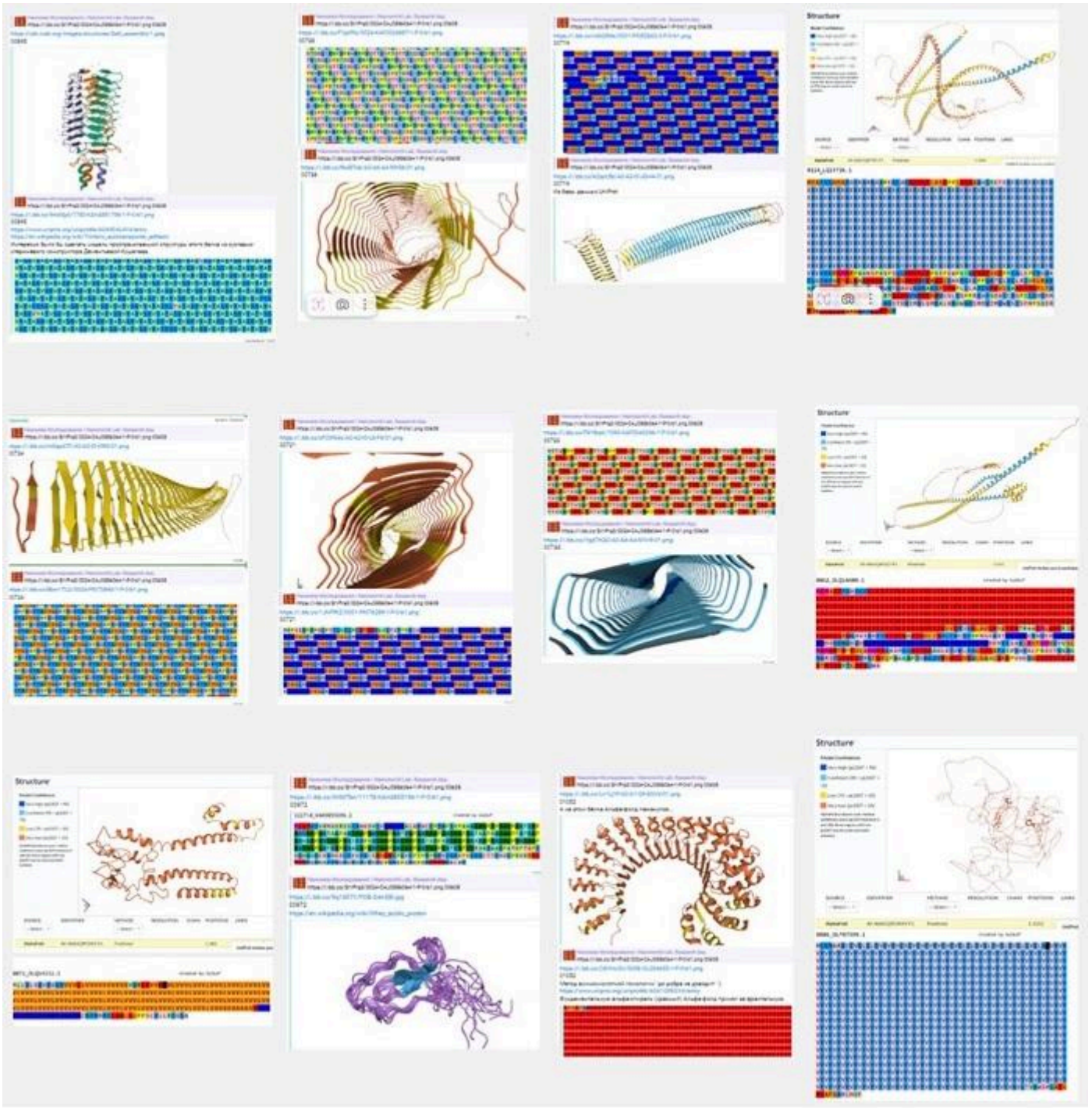
Q-helices

X-ray diffraction and 3D Genetic code

Examples of super-secondary structures

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

1



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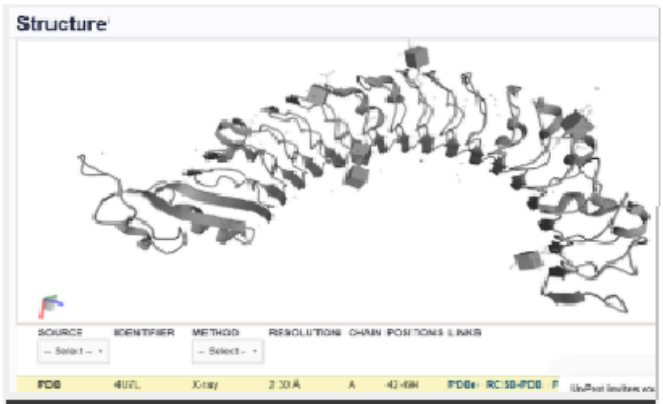
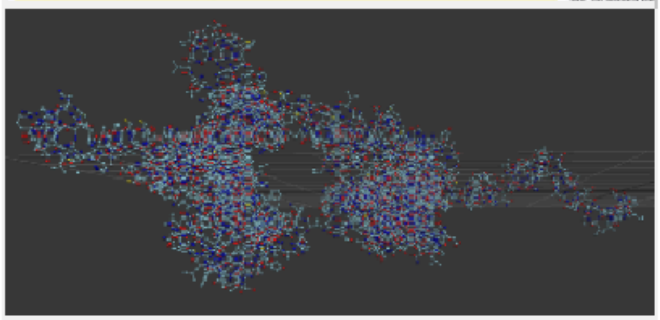
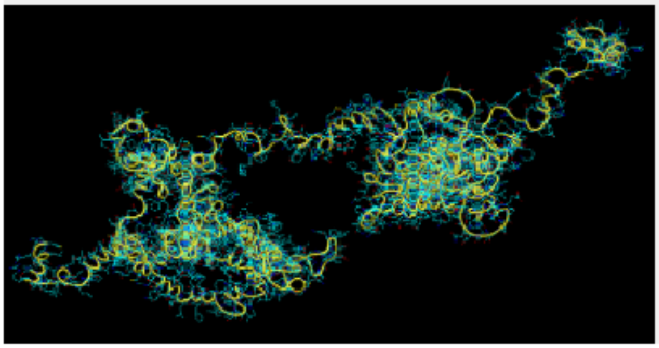

Structure
SOURCE
IDENTIFIER
METHOD
RESOLUTION
CHAIN
POSITIONS
LINKS





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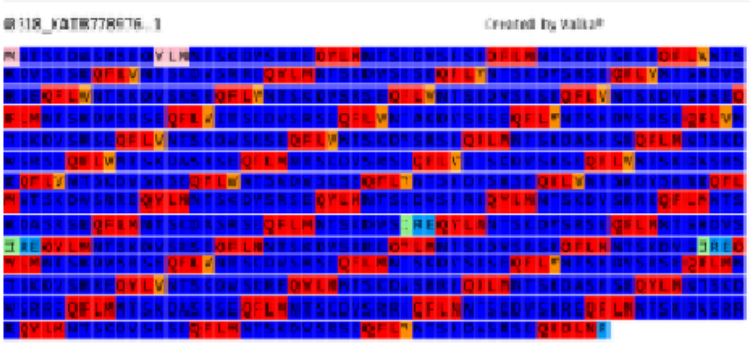
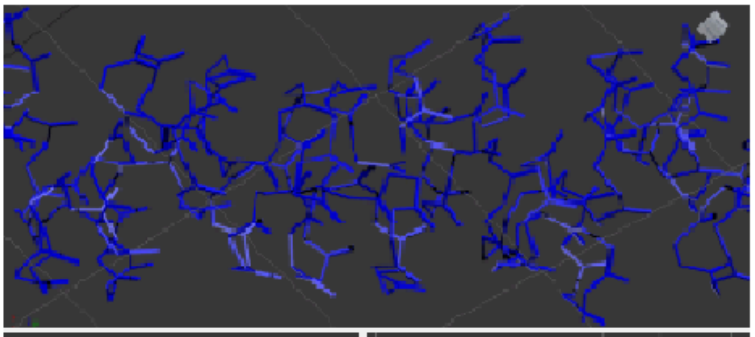
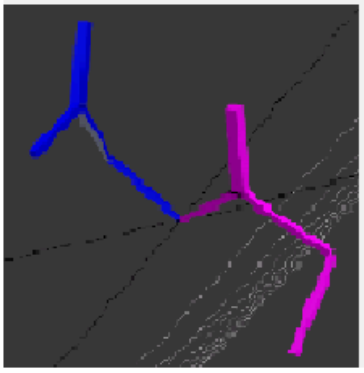
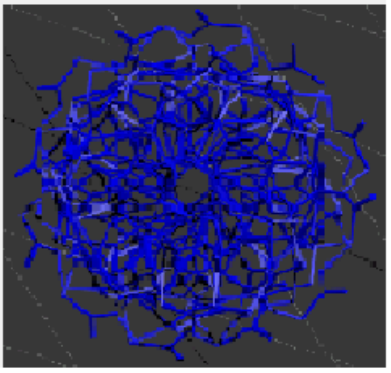


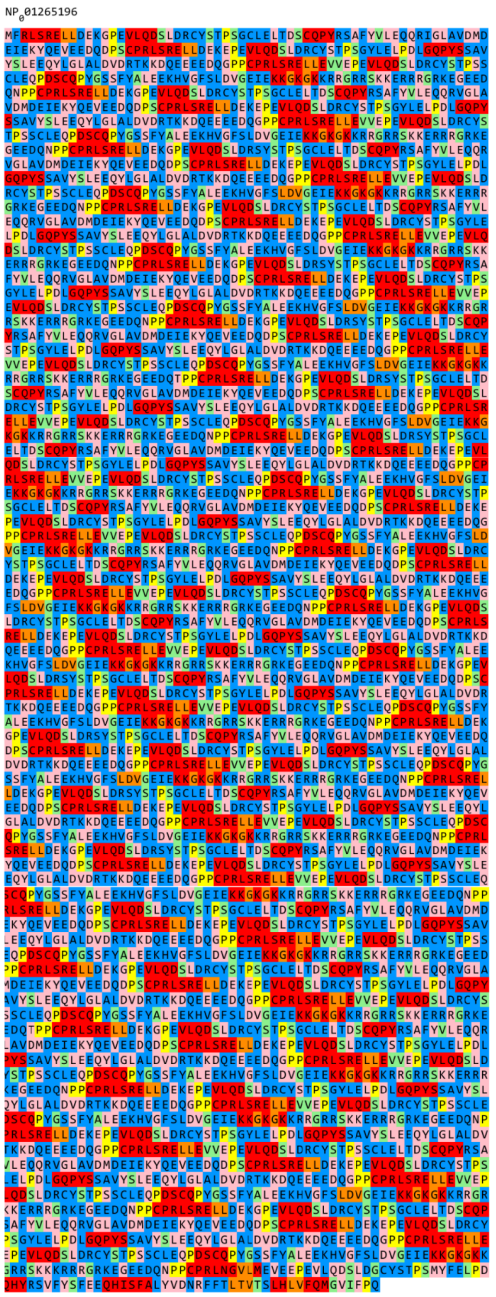


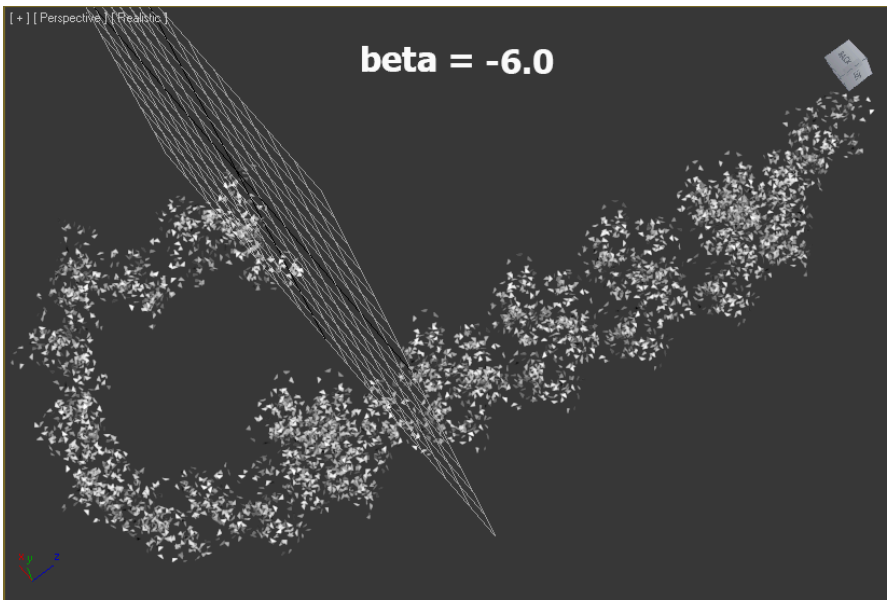




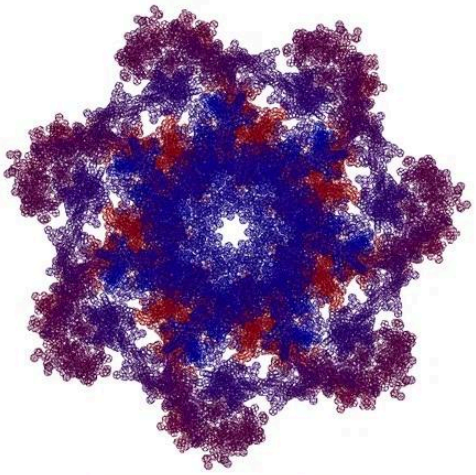
4

Super-secondary structure of the first chromosome (neuroblastoma) and its 3D image

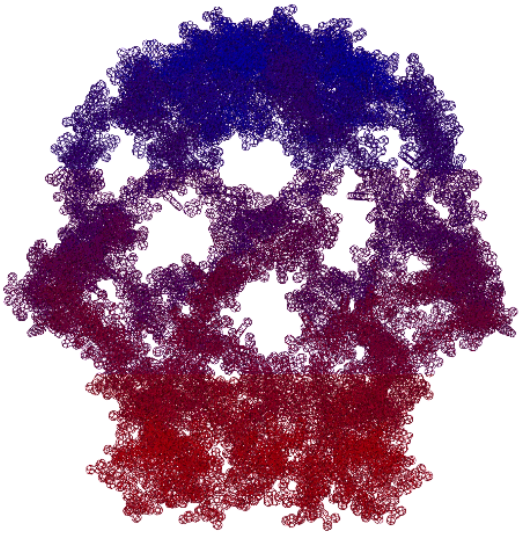


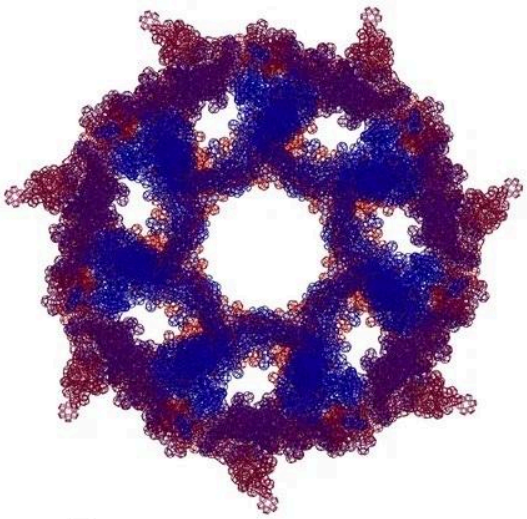


3D Picotech models of chaperones

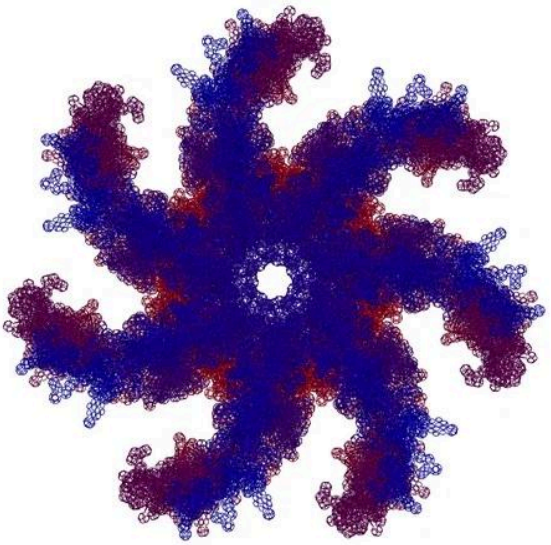


Пикотехнологическая модель
шаперона / chaperone A0KFQ4
Александр Кушелев, лаборатория Наномир 2010(C)

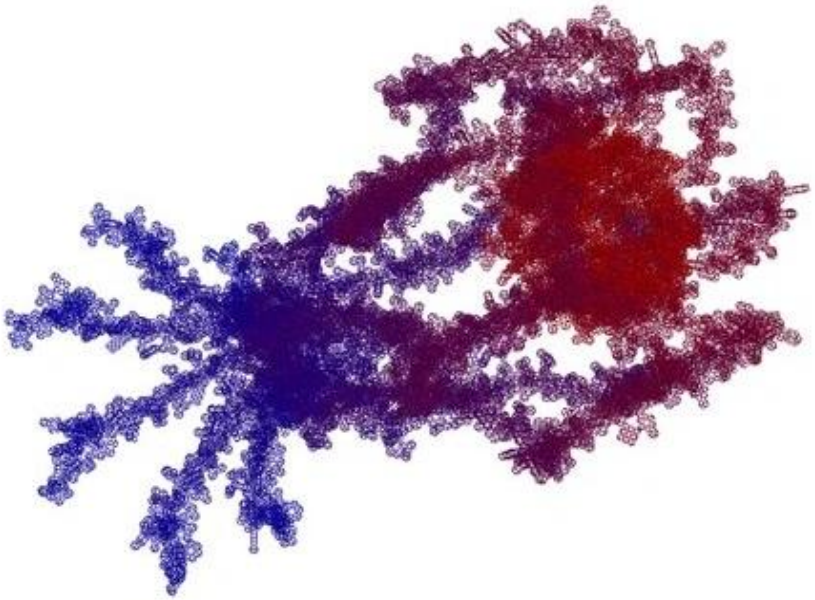




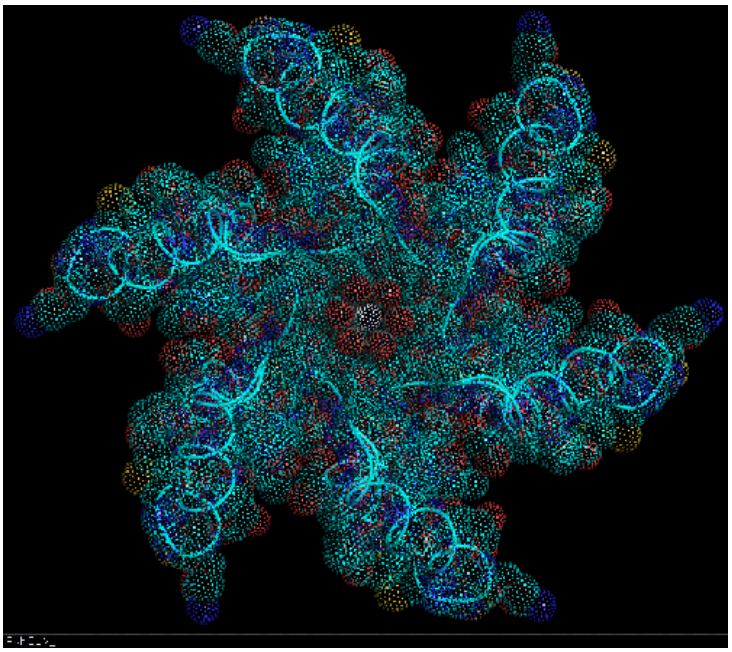
Пикотехнологическая модель
шаперона / chaperone B8GY03
Александр Кушелев, лаборатория Наномир (C)2010

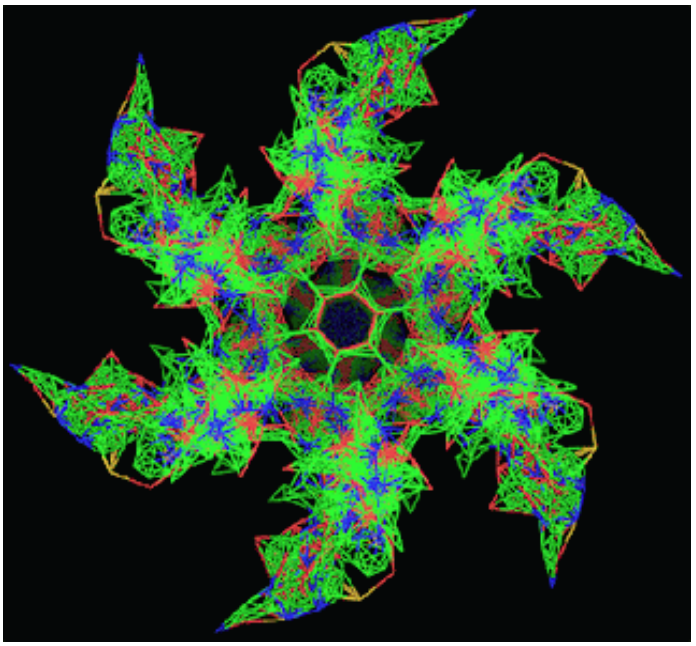


Пикотехнологическая модель
шаперона / chaperone B8H333
Александр Кушелев, лаборатория Наномир (C)2010

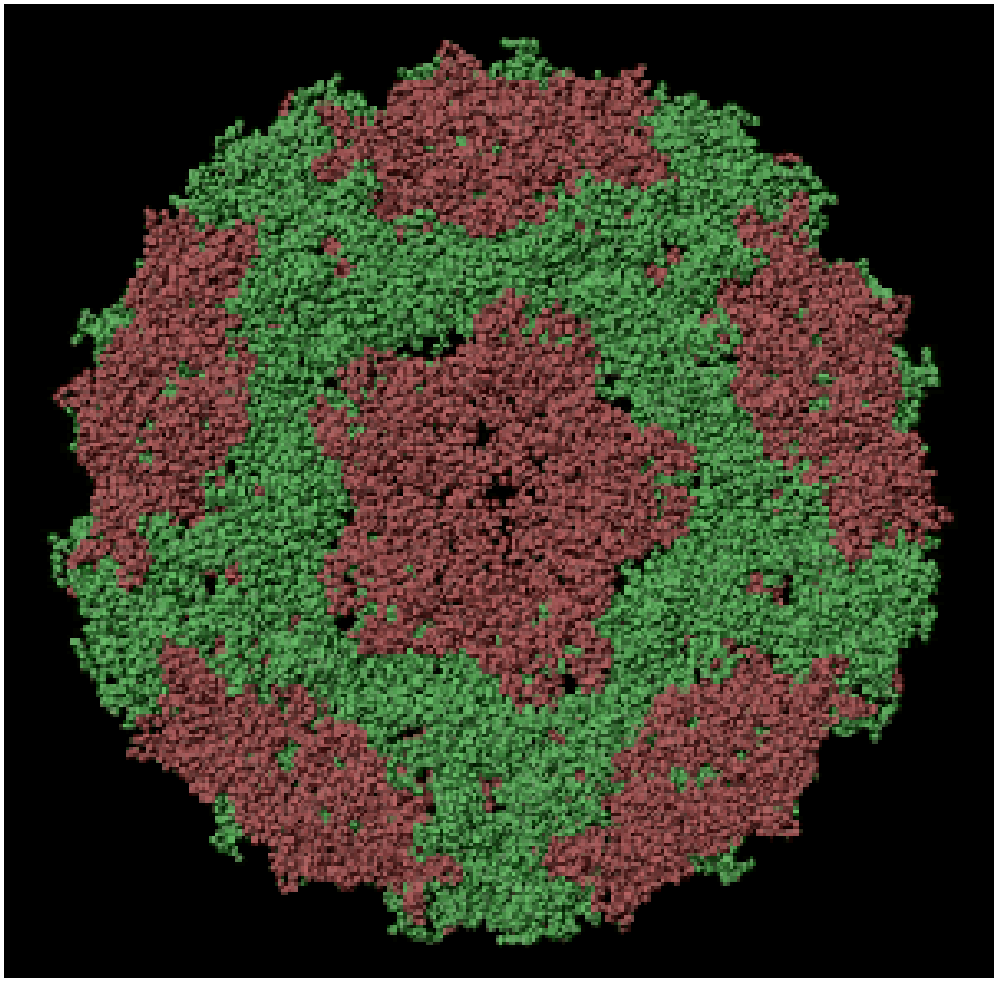


3D model of insulin molecule





3D model of the virus shell



How exactly does this service work?

You send us the coding nucleotide sequence (ideally - in fasta format) of the protein you're interested in via email: **nanoworld_laboratory@mail.ru**.

The key advantages are:

1. Reliability and accuracy of protein secondary structure.

Below the 3D genetic code table, you can see a transcript showing that each triplet of the genetic code corresponds to a specific structure.

2. The size of the protein is irrelevant.

3. The ability of the protein to crystallize is irrelevant.

4. The presence/absence of homologues is irrelevant.

5. The degree of study is irrelevant.

The disadvantages of this method include:

1. It does not account for protein post-processing after ribosome synthesis. The method only identifies the structure resulting from ribosome synthesis. If the protein is subsequently processed by chaperones or enzymes, meaning its secondary structure is altered (fragments are excised), I can only account for this manually by removing the enzyme-excised fragments of the amino acid sequence from the processing results. The client can do this themselves or provide me with data on the excised protein fragments.

2. Only secondary structures are automated. Tertiary structure can be automatically determined only for a narrow class of proteins, such as those consisting of a straight section of any type of helix. Therefore, only the secondary structure is guaranteed.

Tertiary structure and higher structures are "manual work," which can not only take longer but also does not guarantee its determination, for example, if the amino acid sequence contains prolines, which transform the rigid protein structure into a mechanism that can significantly change its conformation. In this case, the client can be provided with partial information on the tertiary and higher structures.

However, there is a high probability of determining both the tertiary and quaternary structures, as well as the protein dynamics

What exactly do clients receive when they contact us?

In what format are the results provided?

1.The client is guaranteed to receive a 2D Picotech diagram of the protein secondary structure.

2. With a certain degree of probability, the client will be able to obtain a 3D model from the joint-rod constructor.

3. If the 3D model is generated automatically or manually, the client will also be able to obtain a standard .pdb file with the coordinates of all protein atoms.

Unlike X-ray diffraction, the new technology has no "blind spots," meaning the PDB file will contain the coordinates of all atoms, from the first to the last amino acid residue.

Also, the client can obtain a dynamic protein model, which provides insight into how the protein performs its functions.

Additionally, clients can receive a consultation in which we demonstrate the correlation between different analysis methods and our data. For example, X-ray diffraction (XRD) or alpha-fold analysis reveal the presence of helical regions, but do not specify their type. We can demonstrate where these methods correctly identified the beginning and end of a helical region, and where they erred, and why. In particular, interpreters often mistake hybrid (alpha-310-) regions of proteins for beta sheets. Picotechnological models can help clients understand why this occurs.

Moreover, we can search for protein active sites using the natural frequencies of amino acid side chains 1, 2, 3 (pp. 29-42). If any are detected, we can attempt to model the mechanism of these active sites at the picomechanical level, i.e., with picometric accuracy.

Thank you very much for your lenient attention !