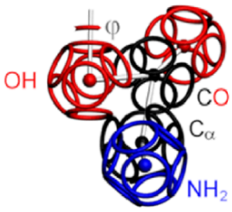
nanoworld_laboratory@mail.ru [3D Genetic Code]

Q-helices

PICOTECHNOLOGY 2D, 3D, 4D SOLUTIONS AND ARTICLES

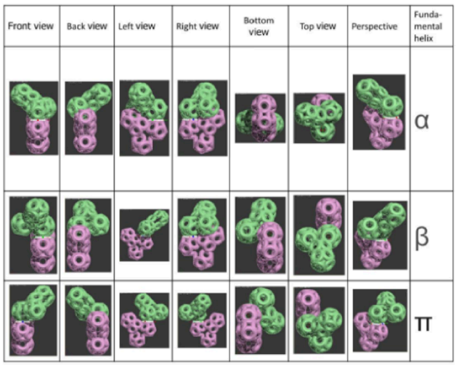
CONVENTIONAL DESIGNATIONS

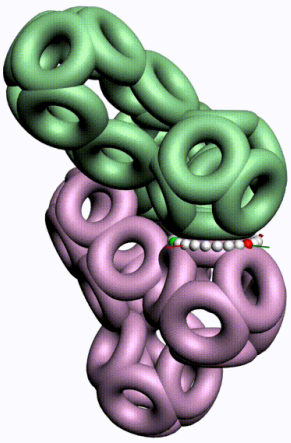
HOW TO READ 2D DIAGRAMS OF PICOTECHNOLOGY

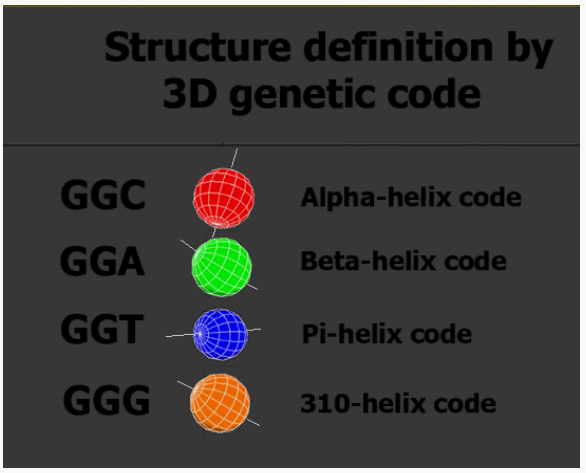


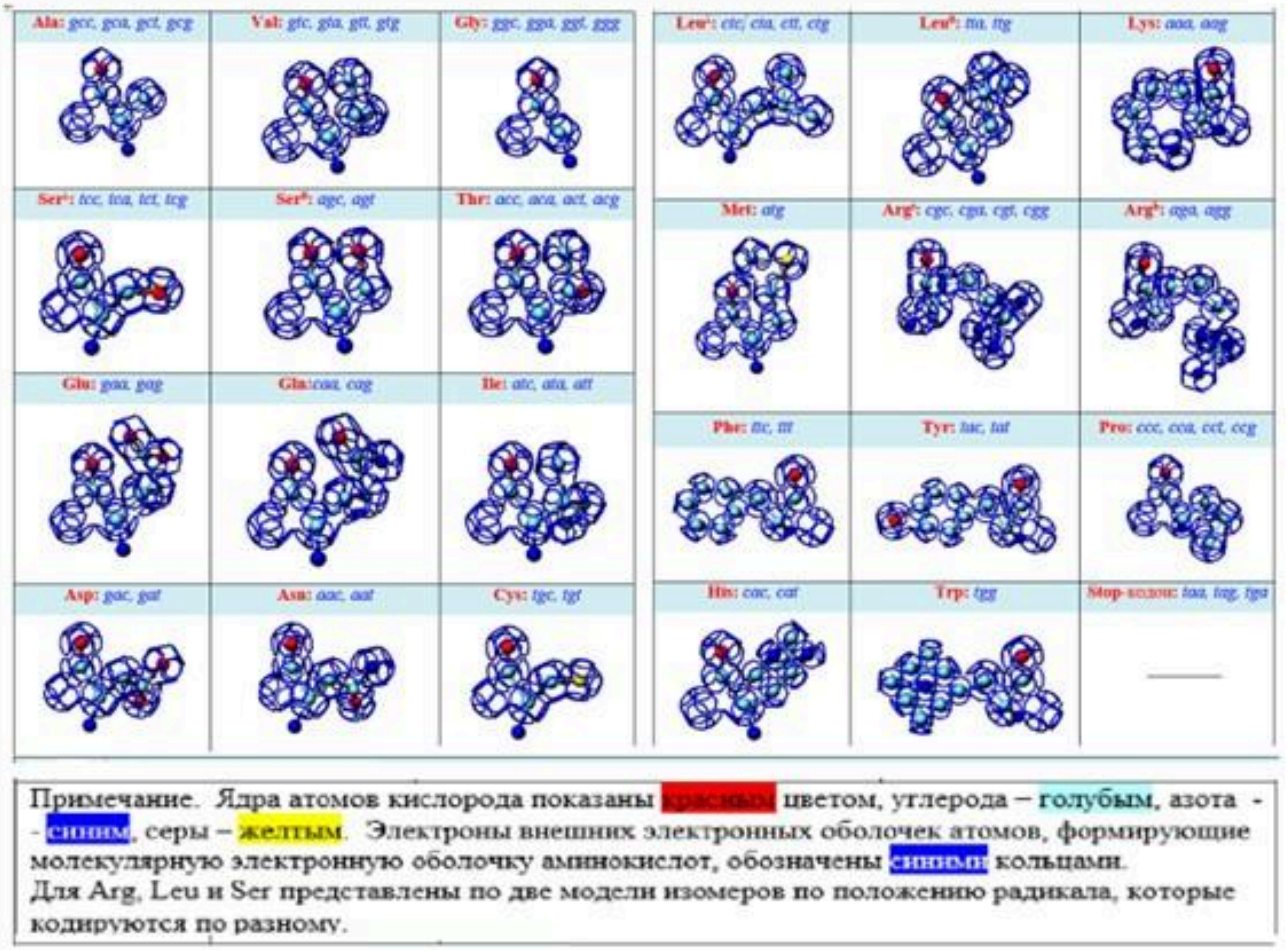
Structural template of amino acid residue

The third letter of the triplet controls the angle of rotation

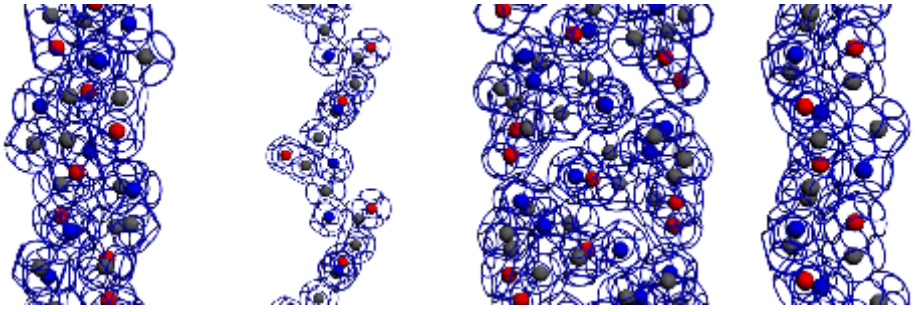








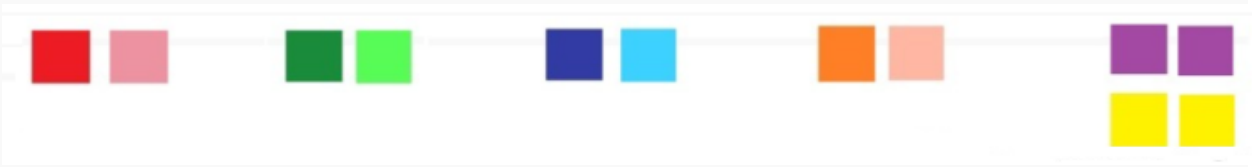
Примечание. Ядра атомов кислорода показаны красным цветом, углерода – голубым, азота - - синим, серы – желтым. Электроны внешних электронных оболочек атомов, формирующие молекулярную электронную оболочку аминокислот, обозначены синими кольцами. Для Arg, Leu и Ser представлены по две модели изомеров по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



Alpha-helix Beta-helix Pi-helix 310-helix

The pitch of the methionine helix is approximately 25% larger than that of a standard alpha helix

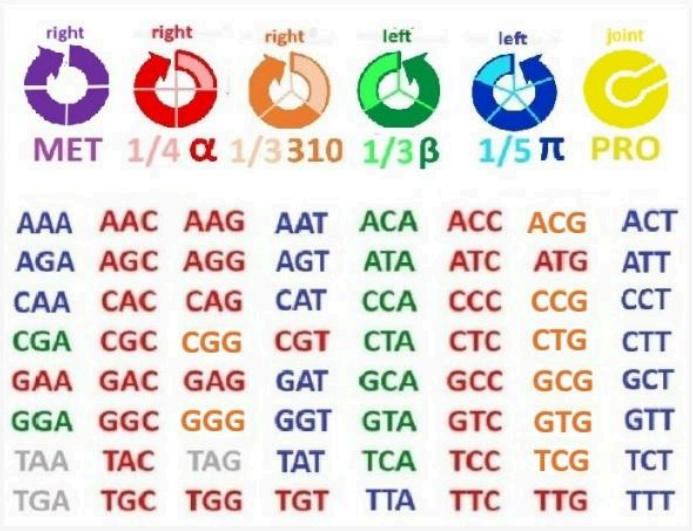
Methionine helix

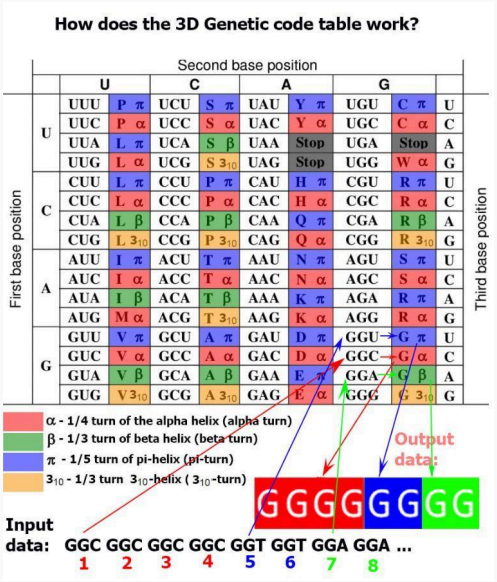


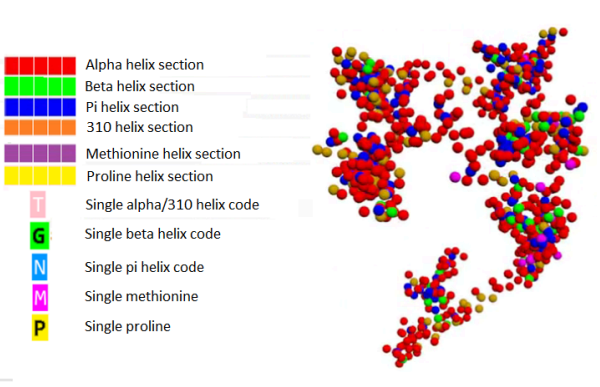
One or more [prolines](#) in a raw

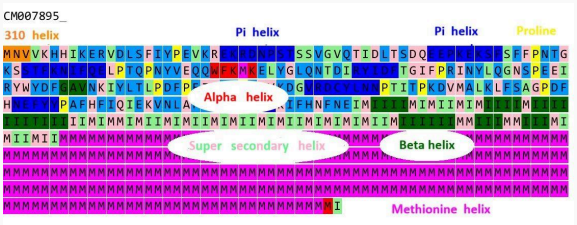
COMPACT 2D PICOTECHNOLOGY DIAGRAM

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.







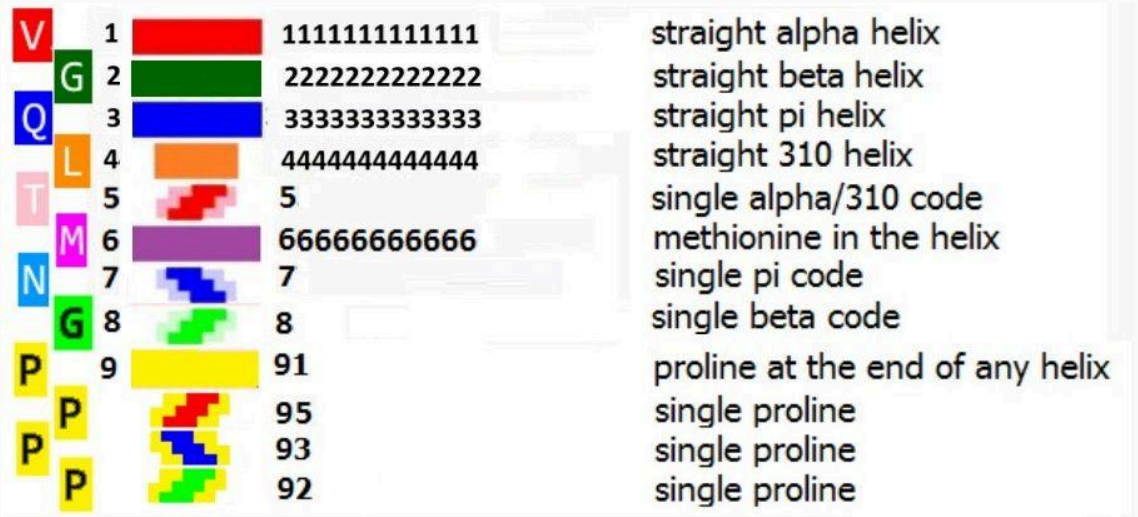


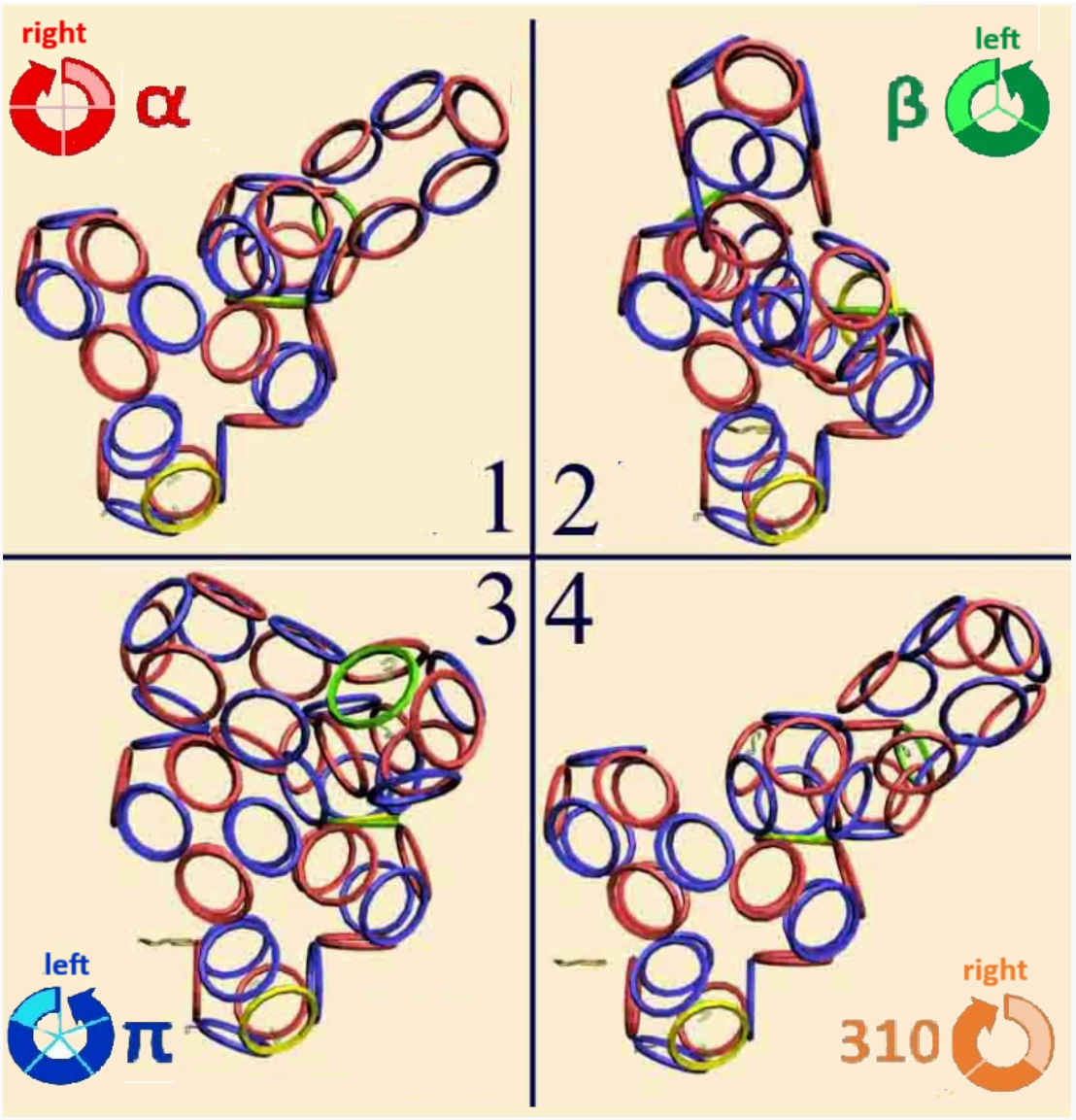
FULL (EXPANDED) DIAGRAM

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)

Composition code Version 9





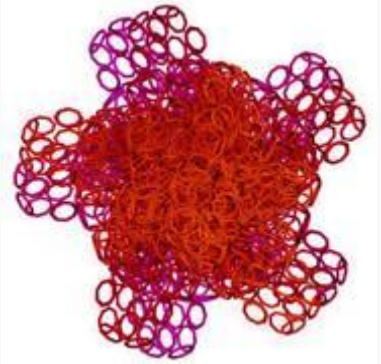
- coil of alpha helix (red) - 4 amino acid residues with the code "1",
- coil of beta-helix (green) - 3 amino acid residues with the code "2",
- 310-heix coil (orange) - 3 amino acid residues with the code "4",
- coil of pi-helix (blue) - 5 amino acid residues with the code "3"
- light gray - stop codon

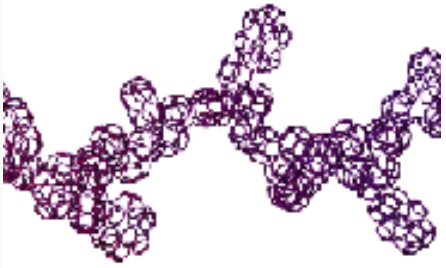
Alpha helix - right,
Pi helix - left,
Beta helix - left,
310 helix - right.

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
44444444444444444444 - straight 310-spiral

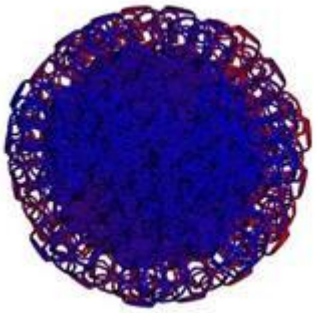
3333333333333333333 - straight pi-helix
2222222222222222222 - direct beta helix
232323 - software 23-helix
141414 - software 14-helix

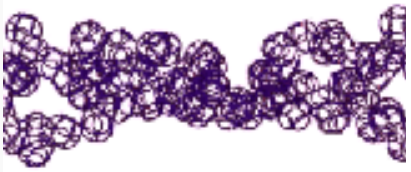
n 3212-helix



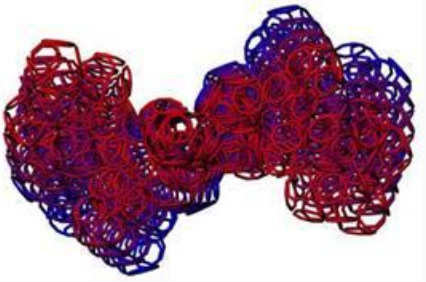


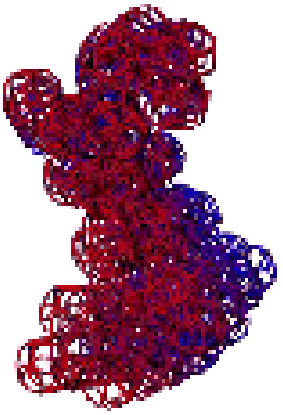
n 233 helix





n 13323 helix





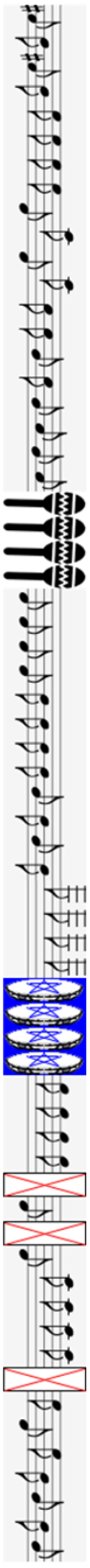
3D-Genetic code

1992

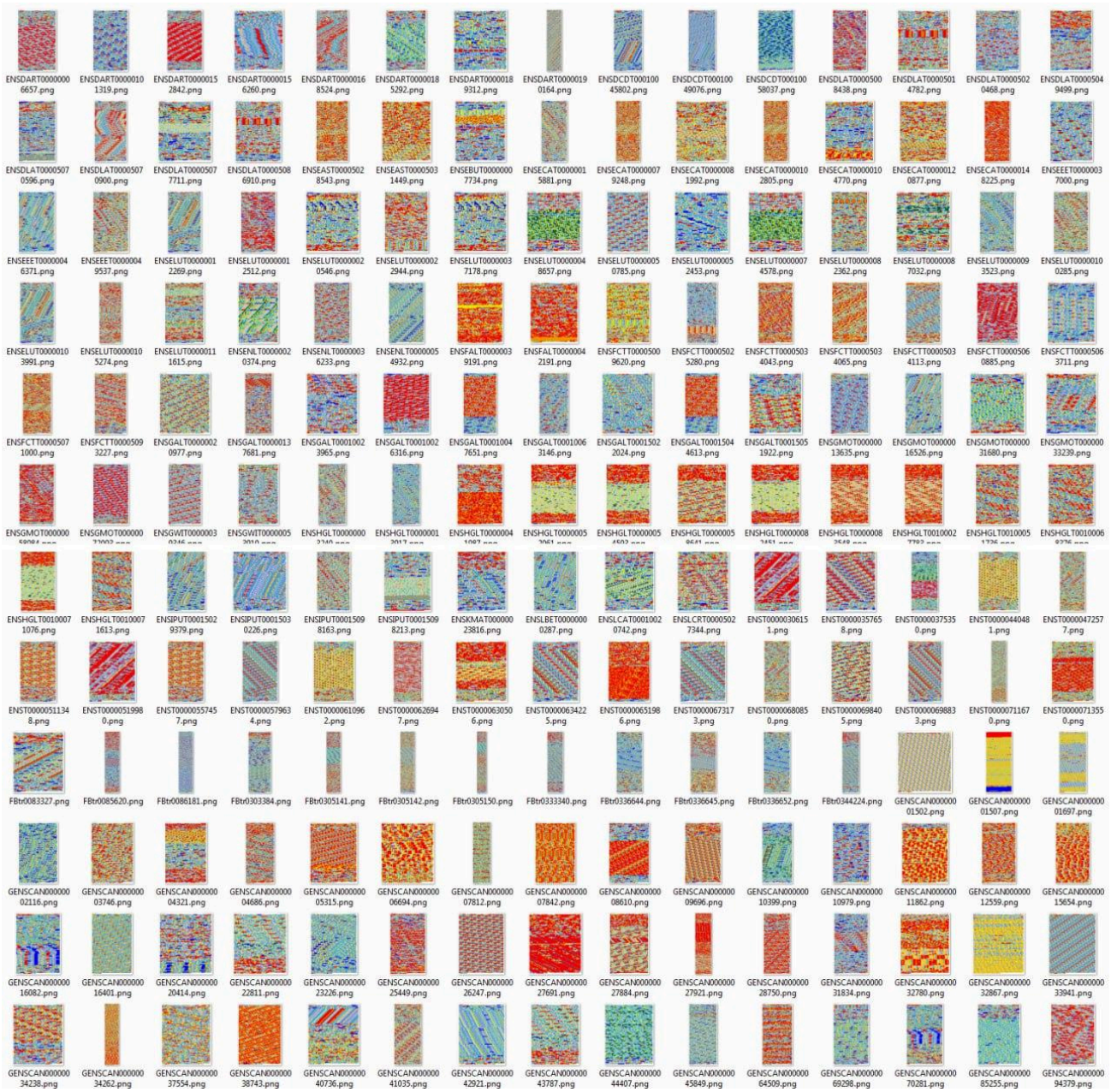
Код	Остаток	Вариант
AAA	Lys	3
AAC	Asn	1
AAG	Lys	1
AAT	Asn	3
ACA	Thr	2
ACC	Thr	1
ACG	Thr	4
ACT	Thr	3
AGA	Arg	3
AGC	Ser	1
AGG	Arg	1
AGT	Ser	3
ATA	Ile	2
ATC	Ile	1
ATG	Met	1
ATT	Ile	3
CAA	Gln	3
CAC	His	1
CAG	Gln	1
CAT	His	3
CCA	Pro	2
CCC	Pro	1
CCG	Pro	4
CCT	Pro	3
CGA	Arg	2
CGC	Arg	1
CGG	Arg	4
CGT	Arg	3
CTA	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

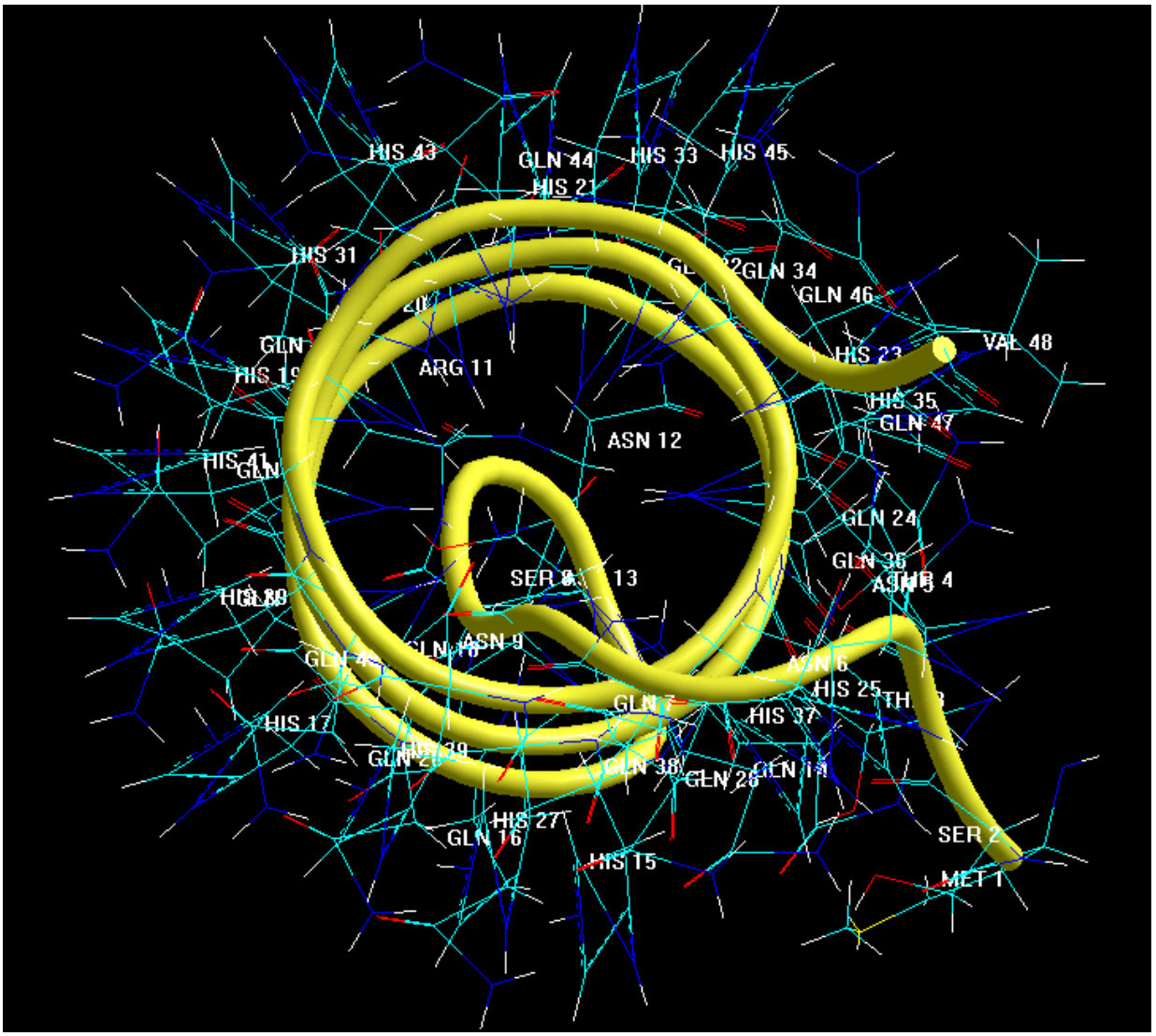
№	DNA	ami	AMI	9var	Score
1	AAA	K	LYS	3	F#1
2	AAC	N	ASN	5	H1
3	AAG	K	LYS	5	F#1
4	AAT	N	ASN	3	H1
5	ACA	T	THR	2	E2
6	ACC	T	THR	5	E2
7	ACG	T	THR	5	E2
8	ACT	T	THR	3	E2
9	AGA	R	ARG	3	D1
10	AGC	S	SER	5	A2
11	AGG	R	ARG	5	D1
12	AGT	S	SER	3	A2
13	ATA	I	ILE	2	C2
14	ATC	I	ILE	5	C2
15	ATG	M	MET	6	G1
16	ATT	I	ILE	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



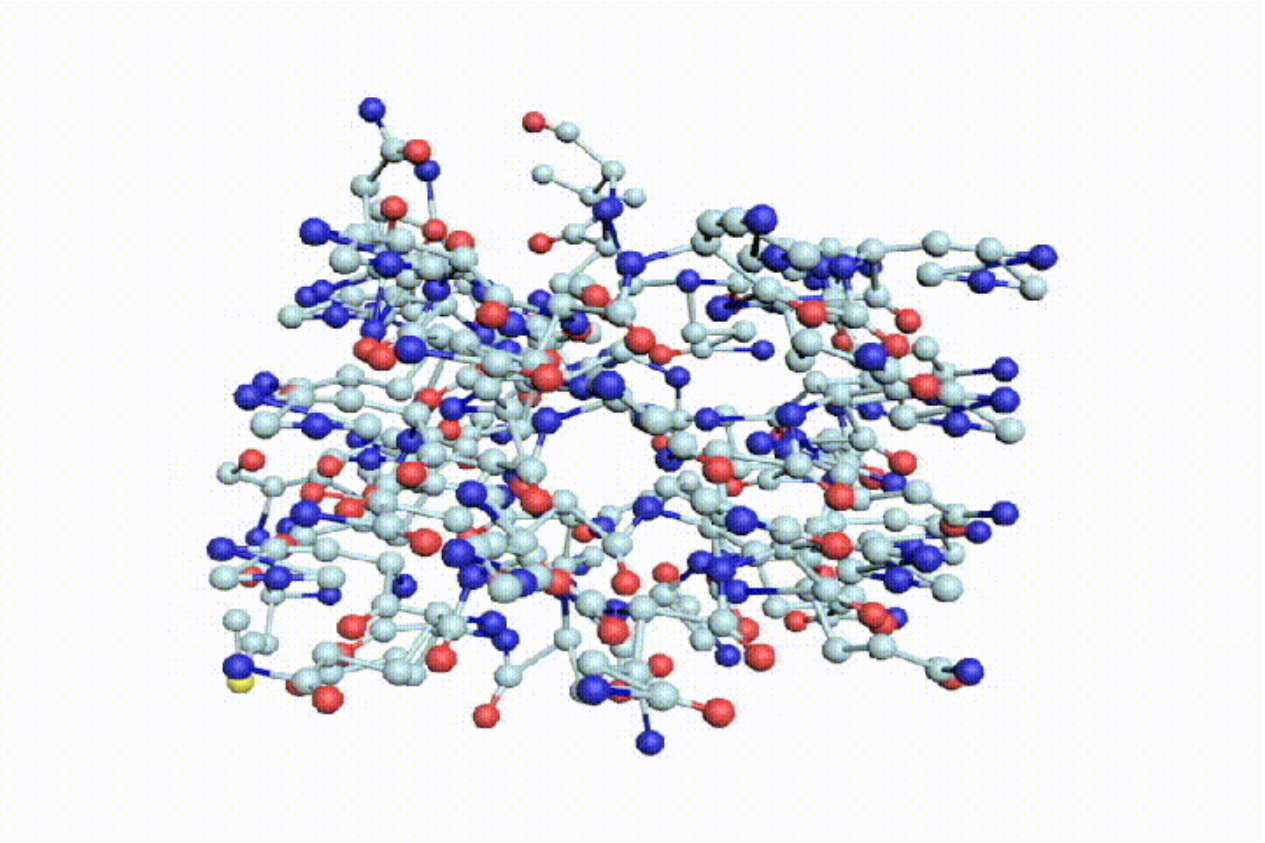
The result of processing 62 genomes (approximately 6 million proteins) was obtained in an hour ‘2025



DATA



Secondary structure of the protein Q-helix 12 amino acid residues per coil



JMNQ01000007 92480 bp DNA linear BCT 06-MAY-2014

№	DNA	Lost	AMI	4var	6var	5clm	6clm
1	atg	M	Met	1	5	G1	
2	agc	S	Ser	1	5	A2	
3	act	T	Thr	3	3	E2	
4	act	T	Thr	3	3	E2	
5	aat	N	Asn	3	3	H1	
6	aat	N	Asn	3	3	H1	
7	caa	Q	Gln	3	3	G1	
8	agc	S	Ser	1	5	A2	
9	aat	N	Asn	3	3	H1	
10	caa	Q	Gln	3	3	G1	
11	cgc	R	Arg	1	5	D1	
12	aac	N	Asn	1	5	H1	
13	aat	N	Asn	3	3	H1	
14	cag	Q	Gln	1	5	G1	
15	cac	H	His	1	5	A1	
16	caa	Q	Gln	3	3	G1	
17	cac	H	His	1	5	A1	
18	caa	Q	Gln	3	3	G1	
19	cac	H	His	1	5	A1	
20	caa	Q	Gln	3	3	G1	
21	cac	H	His	1	5	A1	
22	caa	Q	Gln	3	3	G1	
23	cac	H	His	1	5	A1	
24	caa	Q	Gln	3	3	G1	
25	cac	H	His	1	5	A1	
26	caa	Q	Gln	3	3	G1	
27	cac	H	His	1	5	A1	
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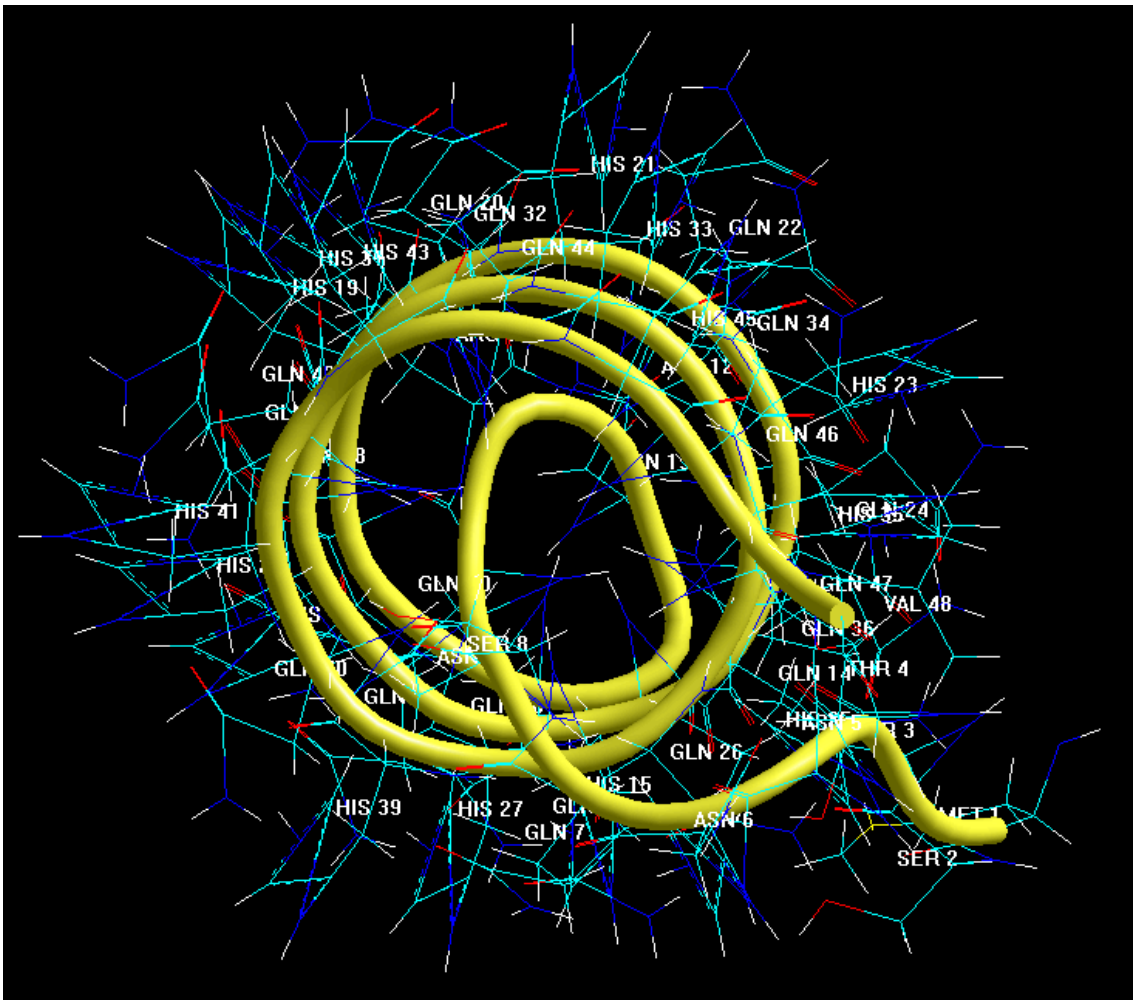
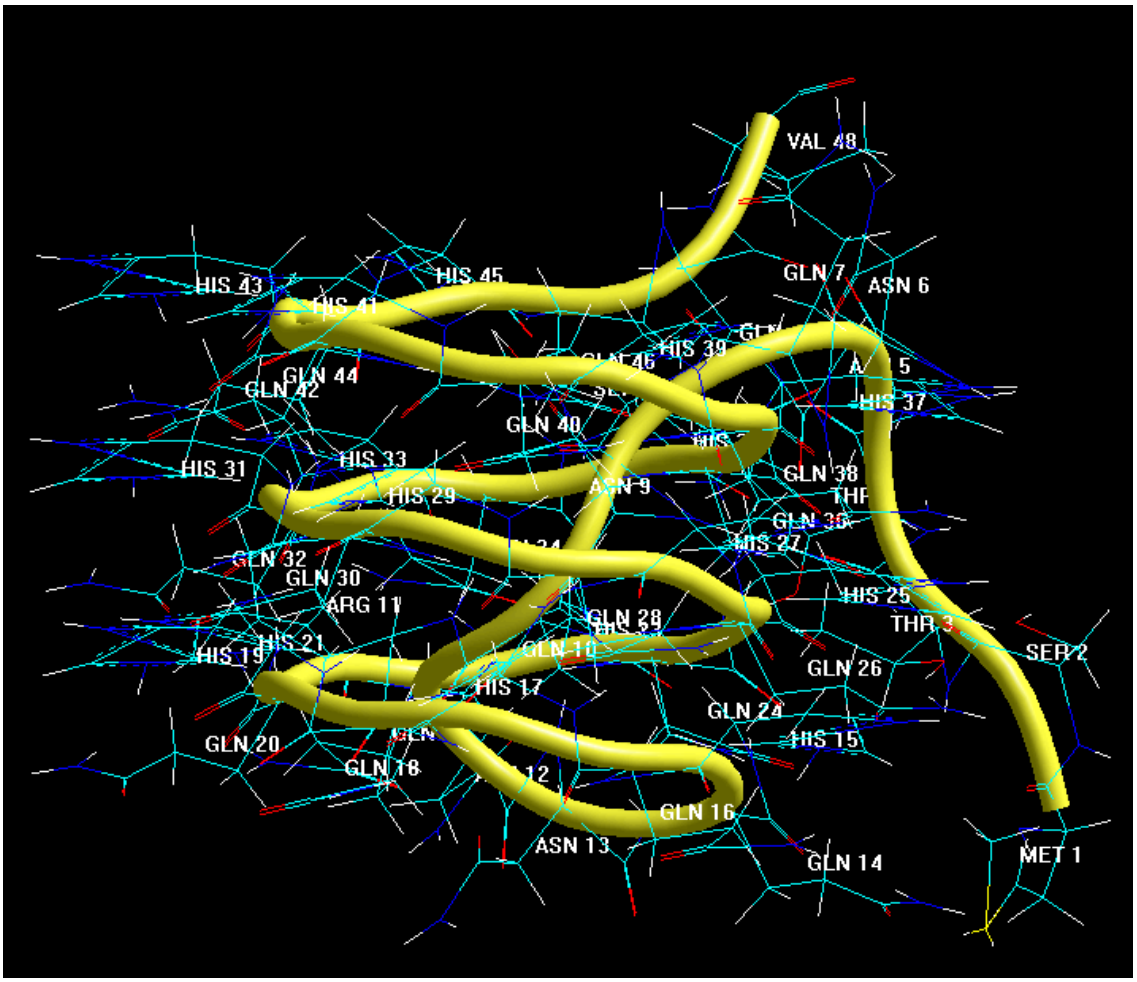
41	cac	H	His	1	5	A1	
42	caa	Q	Gln	3	3	G1	
43	cac	H	His	1	5	A1	
44	caa	Q	Gln	3	3	G1	
45	cac	H	His	1	5	A1	
46	caa	Q	Gln	3	3	G1	
47	caa	Q	Gln	3	3	G1	
48	gtg	V	Val	4	5	G2	
49	tag		TKD	0	0		


HIS 21
GLN 20
GLN 32
HIS 33
GLN 22
GLN 44
HIS 43
HIS 19
GLN 34
HIS 23
GLN 46
HIS 41
GLN 47
VAL 48
SER 8
GLN 14
THR 4
GLN 26
HIS 15
HIS 39
HIS 27
GLN 7
ASN 6
SER 2


VAL 48
HIS 43
HIS 45
GLN 7
ASN 6
HIS 41
HIS 39
GLN 44
GLN 42
HIS 37
GLN 40
HIS 31
HIS 33
GLN 38
HIS 29
GLN 36
HIS 27
GLN 32
GLN 30
HIS 25
ARG 11
THR 3
HIS 21
HIS 19
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HIS 17
GLN 24
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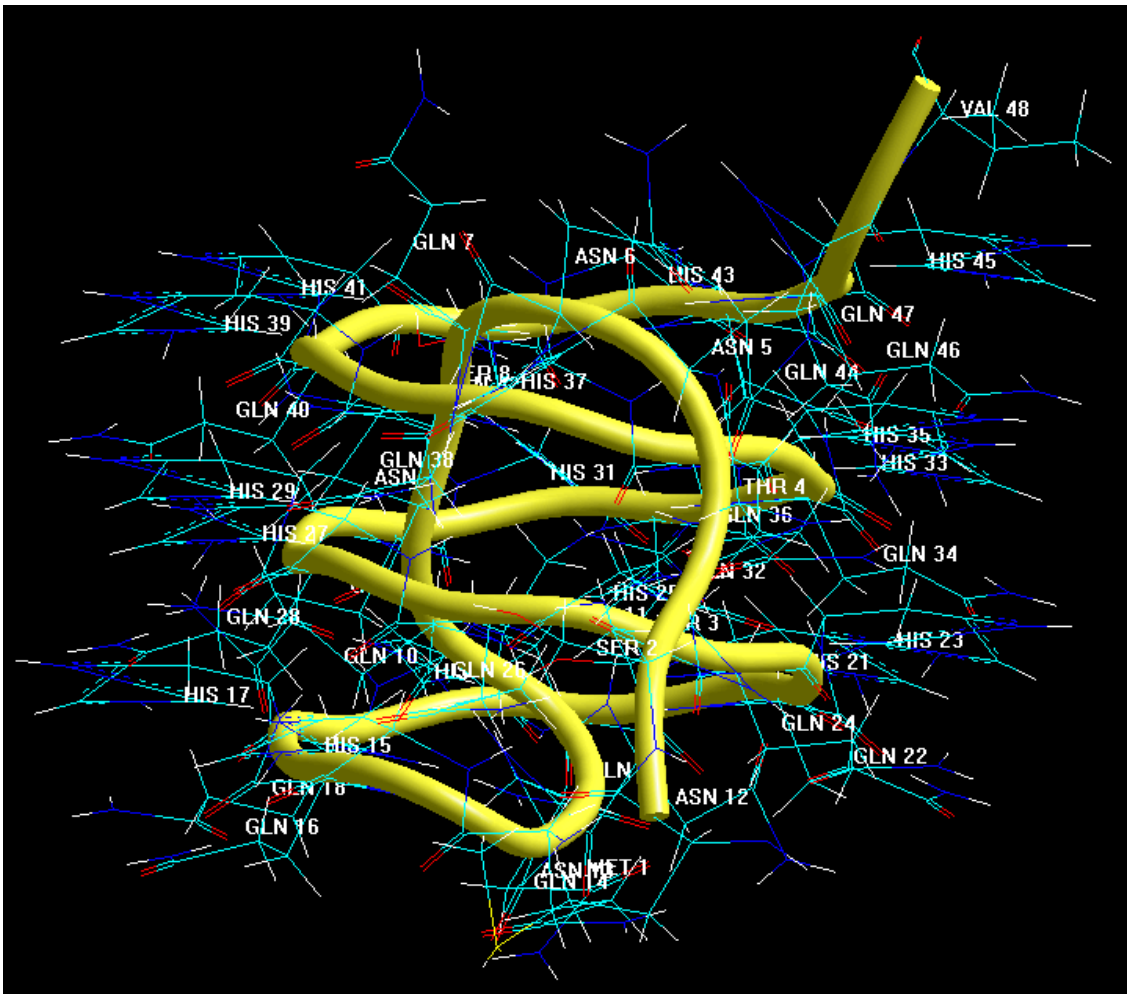
HIS 15
GLN 18
GLN 16
ASN 13
GLN 14
MET 1



Approximately 32 amino acid residues per 11/4 coil turn. 128 amino asid residues for 11 turns. 11.64 amino acid residues per turn.

Kushelev: Let's see how the 3D model of a protein molecule with a Q-helix of 100 amino acid residues will look (from 14 to 114).

This is its 2D structure and assembly notes:

ENA|EFE54881|

№	DNA	ami	AMI	4var	6var	Score	Size
1	GTG	V	VAL	4	5	G2	
2	CTT	L	LEU	3	3	H1	
3	GTA	V	VAL	2	2	G2	
4	TTT	F	PHE	3	3	G1	
5	TAT	Y	TYR	3	3	D1	
6	ACA	T	THR	2	2	E2	
7	GCA	A	ALA	2	2	A3	
8	CTG	L	LEU	4	5	H1	
9	TTT	F	PHE	3	3	G1	
10	TTT	F	PHE	3	3	G1	
11	ATT	I	ILE	3	3	C2	
12	TCT	S	SER	3	3	A2	
13	GGT	G	GLY	3	3	G0	
14	CAA	Q	GLN	3	3	G1	
15	CAC	H	HIS	1	5	A1	
16	CAA	Q	GLN	3	3	G1	
17	CAC	H	HIS	1	5	A1	
18	CAA	Q	GLN	3	3	G1	
19	CAC	H	HIS	1	5	A1	
20	CAA	Q	GLN	3	3	G1	
21	CAC	H	HIS	1	5	A1	
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29	CAC	H	HIS	1	5	A1	
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31	CAC	H	HIS	1	5	A1	
32	CAA	Q	GLN	3	3	G1	
33	CAC	H	HIS	1	5	A1	
34	CAA	Q	GLN	3	3	G1	
35	CAC	H	HIS	1	5	A1	
36	CAA	Q	GLN	3	3	G1	
37	CAC	H	HIS	1	5	A1	
38	CAA	Q	GLN	3	3	G1	
39	CAC	H	HIS	1	5	A1	
40	CAA	Q	GLN	3	3	G1	
41	CAC	H	HIS	1	5	A1	
42	CAA	Q	GLN	3	3	G1	
43	CAC	H	HIS	1	5	A1	
44	CAA	Q	GLN	3	3	G1	
45	CAC	H	HIS	1	5	A1	
46	CAA	Q	GLN	3	3	G1	
47	CAC	H	HIS	1	5	A1	
48	CAA	Q	GLN	3	3	G1	
49	CAC	H	HIS	1	5	A1	
50	CAA	Q	GLN	3	3	G1	
51	CAC	H	HIS	1	5	A1	
52	CAA	Q	GLN	3	3	G1	
53	CAC	H	HIS	1	5	A1	
54	CAA	Q	GLN	3	3	G1	
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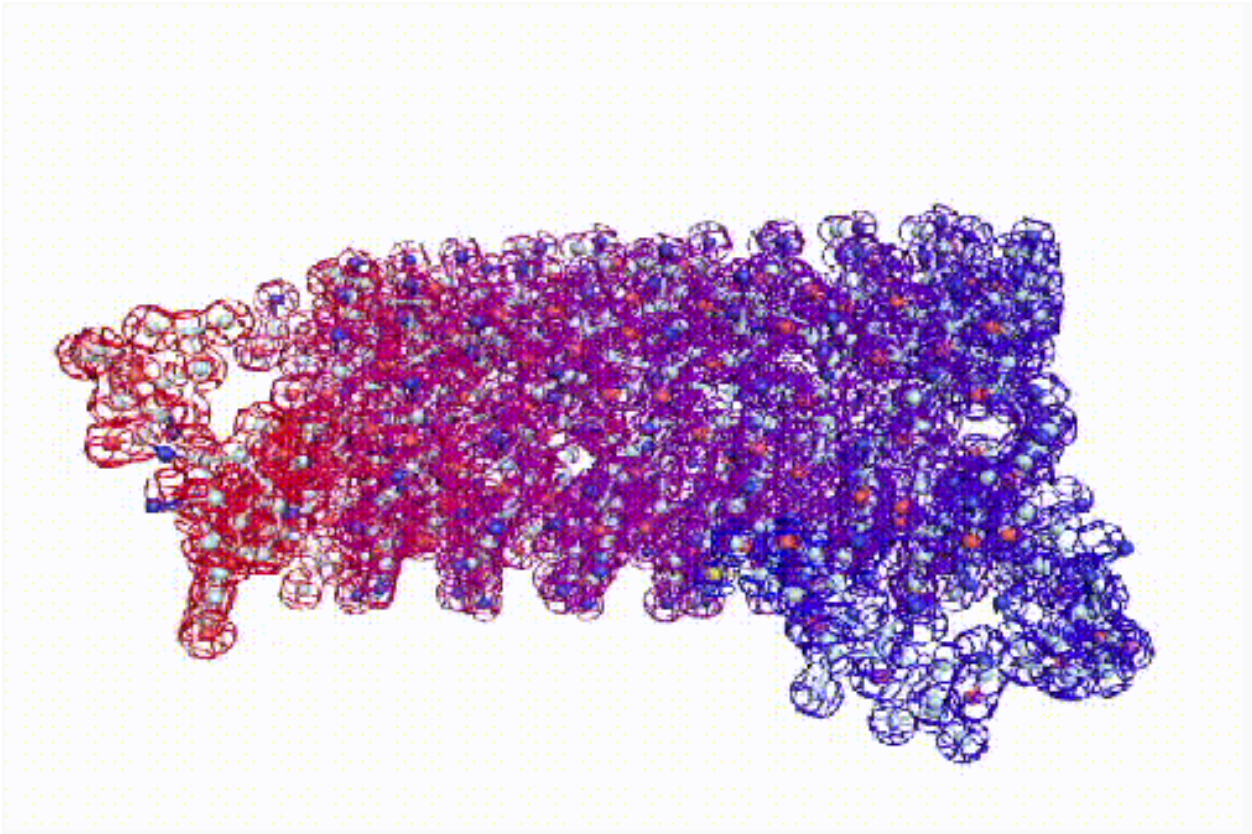

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All these files can be viewed in the folder: https://cloud.mail.ru/public/3urL/EnXBJyzct

34343(Q-helix) и 14141(QVQVQ-helix) in

Thioalkalivibrio nitratireducens DSM 14787 protein

http://www.ebi.ac.uk/ena/data/view/AGA34115&display=text

>ENA|AGA34115|AGA34115.2 Thioalkalivibrio nitratireducens DSM 14787 hypothetical protein

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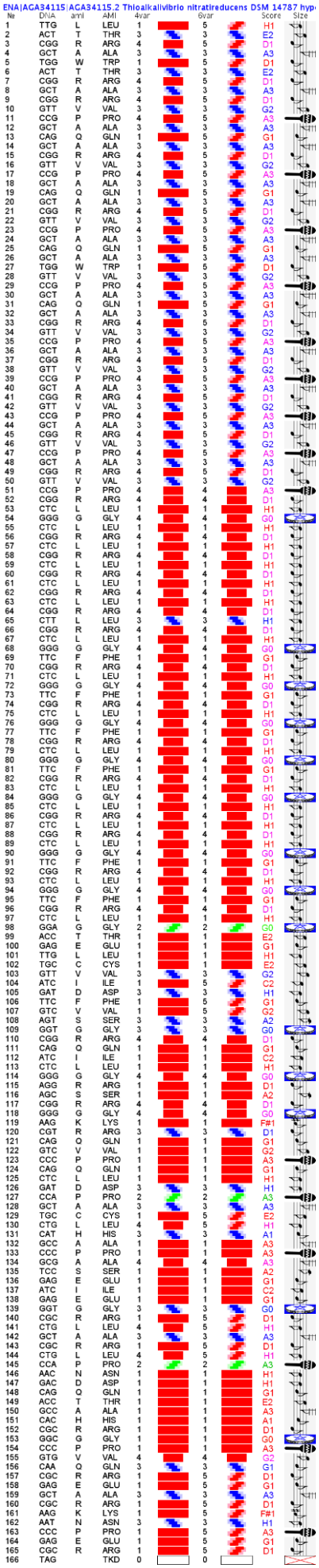
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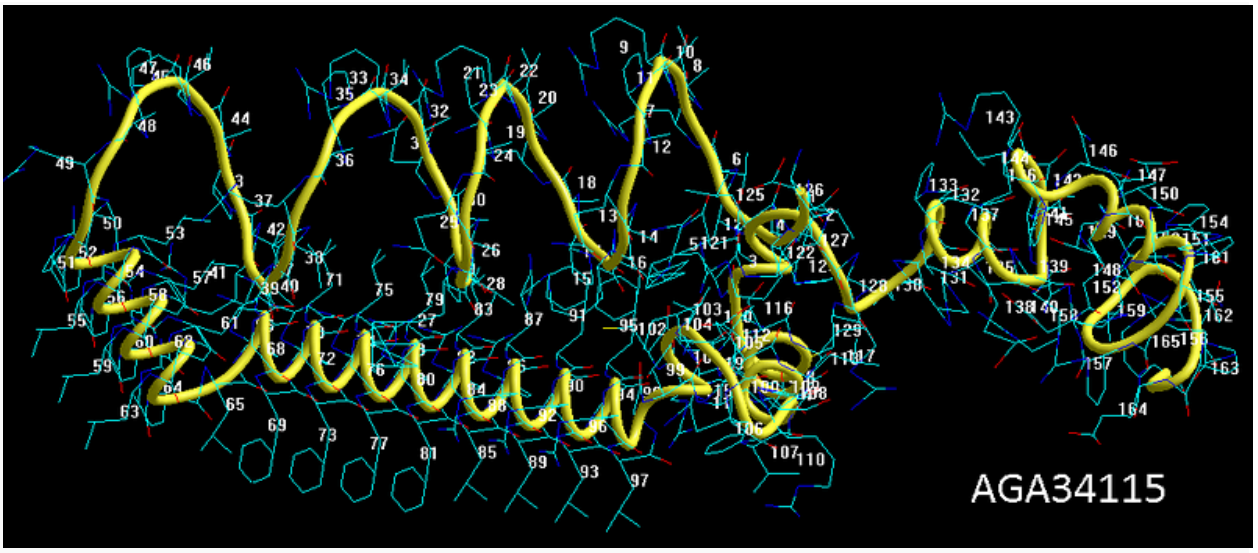
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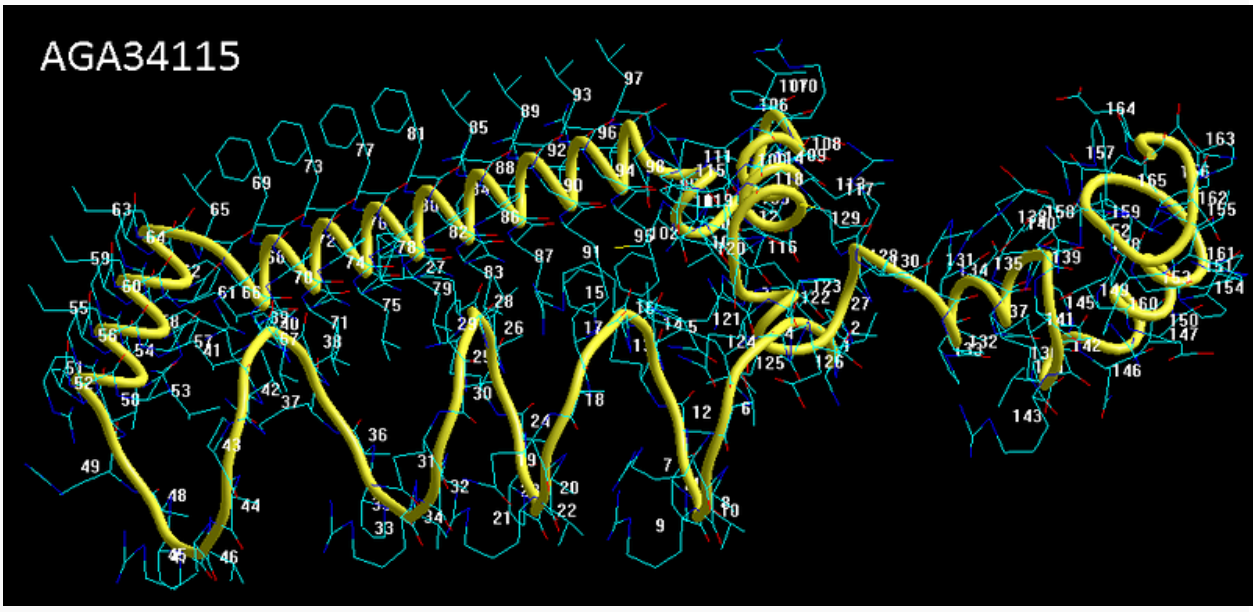
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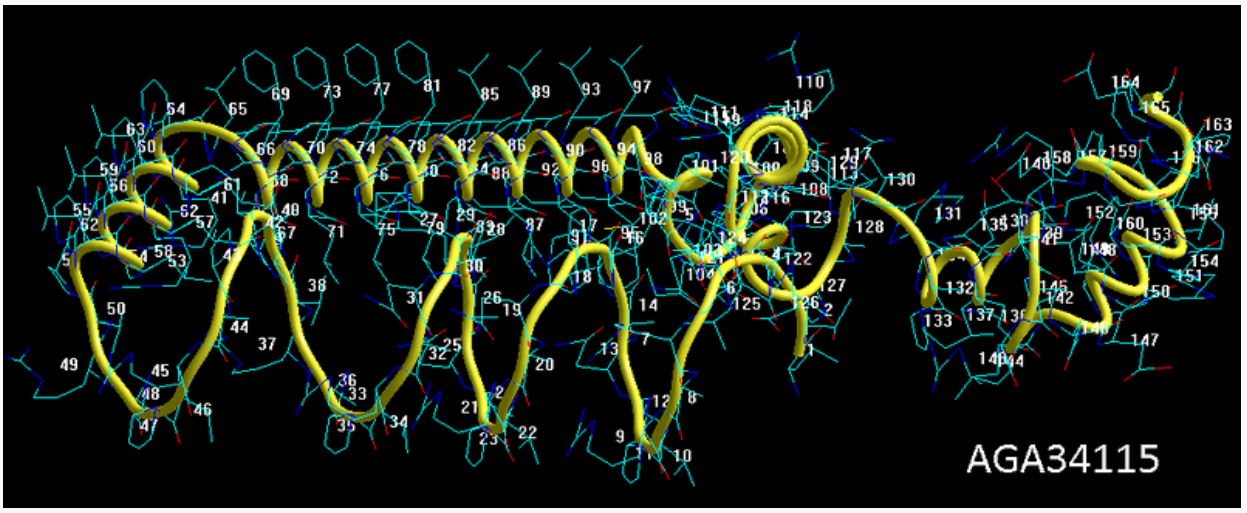
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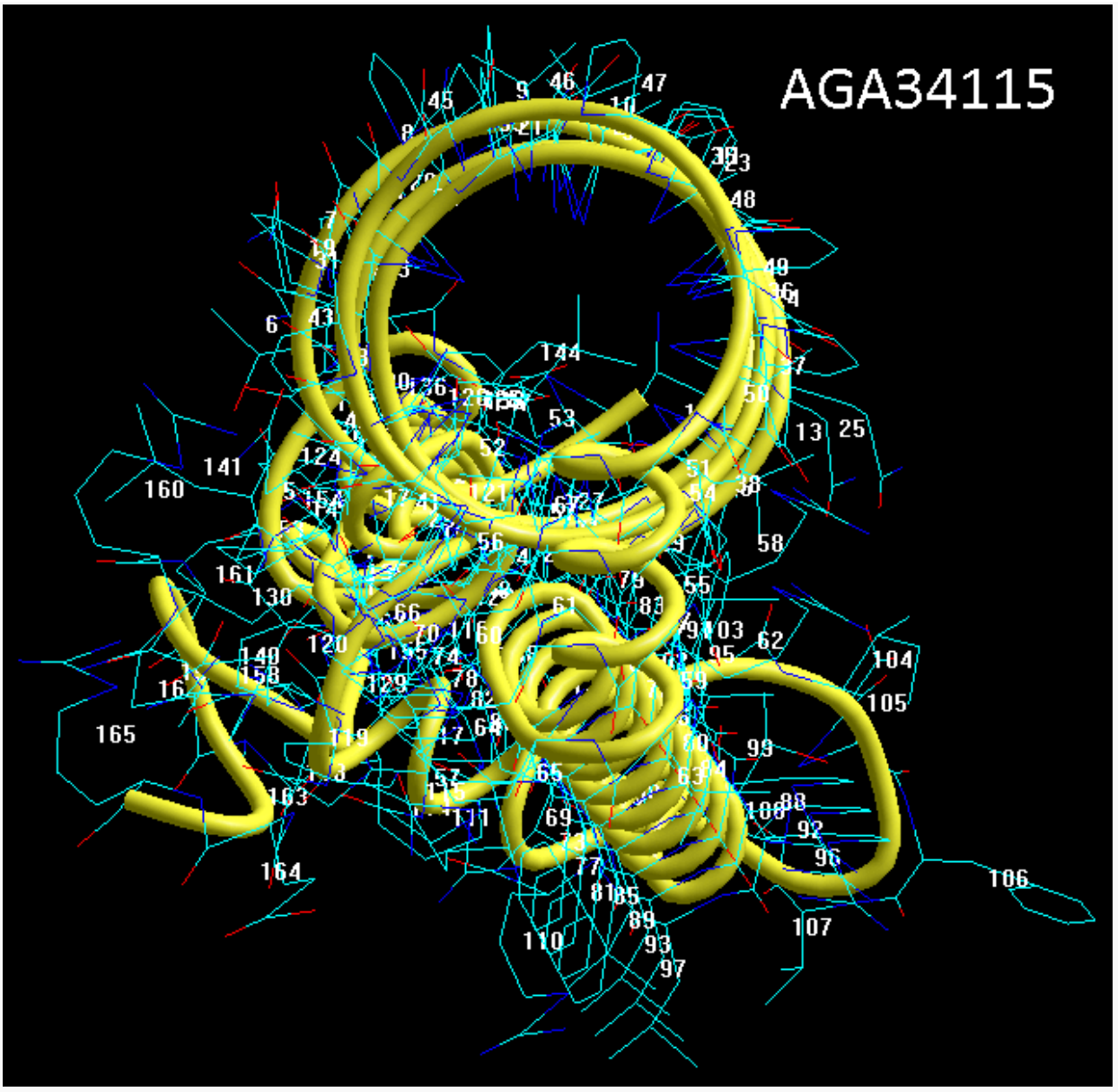
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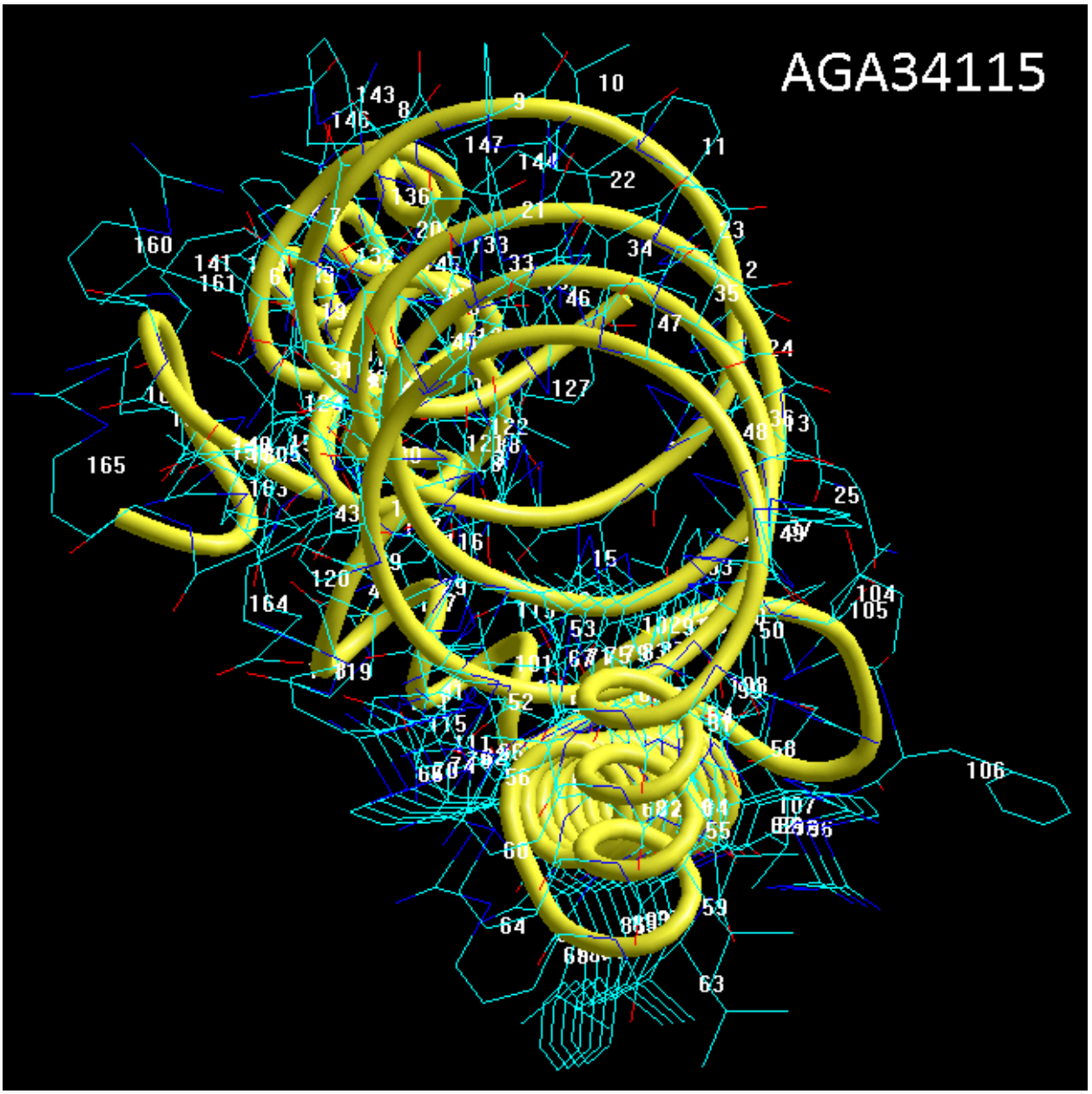
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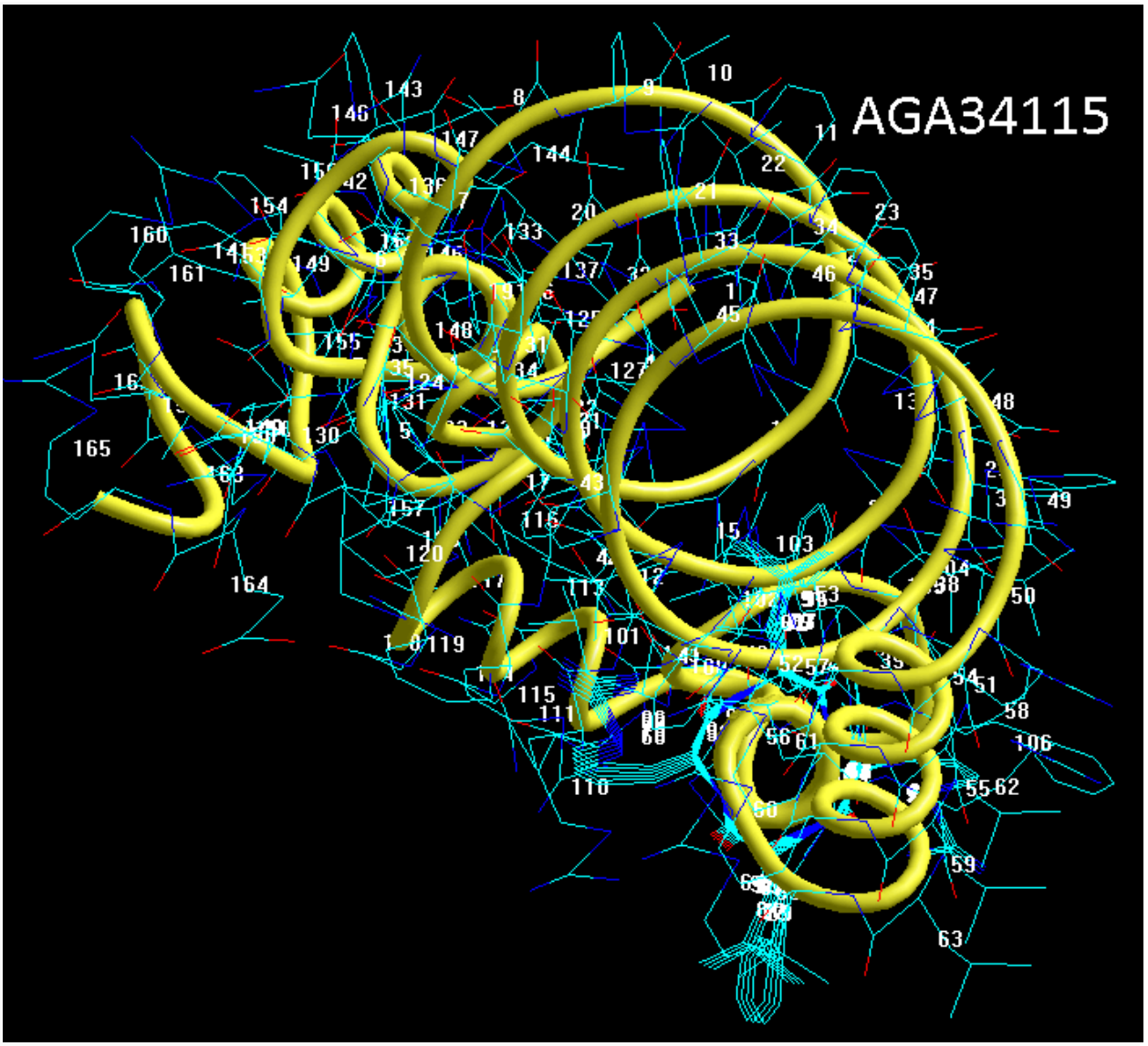
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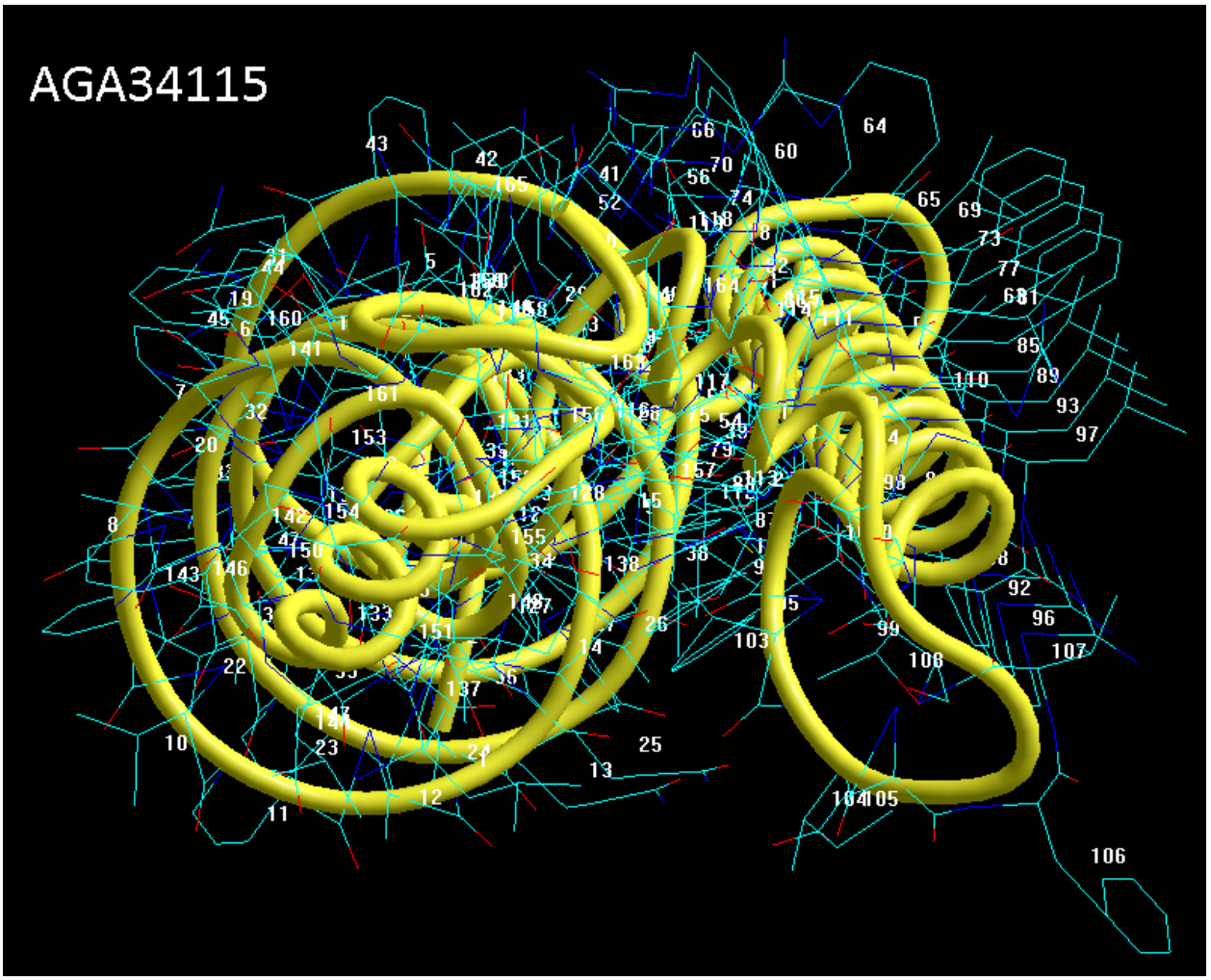
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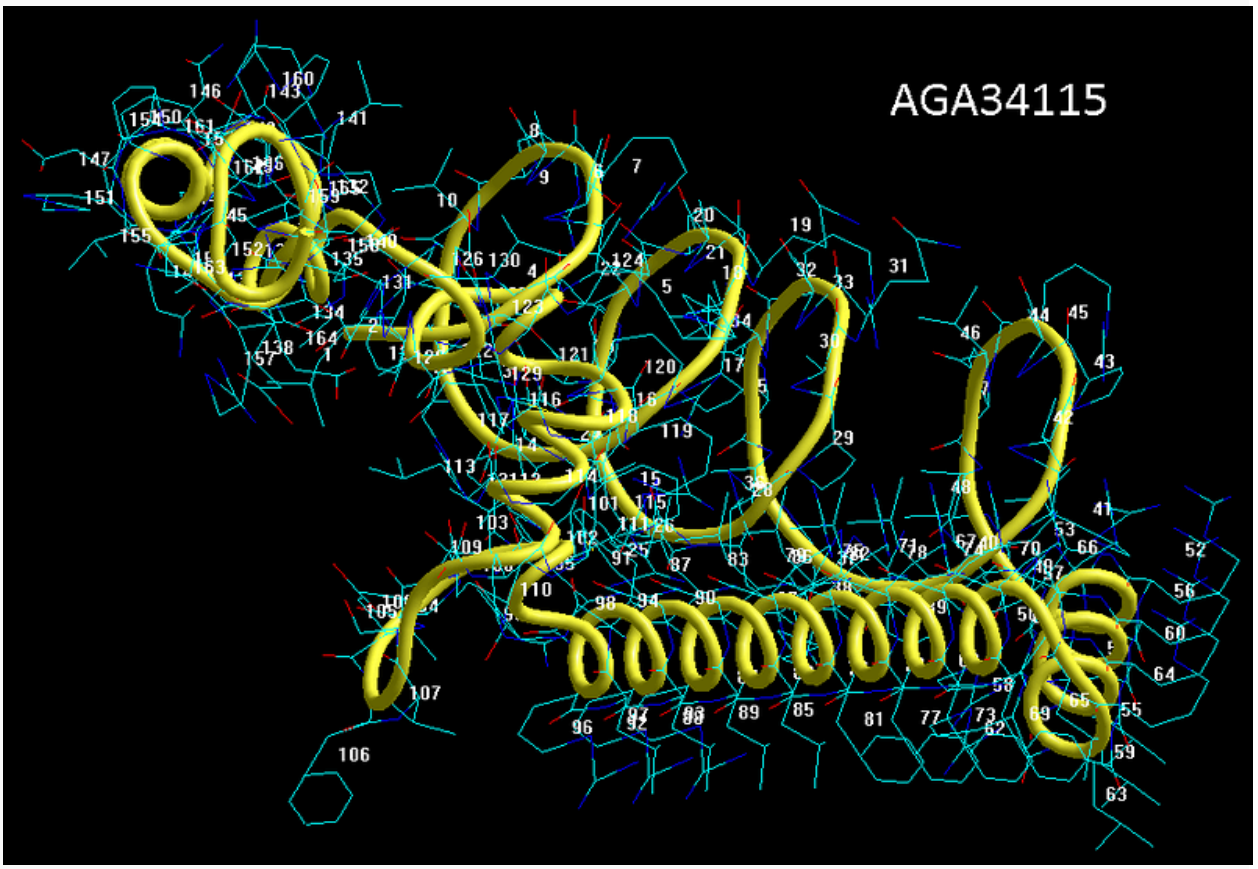
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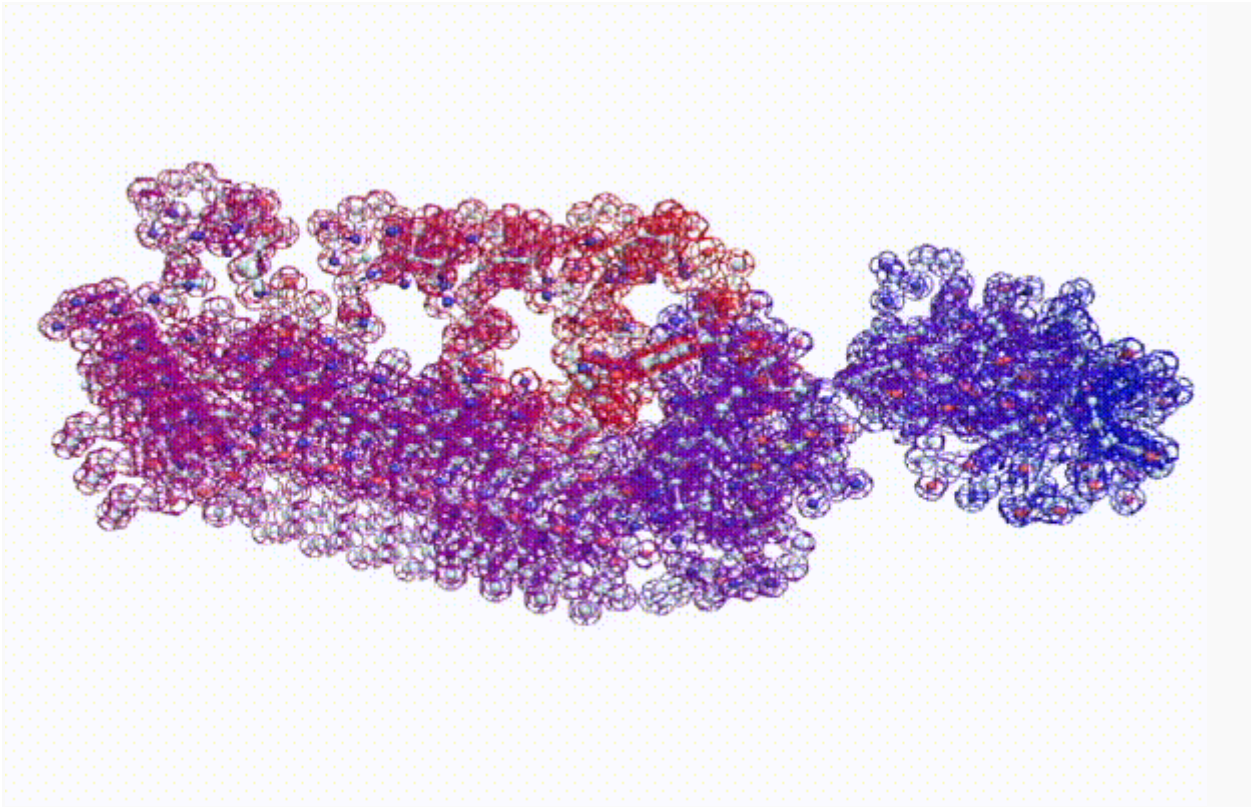

Full set of files: https://cloud.mail.ru/public/2rbQ/1taz9qHr9

https://www.ncbi.nlm.nih.gov/protein/1111467114?report=genbank&log$=prottop&blast_rank=9&RID=DDGPB4AU01R

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Q-helix (13131-helix) A.Kushelev length of more than 200 amino acid residues:

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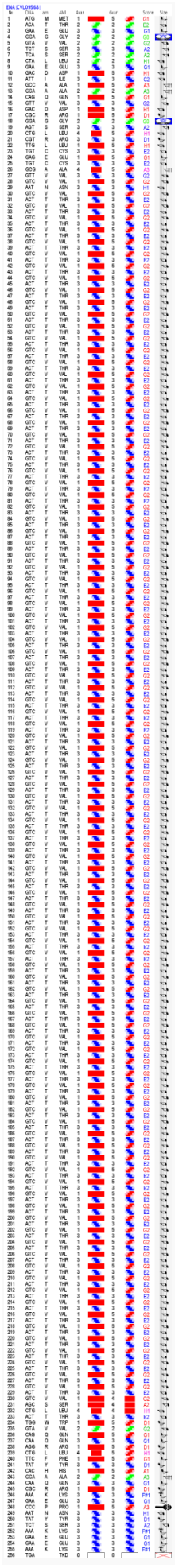

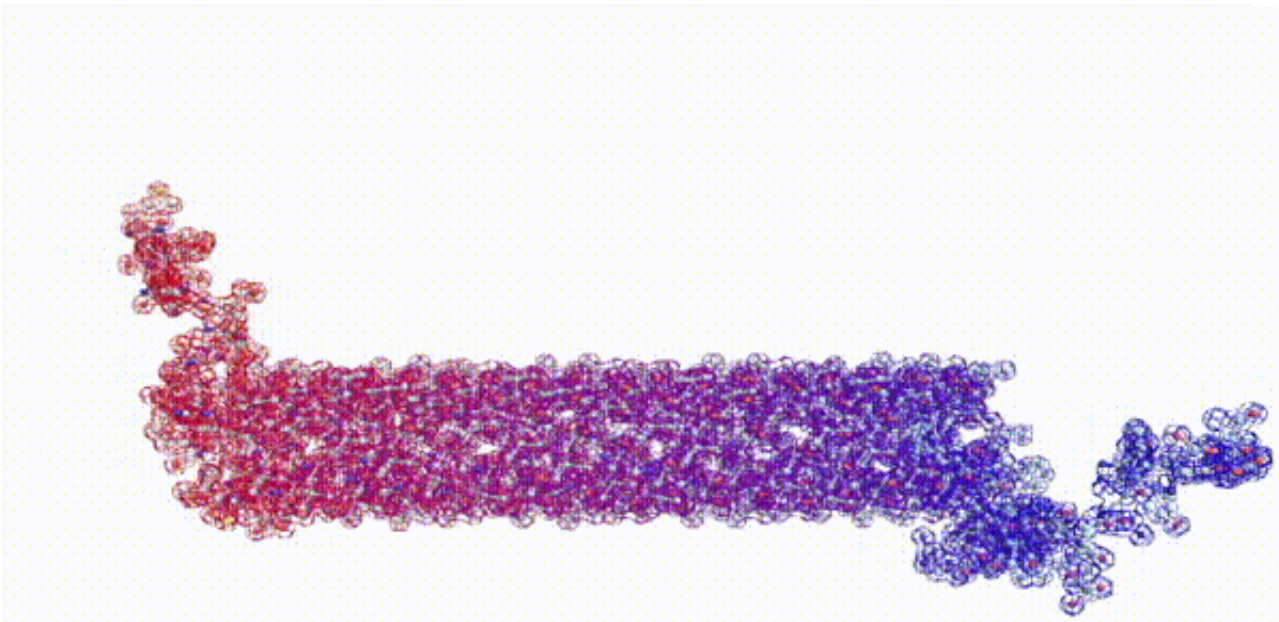

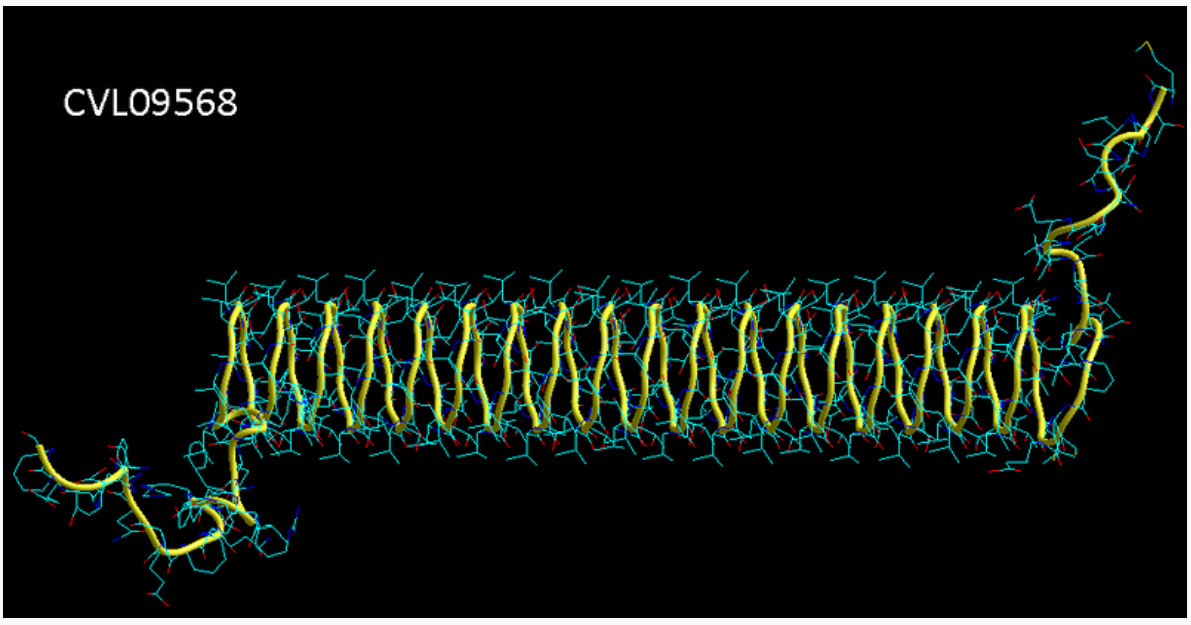
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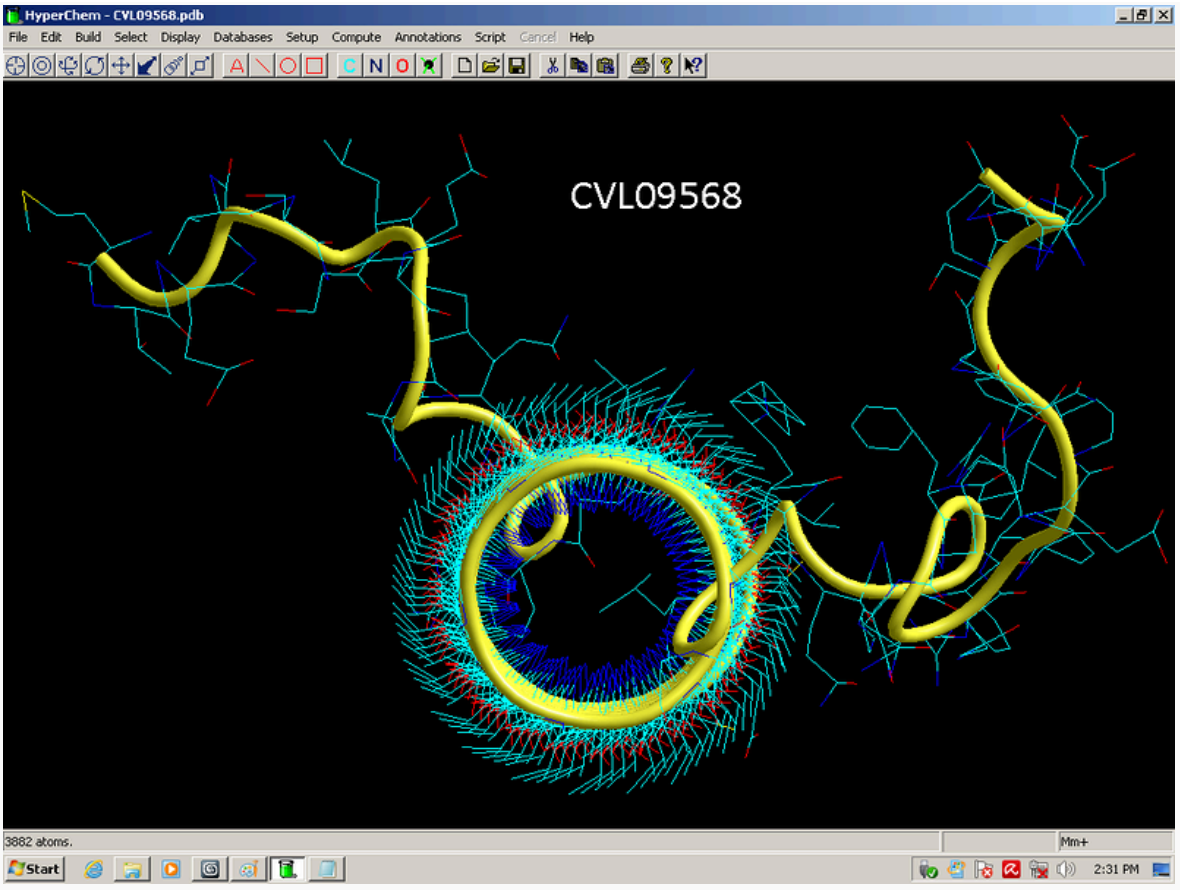
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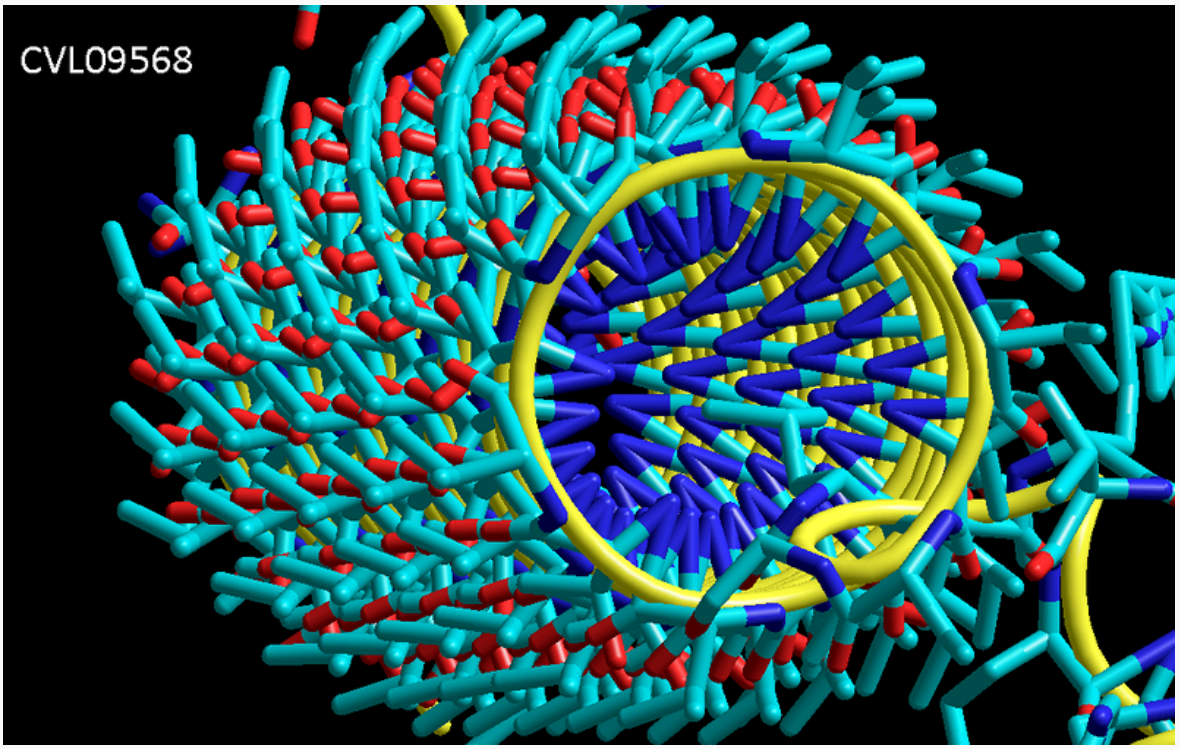
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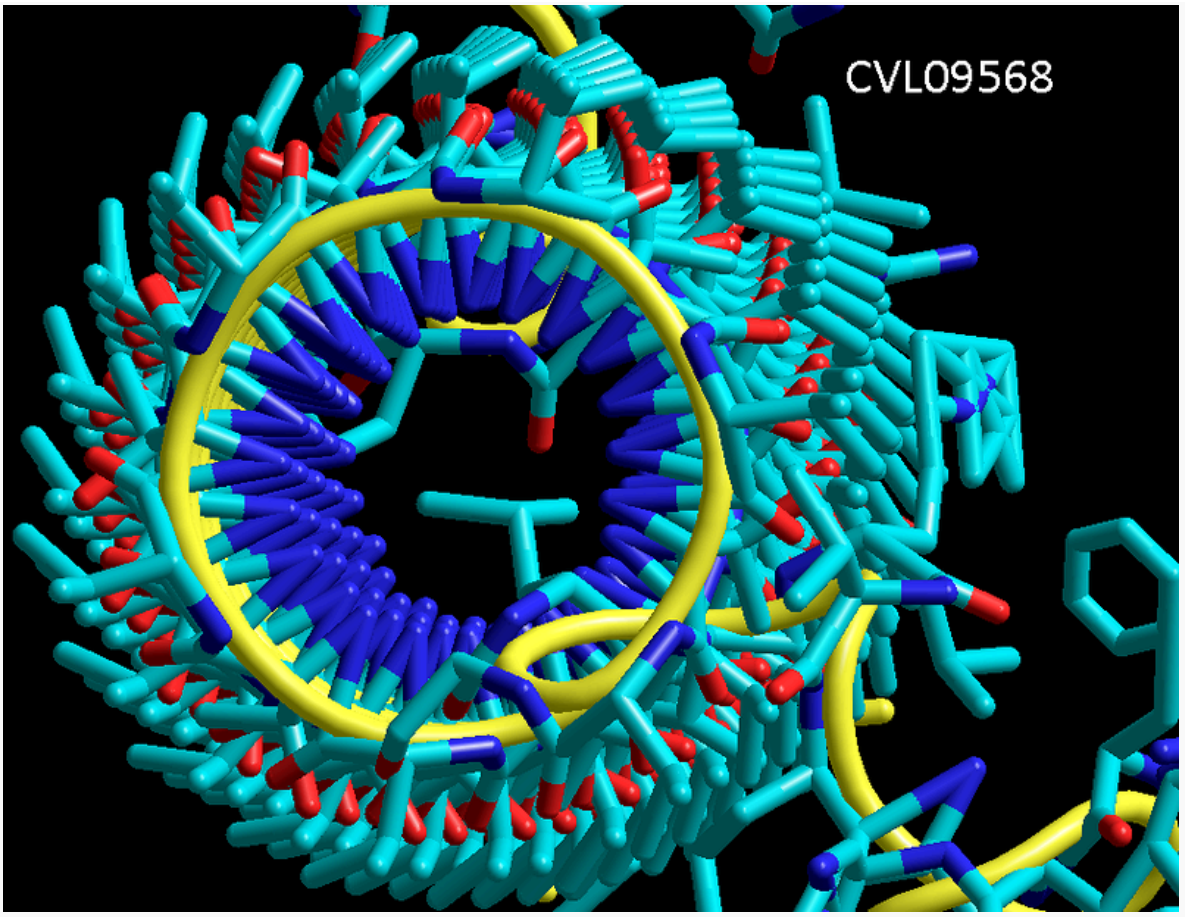
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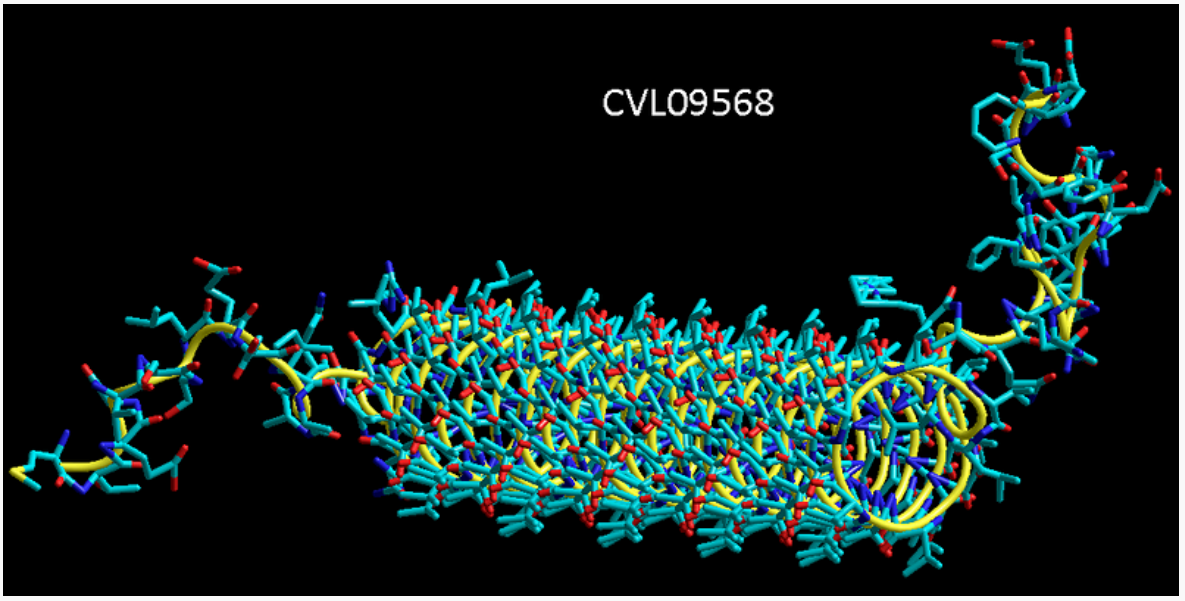
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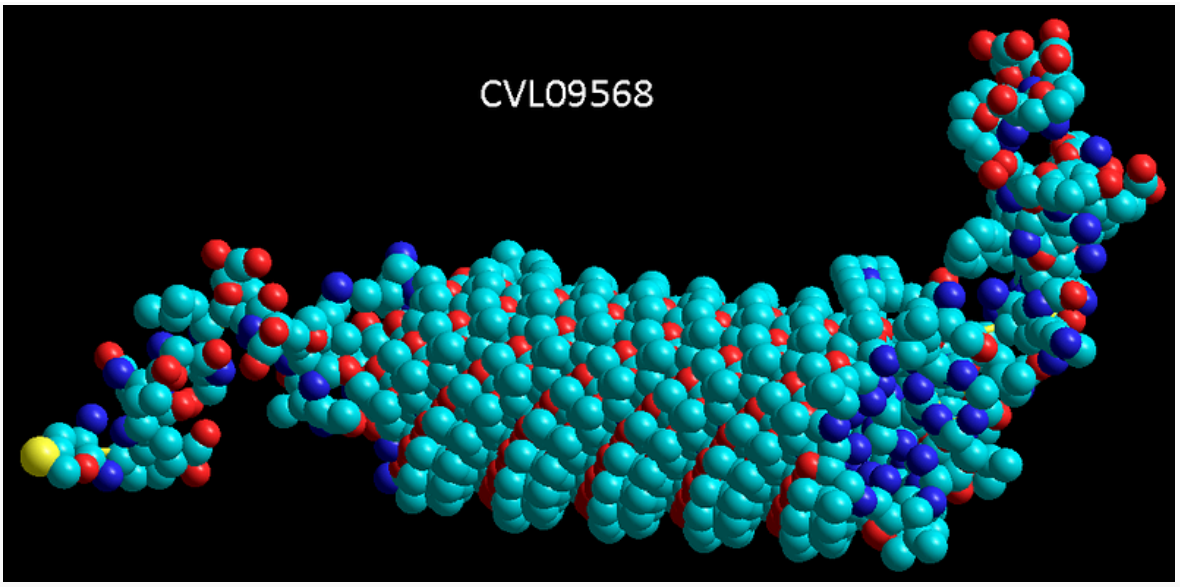
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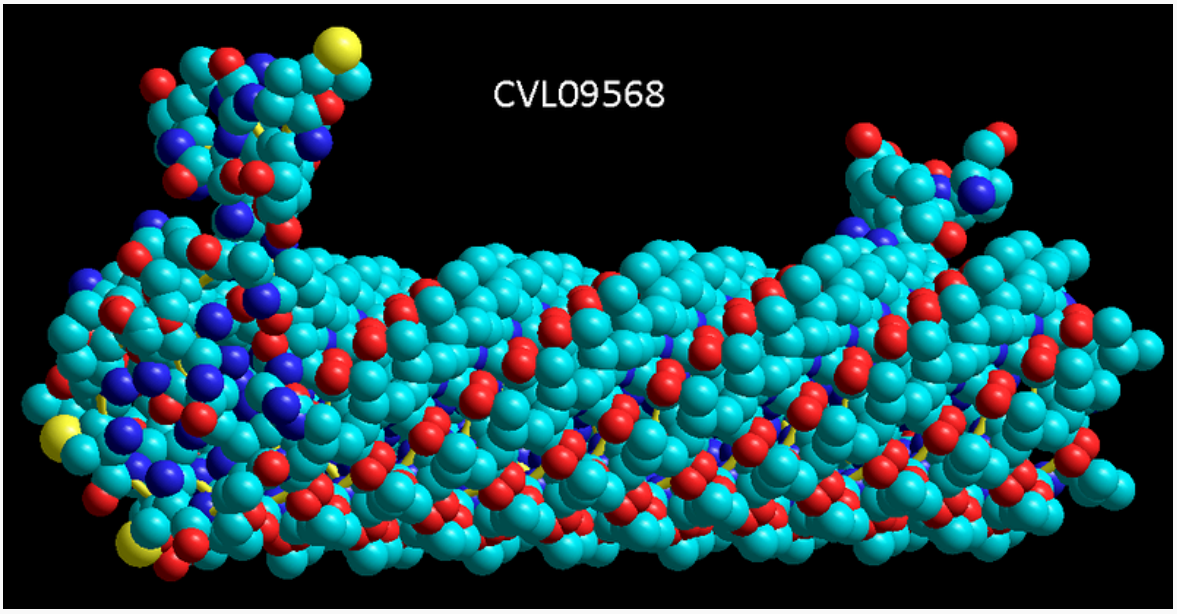
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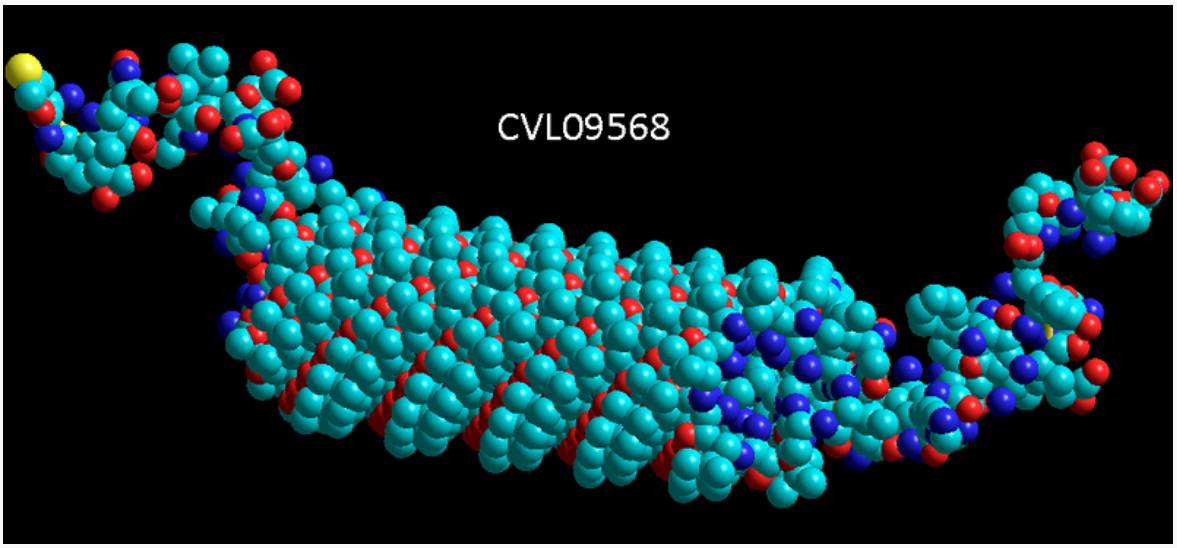
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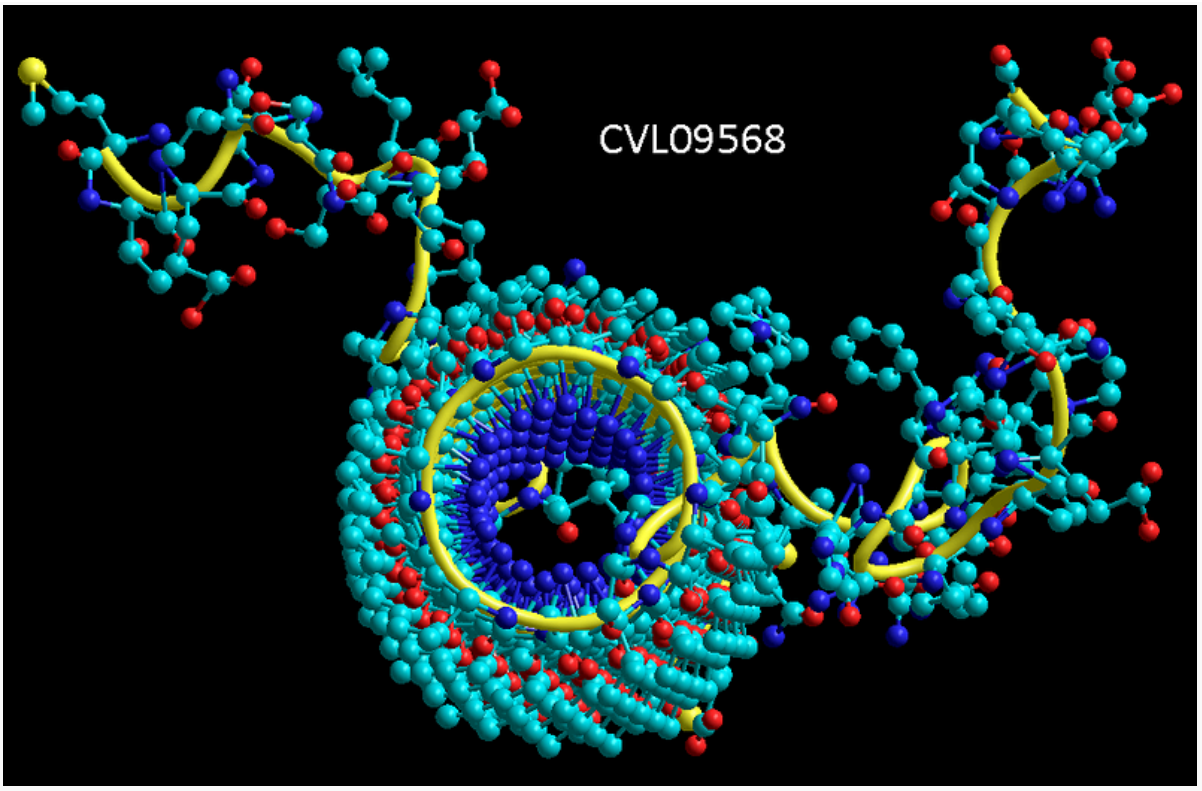
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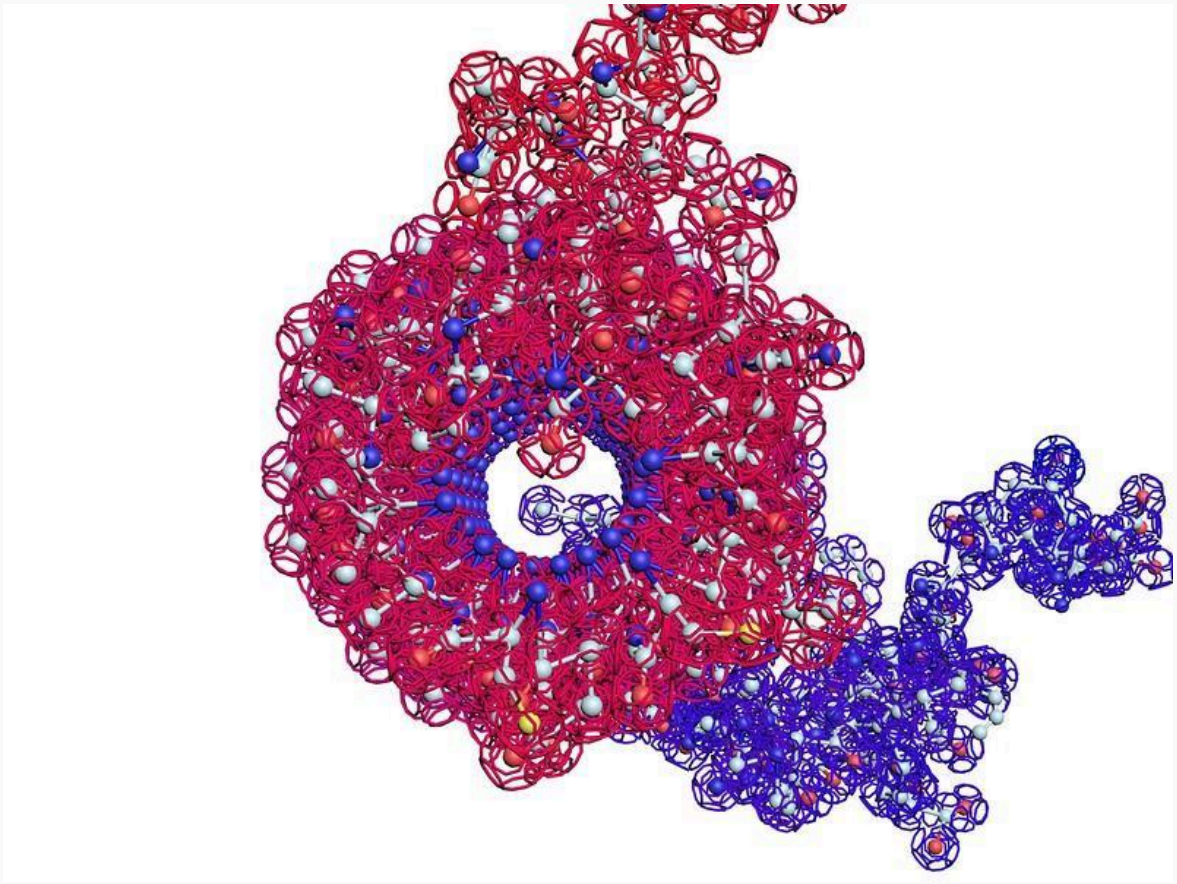

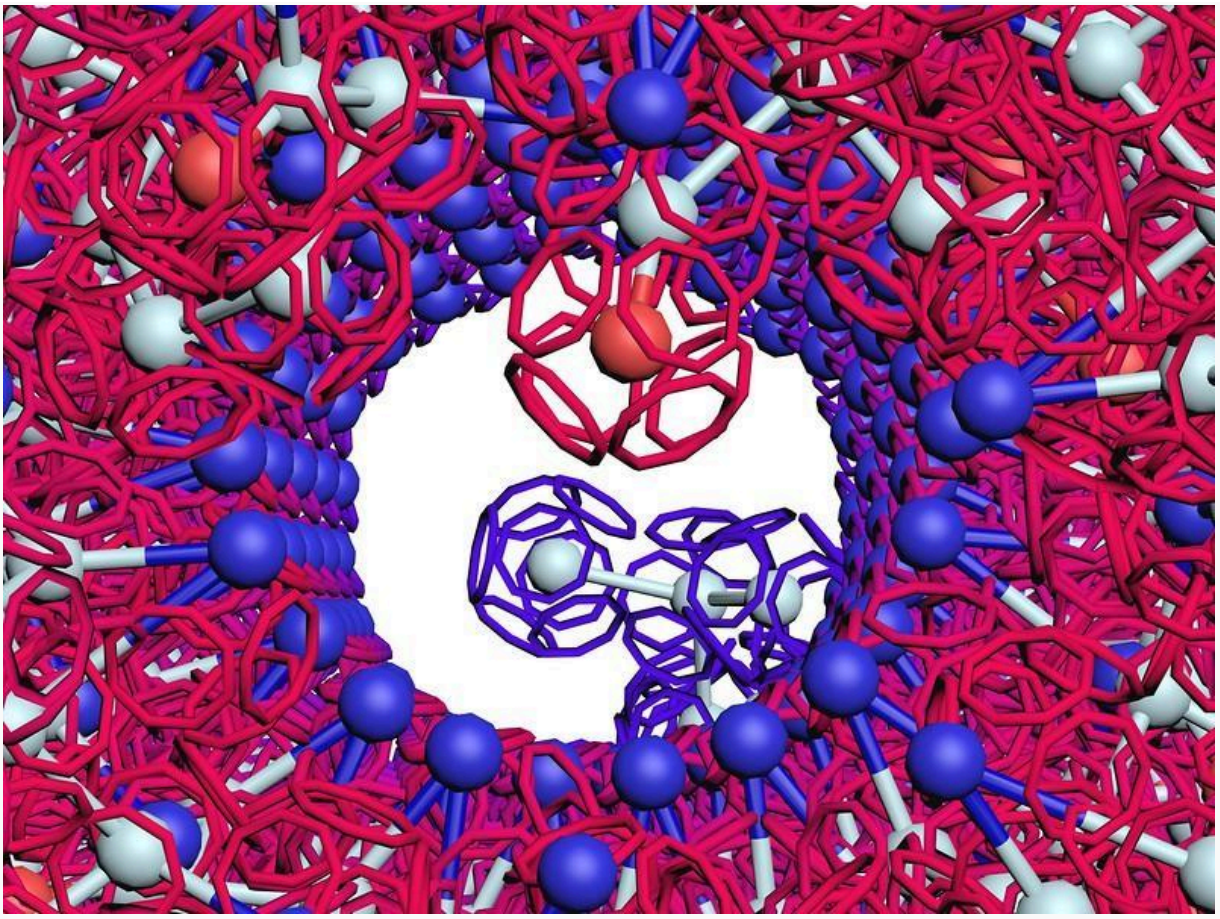

Q-helix is essentially a reactor consisting of nitrogen atoms - [Picotechnological Anisotropic Ultra-High Pressure Reactors](#).

https://www.ncbi.nlm.nih.gov/nuccore/1129213514#

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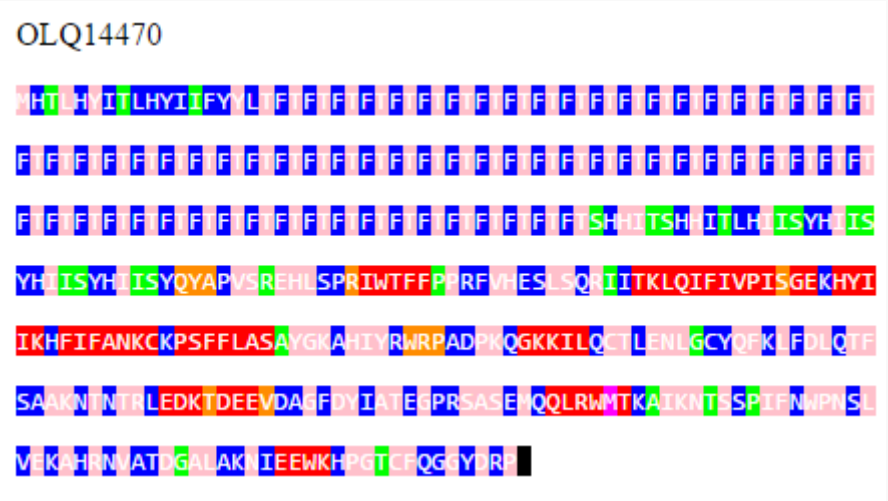

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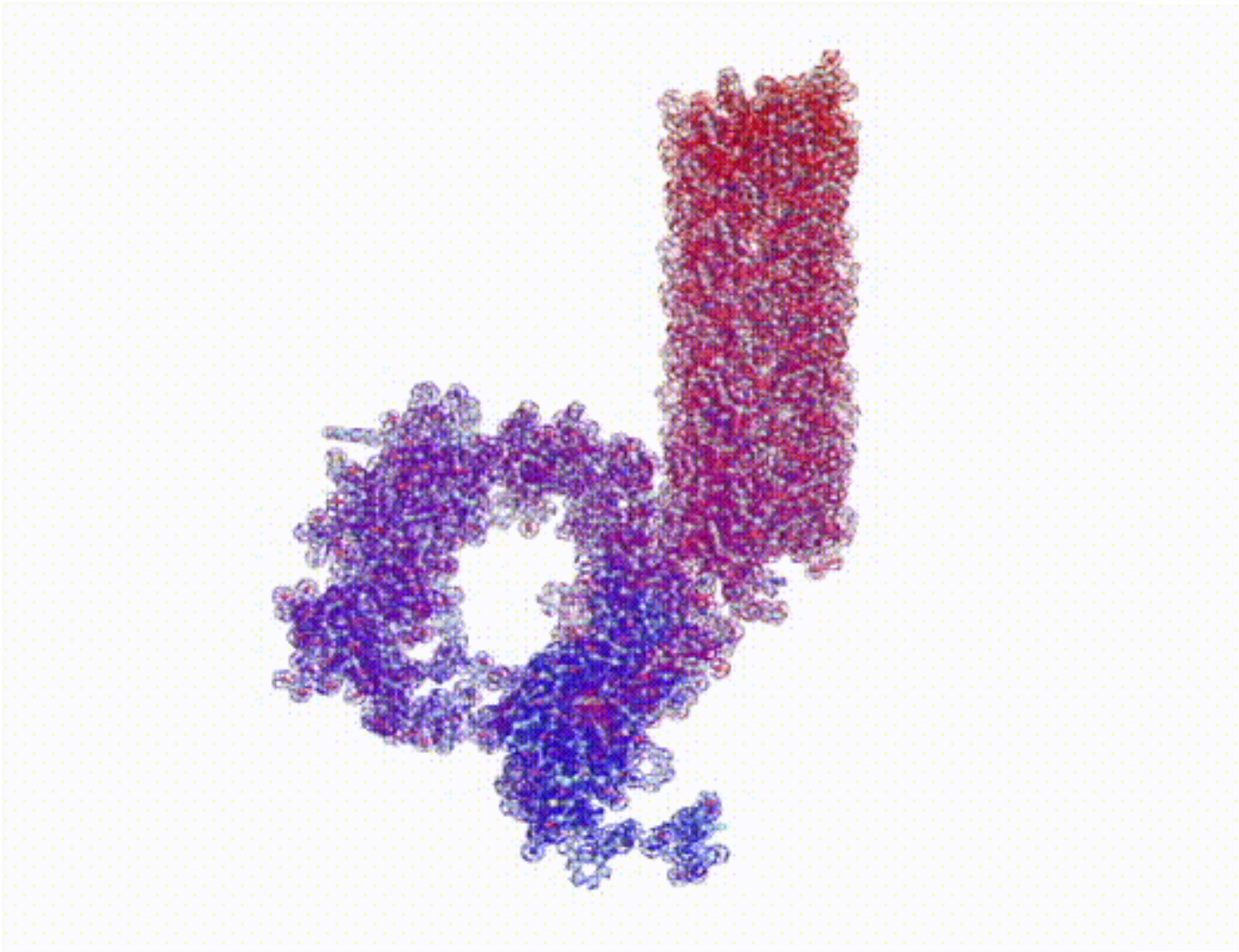

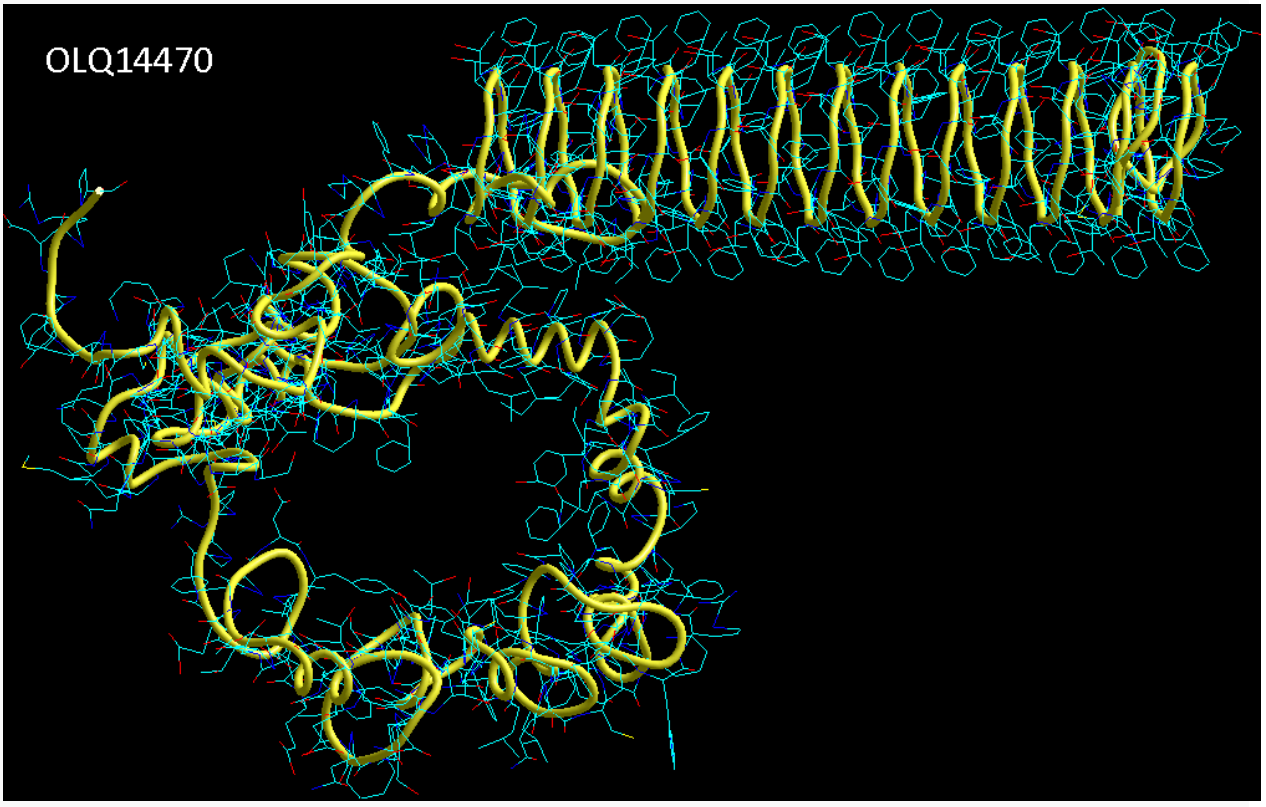
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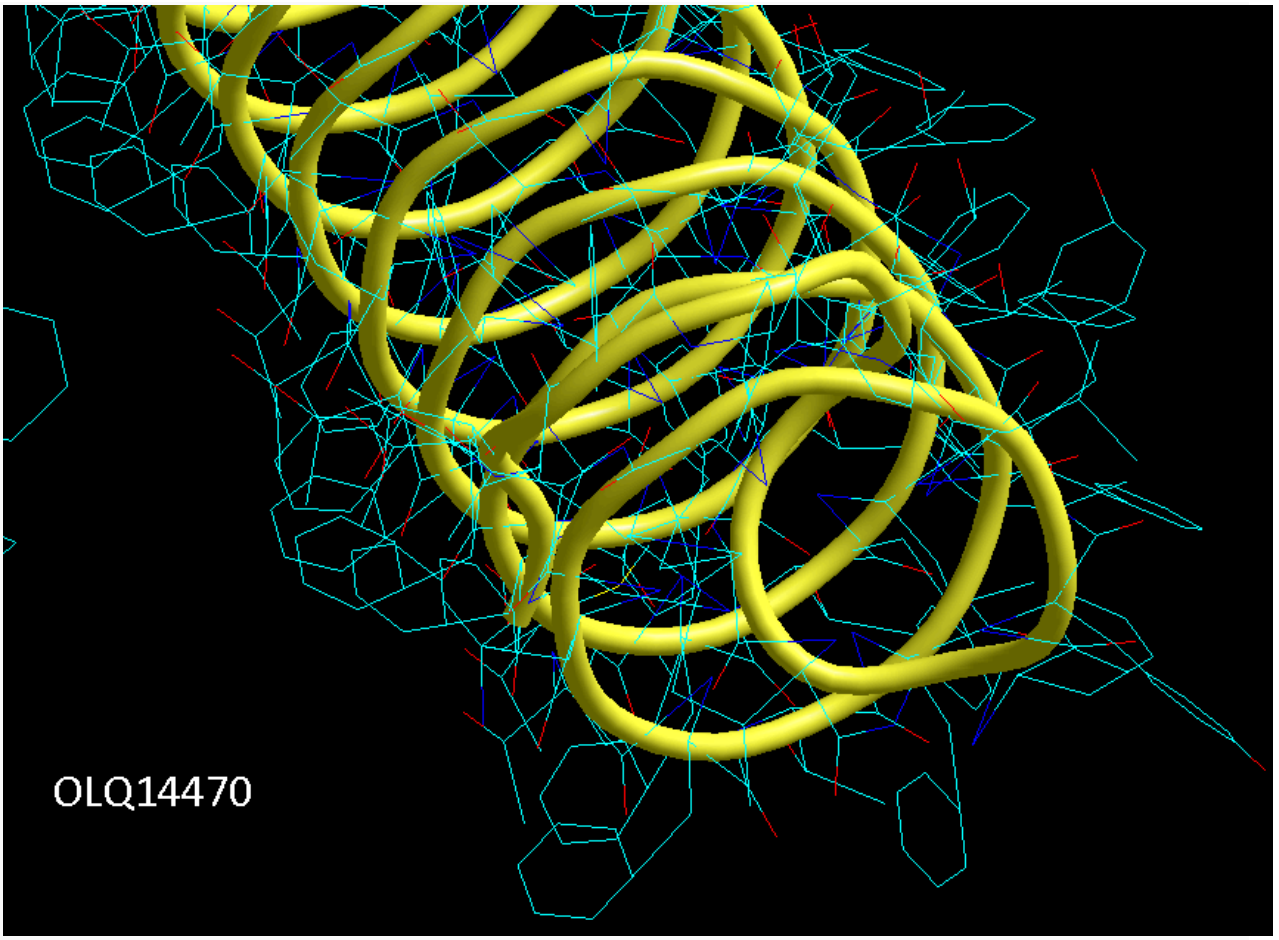
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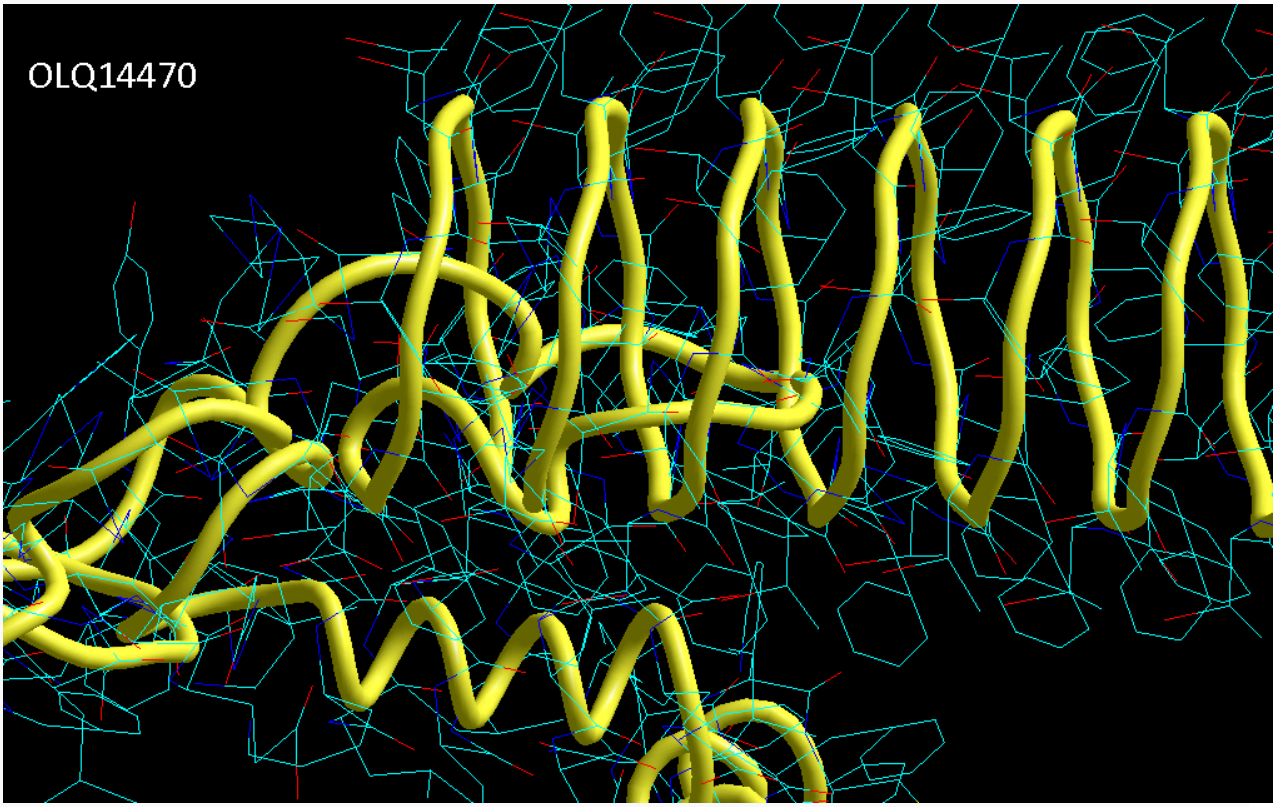
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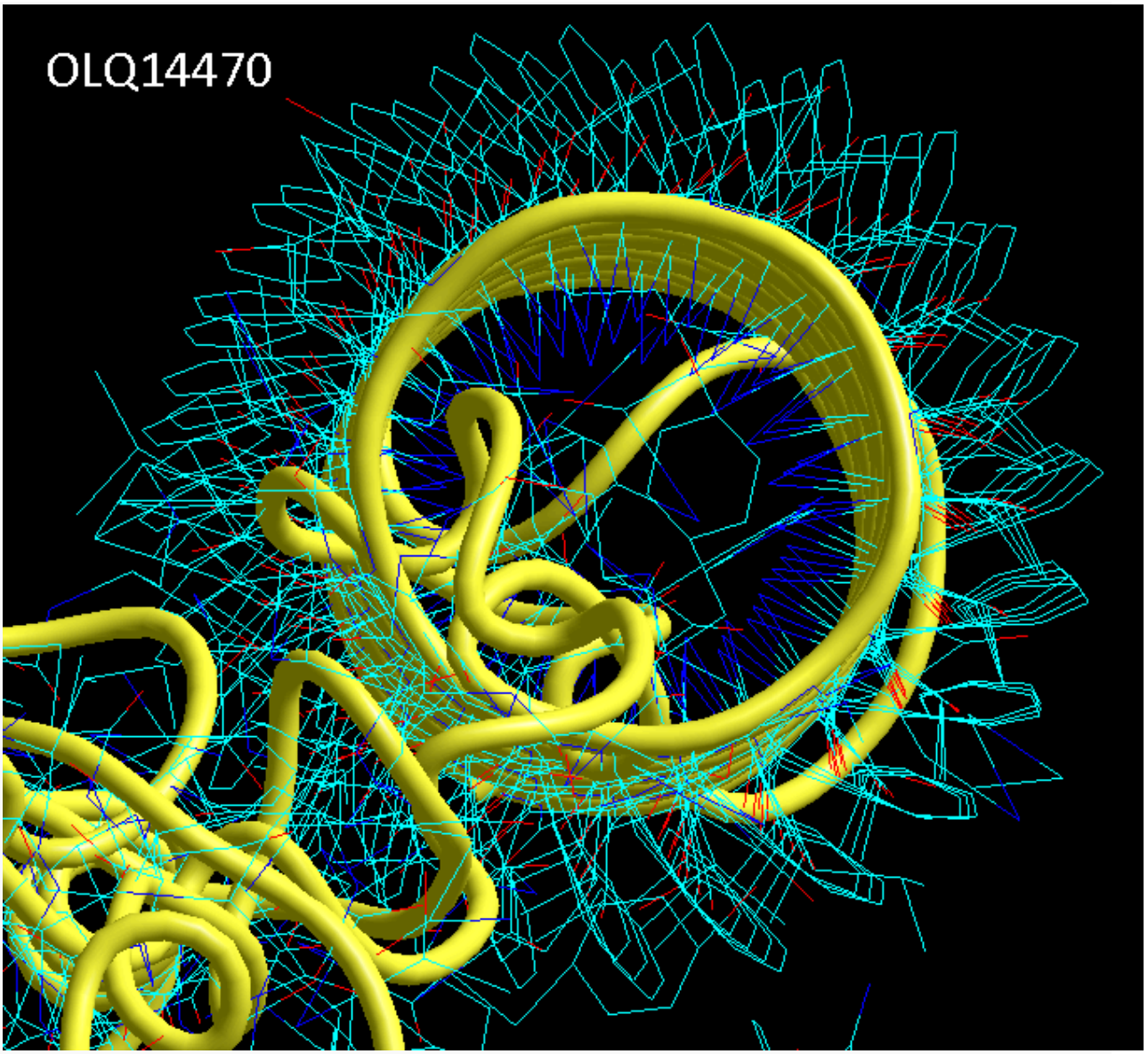


https://img-fotki.yandex.ru/get/404236/ … 8_orig.png

Q-helix parameters determined

Kushelev: Let's try to determine the real parameters of the Kushelev program helix (Q-helix, 57-helix). It would seem that this is not difficult to do. After all, the Q-helix consists of alternating amino acid residues with the codes of alpha- and pi-helices. However, the parameters (compositional, transpositional and proline angles) differ for both types of residues, i.e. from the parameters in the alpha-helix and from the parameters in the pi-helix. Moreover, if we try to make a Q-helix from "frozen" elements of the alpha- and pi-helices, then at the next residue it turns out that it is impossible to add the next residue, since its place is occupied by the residue of the

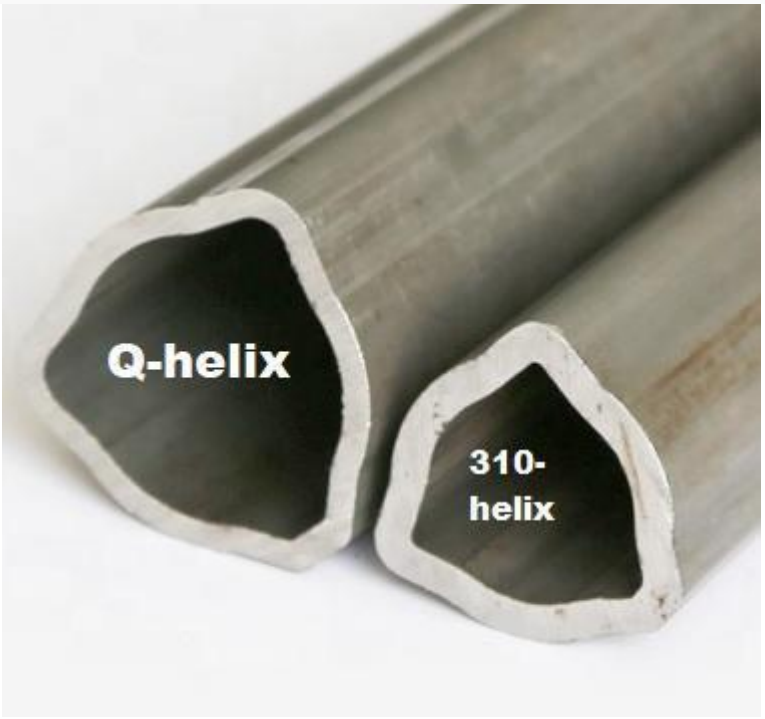
previous turn of the Q-helix. And this means that the Q-helix can be continued only if we change the angles, i.e. "unfreeze" the parameters of the alpha- and pi-elements. What follows from this?

It follows from this that a set of 9 variants with three angles (compositional, transpositional and proline) can describe only a part of protein structures, for example, a straight section of alpha, 310, pi, beta helices, an arbitrary sequence of compositional (3D) codes in the case where there are no restrictions on hydrogen, van der Waals and Hooke bonds. In real proteins, which often contain program helices, such restrictions exist, therefore a set of 9 variants with 3 angles cannot describe most protein structures. Without taking into account physics, i.e. at the level of a geometric algorithm.

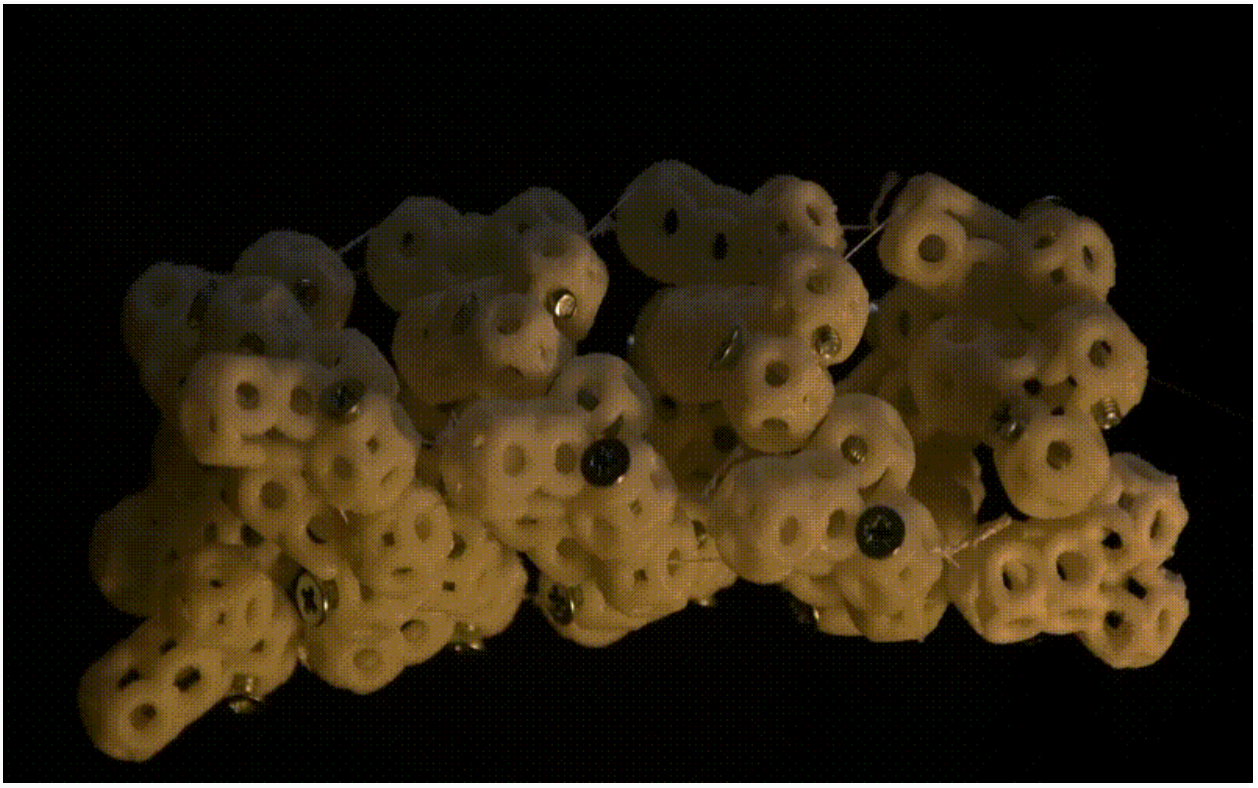
Taking physics into account is labor-intensive, but you can add a database for program spirals, which will greatly expand the capabilities of the geometric algorithm. And although there are a great many program spirals, there are not so many running program spirals, and rare program spirals will have to be studied taking into account physics. For now, in manual mode. The most relevant is the interactive 3D version, where you can visually observe the emergence of various restrictions in the process of constructing a protein model.

And while this version of Picotech 3D Pro interactive is being created, we will define the parameters of some software spirals manually...

I will publish the technology for determining the parameters of program spirals later, but for now I can say that there are ~5.8 amino acid residues per turn of the Q-spiral. The Q-spiral itself (it is right-handed), if it is polyglycine, looks something like this:



For clarity, cross-sections of the larger Q-helix and the smaller 310-helix are shown. By the way, the 310-helix is right-handed and has approximately 3.3 amino acid residues per turn. The pi-helix is left-handed and has approximately 4.4 residues per turn. The alpha-helix is right-handed and has 3.6 residues per turn. The beta-helix is left-handed and has approximately 3 amino acid residues per turn.



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