

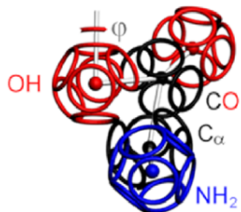


Expanding the antihomologue base

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

CONVENTIONAL DESIGNATIONS

HOW TO READ 2D DIAGRAMS OF PICOTECHNOLOGY



Structural
template of
amino acid
residue

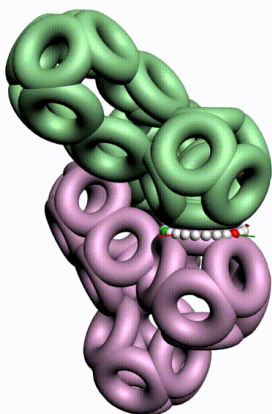
		Second base position									
		U		C		A		G			
First base position	U	UUU	P π	UCU	S π	UAU	Y π	UGU	C π	U	
		UUC	P α	UCC	S α	UAC	Y α	UGC	C α	C	
		UUA	L π	UCA	S β	UAA	Stop	UGA	Stop	A	
		UUG	L α	UCG	S 3_{10}	UAG	Stop	UGG	W α	G	
	C	CUU	L π	CCU	P π	CAU	H π	CGU	R π	U	
		CUC	L α	CCC	P α	CAC	H α	CGC	R α	C	
		CUA	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)

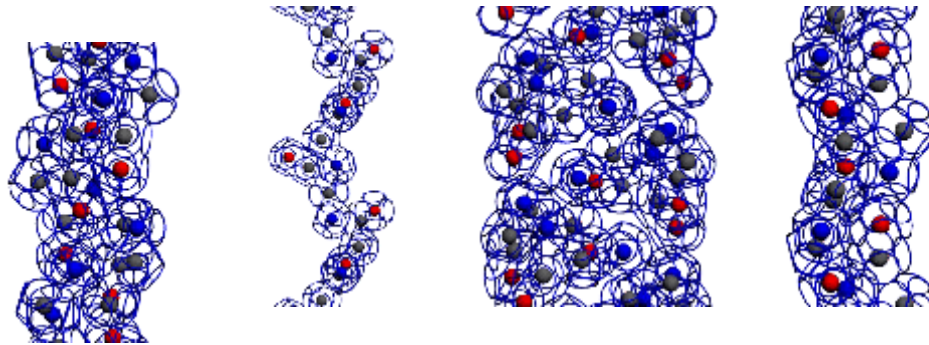
π - 1/5 turn of pi-helix (pi-turn)

3_{10} - 1/3 turn 3_{10} -helix (3_{10} -turn)



Structure definition by 3D genetic code

GGC		Alpha-helix code
GGA		Beta-helix code
GGT		Pi-helix code
GGG		310-helix code



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

Alpha-helix

Beta-helix

Pi-helix

310-helix

[Methionine helix](#)



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

3D STRUCTURES OF AMINO ACID RESIDUES

Ala: gcc, gca, gci, gcg	Val: gtc, gta, gti, gtg	Gly: ggc, gga, ggi, ggg	Leu¹: ctc cta, ctt, ctg	Leu⁶: tta, ttg	Lys: aaa, aag
Ser¹: tcc, tca, tci, tcg	Ser⁶: agc, agt	Thr: acc, aca, aci, acg	Met: atg	Arg¹: cgc, cga, cgt, cgg	Arg⁶: aga, agg
Glu: gaa, gag	Gln: caa, cag	Ile: atc, ata, att	Phe: ttc, ttt	Tyr: tac, tat	Pro: ccc, cca, cct, ccg
Asp: gac, gat	Asn: aac, aat	Cys: tgc, tgt	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.

COMPACT 2D PICOTECHNOLOGY DIAGRAM

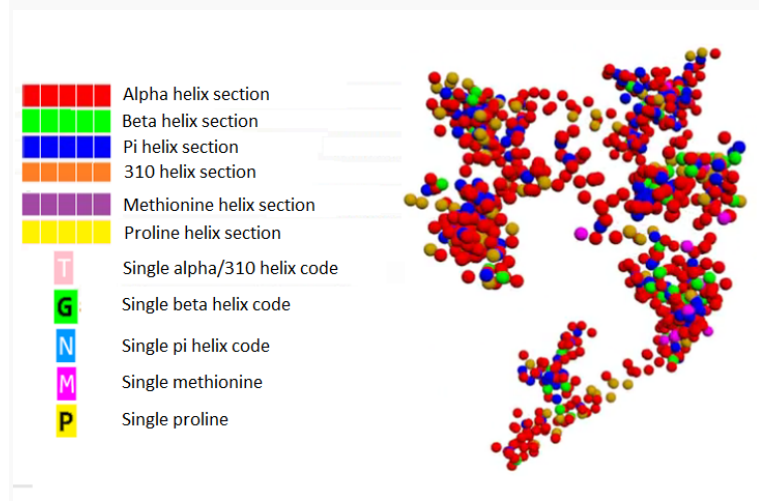
Red is an alpha helix.
The orange is a 310-helix.
Pink is a single alpha / 310 helix code.
Blue is a pi-helix.

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.

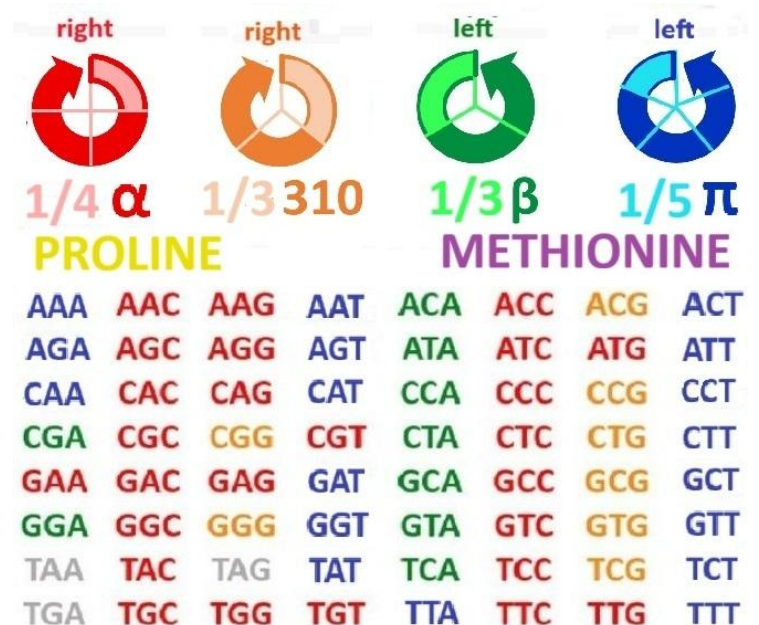


OX530245

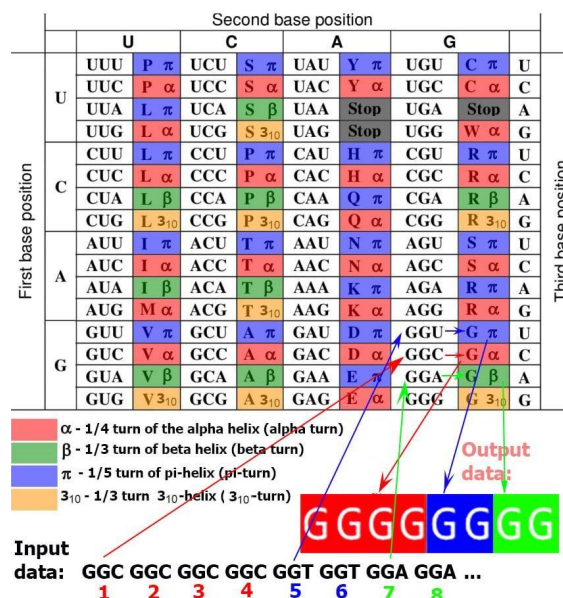
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I H F N GNLVL N VVLDSSQ KPELLNG RIAEE VN A PKERDLSFRLRY
LDSTGELMD I H G E D T WWDLSL NTSI SEETAE DMDEAD GT TDTTDTTDT
D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T
D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T
D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T
D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T
ANTLY S H A I E GGLVRH G E N Q VTFTE NGLI I KNPDDSYWGKDT TLE
SRVDGNTI AQQNDVIHLTG GEOKT AY N IHGDQHTPMY V N S I D G N S
QGN I H DRET L G A N K I L GNDV I I GNT ES YGDAYERR GAKGN LF
VK N DGSV SSL GGGV MYQGV TGGDD T I G S S GE IY D FHAYGNNTGNDR
VE G N TGN I L G D V V N G T D S K Y N D V I G G N S Q G N S I Y L D Y T P S I G K G G D D E L
HISGD T H T L G F R V G M D F G N D N I I G V V T N I R V A G D E Y E V T H Y G D D E L
LGS A N V Y G D C A T G Y N A T G G N I V H D G E R K L I D R A G N D L F I Y N D G H
I I G N D G S V S I D G S N T Y M N T I I N Y E G V G G S A D D I I G N N D N I L G G G N D I L T G G G
G A D A F N R G L D G T I I T D F N S A D D K I Y I A D L D A N G L D L S R L N S T I E N Q L V L N I
N E V O T I O V E R G L V G N Y N F Q F S Q Y G S A S H D S Q N E M N T L L Q L T T E

```



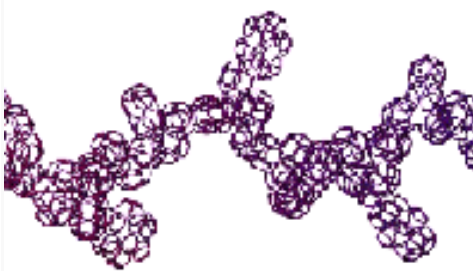
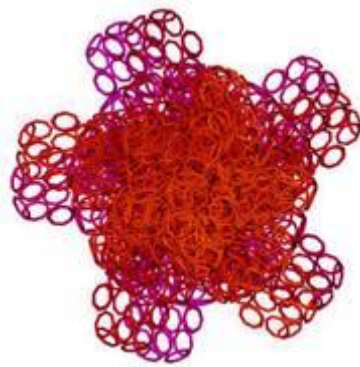
How does the 3D Genetic code table work?



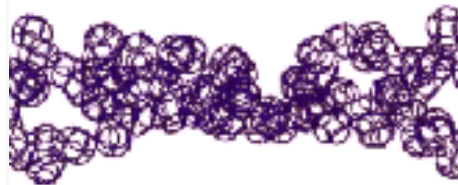
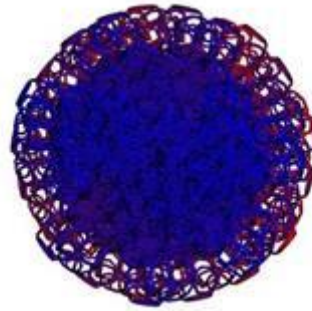
FULL (EXPANDED) DIAGRAM

- 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)

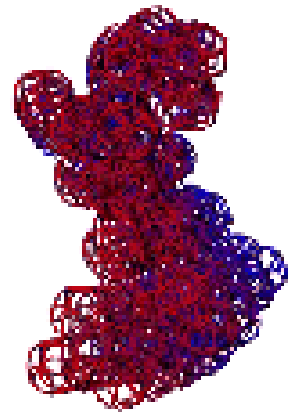
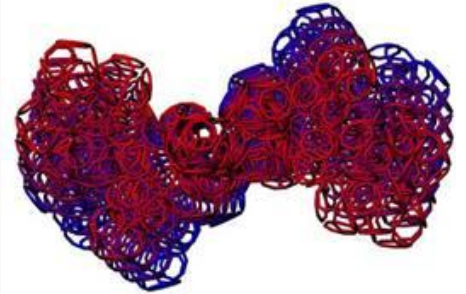
n 3212-helix



n 233 helix



n 13323 helix

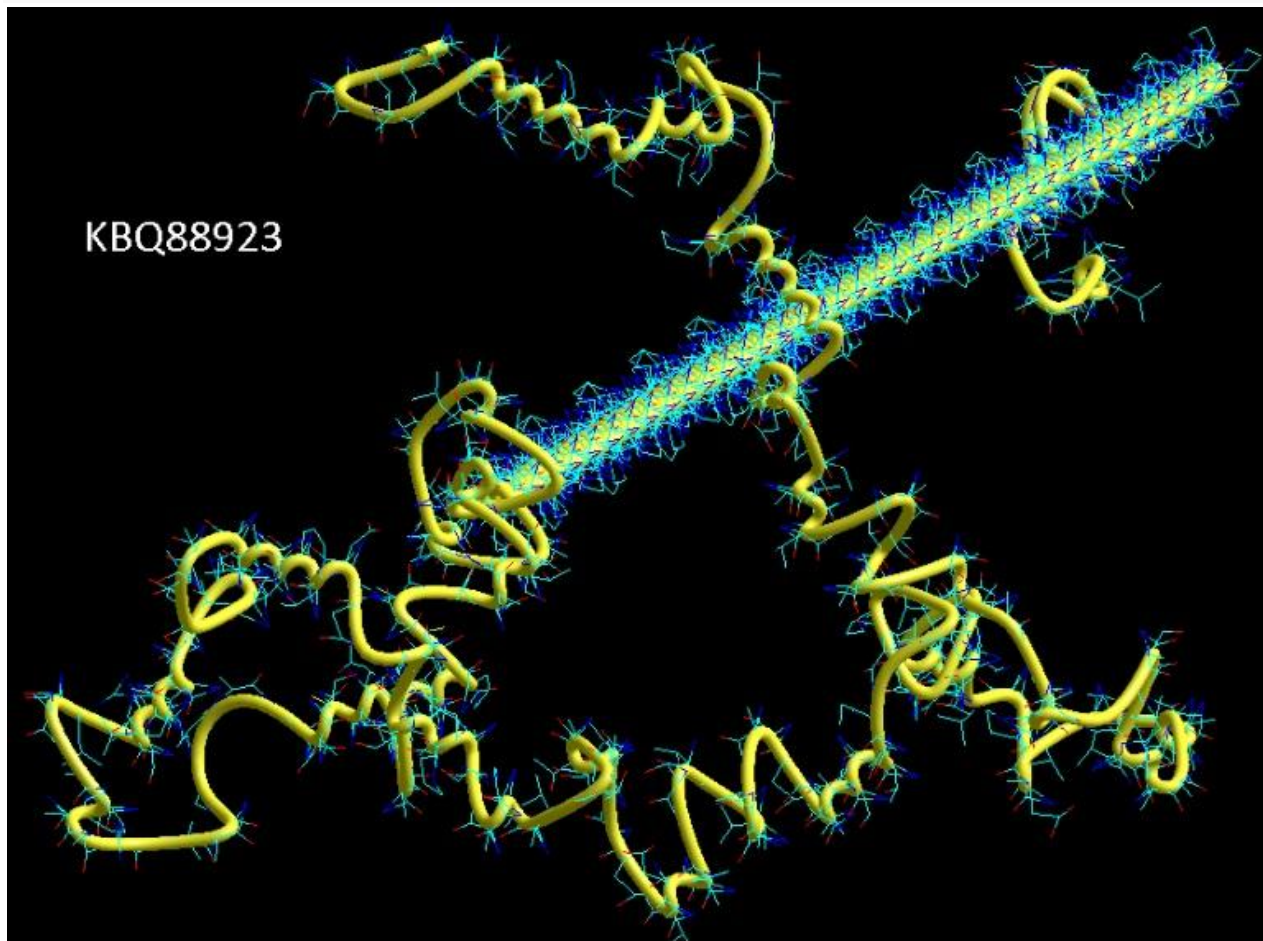
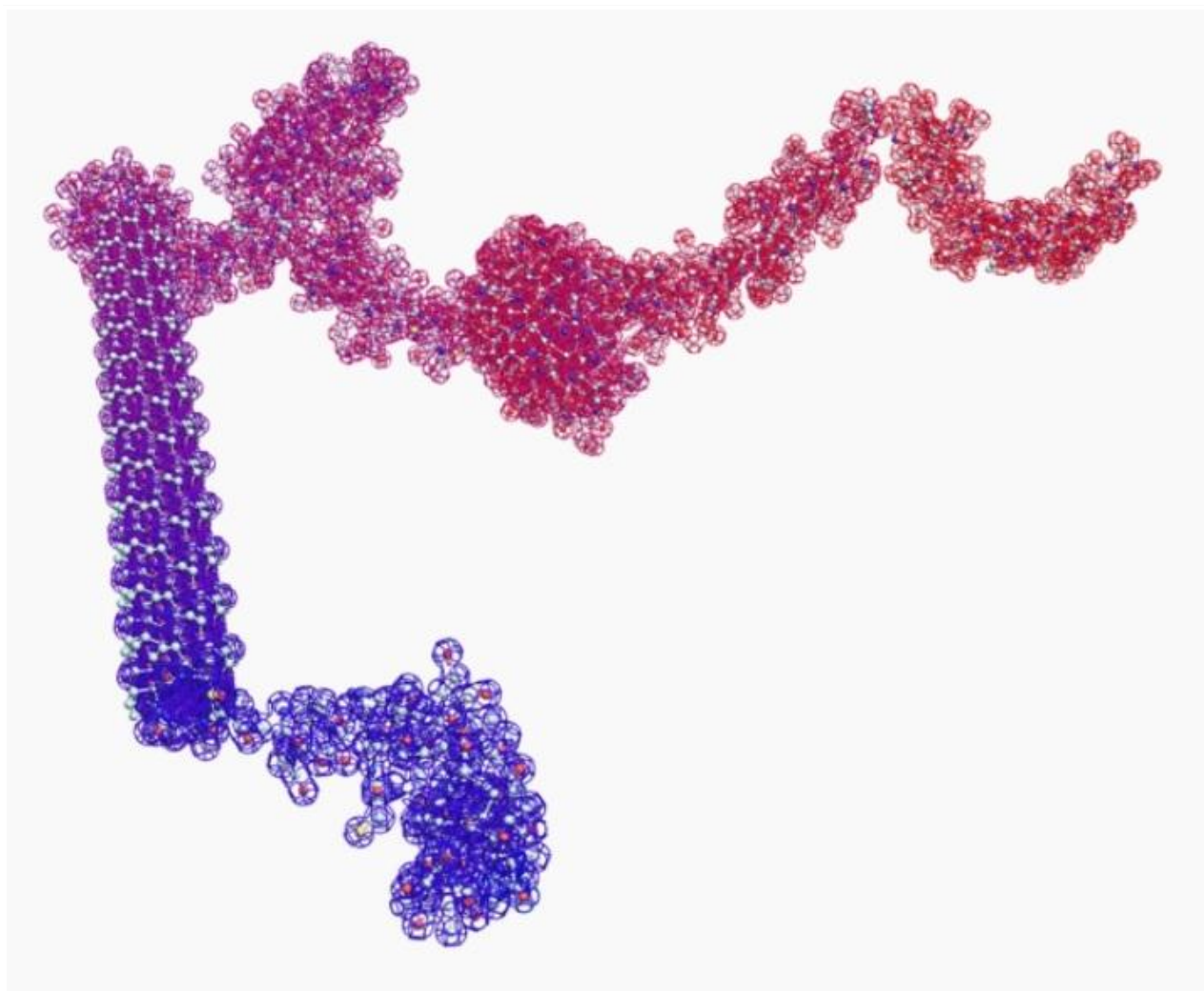


One-to-one correspondence between the sequence and 2D and 3D Picotech diagrams

>ENAKBQ88923|complement 2319 nucleotides

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[illegible]



3D-Genetic code

1992

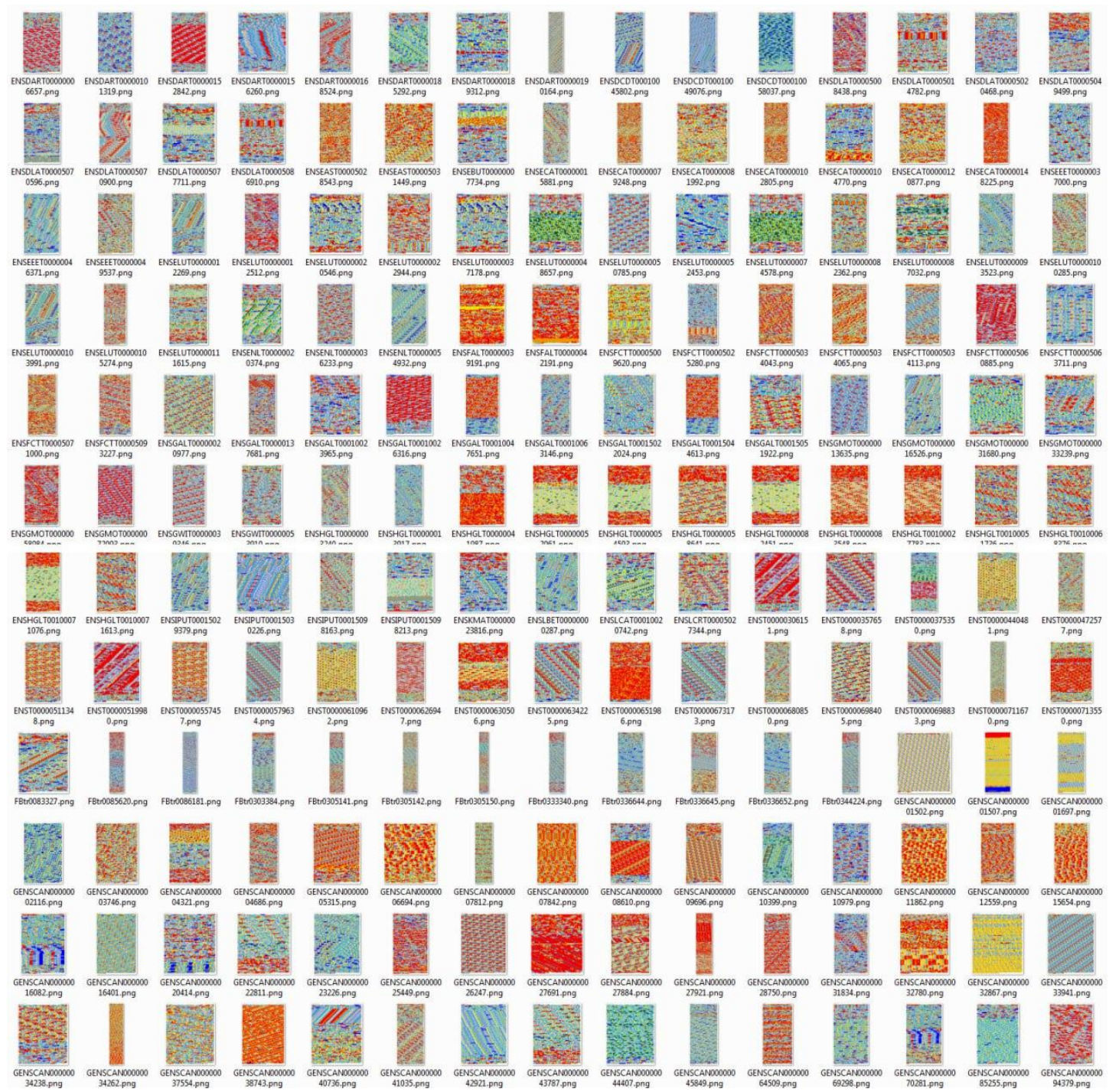
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ACC	Thr	1
ACG	Thr	4
ACT	Thr	3
AGA	Arg	3
AGC	Ser	1
AGG	Arg	1
AGT	Ser	3
ATA	Ile	2
ATC	Ile	1
ATG	Met	1
ATT	Ile	3
CAA	Gln	3
CAC	His	1
CAG	Gln	1
CAT	His	3
CCA	Pro	2
CCC	Pro	1
CCG	Pro	4
CCT	Pro	3
CGA	Arg	2
CGC	Arg	1
CGG	Arg	4
CGT	Arg	3
CTA	Leu	2
CTC	Leu	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

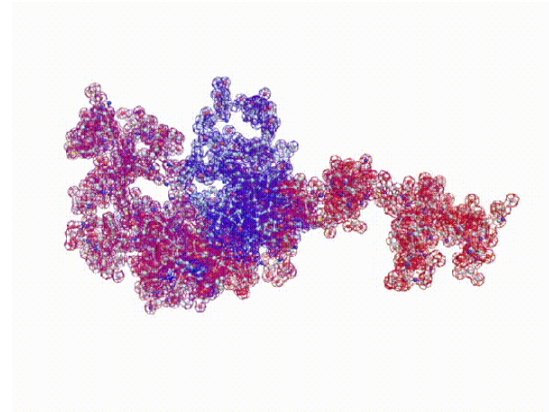


DATA

Kushelev: The presence of antihomologue proteins clearly demonstrates the existence of a 3D genetic code. If it did not exist, proteins with the same amino acid sequence would take the same form. A classic example of antihomologues is binase and barnase.

[Nanoworld Laboratory Newsletters 597](#)

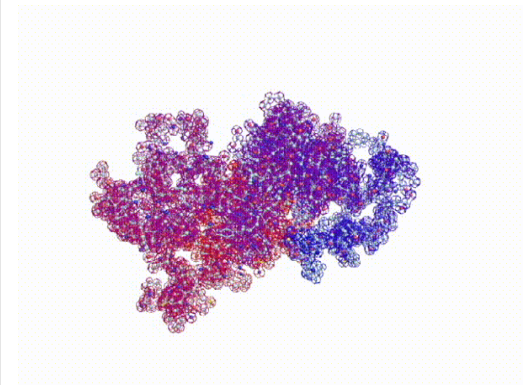
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 TCAGCTTACATAAAGTGTGAATAAATTTTCTCAAACCTGATCGGTCAATTCACTTT



barnase binase

GTT	V	3	GTC	V	5
ATC	I	4	ATT	I	3
AAC	N	4	AAT	N	3
ACG	T	4	ACG	T	5
TTT	F	3	TTT	F	3
GAC	D	5	GAT	D	3
GGG	G	5	GGT	G	3
GTT	V	3	GTA	V	2
GCG	A	3	GCA	A	2
GAT	D	3	GAT	D	3
TAT	Y	3	TAT	Y	3
CTT	L	3	TTA	L	3
CAG	Q	5	ATT	I	3
ACA	T	2	CGC	R	5
TAT	Y	3	TAC	Y	5
CAT	H	3	AAA	K	3
AAG	K	5	CGA	R	2
CTA	L	2	TTG	L	5
CCT	P	3	CCT	P	3
GAT	D	3	GAT	D	3
AAT	N	3	AAC	N	5
TAC	Y	5	TAC	Y	5
ATT	I	3	ATC	I	5
ACA	T	2	ACA	T	2
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TCA	S	2	TCA	S	2
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GCA	A	2	GCA	A	2
CAA	Q	3	AGT	S	3
GCC	A	1	GCT	A	3
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GTG	V	4	GTG	V	5
GCA	A	2	GCA	A	2
TCA	S	2	TCA	S	2
AAA	K	3	AAG	K	5
GGG	G	5	GGA	G	2
AAC	N	5	AAT	N	3
CTT	L	3	CTA	L	2
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GAC	D	5	GAG	E	5
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ATC	I	5	ATC	I	5
GGC	G	5	GGT	G	3
GGA	G	2	GGA	G	2
GAC	D	5	GAT	D	3
ATC	I	5	GTT	V	3
TTC	F	5	TTC	F	5
TCA	S	2	TCT	S	3
AAC	N	5	AAC	N	5
AGG	R	5	CGG	R	5
GAA	E	3	GAG	E	5
GGC	G	5	GGA	G	2
AAA	K	3	CGT	R	3
CTC	L	5	CTT	L	3
CCG	P	5	CCT	P	3
GGC	G	5	TCA	S	2
AAA	K	3	GCA	A	2
AGC	S	5	AGC	S	5
GGA	G	2	GGC	G	5
CGA	R	2	CGA	R	2
ACA	T	2	ACA	T	2
TGG	W	5	TGG	W	5
CGT	R	3	CGT	R	3
GAA	E	3	GAG	E	5
GCG	A	5	GCA	A	2
GAT	D	3	GAT	D	3
ATT	I	3	ATC	I	1
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TAT	Y	3	TAC	Y	1
ACA	T	2	GTC	V	1
TCA	S	2	TCT	S	3
GGC	G	5	GGC	G	5
TTC	F	5	TTC	F	5
AGA	R	3	CGA	R	2
AAT	N	3	AAT	N	3
TCA	S	2	GCT	A	3
GAC	D	5	GAC	D	1
CGG	R	5	CGC	R	1
ATT	I	3	CTC	L	1
CTT	L	3	GTG	V	4
TAC	Y	5	TAT	Y	3
TCA	S	2	TCA	S	2
AGC	S	1	AGT	S	3
GAC	D	1	GAC	D	5
TGG	W	1	TGG	W	5
CTG	L	4	CTC	L	5
ATT	I	3	ATT	I	3
TAC	Y	5	TAC	Y	5
AAA	K	3	AAA	K	3
ACA	T	2	ACA	T	2
ACG	T	5	ACA	T	2
GAC	D	5	GAC	D	5
CAT	H	3	CAT	H	3
TAT	Y	3	TAT	Y	3
CAG	Q	5	GCA	A	2
ACC	T	5	ACT	T	3
TTT	F	3	TTC	F	5
ACA	T	2	ACA	T	2
AAA	K	3	CGT	R	3
ATC	I	5	ATT	I	3
AGA	R	3	CGA	R	2
TAA	0		TAA	0	

>X53697.1 B.intermedius gene for extracellular RNase (binase)
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 CAGACCATATGCAACTTTCACACGATTTCGATAATCAATCAAAAAACAGCCCATTTGACGTAGGGCTG
 TTTTATGCTGCCTATGGC



Today we managed to find several hundred more antihomologue proteins.
 I invite you to the antihomologue exhibition:

Antihomology = Software allotropy

[illegible]

Antihomology = Software allotropy

[illegible]

[illegible]

E E

EEEEEE EE EEE EEE EEE EEE EEE EEE EEE EEE EEE EEE EEE EEE EEE EEE EEE

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EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEYIN
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EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVL

[illegible]

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[illegible]

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E E

EEKEEEEEEE EEEEEEEEEEEEEEEEEEEEEEE EEEFCGEK

EEERNMHCIGKTTPI

[illegible][illegible]

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[illegible]

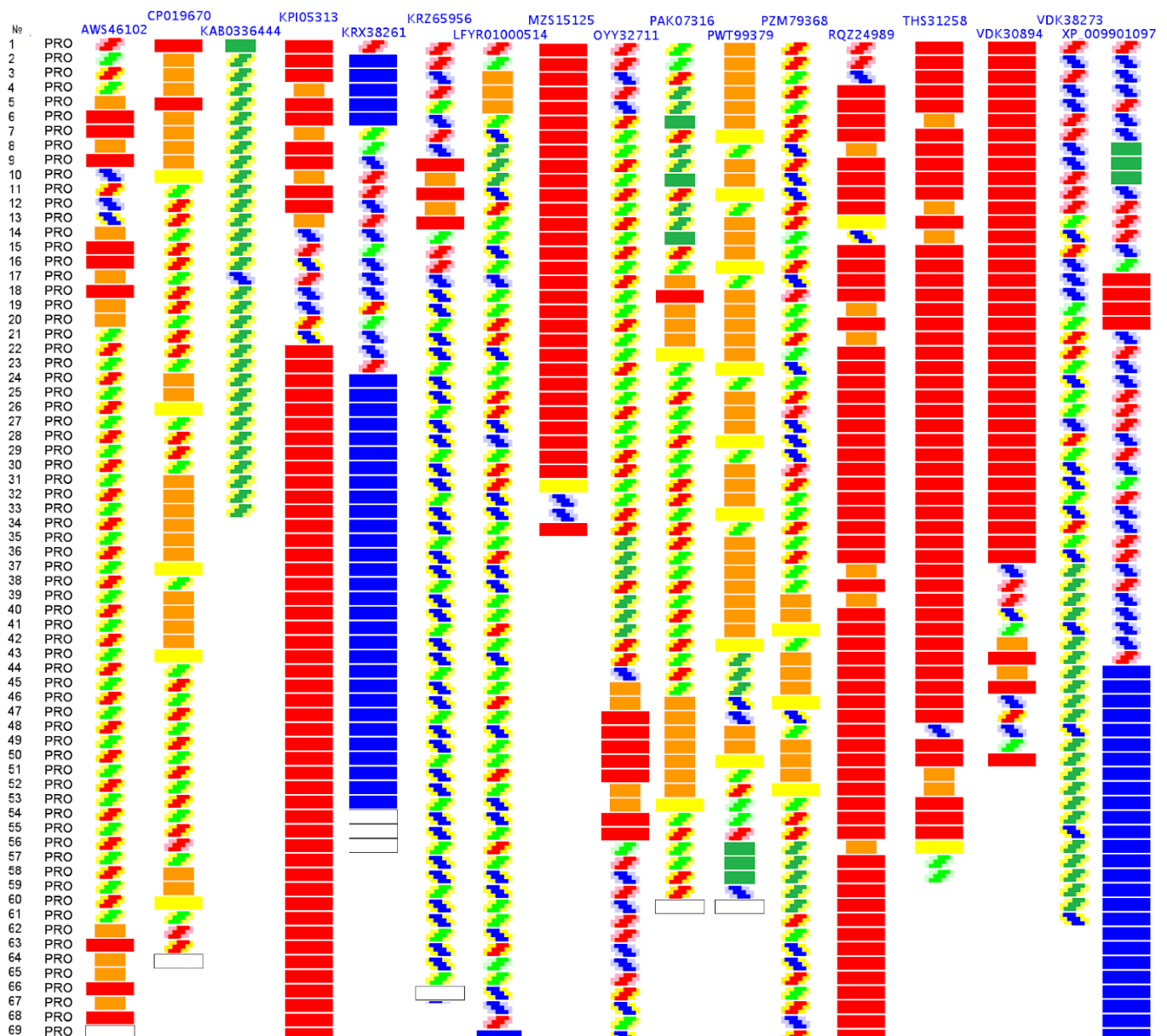
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[illegible][illegible]

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FEEEEEHHHHHSDFFEC

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Antihomology = Software allotropy

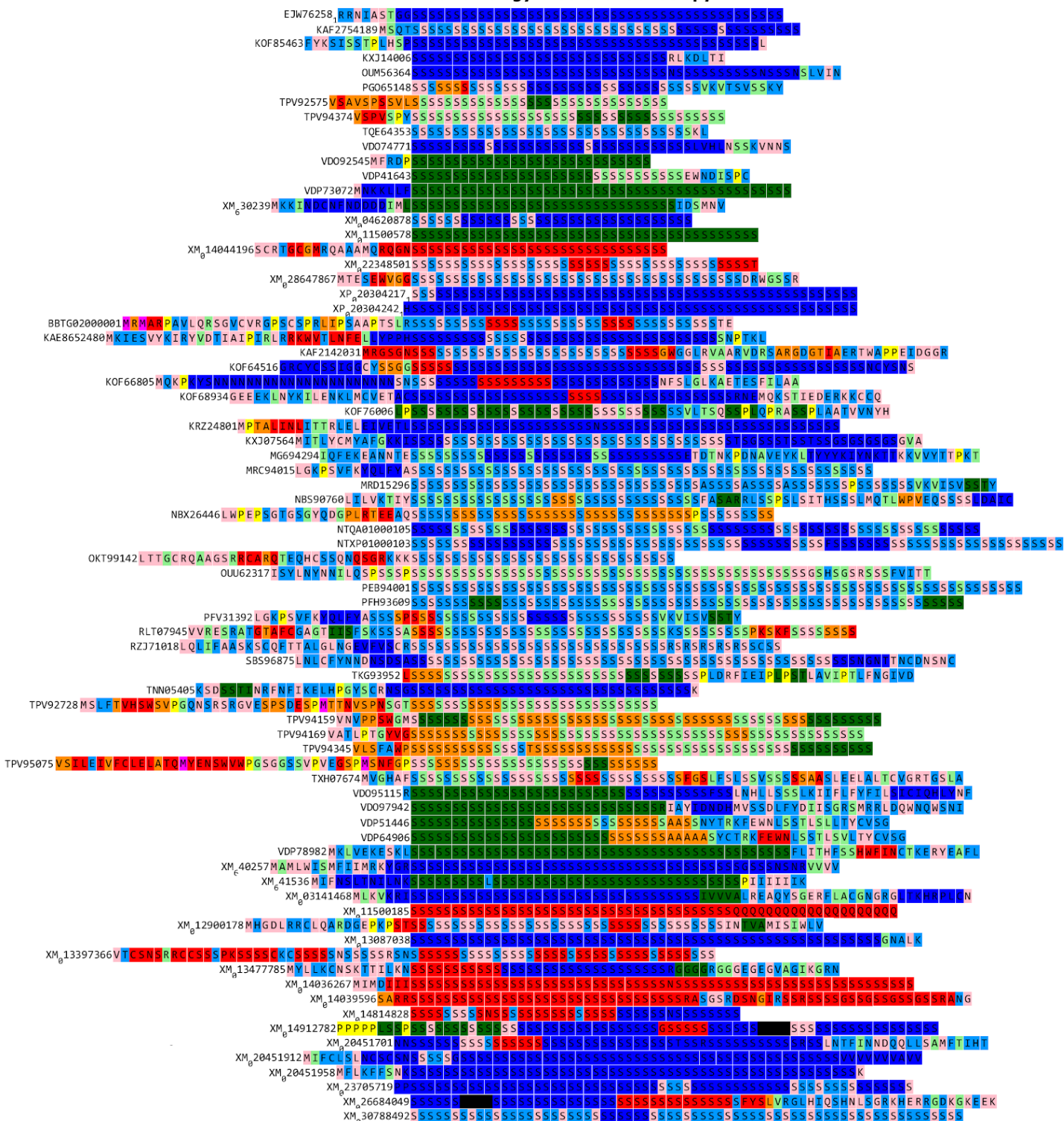


Antihomology = Software allotropy

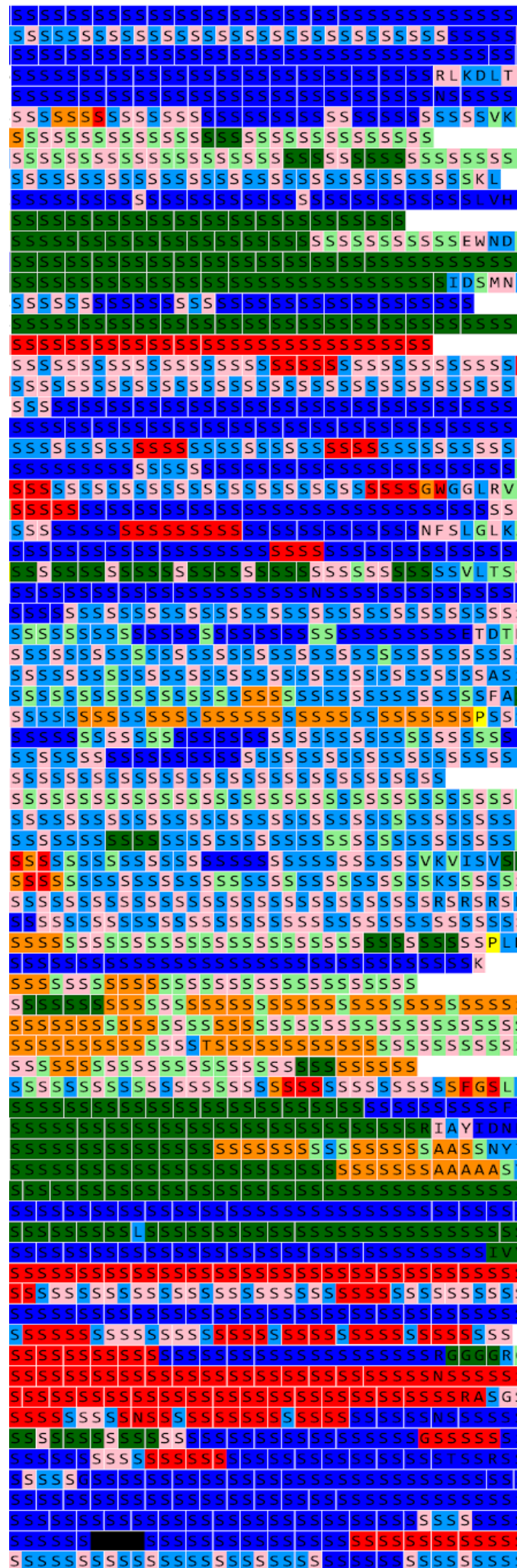
[illegible]

Further evidence for separate coding of amino acid isomers

Antihomology = Software allotropy



Antihomology = Software allotropy



The significantly greater number of secondary structure types of polyserine compared to polyvaline, polyproline, polyglycine, polyglutamine... is additional indirect evidence of coding of different isomers of serine by different triplets. The first indirect evidence is the presence of two groups of triplets coding for serine, arginine and leucine.

The folding hypothesis is refuted by the software
allotropy (compositional coding) of protein structure

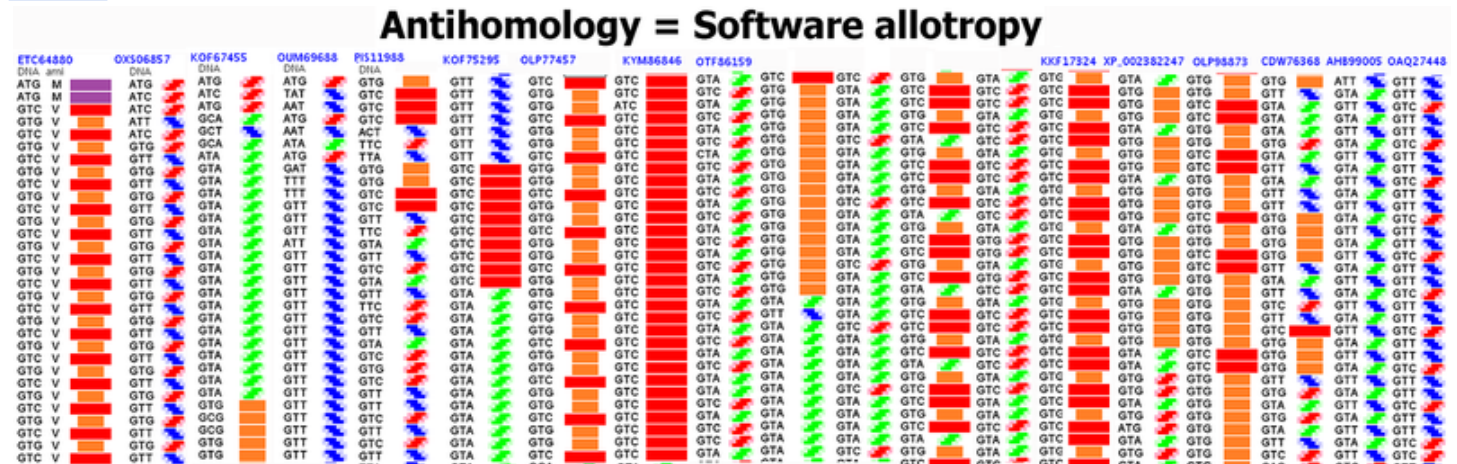
Program protein's allotropy disproves the folding hypothesis

Программная аллотропия белков опровергает гипотезу фолдинга

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1	ATG	ATG	AAA	ATA	ATG	ATG	ATG	ATG	ATG
2	GAG	TAT	GAG	AAC	TAT	TCC	CTG	GAG	CTG
3	AAA	AAG	GTA	AAA	CCA	GGA	CAG	GAG	TCC
4	AAA	AAG	TGT	GAG	AAC	TGG	GAT	GAG	GTA
5	AAA	AAG	ATG	AAA	CCA	ATG	CAG	GAG	ACA
6	AAA	AAG	TAT	GAG	AAC	GAT	AGC	GAG	GTG
7	AAA	AAG	GTA	AAA	CCA	GGA	TAC	GAG	ACA
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9	AAA	AAG	ATG	AAA	CCA	ATG	GAG	GAG	ACA
10	AAA	AAG	TAT	GAG	AAC	GAT	GCC	GAG	TCT
11	AAA	AAG	GTA	AAA	CCA	GGA	ATC	GAG	ACA
12	AAA	AAG	TGT	GAG	AAC	TGG	GCG	GAG	GTG
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34	AAA	AAG	TAT	GAG	AAC	GAT	CAG	GAG	GTA
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37	AAA	AAG	ATG	AAA	CCA	ATG	GTC	GAG	ACA
38	AAA	AAG	TAT	GAG	AAC	GAT	GAG	GAG	GTA
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144	AAA	AAG	TGT	GAG	AAC	TGG	ATG	GAG	GTA
145	AAA	AAG	ATG	AAA	CCA	ATG	TCC	GAG	ACA

The easiest way to test the new technology is by X-ray diffraction on simple structures such as polyvalin:

[Enlarge](#)



ETC64880: <https://www.ncbi.nlm.nih.gov/nucore/564568708>

OXS06857: <https://www.ncbi.nlm.nih.gov/nucore/1226034760>

KOF67455: <https://www.ncbi.nlm.nih.gov/nucore/918287724>

OUM69688: <https://www.ncbi.nlm.nih.gov/nucore/1198313040>

PIS11988: <https://www.ncbi.nlm.nih.gov/nucore/1277217132>

KOF75295: <https://www.ncbi.nlm.nih.gov/nucore/918302080>

OLP77457: <https://www.ncbi.nlm.nih.gov/nucore/1129165616>

KYM86846: https://www.ncbi.nlm.nih.gov/nucore/1009361734?&fmt_mask=65536

OTF86159: <https://www.ncbi.nlm.nih.gov/nucore/CM007906.1?report=fasta&sat=37&satkey=307832265&itemID=1362>

KKF17324: https://www.ncbi.nlm.nih.gov/nucore/808866584?&fmt_mask=65536

XP_002382247: <https://www.ncbi.nlm.nih.gov/nucore/238502026>

OLP98873: <https://www.ncbi.nlm.nih.gov/nucore/1129194414>

CDW76368: <https://www.ncbi.nlm.nih.gov/nucore/678335661>

AHB99005: https://www.ncbi.nlm.nih.gov/nucore/564747871?&fmt_mask=65536

OAQ27448: <https://www.ncbi.nlm.nih.gov/nucore/1032646064>

OUM69730: <https://www.ncbi.nlm.nih.gov/nucore/1198313040>

OGL53990: <https://www.ncbi.nlm.nih.gov/nucore/1084158629>

EIE92391: <https://www.ncbi.nlm.nih.gov/nucore/76151980>

XP_001590524: <https://www.ncbi.nlm.nih.gov/nucore/156049114>

OTG33229: https://www.ncbi.nlm.nih.gov/nucore/CM007891.1?from=7600734&to=7601591&sat=37&sat_key=307832447

OLQ06943: <https://www.ncbi.nlm.nih.gov/nucore/1129204435>

XP_001895277: <https://www.ncbi.nlm.nih.gov/nucore/170580473>

XP_001584576: <https://www.ncbi.nlm.nih.gov/nucore/156030497>

KOF84884: <https://www.ncbi.nlm.nih.gov/nucore/918315370>