ANVIUNPRO-2040$^{(RC)}$

Introduction

After seeing immense sufferings and unbelievable losses incurred from covid-19, I dreamt of a typical concept which I coined as ***"anviunpro-2040^{RC}"***. Its expanded form is given below:

"**An**ti**Vi**ral**Un**iversal**Pro**tein **2040**^{RC}" [RC: Rama Chandran]

No doubt, this is 100% hypothetical and ever existed earlier and I am not sure whether any such product could be possible to synthesize. The previous basic idea behind this concept was 1.5 year old under the name "**RCV-2020**" [***Ramachandran Concept of Virus-2020*** where **2020** is not just the year but **20 polypeptide chains** each having **20 α-amino acid** moieties] where I opined that synthesis of such a typical protein will serve as an antiviral drug/product and I also described all the details of its synthesis in a laboratory by providing all necessary steps.

However, a very recently modified version of RCV-2020 by name **UPUA-2020^{RC}** (universal protein-universal antivirus-2020) in which I proposed a very long polypeptide chain having ***800 α-AA*** moieties which includes almost every possible combination (eg: AA-AG-AQ etc.,).

But, whatever information I got from a number of experts regarding this synthesis is that it is impossible (as on today) to make such a very long polypeptide chain by artificial means with 100% accuracy and a maximum of 50 α-AA based chain alone could be synthesized with suitable 3D-conformation (i.e a small protein like). So, I would like to modify my earlier UPUA-2020 & this present **antiviunpro-2040^{RC}** is just like its eldest child. Here, the four digit numeral **2040** is also just like **2020** but, 20 polypeptide chains & 40 α-AA in each chain with specific sequence. I have arranged 40 α-AA in such a manner that each α-AA likely to pair with every other α-AA (i.e 19) including itself.

I hope, this new protein **antiviunpro-2040^{RC}** may take its birth in near future that opens all possible doors to synthesize many such pharmaceutical drugs which have minimal level of side effects, if any.

Synthesis of Polypeptide Chains [20]

Source: Naturally occurring α-amino acids and respective m-RNA based codons

Proposed Procedure

Step-1: Synthesis of a polypeptide chain which starts with specific α-AA and the chain with all the other 19 α-AA moieties.

Step-2: Synthesis is carried out in such a way that, specific α-AA must pair with itself and also each of other 19 members.

Step-3: Once 20 such polypeptides are ready (*each has 40 α-AA moieties), all samples must be dissolved in suitable non-toxic solvent (water, ethanol etc.,) to prepare 20 samples.

Step-4: Mixing up of all 20 samples to get a mixture by name **antiviunpro-2040^{RC}** where 20 polypeptide chains with definite 3D-conformation exist. There may be or may not be any sort of union (or combination) of two or more such chains to exist as 4^0 (quaternary) type protein.

α-AA Sequences-(m)-RNA Templates

[1] As each polypeptide must be rich in only one α-AA, amount of such α-AA to be selected shall be nearly 19 times that of each of other 19 members in terms of number (*or mole)

Eg: If a polypeptide chain-1 needs Alanine rich, then,

[a] Amount of Alanine needed = 1.90 mol (say)

[b] Amount of each of other 19 α-AA needed = 0.10 mol hence total number of moles (all α-AA together) = 1.90 + 1.90 = 3.80

Table-1

Name of α-AA	Letter Code	Nature	Optical activity	Molar mass
Alanine	[A]	Neutral	Active	89 g/mol
Arginine	[R]	Basic	Active	174 g/mol
Asparagine	[N]	Neutral	Active	132 g/mol
Aspartic acid	[D]	Acidic	Active	133 g/mol
Cysteine	[C]	Neutral	Active	121 g/mol
Glutamine	[Q]	Neutral	Active	146 g/mol
Glutamic acid	[E]	Acidic	Active	147 g/mol
Glycine	[G]	Neutral	Inactive	75 g/mol
Histidine	[H]	Basic	Active	155 g/mol
Isoleucine	[I]	Neutral	Active	131 g/mol
Leucine	[L]	Neutral	Active	131 g/mol
Lysine	[K]	Basic	Active	146 g/mol
Methionine*	[M]	Neutral	Active	149 g/mol
Phenyl alanine	[F]	Neutral	Active	165 g/mol
Proline**	[P]	Basic	Active	115 g/mol
Serine	[S]	Neutral	Active	105 g/mol
Threonine	[T]	Neutral	Active	119 g/mol
Tryptophan	[W]	Basic	Active	204 g/mol
Tyrosine	[Y]	Neutral	Active	189 g/mol
Valine	[V]	Neutral	Active	117 g/mol

Interactions among 20 (or even more) Poly-Peptide-Chains [PPCs]

In each PPC, only one specific amino acid moiety is found rich (by number) and based on number of hydrophobic and hydrophilic moieties in each PPC, the interaction between any two such PPC changes during their folding (from 1^0 to 2^0 to 3^0 levels).

For example, in PPC-1, the chain is rich in Alanine content (in number) and alanine has methyl part (hydrophobic) at α-position (*from COOH) apart from NH_2 functional group.

But in case of PPC-11, 12 & 20, this hydrophobic character is greatly enhanced so, during the formation of 4^0 structure (or even 3^0 structure), these hydrophobic parts usually away from polar ends (i.e aqueous layer) which themselves act as protective shield towards the system but, readily interacts with viral proteinous part (*especially spike), thus does not allow it to interact with m-RNA of host. However, the way how a PPC behaves in the body is really an astonishing aspect.

Observe the following 20 PPC (sequence) where each α-AA is shown by its original single letter symbol only* [**Read each chain from L to R only**]

40 α-AA-PPC-1 [ALANINE rich, % (by number) =52.5] [Solvent: Ethanol]

A	A	A	R	A	N	A	D	A	C	A	Q	A	E	A	G	A	H	A	I
A	L	A	K	A	M	A	F	A	P	A	S	A	T	A	W	A	Y	A	V

40 α-AA PPC-2 [ARGININE rich, % (by number) =52.5] [Solvent: Ethanol]

R	R	R	N	R	D	R	C	R	Q	R	E	R	G	R	H	R	I	R	L
R	K	R	M	R	F	R	P	R	S	R	T	R	W	R	Y	R	V	R	A

40 α-AA PPC-3 [ASPARAGINE rich, % (by number) =52.5] [Solvent: Ethanol]

N	N	N	D	N	C	N	Q	N	E	N	G	N	H	N	I	N	L	N	K
N	M	N	F	N	P	N	S	N	T	N	W	N	Y	N	V	N	A	N	R

40 α-AA PPC-4 [ASPARTIC ACID rich, % (by number) =52.5] [Solvent: Water]

D	D	D	C	D	Q	D	E	D	G	D	H	D	I	D	L	D	K	D	M
D	F	D	P	D	S	D	T	D	W	D	Y	D	V	D	A	D	R	D	N

40 α-AA PPC-5 [CYSTEINE rich, % (by number) =52.5] [Solvent: Water]

C	C	C	Q	C	E	C	G	C	H	C	I	C	L	C	K	C	M	C	F
C	P	C	S	C	T	C	W	C	Y	C	V	C	A	C	R	C	N	C	D

40 α-AA PPC-6 [GLUTAMINE rich, % (by number) =52.5] [Solvent: Water]

Q	Q	Q	E	Q	G	Q	H	Q	I	Q	L	Q	K	Q	M	Q	F	Q	P
Q	S	Q	T	Q	W	Q	Y	Q	V	Q	A	Q	R	Q	N	Q	D	Q	C

40 α-AA PPC-7 [GLUTAMIC ACID rich, % (by number) =52.5] [Solvent: Water]

E	E	E	G	E	H	E	I	E	L	E	K	E	M	E	F	E	P	E	S
E	T	E	W	E	Y	E	V	E	A	E	R	E	N	E	D	E	C	E	Q

40 α-AA PPC-8 [GLYCINE rich, % (by number) =52.5] [Solvent: Water]

G	G	G	H	G	I	G	L	G	K	G	M	G	F	G	P	G	S	G	T
G	W	G	Y	G	V	G	A	G	R	G	N	G	D	G	C	G	Q	G	E

40 α-AA PPC-9 [HISTIDINE rich, % (by number) =52.5] [Solvent: Ethanol]

H	H	H	I	H	L	H	K	H	M	H	F	H	P	H	S	H	T	H	W
H	Y	H	V	H	A	H	R	H	N	H	D	H	C	H	Q	H	E	H	G

40 α-AA PPC-10 [ISOLEUCINE rich, % (by number) =52.5] [Solvent: Ethanol]

I	I	I	L	I	K	I	M	I	F	I	P	I	S	I	T	I	W	I	Y
I	V	I	A	I	R	I	N	I	D	I	C	I	Q	I	E	I	G	I	H

40 α-AA PPC-11 [LEUCINE rich, % (by number) =52.5] [Solvent: Ethanol]

L	L	L	K	L	M	L	F	L	P	L	S	L	T	L	W	L	Y	L	V
L	A	L	R	L	N	L	D	L	C	L	Q	L	E	L	G	L	H	L	I

40 α-AA PPC-12 [ISOLEUCINE rich, % (by number) =52.5] [Solvent: Ethanol]

K	K	K	M	K	F	K	P	K	S	K	T	K	W	K	Y	K	V	K	A
K	R	K	N	K	D	K	C	K	Q	K	E	K	G	K	H	K	I	K	L

40 α-AA PPC-13 [METHIONINE rich, % (by number) =52.5] [Solvent: Ethanol]

M	M	M	F	M	P	M	S	M	T	M	W	M	Y	M	V	M	A	M	R
M	N	M	D	M	C	M	Q	M	E	M	G	M	H	M	I	M	L	M	K

40 α-AA PPC-14 [PHENYL ALANINE rich, % (by number) =52.5] [Solvent: Ethanol]

F	F	F	P	F	S	F	T	F	W	F	Y	F	V	F	A	F	R	F	N
F	D	F	C	F	Q	F	E	F	G	F	H	F	I	F	L	F	K	F	M

40 α-AA PPC-15 [PROLINE rich, % (by number) =52.5] [Solvent: Ethanol]

P	P	P	S	P	T	P	W	P	Y	P	V	P	A	P	R	P	N	P	D
P	C	P	Q	P	E	P	G	P	H	P	I	P	L	P	K	P	M	P	F

40 α-AA PPC-16 [SERINE rich, % (by number) =52.5] [Solvent: Water]

S	S	S	T	S	W	S	Y	S	V	S	A	S	R	S	N	S	D	S	C
S	Q	S	E	S	G	S	H	S	I	S	L	S	K	S	M	S	F	S	P

40 α-AA PPC-17 [THREONINE rich, % (by number) =52.5] [Solvent: Ethanol]

T	T	T	W	T	Y	T	V	T	A	T	R	T	N	T	D	T	C	T	Q
T	E	T	G	T	H	T	I	T	L	T	K	T	M	T	F	T	P	T	S

40 α-AA PPC-18 [TRYPTOPHAN rich, % (by number) =52.5] [Solvent: Ethanol]

W	W	W	Y	W	V	W	A	W	R	W	N	W	D	W	C	W	Q	W	E
W	G	W	H	W	I	W	L	W	K	W	M	W	F	W	P	W	S	W	T

40 α-AA PPC-19 [TYROSINE rich, % (by number) =52.5] [Solvent: Ethanol]

Y	Y	Y	V	Y	A	Y	R	Y	N	Y	D	Y	C	Y	Q	Y	E	Y	G
Y	H	Y	I	Y	L	Y	K	Y	M	Y	F	Y	P	Y	S	Y	T	Y	W

40 α-AA PPC-20 [VALINE rich, % (by number) =52.5] [Solvent: Ethanol]

V	V	V	A	V	R	V	N	V	D	V	C	V	Q	V	E	V	G	V	H
V	I	V	L	V	K	V	M	V	F	V	P	V	S	V	T	V	W	V	Y

[1] This typical protein has sequence of many α-amino acids where the long PPC begins with specific α-amino acid only (eg: Alanine in PPC-1).

[2] The polypeptide chain may begin with N-terminal or C-terminal based on whether free NH_2 or free COOH part is left with the first α-amino acid (eg: alanine).

[3] I always propose that, it is better to use only one possible codon to code any given α-amino acid (eg: GCC = Alanine)

[4] In this long PPC, there exists every possible pair of α-AA moieties so that this typical protein (*if 3D-pattern is clearly known) can fight against all types of viruses in spite of mutations they undergo during their transformation.

[Note: Reading from top to bottom, then moving towards right and again reading in same pattern. Each vertical column has 40 codons]

This typical anviunpro-2040^{RC} must be tested on any R&D platform taking all possible viruses right from simple cold to present Covid-19 (*all variants). The results alone indicate its functionality or effectiveness. As growth of any virus follows 1st order kinetics with specific half-life ($t_{0.5}$), addition of this anviunpro-2040^{RC} must show a gradual or even a rapid decline in the rate of multiplication of viral cells which can be studied as d[N]/dt versus Time (t) graph**

PPC-1	PPC-2	PPC-3	PPC-4	PPC-5	PPC-6	PPC-7	PPC-8	PPC-9	PPC-10	PPC-11	PPC-12	PPC-13	PPC-14	PPC-15
GCC	CGU	AAU	GAC	UGC	CAG	GAG	GGC	CAU	AUU	CUA	AAG	AUG	UUC	CCU
GCU	CGC	AAU	GAC	UGC	CAG	GAG	GGA	CAU	AUC	CUC	AAA	AUG	UUU	CCA
GCA	CGA	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
CGU	AAU	GAU	UGU	CGG	GAG	GGG	CAU	AUU	CUU	AAG	AUG	UUC	CCG	CAG
GCC	CGG	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
AAU	GAU	UGU	CAA	GAA	GGG	CAU	AUU	CUU	AAG	AUG	UUC	CCG	CAG	ACC
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
GAU	UGU	CAA	GAA	GGU	CAU	AUU	CUU	AAG	AUG	UUC	CCG	CAG	ACC	UGG
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
UGU	CAA	GAA	GGU	CAU	AUU	CUU	AAG	AUG	UUC	CCG	CAG	ACC	UGG	UAU
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
CAA	GAA	GGU	CAU	AUU	CUU	AAG	AUG	UUC	CCG	CAG	ACC	UGG	UAU	GUG
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
GAA	GGU	CAU	AUU	CUU	AAG	AUG	UUC	CCG	AGU	ACC	UGG	UAU	GUG	GCA
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
GGU	CAU	AUU	CUU	AAA	AUG	UUC	CCG	AGU	ACU	UGG	UAU	GUG	GCA	CGU
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
CAU	AUU	CUU	AAA	AUG	UUC	CCG	AGU	ACU	UAG	UAU	GUG	GCA	CGU	AAC
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
AUU	CUU	AAA	AUG	UUU	CCG	AGU	ACU	UAG	UAC	GUG	GCA	CGU	AAC	GAC
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
CUU	AAA	AUG	UUU	CCC	AGU	ACU	UAG	UAC	GUG	GCA	CGU	AAC	GAC	UGC
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
AAA	AUG	UUU	CCC	AGU	ACU	UAG	UAC	GUG	GCA	CGU	AAC	GAC	UGC	CAG
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
AUG	UUU	CCC	AGU	ACA	UAG	UAC	GUG	GCA	CGU	AAC	GAC	UGC	CAG	GAG
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
UUU	CCC	AGU	ACA	UGG	UAC	GUG	GCA	CGU	AAC	GAC	UGC	CAG	GAG	GGG
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
CCC	AGU	ACA	UGG	UAU	GUG	GCA	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
AGU	ACA	UGG	UAU	GUG	GCA	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
ACA	UGG	UAU	GUG	GCC	CGU	AAC	GAC	UGC	CAA	GAG	GGG	CAC	AUA	CUG
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
UGG	UAU	GUG	GCC	CGU	AAC	GAC	UGC	CAA	GGG	GGG	CAC	AUA	CUG	AAG
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
UAU	GUG	GCC	CGU	AAU	GAC	UGC	CAA	GGG	GCG	CAC	AUA	CUG	AAG	AUG
GCC	CGU	AAC	GAC	UGC	CAG	GAG	GGG	CAC	AUA	CUG	AAG	AUG	UUC	CCG
GUG	GCC	CGU	AAU	GAC	UGC	CAA	GAA	GCG	CAC	AUA	CUG	AAG	AUG	UUC

PPC-16	PPC-17	PPC-18	PPC-19	PPC-20
AGU	ACG	UGG	UAU	GUC
AGC	ACC	UGG	UAC	GUA
AGU	ACU	UGG	UAU	GUG
ACU	UGG	UAU	GUG	GCA
AGU	ACU	UGG	UAU	GUG
UGG	UAU	GUG	GCA	CGU
AGU	ACU	UGG	UAU	GUG
UAU	GUG	GCA	CGU	AAC
AGU	ACU	UGG	UAU	GUG
GUG	GCA	CGU	AAC	GAC
AGU	ACU	UGG	UAU	GUG
GCA	CGU	AAC	GAC	UGC
AGU	ACU	UGG	UAU	GUG
CGU	AAC	GAC	UGC	CAG
AGU	ACU	UGG	UAU	GUG
AAC	GAC	UGC	CAG	GAG
AGU	ACU	UGG	UAU	GUG
GAC	UGC	CAG	GAG	GGG
AGU	ACU	UGG	UAU	GUG
UGC	CAG	GAG	GGG	CAC
AGU	ACU	UGG	UAU	GUG
CAG	GAG	GGG	CAC	AUA
AGU	ACU	UGG	UAU	GUG

Disclaimer

[1] This antiviunpro-2040^{RC} is purely hypothetical concept and my brain child. I did not know whether similar concept was already existed elsewhere (or) not.

[2] I opine that, this antiviunpro-2040^{RC} if synthesized in any laboratory may be tested on different viral cells to come to any conclusion.

[3] I will be so happy if any Nobel laureate gives a good critic (positive or negative feedback) on this article which itself shall be taken as if I won the Nobel Prize.

[4] A similar article was already published by me in IJSER (2020) for which I received the certificate of publication too.

[5] This article does not have any patent rights (*I tried but patent rights shall not be given to articles, as what they said).

[6] I sent its earlier version (same concept) to many R&D platforms across the globe (*2020).

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GAG	GGG	CAC	AUA	CUG
AGU	ACU	UGG	UAU	GUG
GG	CAC	AUA	CUG	AAG
AGU	ACU	UGG	UAU	GUG
CAC	AUA	CUG	AAG	AUG
AGU	ACU	UGG	UAU	GUG
AUA	CUG	AAG	AUG	UUC
AGU	ACU	UGG	UAU	GUG
UG	AAG	AUG	UUC	CCG
AGU	ACU	UGG	UAU	GUG
AAG	AUG	UUC	CCG	AGU
AGU	ACU	UGG	UAU	GUG
AUG	UUC	CCG	AGU	ACU
AGU	ACU	UGG	UAU	GUG
UUC	CCG	AGU	ACU	UGG
AGU	ACU	UGG	UAU	GUG
CCG	AGU	ACU	UGG	UAU

Polypeptide Chains [40 α-AA units]-Interaction Strengths [*Assumptions]

[1] A simple dipeptide has two possible structures based on the amino acid which contributed OH part [from COOH] (or) H part [from NH_2].
eg: Glycine + Alanine → Glycylalanine [1] + Alanylglycine [2] where in [1], NH_2 of **Gly** is free while in [2], NH_2 of **Ala** is free. So,
[1] has structural formula as : H_2N-CH_2-CO-NH-*$\mathbf{C}$H(Me)-COOH [N to C terminal]
[2] has structural formula as: H_2N-*$\mathbf{C}$H(Me)-CO-NH-CH_2-COOH [N to C terminal]
In both [1] and [2], C* = stereogenic centre (or chiral carbon) and both are optically active.

[2] Secondly, it is [D] or [L] isomer that plays another role. As L-isomer is the natural one in most of cases, problem of [D]-based isomer may be ruled out unless amino acid exists as receimic form [dℓ-pair].

[3] In case of a polypeptide chain, the substituent [say G] on C bearing NH_2 and also COOH may orient itself in space in such a manner so as to minimize torsional type strain (or) steric repulsion type based strain, if any hence such groups are usually protruded from the chain. If this G has hydrophobic part (eg: Isopropyl in case of **Valine**), it prefers non-aqueous systems to develop van der Waal based (or) Dispersion based intermolecular attractions/repulsions based on whether they exist in eclipsed or staggered conformation.

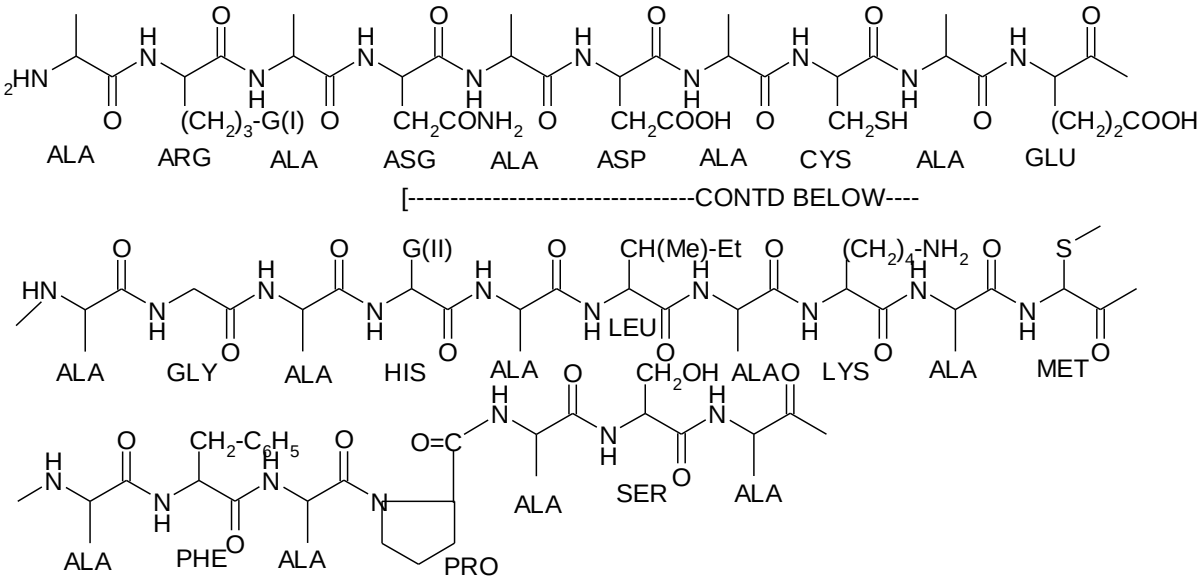
[4] When we observe each of above 20 polypeptide chains, in each chain, only one specific amino acid is found rich (by number) which may even by mass (% by mass too). Since hydrophobic based side chain (substituent = G) interacts less with aqueous system unless stabilized by H-bonding, metal ions such as $Zn^{(II)}$, $Co^{(III)}$, $Fe^{(II)}$, $Mo^{(III)}$ etc.,

[5] When hydrophobic rich polypeptide chain [say X] happens to interact with:
[a] hydrophilic rich polypeptide chain [Y] => [X] -----[Y] interaction is much weaker than [Y]------[Water] interaction so, [Y] prefers to be in soluble state than [X]
[b] hydrophobic rich polypeptide chain [say Z] => [X] ----[Z] interaction is much stronger than [X] -----[Water] (or)[Z] -----[Water] hence such chains prefer to be away from H_2O (polar) ends so remains sparingly soluble state.

[6] When I analyzed covid-19 (sars-cov-19, virus), I found it as hydrophobic rich than other so, action of virus on any specific cell (or organ) prefers hydrophobic rich protein part of such organ so that, its binding ability is enhanced to a greater extent hence causing a great trouble in breathing (eg: Lung infection), digestion (eg: Liver infection) etc.,

[7] Out of 20 such PPC (*polypeptide chain), I assumed that those having Cysteine, Arginine, Histidine, Serine, Glycine, Aspartic acid, Glutamic acid and Threonine **rich** based alone as hydrophilic based and rest, hydrophobic (*relatively more). So, in case, if all these twenty PPC happen to exist as mixture in **50% (v/v)** Ethanol (aqueous) solution, I opine that, only these 8 PPC alone likely to form 4^0 (quaternary) globular protein (***320** AA moieties). The other 12 PPC may give β-pleated (*fibrous based) protein.

[8] As this mixture is **hydrophobic rich**, it may interact with viral protein to cause a greater coagulation since **hydrophilic** based protein protect **hydrophobic** based from coagulation.



Final Word

This hypothesis may not necessarily come true on practical platform due to many and unexpected traits or hurdles. However, my idea may allow other legends in this field to try in a different way to test it or even synthesize it. As per my little knowledge, synthesis of any polypeptide chain of length more than 50 α-AA moieties has not been achieved yet, if any well-known R&D tries to synthesize 20 such separate polypeptide chains (as per specific type of sequence which I shown) and later allow all those to form a complex protein. In such case my view of eradicating any sort of virus may be possible.

I welcome critics from every possible corner across this globe……

Thank you on and all who read this article……

Place: HYDERABAD
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