Modelinig and Simulation of Amino Acide

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ABSTRACT
The study of amino acids was one of the important issues in bioinformatics, and the prediction of the secondary structure of proteins was one of the important steps in the knowledge of the structure and function of the protein. In this research, an algorithm to generate amino acids is suggested using simulation. A software program is build using MATLAB according to the proposed algorithm for the purpose of conducting simulation experiments. Fourteen simulation experiments were performed to generate sequences of different sizes of amino acids of fourteen protein, some of them is private of mitochondria diseases and some other were taken from other types of proteins. Comparisons are performed between the data generated by the proposed algorithm with real data available in international global centers in genetic engineering databases. Percentages of successfulness of similarities and identity between successive cases with those generated by the simulation program were calculated. The practical application of the proposed algorithm indicated that this algorithm gives encouraging results than the similarities proportion between generated data with real data are sometimes exceeds 90%.

Keywords
modeling,simulation, bioinformatics, amino acids, prediction, secondary structure of proteins.

1. INTRODUCTION
The process of identification of the amino acids and genes analysis considered a modernness important concept،and finds a great interest by the searchers .

The huge development in the bimolecular and biochemical science and analysis and study of the anatomical map which illustrates the genes or the hereditary formants carry in human inside the human cells .

In addition to the use of the nuclear acid DNA in achieving trust of people because it is the most important biological formant and the most accurate one، made the need so important to read the chain of the nuclear acid DNA and identify it .

The proteins perform a lot of different functions and in general it consists of 20 different amino acids combined together by peptide bond to determine the proteins by linear sequence from these amino acids ,and this sequence of amino acid determine the final corps and function of the protein .

In general the protein molecules have different levels of composition contains the initial composition level and the secondary composition level and the tertiary .[2]composition level and sometimes the 4th level in some proteins

The reading of the amino acids sequence considered as the most important concept of biological statistics because the most diseases in human should investigated

for their hereditary bases and causes to make it easy for the doctors to treat them , that's why it becomes so important to determine the basic proteins composition ,and also the determination of the first step to build the knowledge and opens the door to design treatments that suits the humans hereditary specs and to understand the elderly health problems . Not all the amino acids leans to get in or involve in the secondary composition and this is because some amino acids are more leaning to get in Alpha _helices composition , in other side some amino acids leans to become Beta – strand and some leans to weakens or destroy the helixes because of the clash of the side chains and in other side some of the amino acids are almost suitable to all the composition Table(1) declines the leaning of the amino acid to get in secondary composition and it is noticed that the favoring of amino acids to get in one of the compositions is not complete [5], [6]

Table (1):Inclination amino acid to enter in to secondary structures.

amino acid	α- helixes	β- strands	Turn
Alanine	1.29	0.90	0.78
Cysteine	1.11	0.74	0.80
Leucine	1.30	1.02	0.59
Methionine	1.47	0.97	0.39
Glutamic Acid	1.44	0.75	1.00
Glutamine	1.27	0.80	0.97
Histidine	1.22	1.08	1.69
Lysine	1.23	0.77	0.96
Valine	0.91	1.49	0.47
Isoleucine	0.97	1.45	0.51
Phenylalanine	1.07	1.32	0.58
Tyrosine	0.72	1.25	1.05
Tryptophan	0.99	1.14	0.75
Threonine	0.82	1.21	1.03
Glycine	0.56	0.92	1.64
Serine	0.82	0.95	1.33
Aspartic Acid	1.04	0.72	1.41

Asparagine	0.90	0.76	1.28
Proline	0.52	0.64	1.91
Arginine	0.96	0.99	0.88

2. PREDICTION OF THE SECONDARY PROTEIN COMPOSITION

The process of prediction of secondary structure of a protein composition from its primary sequence one considered as a special importance in biochemistry . and the prediction of the protein corps according to the sequence of the amino acids is considered as one of the main unsolved problems in bimolecular science . in addition to that the detection of the proteins composition is so important to understand the keys of different functions of these proteins. [11]

The detection of the main (basic) functions of the proteins and their structural composition became one of the great challenges in drug designing field

And with the increase of differences between the amount of knowledge that published by the genome projects and the number of discovered proteins with the function and compositions makes the dependence on computerized informational tools inevitable . The process of creating proteins takes place first by the use of the DNA hereditary material composing genes from the cells as a map for its building , then the second stage of preparing protein will take place in the cell during the protein molecules to certain composition to do the function which is responsible for in the cell , And the type of the taken secondary composition by the protein molecule considered as a key to this preparing process which done through molecular folding by away that determined by its first composition till the final normal composition which will do its function [2]. There are a lot of method s for detection of proteins secondary composition and these methods differ from each other by their accurate intuition to the 2ndory composition and also they differ from generation to generation The enhancements were taken upon the old methods were basically depend on considering the special relationship with protein rolling theory and the inter ship that occurs between the proteins and by these enhancements the special statistics of each residue has returned depending a large number of compositionally detected proteins .

In addition to input of a lot of possible residues inter ship and the most famous method that used in detecting the secondary protein composition which has been suggested by the two researchers Chou and Fasman in the seventies

The chou and fasman methods determine the possibility of Alpha- helices composition and Beta- strands taken by the amino acids depending on the x-ray analysis results of a lot of well-known second compositioning proteins .

The possibility of taking Alpha- helices composition by a residue depends on the possibility of existence of this residue within the Alph- helices composition regions that could be calculated by this equation [5]:

$$f_\alpha = \frac{No.\ of\ x\ residue\ in\ \alpha\ regions}{Total\ No.\ of\ x\ residues} \quad (1)$$

And this gives an example of different residues that exist in Alpha − helices region and usually composition parameter calculated by this equation [6]:

As f_α the probability represent different residues that fall within the snail body area-Alpha,And is usually calculated body spiral parameter of the formula [10]:

$$P_\alpha = \frac{f_\alpha}{< f_\alpha >} \quad (2)$$

The $< f_\alpha >$ represents the average of the possibility of the residues that exists in the Alpha- helices region and in same way the possibility of existence of this residue in Beta –strands composition can be calculated by this equation [5].

$$f_\beta = \frac{No.\ of\ x\ residue\ in\ \beta regions}{Total\ No.\ of\ x\ residues} \quad (3)$$

The parameter of Beta–strand composition can be calculated by this equation [5]

$$P_\beta = \frac{f_\beta}{< f_\beta >} \quad (4)$$

3. SIMULATION AMINO ACIDS

The process of secondary protein composition detection depends basically on the knowledge of the initial protein composition which consist of 20 amino acid, and there are a lot of bases that available in the internet contains proteins and secondary compositions of these proteins and these proteins that exist in these data bases depends on the usage of x-ray and an expensive magnetic resonance imaging

That's why an simulation method has been created to initial the reality and generate an amino acid sequence which represent the initial protein composition and in different sizes and by usage of table (1) which represent the lean of the amino acids to be involved in the secondary protein composition

In this research there is an algorithm suggested to generate a sequence on the available in formation in the previous schedules .For generation of a sequence of amino acids of certain size N we suggest this algorithm :

The algorithm(1): generation of a sequence of amino acids by using simulation.

`Step(1): Entrance of the wanted sequence size in the simulation program N
Step(2): Entrance of table data that represent the lean of the amino acid to be involved in the secondary composition Table (1).
Step(3): formation of amino acid probability matrix P, and the probability law of total has been used for this purpose(*), see[4]:

P(Ala)=P(Ala/Alfa)P(Alfa)+ P(Ala/Beta)P(Beta)+P(Ala/Rot)P(Rot)
P(Cys)=P(Cys/Alfa)P(Alfa)+ P(Cys/Beta)P(Beta)+P(Cys/Rot)P(Rot)
P(Leu)=P(Leu/Alfa)P(Alfa)+ P(Leu/Beta)P(Beta)+P(Leu/Rot)P(Rot)
P(Met)=P(Met/Alfa)P(Alfa)+ P(Met/Beta)P(Beta)+P(Met/Rot)P(Rot)
P(Glu)=P(Glu/Alfa)P(Alfa)+ P(Glu/Beta)P(Beta)+P(Glu/Rot)P(Rot)
P(Gln)=P(Gln/Alfa)P(Alfa)+ P(Gln/Beta)P(Beta)+P(Gln/Rot)P(Rot)
P(His)=P(His/Alfa)P(Alfa)+ P(His/Beta)P(Beta)+P(His/Rot)P(Rot)
P(Iys)=P(Iys/Alfa)P(Alfa)+ P(Iys/Beta)P(Beta)+P(Iys/Rot)P(Rot)
P(Val)=P(Val/Alfa)P(Alfa)+ P(Val/Beta)P(Beta)+P(Val/Rot)P(Rot)
P(Ile)=P(Ile/Alfa)P(Alfa)+ P(Ile/Beta)P(Beta)+P(Ile/Rot)P(Rot)
P(Phe)=P(Phe/Alfa)P(Alfa)+ P(Phe/Beta)P(Beta)+P(Phe/Rot)P(Rot)
P(Tyr)=P(Tyr/Alfa)P(Alfa)+ P(Tyr/Beta)P(Beta)+P(Tyr/Rot)P(Rot)
P(Trp)=P(Trp/Alfa)P(Alfa)+ P(Trp/Beta)P(Beta)+P(Trp/Rot)P(Rot)
P(Thr)=P(Thr/Alfa)P(Alfa)+ P(Thr/Beta)P(Beta)+P(Thr/Rot)P(Rot)
P(Gly)=P(Gly/Alfa)P(Alfa)+ P(Gly/Beta)P(Beta)+P(Gly/Rot)P(Rot)
P(Ser)=P(Ser/Alfa)P(Alfa)+ P(Ser/Beta)P(Beta)+P(Ser/Rot)P(Rot)
P(Asp)=P(Asp/Alfa)P(Alfa)+ P(Asp/Beta)P(Beta)+P(Asp/Rot)P(Rot)
P(Asn)=P(Asn/Alfa)P(Alfa)+ P(Asn/Beta)P(Beta)+P(Asn/Rot)P(Rot)
P(Pro)=P(Pro/Alfa)P(Alfa)+ P(Pro/Beta)P(Beta)+P(Pro/Rot)P(Rot)
P(Arg)=P(Arg/Alfa)P(Alfa)+ P(Arg/Beta)P(Beta)+P(Arg/Rot)P(Rot)

(*) the Probability: Law of Total If, A1, A2, ... Ak are dual negative events and general in sample space S, so for any other event B in S so:

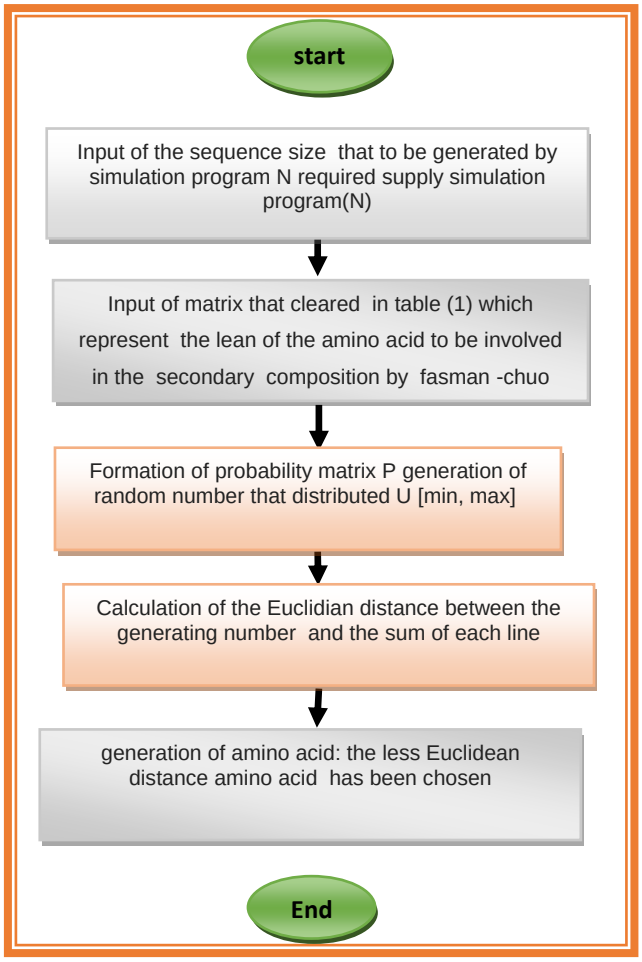
P(B)=P(B|A1)P(A1)+P(B|A2)P(A2)+…+P(B|Ak)P(Ak)

Step 4: generation of random number that follow uniform distribution in the interval [min, max] which is U [min, max] that (min) represents the least value of the sum of each line of the matrix P, which represent the lean of the amino acid to be involved in the secondary composition and (max) represent the largest value of the sum of each line of the matrix p which represent the lean of amino acid to be involved in the secondary composition.

Step5: Calculate the Euclidean distance between the generated number and the sum of each line of the matrix that's obvious in step(2).

Step6:generation of amino acid: the amino acid that has the less Euclidean distance between the sum of each line of the matrix P and the random number that generated will be chosed . the next form clears the stream line chart of algorithm (1)

The following figure shows the flow chart of the algorithm(1)



The Figure 1:the suggested algorithm streamline to generate a sequence of amino acid by using simulation

There is a computer program which has been built by using MATLAB language according to the previous algorithm to do an experiments for simulation .look at the un published ph .Dthesis of the other researcher [3].

4. ALIGNMENT

The pair wise sequence alignment represent its most easiest form that the main target from aligning a pair of sequence is to find the best pair of sequence which has the most number of similar amino acid and one sequence represents the querying sequence that want to search for sequence similar in its database and of known composition and function ,and the process of composition of sequence considered as one of the most important analysis method in biological information, and it is the 1st step in the path of analysis of new sequence structure and function and in which the search for the matched amino acid residue symbol in the related sequence or DNA bases symbol take place.

The pair wise sequence alignment process considered as a main base in the searching in databases for the multiple sequence alignment and this alignment process gives the dual sequence under standing relationship detection possibility that if the two sequences are shared in incorporeal degree of similarity or identify that its so far to this identity to be random and this mean that these two sequences could be descended from combined developmental sources (root or radically matching)

Homologous [10] but also there is a possibility of

mismatching in some regions resulting from amino acids changing processes (in protein form situation)and here the weighting of the possibility of descending of the two sequences from one source (origin) is possible . but they became so far that the radical relation which are not capable to be characterized on the relay level and this appears obviously clear in the fact that the nucleotide in DNA be in two situation either similar or different in comparison with three situation that happens in the amino acids they are either different or similar or different but not matching that's mean that some amino acids are similar in chemical composition like serine and thereonin that each one contain groups of hydroxyl (-OH) and also Lucien and isolucien have similar chemical characters and glutamic and aspartic both are of acidic interaction

The programs outputs differs in the multiply alignment sequences show and most of them depends on colures (in protein form situation)that the colur became specs for each group of amino acids depending on the physiochemical characters but the nitrogen bases have fixed color in most programs of according to the space of the amino acids that have been divided in to many groups which are look also at the next shape [7]:

1.polar amino acids that with green colures are N, Q, C,Y,T,S,G.
2.basic amino acids that with blue colure H, R, K.
3.acidic amino acids that with red colure are E, D.
4. water reluctant amino acid that with black colure are of large number W, P, I, L, V, A, M, F.

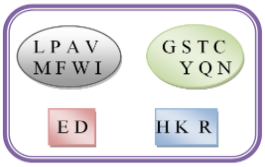


Figure 2: amino acid groups.

It is Also possible to consider the amino acid H as a polar amino acid and according to amino acid characters which b divided in to groups that are similar to the previous groups (Homology)

5. RADICAL MATCHING AND SIMILARITY AND MATCHING OF SEQUENCES

The sequence homology considered a one of the most important bases in sequences analysis when two sequences descended from one origin so it is possible to say that they have sequences homology or they have shared grandfather in versus the sequence similarity represents the alignment ratio and the amino acids residue matching which are similar in their physiochemical characters like size charge and water reluctance there for it was important to distinguish between the term radical matching (homology) and the other related terms like sequence similarity and also sequence identity[9].

That means that the residues are themselves in the two sequences and not from the group and the fact there is a confusion in using of these terms for example : the radical matching clears the relationship of the shared granddads that taken from the sequences comparison that are highly degree similar . but the term similar is a direct result from the observations resulted from sequences alignment and it is possible to determine the quantity of sequences similarity by using percentage .

But the sequences radical matching is a qualitative state (case): for example it is possible to say that the two sequences shared by 40% of similarity and its wrong to say that the two sequences shared by a 40% of radical matching : because there is either a radical matching between them or there is not .

In general if the sequence similarity level is too high so it is possible to conclude that there is a shared developmental relationship .in spite of that sometimes this relationship is not always clear and the answer depends on the type of the below studying and on the length of the sequences .

It is obvious from all what mentioned above that the nucleotide sequences consist of 4 letters which are the number of nitrogenous bases and then the sequences that have no connection between them have the possibility of matching ¼ = 0.25 = 25%, at least as a result of random matching, on the other side the protein sequence have 25% that consist of 20 amino acids which have no matching possibility relationship reach to 1/20= 0.05=5% of matching as a result of random coincidence and in case of gaps usage the percentage increased to reach up to 10-20%

The sequence length considered as an important factor : so the short sequences have a larger chance of matching that caused by random coincidence and that's why it was necessary to put a cut off to the short sequences during identification matching relationships in comparison with long sequences .

For example if a 100 amino acid length sequences aligned so the similarity of 30% or more denotes that the two sequences have convergent similarity and the next shape clears the statistic symbolizing of similar degrees :

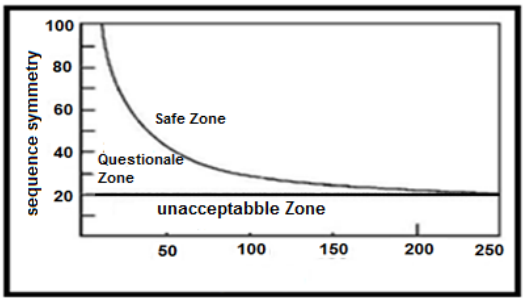


Figure 3: similarity degrees statistic representation.

The matching level of 20-30% indicates that the similarity relationship situated within uncertain region which is called (twilight zone) in which the little similarity intersects with sequences intersections as a result of random relationships but when the similarity percentage is less than 20% so a high percent of sequences appear to be not related sequences and appear symbolized in the shape as called (midnight zone)which are undependable results .

This symbolization couldn't be considered as an accurate measurement to determine the relationship between the sequences especially in the relationship between the sequences especially in the twilight zone and that's why it needs more strong statistic methods to determine the similarity relationship to determine the statistic in corporeal which will be explaining later .

The matching and similarity are used synonymously in the nucleotide sequences and the matching of two sequences refers to the percentage of the same amino acids presences

in the two sequences .but the similarity refers to the percentage of amino acids alignment in the same group . which has similar physiochemical characters which are more liable to be replaced by each other without a big

Influence. there are two methods to calculate the sequences matching and similarity [1]

The first method : This method include the use of the longest sequence so if a and b are sequences and the length of each one is La and Lb, respectively and Ls represents the number of the character similar aligned amino acids in the two sequence so the sequences a ,b similarity percentage calculated by this equation:

$$S= [(Ls \times 2) / (La + Lb)] \times 100\%. \quad (5)$$

And also could be calculated according to this standard equation :

$$S = (Ls / La)\times 100. \quad (6)$$

But the sequencing similarity calculated in similar method as below:

$$I = [(Li \times 2) / (La + Lb)] \times 100\%. \ldots\ldots\ldots (7)$$

Li considered as number of the matched amino acids. It also can be calculated according to this standard equation:

$$I = (Li / La)\times 100. \quad (8)$$

The second method: This method calculation depends on the percentage of each matching and similarity of the amino acid numbers by using this form

$$S= [(Ls \times 2) / (La + Lb)] \times 100\% \quad (9)$$

$$I(S) = Li(S) / La \% \quad (10)$$

That La represents the shorter sequence from the two sequences number study .

6. DATA AND DATA SIMULATION

6.1 Data Description

The data that are used this research are 14 proteins . some of them are special for mitochondrial diseases and especially patients of gram ping chromosome to the rotina sudden spasmodic epilepsy, and the other has been taken from another types of proteins of different sizes of prion . look at the unpublished thesis of 2nd searcher and these information are available in data bases in international centers specialized in genetic engineering and gene function study like NCBI ,Gen Bank ,MBL

6.2 Amino Acids Simulation Experiments

A new program has been built according to suggested algorithm generates an amino acids sequences which represents the initial composition of any protein to be generated .look at the unpublished thesis of the 2nd searcher for details .and in this program the dependence on the available information in the previous table (1) has been done which are a scientific experiments depend on x-ray of proteins group of gaining the lean of the amino acids to be involved in the 2ndory composition a different sized sequences have been generated which are equals to a certain disease specialized proteins size exists in international data bases. and a data similarity of matching percentage has been found which are generated from the simulation program and the factious existent sequence in these data bases . as mentioned below a summary of 14 simulation experiment that carried on 14 international known

First experiment : when choosing a sequence size of N=1075 for mitochondrial brain disuse disease protein simulation which consist of 1075 amino acids the program gives this sequence.

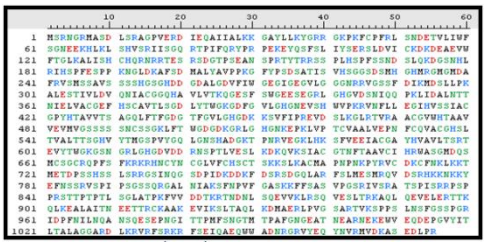
GAGNGRMASDLSRAGPVERDIEQAIIALKKGAYLLKYRLSND
ETVLIWFSSNDETVLIWFSGNEEISGQRTPIFQRYSGQRTPIYPR
PEKEYQSFSLIYSERSLRSLDVICKDKDEAEVWFTGLKALISHC
HQRNRRTESRSDGTPSEANSPRTYTRRSSPLHSPFSSNDSLQKD
GSNHLRIHSPFESPPKNGLDKAFSDMALYAVPPKGFYPSDSATI
SVHSGGSDSMHGHMRGMGMDAFRVSMSSAVSSSSHGSGHDD
GDALGDVFIWGEGIGEGVLGGGNRRVGSSFDIKMDSLLPKAL
ESTIVLDVQNIACGGQHAVLVTKQGESFSWGEESEGRLGHGV
DSNIQQPKLIDALNTTNIELVACGEFHSCAVTLSGDLYTWGKG
DFGVLGHGNEVSHWVPKRVNFLLEGIHVSSIACGPYHTAVVT
SAGQLFTFGDGTFGVLGHGDKKSVFIPREVDSLKGLRTVRAA
CGVWHTAAVVEVMVGSSSSSNCSSGKLFTWGDGDKGRLGHG
NKEPKLVPTCVAALVEPNFCQVACGHSLTVALTTSGHVYTMG
SPVYGQLGNSHADGKTPNRVEGKLHKSFVEEIACGAYHVAVL
TSRTEVYTWGKGSNGRLGHGDVDDRNSPTLVESLKDKQVKSI
ACGTNFTAAVCIHRWASGMDQSMCSGCRQPFSFKRKRHNCY
NCGLVFCHSCTSKKSLKACMAPNPNKPYRVCDKCFNKLKKTE
EKHLKLSHVSSRRGSINTPIFQRYPRPEKEYQSFSLIYSESLMES
MRQVDSRHKKNKKYGGIGHCLSPIPSGSSQGMALNIAKSFNPV
FGNTPGLYGTHMNGGMPTLFFTHPNATMYFVANPTQMPGGN
SASLAGTVGFNFFPGGFLNQFDTMGDSVKLRSQVTRKAQLQE
VELERTTKQLKEALAIGFGGTSSFQNFMLLGTTRLGNGGTLTE
RLPVGSAGSARTVTQGVGGFPAALLMFFANILNQANSQESEPS
EITTPMFSNGSNYFNGQVNFSLQGLIALTGGMFLQNRPPYITLT
GPAGGARYLIDLTIALYGLG

A- when a generated sequence compared with a real protein sequence of (1075) amino acids size a following results may be obtained : that the letter (I) refers (red colour) do residua matching (amino acids) between dates which generated from simulation program with the real data that exist in the international center .

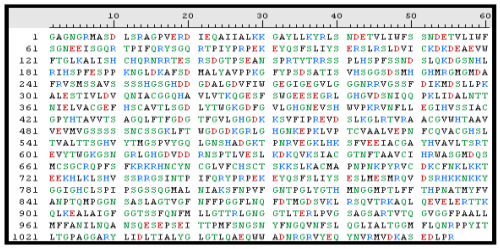
Figure (4): Sequence alignment in sequence generated the first experiment

And for a simulation programs efficacy checking a percentage of matching between areal sequences cases and chose generated from a simulation program calculated and as it is clear from the previous figure so the percentage matching between areal sequences cases with the generated sequences cases from simulation program reach to 77% of cases .And through the existence of such a match between the 1st sequence composition it is possible to predict the position and corp of 2nd protein composition which generated from a simulation program with 77% of success

B. also the similarity percentage between areal sequences cases and the generated sequences cases from a simulation program calculated and the figure (5a) clear areal sequence . but the figure (5b) clears a generated sequence . that the special colures of each group of amino acids depends on physiochemical characters (properties).



figure(5a) areal sequence



figure(5b) generated sequences for the simulation program

And according to the previous symbols so Ls refers to the number of the amino acids that aligned and of similar properties on the other side La , Lb refers to the sum of the length of each sequence separately as a sequence and the computer gave these result :

Ls =870

1075La = Lb =

SimlarityPerc = 81%

As the concluded sequences similarity percentage is 81% so this is an evidence that both have physiochemical properties that similar by 81% and by this there well be a shared evolutional relationship between them which may leads to a generated sequence to be replaced by the real one with success percentage of 81%

While considering the amino acid H as a polar amino acids the computer gave these results .

Ls = 904

1075La = Lb =

SimlarityPerc = 84%

The similarity percentage when considering amino acid H as a polar amino acid increases to be 84% .

2ndexperiment :When closing a sequence size N=818 in order to simulation a mitochondrial brain tissue disease protein which consist of 818 amino acids so the following sequence had been given by the program .

NTGTTTSHAMPHVGYFLLLMALLTACGGGSSSTDAPSEDTYP
VGGTLTGLEQGHTVTLQLNGANDLTLDHTANDNPYSFAVKLP
HGSAYEVTLPAEPSQHHCTIHNATGTVDGAVMNVDVECTTTF
HAHLNLGTGPPHFTGYTPWAWGRNGYGRLGLGDTDDRDVPE
QVGNFGFMGGAVNGGPNTGTYATYGTPALGLNTGAVGPNMS
GDRDEPEQVGVDNDWIALSAGAMGTTGAKADGTLWAWGNF
AYYGGLTHGANHHYTPTNLNLGGLPFFSNSAGRRHSLNMFGL
PSHFFWGDNEYGQLGLGDTDERLTNGGASFPLFGLGTRGDQQ
MPTGFRGGFGPWSWGYMTSGQLGLGDTADRNAPEQVGADT
DWDLVSNFTSLVPNVKADGTLMSLLGPPGGLFLGGDTVSRDA
PVPIASGIDTVAGRNHTVAVNPDGTSGFGGDNEYGQLGLGVM
RYIVTPSQTVTGSYWAAVNGGSFNHSLGLRGQGTLWAWGNN
NGMFGFSMDTDDRATPEQTVPNIDWAAVNAHSYHTLAVKID
GTLWAWGRNSSGQLGLSDTNDRHTPERVGRDTDWATVSVG
QSGLTGVKPDGTLWAWGWNHGTLGGYFFGPNDLSPEQVGGE
MGSGNGCLGLHHTVAVKTDGTLWAFNFTARGQLGLGGFLVG
QTMALTFNPLMQGAVSASGYRTLAVKADGTLWAWGENNNG
QLGLGDTDNRRGTAQVGNDADWAAVSTGLFHTLAFKEDDTL
WAWGRNHDGQLGLGDTDNRDAPVQVGNETDWSTVSCGNGL
YGGTMSDGTLRAWGLNTSGQLGQRTMWFDQNGLYSPC

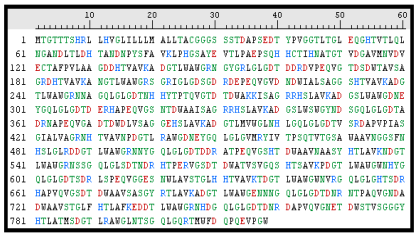
A - when a generated sequence compared with a real protein sequence of (818) amino acids size following results has obtained :

Figure (6) : Sequence alignment in sequence generated the 2nd experiment

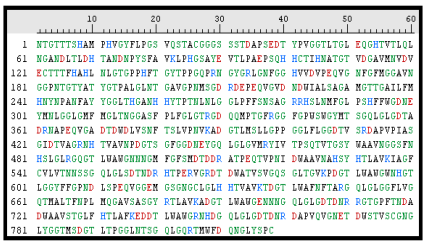
And us it is cleared from the previous figure the matching percentage between a real sequences cases and the generated sequences cases from simulation program reach to 71%of cases .and through the presence of such a match between the primary protein composition so it is possible to predict the position and the crop of the 2ndary protein composition which generational from the simulation program with success percentage of 71%..

B- regarding the similarity percentage between the real sequences cases and the sequences cases that generated from simulation program the figure (7a)clears the real sequence

.but the figure (7b)clears the generated sequence and the computer gave these results. regarding the figure(2):



figure(7a) real sequence



Figure(7b) generated sequences for the simulation program

Ls= 640

La = Lb =818

SimlarityPerc = 78%

As the concluded percentage of two sequence similarity is 78%.so this is an evidence that both have a similar physiochemical properties of about 78%and by this there will

be a shared evolutional relationship between them which leads to liability of the generated sequence to be replaced by the real one success percentage of 78% .

But when considering an amino acid H as a polar amino acid the computer gave these results:

Ls= 661

La = Lb =818

SimlarityPerc = 81%

The similarity percentage when considering an amino acid H as a polar amino acid increase to be 81%.

3rd experiment : when choosing a sequence of N =421 size in order to simulate a mitochondrial brain tissue disease protein which consist of 421 amino acid the program gave those results:

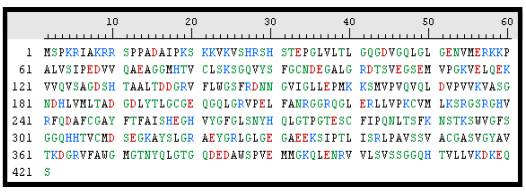
PGPKRIAKRRSPPADAIPKSKKVKVSHRSHSTEPGLVLTLGQG
DVGQLGLGENSHYRKKPALVSIPEDVVQAEAGGMNGLYTFTF
LTVYSFGCNDEGALGRDTSVEGSEMVPGKVELQEKVVQVSA
GDSHTAALTDDGRVFLWGNLFSFGGGIGLLEPMKKSMVPVQ
VQLDVPVVKVASGNDHLVMLTADGDLYTLGCGEQGQPHGV
NTPGHLNRGGRQGLERLLVKCVMLLKSRGSRHVRFQDAFCG
AYFFTDGLLGFFHLVPFTTLCMPNCTGVPFTLFIPQNLTSFKNS
TKSNSFANGVQHHTVCMDSEGKAAYLGRAEYGRLGLGEGAE
EKSIPTLISRRPAVSSVACGASVGYAVTKDGRVFAWGMGTNY
YQLGTGQDEQTSPVEMSSGKQLENRVSVSSGGQHTVLLLVKD
KEQS

A- when a generated sequence compared with a protein real sequence of 421 amino acid size following results had been gotten:

Figure (8): Sequence alignment in sequence generated the 3rd experiment

And as it is clear from the previous figure the matching percentage between the real sequence cases and the generated sequence cases from the simulation program reach up to 73% of cases . and through the presence of such a matching between the primary protein composition so it is possible to predict the position and corp. of the 2ndory protein predict the position and corp of the 2ndory protein composition which generated from simulation . program with success percentage 73% of cases.

B /regarding the similarity percentage between the real sequence cases and the generated sequence cases from simulation program the figure(9a) clears the real sequences while the figure (9b) clear the generated sequences for the simulation sequences



figure(9a) real sequence

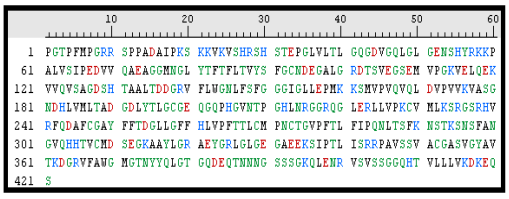


figure (9b) generated sequences for the simulation program

and the computer gave these results. regarding the figure(2): .

Ls = 334

La = Lb = 421

SimlarityPerc = 79%

As the concluded sequences similarity percentage is 79% so this is an evidence that both have physiochemical properties that similar by 79% and by this there well be a shared evolutional relationship between them which may leads to a generated sequence to be replaced by the real one with success percentage of 79%

While considering the amino acid H as a polar amino acids the computer gave these results .

Ls =343

La = Lb = 421

SimlarityPerc = 81%

The similarity percentage when considering amino acid H as a polar amino acid increases to be 81% .

4thexperiment :When closing a sequence size N=1006 in order to simulation a mitochondrial brain tissue disease protein which consist of 1006 amino acids so the following sequence had been given by the program .

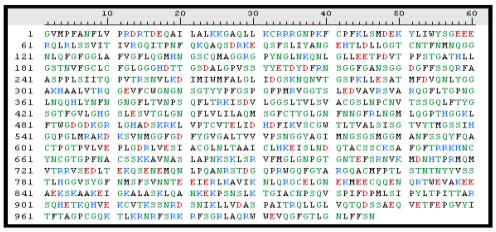
GVMPFANFLVPRDRTDEQAILALKKGAQLLKCRRRGNPKFCP
FKLSMDEKYLIWYSGEEERQLRLSSVITIVRGQITPNFQKQAQS
DRKEQSFSLIYANGEHTLDLLGGTCNTFNMNQGGNLQFGFGG
LAFVGFLQGMHNGSCQMAGGRGPYNGLNKQNLGLLEETPDV
TPFSTGATHLLGSTNVFGCLCFGLGGGHDTTGSDALGPVSSYY
ETDYDFRNSGGFGANSGGDGFFSSQRFAASPPLSIITQPVTRSN
VLKDIMIWMFALGLIDGSKNQNVTGSPKLLESATMFDVQNLY
GGAKHAALVTRQGEVFCWGNGNSGTYYPFGSPGFPMRVGGT
SLEDVAVRSVARQGFLTGPNGLNQQHLYNFNGNGFLTVNPSQ
FLTRKISDVLGGSLTVLSVACGSLNPCNVTSSGQLFTYGSGTFG
VLGHGSLESVTGLGNQFLVLILAQMSGFCTYGLGNFNNGFRL
NGMLQGPTHGGKLFTWGDGDKGRLGHADSKRKLVPTCVTEL
IDHDFIKVSCGWTLTVALSISGTVYTMGSSIHGQPGLMRAKDK
SVNMGGFGDFYGVGALTVVVPSNGGYAGIMNGSGSMGGMA
NFSSQYFQACTPGTPVLVEPLGDRLVESIACGLNLTAAICLHKE
ISLNDQTACSSCKSAFGFTRRKHNCYNCGTGPFNACSSKKAVN
ASLAPNKSKLSRVFMGLGNPGTGNTEFSRNVKMDNHTPRMQ
MVTRRVSEDLTEKQSENEMQNLPQANRSTDGQPRWGQFGYA
RGQACMFPTLSTNTNYYVSSTLHGGVSYGFNMSFSVNNTEEIE
RLKAVIKNLQRGCELGNEKMEECQQENQRTWEVAKEEAEKS
KAAKEIGKALASKLQANKEKPSNSLKTGIACNPSQVSPIFDPM
LSIPYLTPITTARSQHETKQHVEKCVTKSSNRDSNIKLLVDASP
AITRQLLGLVQTQDSSAEQVETFEPGVYITFTAGPCGQKTLKR
NRFSRKRFSGRLAQRWWEVQGFGTLGNLFFSN

A - when a generated sequence compared with a real protein sequence of (1006) amino acids size following results has obtained :

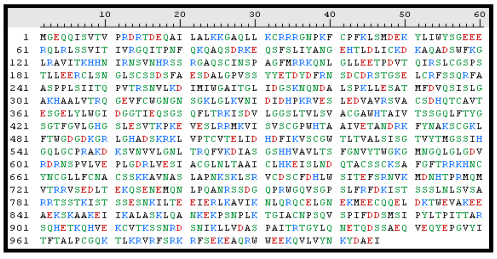
Figure (10):Sequence alignment in sequence generated the 4th experiment

And us it is cleared from the previous figure the matching percentage between a real sequences cases and the generated sequences cases from simulation program reach to 72%of cases .and through the presence of such a match between the primary protein composition so it is possible to predict the position and the crop of the 2ndary protein composition which generational from the simulation program with success percentage of 72%.

B /regarding the similarity percentage between the real sequence cases and the generated sequence cases from simulation program the figure(11a) clears the real sequences while the figure (11b) clear the generated sequences for the simulation sequences



figure(11a) real sequence



figure(11b) generated sequences for the simulation program

and the computer gave these results. regarding the figure(2): .

Ls =770
La = Lb =1006
SimlarityPerc =77%

As the concluded percentage of two sequence similarity is 77%.so this is an evidence that both have a similar physiochemical properties of about 77%and by this there will be a shared evolutional relationship between them which leads to liability of the generated sequence to be replaced by the real one success percentage of77% .

But when considering an amino acid H as a polar amino acid the computer gave these results:

Ls =785

La = Lb =1006

SimlarityPerc =78

The similarity percentage when considering an amino acid H as a polar amino acid increase to be 78%.

5thexperiment :When closing a sequence size N=890 in order to simulation a mitochondrial brain tissue disease protein which consist of N=890 amino acids so the following sequence had been given by the program .

PNGGGKPNSSSNSRDDGNSVFPAKASATGAGPAAAEKRLGTP
PGGGGAGAKEHGNSVCFKVDGGGGGGGGGGGGEEPGFGGM
DAEGPRRQYGFHANNVFNTMTVTGLFPGNMANLQNTPFEKE
QERVKTAGFWIIHPYSDTPMGPNGGNGAYNSVGPFGPTGFTTF
FTEQTTTGTPGFNVASDTVFLLDLIMNFRTGTVNEDSSEIILDP
KVIKMNYLKGNSGGGFISSIPVDYIFLIVEKGMDSEVYKTARA
LRNTHGLAQNTNNTSPGVFTNHCHGGSQTEIFHMTYDLASAV
VRIFNLIGMCPLLCHWDGCLQFLVPLLQDFPPDCWVSLNEMV
NGTYFLGTGFNFINGFPHMLCIGQFLTTPVSMSDLWITMLSMPI
NYSTLRGTGSRSLIVFQSLDSSRRQYQEKYKQVEQYMSPGTLP
ADMRQKIHDYYEHRYQGKIFDEENILNELNDPPPPHVFFHGGG
VIVATMPLFANADPNNPYAMLSKLRFEVFQPGDYIIREVNLPM
PNGLGRNGPQGFGGGSSKEMKLTDGSYFGEICLLIMLVGLFGG
SHNIYCRLYSLSVDNFNEVLEEYPMMRRAFETVAIDRLDFTVQ
CNSILLQKFQKDLNTGVFNNQENEILKQSGKHDREMVQAIA

A - when a generated sequence compared with a real protein sequence of (890) amino acids size following results has obtained :

Figure (12) Sequence alignment in sequence generated the 5th experiment

And us it is cleared from the previous figure the matching percentage between a real sequences cases and the generated sequences cases from simulation program reach to 71%of cases .and through the presence of such a match between the primary protein composition so it is possible to predict the position and the crop of the 2ndary protein composition which generational from the simulation program with success percentage of 71%..

B /regarding the similarity percentage between the real sequence cases and the generated sequence cases from simulation program the figure(13a) clears the real sequences while the figure (13b) clear the generated sequences for the simulation sequences

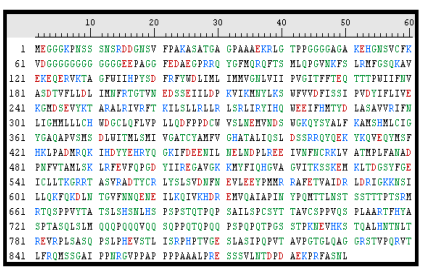


Figure (13a) real sequence

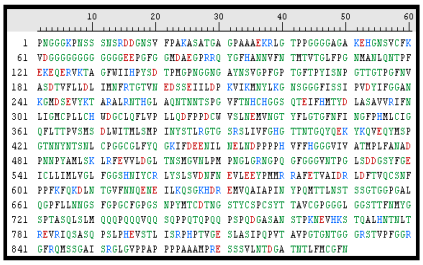


Figure (13b) generated sequences for the simulation program

and the computer gave these results.

Ls =714

La = Lb = 890

SimlarityPerc =80%

As the concluded percentage of two sequence similarity is 80%.so this is an evidence that both have a similar physiochemical properties of about 80%and by this there will be a shared evolutional relationship between them which leads to liability of the generated sequence to be replaced by the real one success percentage of80% .

But when considering an amino acid H as a polar amino acid the computer gave these results:

Ls =726

La = Lb = 890

SimlarityPerc =82%

The similarity percentage when considering an amino acid H as a polar amino acid increase to be 82%.

6th experiment :When closing a sequence size N=774in order to simulation a mitochondrial brain tissue disease protein which consist of 774 amino acids so the following sequence had been given by the program .

TCGGQRPAAGASEGATPGLELGPPVAPPPATAASGGLGSLFPE
PKRRHLGTLLQPTVNKFSLRVFGSHKAVEIEQERVKSAGAWII
HPYSDFRFYWDLCNGFGVLMCTYLGPNTNGPIFTGHCHFGGV
GYPNVNGTTLGPFLLNFRTGIVVEEGAEILLVTMTIRTRYLRT
WFLVDLISSTGTLTIANIIGFEPRLDAEVYKTAPDPTPTTPGNGF
SHFLGLRLSRLIRYIHQWEEFMGTLPANLSAVVRIFNLIGMML
LLCHWDGCLQFLVPMLQDFPPDCWVSINHMVNHSWGQGYSH
ALFKAMSHMLMTRGRLDGQHGNGTHWLTMLSMIVGATCYA
MFIGHATALIQSLDSSRRQYQEKYKQVEQYMSFHKLPADTRQ
RIHEYYEHRYQGKMFDEESILGGAHMPLREEIINFTCRGLVAH
MPLFAHADPSFVTAVLTKLRFEVFQPGDLVVREGSVGRNGFD
PQHGLLSVLLSNTNDTRLTDGSYFGEICLLTRGRRTASVRADT
YCLGFLLSVDHFNAVGEEFPMMRRAFETVAMDMHAVNFGQQ
RGGQRKRSEPSPGSSGGIMESLPPNNIFTLANGVRGRAPSTGA
QLSGKPVLWRGGVHAPLQAAAVTSNVAIALTHQRGPLPLSPD
SPATLLARSAWRSAGSPASPLVPVRAGPWASTSGLPAPPARTL
HASLSRAGRSQVSLLGPPPMMVGPYPGPRGRPLSASQPSLPQR
ATGDGSPGRKGSGSERLTPPGLLAKPPRHAQPPRPPVCFITAAT
QTQLSANM

A - when a generated sequence compared with a real protein sequence of (774) amino acids size following results has obtained :

Figure (14): Sequence alignment in sequence generated the 6th experiment

And us it is cleared from the previous figure the matching percentage between a real sequences cases and the generated sequences cases from simulation program reach to 78%of cases .and through the presence of such a match between the primary protein composition so it is possible to predict the position and the crop of the 2ndary protein composition which generational from the simulation program with success percentage of 78%.

B /regarding the similarity percentage between the real sequence cases and the generated sequence cases from simulation program the figure(15a) clears the real sequences while the figure (15b) clear the figure(13a) generated sequences for the simulation program and the computer gave these results.

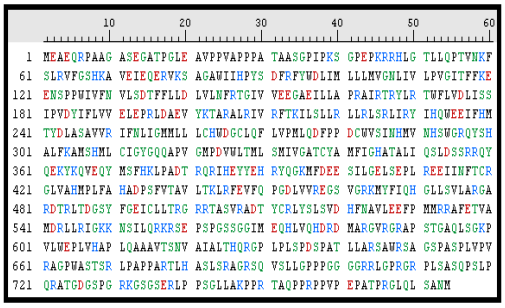


Figure (15a) real sequences

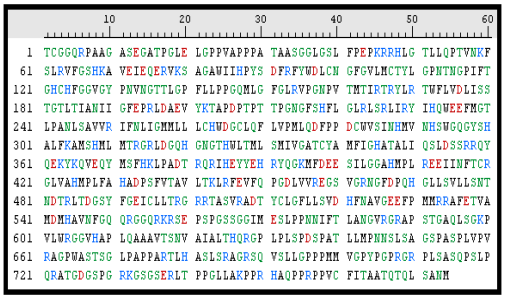


Figure (15b) generated sequences for the simulation program

Ls = 633

La = Lb =774

SimlarityPerc = 82%

As the concluded percentage of two sequence similarity is 82%.so this is an evidence that both have a similar

physiochemical properties of about 82%and by this there will be a shared evolutional relationship between them which leads to liability of the generated sequence to be replaced by the real one success percentage of82% .

But when considering an amino acid H as a polar amino acid the computer gave these results:

Ls = 656

La = Lb =774

SimlarityPerc =% 85

The similarity percentage when considering an amino acid H as a polar amino acid increase to be 85%.

7thexperiment :When closing a sequence size N=888 in order to simulation a mitochondrial brain tissue disease protein which consist of 888 amino acids so the following sequence had been given by the program .

NNFLPPHVAPQNTFLDTIIRKFEGQSRKFIIANARVMGGDGNPG
FLNGSGNGGYSRAEVMQRPCTCDFLHGPRTQRRAAAQIAQAL
LGAEERKVEIAFYRKDGSCFLCLVDVGLHNGILYGQLNFFNN
GHFGLGPTPYGNNDLIFNTQPTLFGNRPMGLYNAPGGKLPALL
ALTARESSVRSGGAGGAGAPGAVGVNVDLTPAAPSSESLALD
EVTAMDNHVAGLGPAEERRAFLNFANSFGVVNNIQYTYSAHS
LNPDASGSSCSLIALTSPVTGMLRRSGGNACMGNTNGNYRTG
PTIPHASTGAMHPLRSLTGTGMALTQGAGPTPMFPYTGTMTN
FVDLKGDPFLASPTSDRELMAPKIKERTHNVTEKVGHNCLYH
NLSPTTNSGNQHNISGLHGGFGSPFKAMGSGNFGVTVIYTAVF
TPYSAAFLLKETEEGPPATECGYACQIFGNHFVFFGNMFIVDIL
INFRTTYVNIPTVNVSHPGRIAVHYFKGWFLIDMVAAIPFDLLI
FGSGSEELIGLLKTARLLRLVPQARKLDRYSEYGAAVLFLLMC
TFALIAHWLACIWYAIGNMEQPHMDSRIGWLHNRNGYQGKP
YNSSGLGGPFLQFPALLNLYFTFSSLTSVGFGNVSPNTNVTTTP
GGFNNLIGSLMYASIFGNVSANMNGPYSGTARYHTQMLRNTG
NLGFHQIPNPLRQRLEEYFGAFGPNSNGIDMNAVLKGGRSYN
VCQFGLHLNRSLLQHCKPFRGATKYMLRALAMKFKTTHAPP
GDTLVHAGDLLTALYFISRGSIEILRGDVVVAILGMGWGAGTG
LEMPSAAFRGASLLNMQSLGLWTWDCLQGHWAPLIHLNSGP
PSGAMERNHTWGEAAELWGSHNQGVGNGRHKQTLFASLK

A - when a generated sequence compared with a real protein sequence of (888) amino acids size following results has obtained :

Figure (16) Sequence alignment in sequence generated the 7thexperiment

And us it is cleared from the previous figure the matching percentage between a real sequences cases and the generated sequences cases from simulation program reach to 70%of cases .and through the presence of such a match between the primary protein composition so it is possible to predict the position and the crop of the 2ndary protein composition which generational from the simulation program with success percentage of 70%..

B /regarding the similarity percentage between the real sequence cases and the generated sequence cases from simulation program the figure(17a) clears the real sequences while the figure (17b) clear the generated sequences for the simulation program

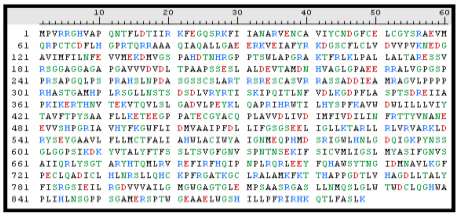


figure (17a) real sequences

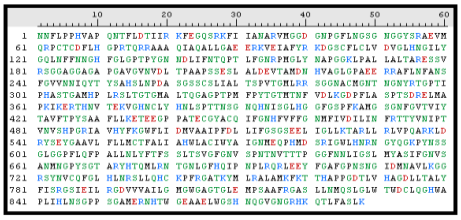


figure (17b) generated sequences for the simulation program

and the computer gave these results.

Ls =682

La = Lb = 888

SimlarityPerc = 77%

As the concluded percentage of two sequence similarity is 77%.so this is an evidence that both have a similar physiochemical properties of about77%and by this there will be a shared evolutional relationship between them which leads to liability of the generated sequence to be replaced by the real one success percentage of77% .

But when considering an amino acid H as a polar amino acid the computer gave these results:

Ls =707

La = Lb = 888

SimlarityPerc = 80%

The similarity percentage when considering an amino acid H as a polar amino acid increase to be 80%.

8thexperiment :When closing a sequence size N=337 in order to simulation aprion protein which consist of 337 amino acids so the following sequence had been given by the program .
TFSTASPAADGGRGPWEGGLVSWPPAPPLTLPWTWMGPSWG
QHPGHWGFPALTDPSASPAASLGIFEVRYVLDASGCSMIFGPG
GGAARFSSYLLSRARKVNGGLPLSPCGVPELCSISTSRATTGY
GMGNMAAMVPFPPQRYHYFLVLDFEATCDKPQIHPQEIIEFPIL
KLNLNPMEIESTFHMYVQPVVHPQLGTFCTELTGIIQAMTDGQ
PSLQQVLERVDWMAKEGGLLDPNVKSIFVTCGDWDLKVMLP
GQCHYLGLPADYFKQWINNLKKAYSFAMGWPKNGGCGDMN
KGLSLQHIGRPHSGIDDCKNANIMGLGLNLYGVGQYQTSKPF

A - when a generated sequence compared with a real protein sequence of (337) amino acids size following results has obtained :

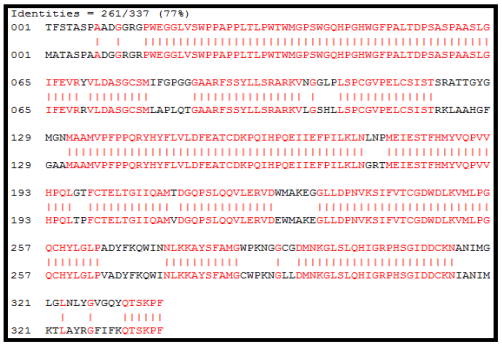


figure (18 **): Sequence alignment in sequence generated the 8thexperiment**

And us it is cleared from the previous figure the matching percentage between a real sequences cases and the generated sequences cases from simulation program reach to 77%of cases .and through the presence of such a match between the primary protein composition so it is possible to predict the position and the crop of the 2ndary protein composition which generational from the simulation program with success percentage of 77%..

B /regarding the similarity percentage between the real sequence cases and the generated sequence cases from simulation program the figure(19a) clears the real sequences while the figure (19b) clear the generated sequences for the simulation program

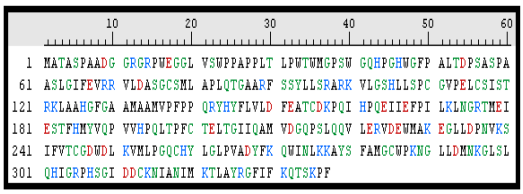


figure (19a)

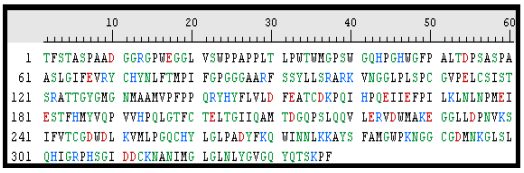


Figure (19b) generated sequences for the simulation program

and the computer gave these results.

Ls =277

La = Lb =337

SimlarityPerc =82%

As the concluded percentage of two sequence similarity is 82%.so this is an evidence that both have a similar physiochemical properties of about82%and by this there will be a shared evolutional relationship between them which leads to liability of the generated sequence to be replaced by the real one success percentage of82% .

But when considering an amino acid H as a polar amino acid the computer gave these results:

Ls =286

La = Lb =337

SimlarityPerc =85%

The similarity percentage when considering an amino acid H as a polar amino acid increase to be 85%.

9thexperiment :When closing a sequence size N=1196 in order to simulation a prion protein which consist of 1196 amino acids so the following sequence had been given by the program .

SVPKKFKLMNSFLDDQPKDPNLVASPFGGYFKNPAADAGSNN
ASKKSSYQQQRNWKQGGNYQQGGYQSYNSNYNNYNNYNN
YNNYNNYNNYNKYNGQGYQKSTYKQSAVTPNQSGTPTPSAS
TTSLTSLNEFNSAGSTSCISQFLSKITFGFGFTDCKNQIKAFFPG
NGGGGNSTGEKIEEWKIVFNGIFLFKPKNPSLVRESAMLIISNIA
QFFSGKPPQEASPLGGNNTFIIFNVMGTHTVKRAAQHAIDSLL
NCFPMEALTCFVLPTILDYLSSGAKWQAKMAALSVVDRIRED
SANDLLELTFKDAVPVLTDVATDFKPELAKQGYKTLLDYVSIL
DNLDLSPRYKLGGGNLQDPSKVPESVKSLSYTIGTNPLTEPSLS
LLVPILNRSLNLSSSSQEQLRQTGGVVENLTRLVNNRNEIESFIP
LLLPGIQKVVDTATRPEVRELANMNLNVLKEDDEADKENKFS
GRLTLEEGRDFLLDHLKDIKADDSCFVKPYMNLETVIKYMSKI
LTVDSNVNDWKRLEDFLTPGHLHRGTTFNGQPNGPQHNLRAL
FYQEKERADEDEGIEIVNTDANGLNRRVNGLNKTNLRLLKGH
RYGLCGRNGAGKSTLMRAIANGQLDGFPDKDTLRTCFVEHKL
QGEEGDLDLVSFIALDEESQSTSREEIAAALTLTIANIIGFFFSVG
SLSGGWKMKLELARAMLQKADILLLDEPGNHLDVSNVKWLE
GTLPAHTDITSLIVSHDSGFLDTVCTDIIHYENKKLAYYNPNLA
AFVEQKPEAKSYYTLTDSNAQMRPPPGILLTGVKSNTRAVAK
MTDVTFSYFLQGNHDDGGAMTNTTGPHGALNLGPNGAGKGL
PVKLLTGELVPNEGKVEKHPNLRTLLLQNVIPQHVNEHKEKT
ANQYLQWRYQFGDDREVLLKEMMTSDHMVRGMMTKEIDID
DGRGKRAIEAIVGRQKLKKSFPNGFFLCCALSNTNPNGTQMT
NLNLFGPAFLQKFDDHEFLYLGLGYRELLSGTYTKHFEDVGV
TSFATQTALPGMMHAGQLVKVVIAGAMWNNPHLLVLDEPTN
YLDRDSLGALAVAIRDWSGGVVMISHNNEFRGALCPEQWIVE
NGKMVQKGSAQVDQSHVGTDVNMARVLLLMPNNSLPSVDD
DTGPANIKVKNFTGPDTRNEKKLMAERRRLRYIEWLSSPKGTP
KPVDTGPYPV

A - when a generated sequence compared with a real protein sequence of (1196) amino acids size following results has obtained :

Figure (20): Sequence alignment in sequence generated the9th experiment

And us it is cleared from the previous figure the matching percentage between a real sequences cases and the generated sequences cases from simulation program reach to 79%of cases .and through the presence of such a match between the primary protein composition so it is possible to predict the position and the crop of the 2ndary protein composition which generational from the simulation program with success percentage of 79%.

B /regarding the similarity percentage between the real sequence cases and the generated sequence cases from simulation program the figure(21a) clears the real sequences

while the figure (21b) clear the generated sequences for the simulation program

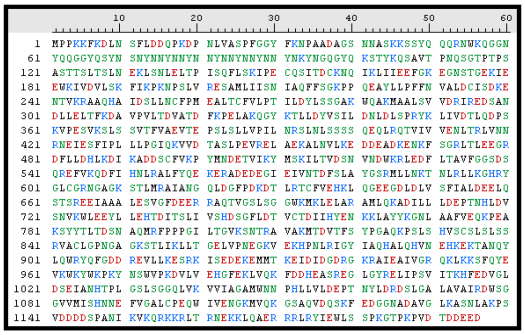


figure (21a) real sequences

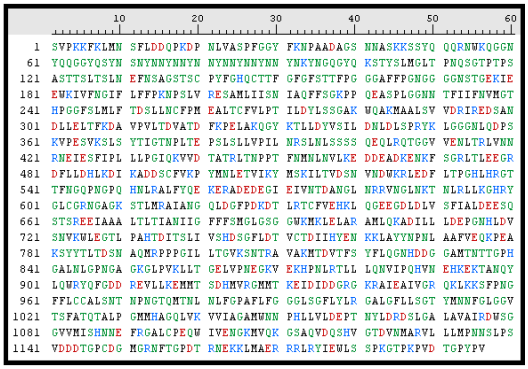


figure (21b) generated sequences for the simulation program

and the computer gave these results .

Ls = 1006

La = Lb = 1196

SimlarityPerc = 84%

As the concluded percentage of two sequence similarity is 84%.so this is an evidence that both have a similar physiochemical properties of about84%and by this there will be a shared evolutional relationship between them which leads to liability of the generated sequence to be replaced by the real one success percentage of84% .

But when considering an amino acid H as a polar amino acid the computer gave these results:

Ls = 1025

La = Lb = 1196

SimlarityPerc = 86%

The similarity percentage when considering an amino acid H as a polar amino acid increase to be 86%.

10ndexperiment :When closing a sequence size N=405 in order to simulation a prion protein which consist of 405 amino acids so the following sequence had been given by the program .

MDTDKLISEAESHFSQGNHAEAVAKLTSAAQSNPNDEQMSTIE
SLIQKIAGYVMDNRSGGSDASQDRAAGGGSSFMNTLMADSK
GSSQTQLGKLALLATVMTHSSNKGSSNRGFDVGTVMSMLSGS
GGGSQSMGASGLAALASQFFKSGNNSQGQGQGQGQGQGQGQG
QGQGQGSFTALASLASSFMNSNNNNQQGQNQSSGGSSFGALA
SMASSFMHSNNNQNSNNSQQGYNQSYQNGNQNSQGYNNQQ
YQGGNGGYQQQQGQSGGAFSSLASMAQSYLGGGQTQSNQQ
QYNQQGQNNQQQYQQQGQNYQHQQQGQQQQQGHSSSFSAL
ASMASSYLGNNSNSNSSYGGQQQANEYGRPQQNGQQQSNEY
GRPQYGGNQNSNGQHESFNFSGNFSQQNNNGNQNRY

A - when a generated sequence compared with a real protein sequence of (405) amino acids size following results has obtained :

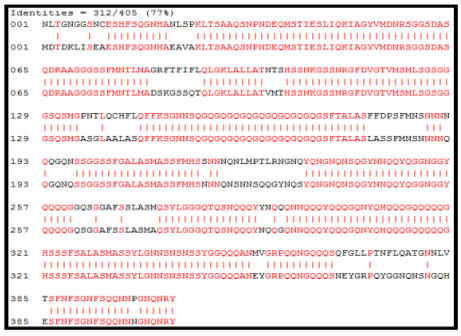


figure (22) Sequence alignment in sequence generated the 10th experiment

And us it is cleared from the previous figure the matching percentage between a real sequences cases and the generated sequences cases from simulation program reach to 77%of cases .and through the presence of such a match between the primary protein composition so it is possible to predict the position and the crop of the 2ndary protein composition which generational from the simulation program with success percentage of 77%.

B /regarding the similarity percentage between the real sequence cases and the generated sequence cases from simulation program the figure(23a) clears the real sequences while the figure (23b) clear the generated sequences for the simulation program .

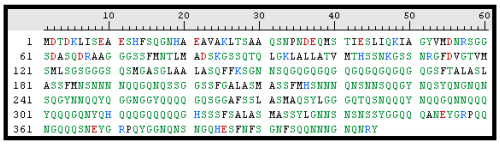


figure (23a) real sequences

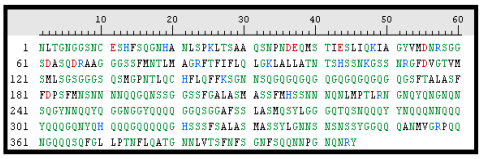


figure (23b) generated sequences for the simulation program

and the computer gave these results

Ls=350

La = Lb =405

SimlarityPerc=86%

As the concluded percentage of two sequence similarity is 86%.so this is an evidence that both have a similar physiochemical properties of about86%and by this there will be a shared evolutional relationship between them which leads to liability of the generated sequence to be replaced by the real one success percentage of86% .

But when considering an amino acid H as a polar amino acid the computer gave these results:

Ls=356

La = Lb =405

SimlarityPerc=88%

The similarity percentage when considering an amino acid H as a polar amino acid increase to be 88%.

11nd experiment :When closing a sequence size N=254 in order to simulation a prion protein which consist of 254 amino acids so the following sequence had been given by the program .

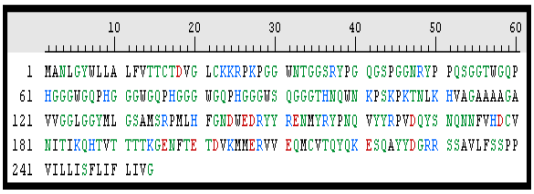
QNNLGYWLLALFVTTCTDVGLCKKRPKPGGWNTGGSRYP GQGSPGGNRYPPQSGGTWGQPHGGGWGQPHGGGWGQP HGGGWGQPHGGGWSQGGGTHNQWNKPSKPKTNLKHVA GAAAAGAVVGGGMFVNAGGQPLAVFFDGGPFWEDRYYR ENMYRYPNQFNNNPVDQYSNQNNFVHDCVNITIKQHTVTT TTKGENFTETGGPGAFGGMPFNQVTQYQKESQAYYDGRR SSAVLFSSPFLNTNVSVFFVGLGL

A - when a generated sequence compared with a real protein sequence of (254) amino acids size following results has obtained :

Figure (24): Sequence alignment in sequence generated the 11th experiment

And us it is cleared from the previous figure the matching percentage between a real sequences cases and the generated sequences cases from simulation program reach to 80%of cases .and through the presence of such a match between the primary protein composition so it is possible to predict the position and the crop of the 2ndary protein composition which generational from the simulation program with success percentage of 80%.

B /regarding the similarity percentage between the real sequence cases and the generated sequence cases from simulation program the figure(25a) clears the real sequences while the figure (25b) clear the generated sequences for the simulation program



figure(25a) real sequences

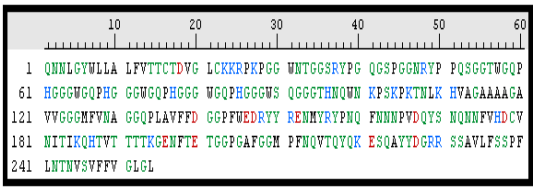


figure (25b) generated sequences for the simulation program

and the computer gave these results

Ls = 215

La = Lb = 254

SimlarityPerc = 85%

As the concluded percentage of two sequence similarity is 85%.so this is an evidence that both have a similar physiochemical properties of about85%and by this there will be a shared evolutional relationship between them which leads to liability of the generated sequence to be replaced by the real one success percentage of 85% .

But when considering an amino acid H as a polar amino acid the computer gave these results:

Ls = 223

La = Lb = 254

SimlarityPerc = 88%

The similarity percentage when considering an amino acid H as a polar amino acid increase to be 88%.

12nd experiment :When closing a sequence size N=151 in order to simulation a prion protein which consist of 151 amino acids so the following sequence had been given by the program .

GNWAPHSNWALLLAAAFLCDSGAAKGGRGGARGSARGG VRGGARGASRVRVRPAQRYGAPGSSLRVAAAGAAAGAAA AGAAAGGLPSGWRRAAGPGERLGLEDEEGVPGGNGTGPG IYSGRAWTPQFTPTRGPRLCLVLGGAFFTVGLLRP

A - when a generated sequence compared with a real protein sequence of (151) amino acids size following results has obtained :

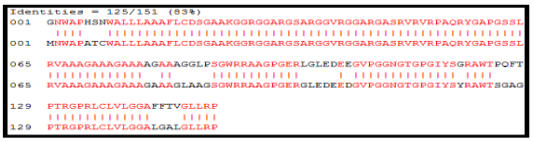


Figure (26):Sequence alignment in sequence generated the 12th experiment

And us it is cleared from the previous figure the matching percentage between a real sequences cases and the generated sequences cases from simulation program reach to 83%of cases .and through the presence of such a match between the primary protein composition so it is possible to predict the position and the crop of the 2ndary protein composition which generational from the simulation program with success percentage of 83%..

B /regarding the similarity percentage between the real sequence cases and the generated sequence cases from simulation program the figure(27a) clears the real sequences while the figure (27b) clear the generated sequences for the simulation program

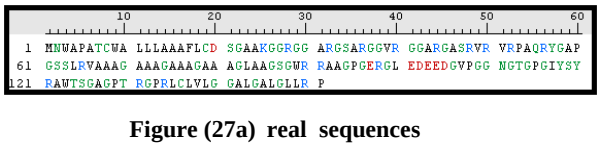


Figure (27a) real sequences

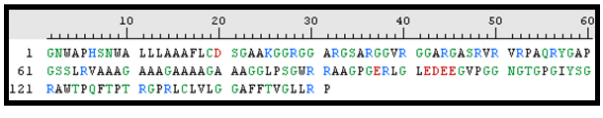


Figure (27b) generated sequences for the simulation program

and the computer gave these results.

Ls = 137

La = Lb =151

SimlarityPerc = 91%

As the concluded percentage of two sequence similarity is 91%.so this is an evidence that both have a similar physiochemical properties of about91%and by this there will be a shared evolutional relationship between them which leads to liability of the generated sequence to be replaced by the real one success percentage of 91% .

But when considering an amino acid H as a polar amino acid the computer gave these results:

Ls = 137

La = Lb =151

SimlarityPerc = 91%

The similarity percentage when considering an amino acid H as a polar amino acid increase to be 91%.

13thexperiment :When closing a sequence size N=89 in order to simulation a prion protein which consist of 89 amino acids so the following sequence had been given by the program .

PQGGGGWGQPHGGGWGQPHGGGWGQPHGGGWGQPHGGGWGQPHGGGWGQPHGGGWGQPHGGGWGQPHGGGWGQPHGGGWGQ

A - when a generated sequence compared with a real protein sequence of (89) amino acids size following results has obtained :

Figure (28): Sequence alignment in sequence generated the 13th experiment

And us it is cleared from the previous figure the matching percentage between a real sequences cases and the generated sequences cases from simulation program reach to 83%of cases .and through the presence of such a match between the primary protein composition so it is possible to predict the position and the crop of the 2ndary protein composition which generational from the simulation program with success percentage of 83%.

B /regarding the similarity percentage between the real sequence cases and the generated sequence cases from simulation program the figure(29a) clears the real sequences while the figure (29b) clear the generated sequences for the simulation sequences

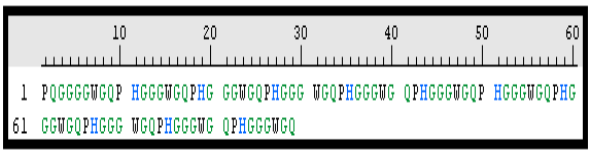


Figure (29a) real sequences

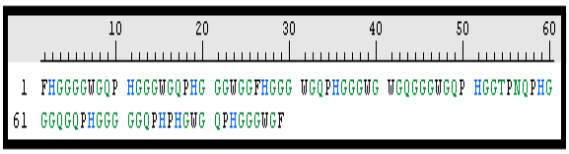


Figure (29b) generated sequences for the simulation program

and the computer gave these results.

Ls = 72

La = Lb =89

SimlarityPerc = 81%

As the concluded percentage of two sequence similarity is 81%.so this is an evidence that both have a similar physiochemical properties of about81%and by this there will be a shared evolutional relationship between them which leads to liability of the generated sequence to be replaced by the real one success percentage of81% .

But when considering an amino acid H as a polar amino acid the computer gave these results:

Ls = 83

La = Lb =89

SimlarityPerc = 93%

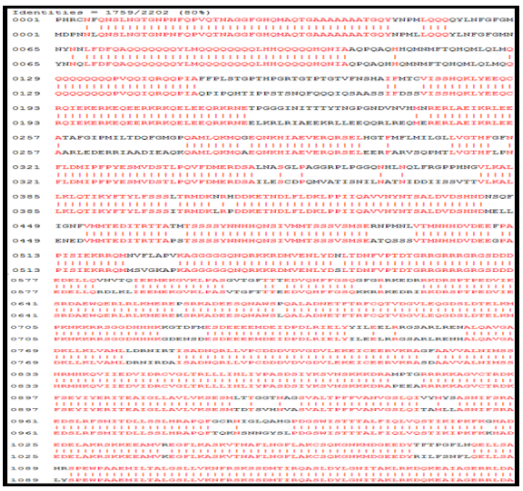
The similarity percentage when considering an amino acid H as a polar amino acid increase to be 93%.

14thexperiment :When closing a sequence size N=2202 in order to prion protein which consist of 2202amino acids so the following sequence had been given by the program .

PHRCNFQNSLNGTGNPNFQPVQTNAGGFGHQMAQTGAAAAA
AATGQYYNPMLQQQQYLNFGFGMNYNNLFDFQAQQQQQQQ
YLMQQQQQQQQLHHQQQQQHQNIAAQPQAQHHQMNMFTQ
HQMLQLMQQQQQQQQQPVQQIQRQQPIAFFPLSTGPTHPGRT
GTPTGTVFNSHAIFMTCVISSHQKLYEEQCRQIEKERKEQEERK
RKQELEEQRKRNETPGGGINITTTYTNGPGNDVNVHMNRERL
AEIKRLEEATAFGIPMILTDQFGMGPQAMLQKMQGEQNKHIA
EVERQRSELHGTFMFLMILGLLVGTHFGFNFLDMIPFPYESMV
DSTLPQVFDMERDSALNASGLPAGGRPLPGGQNHLNQLFRGP
PHNGVLKALLKLQTIKYFTYLFSSSLTRMDKNRHDDKETNDL
FLDKLPPIIQAVVNYNTSALDVDSHNDNSQFIGNFVMMTEDIT
RTTATMTSSSSYNNHHQNSIVMMTSSSVSMSERNPMNLVTMN
HHDVDEEFPAPISIEKRRQMNVFLAPVKAGGGGGQNQRKKRD
MVENLYDNLTDNFVPTDTGRRGRRRGRGSDDDEDELLQVNV
TQIEEMEKGVKLPASGVTGFTTTEDVQHFFGSQGFGRRKEDR
RKDRSPTPEDVIESRDAEWQERLRLKMEREPSRKADEESQNA
WSPQALADNETFTRFCQTVDGVLEQGDSLDTELKMPKNKKR
RSGGDHHHKKGTDFMESDEEEEMDEIDPDLRIELYYILEELRR
GSARLRENALQAVGADKLLKLVAMLLDRNIRTISADNQRLLV
PCDDDVDVGDVLEKEICEERVKRAGFAAVVALNIMSSHRMH
KQVIIEDVIDRCVGLTRLLLIHLIYPASDSIYKSVNSKKKDRAM
PTGRRRKKAGVCTRDKFSEYIYERITEAIGLLAVLVKSESMLTT
GGTNAGSVALTPFFVANVGSLQIVYMYSASNIFSRAEDSLRFS
MITDLLSSLHRAPQFGCRNIGLQAHGPDGSWISTTTALFIQLVQ
STIKIPKFKGHADEDELAKRSKKEEAMVREGFLKASKVTNAFL
NGFLAKCSQKGNKMDGEEDYTFTPGFLNQELLSAHRSPEWPA
AEMILTALGSLLVKNFRSKSSDMTIRQASLDYLGNITAKLRKD
QKEAIAGERRLDAVVKKSFLLLSDKGVEDYESVDISNLKQND
KLKVLETSLIDYLVITNSSDIIVYACNFYVGFPMYEVAEDLESA
RSKLKQTVDTNESEKDVKKAERKYEKIQYRGAEMKVFLSKIL
DKPFLKRRLEKSNKVKMLDSDAFWAVKFLAQSREFTQSFDTY
LKHIVFGAGSETIVALRSKALKCLSSTAVFDSSVLILEDVQQAV
HTRMVDSHAQVRESAVELIGRFVLYDMVLGGGYSQIAERILD
TGVAVDLPVIRIMREICEKFPTFEMIPDMLARMTPRVTDEEGV
KKLVFETFTLLWFQPVDTRIYTNAVGTFTITMCSVAQHCIKDA
MSDYLEQLHLLLNPGFTFGSGMSVANRQIIDSLVDHILNLEQH

KSSGMFLEVELMRRKEQEEKYMAYLSTLAVFSKGARLLLTSH
VEVLLPYLTFSGAKTNAENQVTKCMIGMLERVIPLVPFGDFYV
LDSIDENLCKVIHSLDMALVVNPVSCVASIYKKFKRGATKTID
VFSTYLKHLEVFKRNFDSNPRYDLQYGFFPILSRSIFTLGVLSR
YGQFEEFVKEDPTEEKVEASPNFALLHGGHNSRYHKGGLRQK
ALTAMGHFCAQHSTYLTKRQLTNTYFTPGNAANSPQQQQQR
LLVLQNLEMFLQCEEQKLAASHDKWDENKEAQNLKEMELSG
SGLGSSVIQYWKAVLESYYVDADIQLRRAAQVVWLTLNQGL
GFMPGASIPTLIAMTTDPVDVIRNRIDILKEIIDSKYSGMVQSKA
MQGVRLSYKLHLKLMLTQQEKFVRGFRCDDFHLNTLPNALPE
THDGMAVTLSGLYQSLRTNRQQRRFFLQSMVKLFSEFFSHDK
PQLMEYIFIADNLAMFPYQMDENGNLGNMQIDQNIAQTGQSL
LVQYKLQLRMQESEDEDIVFLDENMMSRLSQLGQIETFYLFLD
SQVPSSLLLYVRTFMHNLYGFNETKVAEYQPSEAAKVYEKAV
TNTQIHMFKPITALEALNFPFEWGSFQHTGTMFGGGPQGRKM
LLSLDQVEEVEVSNTTAANDDYDEEEDGGEDQNNGFMGPGM
HH

A - when a generated sequence compared with a real protein sequence of (2202) amino acids size following results has obtained :



figure(30)**:Sequence alignment in sequence generated the 14th experiment**

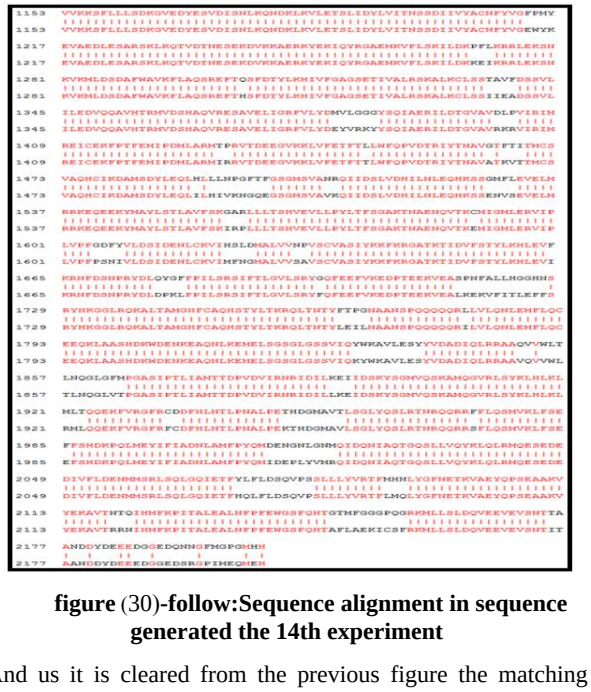


figure (30)**-follow:Sequence alignment in sequence generated the 14th experiment**

And us it is cleared from the previous figure the matching percentage between a real sequences cases and the generated sequences cases from simulation program reach to 80%of cases .and through the presence of such a match between the primary protein composition so it is possible to predict the position and the crop of the 2ndary protein composition which generational from the simulation program with success percentage of 80%.

B /regarding the similarity percentage between the real sequence cases and the generated sequence cases from simulation program the figure(33a) clears the real sequences while the figure (33b) clear the generated sequences for the simulation program

figure (31**a) real sequences**

figure (31**b) generated sequences for the simulation program**

and the computer gave these results.

Ls =1853

La = Lb =2202

SimlarityPerc = 84%

As the concluded percentage of two sequence similarity is 84%.so this is an evidence that both have a similar physiochemical properties of about84%and by this there will be a shared evolutional relationship between them which leads to liability of the generated sequence to be replaced by the real one success percentage of84% .

But when considering an amino acid H as a polar amino acid the computer gave these results:

Ls = 1900

La = Lb =2202

SimlarityPerc = 86%

The similarity percentage when considering an amino acid Has a polar amino acid increase to be 86%.

7. CONCLUSION

The next schedule summarizes the previous experiments results the second column of the schedule clears names of protein that have been simulated by different sized amino acids N (amino acid).and the 4th and 5th column gives the matching /similarity percentage between the factions and generated sequences and the last column gives the similarity percentage when the amino acids H considered as one of the polar amino acids.

Table 2: Summary of amino acids simulation experiments.

similarity percentage of polar amino acids (%)	similarity percentage (%)	matching percentage(%)	Protein size(N)	the name of the simulation Protein	experiment number
84	**81**	**77**	**1075**	brain tissue disease **(1)** protein	**1**
81	**78**	**71**	**818**	brain tissue disease **(2)**protein	**2**
81	**79**	**73**	**421**	brain tissue disease **(3)**protein	**3**
78	**77**	**72**	**1006**	brain tissue disease **(4)**protein	**4**
82	**80**	**71**	**890**	sudden spasmodic **(1)** epilepsy	**5**
85	**82**	**78**	**774**	sudden spasmodic **)2(** epilepsy	**6**
80	**77**	**70**	**888**	sudden spasmodic **(3)** epilepsy	**7**
85	**82**	**77**	**337**	**(1)** Prion protein	**8**
86	**84**	**79**	**1196**	**(2)** Prion protein	**9**
88	**86**	**77**	**405**	**(3)** Prion protein	**10**
88	**85**	**80**	**254**	**(4)** Prion protein	**11**
91	**91**	**83**	**151**	**(5)** Prion protein	**12**
93	**81**	**83**	**89**	**(6)** Prion protein	**13**
86	**84**	**80**	**2202**	**(7)** Prion protein	**14**

From the previous simulation programs a lot of conclusion obtained which are:

1. The simulation program which built for this study is of good efficacy .because it can generates an amino acids sequences simulates to an acceptable degree to the real (factious) sequence to those amino acids .
2. The matching percentage between a factious sequences cases and generated sequences cases from simulation program became between 71%and 83% of cases .
3. The similarity percentage between a factious sequences cases and generated sequences cases from simulation program became between78% and 93%.
4. The matching and simulation good sharing between the factious and generated sequences excludes the random matching and this indicates that the sequences descended from one developmental origin .
5. The detection of the location and corps of secondary protein composition is possible if the proteins 2ndory composition that match's its initial one is known which means that match's its initial one is known . which means that this proteins matching in initial composition leads to make this matching in 2ndory composition and function but if the proteins are matched in composition and function is not necessary leads to matching in initial composition and through the presence of such matching in between the initial compositions so it is possible to detect the 2ndory protein composition position and corps if the 2ndory protein composition that matched with in the initial one is known
6. When amino acids H considered from the polar amino acids so the percentage between the two sequences increase . and this leads to similarity increasing between the physiochemical characters of both sequences which may leads to increase the shared developmental relationship between the sequences and by this the two sequences became more liable to exchange between each other without a great influences

8. REFERENCES

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