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Number of Contiguous Amino Acids in Nanon of 16Å Diameter

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Abstract

Proteins are major source of interactions in living being. Understanding these interactive one is essential in order to elucidate its structure and function. Fundamentally there are some situations where adequate understanding is made in dealing this biomolecule. According to nature of interaction it is reported that carbon alone is main factor of interactions in dealing this structure and function. Following this, new avenues are opening up in recent times. Accordingly it is reported here that carbon factor of fundamental value is deciding the adjoining amino acids in order to maintain structure followed by function. It is revealed that 5 amino acids are crucial in deciding the local structure to stability and all. Otherwise higher number of this value is observed which are minimal and may not be important. Significant arrangements are done at 5 amino acids and accordingly 9 amino acids are crucial in stabilizing this 5 amino acid one. Overall pattern can be identified at lengths of 5, 9 or 27. It is going to be useful in mutational study leading to disease solvation and all.

Keywords: Internal Amino Acid; Carbon Domain; Protein Pattern; Nanon; Carbon value; CARd-3D

Abbreviations: nonCOD: Non-Carbon Optimized Domain.
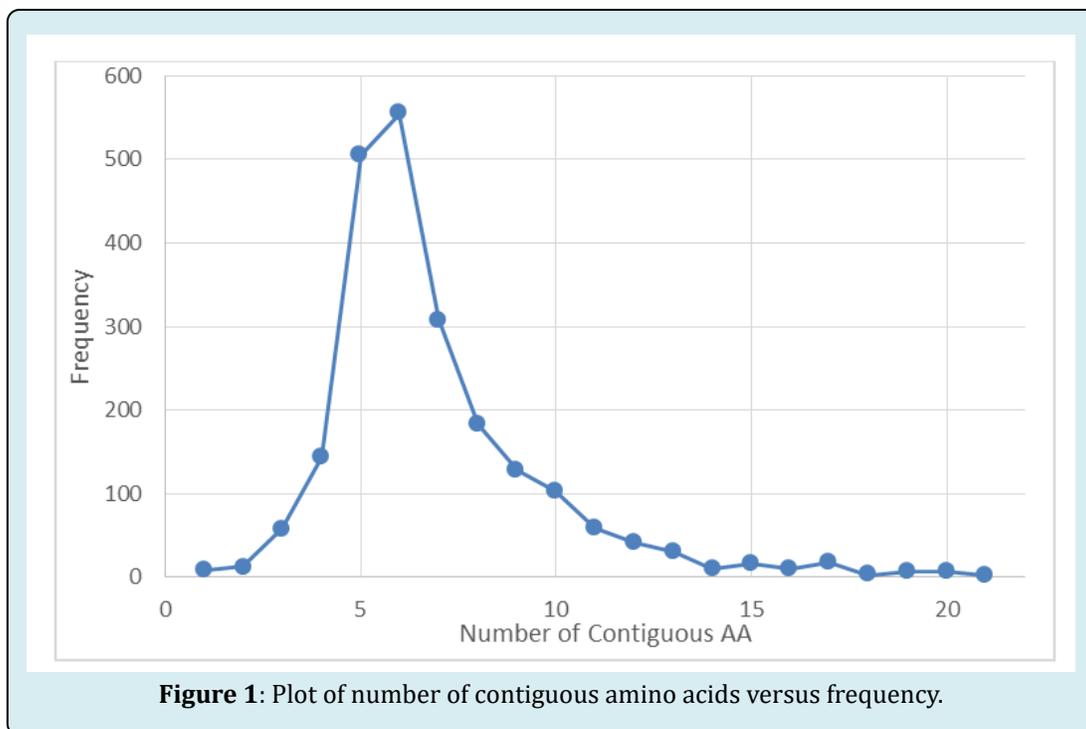
Introduction

According to nature of interactions there are quite a few workouts that seemed good in understanding biomolecules. Recently it has been reported that carbon alone dealing with internals of biomolecules in general [1-5]. Having said that it is mandatory to validate and assess all other factors which are associated with basic carbon force. Dealing so it is said that a diameter of 16Å is determining factor in rounding up a carbon value which will equal to 0.3144 [6-15]. When adopt to this value one would say domain follows [5]. Otherwise call it as non-carbon optimized domain (non COD) where other interacting elements can interfere in its activity which are buried inside mostly. Elements which are good in neighboring residue altogether call it as active for available interaction specifically [1]. In this way one understands the organizations of amino acids in proteins for revealing interactive elements and domain one. One would wonder what will be the extent by which the linear chain of amino acids cooperate carbon value with in the diameter of 16Å. This is taken up here for understanding how long and probable stretch that accommodate within this diameter value. Accordingly it is to be tested for alteration is required and so forth. Given the scenario one can be analyzed for all available proteins. One has to understand that the amino acids are varying in different species. Accordingly analyzed are selected few in example and available in this paper is one. Carbon factor of available interacting elements are captured and revealed here.

Calculations

The number of contiguous amino acids in nanon of diameter 16Å is computed for protein super oxide dismutase. The ID is 1DSW. It is a monomeric protein having 153 amino acids in it. The Card-3D program has been modified for specific calculation of this number of contiguous amino acid which may be domain or non-domain. All elements are considered in evaluation of adjacent amino acids involvement in domain and non-domain. Accordingly it is analyzed for contiguous amino acids for each atom of amino acids with dia of 16Å. Based on the number of amino acids it is grouped. That is to say how many atoms having one amino acid in the dia or in two, three, four, five, six and so forth. These obtained numbers in each group of category is understandably reported by making graph and so forth.

Results and Discussion

Figure 1: Plot of number of contiguous amino acids versus frequency.

The plot of number of contiguous amino acids versus frequency of appearance is shown in figure1. From this it is reported that the value of 5 is probable one. It appears that 5.5 is actual. Given this probable value of 5 amino acids in 16Å understanding can be done accordingly. Otherwise the length goes above 22 amino acids. Understandably it is maximum in domain regions where as it is lower in non-COD regions. One can go on analyzing this number of amino acids in dia of 16Å for probable domain and non-COD.

The probable number of amino acids in domain and non-COD are maximum in 5, 6 and 7. Otherwise it is less important in other higher number of contiguous amino acids. Over and above one may analyze higher end for mutual cooperation among amino acids of adjoining portions. The lower numbers may be fit to water borne amino acid side chains. One can draw inferences from these numbers of amino acids involved in domain and so forth.

The probable 5 leads to assess the adjoining amino acids involvement in stability factor 9 where 5th amino acid may have adjoining 2 amino acids. So totally 9 amino acids be part of this 5 contiguous amino acid. That is contiguous 9 amino acids are in important in understanding 5 amino acid length. A group of nine 9 may have adjoining 9 amino acids that is taken here as pattern of 27 amino acids. Having this fractional value of 5.5 may lead to overall factor of 10 to be considered. At any cost it breaks off at 11. One can understand that any amino acids are taken the adjoining 5 amino acids are important in assessment of its stability factor. Otherwise it's going to be useless in analysis and all.

Pattern can be look upon based on adjoining amino acids. Pattern of carbon value focus may be useful in understanding of mutational one and all. Very many patterns are altered in proteins of disordered one. One can go and check these numbers for any alteration that may give solution for human

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diseases and all. Predominantly protein prefers to have this significant number of carbon score that require to be altered for significant applications. Meanwhile alteration can be done based on domain values but require analysis of 3D structure. Otherwise it's going to be easier here in adjoining one from carbon factor of contiguous one.

Conclusion

The carbon factor protein value has been evaluated in terms of contiguous amino acids length. It is observed to be 5. Otherwise going to be stretch length of 10 is important in local stability. Otherwise going to be amino acid lengths 5 or 9 are crucial in determining stability of local structure. There are wide applications expected to be coming out from this crucial value of pattern length. Patterns are crucial in mutational study leading to stability and all. Pattern of carbon value are crucial in dealing all applications leading to protein stability, function and all. Factors such as protein binding and protein folding are determined from this number of carbon value which can be assessed from neighboring amino acid factor of assessment.

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