

Active Role Carbon by Adjoining Amino Acids in Protein Nature of Interaction



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Submission: January 09, 2023; Published: February 21, 2023

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Abstract

One of the forces coming from carbon has been in discussion for a while. But its full potential is yet to be realized on the applications side. During these phenomena of protein folding and binding action, it is one of the crucial factors in determining the local parameter that and all playing in biological action. In this context it is to be reiterated that carbon does play a role in determining the binding role during action of drug and other molecules to bind. Welcoming this new phenomenon of action during remedial action, it is to be addressed at atomic level and understand it accordingly. While considering this new development, it is again reported with new example that enzymatic protein binding site analysis is carried out to get clear action of force coming from carbon alone and discussed here. When it is realized, it can only be put forth and taken further action accordingly.

Keywords: Active carbon; Binding site; Protein interaction; Cohesive force; Protein-probe; CARd; Carbon domain

Background

One of the forces coming along the amino acid one is the driving force which is crucial in determination of protein nature and all associated calculations [1-5]. It is crucial to determine the role carbon plays in dealing with this active role in proteins and all. Many papers have been written already in references elsewhere [3-6]. One has to be pinpoint in development of active role played by proteins and all. During this analysis of protein nature one can identify active role and all but in vain. With this new development of protein nature during carbon analysis, one may be able to get new way of looking at the structure analysis and all. With the advent of advanced analysis in protein calculations one may find new findings in protein form. Based on new one arriving at all atom consideration in dealing carbon role, it is possible to get the number of interests in leading role played by carbon and all. One can compare sudden development arising out of this carbon one in dealing active as well as advancement of stable mutation for any change that is potential performer of the protein nature. One can be sure that carbon's role is important in dealing with protein nature and all. Otherwise, one can be extended to another system of interest in dealing with this carbon role. But here in interest are with dealing active role played by amino acids in the interest of the pharmaceutical company coming up with solution for any disease or so. Every other molecule in the living being is based on the limit played by carbon and all. Very much in protein which can be tested easily with various parameters of test in theoretical as well as in experimental side.

Many tests have been done in protein nature and reported which can be worth mentioning. Over and above one can go ad

dition to the existing one in development of new product during this advancement of carbon-based analysis which is taken up here in this work of analysis leading to the confirmation of active role played by amino acids and all. One can be sure that protein nature is controlled by amino acid sequence which is crucial in determining 3D structure and role played by adjoining amino acids [7,8]. According to the protein nature of interaction in neighboring amino acid role it of worth mentions that active one is played by not only of single amino acid but of several of them. Clubbed together the amino acids deal with incoming interactive probe of interest. In doing so one has to be causes about the arrangements of these amino acids in the sequence and in structure. Arrangements are crucial in 3D structure as well as in attraction one. Accordingly, the literature values are tested again with new protein of interest here in enzymatic one. Over and above one can be sure to extend further with any other enzyme of interest in several ways. Here in reported for all active role of carbon at atomic level using sequence and 3D structure. The enzyme of protein nature is understood clearly in the role played by carbon. According to the nature of interaction it is a path breaking work carried with carbon role in proteins. Testing can also be extended further with any other protein of interest as shown below.

Methodology

Clear idea on how to get the graphical representation of computed one is given in paper reported already. It is merely the collection of new one here, that enzymatic protein one is treated as an alternative protein sequence which is collected online

for further preparation and all. All other parameters all crucial one in determining the binding site which is characteristic of the emerging program called CARd [9]. It is used here to get this new value of adequacy principle and all. Accordingly, it is computed for entire sequence of event in enzymatic protein. When in need of active exposure, it is to be understood that carbon role is crucial in determining active role as well as stabilizing one. Accordingly, it is to be expected that domain and active elements are crucial here. Otherwise, other elements are either in the interior or exposed one. Over and above, one would look upon domain where critical active part that is few amino acids involved with carbon-rich elements. In this context it is considered to be crucial in determination of the active part of the protein one. Over and above, one would go with a few elements of amino acids that and all involved in active role which are than considered part of domain one accordingly. Otherwise, it is going to be in the interior of protein that is not available for binding and all. One would go on searching for such an element in dealing with active elements.

In this scenario it is recommended that five amino acids may be crucial in determining this factor of binding which are adequate enough to binding the external molecules which are either drug one or in the other amino acids coming from adjacent one. Either way it is reported again that element of carbon does play a role in dealing with such active part and that needs to be taken care in dealing such binding and all. It is reported for enzymatic protein one here which can be extended for any other one in dealing active role dominant calculations and all. Many excellent calculations are yet to be realized in dealing such active role and

development towards enhancement and suppression in crucial development of product development everywhere in phenomena of biological living being. In this context it is crucial in dealing with disease related action of drug and all. One can go on further with either this phenomenon of binding in carbon role or mutational one for healing. It is crucial for both of them. Acting according to the nature of interaction involved by carbon is crucial. Otherwise merely a calculation and have no results. One may go with answers found here in enzymatic protein and deal accordingly in the next one to come.

Carbon and all can be calculated from either 3D structure and/or protein sequence. Here in reported are both sequence analysis and the 3D structure analysis. 3D means again the parameters are crucial in determination of active role played by protein nature. In this role it is of dia 16\AA is crucial again in determination of active role in protein nature. Regarding this active binding site this diameter of carbon nature is going to be the determining factor for all other calculations and all. With this parameter in protein nature is crucial in dealing with such active role played by enzymatic one and others. Accordingly, here again report this parameter-based calculation for the enzyme one. In dealing so it is of cohesive nature in proteins that and all crucial in development of drug and all. Alternatively, one can go with elements of parameter-based mutation in dealing with disease and all [10]. Here again 3D structure analysis based on parameter defined is critically analyzed in enzymatic protein nature which is given below.

Results and Discussion

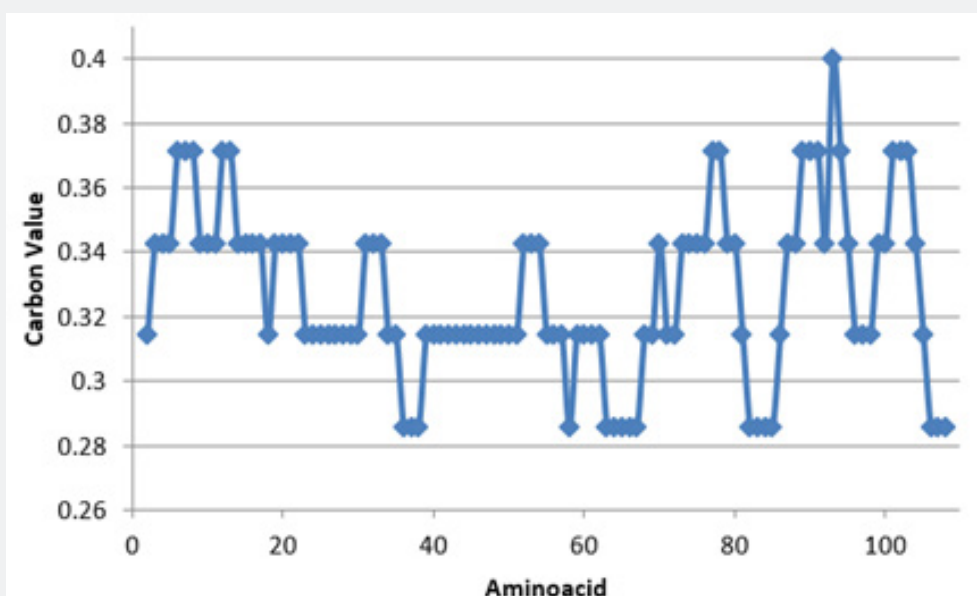


Figure 1: Carbon value in barnase here.

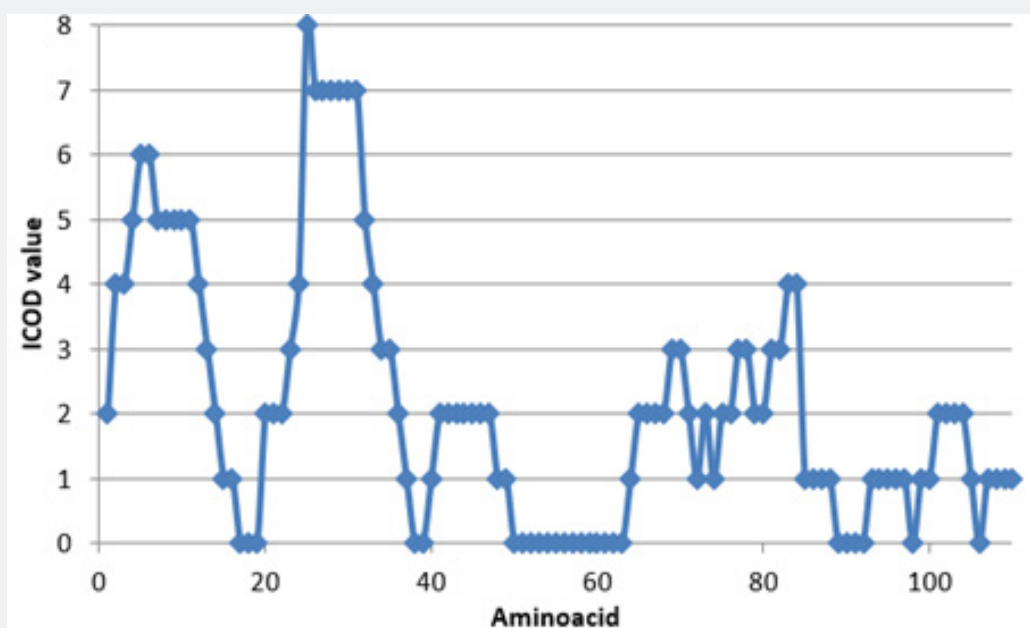


Figure 2: Carbon based domain value for the same barnase protein.

Carbon based protein sequence analysis is done here in protein nature of enzymatic one, barnase one. Other elements are considered in total but in calculation the element of carbon is crucial in determining the factor of binding or so. Dealing so the parameter taken here is 5 amino acid length which is coming around 77 atoms all together. Dealing that 5 amino acid long stretch is crucial in determination of active part played by enzyme protein one. One can go on playing with several parameters in taken care of protein which went in vain. Over and above, it is crucial to work with parameter 5 that works to be in protein nature. One can find from (Figure 1) that the element carbon role is severely playing in this domain one near the active site. That is working out to be near 55. One can identify the domains adjacent to that active portion, say 40-52 and 57-70 which are crucial in development of active role and arrangements of stability factor. Arrangements of amino acids are crucial in dealing active role. Otherwise, it is going to be simply buried or exposed in protein interior or exterior respectively in nature. Over and above one can also identify the other portions of amino acids which are either determined to be buried in protein if carbon-rich or else exposed when less-carbon. The optimum carbon considered to be the domain one will have value of 0.3144. One can test this domain nature of sequence analysis from 3D structure also which are shown below as (Figure 2).

Accordingly, the protein domains are identified either from sequence or in 3D structure. Here in 3D structure, the reports given in figure 2 shows again the domain nature of amino acid. Here in enzymatic one, the amino acids 50-63 are determined to be in active role which in consideration from sequence analysis. The active role can also be identified in this 3D structure as shown here. Accordingly, all others shown are in domain na-

ture with few exceptions around 18 and 90. Otherwise very good agreement in sequence and structure analysis. One can go on analyzing this sort of analysis in protein nature for any reasonable identification and development of amino acid responsible for active role and all. Identified here are very well accord with amino acid analysis. Validation can also be tested and evaluated. Any mutational one helps in identification and development of active role.

Conclusion

Protein analysis leading to protein active role is determined to be of carbon play which again demonstrated here in enzymatic one. One can go on analyzing these amino acid roles in active role for any reasonable understanding and development of enzyme one. Amino acid based mutational one can also be extended here in terms of carbon one which is going to be of crucial one in years to come. Over and above, one has to deal this new development with protein nature for any meaningful play of disease salvation and all. Otherwise it is going to be crucial in human nature of disease and development based on carbon play which is going to be solution for all sufferings.

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DOI: [10.19080/ARR.2023.08.555742](https://doi.org/10.19080/ARR.2023.08.555742)

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