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Carbon Code for Analysis of Protein Stability in Protein Mutation

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Abstract

Carbon mode analysis can be of great use in determining protein stability in the vicinity of protein mutation where carbons alone determine to be involved in mutational part. Varying parameter of interest are determined from this variable analysis where and all code of carbon force determine the mutational one. Varying values of parameter in crucial in determining the fact of carbon mode analysis in mutational one where and all value varies significantly with variable value of carbon mode analysis where values actual in determined parameter alone. Very few instances of parameter changes where variation can included in the calculation. Varying parameter is determined to be of useful in denaturation and all. Very well accord with verifiable value of experimental one reported in the literature. Values are accurate in determining variable value of mutation in protein site of interest where stability is factor of interest in determination. Very well accord with experimental values reported by various method and analysis. Good in terms of carbon mode analysis in determining mutational part for stability and all. One would go for futuristic applications involving carbon mode analysis in determining mutational one leading to vaccine one and stability one.

Keywords: Protein Mutation: Carbon Mode Analysis; Protein Stability; Card; Carbon Code; Collapse Value

Background

Important found from carbon analysis is that carbon force of interaction can be of one of the most fundamental concept arising these days [1-4]. One of main focus of the carbon value is active one where carbon form collapsed carbon at the centre and stabilised at higher order of contribution coming from neighbouring amino acids [5-7]. Given that the active one where and all carbon alone is responsible for activity, it is also proven that stability comes from carbon factor of arrangements in carbon molecules including proteins [8-12]. Very many carbon force analysis were conducted in previous years [10-13]. Given the scenario what could be the deciding force of attraction the vicinity of alternative protein. Based on the previous analysis where and all carbon force of interaction decides binding and internal structure [5,7,12,13], it is extended here to see the role of carbon on mutational one where internal arrangements can be crucial one in deciding stability of the mutated one where a new force of attraction leads to internal force different that may stabilise or destabilise. Initial calculations and all carried out with very many amino acids changes in different proteins [9,14-16]. All in support of the existence of carbon force of interaction in these carbon based molecules. Here an amino acid mutation that stabilises and destabilise a given protein is taken for demonstration. To do the task of mutational value finding an enzymatic protein is taken here.

Methodology

RNA Polymerase Sequence Taken for Carbon Analysis is Shown Below.

MNTINIAKNDFSDIELAAIPFNTLADHYGERLAREQLALEH-
ESYEMGEARFRKMFERQLKAGEVADNAAAKPLITTLLPKMI-
ARINDWFEEVKAKRGKRPTAFQFLQEIKPEAVAYITIKTTLA-
CLTSADNTTVQAVASAIGRAIEDEARFGRIRDLEAKHFKKNVE-
EQLNKRVGHVYKKAFMQVVEADMLSKGLLGGEAWSSWH-
KEDSIHVGVRCIEMLIESTGMVSLHRQNAGVVGQDSETIE-
LAPEYAEAIATRAGALAGISPMFQPCVVPPKPWTGITGGGY-
WANGRRPLALVRTHSKKALMRYEDVYMPEVYKAINIAQN-
TAWKINKKVLAVANVITKWKHCPVEDIPAIEREELPMKPED-
IDMNPEALTAWKRAAAAVYRKDKARKSRRISLEFMLEQANK-
FANHKAIWFPYNMDWRGRVYAVSMFNPQGNDMTKGLLT-
LAKGKPIGKEGYYWLKIHGANCAGVDKVPFPERIKFIEENHEN-
IMACAKSPLENTWWAEQDSPFCFLAFCFEYAGVQHHGLSYNC-
SLPLAFDGSCSGIQHFSAMLRDEVGGRAVNLLPSETVQDIY-
GIVAKKVNEILQADAINGTDNEVVTVTDENTGEISEKVKLGT-
KALAGQWLAYGVTRSVTKRSVMTLAYGSKEFGFRQQVLED-
TIQPAIDSGKGLMFTQPNQAAGYMAKLIWESVSVTVVAA-
VEAMNWLKSAAKLLAAEVKDKKTGEILRKRCAVHWVTPDG-
FPVWQEYKKPIQTRLNLMFLGQFRLQPTINTNKDSEIDAH-
KQESGIAPNFVHSQDGSHLRKTVVWAHEKYGIESFALIHDS-
FGTIPADAANLFKAVRETMVDTYESCDVLADFYDQFADQL-
HESQLDKMPALPAKGNLNLRDILESDFAFA

The amino acids (S430 and H772) marked in colour are taken for mutational study where carbon force of interaction comes from intervening amino acids of neighbour one. It is considered that 3 amino acids may be opting for lowest one for distribution values. Highest may be up to 45 window lengths. Homemade program derived from CARd [17] is taken here for any other substitution is considered whereas for mutational value in the middle of sequence is taken up here in windows where window means amino acid count in to atomic one which means one amino acid counted to 15.55 atoms equally. On obtaining the result from CARd one it is tested with experimental values which is given in Table 1.

T7 RNAP clones with suppressor mutations: activity and stability data						
Variant	**Amino Acid substitution**	**Codon substitution**	**Specific activity (kU/mg)**	**Relative activity (%)**	**$Ti_{1/2}$ 10 min (8ºC)**	**$\Delta Ti_{1/2}$ (8ºC)**
WT			430	100	43.5	
s1	K392M	AAG!ATG	30	7	45	1.5
s2	*S430P*	TCA!CCA	170	40	44.5	1
s3	C510R	TGC!CGC	62	14	44.5	1
s4	*S633P*	TCA!CCA	239	56	44.5	1
s5	K713E	AAG!GAG	110	26	44	0.5
s6r	Q744R	CAG!CGG	589	137	43.5	0
s7	S767G	AGC!GGC	230	53	44	0.5
s8	H772R	CAC!CGC	300	70	43	-0.5
s9	Q786L	CAA!CTA	96	22	46.5	3
s10	*F849I*	TTC!ATC	380	88	45	1.5
s11	*F880Y*	TTC!TAC	160	37	44.5	1

Stabilizing mutations previously described are shown in italics.

Table 1: Mutational stability values are shown here, taken on [16]. Note that mutation S430P is stabilising while H772R is not.

Results and Discussion

Carbon code of operation exist in protein is counted by CARd analysis one in this calculations. Very few incidences are found to be unobvious in this way of finding alteration in amino acid positions. Over and above very well expressed in graphical and end result. Graphically one would go with decision of alteration meeting the stability or not. One may go alternative way of finding stability in terms of carbon mode of operation in the vicinity. Very well represented are the carbon path breaking results of carbon mode analysis in terms of overall mode of operation in terms of carbon value and distribution factor of carbon collapse where and all counted as standard deviation statistically. Very few incidences are found to be intriguing in test results where acceptance based on carbon mode distribution rather than its value where carbon force of interactions varies. Sample mode analysis shown below for a RNA polymerase one where alteration alters stability of protein internally. Accordingly it is known that S430P (Figures 1 & 2) stabilise the local one and H772R (Figures 3 & 4) destabilise other way around. Below one depict the variation on carbon value and also

the carbon distribution factor value. Various parameter and all discussed in code of contact in CARd one. Varying parameters are used to mitigate the inappropriate results obtainable from carbon mode of analysis. Varying values may appropriate to determine the fact of carbon one and all. All these are standardised in this one to determine the stability factor in sequence one. Varying parameters are crucial one to determine the fact of alignment in dealing with varying fact of all atom analysis in carbon one fact.

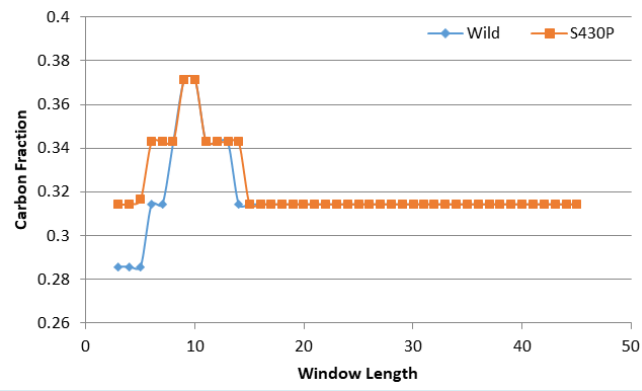

Figure 1: Carbon value for different window lengths are put forth.

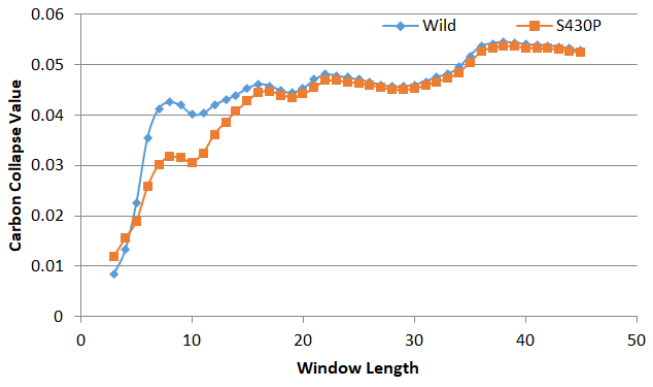

Figure 2: Carbon collapses in windows are given by value.

Carbon point of view there is no change in optimum line in mutation of S430 with P. However the distribution values are reduced which is considered to be stable.

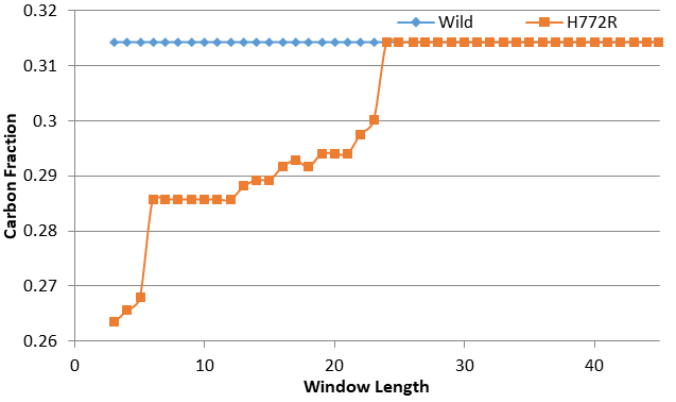

Figure 3: Carbon fraction disturbed by mutation.

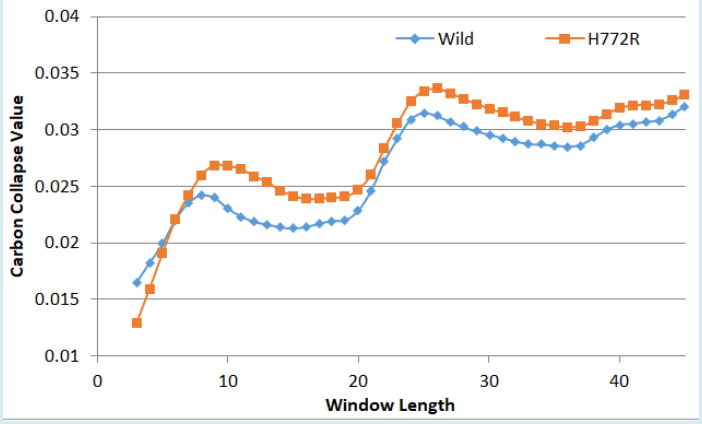

Figure 4: Mutation changes the distribution in different windows.

Both carbon value and distribution protocol are unfavourable in terms of carbon force of interaction in this mutational site H772 where alteration with amino acid R replaces domain with hydrophilic nature. Accordingly in carbon mode alteration all atoms taken into account including hydrogen counts to be 50% in total. Alteration accounts for carbon mode possibilities. Otherwise all atoms are arranged in total with cobweb form nest like structure with the protein 3D structure. According to alteration all atoms are counted but arrangements are equivalent to elemental value coming out to be 0.3144 for carbon. Any alteration accounted in this way in such way that carbon meets out equivalently to substitute in any way for engineered protein one. All and all considered to be equivalent in terms of carbon force of attraction in the vicinity of intended amino acid position equivalent in carbon mode analysis where varying degree of other atoms which are factually ignored in this calculation. Very few incidents of covalent one interfering in the cobweb structure where one neighbour could not come close to one another. Whereas it is in mode operation in vicinity of flexible one where cobweb formation easily favourable very much. The results on other mutations are not discussed here. Otherwise the melting temperature seems to be better in terms of stability is concerned which are reproducible in terms of carbon one.

Conclusion

Carbon mode analysis leading to vicinity alteration is evaluated in this work of carbon based mutational one. It is understood that carbon mode of operation alone is determined to be of great use one and all. Otherwise going to be in operational in any other mode of calculations involving merely bond and non-bonded interactions. Equivalent in way of doing this calculation in mutagenesis one can be operation in this point of view. One should go with carbon force of interaction internally in the vicinity or externally. Interesting to note that carbon based mutation can be very much useful in vaccine generation, validation of proteome mutation and all.

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