

Finding Active Role of Carbon One in Viral Proteins During Association

Ekambaram Rajasekaran^{1*}, Rajasekaran Indupriya² and Rajasekaran Devprakash³

¹V.S.B. Engineering College, Karur – 639111, TN, India

²Andaman & Nicobar Islands Institute of Medical Sciences, Port Blair-744104, Andaman and Nicobar Islands, India

³Lincoln University College, Petaling Jaya, 47301, Malaysia

*Corresponding author: Ekambaram Rajasekaran, V.S.B. Engineering College, Karur – 639111, TN, India



ARTICLE INFO

Received: 📅 December 02, 2022

Published: 📅 December 09, 2022

Citation: Ekambaram Rajasekaran, Rajasekaran Indupriya and Rajasekaran Devprakash. Finding Active Role of Carbon One in Viral Proteins During Association. Biomed J Sci & Tech Res 47(4)-2022. BJSTR. MS.ID.007521.

ABSTRACT

Viral proteins are the assembling blocks that are produced during multiplication. In this process of multiplication, any viral one needs to be in code of order to be intact. In this connection it is important to know the code of order to be in the sequence of protein one and obviously in mRNA or total genetic material. To be precise protein one has to be in specific code of order to get to assemble. Altering this code one might be altering the assembly and all. Alternating this code might be useful from protection point of view. One has to work out a plan that can be incorporated during multiplication. In this connection it is important to know about the role played by carbon in association. It is the Ebola one detailed here for discussion. Adequacy of carbon one leads to association in assembly. According to the nature of association in viral proteins adequacy is prime factor. Analysis were carried out to know where and all adequacy met and not to bind with other. It is reported here in all the proteins of Ebola one accordingly. In this connection it is to be noted that adequacy comes from carbon value. Altering this might be resulting in assembly accordingly. One way or the other, it can also be targeted these active one to deactivate this from assembly. One might want to work out separately in this regard. Otherwise going to be useful in inserting active one in diffusing assembly and all. Ebola, one treated here may be extended to anyone causing human health affected. It is only the program that eliminate all viral one out of existence in the human one and all.

Interestingly it is of carbon one needs to be understood at atomic level by focusing elimination of viral one. Elaborate one needs to be tested in laboratory in the due course.

Keywords: Viral Proteins; Ebola Virus; Active Carbon; Viral Analysis; Carbon Code; ICOD

Introduction

Introducing Ebola one in treatment of viral causing is the main focus of this work. In this study it is of focus that carbon leads to association in assembly of proteins in viral one. It is to be noted that carbon factor of association might be important in diffusing viral propagation. It is to be needed to understand the role played by carbon for formation in the assembly of viral one. In this regard it is utmost important in dealing such a crucial factor in viral one to dealt with. Initial understanding in various active role of carbon in biomolecular association is clearly spelt out earlier [1-8]. It is of application here to extend in viral one to deal severe illness causing diseases in human and all. Earlier works suggest that any carbon rich amino acids surrounded by enlightened one may of active role played in serial action. Otherwise, it is carbon one which and all buried inside the protein one. Any enlightened one may be interior and also exposed exterior one. Anything lacking this carbon role allows water binding one externally. Accordingly, it of important in identify these external one not binding in the overall structure internally. Either this or the one carbon rich with enlightened neighbors interact externally in the functional role played by carbon and all. Anything lacking carbon may be altered to fit in the protein one. Otherwise alteration in the active role of carbon alone to determine to be in assembly of viral one and all. Very many active roles played by protein in the action are put forth during last 5 years. It is here developed in viral treatment in eliminating any active carbon role by inserting appropriate assembly one and all.

In this connection it is taken here the Ebola for instance existing for long time in action in human system of operation. Either eliminate all these Ebola viral one using treatment or end everything alternatively. It is important to think in the direction of carbon role played in protein one and all. Any deviation in altering protein one might be resulting damage to assembly in viral one that may be arrest of the viral proliferation. Encoding these proteins must be carefully altered to meet the assembly to be damaged. Otherwise going to be malfunction in the system of operation in the human body and all. Eliminating these viral proteins must stop propagation all of a sudden. Otherwise arresting this might be evolving to new one that needs to be studied carefully. Code of alteration may be available from the database of known one in the existing system of operation [9,10]. Every alteration may have to adopt to the principle of code of carbon role in protein one. Elimination might supposedly be in action according to new code of arrangement and all. Alteration may have to be thorough in the sense that according to rule of carbon factor needs to be taken care which is governed in principle of carbon code. Alteration according to principle given in nature of action elsewhere in human nature of existence. Eliminating these proteins promote protein of other kind where and all

alteration required which is utmost important in elimination where adjustment need to be accommodated. Overall performance needs to be checked prior to application and all in system of human nature.

Else it is going to operate independently in the system that may evolve separately. Either or the other working inconsistently may be of course to be taken care. Editing these in operation evolving in cell one needs to be taken accordingly. Else everything will be cohesively eliminated inside of it ending operation of removal in the system of human one. Overall performance needs to be tested here and there during elimination when in need where elimination occurs excretive. When elimination occurs that can be available for interfering with system of operation in human one. Existing protein might be interfering in the new one eliminating evolving one. In this connection it is of utmost important to study and understand the nature of protein that needs to be altered according to code of carbon one. Either the code at carbon role in protein or the assembly of altered RNA at the core. Interference need to be effective in the action that comes from viral one eliminating old ineffective that arrest new one from propagation. Elimination may have to be analyzed in the laboratory in the action of cooperation either in new one or else with older one.

Methodology

The viral proteins of Ebola one (P1) glycoprotein, (P2) nucleoprotein, (P3&P4) matrix proteins VP24 and VP40; (P5&P6) non-structural proteins VP30 and VP35; and (P7) polymerase are taken here for carbon role played in it. The NCBI sequences details are given in (Table 1). Role played by carbon was analyzed using COD of Card using computer programming [11]. Inferences are recorded in XY plot as shown in (Figure 1). Understanding the active one and domain regions are crucial in determining role played by carbon in assembly and all. Accordingly it is taken here all adequacy of carbon one are searched in order to find anything lacking carbon one in between domain regions. If it so counted as one active site which may take about 5 to 10 amino acid length and so on. Otherwise call this lack of carbon one counted as hydrophobic one which is not available for any interaction as it obviously buried inside of the global one. Very many interactive these adequacy one in lacking carbon is observed in all these sequences and all. All these are available for interaction in assembly and all. Accordingly it is found out to be very many options in these viral one which interact to bind one another to form viral host. Very many interactive carbons one is in different portion might be interacting with another one to form network of host with assembly including genome material say RNA. Visualizing these might be useful in determination of active role of carbon and alter according to nature of interaction.

Table 1.

No.	Protein	Protein ID	AAs
P1	Envelope glycoprotein	P87666.1	676
P2	Nucleoprotein	O72142.1	739
P3	Membrane-associated protein VP24	Q6V1Q3.1	251
P4	Matrix protein VP40	Q77DJ6.1	326
P5	Minor nucleoprotein VP30 -Transcription activator	Q77DJ5.1	288
P6	Polymerase cofactor VP35	Q6V1Q9.1	340
P7	RNA polymerase L	Q6V1Q2.1	2212

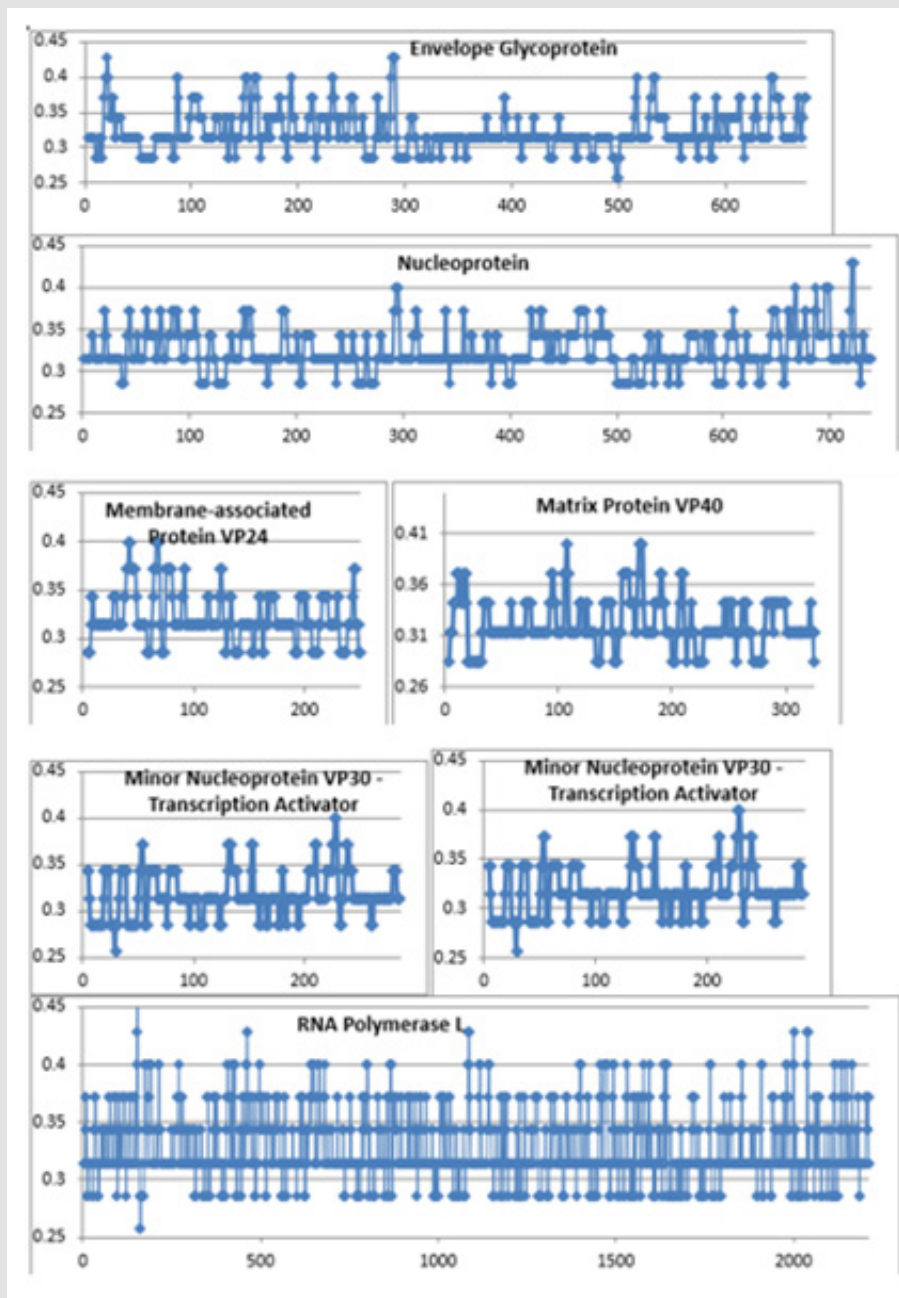


Figure 1: Carbon one computed for viral Ebola.

Very many sites available for such neutralization even though evidence based one would help to determine fact of all that happened in viral disruption from propagation. Even though it is mandatory to unhost viral one, it is crucial to determine which portion might be helpful in disruption. All available seems to be fine but nonetheless verification of these altered one might be of great useful one and all. Alteration one might want to choose in the program to choose from available code contain in the necessitated portion. Nonetheless mandatory one might be pinning in the host of altered one and form another one to continue as viral propagation. Within this chosen one has to be adequacy to be met with all other amino acids within the stretch of available one. Many such instances are occurred to propagate newly formed devised proliferation that may and all available through another system of operation as host (Table 1). Available in the near one host material may have to be inadequate within the domain one formation where are all going to be pinned adequacy in the existing one. Validating these genetic materials through genome one is hope to get new insight in the narrow down of disease and all. Various such available data might be interesting to note gene propagation through these viral genomes and all. Validated one is demonstrated here in Ebola one where and all one can analyze and accelerate these finding in the genome editing in human genome and all.

Various such workout needed at this juncture of accelerating gene one to be part of cure for disease role played by carbon one where and all one has to work out and do the needed one to solve outstanding issues in disease control and propagation. Very many instances are there to maintain adequacy in detail to address these issues and all.

Result and Discussion

Adequacy of all available proteins in Ebola is scanned here in detail. Although one can elaborate in detail, a brief is here to demonstrate the Ebola viral genome in propagation. Very many available source of adequacy are found out here in these proteins which are carbon lacking and having domain one adjacent to these. The list of these host one is given here which are taken further processing of the available sources of adequacy one determined in plot of carbon role as a function of amino acids as shown in figure. One has to be careful in determining these adequacy related parameters for protein scan and all. Very many such instances where and all inadequacy may be occurring but many have not yielded the result of necessary one. In this scenario it is necessary to work out in detail to determine factors of all other parameter intervening in the fact finding. Given the scenario of all available source of protein parameter it is clearly evident from COD of CARd might be interesting to note fact of all available one. When and all adequacy not met with available domain neighbors, address the issue of propagation in cell line. Very many data verification are done to prove this fact

of available parameter coming from COD and CARd one. With this parameter of fact one need to go through either available detail of experiment one or do new to prove. It is verified here detail earlier in the parameter fixing. Parameters found out using these earlier help in determination of active role played by carbon and all in protein of viral one.

Nonetheless it is clear from these observations that active role of all available proteins in the host might be interesting to note for validation and all. One may have to be cautious in dealing such instance in antibody interactions and all. Various other sources may have to be analyzed to get the fact in these encounters. Fact from carbon may have to be dealt at these instances too. Various fact of carbon role is already addressed here in genome and proteome [12]. One may have to look into specific instances to address this carbon fact of binding in dealing such various issues. Varying with amino acid count in determination of active role of carbon may be helpful in early determination of gene therapy. Counting these parameters in terms of carbon may prove to be success in eliminating these defective genes in cure. Very many instances are there to solve all of sudden in the due course of action in the current working actively involved one. Prove to be increasing day by day in the current scenario of defective variation where and all one has to focus to solve the fact of all available sources of carbon role. Role played by carbon and adequacy are given for all of Ebola one which needed to be worked out to demo of eradication of disease in human one and all. Very many instances are given here to choose from where one can stop aggregation in the viral formation where carbon spelt accordingly in the various instances. Verification may have to be done to choose these instances in slowing down the propagation and all in host cell of human one. One can either target these active one or else narrate to add new which eventually eradicate old disease causing line.

Active one in different proteins of Ebola one is given here. In each there is a greater number of such active roles present in the system of protein to fold and act accordingly.

P1: 122-126, 192-197, 248-253, 627-631

P2: 58-67, 186-191, 207-214, 291-296, 309-314, 442-446, 567-576, 604-612, 644-653, 673-678, 719-723

P3: 63-69, 169-173, 195-199, 216-221

P4: 34-38, 71-75, 92-97, 140-146, 169-175, 185-193, 206-210

P5: 20-24, 34-39, 60-67, 78-85, 131-139, 204-211, 220-230, 237-243

P6: 21-29, 41-46, 81-85, 211-216, 258-264, 323-328

P7: 30-36, 61-65, 72-79, 87-92, 98-102, 110-117, 126-133, 148-155, 210-219, 276-283, 296-301, 374-379, 447-452, 562-568, 616-621, 627-631, 693-701, 828-832, 861-867, 913-922, 945-951,

1030-1035, 1082-1091, 1115-1121, 1357-1363, 1379-1383, 1395-1401, 1417-1423, 1451-1459, 1489-1494, 1527-1533, 1573-1581, 1589-1595, 1616-1626, 1634-1643, 1712-1721, 1801-1807, 1819-1827, 1939-1943, 1948-1953, 1979-1987, 2037-2041, 2068-2073, 2129-2136, 2145-2151, 2203-2210.

Similarly the long domain one are listed below which are all considered to be surface one in the system of operation where no other elements interact to participate either in action or replacement.

P1: 309-528

P2: 1-57, 215-290, 315-418, 494-566,

P7: 220-257, 302-373, 569-615, 702-789, 952-1003, 1194-1269, 1644-1711, 1722-1800, 1828-1938, 2152-2202

Anywhere in the protein if more than 5 amino acids occupy less carbon (below 0.3144) one, then there must be instability in the surface of protein. For example in glycoprotein at 52-66, 263-272, 293-303 and 494-502 the less-carbon regions occurs.

Conclusion

Proteins of viral one are analyzed here in order to eliminate viral propagation. Alteration might bring solution to the existing disease in action accordingly. Ebola, one taken here in dealing such a demonstrative one in viral protein's assembly and association. Editing needs to be careful in such a way that alteration brings adequacy in carbon principle of law that govern proteins in operation in human system operation. Either of the applications that come from code of carbon one needs to be tested in the laboratory eliminating viral one from disease cause inside the cell of operation in human one. Either of the operation needed these carbon factor of operation in the protein one which are demonstrated here in Ebola one. Elimination needed to be effective in the sense that no side effect cause during operation. Either probe binding or null operation in protein where assembly stopped is to be careful to meet the adequacy op-

eration exists inside the cell one. Alteration should bring adequacy of action in the cell to function. Any elimination may be adequacy principle that and all used in the system of operation where human nature can adopt to new one and all. Elimination that occur only in diseased one, not elsewhere in the operation.

References

1. Rajasekaran Ekambaram (2021) Nanone interactions in antibody of living systems. *Modern health science* 4(2): 1-5.
2. Senthil Renganathan, Subrata Pramanik, Rajasekaran Ekambaram, Arne Kutzner, Pok-Son Kim, et al. (2021) Identification of a chemotherapeutic lead molecule for the potential disruption of the FAM72A-UNG2 interaction to interfere with genome stability, centromere formation, and genome editing. *Cancers* 13(22): 5870.
3. R Indupriya, R Meenal, E Rajasekaran (2021) Drug in action according to nano force of interaction. *Int J Med Res Health Sci* 10(3): 78-84.
4. Rajasekaran E, J Bioinno (2021) Protein-profen Interaction: The role of carbon in dealing active site interaction 10(2): 666-675.
5. Rajasekaran Ekambaram, Meenal Rajasekaran, Indupriya Rajasekaran (2020) Study on aquaporin proves to be the carbon in protein-protein interface playing in tetramerisation, *High Tech Let* 26(5): 292-298.
6. Manisha Thaker, Ananda Gopu Perumal, Rajasekaran Ekambaram, Naressh Poondla, Markus Schmidt, et al. (2020) Proteomic atomics reveals a distinctive uracil-5-methyltransferase. Subrata Pramanik, *Mol. Info* 39(5): e900135.
7. Rajasekaran Ekambaram, Indupriya Rajasekaran, Meenal Rajasekaran (2019) Domain formation in regions of protein probe interaction. *Int J Mol Biol Open Access* 4(5): 167-169.
8. Indupriya Rajasekaran, Meenal Rajasekaran, Kavitha Velusamy, Rajasekaran Ekambaram (2019) Drug-protein interaction validates the internal COD formed due to cohesive force: Test of bond length variation in amino acids involved. *Int J Mol Biol Open Access* 4(3): 113-117.
9. Rajasekaran Ekambaram (2022) Protein alteration accordance to the carbon interactions internally. *J Cell Science & Therapy* 13(5).
10. R Indupriya, R Devprakash, E Rajasekaran (2021) Mutated protein's stability accordance to carbon force of interaction. *British J Med and Health Sci* 3(6): 977-980.
11. E Rajasekaran (2012) CARd: Carbon distribution analysis program for protein sequences. *Bioinformatics* 8(11): 508-512.
12. E Rajasekaran, R Indupriya (2022) Carbon rule of law that determines

ISSN: 2574-1241

DOI: 10.26717/BJSTR.2022.47.007521

Ekambaram Rajasekaran. Biomed J Sci & Tech Res



This work is licensed under Creative Commons Attribution 4.0 License

Submission Link: <https://biomedres.us/submit-manuscript.php>



Assets of Publishing with us

- Global archiving of articles
- Immediate, unrestricted online access
- Rigorous Peer Review Process
- Authors Retain Copyrights
- Unique DOI for all articles

<https://biomedres.us/>