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Temperature Data in 3d Structure Reveal the Internal Cod Involvement in Molecular Form

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Abstract

Addition of small molecule into force is going to be the task of another rule based activation for any meaningful application in biology of Animalia kingdom of existence. Otherwise it is mandatory to fulfill the norms for adequacy principle arising out of carbon value in force here in protein or other where carbon alone dominates the due course of action and all. Accordingly we have developed an internal one proposal for any meaningful application in carbon based study of intervening elements of interaction arising from carbon value. Additional to existing calculations in modeling, it is going to be the one and only force will dominate the scenario of molecular alteration for many salvations in living organisms. According to rule of law coming from carbon profile, the hydrogen atom also to be the main part of the value calculation and all. According to new force of carbon calculation, it is here calculated to be the internal one of carbon profile found in 3D structure where another part of intervening elements taken into account. As part of this work the internal carbon values are compared to temperature factor value of crystal valuation. Accordingly the tested molecule of super oxide dismutase obeys this internal one and all other parameters needed to incorporate therein. Interestingly the internal values dominate the scenario of uncertainty arising here in temperature factor for protein as well as in RNA or DNA. Very well documented internal values are crucial for any meaningful application where other modifications arising for alteration at the vicinity of active role played by proteins and so on. One can trust these developments for any meaningful applications arising for disease solving or control and also for proteome of future applications. Over and above this evolving newly developed one going to be the task of newly existence of successful run for the future one.

Keywords: Internal Domain; Temperature Factor; Carbon Value; Protein; DNA/RNA; Card3d; Cohesive Force

Introduction

Atomic coordinates of all protein level seems to be clear from the pdb of RCSB. However other parameter that are in play are not yet taken into account here in pdb where only occupancy and temperature factor is listed there against each atom. Additionally other atomic level coordination coming from carbon alone is missing in part. Of course it needed to be worked out for certain application and all. All that happens under universal law of force may represent here in pdb of protein structures. However the uncertainty arising out of carbon value hence forth incorporated in due course of action coming along side of developmental technology of new generation [1-20]. All that needed to be incorporated are how small portion of protein molecule might interact with neighboring one to compensate the needed internal domain formation that and all part of the newly evolving proteomics of allied science yet to be realized.

All that happen in due course of interaction within or

external one may be put forth for meaningful application here in biology or in material science where another type of atoms to be in study of interaction with changing parameters of internal domain values. Whereas it is necessary to monitor or alter these changes along the newly evolving proteome values. Under this circumstance it is very clear that atomic coordinates may represent all that uncertainty related issue of individual atoms. Fact is that internal domain values determine to be part of this new force of interaction which govern in all temperature value or B-factor of individual atoms. When atoms are uncertain according to rule of thermodynamic principle, very essential to take into account of this internal domain activity of individual atoms involved in protein structure or action of other one internally in the structure. Facts being that internal domain values dictate to be in order or disorder which temperature value reveal it. Many such interaction forces arising from carbon force of interaction might be uncertain in individual force of atom altogether in the protein of interest. However very many fact of domains revealed in nature of proteome of pdb one is revealing the all available forces according to rule of law governed by force arising out of carbon fact of adjoining elements arising from neighboring residues of unknown value which again in due course of interaction with other set of amino acids or so. Additionally alteration might be in force with other elements available locally in the vicinity of protein molecule is concerned.

Additional force arising out of carbon value may be computed from domain of all atoms out of CARd program written in PERL. All these happening out of additional force may be intriguing as for as protein structure or available interaction with other of forceful interaction. In the vicinity of interaction it may be noticed to involvement of neighboring one in response to other force of interactive elements. Addition might be intriguing in this in order to improve the additional internal domain at that point of interaction. According to nature of interaction intriguing in the vicinity of elemental adjustment arising here internally may be captured via our internal domain value available from CARd3D one additional to other all atom force available via other packages of modeling stuff. Over and above it is only the carbon value of interaction determined to be interactive elements in the course of structure formation or interaction with other elements of adjoining force of interaction. However it is limited to protein 3D structure availability. All other parameters may be generated for internal domain of available proteins. At the same time additional force might be interested to make any addition or omission of amino acids that and all involved in internal domain formation at the sight of vicinity or long. All that matter to incorporate in due course of action in science of everything where these alone are major player of the game of intervening elements and all. One can go along the way simulating it in terms of carbon force of interaction. However limited to narrow one available for certain applications. All that matter to incorporate in the calculations may not work accordingly in the vicinity of additional force incoming in terms of carbon value. All along the calculations however may refer to additional structural value available from pdb alone help in improving it. Otherwise going to be exhaustive in terms of carbon force calculation for any meaningful applications. Adjoining one is crucial for any addition to take part which is part of available protein structure already in the database. Already available one of course is crucial for any application of mutational study or so. All that available one workout to be part of addition or not. Addition or deletion may be accepted or not in force may be computed based on the available structure one for that event of situation in addition to other force coming from adjoining elements counted from amino acids of interest. Here we prove that addition of small molecule in the vicinity of active stretch in protein of interest may be captured from carbon value alone but comparable to temperature value of additional information available in the crystal structure at pdb via RCSB. According to new table, internal domain can be captured via temperature factor value available via X-ray structure. All the happenings to individual atoms are adequately captured in the value provided for temperature value additional to occupancy which is differently dealing the same concept of uncertainty. According to new line of uncertainty, additional force of interaction is due to carbon value which again in terms of available structure.

Additionally other force that may influence another molecule accordingly in the crystal are needless to incorporate in this value of uncertainty where carbon value arising from internal alone is deterministic in uncertain is concerned. Otherwise temperature factor may or may not influence of another molecule deposited over the other during crystallization. All that happening because additional force arising from internal domain and all that arising out of other may be neglected during consideration of uncertainty in the event that addition or drifting of course be part of carbon value alone where other may be excluded for consideration accordingly. Otherwise going to be significant in terms of carbon of force arising out of additional work counted via internal domain value. For the present the additional forces are calculated to be in accordance to available temperature factor which are demonstrated here in this study. Over and above it is true to be considered as it is and no further arguments needed to be included for any point of consideration. All that happenings in the vicinity or structural one are due to this carbon force of interaction. Accepting it in terms of internal domain preferably be useful. Non adherence of internal domain may be deviation from intervening elements of interest in terms of available sources

for and above the application is concerned. One should go ahead with this newly evolving practice of carbon value for any purposeful deviation in addition to other values coming for object oriented application. Over and above it is to be the true of all that happening in protein science and macromolecule of biologically important. Very well documented elsewhere in the universal problem of doi to be incorporated. Fortunately we have some applications leading to disease solving and all. Incorporation of these newly evolving proteome going to be the part of main source for application where new creature yet to be realized and all. Additional to this force of interaction for several diseases solving, adherence of alternative elements of interaction may be crucial for evolving genome over the current disease oriented omics under influence.

Methodology

Carbon Analysis in 1D

Of course the data for the analysis are always being the pdb under RCSB (Table 1). According to the rule of law governing from carbon fact of adequacy principle the CARd program does take care of everything from sequence read to analysis and report. Overall performances are already reported elsewhere [4-6]. Better combination of analysis and alteration are adjusted to meet the carbon value to be evaluated according to rule of law. Over and above it is significant to involve this analysis for alteration and all. CARd performs operation at outer length of 62, 78, 109, 125, 140, 155, 171, 202, 218, 233, 249, 264, 342 and 700 atoms and average for analysis report. According to carbon rule of law, it is expected to have value of 0.3144 for an internal domain to be achieved or else alternative carbon high or carbon reduction state. According to the principle observed from carbon value, it is noticed that carbon high portions are not accommodated fully at lower dias and is met at higher dias which in turn meet the temperature factor values. Well here we analyzed the temperature factor values which are direct evidence of our internal domain calculations observed elsewhere in the other applications side. Of course it is mandatory to follow the internal domain principle even if the atoms are not arranged accordingly. Otherwise the amino acids are arranged to represent this task. Whereas mandated in it to achieve the proposed structure or selective function. Well this phenomenon is captured in this CARd value reported in the Figure 1. It is a plot of carbon value averaged over the above outer length and amino acids. Of course arranged amino acids are according to needs of the protein of interest; here it is super oxide dismutase. The pdb code of all is 2XJK. Over and above it turns out to be radical change in the overall internal domain formation and alteration occurs only at active region and accordingly the other parameter coming from X-ray values.

S.No.	Macromolecule	PDB ID	Remarks
1	Protein	2XJK	Super oxide dismutase
2	DNA	2M6V	NMR structure
3	RNA	1YFG	Transfer RNA

Table 1: Carbon Analysis in 3D molecules.

Crystal Analysis for Domain One

The other analysis reported earlier to capture the carbon phenomena is the carbon in 3D structure that reveal again internal domain, hydrophobic or hydrophilic regions that are amenable from domain formation. Work has been considerably improved over a period of time to test several phenomena that take place in biology and all. Accordingly the CARd3D program is altered to capture the essence of unattended phenomena that are internal domain relevant. Accordingly we have developed to internal domain parameter in different dias from as low as 4 and high as possible, but here it was 7 to 77 which cover all necessary values. Well said earlier that carbon role of honor is in adequate to if any protein to be active. Accordingly the amino acids are embedded into it. As per adequacy principle the alternative biology of upcoming events are aris ng from carbon alone. Otherwise call it as adequacy of alternative realm adjoining the amino acid of interest. Arranged amino acids are altered according to the carbon value to accommodate in the structure. Otherwise action takes place from carbon alone and none other than this.According to rule of law, adequacy is met, provide it meets the requirement of 31.44% of carbon value provided with circular arrangements. Accordingly the arrangements are met to satisfy this parameter. Otherwise there is going to be altered structure according to dia of different value. Well it is said that the parameter at dia 16Å adequate the principle for lower dias otherwise all other dias are adjoining one to play around. According to new realm the principle has to be met out to accommodate carbon value. Otherwise other molecule of interest might satisfy them to rule the carbon value. Well all these are well captured in the program and averaged for plot as shown in Figure 2. Also the accordance is limited to carbon role and adheres to the norm of carbon value accordingly. Very well documented alterations are applied here to compare with temperature factor of all elements. Otherwise going to be overall performance rather than local parameters which are taken into account of other activity that take place in biology.

Temperature Data Verification for Internal One

As said above the adequacy parameters are alternatively captured from temperature factor value which takes into account of all dias of adequacy value rather than dia at 16Å

alone. Alpha carbon values are arranged according to amino acids as shown in Figure 2 and framed according to internal domain value obtained from average of all dias and so on. According to rule of law one might be expecting the value to be in par with X-ray crystal data alleviate to modernize our internal domain value of all internal domain obtained from lower dia to maximum possible dia. Accordingly the values are extracted to map the parameter with internal domain value obtained from CARd3D program of alternative one to solve different dias. Well one would expect internal domain to be according to nature of interaction coming from carbon role. Accordingly the values are arranged and plotted against to amino acids. Of course the values may be from average of all atoms of individual amino acids to take into account. Interestingly it works well. Otherwise the alpha carbon alone represents this phenomenon of internal domain at all level. Accordingly the arrangements are carried out perform the operation of internal domain and temperature factor value comparison. As shown in Figure 2, the arrangements are neat and alternative to internal domain value. According to rule of law, the internal domain regions are stable over the hydrophobic elements and hydrophilic might be able follow or not. As said in the principle the internal domain portions are expectedly lower temperature factor value and stable over the other disordered unstable portion. Accordingly the results are interpreted. Otherwise internal domains are alternative to temperature factor of all atoms vice versa. Arrangements are to meet the required threshold to say order or disorder and so on. Well said earlier that the hydrophobic portions are less stable over the internal domain regions. But in this case the hydrophobic regions are covered with larger internal domain parameters coming from adjoining elements of interest. Accordingly the temperature factor parameters are valued. Arranged are the average internal domain values and alpha carbon temperature factor value. Otherwise going to yield overall performance of the protein system and may not be the individual role played by intervening elements which are spelt out by internal domain here. Well internal domain may perform better over the conventional value obtainable from X-ray in terms of order or disorder is concern. Otherwise X-ray are arranged values and internal domain are computed value which again superior over one another. Very well those internal domains are comparable to temperature factor values which again alleviate the next level of operation and all.

Results and Discussion

The average hydrophobic domain values for super oxide dismutase is given in Figure 1. As can be seen there the hydrophobic domain portions are having carbon value of 31.4% at 1-12, 21-27, 32-38, 70-124, and 15-19. Super oxide dismutase possesses active site at about 51-62 or hydrophobic part at 15-20, 28-31, 40-56, 59-65 or hydrophilic part at 130-145. As part of the internal domain expectations the carbon rich hydrophobic parts are in disarray or unstable over hydrophobic domain regions. Accordingly occupy higher temperature factor values as part of the sedimentation of crystal of one another. Otherwise the hydrophobic domain regions are highly stable over the other regions, compact and array forming over the rest of the portion. Believe it or not the hydrophobic portions are in disarray and accordingly higher values of temperature factor. Provided the large scale proteins can accommodate these carbon rich portions of internal domain at higher end. Naturally the higher carbon content active regions are accommodated accordingly by neighborhood. Whether or not the active roles are protected by neighboring hydrophobic domain regions accordingly safeguarded during inactive time of intercourse. Over and above the portions which are hydrophilic may take part in domain formation. Otherwise it requires more carbon for internal domain formation. Accordingly one can test with mutational study over the issue. Proof that internal domain of all amino acids exception to carbon high noninternal domain forming regions is stable over the one with high carbon values.

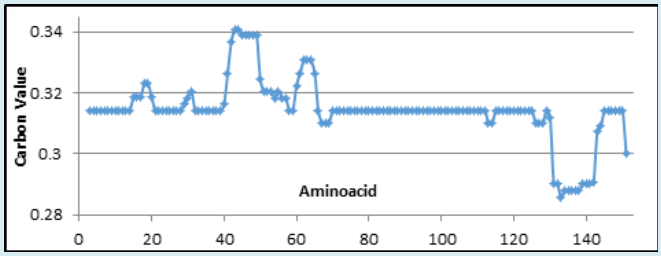

Figure 1: Graph showing carbon value calculated from sequence information. Note that the line on carbon value of 0.3144 is internal domain portion of the protein. Otherwise the noninternal domain having higher carbon value is carbon-rich and carbon reduced portion is hydrophilic in nature.

Accordingly the internal domains of all amino acids are computed using our homemade CARd3D program written in PERL. As seen in Figure 2, the internal domains are plotted against amino acids which are in accordance to internal domain of hydrophobic domain regions that are shown in Figure 1. Also in the plot are temperature factor of alpha carbon of each amino acids taken from crystallographic data (pdb structure). All are in agreement with internal domain value with hoping that higher internal domains are highly stable over the noninternal domain regions. Interestingly, the internal domains are invariably matching with temperature values all along the amino acids of domain or no domain regions. Otherwise hydrophilic stretches may be deviating with negligence for purposeful arrangements to form internal domain. Otherwise all are accordance to internal

domain and only the internal domain determine to stability over the other forces of interaction revealed from various other sources. Well it is clear that carbon alone do match with temperature factor of all atoms and nothing of coming from van der Waals or from electrostatic one. Deliberately it is devised to have internal domain forming elements in the control of cohesive force arising from carbon alone. Nonetheless it is advised to form coherent intervening force to make it an internal domain and all. Otherwise internal domain will be in a position to take over the issue of internal domain formation by mutation or alteration for meaningful applications. Advised to form a noninternal domain stretches for any interactive species to have eventuality of intervening elements in accordance to arrangements already in the available data of pdb structures. Anything arising out of this eventually is useful for non-intervening elements of accordance to follow for future applications. Otherwise going to be in the market for damage control and all.

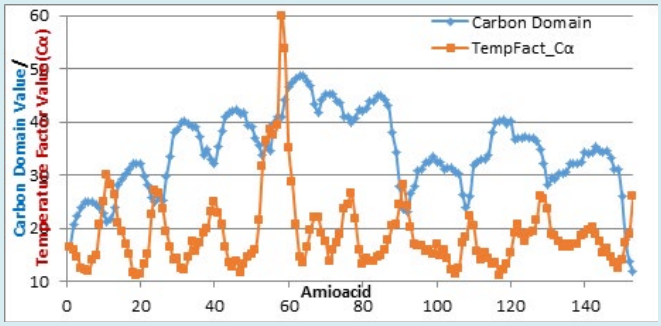

Figure 2: Carbon domain value computed along the protein in different dias are averaged for total carbon domain value which are in comparable to temperature factor of atom Cα. Internal domains are agreeable to temperature factor according to the nature of atom involved with internal domain or carbon-rich or carbon reduced portions.

Many eventualities are coming forward to makeup the disease control and all. Otherwise going to be useful for meaningful application of disease prohibition or stopping of catching of disease formula under the cloud of carbon one. Over and above this may be useful for futuristic application over development in accordance to developmental biology for future creature. Well otherwise going long way of travel with many different eventuality as per demand over space and time. Nurture these phenomena of intervening elements to pursue new kind of research over the development of new creature with adequate knowledge and support. Well known fact that dreaming high is big enough to pursue upcoming one to continue with dedications and test, rather than merely occupying position and above. Over the period of time this has consumed enormous amount of time and effort to come to this stage of knowledge based movement to recruit other elements that can survive in due course of time management. Whereas it is time now to think of this newly evolved force of interaction in the years to come. Whereas it is alpha beta of elemental course of interactions in the year ahead. Well it may be taking part in the event of eventual analysis of intervening elements to construct a robo like platform for other space of interactive elements intervening. Over and above this might be interesting to note the survival of this newly evolved one to take over the existing one during meaningful application as otherwise limited by a factor adjoining force which may not work fine everywhere in the system of approach. Rather it may be better performer over the existing phenomena of interactive elements in dealing situation to situation accordance to fruitful discussion on eventful applications.

Otherwise going to be the wonderful meaning of event that controlled by other passes by newly developed wondering of other of plan work force adjoining the existing one which may fail at one point of time. Accordance to new force of interaction it is a matter time to take over the new plan of action to deliver new variety of actionable applications. Eventually it is matter for moving body to accomplish the task of driven force or less over the conventional one already existing. During this new variety of application it is recommended that popularly known ones are driven away first during due course of interaction. Eventually those occupy the new form of action during initiation and all. Well it will be marketable for many to accomplish the task during failure of the existing condition and above. Overwhelmingly it might solve several such problems during this kind of operation in the universe of meaningful applications. Well in advance one can plan or die hard to establish this newly evolving event to the point that it might be interesting to makeup. Over and above it is a fantastic development over the conventional one during the production stage of interaction. Wellbeing is the key to success of this new force of action taking part in the additional action of force forming from carbon alone. Over a period of time of course all other issue can also be brought up to the meaningful application in the eventuality that may fail to accomplish task oriented problem. Very well done in this case of alteration eventually need of this hour for accordance to the nature of elemental analysis during the process of action. Otherwise going to be big hit in the event that may fail to accomplish the task may be brought forward the reality of working. Well it is a matter of time to come and accomplish this task.

In most of the applications it is going to be the task of calculation the internal domain value at dia of 16Å. Whereas it is counted as the whole lot of dias for the temperature factor is concerned. Accordingly over a larger spectrum accomplishment it may be higher internal domain values for carbon rich regions which are expected for satisfaction. One might even think that the smaller dia internal domain can

be compared for larger dia value adjusted in temperature factor of atoms. Otherwise accomplishments are adjusted for higher carbon value while the internal domain patterns are left out at the higher performance of intervening elements coming from longer neighbors. Eventually it is for the eventual elements to accomplish the task of fulfillment of internal domain formation and all. Otherwise all other are satisfied with lower dias eventually end up with lower internal domain value. Meaningful say that accomplishments are attained at smaller dias and adequacy met at that level, further may not be required to proceed with neighboring value. Over and above it is a matter of time to achieve this task of fulfillment the eventuality of needless carbon out there. Otherwise going to be healing of the carbon rich pattern in the event of hydrophilic pattern that are adjacent to hydrophobic part.

Noninternal domain patterns are filled with atoms of internal domain forming elements. Whereas it is mostly the recovery of this force of interaction the poison that adapt to the biology of living matter. Well one need to spend time on it to win this task of inadequacy. Many are inadequate to meet out the task of other platform in joining force. Only the lower phenomenon of adequacy is important for functional units to work in nature. Many such viral ones are behaving this platform needless adequacy problem. Well one might want to meet out this task of achievement of disease free zone of alteration. Mutational studies may be part this task for meaning application of viral one to achieve the force of action. Well we have reported that cohesive force alters that bond lengths of atoms involved in internal domain. Accordingly the system response but not on the basis of long range interaction as reported for temperature factor. Other evidence of intervening elements is accomplished by superposition of one with or without alteration at active sites. It is clearly explaining the adjoining elements in dealing with internal domain of noninternal domain elements in active one. Over and above it is a matter of time to eliminate the task of nonobedience of internal atoms in the internal domain formation.

Temperature factor is one of the main part of the structural proteins to achieve the structure intact of internal one. Otherwise nothing can be achieved out of other forces of interactions. On order to match the computed internal domain value with temperature factor we have tested for derivative test which are on accomplishment of internal one and all. Derivatives 5-1, 6-2, 7-3 etc. seems to be good in the sense that it is matching with internal domain aligned. Over and above the temperature factor of alpha carbon is taken here for implementation of adequacy principle as it alone neutral to the residue of interest. Overwhelmingly it reproduces the result of matching scale, better than any other atoms at the internal domain comparison. Otherwise all atom involvement can be part of it, which again matching it. But there are side chain portions which may deviate from the regular task of internal domain formation and in particular the lysine which has long tail and electrophilic elements at the last of it. All of this shows disorder from temperature factor value. Removal of this lysine from regular task is expected to have better performance over the conventional one. This is phenomenon of deviation is also observed in temperature factor values of individual atoms and also in internal domain values. Well we may conclude that internal domains are the driving force of attraction in all these intervening elements. With this we derive principle of intervening elements existing from available database of pdb.

According to the nature of interactive elements it seems to a pattern of events that take part accordingly as observed from ups and down of internal domain and its temperature factor values. Well we have work towards these intervening elements in achieving the task of mutational study and all. It appears to be occurs at intervening length of 15 or so. According to principle of carbon principle of adequacy it meets at 16Å which contain about atoms that are coming from neighbor of 15 alone and none are accordance to them. Very well said that the atoms are arranged to meet the philosophy of carbon role. Accordingly arranged are the amino acids. Otherwise call it as adequate amino acids that perform well with carbon profile of attraction. Otherwise going to be other circle of alteration coming from long range interactive elements which may provide adequacy principle as in the case of temperature factor observed for it. Over and above it maintain the law of carbon value adequately and all. One might scale this phenomenon from carbon value of adequacy principle.

One of the interesting phenomena of active site formation due to disulphide bond is unexplained from previous work of other forces. Whereas it is clearly visible from internal domain and comparable to temperature factor value. Carbon phenomenon explains it thoroughly over the active site formation due to cystein-cystein disulphide bond. In fact the neighboring role in fulfilling this demand made out of disulfide bond is felt at the adjoining amino acid instead of that happens at Cys itself. Over and above it is clear evidence of neighbor role in formation of internal domain while in other force is in due.

On analyzing the nucleic acid structures (2M6V and 1YFG) for internal domain formation and comparable to temperature factor values reported therein, it is clear evidence that internal domain alone dominate the scenario of temperature factor and all. It explains atom by atom interaction within the neighborhood. In fact the stacking interaction followed by quadruplex formation by DNA, GGGTTGGGTTTTGGGTGGG is due to domain. There are

unstable and stable elements along the sequence and structure. Accordingly the internal domain and temperature factor varies. It is a clear evidence of internal domain involvement in biomolecular systems that may be the future of study in due course action. Over and above it is evident that the cross check of this value with temperature factor is going to be the use of monumental development of newly proposing developmental creature of application. Of course project on stalking and pairing interactions or exceptions can be planned adequately to meet out the requirements. Stability factor can be adequately met out from this carbon role of interactive elements and species. None other forces can explain this phenomena of intervening elements and all.

Conclusion

According to the rule of law governed from carbon value, the proposed arrangements are altered because of adequacy principle. Otherwise it is evident from internal domain value comparable to temperature factor value observed from X-ray crystallography structure. It is clear that the internal domain coming from carbon role interior to protein or other macromolecule of biological nature are made out of macroscopic scale which again meets out the temperature factor value. Original value of crystallography can be better exploited for purposeful identification and application of internal domain parameter for and above application in living system of interest. Over the period of time it is a matter for every one think in this direction of long livable one arising from carbon value here in this research. Periodic checking and analysis of all such intervening elements of interaction are going to be the pillar of the new developmental creature to come in due course. Over and above it is a matter of time to expose and advance the science of everything coming out from carbon course of interaction.

Well in advance one can think of alternative elements to be imparted for smooth transformation of elemental incorporation. Over and above one might even leave out the old one to cherish the new beginning of advanced technological improvement over the conventional one arising as undesirable. Of course one might even want of alternative events to be incorporated at all level for future happening while old one to go away. Of course one would go on searching for real application of alternative elements at the adjoining course. Purposeful applications are yet to be chartered out to meet out requirements of elements. Overall it is going to be alternative source of interaction in the course of failure or so. Meaningful of this devised application are to be part of the new developmental application in the years to go or vary again in principle. Overall it may hit the supersonic radio wave parameter to meet the people interest in the course of interaction. One would even go ahead with new line work which provides hell lot of achievable task of magnificent research, alternative to the existing one and all. Alternative in the sense that accommodate the newly evolved one go along the evolving radio frequency attractive to one another. All that happens at one time, of course during the evolutionary time development. One may opt for a prolonged application during this devised application of carbon value. Over and above it is new developmental task to reach out to every needy to take part and all. Overall performance can be monitored to meet out the task oriented problem of interest. One can opt out to change the parameter for betterment in the campaign of engaged life platform. One may think twice to meet the loyal one to risk out the old of anarchy. Of course time will tell all about this task oriented activity related to development and all. One should risk this development in due course of action every now and then. Performance can be altered according to the need or the development for purposeful application.

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