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The Sequencing of Particular Amino Acids into Protein

Ratan Kumar Sarkar

Janhavi, Keota, Hooghly, West Bengal, India

Abstract The sequencing of amino acids in context of p53 and human normal hemoglobin alpha and beta chains have been clarified to some extent is a biophysical structural matter in space-time. The molecular points possess a structural biology so mutational events in fundamental structure causes severe disease like sickle-cell-anemia and cancer.

Keywords Hemoglobin, SCA, TP53, Molecular point

1. Introduction

The sequencing of amino acids into protein follows biophysical structural conformation in space-time. The sequencing of amino acids into protein can be determined by structural conformations in normal alpha and beta chains in human hemoglobin that also aligned to p53 protein molecule. A generalized structural matter would be applicable to sequencing of all kind of proteins. The generalizations are as follows:

1. The molecular point '197'(val-p53) is a fundamental structural parameter where 197*0.0019 = 2*0.1872 in space-time. [1]
2. The molecular point of amino acids are related to the core values(C_v) or hidden time of corresponding amino acids in the structure e.g. Met C_v = 149*0.0019 – 0.2124 = 0.0707.
3. The protein molecules would possess structural suppression.
4. The protein molecule bisects on appearing '367' (earth-moon time curvature), if not further amplified since 183*0.0019 = 0.3477(lunar time limit) while 367 = 183 + 184.
5. Glutamine(146.1451) is a vital amino acid acts towards structural conformation.

The understanding of amino acid sequencing is needed as a cancer perspective while it would not be feasible to reinstate mutated protein. As p53 and hemoglobin chains are co-related, sickle-cell-anemia and cancer would thus cause a syndrome.

2. Discussions

The sequencing of amino acids into protein:

The human normal hemoglobin comprises two identical alpha and beta chains are anti-parallel chains showing structural conformations. The causes of two identical alpha hemoglobin(R-141 amino acid long) is to bisection of terminal amino acid(R282-p53) due to appearing '367' curvature of time where 367 = 282 + 85(suppression) as well as bisection of oxy-time(0.0304) and for beta-chain, 368 – 146 = 222 = 393(p53) – 171. The molecular point 146 occupied by His in beta chain of hemoglobin while 146-trp in p53 shows structural conformation i.e. 0.1615(trp core values) – 0.1393(his core values) = 0.0222 = 222 = 257 – 35 where 146(trp-p53) + 111 = 257.

Accordingly, 368 + 292 = 660 = 393 + 267 = 327(tyr-p53) + 3*111 where 333 – 146 = 187 = 197 – 10 where 292 – 282 = 10.

The structural conformation tends to 54-gln and 59-lys from terminal of alpha and beta chains of hemoglobin with 146 – 141 = 59 – 54 = 5 values difference. The molecular point equipoised for alpha and beta chains and ultimately single molecular point difference where glutamine plays an important role.

Mathematically, 0.1494(glu core values, E6-beta) – 0.1323(gln core values) = 0.0171 = 171 where 393(p53) = 222 + 171 in the bi-folded structure.

There is no basic difference between glu(6-beta) and asp(6-alpha) except 0.1495(asp core values) – 0.1494(glu core values) = 0.0001 = 1. Now, 222 – 171 = 51 = 1545(tyr core values) – 1494(glu core values) and suppression values 85 = 51 + 35 with one molecular point difference about commonly seen.

Cys-Glu perspectives in hemoglobin chains:

Since oxy-time(0.0304 = 16*0.0019) is bisected at p53 terminal point(282), cys-glu structural symmetry is applicable to this.

Now, 147.1299(glu) + 121.1590(cys) = 268.2889 where 152*0.0019 = 0.2889 according to formula T(time) = M(mass)*0.0019.

* Corresponding author:
rksarkar36@gmail.com (Ratan Kumar Sarkar)
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Or, 0.2889 – 0.0268 = 0.2621(138) pre-transitional values gives 268 = 138 + 130.

Now, 130 + 152 = 282 = 141*2(alpha chains) and 138 + 152 = 290 = 146*2(beta chains) with 0.0002 adjustable time difference. Since alpha and beta chains are oppositely directed, 146 + 29(approaching value to lunar gravity found as spots in chromatography) = 175 = 327(tyr) – 152 and 122 + 29 = 152 - 1 in the structure.

Cys's are found in positions 93 and 112 in beta chain shows alpha and beta chains interactions i.e. 93 + 29 = 122 and 112 + 29 = 141. Conversely, 122 + 104(cys-alpha or gln-p53) = 226 = 367 – 141 = 292(lys-p53) – 66(t-RNA 'distance of constancy' factor).

Again, 0.1323(gln core values) – 0.0709(cys core values) = 0.0614 where 0.0707(met core values) – 0.0614 = 0.0093 = 93. The met and cys having 0.0002 core values difference.

Met is found in position 55(Hb-beta chain) and in positions 32, 76(Hb-alpha chain).

Structurally, 55 + 29 = 84 = 177 – 93 and 122 + 32 = 154 = 183(lunar time) – 29 = 100 + 55 and 122 + 76 = 198 = 227 - 29 with one molecular point difference that showing a '100' factor in methionine derived from 803(half of lunar gravity) – 703(met core values with 0.0004 adjustable time difference) = 100 and 1254(66) – 551(29) = 703(37) avoiding decimals. Consequently, 136(gln-p53) is associated with met where 3477(183-lunar time) – 803 = 2674 = 2774(146) – 100 avoiding decimals.

The cys and met are differentiated by 0.0002 core values while cys is incorporated into tyr can be found in context of oxy-time(0.0304).

Trans-activated sequencing in p53:

In p53, 1872(197) – 1545(tyr core values) = 327(tyr) = 220(tyr) + 107(tyr) and 327 – 130 = 197 = 131 + 66 and 131(leu vertical time)*0.0019 = 0.2489 where 2489 – 617(V617F) = 1872, avoiding decimals. The values 1545 – 1254(66) = 291(lys) = 184 + 107(tyr). Accordingly, 0.1545(tyr core values) – 0.0893(lys core values) = 0.0652 = 1975(met pre-transitional value) – 1323(gln core values) = 652 = 361 + 291 since 0.1254(66) – 0.0893 = 0.0361 = 361 are structural matters. Biophysically, Tyr and Lys is very systematic since AAA(405) – UAC(358) = 47(a fundamental value) and conversely Met + 29(0.0551) = Phe.

Here, 652 = 552 + 100 = 617 + 35 = 2*326(terminal mutation at C843T R282W) [2] and 1494(glu core values) – 652 = 842 where 367 + 103 = 469 + 1 and 652 – 183(lunar time) = 469(G469T V157F) and also1872 – 1494 = 378(TTT) would cause directional conflicts whenever instability exists. It is seen 327*3 = 981 = 844 + 137 = 2831(149) - 1849 where 844 – 707(met core values) = 137 and 1451 – 982 = 469 are cancer components in biophysical structure.

Furthermore, 327(tyr) + 291(lys) = 618(V617F) and 327 – 156(V157F) = 171 = 136 + 35 where 327 – 291 = 36 = 30 + 6(glu-beta) in biophysical structure that indicates cancer and sickle-cell-anemia are co-related and would be oppositely active. What is the relation between cell de-oxygenation and tumor formation?

Trp positioning in p53 and hemoglobin chains:

Trp found at 23, 53, 91, 146 positions in p53 while 1872 – 1615(trp core values) = 257.

Now, 257 – 146 = 111 = 393(p53) – 282; 257 – 91 = 166 = 393 – 227 where 368 – 227 = 141; 257 – 53 = 204 = 393 – 189 where 189 = 282 – 93 and 146 = 93 + 53; 257 – 23 = 234 = 393 – 159 where 93 + 66 = 159 with 0.0002 time difference.

Again, 37(trp-beta) + 29 = 66 and 257 – 66 = 191 = 282 – 91(trp-p53); 121 + 14(trp-alpha) = 135 = 257 – 122.In directional context of alpha and beta hemoglobin, 29 +146 = 175 = 327(tyr) – 152 while 121 + 141 = 262 = 291(lys) – 29.

3. Conclusions

The clarification of hemoglobin alpha and beta anti-parallel chains structure is biology in space-time. The sequencing of particular amino acids is clarified in biophysical structure. There should be a generalized structure for time motivation forming the sequence of proteins. The cancerous arena has been shown lies in fundamental biophysical structure goes detrimental under structural mutations.

REFERENCES

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