Insight of *Tp53* Mutants and its effect on Protein in Different *Feline* and *Canine* Neoplasms (Saif R, *et al*)

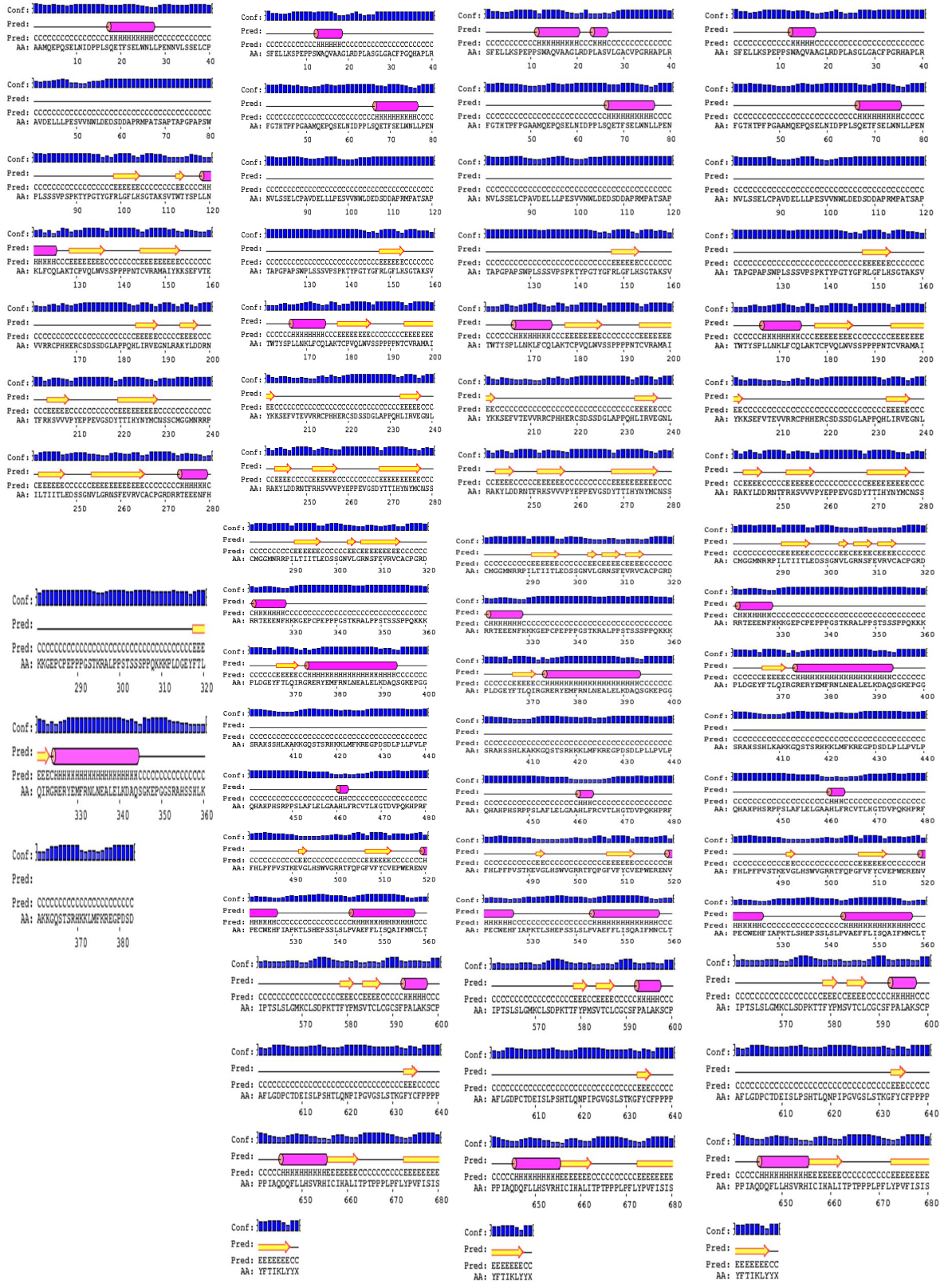


Figure 1: Secondary structure of (a) wild type represents the normal protein. (b) Secondary structure of M1, M2, and M4 as all three mutants showed similar structure. Helices are present from 13-18 and 67-76 a.a which is represented by a cylinder, an arrow represents a strand and a straight line represents a coil. (c) Secondary structure of M3, helices are present at 12-20, 24-26, and 461-463. (d) Secondary structure of M5. Difference in M5 is that only one helix from c.13-17 present and then one at 67-75 amino acids is also present.

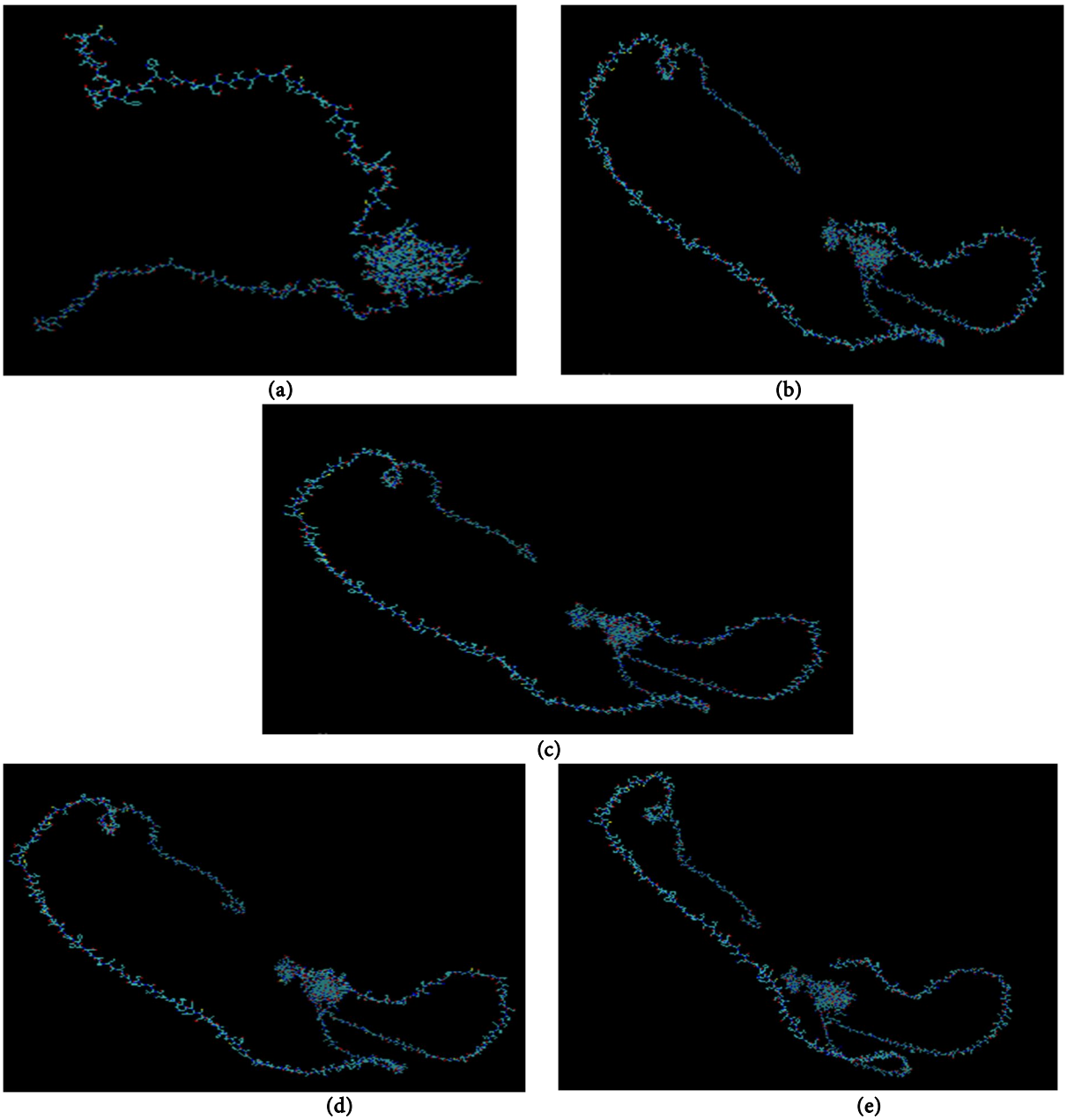


Figure 2: (a) The BioSerf modelling of wild type. (b) M1, M4. (c) M2. (d) M3. (e) M5, M6, M7 by using VMD. Acidic residues are represented by red, basic by blue, polar by green and non-polar by white. Oxygen is represented by red, Nitrogen by blue, Sulphur by yellow and Carbon by cyan colour

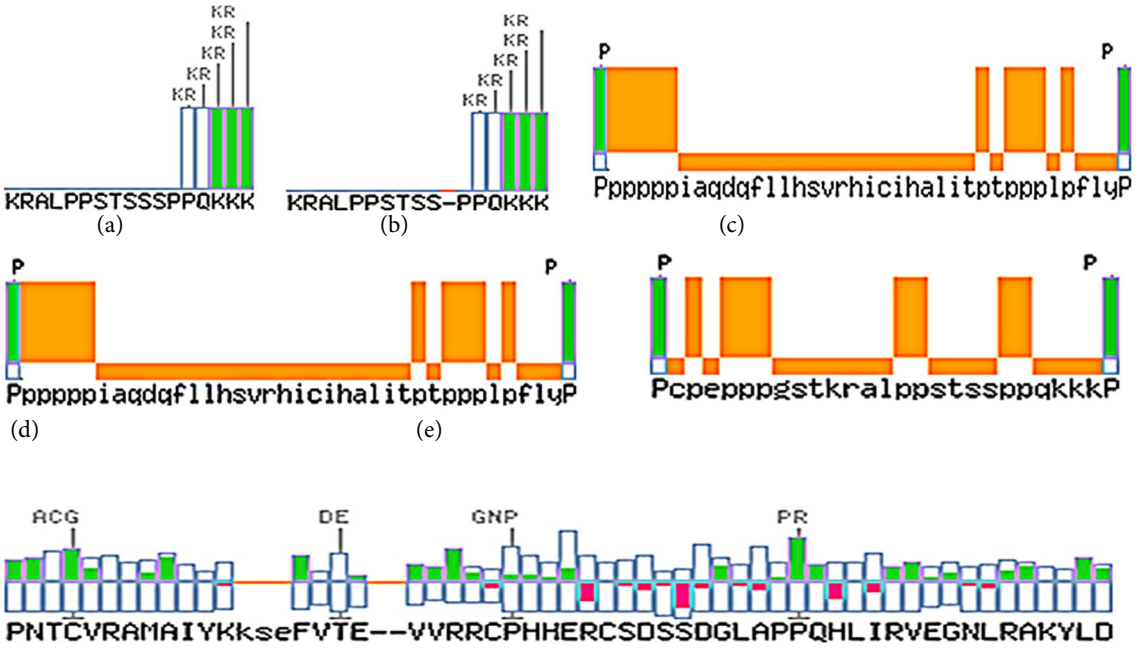


Figure 3: Match details (a) The bipartite nuclear localization signal profile of wild type, M1, M2, M3 & M4 *Tp53* protein. (b) The bipartite nuclear localization signal profile of M5, M6 & M7. (c) The proline rich region profile of *Tp53* protein in M1, M2, M3 & M4. (d, e) The proline rich region profile of M5, M6 & M7. (f) The MVP repeats profile of wild type and mutants of *Tp53* protein. MVP is composed of near to 53 amino acids

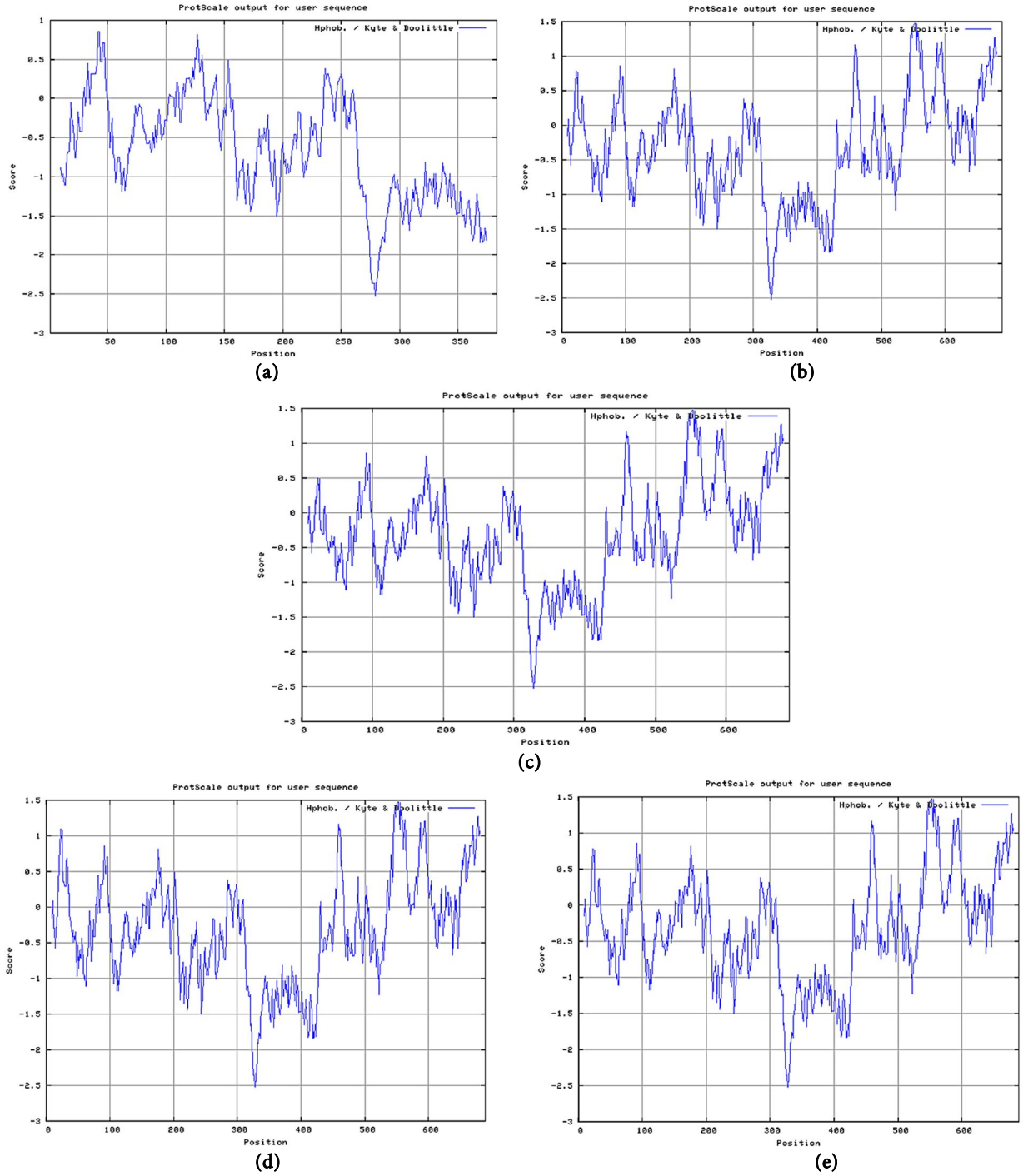
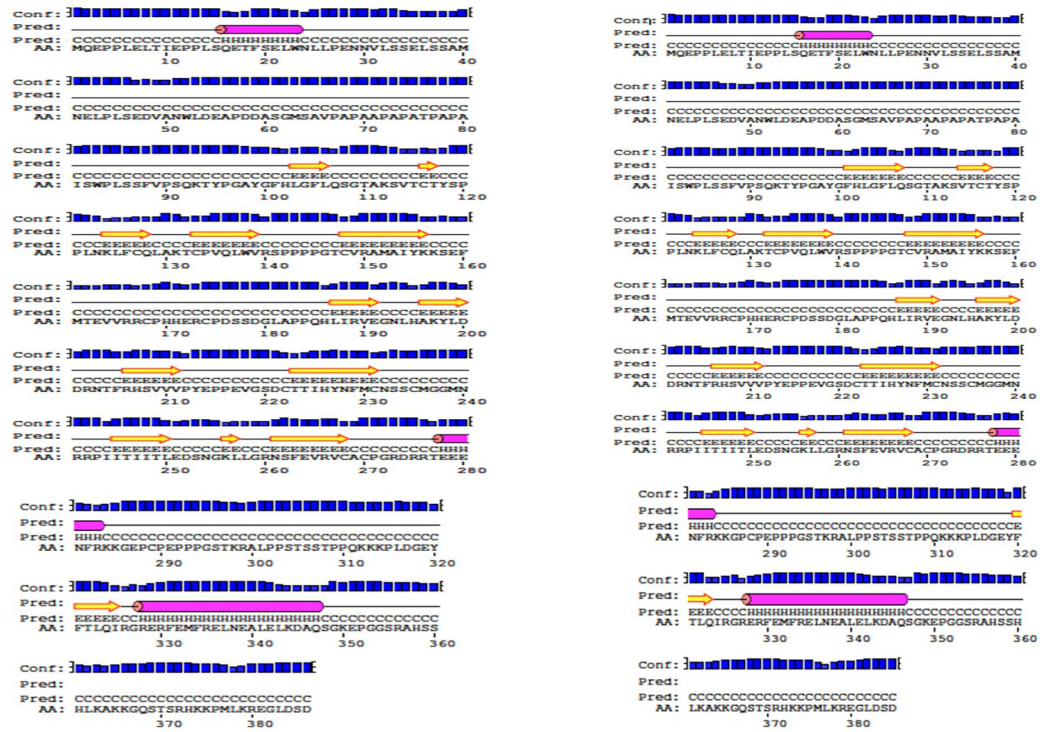
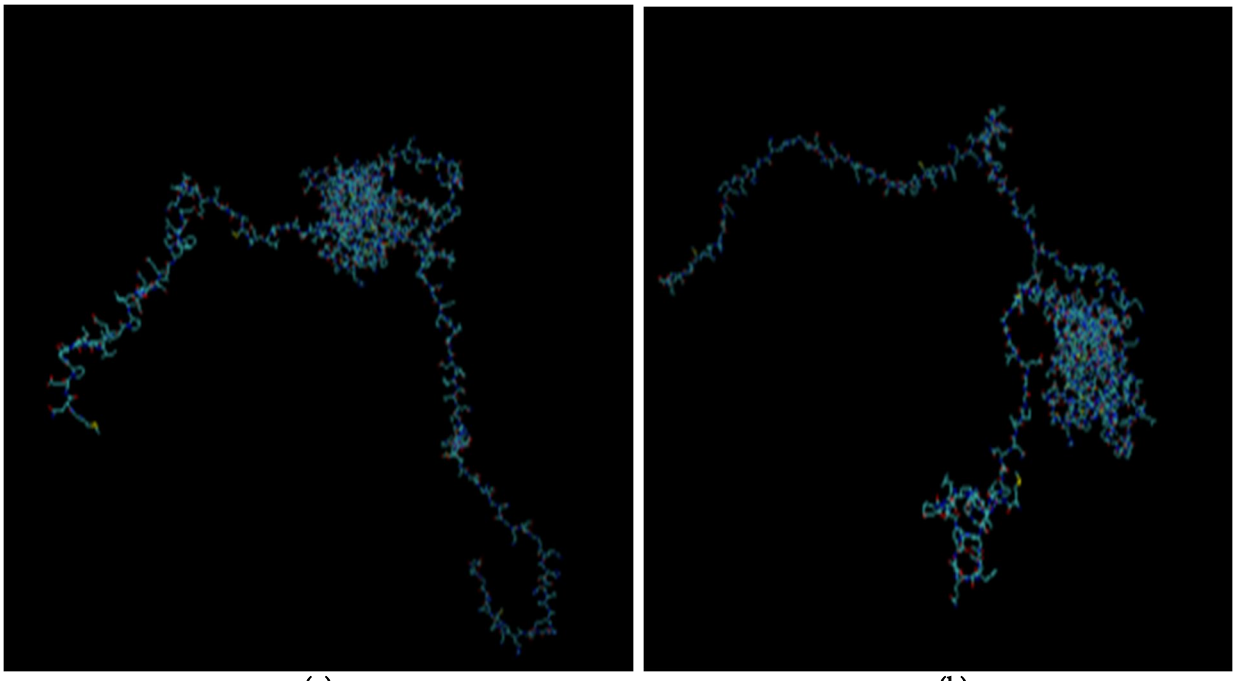


Figure 4: Graphs showing transmembrane structures of, (a) The wild type *Tp53* protein in dog. (b) M1, M4. (c)M2. (d) M3. (e) M5, M 6 & M7. X- axis shows the position of the transmembrane structure in the protein, whereas Y- axis indicates the hydrophobicity score of particular amino acid according to the Kyte & Doolittle algorithm. The positive highest peaks shown in the graph indicate the transmembrane structures in extracellular proteins. On the other hand, strong negative peaks show the surface proteins.



(a) (b)

Figure 5: (a) The secondary structure of wild type M1, M2, M3, M4. In wild type a strand was present from 321-325. The arrow represents a strand, a cylinder represents a helix and a straight line represents a coil. (b) Secondary structure of M5, a strand was present from 321-323.



(a) (b)

Figure 6. (a) Bioserf model of wild type, M1, M2, M3, M4 shows 3075 bonds and 386 residues (b) Model of M5 3066 bonds and 385 residues. Oxygen is represented by red, Nitrogen by blue, Sulphur by yellow and Carbon by cyan color. Acidic residues are represented by red, basic residues by blue, non-polar residues by white and polar residues by green color.

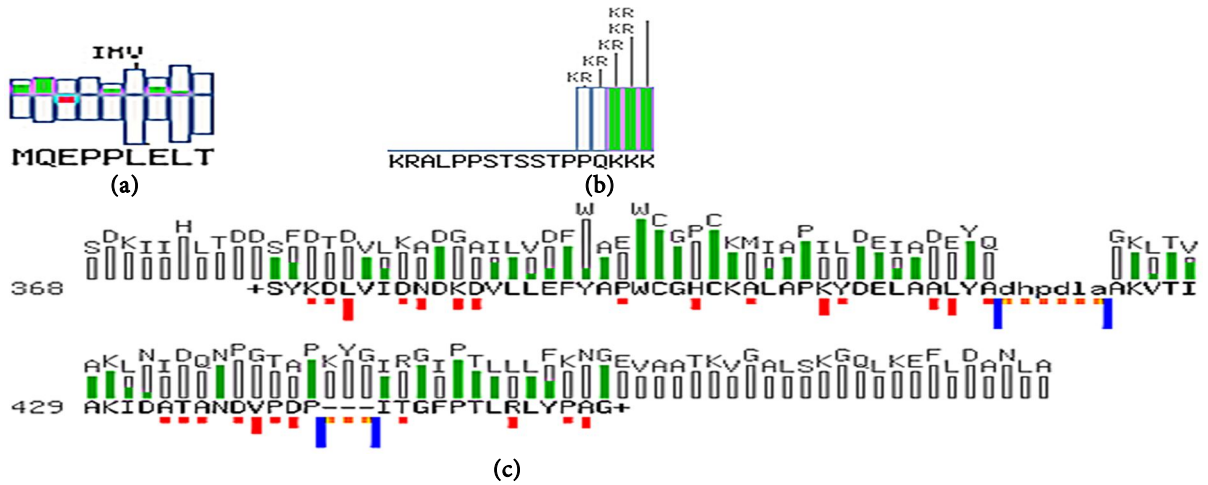


Figure 7: Match details of *Tp53* protein in wild type and mutants of cat. (a) *Big-1* (Bacterial Ig like domain 1) domain profile in wild type and mutant protein sequences of cat. *Big-1* domain is composed of 95 amino acids. Tandem repeats of *Big-1* domain are present in the protein sequences of wild and mutant types of *Tp53* in *Felis catus*. (b) Bipartite nuclear localization signal profile in wild and mutant types of *Tp53* protein. (c) Graphical representation of local alignment of two sequences.

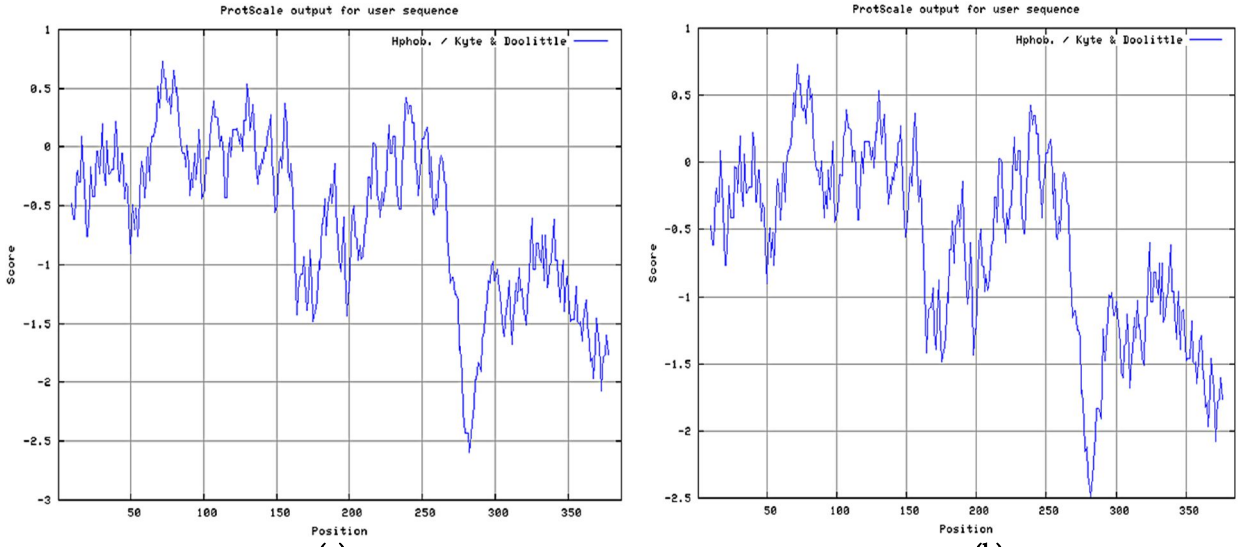


Figure 8: Graphs showing transmembrane structures of, (a) The wild type, M1, M2, M3 and M4 (b) M5. X- axis shows the position of the transmembrane structure in the protein, whereas Y- axis indicates the hydrophobicity score of particular amino acid according to the Kyte & Doolittle algorithm. The highest peaks with the positive score shown in the graph specify hydrophobicity and indicate the transmembrane structures in extracellular proteins whereas negative scores indicate the hydrophilic amino acids.