Correction

Correction: Ali, A., et al. Modeling Novel Putative Drugs and Vaccine Candidates against Tick-Borne Pathogens: A Subtractive Proteomics Approach. *Vet. Sci.* 2020, 7, 129

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check for updates

The authors wish to make the following corrections to this paper [1].

Figure 1 should be replaced due to mislabeling. The correct Figure 1 can be found below.
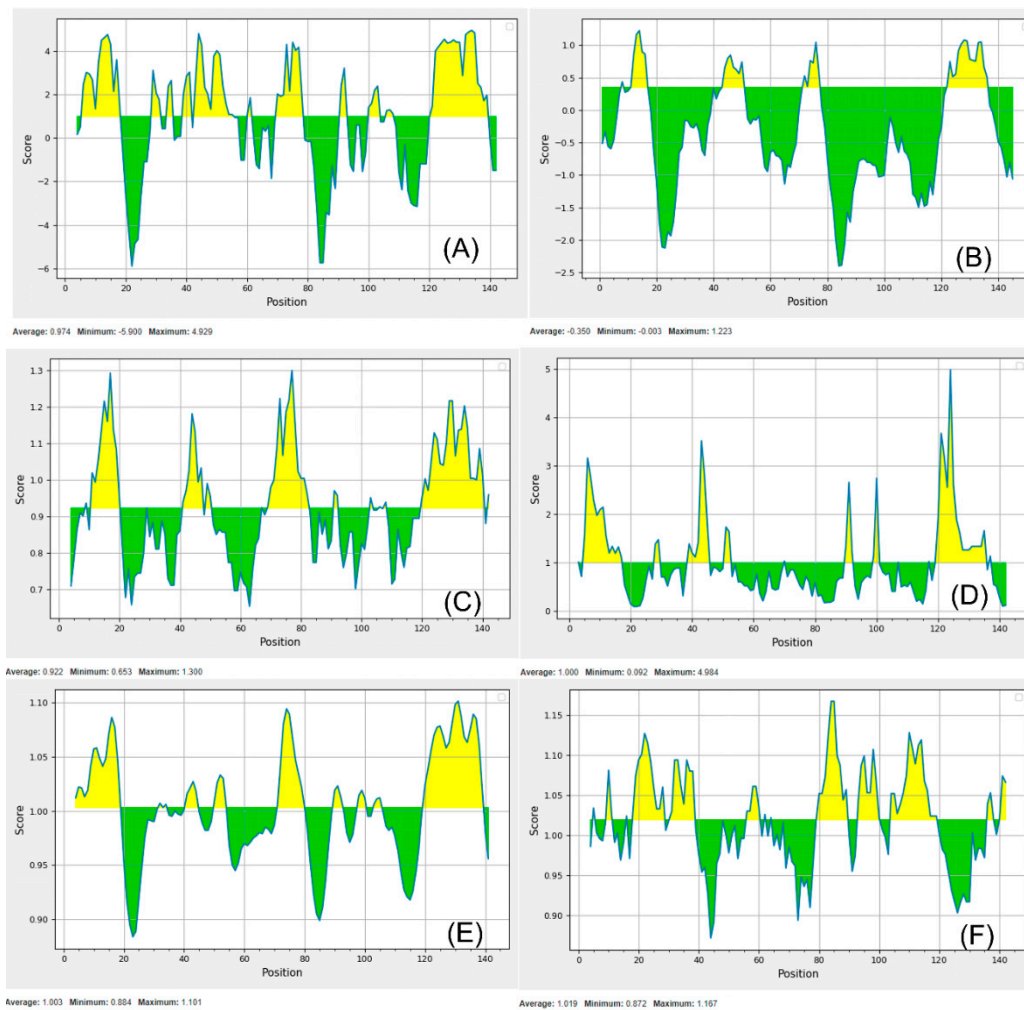
Figure 1. B-cell epitope in the FLiS protein based on Parker hydrophilicity prediction (**A**). Bepipred linear epitope (**B**). Chou and Fasman β-turn prediction (**C**). Emini surface accessibility prediction (**D**). Karplus and Schulz flexibility prediction (**E**). Kolaskar and Tongaonkar antigenicity (**F**). The x axis and y axis represent the sequence position and corresponding antigenic properties score, respectively. The threshold level was set as a default parameter of the server. The regions shown in yellow color above the threshold value were predicted as the B-cell epitope.

The authors would like to apologize for any inconvenience caused to the readers by these changes.

References

1. Ali, A.; Ahmad, S.; Wadood, A.; Rehman, A.U.; Zahid, H.; Qayash Khan, M.; Nawab, J.; Rahman, Z.U.; Alouffi, A.S. Modeling Novel Putative Drugs and Vaccine Candidates against Tick-Borne Pathogens: A Subtractive Proteomics Approach. *Vet. Sci.* **2020**, *7*, 129.