IWIMSM-03: Iberoamerican Workshop on Model. and Simulation Methods, Valencia, Spain, 2019
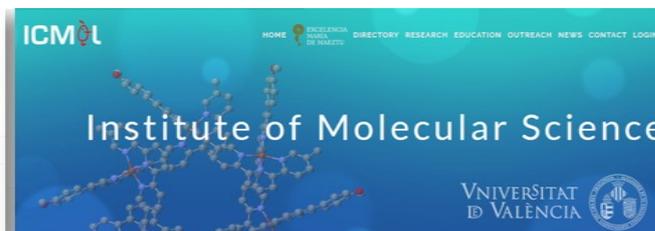
The persistence of the electromagnetic balance in proteins

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Abstract.
In the last six decades a large number of mathematical methods have been developed to determine the predominant function of a protein. This work uses a graphic refinement to one of these methods, the Polarity Index Method. The results show that the polarity/charge profile of a sequence, in addition to having a distinctive profile, is self-modifying to maintain an electromagnetic balance. We consider that this regularity contributes to the understanding of the understanding between the preponderant function of a sequence and its electromagnetic balance.

Results and Discussion
Figure shows the succession of graphs of the polarity/charge profile [1] from the PRO_0000435834 [291AA-790AA] envelope protein (E), constructed according to the Materials and Methods section. It can be observed (**Figure; black ellipse**) that the polarity/charge profile the

polar interaction [P+, N] decreases in a uniform way (not abrupt), and on the contrary in the polar interaction [NP, P−] the polarity/charge profile also grows uniformly (not abrupt). We have a previous annotation about this observation [2].

Polarity/Charge Profile of PRO_0000435834[291aa-790aa] envelope protein (E).
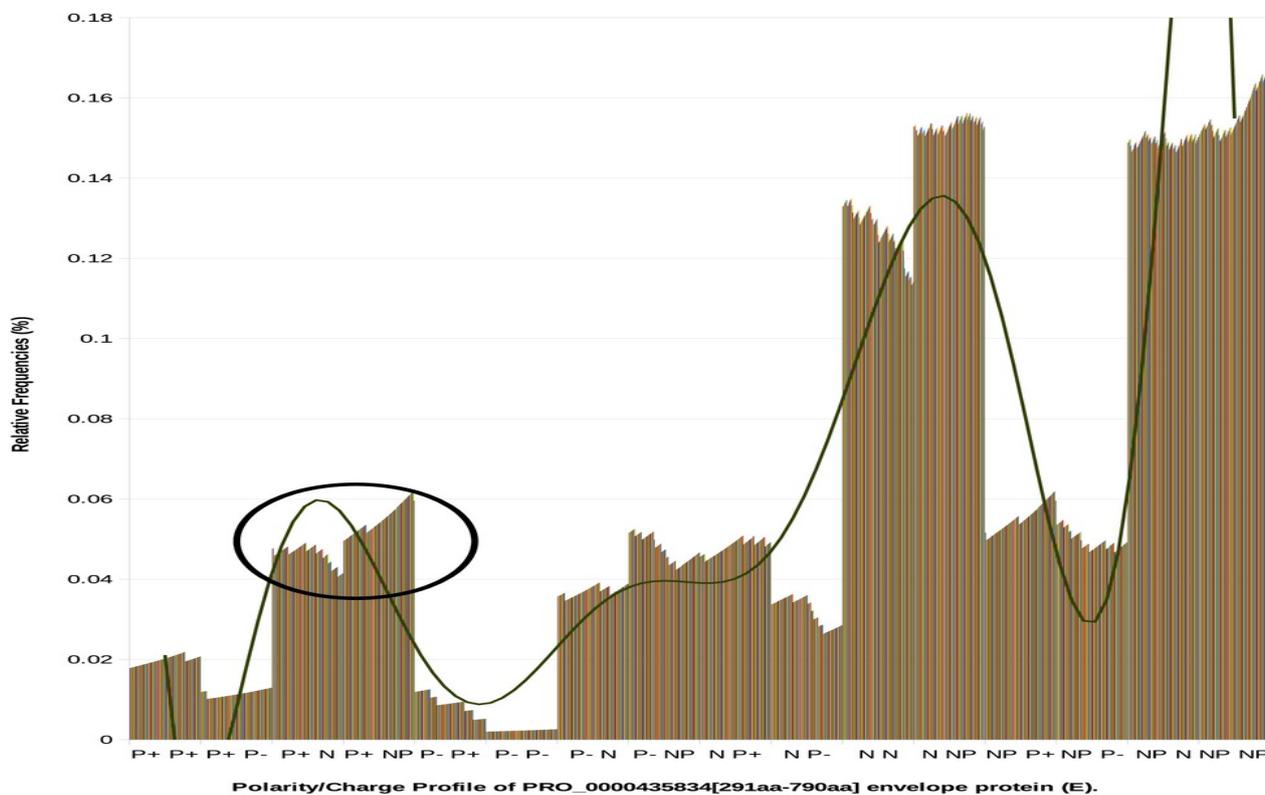
Conclusions

The regularity found in **Figure** allows one to conjecture that the polarity/charge profile of a sequence is adjusted automatically, so that no sudden changes are observed in the polarity/charge profile of the protein.

References

1. Polanco, C. in: Polarity Index in Proteins - A bioinformatics tool., Bentham Science Publishers Sharjah: U.A.E., **2016**.
2. Polanco, C.; Samaniego Mendoza, J.L.; Buhse, T.; Uversky, V.N.; Bañuelos Chao, I.P.; Bañuelos Cedano, M.A.; Tavera, F.M.; Tavera. D.M.; Falconi, M.; Ponce de León, A.V. On the Regularities of the Polar Profiles of Proteins Related to Ebola Virus Infection and their Functional Domains. *Cell Biochem Biophys.*, **2018**, *76*(3), 411-431.