SIMULATION OF PROTEIN MOLECULE FLUCTUATIONS BY IRREGULAR IMPEDANCE NETWORK METHOD

V.I. Akimov, A.V. Shestopalova[1], *V.M. Tulupenko, L. Reggiani*[2]

Donbass State Engineering Academy
(*72, Shkadinov Str., Kramatorsk 84313, Ukraine; e-mail: avi@laser.donetsk.ua*),
[1]A. Usikov Institute for Radiophysics and Electronics, Nat. Acad. Sci. of Ukraine
(*12, Academician Proskura Str., Kharkiv 61085, Ukraine*),
[2]Dipartimento di Ingegneria dell'Innovazione, Università di Lecce
(*Via Arnesano, Lecce 73100, Italy*)

S u m m a r y

The method of irregular impedance network developed by the authors has been applied to studying the electrical fluctuations of a protein molecule located between two ohmic contacts. Specific calculations have been carried out for a bovine rhodopsin molecule. Random fluctuations of distances between amino acids (the link oscillation model) or random fluctuations of amino acids themselves about relevant fixed positions (the node oscillation model) have been analyzed. The mean network impedance and its dispersion have been calculated as functions of the fluctuation amplitude. The similarity and the difference between the results obtained in the framework of these two models have been discussed. A universal dependence of the impedance dispersion on the oscillation amplitude has been found.