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Model of environment dependent amyloid transformation

Structural transformation of proteins producing the amyloid forms is presented. The fuzzy oil drop model allowing assessment of external force field participation in folding process (including structural transformations). This model applied for analysis of WT and amyloid forms identifies the necessary change of environmental conditions as the driving force for this transformation. The influence of environment (external force field) is quantitatively expresses in this model by K parameter. Three scenarios are recognised for fibril formation: 1 – the globular form of native protein representing low K gets changed to amyloid form described by high K values (transthyretin, VL domain of IgG); 2 – the biologically active form of protein characterised by high K value (effect of external force field specificity) changes its status to the form described by low K value (adaptation to water environment) (α-Synuclein) and 3 – the biologically active protein in form of fibril represents the status described by low K for both: individual chain as well as in 6-chains fibril treated as form of reservoir. It is interpreted as self-control for fibril propagation limited to 8 chain in maximum controlled by water environment. The fibrils of higher number of chains represent increasing K value what requires changes in external force field. As long as water is participating in folding process, the increase of fibril length (above 8 chains) is forbidden.

In conclusion: the amyloid transformation is driven by environment changes (external force field) expressed in fizzy oil drop model by the value of K parameter.

Keywords: amyloid; environment; Alpha-synuclein; tranthyretin; endorphin; hydrophobicity

Biography

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Educated in theoretical chemistry. Two years postdoc at Cornell University – H.A. Scheragas group 1987-1989. In 2000-2020 chief of the Department of Bioinformatics and Telemedicine.

Author of fuzzy oil drop model treating the proteins as intelligent micelles with centric hydrophobic core and polar surface. Chief Editor of the journal Bio-Algoriythms and Med-Systems (2000-2020). Author of about 200 publications and books: Systems Biology: 2023, Springer Simulations in Medicine: 2015, Walter de Gruyter (ISBN (978-3-11-04064403), Protein structure: 2019 Elsevier, From Globular Proteins to Amyloids - Elsevier2026 - Simulating Protein Folding in Variable Environmental Conditions. Present on the 2% top scientists list (since 2020)

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