



PAGE: An efficient and reliable software to predict protein aggregation

The computer program PAGE is useful for the reliable identification of aggregating segments in protein sequences and to design mutations to reduce (or improve) aggregation propensity. PAGE is based on a method with improved predictive ability compared to other approaches.

Keywords Polypeptide aggregation, protein expression, amyloid diseases, Alzheimer's disease, prion protein

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Background The reliable identification of aggregating segments (hot spots) in protein sequences is important not only for improving protein expression for biotechnological applications but also for the development of therapeutic agents for Alzheimer's and Parkinson's diseases as well as other pathological conditions associated with protein deposition. It is essential that the software employed to identify those hot spots has a high predictive ability.

Technology PAGE is a very efficient computer program (each run completes within fractions of a second) developed to reliably predict aggregation hot spots and rates. It uses an equation based on physicochemical properties as well as results of detailed (i.e. atomistic) simulations of peptides and proteins. Validation of PAGE on pathological protein sequences and entire proteomes have been published.
PAGE uses an equation derived from first principles in contrast to other published approaches which were calibrated by fitting. Therefore, the predictive ability of PAGE is higher than the one of other methods.

Fields of Use Protein expression, protein design, proteomic studies, design of nanofibrillar materials.

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