Method to Assess Risk of Amyloid Diseases

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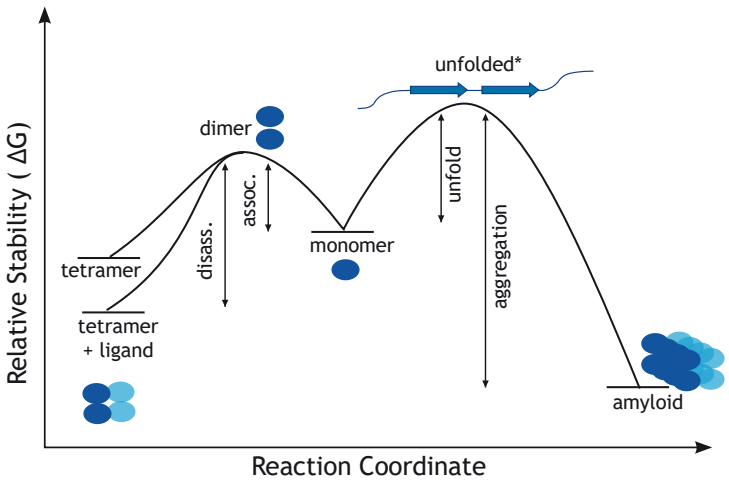
DESCRIPTION

Misfolded protein structures that deposit in tissues and resist normal degradation processes cause amyloid diseases. Development of amyloidosis depends on the protein monomer concentration, proteolysis rate, and conformational stability of the native protein. Researchers at BYU have developed a unifying biophysical model that defines the relationships among the monomer concentration, native monomer stability, and the rate of monomer removal from the proteome. The model suggests the probability of an individual developing an amyloid disease can be estimated from measurements of these variables in serum samples of individuals. Methods for measurements have been developed.



Gibbs energy diagram for dissociation/association reactions of TTR

PROBLEM SOLVED

Many amyloid-driven pathologies have genetic and stochastic components where assessing risk of disease development requires a complex multifactorial calculation. This invention enables simpler measurements of total TTR plasma concentration and tetramer stability in near in vivo conditions allowing quantification of risk for late-in-life amyloidosis and provides the information necessary for development of methods for early diagnosis and prevention.

KEY ADVANTAGES

- ***Simpler measurements***
- ***Enables early diagnosis and prevention***

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APPLICATIONS

This method has the potential to provide the stability measurements needed to assess risk of amyloidosis.

IP Status:
Patent Pending

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BYU TECHNOLOGY transfer

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