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Protein conformational dynamics dictate the binding
Protein conformational dynamics dictate the binding af nity for a ligand Moon-Hyeong Seo1, Jeongbin Park2, conformational dynamics and dissociation constants for maltose. Our results provide direct evidence that the ligand dissociation is determined by the intrinsic opening rate of the protein. DOI: 10.1038/ncomms4724 1Department of Biological Sciences, Korea Advanced Institute of
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Optical tweezers measurements of protein folding unfolding
PROTEIN UNFOLDING APPLICATION NOTE Optical tweezers measurements of protein folding/unfolding & conformational dynamics at the single-protein level.
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Protein dynamics Wikipedia
The study of protein dynamics is most directly concerned with the transitions between these states, but can also involve the nature and equilibrium populations of the states themselves.
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A growing number of studies have suggested that conformational dynamics of proteins govern their role in regulating biological functions, examples of this regulation can be found in signal transduction, molecular recognition, apoptosis, protein / ion / other molecules translocation and gene expression.
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Conformational dynamics of the KcsA potassium channel
The simplest structural definition of ion channel gating is the ability to alternate, in a signal-dependent way, between states that selectively permit the flow of ions (open) or do not (closed).
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Protocol for Molecular Dynamics Simulations of Proteins
Keywords: Molecular dynamics simulations, Conformational studies, Gromacs, Structural studies, Protein dynamics Background While molecular dynamics (MD) simulations are increasingly getting popular in studying protein dynamics in silico , there is a strong need to correlate the results with experimental observations.
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Molecular Simulations of the Fluctuating Conformational
Molecular Simulations of the Fluctuating Conformational Dynamics of Intrinsically Disordered Proteins W. Wendell Smith 1, Carl F. Schreck , Nabeem Hashem1, Sherwin Soltani ,
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channels alter salt induced Topics by Science gov

Sample records for channels alter salt-induced These proteins have evolved independently in different kinds of cold-adapted ectothermic animals, including insects and fish, where they protect against lethal freezing of the body fluids. There is a great variability in the capacity of different kinds of antifreeze proteins to evoke the antifreeze effect, but the basis of these differences is

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Harmonicity and anharmonicity in protein dynamics A

A comparison of a normal mode analysis and principal component analysis of a 200 ps molecular dynamics trajectory of bovine pancreatic trypsin inhibitor in vacuum has been made in order to further elucidate the harmonic and anharmonic aspects in the dynamics of proteins.

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