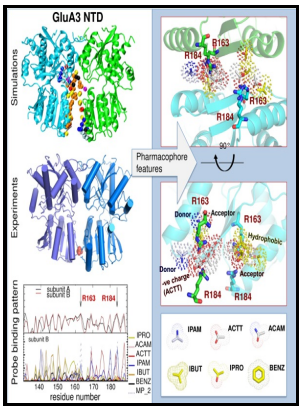
Single molecule dynamics in life science

Wiley-VCH - Single



Description: -
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Amapá (Brazil : Territory) -- Politics and government.
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Molecular Structure
Models, Molecular
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-Single molecule dynamics in life science
Notes: Includes bibliographical references and index.
This edition was published in 2009

Filesize: 27.44 MB

Tags: #Single #molecule #biophysics

Single

Therefore, the range of the accuracy threshold ±20% represents only 30% of the statistical errors. . The diffusion coefficients obtained from the particle tracking revealed a highly dynamic nature of SecA under native conditions in cells.

Single

We also built a simple theoretical model to qualitatively illustrate the difficulty of the dissociation processes by solvent intercalation. The relaxation time of the molecule τ R is estimated by the autocorrelation analysis of A i using the following formula: Conformational dynamics of Charomid DNA.

Single

To study the dynamics of SecA motion within cells in more detail, single-particle tracking of SecA-Yet molecules was used to calculate diffusion rates. A cubic supercell with the lattice constant of 20 Å and a Gamma k-point were employed.

Single Molecule Dynamics in Life Science

We validate our approach by analysing the statistical distribution of diffusion coefficients of fluorescent nanospheres as calculated by the CA method and the distribution as calculated by SMLT. Data availability The data that support the findings of this study are available from the corresponding authors upon reasonable request.

Single Molecule Experiments in Life Sciences

Two questions are usually asked: 1 is the reaction spontaneous? Similar current spikes at the submillisecond level and bimodal distributions were observed at each temperature Fig. The electronic transport simulations were performed by using real-space NEGF techniques implemented in the TranSIESTA package ,. Structures are essential to unravel the binding partners.

Single Molecule Dynamics in Life Science by Toshio Yanagida, Yoshiharu Ishii

Thus, the smaller σ D obtained by the CA method as compared with that obtained by SMLT-MSD analysis corresponds to the smaller statistical error in the former method.

Changes in single

High precision coverslips 75 × 25 × 0. Insets in the histograms amplify the details of the current distributions. The expected diffusion coefficient calculated from the Stokes—Einstein equation is 1.

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Stacked bar chart summarizing the diffusion rates obtained from the CPD analysis. However, single molecule techniques are now mature enough to be used in diverse fields of research, most notably in biology. Detailed discussions of studies on protein enzymes, ribozymes and nucleic acids are also included.

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