عنوان مقاله:

PhiDsc: Protein Hotspot Identification by 3D Structure Comparison

محل انتشار:

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خلاصه مقاله:

Selective pressures involved in cancer initiation and progression shape the mutational landscape of somatic mutations in cancer. Given the limits within which cells are regulated, a growing tumor different cells of origin often harbor identical genetic alterations. Recent expansive sequencing efforts have identified recurrent hospot mutated residues in individual genes. Here, we introduce PhiDsc, a novel statistical method developed based on the hypothesis that hotspot mutations in a recurrently aberrant gene family can guide the identification of mutated residues in the family’s individual genes with potential functional relevance. PhiDsc combines 3D structural alignment of related proteins with recurrence data for their mutated residues to calculate the probability of randomness of the proposed mutation. The application of this approach to the RAS and RHO protein families identified known mutational hotspots as well as previously unrecognized mutated residues with potentially altering effect on protein stability and function. These mutation were located in or at proximity of binding domain and were indicated as protein- altering .according to eight in silico predictors

کلمات کلیدی:

لینک ثابت مقاله در پایگاه سیویلیکا: