

## **Fast pattern recognition of protein three dimensional features using a bit-pattern approach as a prescreen.**

Phillip Yen<sup>1</sup>, Oscar N. Ventura<sup>2</sup>, Stanley K. Burt<sup>1</sup>, Raul E. Cachau<sup>1</sup>.

<sup>1</sup>Advanced Biomedical Computing Center, NCI-Frederick, Frederick, MD, USA, <sup>2</sup>CCPG-DETEMA, Facultad de Química, Universidad de la República, Montevideo, Uruguay.

Three dimensional (structural) pattern recognition has been applied in the past to search new structures for known functions or, conversely, to annotate structural databases. These efforts are frequently limited to exploring known patterns. In this work, we will discuss the implementation of a new, very fast search engine designed primarily for embedding in complex search algorithms (i.e. functional annotation of new structures). The unrestricted nature of the search should be helpful in uncovering hidden effectors. We will discuss the implementation of our engine in parallel and single processor machines and its use in the study of regulatory interactions (Ub domain interactions) and viral ion channels.

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