

Ron Elber (ron@cs.cornell.edu)

In brief

(Cootes, Muggleton et al. 2003; Dantas, G., Kuhlman et al. 2003; Dehouck, Biot et al. 2003; Fang and Wang 2003; Gray, Moughon et al. 2003; Gutteridge, Bartlett et al. 2003; Heger and Holm 2003; Keasar and Levitt 2003; Larson and Pande 2003; Stark, Sunyaev et al. 2003; Yu, Wang et al. 2003; Zhang, Lindstam et al. 2003)

Full list

Cootes, A. P., S. H. Muggleton, et al. (2003). "The automatic discovery of structural principles describing protein fold space." Journal of Molecular Biology 330: 839-850.

Dantas, G., B. Kuhlman, et al. (2003). "A large scale test of computational protein design: Folding and stability of nine completely redesigned globular proteins." Journal of Molecular Biology 332: 449-460.

Dehouck, Y., C. Biot, et al. (2003). "Sequence-structure signals of 3D domain swapping in proteins." Journal of Molecular Biology 330: 1215-1225.

Fang, K. and W. Wang (2003). "What is the minimum number of letters required to fold a protein?" Journal of Molecular Biology 328: 921-926.

Gray, J., J., S. Moughon, et al. (2003). "Protein-protein docking with simultaneous optimization of rigid body displacement and side-chain conformations." Journal of Molecular Biology 331: 281-299.

Gutteridge, A., G. J. Bartlett, , et al. (2003). "Using a neural network and spatial clustering to predict the location of active sites in enzymes." Journal of Molecular Biology 330: 719-734.

Heger, A. and L. Holm (2003). "Exhaustive Enumeration of protein domain families." Journal of Molecular Biology 328: 749-767.

Keasar, C. and M. Levitt (2003). "Designing a physical energy function having local minima with native structure characteristics." Journal of Molecular Biology 329: 159-174.

Larson, S. M. and V. S. Pande (2003). "Sequence optimization for native state stability determines the evolution of folding kinetics of a small protein." Journal of Molecular Biology 332: 275-286.

Stark, A., S. Sunyaev, et al. (2003). "A model for statistical significance of local similarities in structure." Journal of Molecular Biology 326: 1307-1316.

Yu, C. S., J. J. Wang, et al. (2003). "Fine-grained protein fold assignment by support vector machines using generalized npeptide coding schemes and jury voting from multiple-parameter sets." Proteins 50: 531-536.

Zhang, Z., M. Lindstam, et al. (2003). "Potential for dramatic improvement in sequence alignment against structures of remote homologous proteins by extracting structural information from multiple structure alignment." Journal of Molecular Biology 332: 127-142.