HAL
open science

Assessing a novel approach for predicting local 3D protein structures from sequence.

Cristina Benros, Alexandre de Brevern, Catherine Etchebest, Serge A. Hazout

To cite this version:

Cristina Benros, Alexandre de Brevern, Catherine Etchebest, Serge A. Hazout. Assessing a novel approach for predicting local 3D protein structures from sequence.. Proteins - Structure, Function and Bioinformatics, 2006, 62 (4), pp.865-80. 10.1002/prot.20815 . inserm-00133180

HAL Id: inserm-00133180

https://inserm.hal.science/inserm-00133180v1

Submitted on 4 Sep 2009

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

TABLE I. Prediction results function of the maximal number of allowed candidates per target sequence window

MNAC[a]	Mean number of candidates ± sd (median)	Prediction rate (%)			Gain over random (%)		
		1.5 Å	2 Å	2.5 Å	1.5 Å	2 Å	2.5 Å
1	1	13.6	20.6	29.5	12.3	17.7	23.3
2	1.9 ± 0.2 (2)	17.8	27.3	39.6	15.3	21.9	28.1
3	2.8 ± 0.5 (3)	20.1	31.2	45.4	16.6	23.6	29.7
4	3.6 ± 0.8 (4)	21.4	33.6	48.9	16.9	24.2	29.7
5	**4.2 ± 1.2 (5)**	**22.2**	**35.1**	**51.2**	**17.0**	**24.3**	**29.3**
6	4.7 ± 1.6 (6)	22.7	36.1	52.6	17.0	24.2	28.7
7	5.1 ± 2.0 (6)	23.1	36.8	53.6	17.0	24.1	28.3
8	5.4 ± 2.3 (6)	23.3	37.3	54.2	16.9	24.1	27.9
All	6.3 ± 3.8 (6)	23.7	38.3	55.4	16.5	23.8	26.9

[a] Maximal Number of Allowed Candidates (MNAC)