

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

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

MNAC <sup>a</sup>	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
<b>5</b>	<b>4.2 ± 1.2 (5)</b>	<b>22.2</b>	<b>35.1</b>	<b>51.2</b>	<b>17.0</b>	<b>24.3</b>	<b>29.3</b>
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

<sup>a</sup> Maximal Number of Allowed Candidates (MNAC)