Table 2. Comparison of average TM-scores of the structure pools with 100 vs. 200 models.

	Lowest Rosetta Energy[1]			Model with highest TM compared to experimental structure		
	Average TM from 100	Average TM from 200	p-value[2]	Average TM from 100	Average TM from 200	p-value[2]
RaptorX contact only (108)	0.667	0.665	0.320	0.766	0.775	0.04
RaptorX + Distance (108)	0.720	0.737	0.008	0.780	0.786	$7\text{x}10^{-5}$
RaptorX contact only (50)	0.493	0.494	0.831	0.557	0.568	$1\text{x}10^{-5}$
RaptorX + Distance (50)	0.516	0.515	0.850	0.561	0.576	$8\text{x}10^{-5}$

[1] Average TM, compared to experimental structure, of the model with lowest Rosetta energy model for each of the 108 proteins and the 50 proteins in the test sets, when using a pool of 100 or 200 models, per protein, to select from. [2] Paired t-test.