

# Predicting protein flexibility through the prediction of local structures.

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**Table III** – *Confusion matrix between normalised B-factors and normalised RMSF values from MD dataset for the three flexibility classes.*

		RMSF <sub>Norm</sub>			
		1	2	3	Σ
B-factor <sub>Norm</sub>	1	<b>26.47</b>	11.19	2.79	40.45
	2	11.88	<b>16.03</b>	8.78	36.69
	3	2.10	9.47	<b>11.29</b>	22.87
	Σ	40.45	36.69	22.87	<b>100.00</b>