Free energy reaction profile of the desuccinylaiton catalyzed by Sirtuin 5

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Human sirtuin 5 is an NAD⁺ dependent desuccinylase [1,2]. Deregulation of this activity is connected to several human disorders, therefore, it is important to gain in depth knowledge of its reactivity [2]. One major problem is that most techniques to characterize enzymatic reactions, especially non-dynamic schemes, strongly depended on the chosen educt conformation. A start-frame, necessary for all approaches, is usually chosen from an MM-MD simulation. Since not all educt conformations are reactive, one has to identify suitable periods within the MM-MD simulation to obtain a realistic estimate of a reaction mechanism, before applying cost intensive QM/MM methods [3]. Thus, we utilized machine learning to distinguish suitable start-frames and to discover relevant structural features for the initial step of the desuccinlyation. Subsequent umbrella sampling [4] and the weighted histogram analysis method [5,6] were employed to compute the free energy reaction profile. The computational investigation lead to the conclusion that the nicotinamide cleavage, the first step of the desuccinlyation, shows a SN2 type reaction mechanism.

References

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