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Using virus particles scaffolds for imaging proteins at work.

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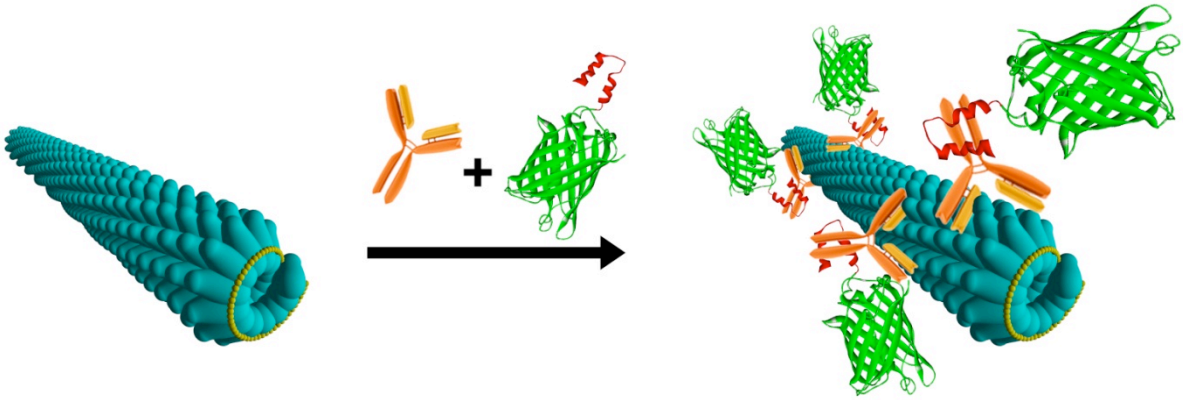
Because of their high degree of organization, natural signaling and metabolitic pathways achieve unsurpassed yields and specificity. Understanding the effect of spatial organization on enzymatic activity in multi-enzyme systems is therefore of fundamental interest. It may also help designing artificial enzymatic systems offering enhanced catalytic performances for the production of useful molecules, or higher sensitivity for bio-sensing applications.
To gain insights into these systems, experimental nanoscale multi-enzymatic platforms need to be designed and their functional behavior interrogated. There are only few methods, all of them very recent, available to construct such multi-enzyme systems and systematically evaluate how spatial factors (e.g., position, orientation) influence enzymatic activity. This limitation notably comes from the fact that the small size of enzymes renders them extremely difficult to organize into fully active supramolecular complexes amenable to experimental studies. The use of DNA scafolds (ie. origami) sounds promising. However this method does not offer a controlled orientation of the enzyme. Besides, these origamis are costly and this strategy remains difficult to upscale beyond the nanometric scale, in order to build robust experimental platforms.
An emerging alternative to origami-based methods is to use engineered protein scaffolds, mimicking natural structures, for designing organized multi-enzyme systems. Following the rule "like attracts like", we reasoned that enzymes of interest could be coupled with a compatible highly ordered protein scaffold. The strategy we propose here, in order to spatially organize biomolecular components at the nanoscale, makes use of robust plant virus nano-carriers as positioning helpers. Various strategies to control the positioning of active proteins on the virus surface will be presented. In the past 10 years our team built strong multidisciplinary collaborations devoted to the developments of techniques allowing to image proteins at work on these virus scaffolds.



Courtesy Mark B. van Eldijk, Univ. Nijmegen

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