

EXPLORING CONSTRAINTS OF SEQUENCE SPACE IN SEARCH OF OPTIMAL ENZYMES

Claes Gustafsson, ATUM, USA
claes@atum.bio
Sridhar Govindarajan, ATUM, USA

Engineering of enzyme variants for improved multidimensional fitness requires balancing the amino acid substitutions number and phylogenetic diversity as a function of the dynamic range of the assays used. Computational tools can be very helpful to visualize and calculate the required diversity of substitutions and proposed size of the available space. This presentation will showcase ATUM-developed computational sequence exploring tools and illustrate with commercial case studies how they can be applied.