Computational design and screening of enzyme enantioselectivity

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Propositions

1. More rapid success in enzyme engineering requires the strengthening of *in silico* tools for screening and ranking enzyme variants (Chapter 1).

2. High-throughput multiple-initialization ultrashort molecular dynamics simulations offer a computationally cheap solution for *in silico* screening of enzyme variants, provided conformational changes are of minor importance (Chapter 2, Chapter 4).

3. Even a simple one-step enzyme reaction involving water may be too complex to predict its regioselectivity (Chapter 3).

4. When discussing enzyme engineering, diastereomers should not be confused with enantiomers (Chapter 4).

5. A good methodology is hard to overcome: Rosetta has been the leading tool for protein redesign for more than 20 years (Chapter 2, Chapter 4).

6. Negative results include useful data that should be shared with the scientific community.

7. Increased computational power can either make scientists more effective or more efficient at being stupid (*modified from J.F. Wells (1984) The survival advantage of stupidity, Speculations in Science and Technology 7, 17-21.*)

8. The impressive progress in protein structure prediction offered by AlphaFold and the abuse of "machine learning" terminology are two faces of the same coin.