

Abstract Submitted
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Mutational robustness emerges in a microscopic model of protein evolution¹ KONSTANTIN ZELDOVICH, University of Massachusetts Medical School, EUGENE SHAKHNOVICH, Harvard University, Department of Chemistry and Chemical Biology — The ability to absorb mutations while retaining structure and function, or mutational robustness, is a remarkable property of natural proteins. We use a computational model of organismic evolution [Zeldovich et al, PLOS Comp Biol 3(7):e139 (2007)], which explicitly couples protein physics and population dynamics, to study mutational robustness of evolved model proteins. We compare evolved sequences with the ones designed to fold into the same native structures and having the same thermodynamic stability, and find that evolved sequences are more robust against point mutations, being less likely to be destabilized, and more likely to increase stability upon a point mutation. These results point to sequence evolution as an important method of protein engineering if mutational robustness of the artificially developed proteins is desired. On the biological side, mutational robustness of proteins appears to be a natural consequence of the divergence-mutation-selection evolutionary process.

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