Title:	Complex network analysis of thermostable mutants of Bacillus subtilis Lipase A
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Abstract:	Three-dimensional structures of proteins that regulate their functions can be modelled using complex network based approaches for understanding the structure-function relationship. The six mutants of the protein Lipase A from Bacillus subtilis, harbouring 2 to 12 mutations, retain their function at higher temperatures with negligible variation in their overall three-dimensional crystallographic structures. This enhanced thermostability of the mutants questions the structure-function paradigm. In this paper, a coarse-grained complex network approach is used to elucidate the structural basis of enhanced thermostability in the mutant proteins, by uncovering small but significant local changes distributed throughout the structure, rendering stability to the mutants at higher temperatures. Community structure analysis of the six mutant protein networks uncovers the specific reorganisations among the nodes/residues that occur, in absence of overall structural variations, which induce enhanced rigidity underlying the increased thermostability. This study offers a novel and significant application of complex network analysis that proposes to be useful in the understanding and designing of thermostable proteins.
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