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Title:	Probe into a multi-protein prokaryotic organelle using thermal scanning assay reveals distinct properties of the core and the shell
Authors:	Hazra, J.P. (/jspui/browse?type=author&value=Hazra%2C+J.P.)
Keywords:	Bacterial microcompartments Globular proteins Self-assembly Shell proteins
Issue Date:	2020
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Citation:	Biochimica et Biophysica Acta - General Subjects, 1864(10)
Abstract:	Background: Bacterial microcompartments represent the only reported category of prokaryotic organelles that are capable of functioning as independent bioreactors. In this organelle, a biochemical pathway with all the enzyme machinery is encapsulated within an all protein shell. The shell proteins and the enzymes have distinct structural features. It is hypothesized that flat shell proteins align sideways to form extended sheets and, the globular enzymes fill up the central core of the organelle. Methods: Using differential scanning fluorimetry, we explored the structure and functional alteration of Pdu BMC, involving tertiary or quaternary structures. Results: Our findings exhibit that these intact BMCs as a whole behave similar to a globular protein with a rich hydrophobic core, which is exposed upon thermal insult. The encapsulated enzymes itself have a strong hydrophobic core, which is in line with the hydrophobic-collapse model of protein folding. The shell proteins, on the other hand, do not have a strong hydrophobic core and show a significant portion of exposed hydrophobic patches. Conclusion: We show for the first time the thermal unfolding profile of the BMC domain proteins and the unique exposure of hydrophobic patches in them might be required for anchoring the enzymes leading to better packaging of the micro-compartments. General significance: These observations indicate that the genesis of these unique bacterial organelles is driven by the hydrophobic interactions between the shell and the enzymes. Insights from this work will aid in the genetic and biochemical engineering of thermostable efficient enzymatic biomaterials.
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