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Structural characterization of a mitochondrial intermembrane domain

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Our object of study is a human protein anchored at the mitochondrial inner membrane. This protein consists of three domains whose function is still unknown. The N-terminal domain (N) spans through the intermembrane space, whereas the C-terminal domain (C) faces the mitochondrial matrix, both regions being connected by a transmembrane helix embedded in the inner membrane. Several constructs of both the N and C domains were generated to obtain stable protein fragments suitable for expression and crystallization. However, only a few N-terminal constructs were soluble, but most of them aggregated during purification. Construct N4 showed the highest expression levels in Escherichia coli and could be reasonably purified. Nevertheless, once pure, N4 had a high tendency to precipitate, which led us to explore new approaches to improve its stability. We will present the re-design approaches of the constructs to improve solubility and solve aggregation and precipitation.

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Yes

Primary author: ILLANES VICIOSO, Ramiro (IBMB-CSIC)

Co-authors: RUIZ LÓPEZ, Elena (IBMB-CSIC); SOLA, Maria (IBMB-CSIC)

Presenter: ILLANES VICIOSO, Ramiro (IBMB-CSIC)

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