Optimization of crystallization conditions for PfActII in complex with fragmin F1 domain

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Actins are among the most abundant proteins in cells. They form filaments, which are involved in essential processes in the cell, including cell division, transport, motility, and structural functions. Polymerization involves a transition of monomeric (G-form) actin to the filamentous F-form. Conformational changes upon this transition activate ATP hydrolysis in the actin protomer. In apicomplexan parasites, actin filaments are essential for motility and host cell invasion. Unlike other apicomplexan parasites, including Toxoplasma gondii, which have only a single actin isoform, there are two actin isoforms in Plasmodium spp. (ActI and ActII). Plasmodium falciparum (Pf) ActII is one of the most divergent actins in eukaryotes. PfActII is expressed only during gametogenesis and insect cell stages. PfActI is the most studied isoform. Currently, there are no available atomic details of the PfActII filaments. To understand the mechanisms of F-actin ATP hydrolysis, structures at atomic resolution are indispensable. We have obtained crystals of Mg-ADP-PfActII in complex with fragmin domain F1 from Physarum polycephalum. Fragmin belongs to the gelsolin superfamily, and the interaction with actin is Ca2+ dependent. This protein binds to the barbed end actin subunit and induces an F-like conformation in monomeric actin. We are in the process of optimizing the crystallization conditions of Mg-ADP-PfActII-F1. Additionally, we intend to obtain crystals with PfActII in different nucleotide states.