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ARTICLE

Backbone and side chain NMR assignments for the ribosome Elongation Factor P (EF-P) from *Staphylococcus aureus*

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Abstract

Elongation Factor P (EF-P) is a 20.5 kDa protein that provides specialized translation of special stalling amino acid motifs. Proteins with stalling motifs are often involved in various processes, including stress resistance and virulence. Thus it has been shown that the virulent properties of microorganisms can be significantly reduced if the work of EF-P is disrupted. In order to elucidate the structure, dynamics and function of EF-P from *Staphylococcus aureus* (*S. aureus*), here we report backbone and side chains ^{1}H, ^{13}C and ^{15}N chemical shift assignments of EF-P. Analysis of the backbone chemical shifts by TALOS+ suggests that EF-P contains 1 α-helix and 13 β-strands (β1-β2-β3-β4-β5-β6-β7-α1-β8-β9-β10-β11-β12-β13). The solution of the structure of this protein by NMR and X-ray diffraction analysis, as well as the structure of the ribosome complex by cryo-electron microscopy, will allow further screening of highly selective inhibitors of the translation of the pathogenic bacterium *S. aureus*. Here we report the almost complete ^{1}H, ^{13}C, ^{15}N backbone and side chain NMR assignment of a 20.5 kDa EF-P.

Keywords EF-P · Staphylococcus aureus · Ribosome · Protein · NMR · Resonance assignment

Abbreviations

S. aureus	*Staphylococcus aureus*
EF-P	Elongation Factor P
Cryo-EM	Cryo-electron microscopy
SEC	Size-exclusion chromatography
IMAC	Immobilized metal affinity chromatography

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Biological context

Staphylococcus aureus (*S. aureus*) is a gram-positive bacteria that causes various human diseases. Despite the presence of different types of antibiotics, it is still a significant threat for human health. Growing antibiotic resistance of *S. aureus* is a major threat for the national health systems (Lowy 1998).

Protein synthesis is a key process for living organisms, so the protein synthesis machinery is often the target for the action of antimicrobial agents. In recent decades a significant progress has been made in the research area of the mechanisms of protein synthesis and its structural organization. The structures of the ribosome and several functional complexes with translation factors and ligands modeling various stages of protein synthesis were determined by X-ray diffraction analysis with atomic resolution. These data created the basis for our understanding of biochemical processes taking place during the protein synthesis, allow to determine causes of inhibitory effects for certain antibiotics on protein synthesis (Khusainov et al. 2016, 2017) and also could be used to predict and develop new antimicrobial agents.