Polihistydylowe sekwencje z motywem His-tag - ich rola i biologiczne znaczenie oddziaływania z jonami metali = Polyhistidine sequences with His-tag motif - their role and biological significance of interaction with metal ions.

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Streszczenie

His-tags are specific sequences containing six to nine subsequent histydyl residues and they are used commercially in immobilized metal affinity chromatography
(IMAC) as molecular ‘anchors’ that bind to a metal ion (usually nickel), immobilized by chelation with nitrilotriacetic acid (NTA) bound to a solid support [37, 38]. Con
secutive histidines are the common denominator for both His-tags used in molecular biology and for quite remote biological phenomena – more than 2000 histi
dine-rich proteins (HRPs) are found in microorganisms including 60% and 82% of archaeal and bacterial species, respectively and their roles are not well characterized[73].
The physicochemical properties of histidine make it a versatile amino acid that influences protein conformation and enzymatic activity [15]. Many natural proteins with a
His-tag domain are assigned to different functions, for example: most bacterial proteins, containing this motif are probably involved in the homeostasis of nickel ions [68, 76],
while others, e.g.newly isolated peptides from the venom of the snake genus Atheris contain poly-histidyl-poly-glycyl sequences (pHpG) can act on the cardiovascular system
by inhibiting snake venom metalloproteinases and affect ts function by acting on specific receptors [58, 62]. His-rich motifs have been found also e.g.in Zn2+transporters,
prion proteins, His-rich glycoproteins, transcription factors or numerous copper-binding proteins [56, 67, 84]. Binding mode and the thermodynamic properties of the system
depends on the specific metal ion and the histidine sequence. Despite the wide application of the His-tag for purification of proteins, little is known about the properties of metal-
binding to such tag domain. Recent experimental and theoretical studies have shown that metal ions, e.g. Cu2+ can

bind to various sets of imidazoles depending on the number of histidine residues that are located in His-rich sequences. The occurrence of polymorphic binding states and the formation of an α-helical structure induced by metal ion coordination suggest that proteins with a His-tag domain may serve as the dynamic site able to ‘move’ metal ions along the tag Ni^{2+}sequence [99, 100].

This might explain the frequent occurrence of such sequences in bacterial Ni2+ chaperones, which transfer the metal ion between different proteins.

Słowa kluczowe

histidine, His-tag motif, metal ions, proteins