Poster Presentation

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A closed-homodimer structure of human importin-α1

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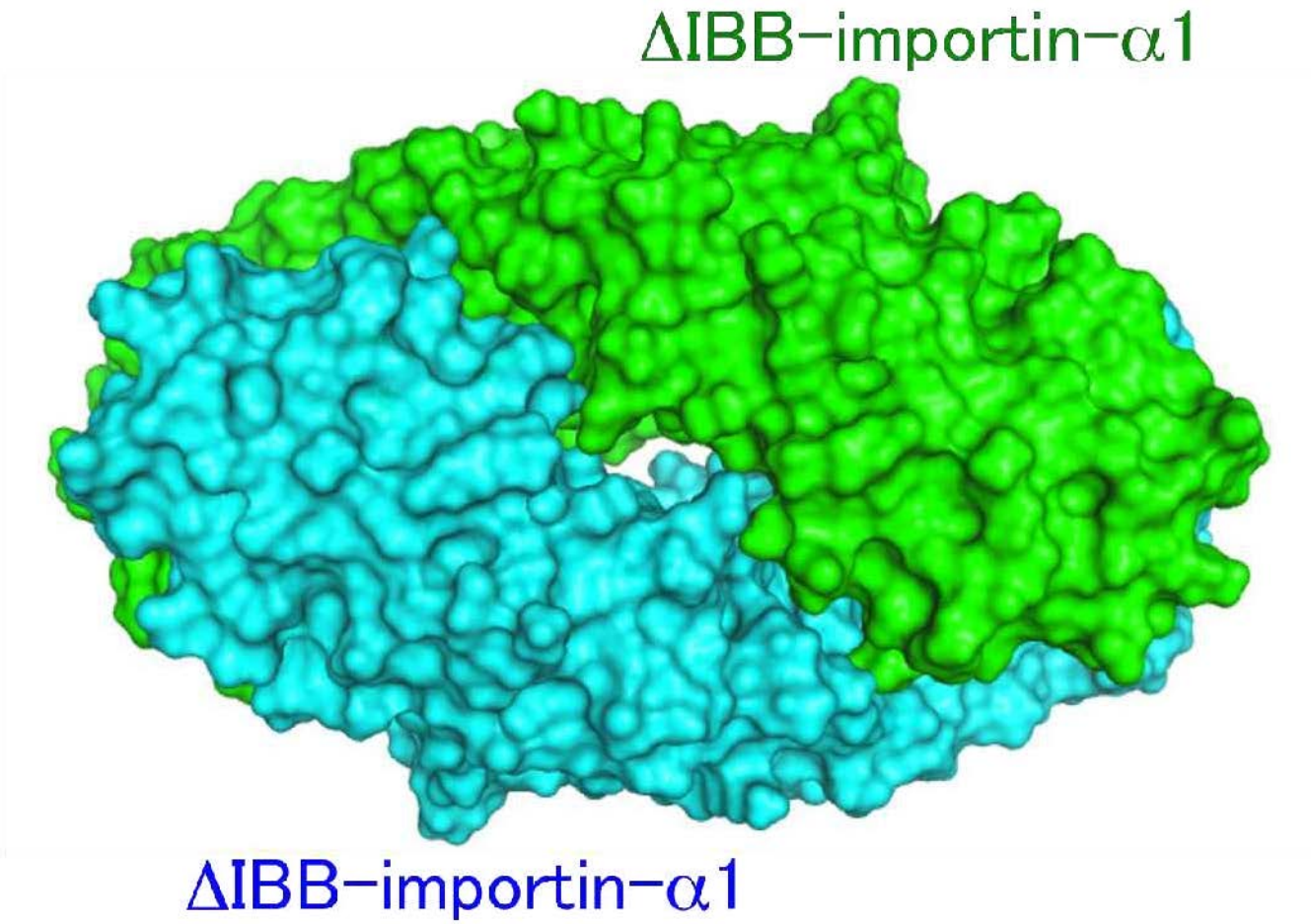
We determined the crystal structure of N-terminal importin-β-binding (IBB) domain truncated human importin-α1 (ΔIBB-importin-α1) at 2.63Å resolution. The crystal structure of ΔIBB-importin-α1 is a novel closed-homodimer. The homodimer exists in an autoinhibition state in which both of the major and minor NLS-binding sites are completely buried in the homodimerization interface to avoid NLS binding. Importin-α1 is in dimer-monomer equilibration in solution. In the dimerization sate, the P1'-binding pocket in the minor NLS binding site plays a role to stabilize the dimer formation. The external K108 binds into the P1'-binding pocket that results in the autoinhibition of the NLS binding. The present closed-homodimer of ΔIBB-importin-α1 conjured the functional aspects of multimerization of importin-α1. The further physicochemical studies using full- and ΔIBB- importin-α1 reveal that the IBB domain is involved in the monomer-dimer equilibration; thereby the NLS binding affinity is kept even in the higher concentration of importin-α1. Owing to the multimerization property, importin-αs can autoinhibition the NLS binding, that may result in a variety of NLS recognition way.



Keywords: importin-α1, closed-homodimer, autoinhibition