Poster Presentation

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Structural analysis of Pore-Forming CEL-III

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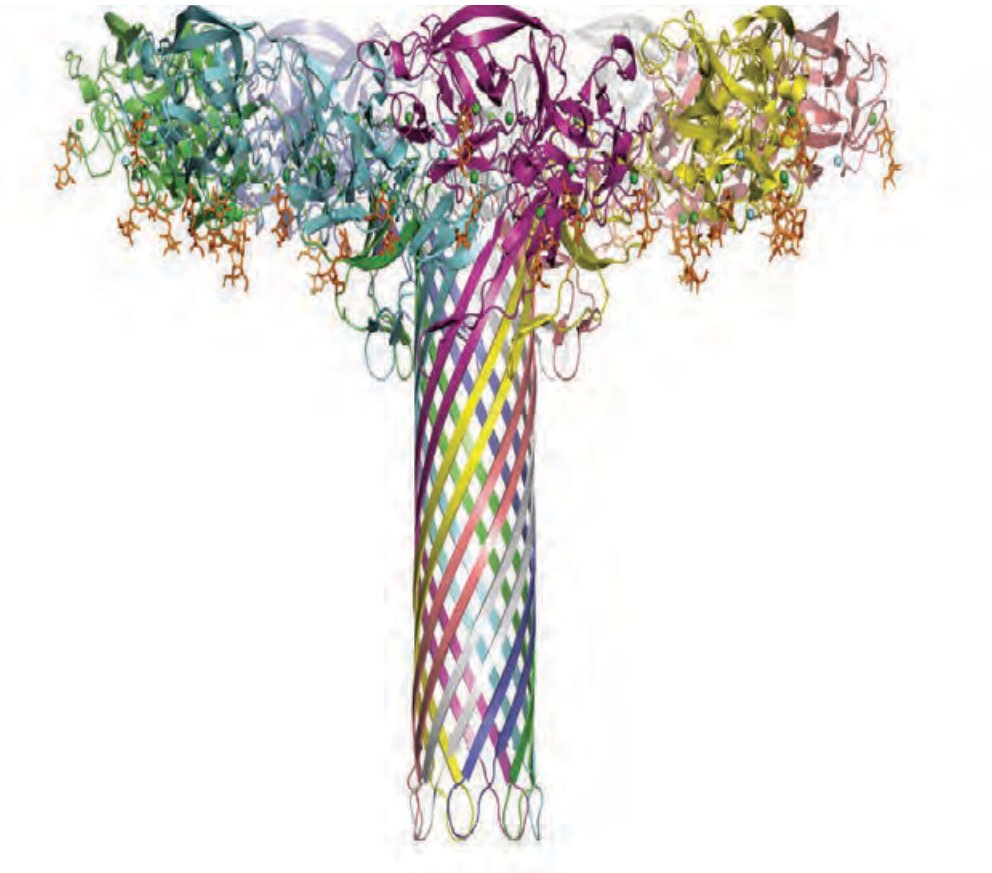
CEL-III is a hemolytic lectin isolated from the sea cucumber Cucumaria echinata. This lectin is composed of two carbohydrate-binding domains (domains 1-2) and one oligomerization domain (domain 3). After binding to the cell surface carbohydrate chains through domains 1-2, domain 3 self-associates to form transmembrane pores, leading to cell lysis or death, which resembles other pore-forming toxins of diverse organisms. To elucidate the pore-formation mechanism of CEL-III, the crystal structure of the CEL-III oligomer was determined. The CEL-III oligomer has a heptameric structure with a long β-barrel as a transmembrane pore. This β-barrel is composed of 14 β-strands resulting from a large structural transition of α-helices accommodated in the interface between domains 1-2 and domain 3 in the monomeric structure, suggesting that the dissociation of these α-helices triggered their structural transition into a β-barrel. After heptamerization, domains 1-2 form a flat ring, in which all carbohydrate- binding sites remain bound to cell surface carbohydrate chains, stabilizing the transmembrane β-barrel in a position perpendicular to the plane of the lipid bilayer.



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