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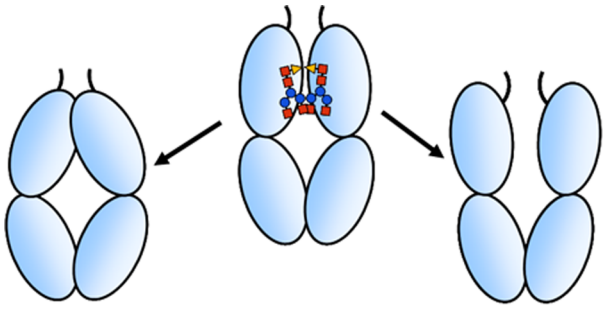
SMALL ANGLES, BIG INFORMATION

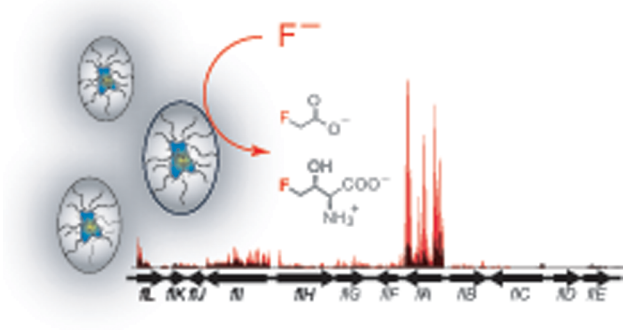
Immunoglobulin G antibodies are key components of the immune system, galvanizing various types of white blood cells to attack foreign invaders. Their Fragment crystallizable (Fc) portion, the part that directly interacts with receptors on white blood cells, is made up of two C_H2 domains and two C_H3 domains. The C_H2 domains are glycosylated, a modification known to be important for binding to Fc receptors. Borrok *et al.* (DOI: 10.1021/cb300130k) now use X-ray crystallization and small-angle X-ray scattering to explore just how the glycan promotes the active conformation of the receptor.



After uncovering discrepancies in the X-ray structures of different aglycosylated Fc molecules, the authors employed small-angle X-ray scattering to probe the structure of the protein in solution, which is likely more physiologically relevant. They characterize solution structure as well as interactions at the interface of the C_H2 and C_H3 domains important for receptor binding. Taken together, their results offer compelling new evidence for how the glycan likely stabilizes the otherwise dynamic nature of the Fc domain.

TOWARD THE FLOURISHING PRODUCTION OF ORGANOFLUORINES

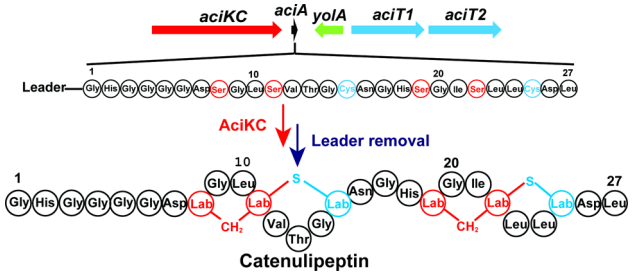
Though fluorine-containing organic compounds are scarcely found in nature, their unique biological properties have made synthetic organofluorines of increasing interest as drug candidates. The bacteria *Streptomyces cattleya* is the only organism known to synthesize organofluorine compounds, and a better understanding of the biosynthetic pathways involved could lead to improved methods for the generation of novel fluorine-containing molecules. To this end, Walker *et al.* (DOI: 10.1021/cb3002057) elegantly combine genomic, genetic, and biochemical methods to explore the biochemistry and physiology of fluorine in *S. cattleya.*



They discover that the biosynthesis of organofluorines in *S. cattleya* is dependent both on the presence of fluoride as a fluorine donor and the growth phase of the bacteria. The growth phase dependence is especially important, because it enables the bacteria to circumvent the toxicity of the very fluorine-containing compounds that it produces. The insights into fluorine metabolism gained in this study will guide future bioengineering strategies for incorporating fluorine into various small molecules.

CHARACTERIZING CATENULIPEPTIN

Lantipeptides are a family of polycyclic peptides characterized by the presence of thioether cross-links. They are produced by various bacteria and have diverse biological activities ranging from promoting the formation of branching filamentous structures called hyphae in bacteria to functioning as potent antibiotics. A new class of lantipeptides has been discovered recently that contains unusual cyclic structures called labionins, in which two serines and a cysteine are linked through the activity of multifunctional enzymes containing both kinase and cyclase activities, called LabKCs. Now, Wang and van der Donk (DOI: 10.1021/cb3002446) explore a previously uncharacterized LabKC in the bacteria *Catenulispora acidiphila*, referred to as AciKC.



They discover that AciKC is responsible for several key steps in the biosynthesis of novel labionin-containing lantipeptide called catenulipeptin, including dehydration and cyclization of the peptide substrate as well as installation of the labionin moieties. Examination of the biological activity of catenulipeptin demonstrated its ability to restore hyphae growth in the bacteria *Streptomyces coelicolor*.

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