

The structure of resistance

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A team of scientists from the University Paris Descartes has solved the structure of two proteins that allow bacteria to gain resistance to multiple types of antibiotics, according to a report in EMBO reports this month. This work provides new clues as to how bacteria adapt to resist antibiotics and how to design new drugs that counteract this defense mechanism.

Frédéric Dardel and colleagues crystallized both the narrow and broad-spectrum resistance forms of the antibiotic-modifying acetyltransferase enzyme. Their report reveals that the enzyme has a flexible active site that can evolve to accommodate new antibiotics, allowing the bacteria to break them down and render them useless. This explains why this type of enzyme is now carried by many bacteria struggling for survival in the antibiotic age.

More importantly, the research provides new insight for the design of new antibiotics that could evade this form of resistance, and new inhibitors that would extend the effectiveness of current antibiotics, both of which could help in the fight against the deadly infections becoming more frequent in hospitals.

Article: www.nature.com/embor/journal/v.../abs/embor20089.html

Source: European Molecular Biology Organization

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