Beamlines: AMX & FMX

Revealing the Basis for Metacaspase Activation



The image shows the structure of MC4, which contain three different domains with a large linker domain (green). The side chain in the linker domain blocks the active site, thus insuring the tight regulation of this protease from inappropriate activation.

P. Zhu, X.-H. Yu, C. Wang, Q. Zhang, W. Liu, S. McSweeney, J. Shanklin, E. Lam, Q. Liu. *Nature Communication* **11** (1), 2249 (2020). doi:10.1038/s41467-020-15830-8.

Work was performed in part at Brookhaven National Laboratory





Scientific Achievement

Scientists determined the structure of Metacaspase 4 (MC4) and identified the linker that can block its activation.

Significance and Impact

Metacaspases mediate many important cellular functions such as stress and immune responses in plants. Understanding mechanisms of these responses offers a basis for future engineering to enable design of more sustainable crops and biofuels.

Research Details

- Damage-induced intracellular Ca²⁺ flux activates MC4 in *Arabidopsis thaliana*, a weed/ model organism.
- Structures were determined of inactive and Ca²⁺⁻ activated MC4 structures.
- In vivo activity was analyzed using tobacco plants.
- Results identified the structural basis for MC4 activation via linker cleavage.
- X-ray diffraction data collected at the AMX and FMX beamlines at NSLS-II were essential for this work.

