
Contribution ID: **191** Type: **Talk**

# Crystal structure and function of the CRISPR-Lon protease

*Wednesday, 16 March 2022 10:00 (20 minutes)*

We report the crystal structure of CRISPR-Lon, a type-III CRISPR related protease that is activated by cyclic oligoadenylates. The protein is a soluble monomer and contains a SAVED domain that accommodates cA4. Further, we show that CRISPR-Lon forms a stable complex with the 34 kDa CRISPR-T protein. Upon activation by cA4, CRISPR-Lon specifically cleaves CRISRP-T, releasing CRISPR-T23, a 23 kDa fragment that is structurally very similar to MazF toxins and is likely a sequence specific nuclease.

**Primary authors:** ROUILLON, Christophe (University of Bonn); SCHNEBERGER, Niels (University of Bonn); CHI, Haotian (University of St Andrews); PETER, Martin (University of Bonn); GEYER, Matthias (University of Bonn); BOENIGK, Wolfgang (3Center of Advanced European Studies and Research (caesar)); SEIFERT, Reinhard (3Center of Advanced European Studies and Research (caesar)); WHITE, Malcolm (University of St Andrews); HAGELUEKEN, Gregor (University of Bonn)

**Presenter:** HAGELUEKEN, Gregor (University of Bonn)

**Session Classification:** Biocrystallography: Signalling and Macromolecular Complexes

**Track Classification:** Main conference: Biologic Structure, Function, Reactivity, and Regulation