



**Symposium: Beyond Sequence Alignment | 2017-10-16 | Abstracts**

**UNDERSTANDING VULNERABILITY TO PROTEIN OXIDATION IN BACTERIA**

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Vulnerability to reactive oxygen species stratifies within proteomes based on undetermined biomolecular properties. Experimental identification of targets forming protein carbonyls, the standard marker for proteome oxidation, is limited by inherent transience and low sampling rate.

We predict protein carbonyls that we measured forming in *Escherichia coli* and *Deinococcus radiodurans* under lethal-dose gamma-irradiation by integrating structural systems biology with machine learning, comprising a biomolecular basis for understanding vulnerability and robustness to protein oxidation in bacteria. Our analysis shows that ribosomal proteins are especially vulnerable to oxidation. We highlight *D. radiodurans* orthologs likely to contribute to radioresistance.

These findings provide mechanistic insight into proteome oxidation and are applicable to understanding cytotoxicity associated with oxidative stress from the environment, cellular respiration, and human diseases.

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