

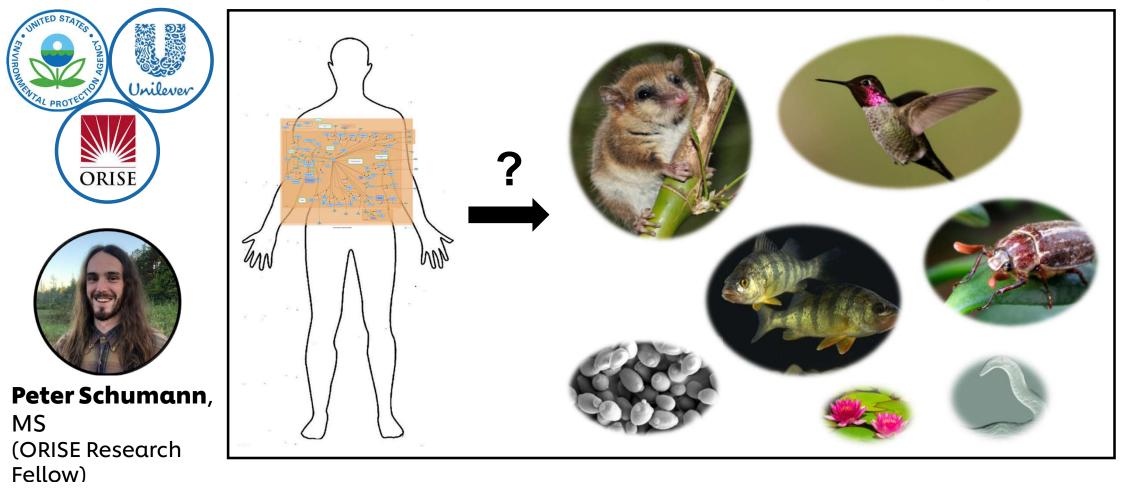
Combination of Computational New Approach Methodologies for Enhancing Evidence of Biological Pathway Conservation Across Species

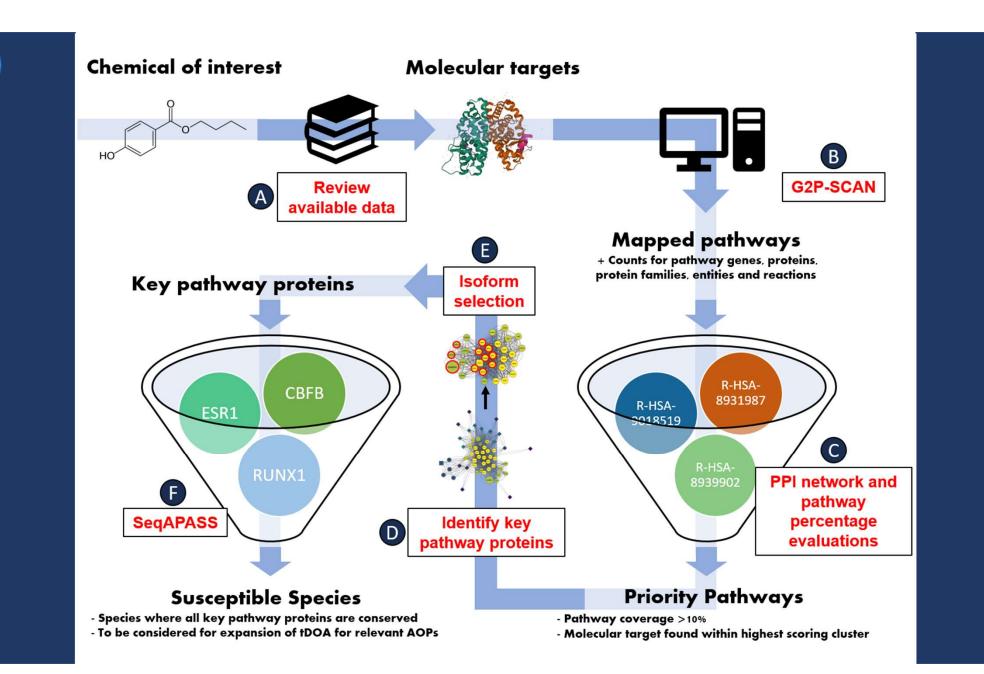
P. Schumann¹, C. Rivetti², J. Houghton², B. Campos², G. Hodges², and C. LaLone³

www.epa.gov

¹Oak Ridge Institute for Science and Education, Duluth, MN ²Safety and Environmental Assurance Centre, Unilever, Colworth Science Park, Sharnbrook, Bedfordshire, UK ³U.S. Environmental Protection Agency, Office of Research and Development, Mid-continent Ecology Division, Duluth, MN

Peter Schumann | schumann.peter@epa.gov | 414-687-7552



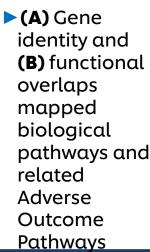


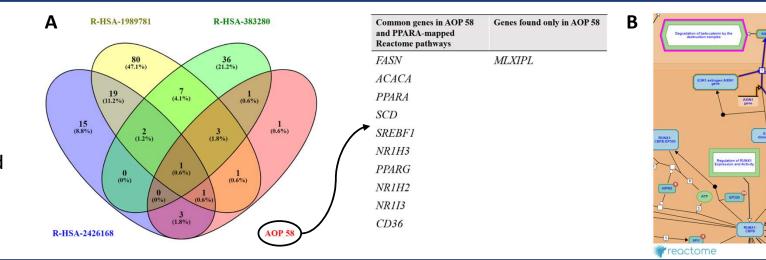


Conclusions and Next Steps



KCTDS ON





An Eshibination, it was demonstrated that these tools can be used to:

- > Expand the prediction of biological pathway conservation across species (several additional lines of evidence are generated through the use of G2P-SCAN)
- > Aid in the prediction of cross-species chemical susceptibility (approaching a systems perspective)
- > Potentially extend the biologically plausible tDOA of relevant AOPs
- > Provide additional biological information to help further characterize certain KEs and KERs
- Areas of improvement:
 - Additional factors such as life stage, life history, biological sex, and toxicokinetic factors like absorption, distribution, metabolism, excretion (ADME) may be incorporated to yield a more complete understanding of the chemical exposure and resulting biological impacts
 - > Incorporation of quantitative pathway information through the use of (high-throughput) transcriptomics or proteomics would allow for pathway topology evaluations for molecular target and pathway prioritizations