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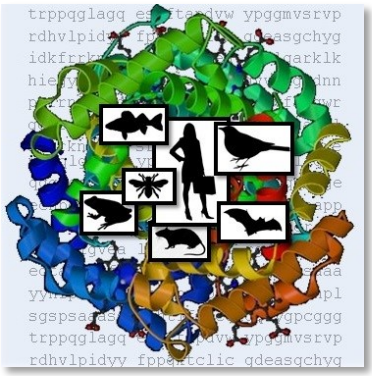
INNOVATIVE RESEARCH FOR A SUSTAINABLE FUTURE

SeqAPASS

Sequence Alignment to Predict Across Species Susceptibility



What is SeqAPASS?

Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS) is a fast, online screening tool that allows researchers and regulators to use available information about species' sensitivity to chemicals to consistently predict chemical susceptibility for hundreds of other species. SeqAPASS uses available protein sequence and structural information to understand species susceptibility at the molecular level. Using existing data from model organisms to inform predictions reduces the need for additional resource-intensive toxicity testing. SeqAPASS minimizes the complexity of protein sequence and structural comparisons for species extrapolation, making the process more rapid and less daunting for scientists and regulators alike to help guide research and inform risk assessments.

How SeqAPASS works

IDs chemical interaction with protein targets of species known to be sensitive to the chemical

→

Evaluates protein target similarities in other species

→

Predicts likely or unlikely chemical interaction for untested species

Why SeqAPASS?

By necessity, human and environmental risk assessments for chemicals use a limited number of models to generate toxicity test data, which are then extrapolated to species of concern. Decreasing testing resources, international interest in reducing animal use, and increasing demand to evaluate chemicals in a more timely manner means increased demand for good predictive approaches to maximize the use of existing data. For some species, EPA has data regarding toxicity to certain chemicals. SeqAPASS uses this data along with publicly available protein sequence and structure information to better understand the effects of chemicals on non-target species. For example, if a chemical is known to interact with a protein in one organism, SeqAPASS can help efficiently 1) identify whether that protein sequence/structure is present in other species of interest, and 2) use this information as an initial, screening level, line of evidence to predict chemical susceptibility to hundreds of other species where limited or no toxicity information exists. SeqAPASS is a unique application that is:

ROBUST: Pulls information from the National Center for Biotechnology Information (NCBI) protein database, which has information on over 125,000,000 proteins representing more than 85,000 organisms.

FLEXIBLE: Flexibility in the analysis, moving from primary amino acid sequence evaluations to structural consideration, allows users to capitalize on any existing information pertaining to chemical-protein interactions in known sensitive species.

INNOVATIVE: Allows users to extrapolate from any species to all other species for which protein sequence data exist.

For More Information, Contact
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How To Access

1. Go to seqapass.epa.gov/seqapass/
2. Request the free user account

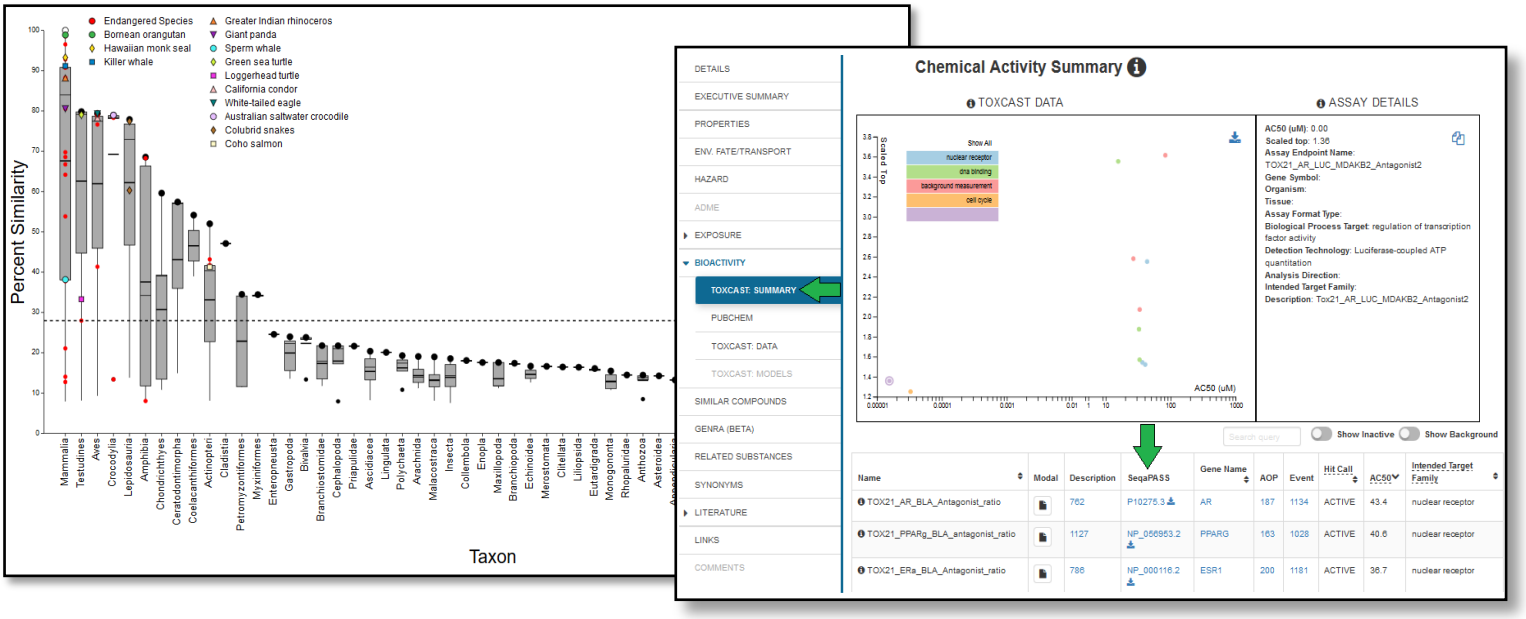
Data Visualization

Interactive data visualization and synthesis features such as customizable box-plot graphics, make the interpretation of results easier for users.

SeqAPASS data visualizations and summary tables are downloadable for use in presentations and publications.

Interoperability

SeqAPASS is interoperable with the CompTox Chemicals Dashboard (comptox.epa.gov/dashboard), where SeqAPASS results from ToxCast Assay targets can be obtained for use as an initial line of evidence for extrapolating mammalian-based high-throughout assay data across species.



SeqAPASS in ACTION

Multiple case studies demonstrate the applicability and utility of SeqAPASS to predict cross species susceptibility to chemicals that have the potential to effect:

THE ENDOCRINE SYSTEM IN HUMANS AND WILDLIFE:

human estrogen receptor: EPA's Endocrine Disruptor Screening Program (EDSP) is charged with examining the effects of over 10,000 chemicals on the endocrine system. Scientists used SeqAPASS to help determine the degree to which data generated to evaluate chemical activation in mammalian systems (e.g., the human estrogen receptor) can be translated to non-mammalian species (e.g., fish, amphibians and birds). This information will help prioritize testing to assess the human health and ecological risks of estrogenic chemicals. https://doi.org/10.1002/etc.3456 and https://doi.org/10.1021/acs.est.8b04587

MOLTING PROCESSES IN INSECTS AND INVERTEBRATES:

tobacco budworm ecdysone receptor: Various synthetic chemicals were designed to mimic the hormones that control molting, a necessary process for proper growth and development in insects and other invertebrates. These chemicals work to interfere with this process to cause specific toxicity to larval pests such as armyworms, budworms, moths, and corn borers. Yet, these same chemicals do not harm non-target species, such as honey bees and earthworms. Scientists used SeqAPASS for a cross-species comparison of the protein sequence in the tobacco budworm, a known target organism, to predict the potential susceptibility of these chemicals in other species. https://doi.org/10.1093/toxsci/kfw119

SURVIVAL OF HONEY BEE COLONIES:

honey bee nicotinic acetylcholine receptor: The decline in honey bee colonies is a widespread concern because of their key function in pollinating crops. Both chemical and non-chemical stressors have been implicated in the loss of some pollinators. SeqAPASS was used to evaluate the potential chemical susceptibility of honey bees, other bee species, and insects for which toxicity information is lacking. https://doi.org/10.1093/toxsci/kfw119 and https://dx.doi.org/10.1016%2Fj.scitotenv.2017.01.113

U.S. Environmental Protection Agency
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