

A Fathead Minnow Genome Browser Provides Simplified Access to Annotated Genomic Sequences

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**CONTENTS OF THIS PRESENTATION NEITHER CONSTITUTE, NOR NECESSARILY REFLECT, OFFICIAL US EPA POLICY*

FATHEAD MINNOW GENOME BROWSER

BACKGROUND

- The fathead minnow (*Pimephales promelas*) is a widely used model laboratory organism
 - Long history of use in research and regulatory toxicity testing
 - Biological responses to chemical exposures relatively well-documented
- However, until recently, genome scale information was lacking for this species
 - Limited the utility of the species for pathway-based toxicity testing and research
 - 'omics' technologies proven to be powerful tools



DEVELOPMENT

- Next generation sequencing was applied to generate a draft fathead minnow genome assembly (Burns et al., 2016).
- First generation genome annotation was developed using AUGUSTUS *Ab initio* gene prediction
- Developed into a user-friendly browser, accessible to the research community (Saari et al., 2017)



FATHEAD MINNOW GENOME BROWSER

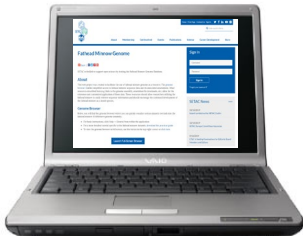
PURPOSE OF THE TOOL

- Provides simplified access to the annotations for the fathead minnow genome
- Allows the user to:
 - Search for genes of interest
 - Extract corresponding sequence
 - Identify intron and exon boundaries
 - Align the predicted genes with supporting evidence

TOOL FORMAT/ACCESSIBILITY

- Web-based tool hosted by SETAC
- Accessed at:

www.setac.org/fhm-genome

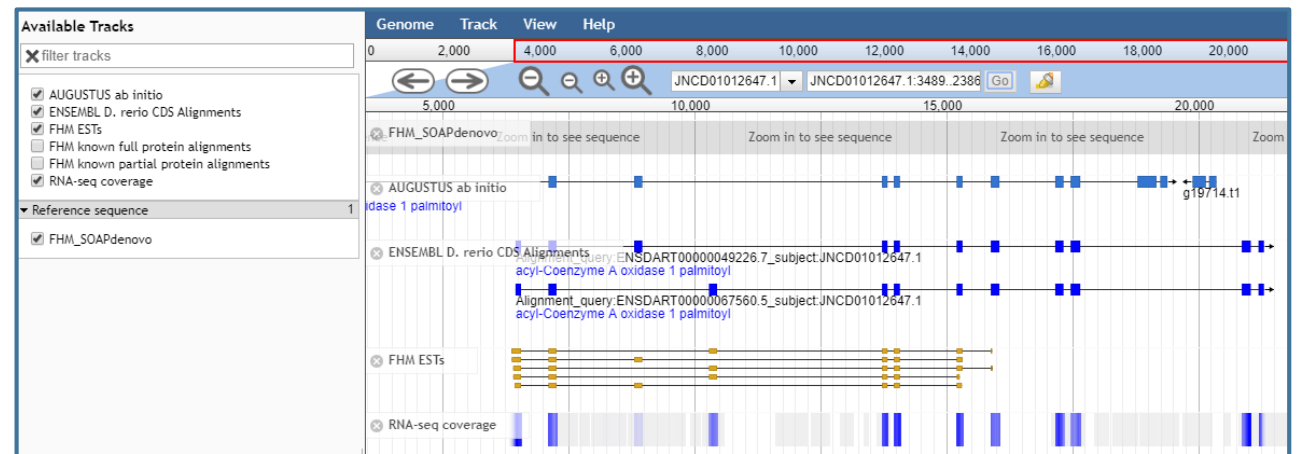


The screenshot shows the homepage of the Fathead Minnow Genome Browser. At the top, there is a navigation bar with links for Home, Print Page, Contact Us, Sign In, and social media icons. The main header features the SETAC logo and the URL www.setac.org/fhm-genome. Below this is a secondary navigation bar with links for About, Membership, Get Involved, Events, Publications, Science, Career Development, and Store. The main content area is titled 'Fathead Minnow Genome' and includes a 'Share' button with social media icons. A paragraph states that SETAC supports open science by hosting the database. An 'About' section explains the project's goal to facilitate the use of the fathead minnow genome as a resource. A 'Genome Browser' section describes the tool's functionality and provides links for help, a practical guide, and a full-screen browser button. On the right side, there is a 'Sign In' form with fields for Username and Password, and a 'Sign In' button. Below the sign-in form is a 'SETAC News' section with a 'more' link and three news items dated 10/10/2019 and 9/18/2019.

INTENDED AUDIENCE

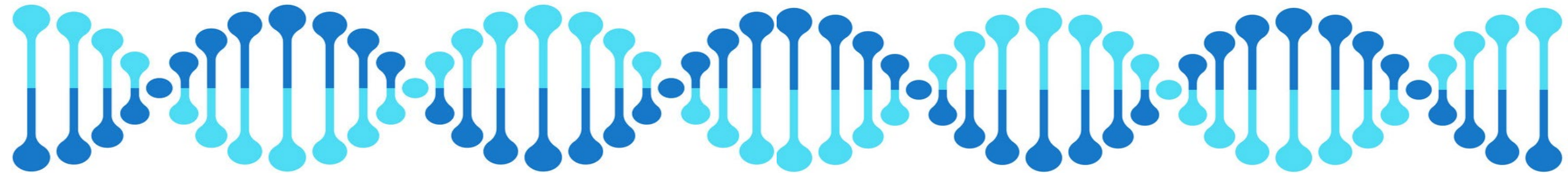
USERS/PRACTICAL APPLICATIONS:

- The ecotoxicology community
- Any application for which an annotated fathead genome is required/desired
- Primer and probe design (QPCR, WISH, RNAseq, etc...)
- CRISPR guide strands
- 'omics' research
- Opens up a wide array of new research opportunities with the fathead minnow



REFERENCES

- Burns, F.R., Cogburn, A., Ankley, G.T., Villeneuve, D.L., Waits, E., Chang, Y.-J., Llaca, V., Deschamps, S.D., Jackson, R.E., Hoke, R.A. 2016. Sequencing and de novo draft assemblies of a fathead minnow (*Pimephales promelas*) reference genome. *Environmental Toxicology and Chemistry* 35: 212-217.
- Saari, T.W., Schroeder, A.L., Ankley, G.T., Villeneuve, D.L. 2017. First-generation annotations for the fathead minnow (*Pimephales promelas*) genome. *Environmental Toxicology and Chemistry* 36: 3436-3442.



ACKNOWLEDGMENTS



Thank you!

Du Pont de Nemours

Frank R Burns
Amarin L Cogburn
Stephane D Deschamps
Raymond E Jackson
Robert A Hoke

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