



Quarterly Newsletter: Winter 2022-23



A snapshot of some proud moments of 2022

Last year, we continued exploring genomic interactions and refining methods to assemble the most complete genomes. These advancements have the potential to revolutionize the way we approach a wide range of medical conditions and open doors to novel research spanning viral infections, antimicrobial resistance, and cancer. As we move into the new year, we can look forward to even more exciting advances in genomics that will help us to close gaps in understanding and facilitate discoveries.

Read our recent blog to discover research highlights, company updates, and news-worth events that took place in 2022.

READ HERE

Over 150 Publications!

Last year, we surpassed 150 papers published using our genome assembly technology. Here are some research highlights from 2022.



Mobile Element Host Attribution

Published in Nature Biotechnology, [breakthrough metagenomic research](#), featuring ProxiMeta Hi-C data, assembled over 400 high-quality MAGs and hundreds of host-viral/plasmid associations from a single fecal sample.

AMR Tracking

[A study](#) using ProxiMeta linked AMR genes to their genomic, plasmid, or viral host in microbiome samples. Their data was used to track horizontal gene transfer of antimicrobial resistance to Salmonella in chickens.

Evolution

Genomic sequencing techniques unearthed surprises about life and evolution. [This article](#) features new studies that illuminate a rarely-seen evolutionary transition in sex chromosomes.

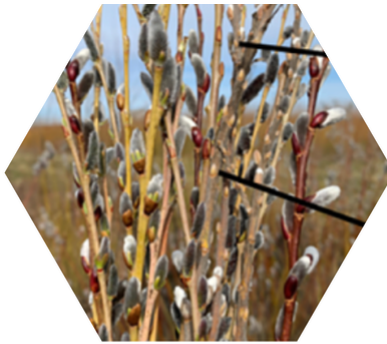
Recent Research



A chromosome-level genome assembly reveals genomic characteristics of the American mink (*Neogale vison*)



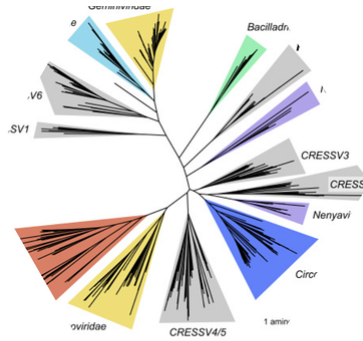
Chromosome-scale genome assembly of *Eustoma grandiflorum*, the first complete genome sequence in the genus *Eustoma*



De Novo Assembly and Annotation of 11 Diverse Shrub Willow (*Salix*) Genomes Reveals Novel Gene Organization in Sex-Linked Regions



The telomere-to-telomere, gapless, phased diploid genome and methylome of the green alga *Scenedesmus obliquus* UTEX 3031 reveals significant heterozygosity and functional separation of the haplotypes



Widespread, human-associated
redondoviruses infect the
commensal protozoan *Entamoeba
gingivalis*

MORE PAPERS

Catch us at a Conference

[Precision Medicine World Conference](#) – Santa Clara, CA (Jan 25-27)

[Advanced in Genome Biology and Technology](#) – Hollywood, FL (Feb. 6-9)

[American College of Medical Genetics and Genomics](#) – Salt Lake City (Mar 14-18)

Have a project in mind?

Contact Us

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