



Next-Generation Sequencing Services

OVERVIEW

The myReads[®] team at Arbor has decades of combined experience in planning and successfully executing a wide variety of custom NGS projects, including our speciality, targeted sequencing with hybridization capture. We have worked with hundreds of non-model species in a variety of preservation levels, including herbarium, ancient and museum DNA. Our team has honed library prep, hybridization capture, and sequencing procedures for maximum efficiency, allowing us to tackle projects of any size successfully and cost-effectively. We provide dedicated customer support and project management to all of our clients, regardless of project scale, and are committed to delivering the highest quality data that translates immediately to your publishable results.

FEATURES & BENEFITS

Proven System – Consistent results from high-complexity NGS library preparation
 Fast Turn-Around – From DNA or RNA to sequencing data in weeks
 Collaborative – Design consultation to meet project budget and goals
 Virtually Any Sample – Utilize fresh, degraded, metagenomic, or ancient DNA
 Any Sequencing Platform – Select Illumina[®], PacBio[®], or Oxford Nanopore[®]
 Volume Discounts – Tiered per-sample pricing for larger projects

OUR SERVICES

- Next-Generation Sequencing (NGS)
- Targeted Sequencing via Hybridization Capture
- DNA-seq and RNA-seq
- Whole Genome Sequencing
- Transcriptome Sequencing
- Short- and Long-Read Platforms
 (Illumina[®], Ion Torrent[®], PacBio[®], Oxford Nanopore[®])
- Fresh or Degraded DNA Services Available
- Bioinformatics Services Available for Special Applications





myReads – Flexible, Collaborative Services to Fit Your Experimental Goals

SERVICES OVERVIEW

We will help you design a project that meets your research needs, whether you need library preparation, hybridization capture, sequencing, or all three! The myReads team offers a variety of library preparation options to best fit your sample type and research goals. Combine your project with a customized or predesigned targeted sequencing myBaits hybridization capture kit from Arbor Biosciences to enhance the efficiency and cost-effectiveness of your NGS project. Alternatively, proceed directly to sequencing on an array of major NGS platforms.

NGS Library Preparation

- Short-insert DNA or RNA library preparation
- Long-insert DNA or cDNA library preparation
- Specialized double or single-stranded chemistry for degraded/ancient DNA

Target Enrichment with myBaits[®]

- New Custom panels with free design assistance
- Predesigned Expert panels for special applications: UCEs, Wheat Exome, and more!

Sequencing – Short and Long Read Platforms

- Illumina[®] NovaSeq and MiSeq
- Ion Torrent® Proton
- PacBio[®] Sequel II
- Oxford Nanopore

CASE STUDIES

myReads Projects Result in Top-Quality Publications

Marchal *et. al* (2018) identified genes that provide resistance to yellow rust in hexaploid wheat *(Triticum aestivum)* using MutRenSeq. They characterized three genes *(Yr7, Yr5, and YrSP)* belonging to a gene cluster on chromosome 2B which contains a non-canonical N-terminal zinc-finger BED domain.



Marchal, C., Zhang, J., Zhang, P. et al. (2018). **BED-domain-containing** *immune receptors confer diverse resistance spectra to yellow rust.* Nature Plants 4: 662–668

Ruane & Austin (2017) targeted ultraconserved elements (UCEs) from 10 snake samples that had been formalin-preserved, including the never-before sequenced *Xylophis sternohynchus*. They placed the formalin-preserved samples in a phylogeny including modern snakes and recovered the expected taxonomic relationships.



Ruane, S. and Austin, C.C. (2017). *Phylogenomics using formalinfixed and 100+ year- old intractable natural history specimens. Molecular Ecology Resources 17: 1003-1008*

FLEXIBLE OPTIONS FOR ANY APPLICATION AND BUDGET



OUR SPECIALITIES

- · Genotyping, Marker Resequencing, and Marker Discovery
- Variant Discovery in Non-Model Organisms
- · Herbarium, Ancient, and Museum DNA Sequencing
- Phylogenetically Informative Region Sequencing (e.g. Ultraconserved Elements / UCEs)
- Disease Resistance Gene Sequencing (RenSeq)
- Long-Insert Targeted Sequencing for PacBio and Oxford Nanopore
- Target Enrichment for Methylation Analysis

WHY ARBOR BIOSCIENCES?

- Competitive pricing
- Dedicated scientific team
- Experience with a broad range of sample types
- Proven results

Expert Scientists Are Here for You

Our team of expert scientists have extensive experience working with a wide range of NGS project types, including fresh and degraded specimens, DNA- and RNA-seq, targeted sequencing with hybridization capture, all major NGS platforms including short- and long-read sequencing, and more. We take great pride in consulting and handling your project as we would if it were our own research project, and will confer with you about any recommended or necessary changes along the way in order to maximize the success of your project.

HOW IT WORKS

- 1. Contact myReads scientists for customized project conferral and estimate
- 2. Provide sequences for custom myBaits design (if applicable)
- 3. Ship DNA or RNA samples following Arbor's sample preparation and submission guidelines
- 4. Receive back either enriched or shotgun NGS libraries or digital NGS FASTQ read data

GETTING STARTED

web

Contact us today via email, phone, or our website to start the conversation about your next NGS project goals. Our team of experts has experience with a wide range of project types and applications, and will work with you to find a solution that fits your research aims as well as your budget. We accept projects from researchers all over the world and look forward to ensuring that your next project is a success.

Illumina, PacBio and Oxford Nanopore are registered trademarks of Illumina, Inc., Pacific Biosciences, and Oxford Nanopore Technologies Limited, respectively.



www.arborbiosci.com info@arborbiosci.com email 1-734-998-0751 phone twitter @ArborBio

Targeted Sequencing Services www.arborbiosci.com/myReads

