



myReads® NGS Service Packages

Flexible, customizable options for different types of samples and projects

- Mix and match to meet your needs or choose services à la carte
- Easily decide which samples to keep, drop, or supplement
- Free QC report with all packages

Packages for hybridization capture with myBaits Custom Kits:

Degraded DNA

Appropriate for older specimens, herbarium material, or samples of unknown quality

- Includes extended QC, fragmentation where necessary, library preparation with specialized chemistry (where necessary), 4-to-6-plex captures, and 1Gbp of PE150 sequencing data per sample
- Samples may have a range of molecular weights, UV 260:280 values, and mass (>10 ng)
- Perfect for samples for which you have no information or are unsure about gDNA quality/quantity!

Ancient DNA

Appropriate for museum, historical, ancient DNA; single-stranded option for cfDNA, single-stranded cDNA

- Includes QC, library preparation with specialized single- or double-stranded chemistry, 2-to-4-plex dual-round captures, and 1Gbp of PE150 sequencing data per sample
- All samples must be low molecular mass (<1kbp)

Standard DNA

Appropriate for freshly-extracted, good quality DNA

- Includes QC, fragmentation, library preparation, 8-to-12-plex captures, and 1Gbp of PE150 sequencing data per sample
- All samples must be high molecular weight (>10kbp modal length), high quality (UV 260:280 1.7-1.9), and high mass (>500 ng of gDNA).
- Library preparation performance commitment* for samples meeting our guidelines

Long Insert DNA

Appropriate for DNA or ds-cDNA intended for PacBio sequencing

- Includes QC, long-insert precursor library preparation, 3-plex captures, and 1 SMRTbell preparation & PacBio Vega cell per 12 samples
- All samples must be high molecular weight (>10kbp modal length), high quality (UV 260:280 1.7-1.9), and high mass (>5000 ng of gDNA)
- Library preparation performance commitment* for samples meeting our guidelines

Standard RNA

Appropriate for high-quality RNA or mRNA

- Includes QC, DNase treatment, purification, fragmentation, directional library preparation, 8-to-12-plex captures, and 1Gbp of PE150 sequencing data per sample
- All samples must be high quality (UV 260:280 1.9-2.1), and high mass (>=250 ng of RNA)
- Additional options for mRNA capture & rRNA depletion from human/mouse/rat samples
- Library preparation performance commitment* for samples meeting our guidelines

- Samples must meet standard DNA criteria for Expert, Community, & WGS Packages
- For degraded samples, add our handling fee to apply degraded criteria and handling

Packages for hybridization capture with myBaits Expert Catalog Kits:

Ultra Conserved Elements or Angiosperms-353

- Includes QC, fragmentation, library preparation, multiplexed captures, and 0.6Gbp of PE150 sequencing data per sample
- All samples must be high molecular weight (>10kbp modal length), high quality (UV 260:280 1.7-1.9), and high mass (>500 ng of gDNA)
- Library preparation performance commitment* for samples meeting our guidelines

16S-Hyb

- Includes QC, fragmentation, library preparation, multiplexed captures, and 3Gbp of PE150 sequencing data per sample
- All samples must be high molecular weight (>10kbp modal length), high quality (UV 260:280 1.7-1.9), and high mass (>500 ng of gDNA)
- Library preparation performance commitment* for samples meeting our guidelines

Wheat exome and/or promoters

- Includes QC, fragmentation, library preparation, multiplexed captures, and 18Gbp of PE150 sequencing data per sample (per bait set)
- All samples must be high molecular weight (>10kbp modal length), high quality (UV 260:280 1.7-1.9), and high mass (>1000 ng of gDNA)
- Library preparation performance commitment* for samples meeting our guidelines

myBaits reactions are included in the Expert and Community packages

Respiratory viruses – dsDNA, ssDNA, RNA, or DNA + RNA

DNA

- Includes QC, fragmentation, double-or single-stranded DNA library preparation, multiplexed captures, and 1Gbp of PE150 sequencing data per sample
- All samples must be high molecular weight (>10kbp modal length), high quality (UV 260:280 1.7-1.9), and high mass (>500 ng of gDNA)
- DNA + RNA includes everything from the ssDNA & RNA packages
- Library preparation performance commitment* for samples meeting our guidelines

RNA

- Includes QC, DNase treatment, purification, fragmentation, directional RNA library preparation, multiplexed captures, and 1Gbp of PE150 sequencing data per sample
- All samples must be high quality (UV 260:280 1.9-2.1), and high mass (>=250 ng of RNA)

Packages for hybridization capture with myBaits Community Panels:

Base package – DNA

- Includes QC, fragmentation, library preparation, multiplexed captures, and 1Gbp of PE150 sequencing data per sample
- All samples must be high molecular weight (>10kbp modal length), high quality (UV 260:280 1.7-1.9), and high mass (>500 ng of gDNA)
- Library preparation performance commitment* for samples meeting our guidelines

Base package – RNA

- Includes QC, DNase treatment, purification, fragmentation, directional library preparation, multiplexed captures, and 1Gbp of PE150 sequencing data per sample
- All samples must be high quality (UV 260:280 1.9-2.1), and high mass (>=250 ng of RNA)
- Additional options for mRNA capture & rRNA depletion from human/mouse/rat samples
- Library preparation performance commitment* for samples meeting our guidelines

Jumpstart your next NGS project with our collection of Community Panels



Packages for whole genome sequencing (WGS):

All packages

- Include QC, fragmentation, library preparation, and PE150 sequencing data
- All samples must be high molecular weight (>10kbp modal length), high quality (UV 260:280 1.7-1.9), and high mass (>500 ng of gDNA)
- Library preparation performance commitment* for samples meeting our guidelines

Per sample sequencing amount	Appropriate for:
0.5Gbp	Low pass or screen sequencing, viral genomes, small bacterial genomes, mtDNA, plasmids
1Gbp	Low pass or screen sequencing, metagenomics, large bacterial genomes (<33Mbp)
6Gbp	Small plant, insect, fungal genomes (<200Mbp)
25Gbp	Mid-size plant genomes, large insect & fungal genomes(<1Gbp)
100 Gbp	Human, mouse, fish, birds, reptiles (<3.3Gbp)

A la carte services

Need fewer samples per capture? DNA extraction? More sequencing? Bioinformatics? Talk to our dedicated team of scientists about the best custom options for your project today.

Your project, your way

Learn more about
**myReads NGS
Service Packages**



*See **myReads Service Policies** document for additional details



Web: www.arborbiosci.com
 Email: info@arbor.daicel.com
 Phone: 1-734-998-0751
 Twitter: @ArborBio

