

Non-coding RNA and Epitranscriptomic Solutions

| GlycoRNA Arrays **NEW !**

Cover Y-RNA/Y-RNA fragment, tRNA, tiRNA&tRF, pre-miRNA, miRNA & more

| Downstream-of-Gene Transcript (DoG RNA) Arrays **NEW !**

Profile DoG RNAs and all their target RNA types simultaneously

| R-loop Profiling **NEW !**

Profile the lncRNA/mRNA/circRNA organized R-loops in gene regulation by DRIPc-seq

| Circular RNA Arrays

Accurately profile circular RNAs by highly specific circular junction probe design

| LncRNA Arrays

Overcome the limitations of RNA-seq for lncRNAs often at low abundance

| Small RNA Arrays

Accurately profile miRNA, pre-miRNA, tRNA, tsRNA, and snoRNA simultaneously

| Epitranscriptomic Arrays

Quantify the percentage of m6A modifications at the transcript specific level

| m6A Single Nucleotide Arrays

Locate and quantify the exact m6A site at single nucleotide resolution

| Small RNA Modification Arrays **NEW !**

Quantify o8G/m7G/m6A/Ψ/m5C in miRNAs, pre-miRNAs & tsRNAs



Get Your Free eBook



Functionality,
reimagined.



The New Vortex Mixer

- Mix and vortex in one compact device
- Precisely set speed and duration controls
- Glove compatible touchscreen
- Quickly vortex tubes with just one touch

The Vortex Mixer is ideally suited for assay protocols that require gentle mixing, all the way up to resuspensions that require vigorous vortexing. Find out more at usascientific.com/vortex_mixer.



Schedule a
demo!

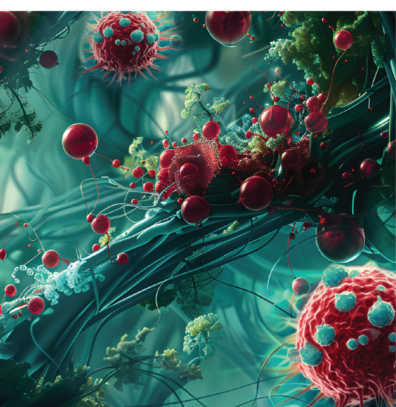
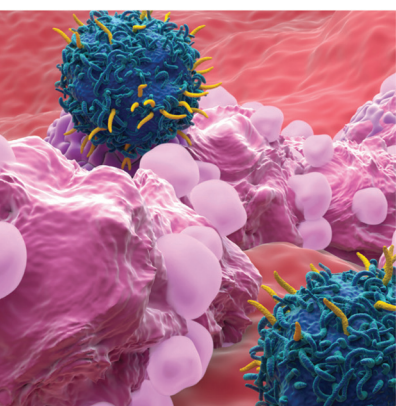
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AACR American Association
for Cancer Research®

2025-2026 SCIENTIFIC CONFERENCES

Presenting the most significant research on cancer etiology, prevention,
diagnosis, and treatment



INTERNATIONAL CONFERENCE ON MALIGNANT LYMPHOMA (ICML)

June 17-21 | Lugano, Switzerland

ARTIFICIAL INTELLIGENCE AND MACHINE LEARNING

July 10-12 | Montreal, QC, Canada

18TH AACR CONFERENCE ON THE SCIENCE OF CANCER HEALTH DISPARITIES IN RACIAL/ETHNIC MINORITIES AND THE MEDICALLY UNDERSERVED

September 18-21 | Baltimore, MD

ADVANCES IN OVARIAN CANCER RESEARCH

September 19-21 | Denver, CO

MECHANISMS OF CANCER IMMUNITY AND CANCER-RELATED AUTOIMMUNITY

September 24-27 | Montreal, QC, Canada

ADVANCES IN PEDIATRIC CANCER RESEARCH

September 25-28 | Boston, MA

ADVANCES IN PANCREATIC CANCER RESEARCH

September 28-October 1 | Boston, MA

AACR-NCI-EORTC INTERNATIONAL CONFERENCE ON MOLECULAR TARGETS AND CANCER THERAPEUTICS

October 22-26 | Boston, MA

AACR-KCA JOINT CONFERENCE ON PRECISION MEDICINE IN CANCER

November 13-14, 2025 | Busan, Korea

CANCER EVOLUTION

December 4-6 | Albuquerque, NM

SAN ANTONIO BREAST CANCER SYMPOSIUM

December 9-12 | San Antonio, TX

THE RISE IN EARLY ONSET CANCERS – KNOWLEDGE GAPS AND RESEARCH OPPORTUNITIES

December 10-13 | Montreal, QC, Canada

FUSION-POSITIVE CANCERS

January 13-15, 2026 | Philadelphia, PA

AACR IO DISCOVERY AND INNOVATION IN CANCER IMMUNOLOGY: REVOLUTIONIZING TREATMENT THROUGH IMMUNOTHERAPY

February 18-21, 2026 | Los Angeles, CA

ADVANCES IN KIDNEY CANCER RESEARCH

March 1-16, 2026 | Philadelphia, PA

Learn more
and register



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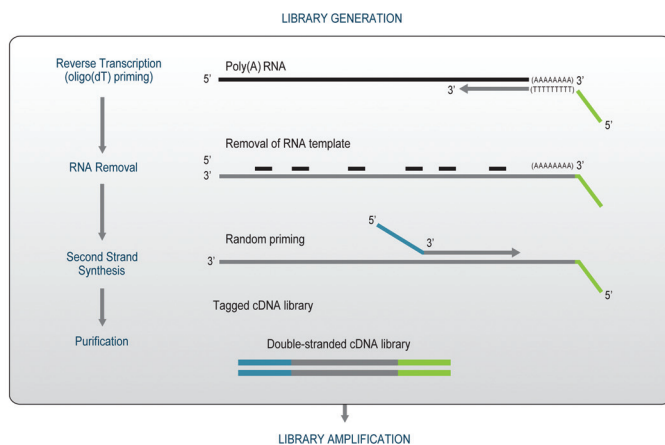
Unlock Alternative Polyadenylation with Ease!

QuantSeq REV V2



Accelerate your Discoveries with Lexogen Solutions for APA Studies!

Alternative polyadenylation (APA) is a fundamental mechanism that regulates eukaryotic gene expression through the generation of distinct mRNA isoforms. Alternative poly(A) site usage is of utmost importance for diverse biological processes, e.g., development and disease. QuantSeq REV V2 allows you to investigate APA, and to deepen understanding of cellular regulation and can even open new paths for exploring therapeutic interventions.



QuantSeq REV allows to precisely pinpoint the 3' end of poly(A) RNA following a fast and streamlined 5-step workflow: 1) oligo(dT) priming and reverse transcription to generate cDNA directly downstream of the poly(A) site, 2) RNA removal and second strand synthesis, 3) purification, 4) library amplification and indexing, and 5) final purification (Fig. 1).

Gene expression, alternative polyadenylation events, and accurate information about a transcripts' 3' UTR can be detected globally using QuantSeq REV (Fig. 2).

Figure 1 | QuantSeq REV V2 workflow: generate ready-to-sequence libraries in only 4.5 hours.

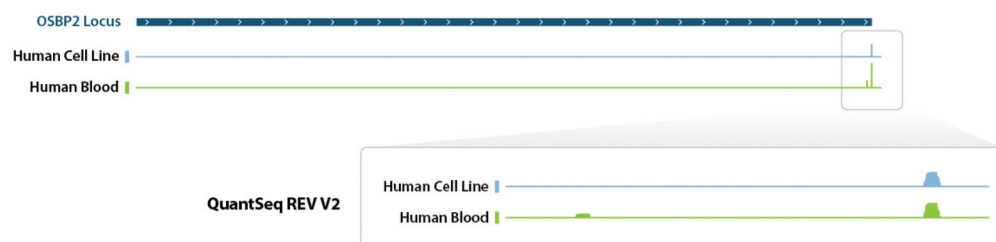


Figure 2 | Alternative polyadenylation of OSBP2 in human blood detected with QuantSeq REV V2 (with Hs Globin Block for blood sample preparation). Alternative polyadenylation site detection revealed two distinct transcript end sites for OSBP2 (human Oxysterol Binding Protein 2).

Interested to learn more?

Scan the QR-code or visit our [webpage](#) for more information.

