www.purigenbio.com

NUCLEIC ACID PURIFICATION – PURE AND SIMPLE™

Finally, get what you need from your FFPE samples

The revolutionary Ionic™ Purification System from Purigen Biosystems uses isotachophoresis to extract, purify, and concentrate nucleic acid from biological samples. Nucleic acids remain in their native form, not denatured or dehydrated, and there is also no binding to, or stripping from, fixed surfaces. Get pure, abundant, and ready-to-use nucleic acid with < 3 minutes of hands-on time per sample.

A better way to extract nucleic acid from FFPE samples

- **More Quantity**
  3.5x higher yield on average from FFPE
- **No Beads, Columns, or Surface-binding**
  Less fragmentation and no risk of contamination from beads or wash solvents
- **More Efficiency**
  Fewer manual steps with <3 minutes of hands-on time per FFPE sample
- **Better Data**
  More material with no bias towards length or GC content means more actionable data

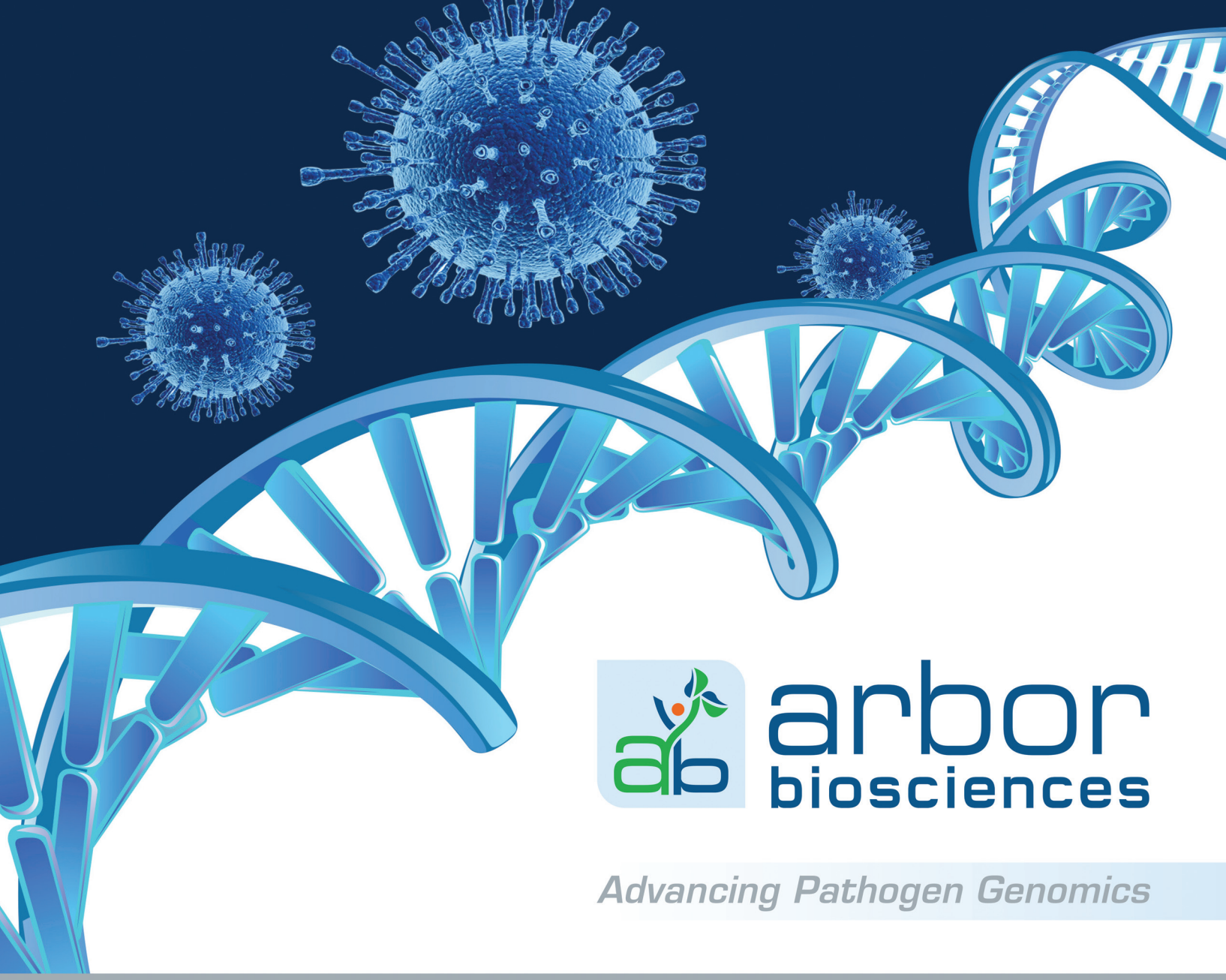
For more information, please contact **info@purigenbio.com**.

Visit us at
ABRF 2020 | BOOTH 106

PURIGEN™ BIOSYSTEMS

FOR RESEARCH USE ONLY. Not for use in diagnostic procedures.

NUCLEIC ACID PURIFICATION – PURE AND SIMPLE™



arbor biosciences

Advancing Pathogen Genomics

myBaits®

myBaits® Custom Panels for Pathogen Sequencing

Whole genome enrichment of pathogens from native environments

Generate orders of magnitude enrichment of pathogen DNA or RNA from naturally complex samples, including bacterial, fungal, and viral pathogens, with hybridization-based target capture kits.

- Generate whole genome sequences of bacteria, fungi, and viruses
- Achieve >250-fold enrichment of pathogens from NGS libraries
- Easily detect any type of mutation; SNPs, indels, rearrangements

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SBS Genetech Co.,Ltd.

◎ Thermo-stable M-MLV (H-) Reverse Transcriptase US$1.5 per KU for more than 1,000 KU

• H minus Moloney Murine Leukemia Virus (M-MLV) Reverse Transcriptase is a recombinant M-MLV reverse transcriptase. RNase H activity has been eliminated by a point mutation in the RNase H domain of M-MLV RTase, ensuring high yields.

• Deficient RNase H activity to reduce RNA template degradation during the first-strand cDNA synthesis.

• Thermal stability of the reverse transcriptase is improved and the optimal reaction temperature is therefore 50℃.

◎ RNasin (RNase inhibitor) US$10 per KU for more than 100 KU

RNasin is a ribonuclease inhibitor extracted from human placenta with a molecular weight 51 kDa. It inhibits the activity of RNase by specifically binding up to RNase with a non-covalent bond. RNasin, free of RNase or Nickase, can maintain its activity at pH from 5 to 8, and the highest one at pH7.8.

Beijing SBS Genetech Co. Ltd.
Phone: +86-10-62969345,62969346
Email: order@sbsbio.com
Website: www.sbsbio.com

TURNING SCIENCE INTO LIFESAVING CARE

Join us in San Diego for the latest innovative and inspiring cancer research from around the world...**the AACR ANNUAL MEETING 2020!**

REGISTER TODAY!

Become a Member!
Join the AACR and receive a discount on registration.

ABIM CME MOC ACCREDITED
Continuing Medical Education Activity - *AMA PRA Category 1 Credits*™ available

The AACR Annual Meeting highlights the work of the greatest minds in cancer science and medicine from institutions all over the world. This meeting presents the many scientific discoveries across the breadth of cancer research—from prevention, early detection, and interception; to cancer biology, translational, and clinical studies; to survivorship, population science, and advocacy. This year's program, with the theme of "Turning Science into Lifesaving Care," will be a comprehensive, cutting-edge scientific event that you will not want to miss!

We look forward to seeing you!

AACR.ORG • #AACR20

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Cold Spring Harbor Laboratory 2020 Meetings & Courses

Meetings

Systems Biology: Global Regulation of Gene Expression March 11 - 14 / January 20

Neuronal Circuits March 18 - 21 / January 10

From Neuroscience to Artificially Intelligent Systems March 24 - 28 / January 10

Celebrating the Life and Science of Sydney Brenner March 29 - 31 / January 31

The PARP Family & ADP-ribosylation
April 1 - 4 / January 17

JAK-STAT Pathways in Health & Disease
April 6 - 9 / January 17

Gene Expression and Signaling in the Immune System April 14 - 18 / January 24

Protein Homeostasis in Health & Disease
April 21 - 25 / January 31

Genome Organization & Nuclear Function
April 28 - May 2 / February 7

The Biology of Genomes
May 5 - 9 / February 14

Regulatory & Non-Coding RNAs
May 12 - 16 / February 21

Retroviruses May 18 - 23 / February 28

85th Symposium: Genome Stability & Integrity
May 27 - June 1 / March 6

Glia in Health & Disease July 16 - 20 / May 1

Mechanisms & Models of Cancer
August 11 - 15 / May 22

Genome Engineering: CRISPR Frontiers
August 19 - 22 / May 29

Single Biomolecules & their Cellular Context
August 25 - 29 / June 5

Translational Control September 1 - 5 / June 12

Molecular Mechanisms of Neuronal Connectivity September 8 - 12 / June 19

Epigenetics & Chromatin
September 14 - 18 / June 26

Mechanisms of Aging
September 21 - 25 / July 3

Germ Cells
September 29 - October 3 / July 10

Transposable Elements
October 6 - 10 / July 17

Microbiome October 20 - 24 / July 31

Fifty Years of Reverse Transcriptase
October 28 - 31 / August 7

Biological Data Science
November 4 - 7 / August 14

Neurodegenerative Diseases: Biology & Therapeutics
December 2 - 5 / September 18

Courses

Cryoelectron Microscopy
March 9 - 22 / January 15

Quantitative Imaging: From Acquisition to Analysis March 24 - April 7 / January 31

Cell & Dev Biology of *Xenopus*: Gene Discovery & Disease
March 25 - April 7 / January 31

Expression, Purification & Analysis of Proteins & Protein Complexes
March 25 - April 7 / January 31

Advanced Bacterial Genetics
June 2 - 22 / March 1

Ion Channels in Synaptic & Neural Circuit Physiology June 2 - 22 / March 1

Schizophrenia & Related Disorders
June 3 - 10 / March 1

Mouse Development, Stem Cells & Cancer
June 3 - 22 / March 1

Metabolomics
June 6 - 22 / March 1

Pancreatic Cancer
June 15 - 21 / March 1

Statistical Methods for Functional Genomics
June 26 - July 9 / March 15

Advanced Techniques in Molecular Neuroscience June 26 - July 11 / March 15

Single Cell Analysis
June 26 - July 11 / March 15

Drosophila Neurobiology: Genes, Circuits & Behavior June 26 - July 16 / March 15

Frontiers & Techniques in Plant Science
June 26 - July 16 / March 15

Computational Neuroscience: Vision
July 12 - 25 / March 15

Synthetic Biology July 21 - August 3 / April 1

Chromatin, Epigenetics and Gene Expression
July 21 - August 9 / April 1

Imaging Structure & Function in the Nervous System July 21 - August 10 / April 1

Yeast Genetics & Genomics
July 21 - August 10 / April 1

Genetics & Neurobiology of Language
July 27 - August 2 / April 1

Brain Tumors August 4 - 10 / April 1

Proteomics August 5 - 18 / April 1

Neuroscience of Addiction
September 27 - October 4 / May 31

Macromolecular Crystallography
October 13 - 28 / June 15

Programming for Biology
October 13 - 28 / July 15

Antibody Engineering, Phage Display & Immune Repertoire Analysis
October 15 - 28 / July 15

Advanced Sequencing Technologies & Bioinformatics Analysis
November 3 - 15 / August 15

Scientific Writing Retreat
November 11 - 15 / August 15

Computational Genomics
December 2 - 9 / August 15

The Genome Access Course
April 26 - 28 & November 17 - 18 / rolling

Postdoctoral Positions

About SCISSOR
Single-Cell In Situ Spatial Omics at subcellular Resolution (SCISSOR) is a well-supported multidisciplinary program that aims to introduce new paradigms for cancer biology and diagnostics, using spatial and non-spatial omics technologies. Our team comprises of computational biologists (lead: Shyam Prabhakar), oncologists (lead: Iain Tan), biotechnologists (lead: Kok Hao Chen), and pathologists (lead: Tony Lim) with a track record of combining cutting-edge computational and experimental approaches to infer disease mechanisms and develop clinical applications (Chen et al., Science 2015; Li et al., Nat Genet 2017; Sun et al., Cell 2016; Fukawa et al., Nat Med 2016; del Rosario et al., Nat Methods 2015; Kumar et al., Nat Biotechnol 2013; Ku et al., Lancet Oncol 2012).

We are looking for bright, motivated individuals who are interested in working on cutting-edge research projects that leverage single cell and spatial omics. Our interdisciplinary team combines experimental biology, technology development and computational biology to address major questions in cancer biology.

Position 1
Postdoctoral fellow: Machine Learning and Mathematical Analysis of Spatial Transcriptomics Data

Successful candidates will develop and apply algorithms for the analysis of large-scale cancer data. This will be a unique opportunity to lead computational analysis of new types of data in the nascent field of spatial transcriptomics.

Requirements:

- Strong programming skills
- Expertise in mathematics, computer science, statistics, engineering, machine learning, signal processing, computational genomics, or a related field
- General quantitative intuition
- Strong publication record
- Strong communication skills
- The ability to work closely with clinicians and experimental biologists

Position 2
Postdoctoral fellow: Assay Development, Cancer Markers and Mechanisms

Successful candidates will have the opportunity to lead experimental design and execution for a spatial transcriptomics study looking at DNA and RNA changes in a variety of human cancers at subcellular resolution.

Requirements:

- Expertise in cancer biology, immunology, genomics or related fields
- Skilled in molecular and cellular assays
- Strong publication record
- Team player and strong communication skills (oral and written)
- The ability to work closely with clinicians and computational biologists

Benefits:
The Genome Institute of Singapore offers a competitive salary and a complete benefits package that ensures a very high living standard in one of the most modern cities in the world.

About the Organisation
The Genome Institute of Singapore (GIS), A*STAR Research Entities is the national flagship program for genomic science in Singapore. GIS is located within the Biopolis, the biomedical research hub of Singapore, which houses in close proximity research institutes under the Agency of Science, Technology and Research (A*STAR), biotech startups and international pharmaceutical corporations. The applicant would have the opportunity to interact with scientists, bioinformaticians, clinicians, engineers and other professionals from all over the world in a vibrant, intellectually stimulating and scientifically curious setting. You will be part of a vibrant scientific community where you will have the opportunity to share your ideas and demonstrate your skills and passion for scientific research. You can find out more about the Genome Institute of Singapore online: https://www.a-star.edu.sg/gis/.

Why Singapore?
Singapore, a city-state with one of the highest standards of living in the world, is an international hub for the biomedical sciences. Singapore is a tropical city with a rich Asian heritage and modern style of living, and is an ideal gateway to explore Asia providing a unique experience and an excellent quality of life.

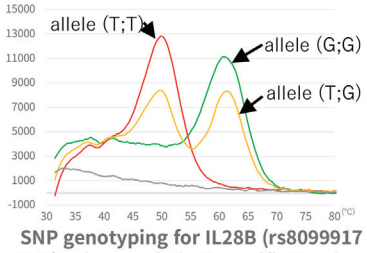
How to Apply
To apply, please email your CV and names of references to: prabhakars@gis.a-star.edu.sg, arulrayan@gis.a-star.edu.sg

Eprobe® / Eprimer™ fluorescent probe

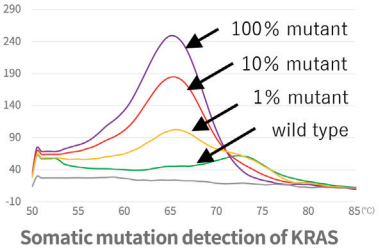
A novel solution for SNP/somatic mutation detection

Eprobe is a DNA-based fluorescent probe which emits fluorescence when specifically binding to a complementary strand. Melting curve analysis after PCR can detect SNP genotype and somatic mutations. Two fluorescent dyes (thiazole orange and thiazole pink) are available.

- **High resolution SNP detection**—Increased Tm (approx.10°C) by the thiazole orange enables a shorter probe design and a clearer distinction of SNPs
- **Simple and highly sensitive somatic mutation detection**—sensitive detection of somatic mutations (down to 0.1%) can be achieved by suppression of PCR amplification of wild-type alleles by Eprobe (PCR clamping)
- **Compatible with most real time PCR instruments**—fluorescence emitted by Eprobe can be detected using a filter for SYBR® Green I* *SYBR® is a registered trademark of Molecular Probes, Inc.
- **Easy to use online design tools**—a design tool for a primer/Eprobe (E-design, www.dnaform.com/edesign2/) and a thermodynamic calculation tool (ECHO, www.dnaform.com/devel/echo/thermodynamics/) are available



SNP genotyping for IL28B (rs8099917 T;G) using an allele G specific Eprobe



Somatic mutation detection of KRAS G12D using an wildtype specific Eprobe.

Fluorphore (excitation/emission)	1.5 nmol	3.0 nmol	5.0 nmol	10.0 nmol
Thiazole orange (510 nm / 530 nm)	19,000 JPY ~~38,000 JPY~~	30,000 JPY ~~60,000 JPY~~	45,000 JPY ~~90,000 JPY~~	70,000 JPY ~~140,000 JPY~~
Thiazole pink (570 nm / 590 nm)	45,000 JPY	70,000 JPY	110,000 JPY	170,000 JPY

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50% OFF the list price!

All Thiazole orange-labeled products

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DISCOVER NEXT

REVEAL STRUCTRUAL VARIATION LIKE NEVER BEFORE WITH BIONANO GENOME IMAGING

The Saphyr System images and analyzes ultra-long, linearized DNA molecules labeled at specific sequence motifs for ultra-sensitive, ultra-specific structural variant detection.

Unparalleled Structural Variation Detection

Genome-wide detection of SVs >500 bp to chromosome-arm length at up to 99% sensitivity and <2% false positive rate

Powerful Complement to Sequencing

Discover novel disease-associated SVs missed by NGS and long-read sequencers with sensitivities down to 1% allele frequency

Confident Answers

High concordance to SVs reported by FISH, karyotyping and chromosomal microarrays

Comprehensive Workflow

Robust and streamlined assay, automated for a short turnaround time as little as 4 days

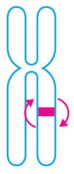
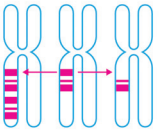
VISIT US AT AACR BOOTH #637

Attend our workshop at AACR to see how Genome imaging is a new breakthrough genomics tool for evaluating the molecular basis of cancer and for studying ecDNA

MONDAY, APRIL 27 | 10:00AM – 11:00 AM

SPOTLIGHT THEATER C

SAPHYR SYSTEM DETECTS VARIANTS OTHER TECHNOLOGIES MISS

				
Homozygous insertions/deletions larger than 500 bp	**Balanced and unbalanced translocations** larger than 50 kbp	**Inversions** large than 30 kbp	**Duplications** larger than 30 kbp	**Copy number variations** larger than 500 kbp
99% sensitivity	**95% sensitivity**	**99% sensitivity**	**97% sensitivity**	**97% sensitivity**

False-positive as low as 2%

Learn more at **www.bionanogenomics.com**.