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small RNA sequencing, De Novo transcriptome assembly, and variant calling & transcriptome epigenetics. In 2018, the expression profiling analysis segment accounted for the largest share of the RNA ...

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NGS-Based RNA-Sequencing Market To Reach USD 4.2 Billion - Applications Of RNA-Seq In Research Industry

Osteocytes are the master regulatory cells within the skeleton. Here, the authors map the transcriptome of osteocytes from diverse skeletal sites, ages and between sexes and

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identify an osteocyte ...

Osteocyte transcriptome mapping identifies a molecular landscape controlling skeletal homeostasis and susceptibility to skeletal disease

These HMM-derived TARs capture the transcriptional activity in the sample,

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limited only by the scRNA-seq
measurement and quality of the genome
assembly ... 1: Generating de novo
features based ...

**Uncovering transcriptional dark
matter via gene annotation
independent single-cell RNA
sequencing analysis**

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We applied sci-RNA-seq to profile nearly 50,000 cells from the nematode ...
Single-molecule combinatorial indexing can be used for haplotype-resolved genome sequencing and de novo genome assembly (20, ...

**Comprehensive single-cell
transcriptional profiling of a**

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multicellular organism

Individuals will be expected to perform routine and project specific data analysis including, but not limited to, de novo assembly, gene prediction and annotation, RNA-Seq, ChIP-Seq, metagenomics ...

Open Position - Postdoctoral

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Researcher

[22,23] Directly sequencing RNA/cDNA offers an alternative approach for high-throughput transcriptome analysis. [37] RNA-Seq is revolutionary in its abilities to provide precision in measuring ...

Next-generation Sequencing and its Applications in Molecular

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Diagnostics

Abstract Recently, long-read sequencing with high accuracy has become a reality. Previous technologies allowed for the detection of particular classes of genetic variation and/or have focused on ...

Application of Long-read Sequencing in Human Genetics

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Mar 23, 2021 (Heraldkeepers) -- Global NGS-based RNA-seq Market Overview: Global NGS-based RNA-seq Market Report 2020 comes with the extensive industry analysis of development components ...

Global NGS-based RNA-seq Market Insights, Overview, Analysis and

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forecast 2021

Sakai H, Naito K, Ogiso-Tanaka E,
Takahashi Y, Iseki K, Muto C, Satou K,
Teruya K, Shiroma A, Shimoji M, Hirano
T, Itoh T, Tomooka N (2015) The power
of single molecule real-time sequencing
technology ...

Bioinformatics Research Unit

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(MENAFN - America News Hour)The global NGS-based RNA-seq Market was valued at USD 0.89 billion in 2016 and is projected to reach USD 4.65billion by 2025, growing at a CAGR of 20.17% from 2017 to 2025.

**NGS-based RNA-Seq Market Is
Projected To Grow At A Moderate**

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CAGR During The Period 2020-2025

1 Howard Hughes Medical Institute, Boston Children's Hospital, Boston, MA 02115, USA. 2 Program in Cellular and Molecular Medicine, Boston Children's Hospital, Boston, MA 02115, USA. 3 Division of ...

Allelic H3K27me3 to allelic DNA

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methylation switch maintains noncanonical imprinting in extraembryonic cells

Obtaining ultra-large DNA molecules is essential for exploiting third generation long-read sequencing technologies ...

This platform can be used to maximise de novo assembly, and has additional ...

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Genomics facility

RNA) under nanoplatfrom using advanced physical and chemical methods. One of such unique and innovative techniques, genome mapping, has been demonstrated in assisting the de novo assembly of ...

Ming Xiao, PhD

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However, by using real-time reverse transcription PCR targeting the gene that encodes the precursor of membrane protein, we detected ZIKV RNA in the ... obtained from de novo assembly and blastn ...

**Zika Virus Infection, Philippines,
2012**

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These results support models in which the timing of chromatin replication and thus assembly plays a key role in maintaining ... Histone modifications are both recycled from parental chromatin and ...

Replication timing maintains the global epigenetic state in human

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cells

Major NGS applications in the characterization of DNA, RNA, methylation, ChIP, and chromatin structure analysis will be described. Topics will cover alignment, whole genome de novo assembly, variant ...

Bioinformatics Track

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Major NGS applications in the characterization of DNA, RNA, methylation, ChIP, and chromatin structure analysis will be described. Topics will cover alignment, whole genome de novo assembly, variant ...

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