IIeasy

Introducing the Genome Analyzer IIe

Easy workflow. Easy data analysis. Easy access to next-gen sequencing. The Illumina® Genome Analyzer IIe delivers proven Illumina technology and industry-leading data quality at an affordable cost.

- Up to 40 Gb of output per run with 2 x 150 bp reads enables an expansive range of applications—including targeted resequencing, RNA-Seq, ChIP-Seq, and small- to medium-sized genome resequencing
- Simplest next-gen sequencing workflow
- Easy-to-us sample prep kits and simplified data analysis
- Flexibility to upgrade to Genome Analyzer IIx performance as your research needs expand

Learn more at www.illumina.com/GAIIe

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Introducing HiSeq™ 2000

Redefining the trajectory of sequencing.

What if you could:

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- Perform gene expression profiling on 200 samples?
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Each in a single run?

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Sequence on a scale never before possible.

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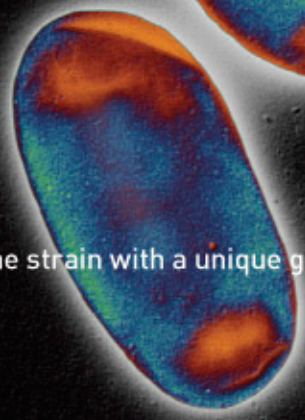
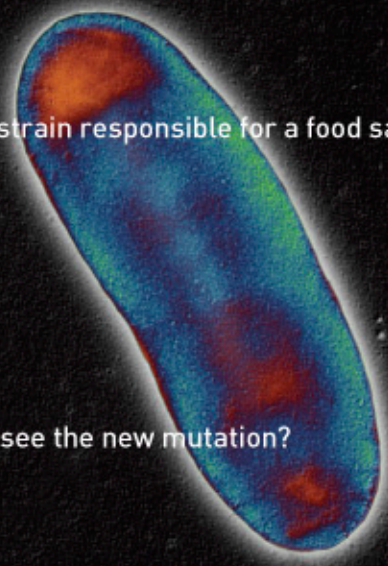
Can you see the pathogenic strain?

SOLiD™ 4
SYSTEM SEQUENCING

Can you see the drug-resistant strain?



Can you see the strain with a unique genetic fingerprint?



Can you see the strain responsible for a food safety outbreak?

Can you see the new mutation?

Introducing the new, more accurate, higher throughput SOLiD™ 4 System.

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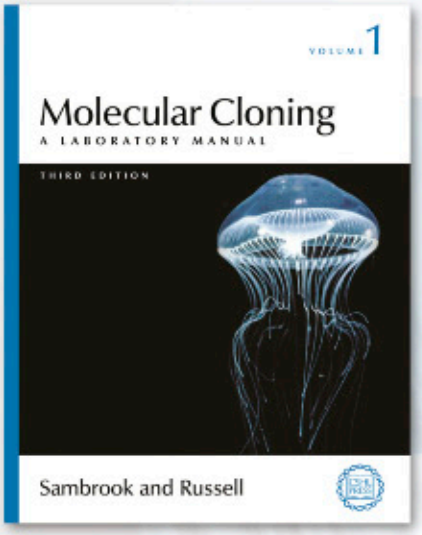

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Position 1 (Molecular/Cellular Bone Biology): The successful candidate will participate in molecular bone biology research projects aimed to identify novel mechanisms of gene regulation for bone formation. Major responsibilities will include performing in vitro and in vivo experiments, such as cell culture, DNA manipulation, Western blot, qPCR, IHC, IF, EMSA. ChIP, genotyping and characterizing knockout and transgenic mice, and analyzing research data. Experience in advanced molecular and cellular biology and genetic mouse models is a plus.

Position 2 (Statistical Genetics and Bioinformatics): The successful candidate will involve in data analysis and method development for genome-wide association studies using genomic and sequence data, data modeling and analysis for epigenomic studies, and integrative analysis of genetic variation at multiple biological levels. Applicants must have background in statistical genetics, bioinformatics, or related areas.

Position 3 (Functional Genomics and Proteomics): The successful candidate will participate in functional genomics and/or proteomics research projects for osteoporosis and related diseases (e.g., genome-wide gene expression analyses using microarrays and proteomics analyses using liquid chromatography and mass spectrometry, etc).

Position 4 (Epigenetics and Epigenomics): The successful candidate will involve in developing and executing research projects related to identification and characterization of epigenetic / epigenomic factors associated with osteoporosis and related diseases. Prior experience in chromatin immunoprecipitaion (ChIP) and/or related techniques (e.g., ChIP-chip, ChIP-seq, reporter assay, etc) is necessary.

Position 5 (Genetic Epidemiology): The successful candidate will participate in genetic epidemiological research projects for osteoporosis and related diseases (e.g., candidate gene and/or genome-wide association studies, DNA re-sequencing studies, nutrigenetic or nutrigenomic studies, etc).

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