# Genome Analyzer$_{IIx}$ System

Illumina's highly scalable Genome Analyzer platform offers an unmatched combination of read lengths, number of reads, and paired-end insert size ranges. With greater output and walk-away simplicity, the Genome Analyzer$_{IIx}$ is even more powerful and easier to use.

## A REVOLUTION IN GENOMICS

Illumina's Genome Analyzer, a proven platform for genetic analysis and functional genomics, has transformed the way experiments are developed and executed. Massively parallel sequencing technology leverages clonal cluster formation and proprietary reversible terminator chemistry to dramatically improve the speed, and reduce the cost, of large-scale sequencing.

## BROADEST APPLICATIONS FLEXIBILITY

The Genome Analyzer supports a wide range of applications, including whole-genome and candidate region

resequencing, transcriptome analysis, small RNA discovery, methylation profiling, and protein-nucleic acid interaction analysis at a genome-wide scale.

## SIMPLE, FAST, AND AUTOMATED

The Genome Analyzer system offers the simplest and fastest workflow for a broad range of high-throughput sequencing applications. Sample libraries are prepared in just a few hours with ready-to-use kits. Clonal clusters are automatically generated on Illumina Genome Analyzer flow cells using the Cluster Station. In less than five hours, up to twelve multiplexed samples can be isothermally amplified in each flow cell channel.

Illumina Sequencing technology provides an easy-to-use protocol that does not require emulsion PCR. This allows for a self-contained system that minimizes handling errors and contamination concerns, eliminating the need for robotics or clean rooms. The system is designed to fit in any lab, from individual research labs to core labs and genome centers. The streamlined workflow of the Genome Analyzer$_{IIx}$ system enables generation of meaningful data quickly and efficiently, while reducing project timelines and costs (*Figure* 1). Walk-away automation is available for reads in excess of 100 bp.

## SCALABLE ULTRA-HIGH OUTPUT

The scalable nature of Illumina's sequencing technology delivers

**FIGURE 1: GENOME ANALYZER$_{IIx}$ SYSTEM**

The Genome Analyzer$_{IIx}$ provides an improved reagent cooler system for a faster, easier workflow and a new manifold designed to increase the imaging area by 20%.

unmatched data densities and output, supporting more complex projects at lower costs. Cluster density improvements, sequencing chemistry modifications, and informatics advances allow for future sequencing yield expansion on the Genome Analyzer.

## HIGHEST YIELD OF QUALITY DATA

The quality of raw data generated by a sequencing system is the most fundamentally important factor in the success of an experiment. The high accuracy of Genome Analyzer data, with quality metrics available for each base sequenced, allows a given experiment to be conducted with fewer runs and with higher confidence.

---

### GENOME ANALYZER HIGHLIGHTS

- **Broadest Applications Flexibility**: Study the genome, epigenome, and transcriptome

- **Simplest Workflow**: Reduce hands-on time with easy-to-use reagents and walk-away automation for > 100 sequencing cycles

- **Broadest Spectrum of Genomic Variation:** Characterize short- and long-insert paired-end reads with insert sizes from 200 bp to 5 kb

- **Unmatched Combination of Read Length and Number of Reads:** Achieve 2 × 75 bp reads and > 300 million reads per paired-end run

- **Unrivaled Output**: Generate the highest throughput per day and highest output of perfect reads per run

---

illumina®

## NOVEL SEQUENCING CHEMISTRY

The Genome Analyzer uses sequencing by synthesis (SBS) to support massively parallel sequencing. Based on novel reversible fluorescently labeled terminators, this technology allows detection of single-base incorporation events into growing DNA strands. Since all four reversible-terminator dNTPs are present during each sequencing cycle, natural competition minimizes incorporation bias. Homopolymers pose no problem because each cycle interrogates only one base at a time per template. The reversible terminator chemistry ensures strict base-by-base sequencing.

## SINGLE OR PAIRED-END SUPPORT

The Genome Analyzer system supports sequencing of both single-read and paired-end libraries. It is the only platform available that offers a short-insert paired-end capability for high-resolution sequencing as well as long-insert paired-end reads for efficient sequence assembly, *de novo* sequencing, and large-scale structural variation detection. Illumina's simple library construction protocol minimizes the time from sample isolation to usable results. Single-read or short-insert paired-end sample preparation of genomic DNA takes as few as six hours with only three hours of hands-on time. The combination of short inserts and 2 × 75 bp or longer reads increases the ability to align and sample the genome, expanding the Genome Analyzer's utility for other applications.

## LOW INPUT REQUIREMENTS

The Genome Analyzer System requires sample inputs as low as 100 ng, enabling a host of applica-

## AUTOMATED WORKFLOW

### 1. SAMPLE PREPARATION

~6 hours (~3 hours hands-on)

- Sample collection, genomic DNA sheared
- DNA end-repair
- Adapter ligation

### 2. CLUSTER GENERATION

~5 hours (~10 min. preparation)

- Flow cell and pre-filled reagents placed into Cluster Station
- Samples applied to flow cell
- Complete walk-away automation

### 3. SEQUENCING BY SYNTHESIS

~5 days for 2 × 35 bp  (~10 min. preparation)

- Flow cell and pre-filled reagents placed on Genome Analyzer
- Complete walk-away automation, including support for longer reads

### 4. PAIRED-END MODULE

- Add-on module for automated reagent delivery
- Second read prepared and sequenced while flow cell remains on Genome Analyzer

### 5. DATA ANALYSIS
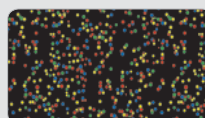
~1–2 days

- Real-time image analysis
- Data transfer to automated analysis pipeline
- Automated base calling
- Paired-end alignment
- Polymorphism detection

---

tions where sample is limited (e.g., immunoprecipitates, laser-dissected materials, and small model systems).

## DATA ANALYSIS SUPPORT

The analysis software and hardware included with the Genome Analyzer contribute to an end-to-end sequencing approach that enables researchers to rapidly move from raw data acquisition to publishable, biologically meaningful results. Illumina's Sequencing Control Software (SCS) offers real-time analysis processing that automatically produces image

intensities and quality-scored base calls directly on the instrument computer. These reads can be aligned to a reference sequence and analyzed using the Pipeline analysis software. In combination with the Consensus Assessment of Sequence and Variation (CASAVA) software, GenomeStudio™ data analysis software provides intuitive, graphical analysis and interaction with DNA and RNA data.

## PRODUCTS AND CATALOG NUMBERS FOR GENOME ANALYZER$_{IIx}$ APPLICATIONS

| APPLICATION | LIBRARY PREPARATION | CLUSTER GENERATION | SEQUENCING |
|---|---|---|---|
| **DNA Sequencing** | | | |
| **Genomic DNA Paired-End Library Sequencing (200 bp–500 bp inserts)** | Paired-End Genomic DNA Sample Prep Kit | Paired-End Cluster Generation Kit | Standard Sequencing Kit (36 cycle) |
| *Catalog Number* | *PE-102-1001* | *PE-203-2001* | *FC-104-3002* |
| **Mate Pair Library Sequencing (2 kb–5 kb inserts)** | Mate Pair Library Prep Kit | Paired-End Cluster Generation Kit | Standard Sequencing Kit (36 cycle) |
| *Catalog Number* | *PE-112-1002* | *PE-203-2001* | *FC-104-3002* |
| **Genomic DNA Single-Read Sequencing** | Genomic DNA Sample Prep Kit | Single-Read Cluster Generation Kit | Standard Sequencing Kit (36 cycle) |
| *Catalog Number* | *FC-102-1001* | *GD-203-2001* | *FC-104-3002* |
| **Transcriptome Analysis** | | | |
| **mRNA-Seq (full-length cDNA sequencing)** | mRNA-Seq Sample Prep Kit | Single-Read Cluster Generation Kit | Standard Sequencing Kit (36 cycle) |
| *Catalog Number* | *RS-100-0801* | *GD-203-2001* | *FC-104-3002* |
| **mRNA Tag Profiling (16 or 17 bp mRNA tags)** | Tag Profiling Sample Prep Kit | Tag Profiling Cluster Generation Kit | Standard Sequencing Kit (18 cycle) |
| *Catalog Number* | *FC-102-1007 (DpnII)* *FC-102-1005 (NlaIII)* | *RS-410-0122 (DpnII)* *RS-310-0122 (NlaIII)* | *FC-104-3001* |
| **Small RNA Discovery and Analysis** | Small RNA Sample Prep Kit | Small RNA Cluster Generation Kit | Standard Sequencing Kit (36 cycle) |
| *Catalog Number* | *FC-102-1009* | *RS-220-0122* | *FC-104-3002* |
| **Gene Regulation and Control Analysis** | | | |
| **Protein-Nucleic Acid Interaction Analysis** | ChIP-Seq Sample Prep Kit | Single-Read Cluster Generation Kit | Standard Sequencing Kit (36 cycle) |
| *Catalog Number* | *IP-102-1001* | *GD-203-2001* | *FC-104-3002* |
| **Sample Multiplexing** | | | |
| **Multiplex up to 12 samples per flow cell channel** | Multiplexing Sample Prep Oligonucleotide Kit | Single-Read or Paired-End Cluster Generation Kit | Standard Sequencing Kits (36 cycle) FC-104-3002 |
| *Catalog Number* | *PE-400-1001* | *GD-203-2001* *PE-203-2001* | Multiplexing Sequencing Primer Kit *PE-400-2002* |

## PERFORMANCE PARAMETERS*

| READ LENGTH† | RUN TIME (DAYS) | # OF READS (PER FLOW CELL) | HIGH-QUALITY OUTPUT (GB)‡ | HIGH-QUALITY OUTPUT (GB PER DAY)‡ | BASE CALLS WITH Q ≥ 30 | PER BASE READ ACCURACY | % PERFECT READS |
|---|---|---|---|---|---|---|---|
| 1 × 35 bp | ~ 2.5 | 138–168 million | 4.5–6 | ~ 1.8–2.4 | 70–85% | ≥ 99% | ≥ 90% |
| 2 × 35 bp | ~ 5 | 138–168 million | 9.5–11.5 | ~ 1.9–2.3 | 70–85% | ≥ 99% | ≥ 90% |
| 2 × 50 bp | ~ 6.5 | 138–168 million | 13.5–16.5 | ~ 2.0–2.5 | 70–85% | > 98.5% | ≥ 80% |
| 2 × 75 bp | ~ 9.5 | 138–168 million | 20.5–25 | ~ 2.1–2.6 | > 70% | ≥ 98.5% | ≥ 70% |

### SAMPLES

**Throughput:** eight channels per flowcell, up to 12 samples per channel
**Input requirement:** 0.1–1.0 µg (single- and paired-end reads), 10 µg (Mate Pair reads)
**Genomic DNA sample prep:** 3 hours hands-on, 6 hours total for single or paired-end libraries
**Flow cell:** Genome Analyzer$_{IIx}$ uses 1.4 mm channel flow cell

### SERVICE AND SUPPORT

Illumina will ensure that your Genome Analyzer system is properly installed and qualified, and will provide ongoing maintenance and service. This industry-leading support is available in North America, Europe, and Asia.

\* gDNA sequencing output generated with cluster densities between 144,000 and 176,000 clusters per tile that pass filtering on a Genome Analyzer$_{IIx}$ using Sequencing Control Software (SCS) 2.4 and SBS v3 kits with data analyzed using Pipeline software v1.4.

† 2 × 75 bp reads supported.

‡ Data generated from clusters that pass Pipeline software v1.4 quality filters.

## SPECIFICATIONS FOR THE GENOME ANALYZER$_{IIx}$ SYSTEM

| ILLUMINA GENOME ANALYZER | ILLUMINA CLUSTER STATION | ILLUMINA PAIRED-END MODULE |
|---|---|---|
| **CATALOG NUMBER** | | |
| SY-301-1301 | SY-301-2001 | SE-301-1002 |
| **INSTRUMENT CONFIGURATION** | | |
| CE Marked and ETL Listed instrument | CE Marked and ETL Listed instrument | CE Marked and ETL Listed instrument |
| Computer and flat panel display | Computer and flat panel display | Installation setup and accessories |
| Installation setup and accessories | Installation setup and accessories | |
| Data collection and analysis software | | |
| **INSTRUMENT CONTROL COMPUTER** | | |
| Base Unit: 3.6 GHz Dual Processor | Base Unit: 2.8 GHz Processor | |
| Memory: 4 GB RAM | Memory: 512 MB RAM | |
| Hard Drive: 4 × 300 GB SCSI | Hard Drive: 80 GB | |
| Operating System: Windows XP | Operating System: Windows XP | |
| Monitor: 19" LCD flat panel | Monitor: 17" LCD flat panel | |
| Note: The computer specifications may be regularly upgraded. Contact your local Account Manager for current configuration. | | |
| **OPERATING ENVIRONMENT** | | |
| Temperature: 22°C ± 3°C | Temperature: 22°C ± 3°C | Temperature: 22°C ± 3°C |
| Humidity: Non-Condensing 20%–80% | Humidity: Non-Condensing 20%–80% | Humidity: Non-Condensing 20%–80% |
| Altitude: Less than 2,000 m (6,500 ft) | Altitude: Less than 2,000 m (6,500 ft) | Altitude: Less than 2,000 m (6,500 ft) |
| Air Quality: Pollution Degree Rating of II | Air Quality: Pollution Degree Rating of II | Air Quality: Pollution Degree Rating of II |
| Ventilation: Maximum of 3400 Btu/h (1000W) | | |
| For Indoor Use Only | For Indoor Use Only | For Indoor Use Only |
| **LASER** | | |
| 3 laser system: 660, 635, and 532 nm | | |
| **DIMENSIONS** | | |
| W×D×H: 102 cm × 67 cm × 92 cm | W×D×H: 58 cm × 62 cm × 38 cm | W×D×H: 24 cm × 61 cm × 44 cm |
| Weight: 187 kg | Weight: 27 kg | Weight: 13 kg |
| Crated Weight: 232 kg | Crated Weight: 41 kg | Crated Weight: 34 kg |
| **POWER REQUIREMENTS** | | |
| 100–240V AC 50/60 Hz, 20A, 900 Watts | 100–240V AC 50/60 Hz, 15A, 750 Watts | 100–240V AC 50/60 Hz, 3A Max, 250 Watts |
| Illumina recommends an uninterruptible power supply (UPS) with an output capacity of at least 3 kVA. | | |
| **INSTRUMENT BENCH** | | |
| Illumina recommends a movable table with locking casters capable of supporting the weight of the instrument and computers. | | |

### ADDITIONAL INFORMATION

Visit our website or contact us to learn more about Illumina Sequencing products and services. Contact Customer Solutions for the most up-to-date throughput specifications.

**Illumina, Inc.**
**Customer Solutions**
9885 Towne Centre Drive
San Diego, CA 92121-1975
1.800.809.4566 (toll free)
1.858.202.4566 (outside the U.S.)
techsupport@illumina.com
www.illumina.com

**FOR RESEARCH USE ONLY**

illumina®