

Genome Sequencer FLX System

More Flexibility, More Applications, More Publications



ChIP Sequencing/Epigenetics

Albert, I. *et al.* "Translational and rotational settings of H2A.Z nucleosomes across the *Saccharomyces cerevisiae* genome." *Nature* **446** (7135), 572-576 (2007).

Bhinge, A.A. *et al.* "Mapping the chromosomal targets of STAT1 by Sequence Tag Analysis of Genomic Enrichment (STAGE)." *Genome Research* **17** (6), 910-916 (2007).

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Dostie, J. *et al.* "Chromosome conformation capture carbon copy (5C): a massively parallel solution for mapping interactions between genomic elements." *Genome Research* **16** (10), 1299-1309 (2006).

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Swaminathan, K., Varala, K., and Hudson, M.E. "Global repeat discovery and estimation of genomic copy number in a large, complex genome using a high-throughput 454 sequence survey." *BMC Genomics* **8**, 132 (2007).



In a single instrument run, the Genome Sequencer FLX System generates over 400,000 reads of 250 to 300 bases with 99.5% accuracy per read.

Ancient DNA

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Noonan, J.P. *et al.* "Sequencing and analysis of Neanderthal genomic DNA." *Science* **314** (5802), 1113-1118 (2006).

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Andries, K. *et al.* "A diarylquinoline drug active on the ATP synthase of *Mycobacterium tuberculosis*." *Science* **307** (5707), 223-227 (2005).

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- Highlander, S.K. *et al.* "Subtle genetic changes enhance virulence of methicillin resistant and sensitive *Staphylococcus aureus*." *BMC Microbiology* **7**, 99 (2007).
- Hiller, N.L. *et al.* "Comparative genomic analyses of seventeen *Streptococcus pneumoniae* strains: insights into the pneumococcal supragenome." *Journal of Bacteriology* **189** (22), 8186-8195 (2007).
- Hofreuter, D. *et al.* "Unique features of a highly pathogenic *Campylobacter jejuni* strain." *Infection and Immunity* **74** (8), 4694-4707 (2006).
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- Pol, A. *et al.* "Methanotrophy below pH 1 by a new *Verrucomicrobia* species." *Nature* **450** (7171), 874-878 (2007).
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- Thomas, J.A. *et al.* "Complete genomic sequence and mass spectrometric analysis of highly diverse, atypical *Bacillus thuringiensis* phage 0305varphi8-36." *Virology* **368** (2), 405-421 (2007).
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- Velicer, G.J. *et al.* "Comprehensive mutation identification in an evolved bacterial cooperater and its cheating ancestor." *Proc. Natl. Acad. Sci. USA* **103** (21), 8107-8112 (2006).
- Velasco, R. *et al.* "A high quality draft consensus sequence of the genome of a heterozygous grapevine variety." *PLoS One* **2** (12), e1326 (2007).
- Wackett, L.P. *et al.* "Genomic and biochemical studies demonstrating the absence of an alkane-producing phenotype in *Vibrio furnissii* M1." *Applied and Environmental Microbiology* **73** (22), 7192-7198 (2007).
- Zuber, S. *et al.* "Genome analysis of phage JS98 defines a fourth major subgroup of T4-like phages in *Escherichia coli*." *Journal of Bacteriology* **189** (22), 8206-8214 (2007).

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NEW indicates journal articles that have been published since December 21, 2007.

Transcriptomes

- Bainbridge, M.N. *et al.* "Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach." *BMC Genomics* **7**, 246 (2006).
- Barbazuk, W.B. *et al.* "SNP discovery via 454 transcriptome sequencing." *The Plant Journal* **51** (5), 910-918 (2007).
- Cheung, F. *et al.* "Sequencing *Medicago truncatula* expressed sequenced tags using 454 Life Sciences technology." *BMC Genomics* **7**, 272 (2006).
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- Gowda, M. *et al.* "Robust analysis of 5'-transcript ends (5'-RATE): a novel technique for transcriptome analysis and genome annotation." *Nucleic Acids Research* **34** (19), e126 (2006).
- Jones-Rhoades M.W., Borevitz J.O., and Preuss, D. "Genome-wide expression profiling of the *Arabidopsis* female gametophyte identifies families of small, secreted proteins." *PLoS Genetics* **3** (10), e171 (2007).
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Albert, T.J. *et al.* "Direct selection of human genomic loci by microarray hybridization." *Nature Methods* **4** (11), 903-905 (2007).

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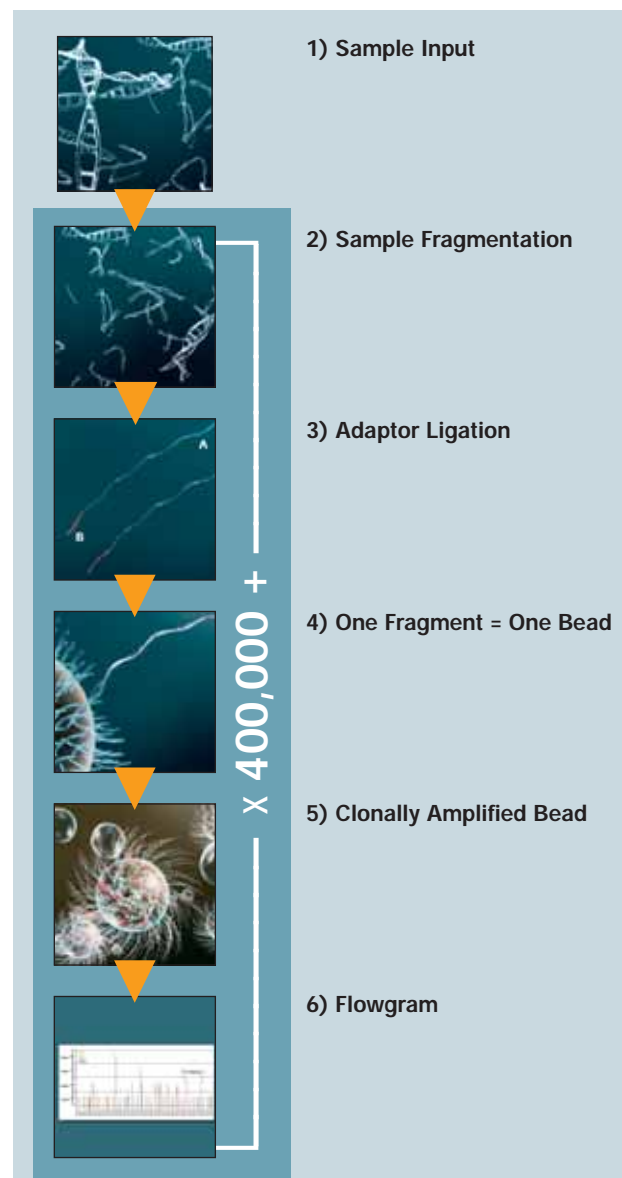
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