

Genome Sequencer FLX System

More Flexibility, More Applications, More Publications



HIV Studies

Hoffmann, C. *et al.* "DNA bar coding and pyrosequencing to identify rare HIV drug resistance mutations." *Nucleic Acids Research* **35** (13), e91 (2007).

Wang, C. *et al.* "Characterization of mutation spectra with ultra-deep pyrosequencing: Application to HIV-1 drug resistance." *Genome Research* **17** (8), 1195-1201 (2007).

Wang, G.P. *et al.* "HIV integration site selection: Analysis by massively parallel pyrosequencing reveals association with epigenetic modifications." *Genome Research* **17** (8), 1186-1194 (2007).

BACs/Plastids/Mitochondria/*etc.*

NEW Baker, S. *et al.* "A novel linear plasmid mediates flagellar variation in *Salmonella Typhi*." *PLoS Pathogens* **3** (5), e59 (2007).

Cai, Z. *et al.* "Complete plastid genome sequences of *Drimys*, *Liriodendron*, and *Piper*: implications for the phylogenetic relationships of magnoliids." *BMC Evolutionary Biology* **6**, 77 (2006).

Cuadros-Orellana, S. *et al.* "Genomic plasticity in prokaryotes: the case of the square haloarchaeon." *The ISME Journal* **1** (3), 235-245 (2007).

NEW Jex, A.R. *et al.* "Using 454 technology for long-PCR based sequencing of the complete mitochondrial genome from single *Haemonchus contortus* (Nematoda)." *BMC Genomics* **9**, 11 (2008).

Meyer, M. *et al.* "Targeted high-throughput sequencing of tagged nucleic acid samples." *Nucleic Acids Research* **35** (15), e97 (2007).

Moore, M.J. *et al.* "Rapid and accurate pyrosequencing of angiosperm plastid genomes." *BMC Plant Biology* **6**, 17 (2006).

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

Metagenomics and Microbial Diversity

Angly, F.E. *et al.* "The marine viromes of four oceanic regions." *PLoS Biology*, **4** (11), e368 (2006).

Cox-Foster, D.L. *et al.* "A metagenomic survey of microbes in honey bee colony collapse disorder." *Science* **318** (5848), 283-287 (2007).

Edwards, R.A. *et al.* "Using pyrosequencing to shed light on deep mine microbial ecology." *BMC Genomics* **7**, 57 (2006).

Huber, J.A. *et al.* "Microbial population structures in the deep marine biosphere." *Science* **318** (5847), 97-100 (2007).

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Krause, L. *et al.* "Finding novel genes in bacterial communities isolated from the environment." *Bioinformatics* **22** (14), e281-e289 (2006).

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NEW Palacios, G. *et al.* "A new arenavirus in a cluster of fatal transplant-associated diseases." *The New England Journal of Medicine* **358**; published at www.nejm.org on February 6, 2008; doi:10.1056/NEJMoa073785 (2008).

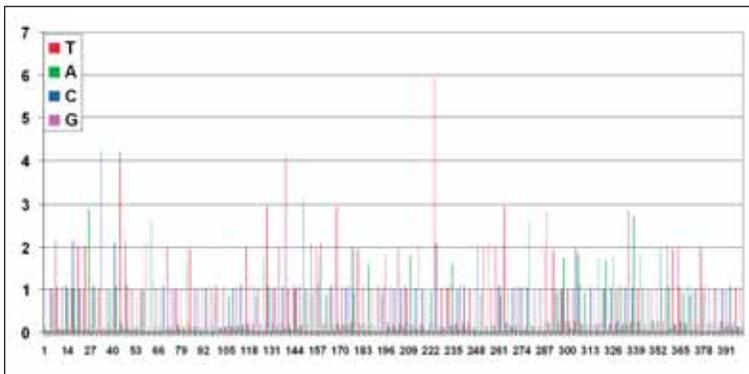
Sogin, M.L. *et al.* "Microbial diversity in the deep sea and the underexplored 'rare biosphere'." *Proc. Natl. Acad. Sci. USA* **103** (32), 12115-12120 (2006).

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Warnecke, F. *et al.* "Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite." *Nature* **450** (7169), 560-565 (2007).

Wegley, L. *et al.* "Metagenomic analysis of the microbial community associated with the coral *Porites astreoides*." *Environmental Microbiology* **9** (11), 2707-2719 (2007).



Flowgram showing a single read of 256 bases. Each bar represents a discrete base (A, T, C, or G), and the height of a bar correlates to the number of bases in a specific position.

ChIP Sequencing/Epigenetics

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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).

NEW Boyle, A.P. *et al.* "High-resolution mapping and characterization of open chromatin across the genome." *Cell* **132** (2), 311-322 (2008).

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).

Johnson, S.M. *et al.* "Flexibility and constraint in the nucleosome core landscape of *Caenorhabditis elegans* chromatin." *Genome Research* **16** (12), 1505-1516 (2006).

Korbel, J.O. *et al.* "Paired-end mapping reveals extensive structural variation in the human genome." *Science* **318** (5849), 420-426 (2007).

Nagel, S. *et al.* "Activation of *TLX3* and *NKX2-5* in t(5;14)(q35;q32) T-Cell acute lymphoblastic leukemia by remote 3'-*BCL11B* enhancers and coregulation by PU.1 and HMGA1." *Cancer Research* **67** (4), 1461-1471 (2007).

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

Briggs, A.W. *et al.* "Patterns of damage in genomic DNA sequences from a Neandertal." *Proc. Natl. Acad. Sci. USA* **104** (37), 14616-14621 (2007).

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Green, R.E. *et al.* "Analysis of one million base pairs of Neanderthal DNA." *Nature*, **444** (7117), 330-336 (2006).

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

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Whole Genome Sequencing

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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Chen, Y. *et al.* "The genome of non-O1 *Vibrio cholerae* NRT36S demonstrates the presence of pathogenic mechanisms that are distinct from O1 *Vibrio cholerae*." *Infection and Immunity*, **75** (5), 2645-2647 (2007).

Deng, L. *et al.* "Identification of novel antipoxviral agents: mitoxantrone inhibits vaccinia virus replication by blocking virion assembly." *Journal of Virology* **81** (24), 13392-13402 (2007).

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Hallen, H.E. *et al.* "Gene family encoding the major toxins of lethal *Amanita* mushrooms." *Proc. Natl. Acad. Sci. USA* **104** (48), 19097-19101 (2007).

Whole Genome Sequencing (continued)

- 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).
- Hogg, J.S. *et al.* "Characterization and modeling of the *Haemophilus influenzae* core- and supra-genomes based on the complete genomic sequences of Rd and 12 clinical nontypeable strains." *Genome Biology* **8** (6), R103 (2007).
- Lasken, R.S. and Stockwell, T.B. "Mechanism of chimera formation during the Multiple Displacement Amplification Reaction." *BMC Biotechnology* **7**, 19 (2007).
- Macas, J., Neumann, P., and Navratilova, A. "Repetitive DNA in the pea (*Pisum sativum* L.) genome: comprehensive characterization using 454 sequencing and comparison to soybean and *Medicago truncatula*." *BMC Genomics* **8**, 427 (2007).
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- NEW** Mouton, L. *et al.* "Variable-number tandem repeats as molecular markers for biotypes of *Pasteuria ramosa* in *Daphnia* spp." *Applied and Environmental Microbiology* **73** (11), 3715-3718 (2007).
- Mußmann, M. *et al.* "Insights into the genome of large sulfur bacteria revealed by analysis of single filaments." *PLoS Biology* **5** (9), e230 (2007).
- Oh, J.D. *et al.* "The complete genome sequence of a chronic atrophic gastritis *Helicobacter pylori* strain: evolution during disease progression." *Proc. Natl. Acad. Sci. USA* **103** (26), 9999-10004 (2006).
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- Pinard, R. *et al.* "Assessment of whole genome amplification-induced bias through high-throughput, massively parallel whole genome sequencing." *BMC Genomics* **7**, 216 (2006).
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- Poly, F. *et al.* "Genome sequence of a clinical isolate of *Campylobacter jejuni* from Thailand." *Infection and Immunity* **75** (7), 3425-3433 (2007).
- Raymond, J.A., Fritsen, C., and Shen, K. "An ice-binding protein from an Antarctic sea ice bacterium." *FEMS Microbiology Ecology* **61** (2), 214-221 (2007).
- Smith, M.G. *et al.* "New insights into *Acinetobacter baumannii* pathogenesis revealed by high-density pyrosequencing and transposon mutagenesis." *Genes & Development* **21** (5), 614 (2007).
- NEW** Swingley, W.D. *et al.* "Niche adaptation and genome expansion in the chlorophyll *d*-producing cyanobacterium *Acaryochloris marina*." *Proc. Natl. Acad. Sci. USA* **105** (6), 2005-2010 (2008).
- 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).
- Thomson, N.R. *et al.* "*Chlamydia trachomatis*: genome sequence analysis of lymphogranuloma venereum isolates." *Genome Research* **18** (1), 161-171 (2008).
- Velicer, G.J. *et al.* "Comprehensive mutation identification in an evolved bacterial cooperator 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).
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- Cheung, F. *et al.* "Sequencing *Medicago truncatula* expressed sequenced tags using 454 Life Sciences technology." *BMC Genomics* **7**, 272 (2006).
- Emrich, S.J. *et al.* "Gene discovery and annotation using LCM-454 transcriptome sequencing." *Genome Research* **17** (1), 69-73 (2007).
- Eveland, A.L., McCarty, D.R., and Koch, K.E. "Transcript profiling by 3'-untranslated region sequencing resolves expression of gene families." *Plant Physiology* **146** (1), 32-44 (2008).
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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).
- Ng, P. *et al.* "Multiplex sequencing of paired-end ditags (MS-PET): a strategy for the ultra-high-throughput analysis of transcriptomes and genomes." *Nucleic Acids Research* **34** (12), e84 (2006).
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- Robb, S.M., Ross, E., and Alvarado, A.S. "SmedGD: the *Schmidtea mediterranea* genome database." *Nucleic Acids Research* **36** (Database issue), D599-D606 (2008).
- Ruan, Y. *et al.* "Fusion transcripts and transcribed retro-transposed loci discovered through comprehensive transcriptome analysis using Paired-End diTags (PETs)." *Genome Research* **17** (6), 828-838 (2007).

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Amplicons and Methylation

- Binladen, J. *et al.* "The use of coded PCR primers enables high-throughput sequencing of multiple homolog amplification products by 454 parallel sequencing." *PLoS ONE* **2** (2), e197 (2007).
- Dahl, F. *et al.* "Multigene amplification and massively parallel sequencing for cancer mutation discovery." *Proc. Natl. Acad. Sci. USA* **104** (22), 9387-9392 (2007).
- Korshunova, Y. *et al.* "Massively parallel bisulphite pyrosequencing reveals the molecular complexity of breast cancer-associated cytosine-methylation patterns obtained from tissue and serum DNA." *Genome Research* **18** (1), 19-29 (2008).
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- Thomas, R.K. *et al.* "Sensitive mutation detection in heterogeneous cancer specimens by massively parallel picoliter reactor sequencing." *Nature Medicine* **12** (7), 852-855 (2006).
- Thomas, R.K. *et al.* "High-throughput oncogene mutation profiling in human cancer." *Nature Genetics* **39** (3), 347-351 (2007).

Technology and Bioinformatics

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Sequence Capture Arrays (Sample Enrichment)

Albert, T.J. *et al.* "Direct selection of human genomic loci by microarray hybridization." *Nature Methods* **4** (11), 903-905 (2007).

Small RNA

Aravin, A.A. *et al.* "Developmentally regulated piRNA clusters implicate MILI in transposon control." *Science* **316** (5825), 744-747 (2007).

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Berezikov, E. *et al.* "Diversity of microRNAs in human and chimpanzee brain." *Nature Genetics* **38** (12), 1375-1377 (2006).

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Burnside, J. *et al.* "Marek's disease virus encodes microRNAs that map to *meq* and the latency-associated transcript." *Journal of Virology* **80** (17), 8778-8786 (2006).

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Girard, A. *et al.* "A germline-specific class of small RNAs binds mammalian Piwi proteins." *Nature* **442** (7099), 199-202 (2006).

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Lau, N.C. *et al.* "Characterization of the piRNA complex from rat testes." *Science* **313** (5785), 363-367 (2006).

Lu, C. *et al.* "MicroRNAs and other small RNAs enriched in the *Arabidopsis* RNA-dependent RNA polymerase-2 mutant." *Genome Research* **16** (10), 1276-1288 (2006).

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Pak, J. and Fire, A. "Distinct populations of primary and secondary effectors during RNAi in *C. elegans*." *Science* **315** (5809), 241-244 (2007).

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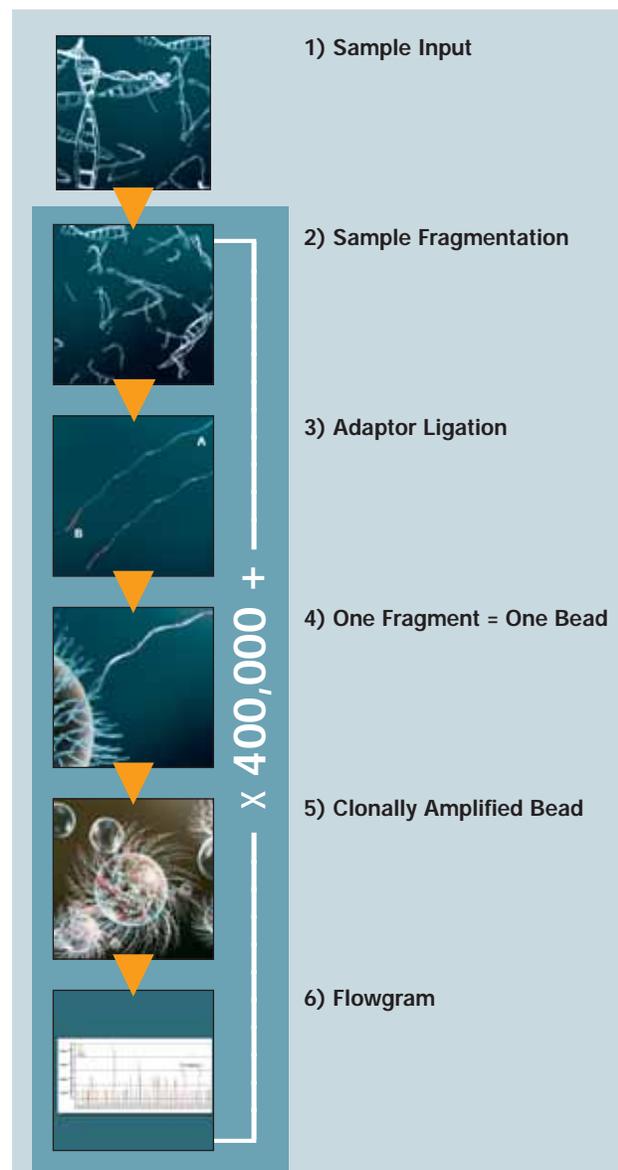
Zhang, X. *et al.* "Role of RNA polymerase IV in plant small RNA metabolism." *Proc. Natl. Acad. Sci. USA* **104** (11), 4536-4541 (2007).

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