# SOLiD® Next Generation Sequencing Publications & Literature

All the latest scientific publications using the SOLiD System, as well as brochures, application notes, protocols, and other product literature from Applied Biosystems.

## Platform/Technology

**NGSQC: cross-platform quality analysis pipeline for deep sequencing data**
Publication: BMC Genomics
Authors: Dai, et al.

**Applied Biosystems SOLiD™ System: Ligation-Based Sequencing**
Publication: Next Generation Genome Sequencing: Towards Personalized Medicine
Authors: Pandey V, Nutter RC, Prediger E (2008), Wiley, pages 29-41

**New Frontiers in Plant Functional Genomics Using Next Generation Sequencing Technologies**
Publication: New Frontiers in Plant Functional Genomics Using Next Generation Sequencing Technologies

## Accuracy of the SOLiD™ System

**Large-scale detection and analysis of RNA editing in grape mtDNA by RNA deep-sequencing**
Publication: Acids Research (2010)
Authors: Picardi, et al.

**U87MG Decoded: The genomic sequence of a cytogenetically aberrant human cancer cell line**
Authors: Smith, et al.

[View more](http://www.lifetechnologies.com/uk/en/home/life-science/seq...

## Automation

**Semi-Automated library preparation for high-throughput DNA sequencing platforms**
Publication: Journal of Biomedicine and Biotechnology, Volume 2010, Article ID 617469
Authors: Farias-Hesson, et al.

## Bioinformatics

**ZOOM Lite: next-generation sequencing data mapping and visualization software**
Publication: Nucleic Acids Research (2011)
Authors: Zhang Z. et al.

**Sniper: Improved SNP discovery by multiply mapping deep sequenced reads**
Publication: Genome Biology (2011)
Authors: Simola D. et al.

**A framework for variation discovery and genotyping using next-generation DNA sequencing data**
Publication: Nature Genetics (2011)
Authors: De Pristo M. A, et al.

**HapEdit: an accuracy assessment viewer for haplotype assembly using massively parallel DNA-sequencing technologies**
Publication: Nucleic Acids Research (2011)
Authors: Kim et al.

**Analysis of quality raw data of second generation sequencers with Quality Assessment Software**
Publication: BMC Research Notes (2011)
Authors: Ramos R. et al.

**SHRiMP2: Sensitive yet Practical Short Read Mapping**
Publication: Bioinformatics (2011)
Authors: David M. et al.
## Whole Genome Resequencing

- **Fosmid-based whole genome haplotyping of a HapMap trio child: evaluation of single individual haplotyping techniques**  
  Publication: Nucleic Acids Research (2011)  
  Authors: Duitama J. et al.
- **Comparative analysis of the complete genome sequences of two Australian origin live attenuated vaccines of infectious laryngotracheitis virus**  
  Publication: Vaccine (2011)  
  Authors: Lee Sang-Won et al.
- **Multiple emergences of genetically diverse amphibian-infecting chytrids include a globalized hypervirulent recombinant lineage**  
  Publication: PNAS (2011)  
  Authors: Farrer R.A. et al.
- **Chromothripsis as a mechanism driving complex de novo structural rearrangements in the germline**  
  Publication: Human Molecular Genetics (2011)  
  Authors: Kloosterman, et al.
- **Extensive genomic and transcriptional diversity identified through massively parallel DNA and RNA sequencing of eighteen Korean individuals**  
  Publication: Nature Genetics (2011)  
  Authors: Ju. et al.
- **Global analysis of disease-related DNA sequence variation in 10 healthy individuals: Implications for whole genome-based clinical diagnostics**  
  Publication: Genetics in Medicine (2011)  
  Authors: Moore. et al.
- **Demographic history and rare allele sharing among human population**  
  Publication: Gravel S et al, 2011  
  Authors: PNAS
- **Next-generation sequencing of Coccidioides immitis isolated during cluster investigation**  
  Publication: Emerging Infectious Diseases (2011)  
  Authors: Engelthaler, et al.

## Targeted Resequencing

- **Multiplexed array-based and in-solution genomic enrichment for flexible and cost-effective targeted next-generation sequencing**  
  Publication: Nature Protocols (2011)  
  Authors: Harakalova M. et al.
- **Frequent somatic mutations in MAP3K5 and MAP3K9 in metastatic melanoma identified by exome sequencing**  
  Publication: Nature Genetics (2011)  
  Authors: Stark M.S. et al.
- **Decoding cell lineage from acquired mutations using arbitrary deep sequencing**  
  Publication: Nature Methods (2011)  
  Authors: Carlson C. A. et al.
- **Comparison of Three Targeted Enrichment Strategies on the SOLiD Sequencing Platform**  
  Publication: Plos One (2011)  
  Authors: Hedges D.J. et al.
- **Population genetics in non-model organisms: II. Natural selection in marginal habitats revealed by deep sequencing on dual platforms**  
  Publication: Molecular Biology and Evolution (2011)  
  Authors: Zhou R. et al.
De Novo Sequencing

First complete genome sequence of infectious laryngotracheitis virus
Publication: BMC Genomics (2011)
Authors: Lee S. et al

Whole-Genome Shotgun Sequencing of the Sulfur-Oxidizing Chemoautotroph Tetrathiobacter kashmirensis
Publication: Journal of Bacteriology (2011)
Authors: Ghosh W et al

Whole genome sequencing of environmental Vibrio cholerae 01 from 10 nanograms of DNA using short reads
Publication: Journal of Microbiological Methods (2011)
Authors: Chaparro P, et al.

Rapid hybrid de novo assembly of a microbial genome using only short reads: Corynebacterium pseudotuberculosis I19 as a case study
Publication: Journal of Microbiological Methods (2011)
Authors: Cerdeira L, et al.

Comparative genomics of the bacterial genus Listeria: Genome evolution is characterized by limited gene acquisition and limited gene loss
Publication: BMC Genomics (2010)
Authors: den Bakker, et al.

Genome expansion and gene loss in powdery mildew fungi reveal tradeoffs in extreme parasitism
Publication: Science (2010)
Authors: Spanu, et al.

Chromatin Immunoprecipitation Sequencing (ChIP-Seq)

Chromosome length influences replication-induced topological stress
Publication: Nature (2011)
Authors: Kegel, et al.

Efficient double fragmentation ChIP-Seq provides nucleotide resolution protein-DNA binding profiles
Authors: Mokry, et al.

Methylation Analysis
Increased methylation variation in epigenetic domains across cancer types
Publication: Nature Genetics (2011)
Authors: Edwards, et al.

High Resolution Detection and Analysis of CpG Dinucleotides Methylation Using MBD-Seq Technology
Authors: Lan L, et al.

Identification of methylated regions with peak search based on Poisson model from massively parallel methylated DNA immunoprecipitation-sequencing data
Publication: Electrophoresis (2010)
Authors: Yang, et al.

An alignment algorithm for bisulfite sequencing using the Applied Biosystems SOLiD™ System
Publication: Bioinformatics Advance Access (June 18, 2010)
Authors: Ondov, et al.

Whole Transcriptome Analysis

Analysis of HIV-1 expression level and sense of transcription by high-throughput sequencing of the infected cell
Publication: Journal of Virology (2012)
Authors: Lefebvre G. et al

Genome wide full-length transcript analysis using 5’and 3’ paired-end-tag next generation sequencing (RNA-PET)
Authors: Xiaoa Ruan and Yijun Ruan

Programmed fluctuations in sense/antisense transcript ratios drive sexual differentiation in S. pombe
Publication: Molecular Systems Biology (2011)
Authors: Bitton D. A. et al.

Deep-transcriptome and ribonome sequencing redefines the molecular networks of pluripotency and the extracellular space in human embryonic stem cells
Publication: Genome Research (2011)
Authors: Kolle G. et al.

Whole-Genome Sequencing for Optimized Patient Management
Publication: Science Translational Medicine (2011)
Authors: Bainbridge M. et al.

Genome-wide Analysis of the 5’ and 3’ Ends of Vaccinia Virus Early mRNAs Delineates Regulatory Sequences of Annotated and Anomalous Transcripts
Publication: Journal of Virology (2011)
Authors: Yang Z., et al.

The Cluster 1 Type VI Secretion System Is a Major Virulence Determinant in Burkholderia pseudomallei
Publication: Infection and Immunity (2011)
Authors: Burtnick M., et al.

Maternal Epigenetic Pathways Control Parental Contributions to Arabidopsis Early Embryogenesis
Publication: Cell (2011) Authors: Autran D. et al.

NanoRNAs Prime Transcription Initiation In Vivo
Publication: Molecular Cell (2011)
Authors: Goldman et al.

Characterization and improvement of RNA-Seq precision in quantitative transcript expression profiling
Publication: Bioinformatics (2011)
Authors: Labaj P. et al.

A tissue-specific landscape of sense/antisense transcription in the mouse intestine
Publication: BMC Genomics (2011)
Authors: Klostermeier U. et al.

Metatranscriptomics of a hot-spring microbial mat
Publication: The ISME Journals (2011)
Authors: Z Liu et al.

Deterministic and Stochastic Allele Specific Gene Expression in Single Mouse Blastomeres
Authors: Tang F. et al.

Whole-transcriptome RNSseq analysis from minute amount of total RNA
Publication: Nucleic Acids Research (2011)
Authors: Tariq M. et al.

XUTs are a class of Xrn1-sensitive antisense regulatory non-coding RNA in yeast
Publication: Nature (2011)
Authors: Dijk E. et al.

Zebrafish mRNA sequencing decipher novelties in transcriptome dynamics during maternal to zygotic transition
Publication: Genome Research (2011)
Authors: Aanes H. et al.
Short reads and nonmodel species: exploring the complexities of next-generation sequence assembly and SNP discovery in the absence of a reference genome
Publication: Molecular Ecology Resources (2011)
Authors: Everett M.V. et al.

Massive-Scale RNA-Seq Analysis of Non Ribosomal Transcriptome in Human Trisomy 21
Authors: Costa V. et al.

Development and applications of single-cell transcriptome analysis
Publication: Nature Methods (2011)
Authors: Tang F. et al.

Transcriptional consequences of genomic structural aberrations in breast cancer
Publication: Genome Research (2011)
Authors: Inaki K. et al.

Deep sequencing-based analysis of the anaerobic stimulon in Neisseria gonorrhoeae
Publication: BMC Genomics (2011)
Authors: Isabella V. M., et al.

Hyperactivation of anandamide synthesis and regulation of cell-cycle progression via cannabinoid type 1 (CB1) receptors in the regenerating liver
Publication: PNAS (2011)
Authors: Mukhopadhyay B. et al.

Breaking the 1000-gene barrier for Mimivirus using ultra-deep genome and transcriptome sequencing
Publication: Virology journal (2011)
Authors: Legendre M. et al.

RNA-Seq analysis of two closely related leukemia clones that differ in their self-renewal capacity
Publication: Blood (2010)
Authors: Wilhelm, et al.

Evolution of yeast noncoding RNAs reveals an alternative mechanism for widespread intron loss
Publication: Science (2010)
Authors: Mitrovich, et al.

FragSeq: transcriptome-wide RNA structure probing using high-throughput sequencing
Authors: Underwood, et al.

The exon junction complex controls the splicing of mapk and other long intron-containing transcripts in drosophila
Publication: Cell (2010)
Authors: Ashton-Beaucage, et al.

A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk
Authors: Heining, et al.

Identification of novel exons and transcribed regions by chimpanzee transcriptome sequencing
Publication: Genome Biology (2010)
Authors: Wetterbom, et al.

Constitutively active androgen receptor splice variants expressed in castration-resistant prostate cancer require full-length androgen receptor
Publication: PNAS (2010)
Authors: Watson, et al.

Roles of xanthophyll carotenoids in protection against photoinhibition and oxidative stress in the cyanobacterium Synechococcus sp. strain PCC 7002
Publication: Archives of Biochemistry and Biophysics (2010)
Authors: Zhu et al.

Functional and structural characterization of the 2/2 hemoglobin from Synechococcus sp. PCC 7002
Publication: Biochemistry (2010)
Authors: Scott et al.

The transcriptomes of two heritable cell types illuminate the circuit governing their differentiation
Authors: Tuch, et al.

Simultaneous high-resolution analysis of vaccinia virus and host cell transcriptomes by deep RNA sequencing
Publication: PNAS, published online (June 7, 2010)
Authors: Yang, et al.

Genome-wide misexpression of X-linked versus autosomal genes associated with hybrid male sterility
Publication: Genome Res., published online (May 28, 2010)
Authors: Lu, et al.

Widespread transcription at neuronal activity-regulated enhancers
Authors: Kim et al.

RNA-Seq analysis to capture the transcriptome landscape of a single cell.
Publication: Nature Protocols, 5, -516-535. 25 Feb 2010
Authors: Tang, F., et al.

Tumor transcriptome sequencing reveals allelic expression imbalances associated with copy number alterations.
Authors: Tuch, T., et al.
Small RNA Analysis

Pair-barcode high-throughput sequencing for large-scale multiplexed sample analysis
Publication: BMC Genomics (2012)
Authors: Tu J. et al.

Deep-sequencing of endothelial cells exposed to hypoxia reveals the complexity of known and novel microRNAs
Publication: RNA (2012)
Authors: Voellenkle C. et al.

Effecter identification in the lettuce downy mildew Bremia lactucae by massively parallel transcriptome sequencing
Publication: Molecular Plant Pathology, (2012)
Authors: Stassen J. et al.

Sequencing circulating miRNA in maternal plasma with modified library preparation
Publication: Clinica Chimica Acta(2011)
Authors: Ge Q. et al.

Assessment of nanomaterial cytotoxicity with SOLiD sequencing-based microRNA expression profiling
Publication: Biomaterials (2011)
Authors: Li S. et al.

Characterization of the small RNA transcriptome of the diatom, Thalassiosira pseudonana
Authors: Norden-Krichmar T. et al

Deep Sequencing of virus-infected cells reveals HIV-encoded small RNAs
Publication: Nucleic Acids Research (2011)
Authors: Shopman N. et al.

A Comprehensive Survey of miRNA Repertoire and 39 Addition Events in the Placentas of Patients with Pre- Eclampsia from High-Throughput Sequencing
Publication: PloS One (2011)
Authors: Guo, et al.

Next-Generation Sequencing of MicroRNAs for Breast Cancer Detection
Publication: Journal of Biomedicine and Biotechnology (2011)
Authors: Qu Q. et al.

Sequencing circulating miRNA in maternal plasma with modified library preparation
Publication: Clinica Chimica Acta(2011)
Authors: Ge Q. et al.

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Characterization of the small RNA transcriptome of the diatom, Thalassiosira pseudonana
Authors: Norden-Krichmar T. et al

Small RNA profiling of Dengue virus-mosquito interactions implicates the PIWI RNA pathway in anti- viral defense
Publication: BMC Microbiology (2011)
Authors: Hess A.M. et al.

MicroRNAs as participants in cytotoxicity of CdTe quantum dots in NIH/3T3 cells
Publication: Biomaterials (2011)
Authors: Li, et al.

Evolution of yeast noncoding RNAs reveals an alternative mechanism for widespread Intron loss
Publication: Science (2010)
Authors: Quinn, et al.
Gene Expression

Variation in the Large-Scale Organization of Gene Expression Levels in the Hippocampus Relates to Stable Epigenetic Variability in Behavior.
Authors: Alter et al.

High-Resolution Analysis of the 5'-End Transcriptome Using a Next Generation DNA Sequencer.
Authors: Hashimoto, et al.

RNA Structure

Genome-wide measurement of RNA secondary structure in yeast
Authors: Kertesz, et al.

Long noncoding RNA as modular scaffold of histone modification complexes
Publication: Science, Published online (July 8, 2010)
Authors: Tsai, et al.

Metagenomics

Metatranscriptomic analyses of chlorophototrophs of a hot-spring microbial mat
Publication: The ISME Journal (2011)
Authors: Liu Z. et al.

Confirmation of the Sequence of 'Candidatus Liberibacter asiaticus' and Assessment of Microbial Diversity in Huanglongbing-Infected Citrus Phloem Using a Metagenomic Approach.
Publication: Molecular Plant-Microbe Interactions, Vol. 22, No. 12, 2009
Authors: Tyler et al.

The carnivorous bladderwort (Utricularia, Lentibulaiceae) a system inflates.
Publication: Journal of Experimental Botany, vol. 61, No1, pp 5-9, 2010
Authors: Albert, et al.

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