+44 20 8123 2220
info@marketpublishers.com

DNA Sequencing Markets: Global Analysis and Opportunity Evaluation 2016 - 2020

https://marketpublishers.com/r/D753717B0FDEN.html
Date: October 2016
Pages: 118
Price: US$ 5,799.88 (Single User License)
ID: D753717B0FDEN

Abstracts

This market report gives a comprehensive and easy-to-review analysis of the DNA sequencing market 2016 – 2020. It provides key market data and identifies new and emerging opportunities across this growing field. The analysis is based on primary data disclosed by experienced end-users' on their current sequencing practices and their plans over the next three. Its findings provide a wealth of market information on the sequencing market and enables suppliers to reduce costs, identify new markets and compete more effectively in the global marketplace.

Current and 3-year market estimates provided by experienced end-users

Recent Growth in sequencing and estimated growth over the next 3 years (±% change)

Sequencing laboratory locations and preferred external laboratories

Sequencing techniques used currently and anticipated in 3 years (±% change)

Sequencing instruments used currently and anticipated in 3 years (±% change)

Current sequencing suppliers and anticipated suppliers in 3 years (±% change)

Current sequencing applications and anticipated applications in 3 years (±% change)

Clonal amplification methods

+44 20 8123 2220
info@marketpublishers.com

Read lengths, accuracy, reads per run, time per run and sequencing costs.

Disease areas relating to sequencing now and in 3 years (±% change)

Nucleotide types currently sequenced and anticipated in 3 years (±% change)

Software used by sequencers

Costs of sequencing per sample and associated nucleotide lengths

Numbers of samples sequenced per month

Disease biomarkers investigated using sequencing

Biomarker disease areas and molecular types

Sample preparation methods used in sequencing

Purpose, fields or sectors

Global regions, countries and organisation types

This Report

The last decade has seen remarkable innovation and development in the nucleotide sequencing field. Today, a number of powerful high–throughput sequencing technologies are available and are being used to address an increasingly diverse range of biological problems. The quantitative scale and efficiencies of next-generation sequencing platforms are also seeing unprecedented progress and growth in many areas of fundamental research. Also, dramatic reductions in the associated costs and the operational complexities of these techniques are opening up applications in areas that would have been unimaginable just a decade ago.

This report presents the findings of a new global study of nucleotide sequencing, which profiled the use of these techniques from the end-user’s perspective. This study, which evaluated end-users' current sequencing practices and three-year plans, investigated market growth, the competitive positions of global sequencing suppliers, sequencing

+44 20 8123 2220
info@marketpublishers.com

laboratory location, preferred external Laboratories, sequencing methods, sequencing laboratory instruments, company suppliers, applications, clonal amplification, diseases, nucleotide types, software, sequencing performance, numbers of samples, disease Biomarkers, study samples, sample preparation, advantages and disadvantages, fields, participant roles, organisation type, experience, countries and regions.

Biopharm Reports' specialised market studies are designed to assist suppliers and developers to profile current and evolving market opportunities. All of our studies are carried out through specialist groups of experienced researchers and clinicians, and therefore findings are based on 'real world' market data. By providing new insights and a better understanding of end-user practices, needs and future plans, our studies assist suppliers to sell into these markets, and also support innovation and strategic planning. The following study areas were investigated:

Companies mentioned

More than 60 companies are mentioned in this report, namely 5-Prime, Affymetrix, Agencourt (Beckman Coulter), Agilent, AGRF, Ambion (Lifetech), AppliChem, Applied Biosystems, BD, Beckman, BGI, Bioline, Biomerieux, Biometra, Bio-Rad, Celera, Complete Genomics, DNA Technologies, Eppendorf, Eurofins, Exiqon, Fermentas, Fisher Scientific, Fluidigm, GE, Illumina, In-House, Integrated DNA Technologies (IDT), Invitrogen (Lifetech), Ion Torrent (LifeTech), Kapa Biosystems, Labgene, LGC Genomics, Li-Cor, Life technologies, Lucigen, Macherey-Nagel, Macrogen, Mallinckrodt Baker, Millennium Bioscience, MO BIO, Molecular Research Center, MP Biomedical, MWG Operon, New England Biolabs, Nugen, Orion Genomics, Oxford Nanopore, Pacific Biosciences, Perkin Elmer, Promega, Qiagen, Roche (454), Roche Diagnostics, Sangon Biotech, Seegene, Sequenom, Sigma-Aldrich, Solis BioDyne, Takara/Clontech, Tecan, Thermo Scientific, USB Corp and Zymo Research.

Sequencing Location: The locations of the laboratory where Sequencer's sequencing work are carried out, where the options considered were their own laboratory, and external laboratory or both own laboratory and external laboratory.

Preferred External Laboratories: Those sequencers who indicated that they contracted-out their sequencing activities to external laboratories were asked to indicate their preferred laboratories for this activity.

Growth: Based on recent trends in the numbers of sequencing studies carried out in their laboratories, end-users' estimates of by how much (% increase or % decrease)

+44 20 8123 2220
info@marketpublishers.com

their laboratory use of sequencing has changed over the last three years. Also, based on current trends in the numbers of sequencing studies carried out in their laboratories, end-users' estimates of by how much (% increase or % decrease) they anticipate their laboratory use of sequencing will change over the next three years.

Sequencing methods: Sequencer's main use of specific sequencing techniques, both currently and anticipated in three years from now, where the techniques considered (23 different methods) were 454 Pyrosequencing (Roche), Chain Termination Method (Sanger Sequencing), DArT Seq (Diversity Array Technology), DNA Nanoball Sequencing (Complete Genomics), DNA Nanopore Sequencing (Oxford Nanopore Technologies), Electron Microscopy-Based Sequencing (ZS Genetics), Gene Electronic Nano-Integrated Ultra-Sensitive Technology (Geneapsys), Ion Torrent (Thermo Fisher), Massively Parallel Signature Sequencing (Illumina), Microfluidic Sequencing (GnuBIO), Nanowire Biosensor Sequencing Technology (Quantumdx), RAD Sequencing (University Oregon/Floragenex), Sequencing by Hybridization (Affymetrix), Sequencing by Hybridization-Assisted Pore-Based sequencing (NABsys), Sequencing by mass spectrometry, Sequencing by Reversible-Hybridization (Complete Genomics), Sequencing by Synthesis (Illumina/Solexa), Shotgun Sequencing/Chain Termination (Sanger), Single Molecule Nanopore Sequencing (Noblegen Biosciences), Single Molecule Real-Time Sequencing (Pacific Biosciences), Single-molecule Semiconductor-Based Sequencing (Genia/Roche), SOLiD Sequencing (Applied Biosystems), Tunnelling Current DNA sequencing and any others.

Sequencing Instruments: Sequencer's use of specific sequencing instruments, both currently and anticipated in three years from now, where the instruments considered (26 different systems) were Applied Biosystems: 3500 Genetic Analyzer, Applied Biosystems: 3500xL Genetic Analyzer, Applied Biosystems: 3730 DNA Analyzer, Applied Biosystems: 3730xl DNA Analyzer, Applied Biosystems: SOLiD Next-Generation System, BGI: BGISEQ-500 NGS System, Diversity Array Technology: Scanner (DArT Seq), Geneapsys: GENIUS, GnuBio: GnuBIO instrument, Illumina: HiSeq 2500, Illumina: HiSeq 3000/HiSeq 4000, Illumina: HiSeq X Five, Illumina: HiSeq X Ten, Illumina: MiniSeq, Illumina: MiSeq, Illumina: MiSeq FGx, Illumina: MiSeqDx, Illumina: NextSeq 500, Oxford Nanopore: GridION System, Oxford Nanopore: MinION, Oxford Nanopore: PromethION, Pacific Biosciences: PacBio RS II, Pacific Biosciences: Sequel System, Thermo Fisher: 3500 Genetic Analyser (Sanger), Thermo Fisher: Ion PGM System Ion PGM System, Thermo Fisher: Ion Proton System for NGS and any others.

External Laboratory Sequencing Service Providers: As part of this market study,

+44 20 8123 2220
info@marketpublishers.com

external laboratories that provide nucleotide sequencing services to the end-users profiled, were also invesigated and are identified in this report.

Company Suppliers: End-users' current main suppliers of sequencing instruments, products or consumables, as well as those companies they anticipate will be supplying these products to their laboratories in three years from now, where 93 companies are considered, namely, 5-Prime, Abbott, Affymetrix, Agencourt (Beckman Coulter), Agilent, AGRF, Ambion (Lifetech), Anatech, Answer Choices, AppliChem, Applied Biosystems, BD, Beckman, BGI, Bioline, Biomerieux, Biometra, BioNanomatrix, Bioneer, Bionobile, Bionobile, Bio-Rad, Celera, Chemagen (PE), Complete Genomics, DNA Technologies, Eppendorf, Eurofins, EURx, Exiqon, Fermentas, Fisher Scientific, Fluidigm, FugiFilm, GE, GenDx, Halcyon Molecular, Illumina, In-House, Inqaba Biotechnology, Integrated DNA Technologies (IDT), Intelligent BioSystems, Invitek, Invitrogen (Lifetech), Ion Torrent (LifeTech), Kapa Biosystems, Labgene, LGC Genomics, Li-Cor, Life technologies, Lucigen, Macherey-Nagel, Macrogen, Mallinckrodt Baker, Millennium Bioscience, MO BIO, Molecular Research Center, MP Biomedical, MWG Operon, NABsys, New England Biolabs, Nexttec, Nippon Gene, Nugen, Orion Genomics, Oxford Nanopore, Pacific Biosciences, Panomics,
Perkin Elmer, Phoenix (Microarray), Primm Biotech, Promega, Qiagen, r-Biopharm, Roche, Roche (454), Roche Diagnostics, Roth, Sangon Biotech, Seegene, SeqLL, Sequenom, Sequiserve, Siemens, Sigma-Aldrich, Solis BioDyne, Stab Vida, Takara/Clontech, Tecan, Thermo Scientific, USB Corp, Vivantis, Zymo Research and any others.

Applications: End-users' current main applications of sequencing as well as the applications they anticipate using in three years from now, where the applications considered were Allele size detection, Aneuploidy and CNV analysis, Antibacterial resistance analysis, Antiviral resistance analysis, Bacterial typing, ChIP-Seq, Cloning, Complex populations, De Novo Sequencing, Detection, identification of bacteria, Detection, identification of viruses, Diverse gene polymorphisms, DNA barcoding, species identifications, DNA quantification, Epigenome characterization, Exome sequencing, Fragment analysis for epidemiological analysis, Full 16S sequencing for identification and phylogeny, Gene expression (mRNA), Gene mutations or alterations, Gene variants in disease, Genetic mapping, Genome Resequencing, Genotyping by Sequencing, Genotyping of microorganisms, Haplotypes, Immune diversity, Metagenomics, Methylation Sequencing, Microbial Sequencing, MicroRNA Studies, Microsatellites, Phylodynamic analyses, Rapid Diagnostic - Genetic Markers, Regulatory elements, Ribosomal DNA (rRNA) Studies, RNA Sequencing, Short Tandem Repeat Analysis, Single Nucleotide Polymorphisms, Single-Strand Conformation

+44 20 8123 2220
info@marketpublishers.com

Polymorphism, Small insertions or deletions, Small Interfering RNA (siRNA) Studies, Small Nuclear RNA (snRNA) Studies, Small RNA and miRNA Sequencing, Targeted DNA sequencing, Targeted Resequencing, Tissue typing, Total RNA Sequencing (Transcriptome), Transfer RNA (tRNA) Studies, Ultra-Low-Input/Single-Cell RNA-Seq, Viral Typing, Whole-Genome Sequencing and any others.

Clonal Amplification: End-users' clonal amplifications methods used in their nucleotide sequencing, both currently and anticipated in three years, where the methods considered were Bridge PCR Amplification, Emulsion PCR Amplification, Rolling Circle Amplification and None (e.g. Single Molecule Sequencing).

Diseases: End-user's current sequencing activities, and those sequencing activities they anticipate in three years from now, relating to specific disease areas, namely Antimicrobial resistance, Arthritis, Asthma and allergy, Autoimmune Diseases, Bone Metabolism, Cancer, Cardiovascular, Central Nervous System, Dentistry, Dermatology, Endocrine, Gastrointestinal, Genetic diseases, Genito-Urinary System, Haematology, Hearing Loss, Immunodeficiency, Infections, Infertility, Inflammation, Liver disease, Metabolic Disorders, Musculoskeletal Disorders, None, Nutrition, Obstetrics and Gynaecology, Ophthalmology, Pain, Phytopathology, Psychiatry, Rare diseases, Reproduction, Respiratory, Sexually transmitted infections, Skin, Stem cells, Transplantation medicine, Vector borne disease, Virus diseases and any others.

Nucleotide Types: Main nucleic acid types currently sequenced, as well as those anticipated to be sequenced in three years from now, where the nucleic acids considered were Archaeal DNA, Bacterial DNA, Bacterial PCR amplicons, Bisulfite-converted DNA, cDNA, cell free miRNA, fungal DNA, Genomic DNA, ITS region, Metagenomic DNA, MicroRNA, Mitochondrial DNA, mRNA, Noncoding RNA, Nuclear DNA genes, Pathogen RNA/DNA, piRNA, Plant viral RNA or DNA, Plasma Cell Free DNA, Plasmid DNA, Prokaryotic small RNA, Protist DNA, Ribosomal RNA (rRNA), Small interfering RNA (siRNA), Small nuclear RNA (snRNA), Total RNA, Transfer RNA (tRNA), Tumour Cell DNA, Viral DNA, Viral PCR amplicons, Viral RNA and any others.

Software: Sequencers main software programs used for their nucleotide sequencing activities and those considered (n = 387) were ABA (Raphaelet al.), ABySS (Simpson et al.), ACANA (Huang et al.), ACT (Sanger), Alamut (Interactive Biosoftware), ALE (Blandy et al.), AlignMe (Stamm et al.), ALLPATHS (Broad Institute), Alta-cyclic (Omictools), AMAP (Schwartz et al.), AnnHyb (MyBiosoftware), Annovar (Open Bioinformatics), anon. (Powell et al.), Answer Choices, Artemis (Sanger), Augustus (Gottingen), AVID (Vista), BAliBASE (Thompson et al.), BAli-Phy (Redelings et al.),

+44 20 8123 2220
info@marketpublishers.com

BarraCUDA (GPL), Base-By-Base (Brodie et al.), BBMap (Source Forge), Beast (Drummond et al.), Belvu (Sanger), BFAST (GPL), BigBWA (Omictools), Bioconductor (Aboyoun et al.), BioEdit (Ibis), BioLinux (EON), Biomart (Ensembl), BioNumerics (Applied Maths), BioPerl dpAlign (Chan et al.), Biopieces (Biostars), BisMark (Babraham), BLAST (Altschul et al.), BLASTN (NCBI), BLASTZ,LASTZ (Schwartz et al.), BLAT (Non-Commercial Academic), BLOCKS (Molbio-Tools), Bowtie (Artistic License), BS-Seq (UCLA), Bustard (Illumina), BWA (GPL), BWA-PSSM (Bio-BWA), Cap3 (Genome), Casava (Illumina), CASHX (Non-Commercial Academic), CEQ (Beckman et al.), CHAOS/DIALIGN (Brudno et al.), ChIP-Seq (DNASTar), Chromas (Technelysium), Clarity (Genologics), CLC Genomic Workbench (CLCBio), Clone Manager (CLCBio), Cloudburst (Artistic License), ClustalW (Thompson et al.), CNVnator (Omictools), CNV-Seq (Chao et al.), CodonCode Aligner (Richterich et al.), Compass (Sadreyev, et al.), Contig Express (Contig), CS-BLAST (Angermueller et al.), CUDA-EC (Omictools), CUDAlign (Source Forge), CUDA-MEME (MyBiosoftware), CUDASW++ (Liu et al.), Cufflinks (Cole-trapnell), CUSHAW (GPL), CUSHAW2 (GPL), CUSHAW2-GPU (GPL), CUSHAW3 (Source Forge), Custom Designed (In-House), Dalliance (Omictools), dbSNP (Open Source), DECIPHER (DecipherProject), DESeq (Bioconductor), DIALIGN-TX and DIALIGN-T (Subramanian et al.), DIAMOND (GitHub), DNA Alignment (Roehl et al.), DNA Baser Sequence Assembler (Heracle BioSoft), DNADot (Bowen et al.), DNAsp (UBEdu), DNASTAR (DNAStar), DOTLET (Pagni et al.), dpAlign (BioPerl), drFAST (BSD), EagleView (Boston College), Edena (Hernandez), EDNA (Salama et al.), ELAND (Illumina), EMBL-EBI (EBI Ac), eMOTIF (Stanford), Ensemble (Ensembl), ERANGE (Wold Lab), ERNE (GPL), EULER-SR (Chaisson), Excel (Open Source), Exonerate (Guy St C Slater et al.), ExpressionSuite (Thermo Fisher), FASTA (Faster Biotech), Fastpcr (PrimerDigital), FastQC (Babraham), fastseq (Helical), fastx-tools (Hannon), FEAST (Hudek et al.), FindPeaks (Bainbridge et al.), FMM (Open Source), FreeBayes (Omictools), FSA (Bradley et al.), Galaxy (Galaxy), GapMis (Frousios et al.), GASSST (Omictools), GATK (Broad Institute), GEM (Non-Commercial Academic), GenAlex (BiologyAssets), Genalice MAP (Genalice), GenDB (Open Source), Gene Construction Kit (Textco), Gene Mapper (ABI), Gene tex (Genetex), GeneInsight (Geneinsight), Geneious (Drummond et al.), Geneious Assembler (Geneious), GeneMapper® Software (ABI), Genologics (Illumina), Genomatix (Genomatix), Genome Browser (UCSC), Genome Compiler (Genome Compiler), GenomeMapper (1001 Genomes project), GenomeStudio Software (Illumina), Genomics Workbench (CLCBio), Genoogle (Genoogle), Genotyper (ABI), GenSearch (Phenosystems), GensearchNGS (Omictools), Geospiza (Geospiza et al.), GGSEARCH, GLSEARCH (Pearson et al.), Gibbs motif sampler (Omictools), Glimmer (CBCD), GLProbs (Omictools), GMAP and GSNAP (Non-Commercial Academic), G-Mo.R-Se (CNS, France), GNUMAP (Omictools), G-PAS (Frohmberg et al.), GS

+44 20 8123 2220
info@marketpublishers.com

Amplicon Variant Analyzer (Roche), HapCompass (Omictools), HGMD (Biobase), HHpred / HHsearch (Soding et al.), HiSeq Software (Illumina), HIVE-hexagon (Hive), HMMER (Durbin et al.), HMMTOP (SACS), HOMSTRAD (Mizuguchi et al.), Htseq (Huber et al.), HyPhy (Hyphy et al.), Ibis (Ibis), IDF (CSUni), IGV (Broad Institute), IMEX (Omictools), IMGT (IMGT), Infernal (Eddy), Ingenuity (Ingenuity), In-House (In-House), Ion Reporter (Thermo Fisher), Ion torrent (Thermo Fisher), iSAAC (Non-Commercial Academic), I-sites (Open Source), JAligner (Moustafa et al.), Jalview (Jalview), JCoils (CHEmbnet), KSync (Chivian et al.), Kalign (Lassmann et al.), KLAST (CLCBio), Kodon (Applied Maths), LALIGN (Pearson et al.), Lasergene (DNAStar), LAST (GPL), LASTZ (NCBI), LookSeq (Sanger), MACS (Zhang et al.), MacVector (MacVector), MAFFT (Katoh et al.), Mage Platform (Genoscope), mAlign (Powell et al.), Manattee (Manattee), MapNext (Sun-Yat Sen Univ), MapView (Sun-Yat Sen Univ), MAQ (GPL), MARNA (Siebert et al.), Matcher (Longden et al.), Mauve (Darlinglab), MAVID (Bray et al.), MCALIGN2 (Wang et al.), MEGA (Megasoft), MEME/MAST (Meme), MERCI (Bioinfo), Metacore (Omictools), MG RAST (Metagenomics), MGA (Omictools), Mira (Omictools), MIRA2 - MIRA (Source Forge), MirCheck (Mybiosoftware), Mirdeep2 (MDC Berlin), miREvo (Omictools), MiSeq (Illumina), MiSeq Software (Illumina), MOM (CS.CMU), MOSAIK (Stromberg et al.), Mothur (Mothur), MPscan (Omictools), MrBayes (MrBayes), mrFAST and mrsFAST (BSD), MSA (Lipman et al.), MSAProbs (Liu et al.), MSeqDR (Open Source), Mulan (Mulan), MULTALIN (Corpet et al.), Multi-LAGAN (Brudno et al.), Multiz (Mybiosoftware), MUMmer (Kurtz et al.), MUSCLE (Edgar et al.), Mutation Surveyor (Softgenetics), mVista (Genome), MyRAST (Mybiosoftware), NCBI (Open Source), Needle (Bleasby et al.), NETGLYC (CBS), NetPrimer (PremierBiosoft), Newbler (Roche), NextGENe (Softgenetics), NextGenMap (Omictools), Ngila (Cartwright et al.), NISC (NIH), Novoalign & NovoalignCS (Non-Commercial Academic), NW-align (Zhang et al.), Omixon (Omixon), Opal (Wheeler et al.), Oxbench (Raghava et al.), PAL_finder (Source Forge), PALMapper (GPL), Pandaseq (Github), Panther (Omictools), Parasail (BMC), Partek (Partek), Pasa (Pasa), PASS (CRIBI), Path (Girdea et al.), PathSeq (Broad Institute), PatternHunter (Ma et al.), PAUP (Evolution), PeakSeq (Rozowsk et al.), Pecan (Paten et al.), PerM (GPL), PFAM (Sanger), PHI-Blast (NCBI), Phylo (McGill Bioinformatics), Phylogeny (Evolution), Phyloscan (NCBI), phyML (ATGC), Picard (Broad Institute), PicXAA (Omictools), PLAST-ncRNA (NCBI), PMS (Open Source), POA (Lee et al.), PolyBayesShort (Boston College), Polyphen (Harvard), Praline (Heringa et al.), PRATT (EBI Ac), PREFAB (Edgar et al.), Primer 3 (PremierBiosoft), PRIMEX (Open Source), Prism (ABI), ProbA (also propA) (Muckstein et al), Probalign (Roshan et al.), ProbCons (Do et al.), Prodigal (Omictools), PROMALS3D (Pei et al.), Proseq (Biosoft), PRRN/PRRP (Totoki et al), PSAlign (Sze et al.), PSI-BLAST (Altschul et al.), PSI-Search (Li et al.), PyMOL (DeLano et al.), PyroBayes (Boston College), Python (DigitalBiol), QIIME (QIIME),

+44 20 8123 2220
info@marketpublishers.com

Qpalma (De Bona et al.), QuEST (Stanford), R (Open Source), RAST (Molbiotools), Ray (Denovo), RazerS (LGPL), RDP (NCBI), REAL, cREAL (GPL), REPuter (Kurtz et al.), Responses, Responses, RevTrans (Wernersson et al.), RMAP (GPL), rNA (GPL), RNASAT (Stanford), Rolexa (Bioconductor), RTG Investigator (Non-Commercial Academic), SABERTOOTH (Teichert et al.), SABmark (Van Walle et al.), SAGA (Notredame et al.), SAM (Krogh et al.), Satsuma (Grabherr et al.), ScalaBLAST (Oehmen et al.), ScanProsite (Prosite), Se-Al (Rambaut et al.), Seaview (Mybiosoftware), Segemehl (Non-Commercial Academic), SEQALN (Waterman et al.), SEQAN (Rausch et al.), SeqMan (DNAStar), SeqMap (Jiang et al.), SeqScape (Thermo Fisher), Sequence Scanner Software (ABI), Sequences Studio (Meskauskas et al.), Sequencher (Gene Codes Corp), Sequencing Analysis Software (ABI), Sequencing Analysis Viewer (Illumina), Sequerome (Bioinformatics.org), Sequilab (Lifescisoft), Serial Cloner (SerialBasics), SHARCGS (Dohm et al.), SHORE (1001 Genomes project), Shrec (Omictools), SHRiMP (Brudno et al.), Shuffle-LAGAN (Stanford), SIBsim4 / Sim4 (NEBC), SIM, GAP, NAP, LAP (Huang et al.), SISSRs (Jothi et al.), Slider (BCGSC), SlimSearch (EdwardsLab), SMART (Letunic et al.), SOAP, SOAP2, SOAP3 and SOAP3-dp (GPL), SOCS (Ondov et al.), SOLiD™ Software (ABI), SPA (Shen et al), SPAdes (Open Source), Splign (Open Source), SSAHA and SSAHA2 (Non-Commercial Academic), SSAKE (Omictools), SSEARCH (Pearson et al.), Staden (Source Forge), Stampy (Non-Commercial Academic), StatAlign (Novak et al.), Stemloc (Holmes et al.), SToRM (Omictools), stretcher (Longden et al.), Subread and Subjunc (GPL), SureCall (Agilent), SWAPHI (Open Source), SWAPHI-LS (Open Source), SWIFT suit (Rasmussen et al.), SWIPE (GNU), SXOligoSearch (Synamatix), Syngene (GeneTools), Tablet (Omictools), Taipan (Non-Commercial Academic), T-Coffee (Notredame et al.), TEIRESIAS (IBM), TopHat (Univ's Maryland/California), Torrent (Thermo Fisher), tranalign (Williams et al.), Trinity (Strozzi et al.), UCHIME (Mothur), UCLUST (NEBC), UGENE (GPL), USEARCH (Drive5), VarScan (Source Forge), VCAKE (Omictools), Vector NTI (Thermo Fisher), VectorFriends (BioFriends team), VelociMapper (Omictools), Velvet (Zerbino et al), Vmatch (VMatch), water (Bleasby et al.), wordmatch (Longden et al.), XMatchView (Warren et al.), XpressAlign (Non-Commercial Academic), YASS (Noe et al), Zenbu (Omictools), ZOOM (Omictools) and any Others.

Sequencing Performance: Five areas of the performance of end-users' sequencing activities were investigated namely read length (bp) that they typically achieve in your sequencing work, the accuracy (%, single read, not consensus) that they believe they achieve in their work, the reads per run (in millions of bases) that they typically achieve in their work, the typical time per run (minutes, hours, days, weeks or months) in their sequencing work and the sequencing costs in terms of US$ per 1 million bases.

+44 20 8123 2220
info@marketpublishers.com

Numbers of samples: Sequencers estimates of the number of study samples they sequence in their laboratory, where the options were

+44 20 8123 2220
info@marketpublishers.com

Contents

+44 20 8123 2220
info@marketpublishers.com

+44 20 8123 2220
info@marketpublishers.com

12. SEQUENCING PERFORMANCE

13. NUCLEIC ACID TYPES

14. TRENDS AND GROWTH

15. SUPPLIERS

16. STUDY SAMPLES

+44 20 8123 2220
info@marketpublishers.com

17. SAMPLE PREPARATION

18. SAMPLE PREPARATION KITS

19. DISEASE BIOMARKERS

20. COSTS AND THROUGHPUT

21. DISCUSSION (P.180)

+44 20 8123 2220
info@marketpublishers.com

Figures

FIGURES

+44 20 8123 2220
info@marketpublishers.com

+44 20 8123 2220
info@marketpublishers.com

+44 20 8123 2220
info@marketpublishers.com

Tables

TABLES

+44 20 8123 2220
info@marketpublishers.com

+44 20 8123 2220
info@marketpublishers.com

+44 20 8123 2220
info@marketpublishers.com

I would like to order

Product name: DNA Sequencing Markets: Global Analysis and Opportunity Evaluation 2016 - 2020
Product link: https://marketpublishers.com/r/D753717B0FDEN.html
Price: US$ 5,799.88 (Single User License / Electronic Delivery)

If you want to order Corporate License or Hard Copy, please, contact our Customer Service:
info@marketpublishers.com

Payment

To pay by Credit Card (Visa, MasterCard, American Express, PayPal), please, click button on product page https://marketpublishers.com/r/D753717B0FDEN.html

To pay by Wire Transfer, please, fill in your contact details in the form below:

First name:
Last name:
Email:
Company:
Address:
City:
Zip code:
Country:
Tel:
Fax:
Your message:

**All fields are required

Custumer signature _____

Please, note that by ordering from marketpublishers.com you are agreeing to our Terms & Conditions at https://marketpublishers.com/docs/terms.html

To place an order via fax simply print this form, fill in the information below and fax the completed form to +44 20 7900 3970