

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE PATENT TRIAL AND APPEAL BOARD

INTEGRATED DNA TECHNOLOGIES, INC.,
Petitioner,

v.

TECAN GENOMICS, INC.,
Patent Owner

Case No. IPR2025-00015
U.S. Patent No. 10,036,012

PATENT OWNER'S UPDATED EXHIBIT LIST

Ex.	Short Name	Description
2001	Evans 2009	Mark F. Evans, <i>The Polymerase Chain Reaction and Pathology Practice</i> , 15 DIAGN. HISTOPATHOL. 344 (2009)
2002	N/A	<i>The Cost of Sequencing a Human Genome</i> , NAT'L INST. OF HEALTH NAT'L HUMAN GENOME RESEARCH INST., https://www.genome.gov/about-genomics/fact-sheets/Sequencing-Human-Genome-cost (last visited July 18, 2025)
2003	Goodwin 2016	Sara Goodwin et al., <i>Coming of Age: Ten Years of Next-Generation Sequencing Technologies</i> , 17 NAT. REV. 333 (2016).
2004	Mardis 2017	Elaine R. Mardis, <i>DNA Sequencing Technologies: 2006-2016</i> , 12 NAT. PROTOC., 213 (2017).
2005	Fuller 2009	Carl W. Fuller et al., <i>The Challenges of Sequencing by Synthesis</i> , 27 NAT. BIOTECHNOL. 1013 (2009).
2006	Marguiles 2005	Marcel Margulies et al., <i>Genome Sequencing in Open Microfabricated High Density Picoliter Reactors</i> , 437 NATURE 376 (2005).
2007	Luo 2012	Chengwei Luo et al., <i>Direct Comparisons of Illumina vs. Roche 454 Sequencing Technologies on the Same Microbial Community DNA Sample</i> , 7 PLOS ONE 1 (2012).
2008	Hert 2008	Daniel G. Hert et al., <i>Advantages and Limitations of Next-Generation Sequencing Technologies: A Comparison of Electrophoresis and Non-Electrophoresis Methods</i> , 29 ELECTROPHORESIS 4618 (2008).
2009	N/A	<i>Six Years After Acquisition, Roche Quietly Shuttles 454</i> , BioIT World (Oct. 16, 2013), https://www.bio-itworld.com/news/2013/10/16/six-years-after-acquisition-roche-quietly-shuttles-454 .
2010	Mamanova 2010	Lira Mamanova et al., <i>Target-Enrichment Strategies for Next-Generation Sequencing</i> , 7 NAT. METHODS 111 (2010).

Ex.	Short Name	Description
2011	Treangen 2011	Todd J. Treangen et al., <i>Repetitive DNA and Next-Generation Sequencing: Computational Challenges and Solutions</i> , 29 NAT. REV. GENET. 36 (2012).
2012	Brownie 1997	Jannine Brownie et al., <i>The Elimination of Primer-dimer Accumulation in PCR</i> , 25 NUCLEIC ACIDS RES. 3235 (1997).
2013	Tewhey 2009	Ryan Tewhey et al., <i>Microdroplet-based PCR Enrichment for Large-scale Targeted Sequencing</i> , 27 NAT. BIOTECHNOL. 1025 (2009).
2014	Link 2012	U.S. Patent Application No. 2012/0309002 (published Dec. 6, 2012).
2015	Franck 1998	Sophia M. Franck et al., <i>Multiplex PCR for Enterotoxigenic, Attaching and Effacing, and Shiga Toxin-Producing Escherichia coli Strains from Calves</i> , 36 J. CLIN. MICROBIOL. 1795 (1998).
2016	AmpliTaq Gold	Applied Biosystems, <i>AmpliTaq Gold, with GeneAmp® 10X PCR Buffer or GeneAmp 10X PCR Buffer II & MgCl₂ Solution or GeneAmp 10X PCR Gold Buffer & MgCl₂ Solution</i> (2000).
2017	Fool 2002	University of Hawaii, <i>The Simple Fool's Guide to PCR</i> (2002).
2018	Ying 2019	Hua Ying et al., <i>The Whole-Genome Sequence of the Coral Acropora Millepora</i> , 1 GENOME BIOL. Genome Biology 1374 (2019).
2019		Office Action Summary, Application No. 13/750,768 (U.S. Patent & Trademark Office July 15, 2015).
2020	Singleton 2011	A. Singleton, <i>Exome sequencing: a transformative technology</i> , 10 Lancet Neurol. 942-46 (2011).
2021	Former Bustamante Declaration	Declaration of Carlos D. Bustamante, Ph.D. for Patent Owner's Preliminary Response
2022-2035		<i>Reserved</i>

Ex.	Short Name	Description
2036	Sims Deposition 1	Transcript for the June 26, 2025 Deposition of Dr. Peter A. Sims
2037	Sims Deposition 2	Transcript for the June 27, 2025 Deposition of Dr. Peter A. Sims
2038	Bustamante Declaration	Declaration of Carlos D. Bustamante, Ph.D.
2039	Matz Declaration	Declaration of Mikhail V. Matz, Ph.D.
2040	Mullis 1986	K.Mullis et al., <i>Specific Enzymatic Amplification of DNA In Vitro: The Polymerase Chain Reaction</i> , 51 COLDSPRING HARBOR SYMPOSIA QUANTITATIVE BIOL. 1(1986)
2041	Kanagawa 2003	Takahiro Kanagawa, <i>Bias and Artifacts in Multitemplate Polymerase Chain Reactions (PCR)</i> , 96 J. BIOSCI. & BIOENG 4 (2003)
2042	Aird 2011	Daniel Aird et al., <i>Analyzing and minimizing PCR amplifications bias in Illumina sequencing libraries</i> , 12 GENOME BIOL. (2011)
2043	Chenchik 1996	A. Chenchik et al., <i>Full-Length cDNA Cloning and Determination of mRNA 5' and 3' Ends by Amplification of Adaptor-Ligated cDNA</i> , 21 BIOTECHNIQUES 3 (1996)
2044	Devon 1995	Rebecca S. Devon et al., <i>Splinkerettes—improved vectorettes for greater efficiency in PCR walking</i> , 23 NUCLEIC ACIDS RES. 9 (1995)
2045	Padegimas 1998	Linus S. Padegimas & Nancy A. Reichert, <i>Adaptor Ligation-Based Polymerase Chain Reaction-Mediated Walking</i> , 260 ANALYTICAL BIOCHEMISTRY (1998)
2046	Arnold 1991	C. Arnold & I.J. Hodgson, <i>Vectorette PCR: A Novel Approach to Genomic Walking</i> , PCR METHODS & APPLICATIONS (1991)
2047	Miura 2005	Fumihito Miura et al., <i>A novel strategy to design highly specific PCR primers based on stability and uniqueness of 3'-end subsequences</i> , 21 BIOINFORMATICS 24 (2005)

Ex.	Short Name	Description
2048	Tsoktouridis 2005	Georgios Tsoktouridis et al., <i>Adaptor Long-Range PCR Procedure for Clone-Specific Characterization and Chromosomal Localization</i> , 38 BIOTECHNIQUES 6 (2005)
2049	Bower 2010	Neil I. Bower & Ian A. Johnston, <i>Targeted rapid amplification of cDNA ends (T-RACE)—an improved RACE reaction through degradation of non-target sequences</i> , 38 NUCLEIC ACIDS RES. 21 (2010)
2050	Sohn 2011	Jung-Hoon Sohn, <i>A Novel Genome Walking Method for Cloning of Unknown DNA Sequences Adjacent to Known Sequence</i> , Application No. WO 2011/004994
2051	Almomani 2011	Rowida Almomani et al., <i>Experiences with array-based sequence capture; toward clinical applications</i> , 19 EURO. J. HUMAN GENETICS (2011)
2052	Myllykangas 2011	Samuel Myllykangas et al., <i>Targeted sequencing library preparation by genomic DNA circularization</i> , 11 MCB BIOTECH. 122 (2011)
2053	Quail 2008	Michael A. Quail et al., <i>A large genome center's improvements to the Illumina sequencing system</i> , 5 NAT. METHODS 12 (2008)
2054	Kozarewa 2009	Iwanka Kozarewa et al., <i>Amplification-free Illumina sequencing-library preparation facilitates improved mapping and assembly of (G+C)-biased genomes</i> , 6 NAT. METHODS 4 (2009)
2055	Syvänen 2001	Ann-Christine Syvänen, <i>Accessing Genetic Variation: Genotyping Single Nucleotide Polymorphisms</i> , 2 NAT. REV. (2001)
2056	Grunenwald 2010	Haiying Gruenwald et al., <i>Rapid, high-throughput library preparation for next-generation sequencing</i> , NAT. METHODS (2010)
2057	Glenn 2011	Travis C. Glenn, <i>Field guide to next-generation DNA sequencers</i> , MOLECULAR ECOLOGY RES. (2011)
2058	Zhang 2021	Lu Zhang, <i>Advances in Metagenomics and Its Application in Environmental Microorganisms</i> , 12 FRONTIERS IN MICROBIOL. (2021)

Ex.	Short Name	Description
2059	2008 GS-Flx Operating Manual	<i>Genome Sequencer FLX Operator's Manual</i> , ROCHE (2008)
2060	Niedringhaus 2011	Thomas P. Niedringhaus, <i>Landscape of Next-Generation Sequencing Technologies</i> , 83 ANALYTICAL CHEMISTRY (2011)
2061	Thoma 2011	Generation of Stable mRNA Fragments and Translation of N-Truncated Proteins Induced by Antisense Oligodeoxynucleotides
2062	Ernani 2009	Fred Ernani et al., <i>Bringing Cost and Process Efficiency to Next Generation Sequencing</i> , DDW (2009)
2063	Irwin 2011	Jodi Irwin et al., <i>Assessing the potential of next generation sequencing technologies for missing persons identification efforts</i> , 3 FORENSIC SCI. J. (2011)
2064	Lange 2010	Julia Lange, <i>Targeted resequencing for large-scale genomic studies: accelerating NGS throughput using molecular barcodes</i> , NAT. METHODS (2010)
2065	Barchi 2019	Lorenzo Barchi, <i>Single Primer Enrichment Technology (SPET) for High-Throughput Genotyping in Tomato and Eggplant Germplasm</i> , 10 FRONTIERS IN PLANT SCI. (2019)
2066	Gnirke 2009	Andreas Gnirke et al., <i>Solution Hybrid Selection with Ultra-Long Oligonucleotides for Massively Parallel Targeted Sequencing</i> , 27 NAT. BIOTECH. 182 (2009)
2067	Smith 2021	Caitlin Smith, <i>Growing Options for Enriching Target DNA</i> , FUTURELABS, June 17, 2021, https://www.biocompare.com/Editorial-Articles/576645-Growing-Options-for-Enriching-Target-DNA/ .
2068	Scaglione 2019	Davide Scaglione et al., <i>Single primer enrichment technology as a tool for massive genotyping: a benchmark on black poplar and maize</i> , 124 ANNALS OF BOTANY (2019)
2069	Benjamino 2021	Jacquelynn Benjamino et al., <i>Genome-Based Targeted Sequencing as a Reproducible Microbial Community Profiling Assay</i> , 6 MSPHERE 2 (2021)

Ex.	Short Name	Description
2070	Knierim 2011	Ellen Knierim, <i>Systematic comparison of three methods for fragmentation of long-range PCR products for next generation sequencing</i> , 6 PLoS ONE 11 (2011)
2071	Quail 2011	Michael A. Quail et al., <i>Optimal enzymes for amplifying sequencing libraries</i> , 9 NAT. METHODS 1 (2012)
2072	Whiley 2005	David M. Whiley et al., <i>Sequence variation in primer targets affects the accuracy of viral quantitative PCR</i> , 34 J. CLINICAL VIROLOGY (2005)
2073	Ghedira 2009	Rim Ghedira et al., <i>Assessment of Primer/Template Mismatch Effects on Real-Time PCR Amplification of Target Taxa for GMO Quantification</i> , 57 J. AGRICULTURAL & FOOD CHEMISTRY (2009)
2074	Matz 2002	Mikhail V. Matz, <i>Amplification of Representative cDNA Samples from Microscopic Amounts of Invertebrate Tissue to Search for New Genes</i> , in GREEN FLUORESCENT PROTEIN: APPLICATIONS AND PROTOCOLS 3 (Barry W. Hicks ed., 2002)
2075	Bielas 2013	International Publication No. WO 2013/123442 A1
2076	JPMorgan Report	Tycho W. Peterson et al., <i>Next Gen Sequencing Survey</i> , J.P. MORGAN (2010)
2077	Ambion 2008	<i>Ambion® RNA Fragmentation Reagents</i> , APPLIED BIOSYSTEMS (2008)
2078	Illumina 2008	<i>Preparing Samples for Sequencing of mRNA</i> , ILLUMINA (2008)
2079	Additional File 3	Additional File 3 to EX1006
2080	Lewin 1994	Benjamin Lewin, <i>The eukaryotic gene: conserved exons and unique introns</i> , in GENES V 677 (1994)
2081	Evrogen Trimmer Kit Manual	<i>Trimmer-Direct cDNA Normalization Kit User Manual</i> , EVROGEN (2012)
2082	Nugen Nature	<i>Accelerating Genomics with Advanced Sample Preparation Solutions</i> , NATURE RESEARCH CUSTOM MEDIA

Ex.	Short Name	Description
2083	Scolnick 2015	Jonathan A. Scolnick et al., <i>An Efficient Method for Identifying Gene Fusions by Targeted RNA Sequencing from Fresh Frozen and FFPE Samples</i> , PLOS ONE (2015)
2084	Nugen BioSpace	Priya Balachandran, <i>NuGEN Announces Issuance of U.S. Patent For Its Single Primer Target Enrichment Technology (SPET) For Next Generation Sequencing Applications</i> , BIOSPACE, https://www.biospace.com/nugen-announces-issuance-of-u-s-patent-for-its-single-primer-target-enrichment-technology-spet-for-next-generation-sequencing-applications (last visited July 18, 2025)
2085	Allegro V2	<i>Allegro® Targeted Genotyping V2 Product Sheet</i> , TECAN GENOMICS, INC. (2019)
2086	Feng 2016	Weixing Feng et al., <i>Improving Alignment Accuracy on Homopolymer Regions for Semiconductor-Based Sequencing Technologies</i> , 17 BMC GENOMICS 521 (2016)
2087	Nakamura 2011	Kensuke Nakamura et al., <i>Sequence-Specific Error Profile of Illumina Sequencers</i> , 39 NUCLEIC ACIDS RES. 90 (2011)
2088	Sambrook 2006	Joseph Sambrook et al., <i>Fragmentation of DNA by Nebulization</i> , COLD SPRING HARB. PROTOC. (2006)
2089	QIAGEN 2010	<i>QIAGEN® Multiplex PCR Handbook</i> , QIAGEN (2010).
2090	Han 2006	Sangjo Han et al., <i>AtRTPrimer: Database for Arabidopsis Genome-Wide Homogeneous and Specific RT-PCR Primer-Pairs</i> , 7 BMC BIOINFORMATICS 179 (2006).
2091	Matz 1999	Mikhail V. Matz et al., <i>Amplification of cDNA Ends Based on Template-Switching Effect and Step-out PCR</i> , 27 NUCLEIC ACIDS RES. 1558 (1999).
2092	Bru 2008	D. Bru et al., <i>Quantification of the Detrimental Effect of a Single Primer-Template Mismatch by Real-Time PCR Using the 16S rRNA Gene as an Example</i> , 74 APPL. ENVIRON. MICROBIOL. 1660 (2008).

Ex.	Short Name	Description
2093	Bustin 2005	Stephen A. Bustin et al., <i>Quantitative Real-time RT-PCR – A Perspective</i> , 34 J. MOL. ENDOCRINOL. 597 (2005).
2094	Duncavage 2011	Eric J. Duncavage et al., <i>Hybrid Capture and Next-Generation Sequencing Identify Viral Integration Sites from Formalin-Fixed, Paraffin-Embedded Tissue</i> , 13 J. MOL. DIAGNOSTICS. 325 (2011).
2095	Mertes 2011	Florian Mertes et al., <i>Targeted Enrichment of Genomic DNA Regions for Next-Generation Sequencing</i> , 10 BRIEF. FUNCT. GENOM. 374 (2011).
2096	Shen 2010	Zhiyong Shen et al., <i>MPrimer: A Program for Reliable Multiplex PCR Primer Design</i> , 11 BMC BIOINFORMATICS FUNCT. GENOM. 143 (2010).
2097	Deutsche 2011	Ulla Deutsch et al., <i>Streamlining Multiplex PCR Analysis</i> , GENETIC ENGINEERING & BIOTECHNOLOGY, Dec. 1, 2011, https://www.genengnews.com/insights/streamlining-multiplex-pcr-analysis/ .
2098	Bragg 2013	Lauren M. Bragg et al., <i>Shining a Light on Dark Sequencing: Characterising Errors in Ion Torrent PGM Data</i> , 9 PLOS COMPUT. BIOL. 1 (2013)
2099	Stapleton 2002	Mark Stapleton et al., <i>The Drosophila Gene Collection: Identification of Putative Full-Length cDNAs for 70% of D. melanogaster Genes</i> , 12 COLD SPRING HARB. LAB. 1294 (2002)
2100	Infinitives	Evin de Leon Sanchez, <i>Infinitives</i> , SAN JOSE STATE UNIVERSITY WRITING CENTER, https://www.sjsu.edu/writingcenter/docs/handouts/Infinitives.pdf (last visited July 18, 2025)
2101	Meyer Comparison	Redline document comparing Exhibits 2103 and 2039
2102	Matz Email 1	Email thread between counsel and Petitioner’s counsel
2103	Meyer Declaration	Declaration of Eli Meyer, Ph.D.

Ex.	Short Name	Description
2104	Matz Email 2	Email thread between counsel and Petitioner's counsel
2105	Matz Email 3	Email thread between counsel and Petitioner's counsel
2106	Matz Email 4	Email thread between counsel and Petitioner's counsel
2107-2199		<i>Reserved</i>
2200		Privileged & Confidential Correspondence (submitted <i>in camera</i>)
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2284		Privileged & Confidential Correspondence (submitted <i>in camera</i>)
2285		Privileged & Confidential Declaration and Timeline Submitted Under Seal for <i>In Camera</i> Review

Dated: September 26, 2025

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CERTIFICATE OF SERVICE

The undersigned hereby certifies that a copy of the foregoing **PATENT OWNER'S UPDATED EXHIBIT LIST** was served on September 26, 2025 via email to Petitioner by serving the correspondence addresses of record as follows:

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