Paper No. 26
Filed: July 3, 2025

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE PATENT TRIAL AND APPEAL BOARD

ILLUMINA INC.,
Petitioner,

v.

MOLECULAR LOOP BIOSCIENCES, INC.,
Patent Owner.

Case No. IPR2024-00964
Patent No. 11,041,852

PETITIONER'S UPDATED EXHIBIT LIST

Pursuant to 37 C.F.R. § 42.63(e), Petitioner Illumina Inc. hereby submits a current listing of Petitioner exhibits. Exhibits 1046-1068 are being filed today.

Exhibit	Description
1001	U.S. Patent No. 11,041,852
1002	Declaration of Gregory B. Gloor, Ph.D.
1003	Declaration of Paul T. Spellman, Ph.D.
1004	P. Parameswaran, et al., *A pyrosequencing-tailored nucleotide barcode design unveils opportunities for large-scale sample multiplexing*, 35 NUCLEIC ACIDS RSCH. 19(e130) (2007).
1005	G.B. Gloor, et al., *Microbiome profiling by Illumina sequencing of combinatorial sequence-tagged PCR products*, *Cornell University Library* arXiv:1007.5075v1 (2010).
1006	D.R. Bentley, et al., *Accurate whole human genome sequencing using reversible terminator chemistry*, 456 NATURE 6, 53-59 (2008).
1007	File History of U.S. Patent No. 11,041,852
1008	U.S. Provisional Application No. 61/426,817
1009	F. Sanger, et al., *DNA sequencing with chain-terminating inhibitors*, 74 PROC. NAT'L. ACAD. SCI. USA 12, 5463-5467 (1977).
1010	M. Kircher & J. Kelso, *High-throughput DNA sequencing – concepts and limitations*, 32 BIOESSAYS 6, 524-536 (2010).
1011	M.L. Metzker, *Sequencing technologies—the next generation*, 11 NATURE REVIEWS | GENETICS 31-46 (2010).
1012	J. Shendure & H. Ji, *Next-generation DNA sequencing*, 26 NATURE BIOTECH. 10, 1135-1145 (2008).
1013	G. Wiley, et al., *Methods for generating shotgun and mixed shotgun/paired-end libraries for the 454 DNA sequencer*, 61 CURRENT PROTOCOLS IN HUMAN GENETICS 1, 18.1.1-18.1.21 (2009).
1014	M. Meyer, et al., *Parallel tagged sequencing on the 454 platform*, 3 NATURE PROTOCOLS 2, 267-278 (2008).

Exhibit	Description
1015	M. Meyer & M. Kircher, *Illumina sequencing library preparation for highly multiplexed target capture and sequencing*, 2010, COLD SPRING HARBOR PROTOCOL 6 (2010).
1016	U.S. Application Publication No. 2012/0028814
1017	S.J.G. Lahr & L.A. Katz, *Reducing the impact of PCR-mediated recombination in molecular evolution and environmental studies using a new-generation high-fidelity DNA polymerase*, 47 BIOTECHNIQUES 4, 857-866 (2009).
1018	A. Meyerhans, et al., *DNA recombination during PCR*, 18 NUCLEIC ACIDS RSCH. 7, 1687-1691 (1990).
1019	S. Paabo, et al., *DNA damage promotes jumping between templates during enzymatic amplification*, 265 J. OF BIOL. CHEM. 8, 4718-4721 (1990).
1020	S.J. Odelberg, et al., *Template-switching during DNA synthesis by Thermus aquaticus DNA polymerase I*, 23 NUCLEIC ACIDS RSCH. 11, 2049-2057 (1995).
1021	D.W. Craig, et al., *Identification of genetic variants using bar-coded multiplexed sequencing*, 5 NATURE METHODS 10, 887-893 (2008).
1022	R. Li, et al., *SNP detection for massively parallel whole-genome resequencing*, 19 GENOME RSCH. 1124-1132 (2009).
1023	M. Choi, et al., *Genetic diagnosis by whole exome capture and massively parallel DNA sequencing*, 106 PNAS 45, 19096-19101 (2009).
1024	G.B. Gloor, et al., *Microbiome profiling by Illumina sequencing of combinatorial sequence-tagged PCR products*, 5 PLOS ONE 10(e15406) (2010).
1025	*DNA Sequencing With Solexa® Technology*, Technology Spotlight, Illumina® Systems & Software, Pub. No. 770-2007-002 (2007).
1026	(Intentionally left blank)
1027	Illumina Press Release, *Illumina Announces New TruSeq™ SBS Sequencing Kit for the Genome Analyzer*, ILLUMINA (July 26, 2010), accessed at https://emea.illumina.com/cmopany/news-center/press-releases/2010/1451638.html on June 1, 2024.

Exhibit	Description
1028	*Genome Sequencer 20 System First to the Finish*, Roche Diagnostics®, Pub. No. 04866452990 (2006).
1029	J. Binladen, et al., *The use of coded PCR primers enables high-throughput sequencing of multiple homolog amplification products by 454 parallel sequencing*, 2 PLoS ONE 2:e197 (2007).
1030	(Intentionally left blank)
1031	Bruce Alberts, et al., Molecular Biology of the Cell 4, GARLAND SCIENCE (2002).
1032	*Polymerase Chain Reaction (PCR)*, NATIONAL HUMAN GENOME RESEARCH INSTITUTE (updated June 26, 2024), https://www.genome.gov/genetics-glossary/Polymerase-Chain-Reaction.
1033	M. Dai, et al., *NGSQC: cross-platform quality analysis pipeline for deep sequencing data*, 11 BMC GENOMICS 11(Suppl 4):S7 (2010).
1034	S. Creer, et al., *Ultrasequencing of the meiofaunal biosphere: practice, pitfalls and promises*, 19 MOLECULAR ECOLOGY (Suppl. 1) 4-20 (2010).
1035	The Cancer Genome Atlas Research Network, *Comprehensive genomic characterization defines human glioblastoma genes and core pathways*, 455 NATURE 23 (2008).
1036	U.S. Application Publication No. 2009/0226975
1037	International Patent Publication No. WO 2010/056728
1038	P. Maughan, et al., *Single-Nucleotide Polymorphism Genotyping in Mapping Populations via Genomic Reduction and Next-Generation Sequencing: Proof of Concept*, 3 PLANT GENOME (3) 166-178 (2010).
1039	Correspondence between Petitioner's counsel and arXiv, dated between February 22, 2024 and March 1, 2024.
1040	Correspondence between Petitioner's counsel and Patent Owner's counsel, dated between February 12, 2025 and February 25, 2025.
1041	Declaration of Simeon Warner, filed in Case IPR2015-01706.

Exhibit	Description
1042	Correspondence from Petitioner's counsel to arXiv, dated February 7, 2025 and February 14, 2025.
1043	Correspondence from arXiv to Petitioner's counsel, dated February 17, 2025.
1044	Correspondence from Petitioner's counsel to Simeon Warner, dated February 11, 2025.
1045	About arXiv, https://info.arxiv.org/about/index.html.
1046	Reply Declaration of Gregory B. Gloor, Ph.D.
1047	To submit an article, arXiv.org, http://arxiv.org/help/submit, captured on June 23, 2010 by Internet Archive Wayback Machine.
1048	To submit an article, arXiv.org, http://arxiv.org/help/submit, captured on September 17, 2010 by Internet Archive Wayback Machine.
1049	Declaration of Mina Ching (Internet Archive).
1050	Correspondence from arXiv to Gregory B. Gloor, Ph.D., dated March 31, 2025.
1051	Search results from arXiv.org, https://arxiv.org/search/?query=microbiome+illumina&searchtype=all&source=header, retrieved on May 20, 2025.
1052	Paired-ended reads pipeline (Illumina), mothur.org, https://forum.mothur.org/t/paired-end-reads-pipeline-illumina/373, retrieved on Mach 28, 2025.
1053	P.D. Schloss, et al., *Introducing Mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities*, 75 APPLIED & ENV'T MICROBIOLOGY (23) 7537-7541 (2009).
1054	Reply Declaration of Paul T. Spellman, Ph.D.
1055	Deposition Transcript of Viktor Adalsteinsson, Ph.D.
1056	M.W. Anderson et al., *Next Generation DNA Sequencing and the Future of Genomic Medicine*, 1 GENES 38-69 (2010).
1057	P.J. Campbell et al., *Identification of Somatically Acquired Rearrangements in Cancer Using Genome-Wide Massively*

Exhibit	Description
	Parallel Paired-End Sequencing, 40 NATURE GENETICS (6) 722-729 (2008).
1058	M. Delseny et al., *High Throughput DNA Sequencing: The new Sequencing Revolution*, 179 PLANT SCI. 407-422 (2010).
1059	C.W. Fuller et al., *The Challenges of Sequencing by Synthesis*, 27 NATURE BIOTECHNOLOGY (11) 1013-1023 (2009).
1060	I. Gorzer et al., *The Impact of PCR-Generated Recombination on Diversity Estimation of Mixed Viral Populations by Deep Sequencing*, 169 J. VIROLOGICAL METHODS 248-252 (2010).
1061	C.A. Maher et al., *Chimeric Transcript Discovery by Paired-End Transcriptome Sequencing*, 106 PNAS (30) 12353-12358 (2009).
1062	M.E. Pfrender et al., *Assessing Macroinvertebrate Biodiversity in Freshwater Ecosystems: Advances and Challenges in DNA-Based Approaches*, 85 Q. REV. BIOLOGY (3) 319-340 (2010).
1063	R.P. Smyth et al. *Reducing Chimera Formation During PCR Amplification to Ensure Accurate Genotyping*, 469 GENE 45-51 (2010).
1064	Defendant's Answer and Counterclaims to the Complaint, *Molecular Loop Biosciences, Inc. v. Illumina, Inc.*, C.A. No. 24-680-RGA (D. Del. Sept. 13, 2024).
1065	K.H. Taylor et al., *Next Generation Sequencing: Advances in Characterizing the Methylome*, 1 GENES 143-165 (2010).
1066	I. Varela et al., *Somatic Structural Rearrangements in Genetically Engineered Mouse Mammary Tumors*, 11 GENOME BIOLOGY R100, 1-12 (2010).
1067	N. Whiteford et al., *Swift: Primary Data Analysis for the Illumina Solexa Sequencing Platform*, 25 BIOINFORMATICS (17) 2194-2199 (2009).
1068	X. Wu et al., *SNP Discovery by High-Throughput Sequencing in Soybean*, 11 BMC GENOMICS 469, 1-12 (2010).

Respectfully submitted,

Dated: July 3, 2025

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CERTIFICATE OF SERVICE

The undersigned hereby certifies that a copy of the foregoing **PETITIONER'S UPDATED EXHIBIT LIST** and **EXHIBITS 1046-1068** were served on July 3, 2025, via e-mail directed to counsel of record for the Patent Owner at the following:

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