

UNITED STATES PATENT AND TRADEMARK OFFICE

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BEFORE THE PATENT TRIAL AND APPEAL BOARD

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INTEGRATED DNA TECHNOLOGIES, INC.,  
Petitioner,

v.

TECAN GENOMICS, INC.,  
Patent Owner

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Case No. IPR2025-00016  
U.S. Patent No. 10,876,108

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**PATENT OWNER'S OPPOSITION TO PETITIONER'S MOTION TO  
DISQUALIFY MIKHAIL V. MATZ AS PATENT OWNER'S EXPERT  
WITNESS**

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| <i>FujiFilm Corp. v. Sony Corp.</i> ,<br>IPR2017-01267, IPR2017-01268, Paper 9 (P.T.A.B. July 10, 2017) .....     | 7, 9           |
| <i>Galderma S.A. v. Medy-Tox, Inc.</i> ,<br>PGR2019-00062, Paper 56 (P.T.A.B. Feb. 11, 2021) .....                | <i>passim</i>  |
| <i>Hewlett-Packard Co. v. EMC Corp.</i> ,<br>330 F. Supp. 2d 1087 (N.D. Cal. Aug. 10, 2004).....                  | 6, 7           |
| <i>Koch Ref. Co. v. Jennifer L. Boudreau M/V</i> ,<br>85 F.3d 1178 (5th Cir. 1996) .....                          | 7, 9           |
| <i>Packet Intelligence LLC v. Juniper Networks Inc.</i> ,<br>2020 WL 4001460 (N.D. Cal. July 25, 2020) .....      | 5              |

**TABLE OF EXHIBITS**

| <b>Ex.</b> | <b>Short Name</b> | <b>Description</b>                                                                                                                                                                                                                                                                                               |
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| 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., <a href="https://www.genome.gov/about-genomics/fact-sheets/Sequencing-Human-Genome-cost">https://www.genome.gov/about-genomics/fact-sheets/Sequencing-Human-Genome-cost</a> (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 Shuts 454</i> , BioIT World (Oct. 16, 2013), <a href="https://www.bio-itworld.com/news/2013/10/16/six-years-after-acquisition-roche-quietly-shutters-454">https://www.bio-itworld.com/news/2013/10/16/six-years-after-acquisition-roche-quietly-shutters-454</a> . |
| 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 &amp; MgCl<sub>2</sub> Solution or GeneAmp 10X PCR Gold Buffer &amp; MgCl<sub>2</sub> 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                                                                                                                         |

| Ex.       | Short Name             | Description                                                                                                                                                        |
|-----------|------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 2022-2035 |                        | <i>Reserved</i>                                                                                                                                                    |
| 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. Bustamente, 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         | Linas S. Padegimas & Nancy A. Reichert, <i>Adaptor Ligation-Based Polymerase Chain Reaction-Mediated Walking</i> , 260 ANALYTICAL BIOCHEMISTRY (1998)              |

| Ex.  | Short Name        | Description                                                                                                                                                                                        |
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| 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)                        |
| 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)                                                                   |

| Ex.  | Short Name                   | Description                                                                                                                                                                                                                                                                                               |
|------|------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 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)                                                                                                                                                                         |
| 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, <a href="https://www.biocompare.com/Editorial-Articles/576645-Growing-Options-for-Enriching-Target-DNA/">https://www.biocompare.com/Editorial-Articles/576645-Growing-Options-for-Enriching-Target-DNA/</a> . |

| Ex.  | Short Name      | Description                                                                                                                                                                                                                          |
|------|-----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 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)                                                                                      |
| 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)                                                                                                                                                                    |

| Ex.  | Short Name                 | Description                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|------|----------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| 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, <a href="https://www.biospace.com/nugen-announces-issuance-of-u-s-patent-for-its-single-primer-target-enrichment-technology-spet-for-next-generation-sequencing-applications">https://www.biospace.com/nugen-announces-issuance-of-u-s-patent-for-its-single-primer-target-enrichment-technology-spet-for-next-generation-sequencing-applications</a> (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).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |

| Ex.  | Short Name     | Description                                                                                                                                                                                                                                                                            |
|------|----------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 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).                                                                                 |
| 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, <a href="https://www.genengnews.com/insights/streamlining-multiplex-pcr-analysis/">https://www.genengnews.com/insights/streamlining-multiplex-pcr-analysis/</a> . |
| 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,                                                                                                                                                                                                   |

| <b>Ex.</b> | <b>Short Name</b> | <b>Description</b>                                                                                                                                                           |
|------------|-------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|            |                   | <a href="https://www.sjsu.edu/writingcenter/docs/handouts/Infinitives.pdf">https://www.sjsu.edu/writingcenter/docs/handouts/Infinitives.pdf</a> (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.                                                                                                                                              |
| 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                                                                                                                        |

## I. INTRODUCTION

Petitioner improperly seeks to exclude testimony from the authors of the publication that Petitioner alleges anticipates the claims of the '108 patent, namely the Meyer reference. Without conceding the basis for Petitioner's motion regarding Dr. Matz, Tecan repeatedly sought to address Petitioner's alleged concerns, only to have Petitioner change its position at every turn. To avoid the dispute regarding Dr. Matz's involvement and reduce the prejudice to Tecan, Tecan secured a substitute expert—another author of the Meyer reference, Dr. Eli Meyer. Dr. Meyer has reviewed the materials and agreed to adopt the opinions in Dr. Matz's declaration as his own.<sup>1</sup> This solution resolves Petitioner's objections regarding Dr. Matz while preserving testimony that is crucial to properly understanding the Meyer reference. This is the exact recourse ordered by the Board in *Galderma*, and the kind of solution that Petitioner itself proposed. *Galderma S.A. v. Medy-Tox, Inc.*, PGR2019-00062, Paper 56, at 9 (P.T.A.B. Feb. 11, 2021). Now, however, Petitioner has indicated that it will oppose the substitute declarant.

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<sup>1</sup> Attached hereto as Exhibit 2103 is the substitute declaration of Dr. Eli Meyer. Dr. Meyer's declaration has the same opinions about the public disclosure in Meyer as those provided by Dr. Matz. See Exhibit 2101 (comparison of Dr. Meyer's Declaration (EX2103) to Dr. Matz Declaration (EX2039)).

Petitioner's aim appears to be nothing more than keeping the Board in the dark as to misstatements it made in its Petition regarding the contents of Meyer. Rather than simply cross-examine the author on his sworn testimony, Petitioner concocts a false pretext for its motion based on a few hours of background conversation *where Dr. Matz, not Petitioner*, allegedly shared information about his public disclosures in Meyer to preclude this testimony in its entirety.

Petitioner has not articulated any explanation or justification for now objecting to the substitute declaration, beyond suggesting that Dr. Meyer's declaration would be "tainted" if it were the same as Dr. Matz's declaration or because of Dr. Matz's relationship with Dr. Meyer. In essence, Petitioner seeks to manufacture any basis to oppose the kind of compromise it itself proposed. But the relevant facts are simple. Dr. Meyer has no connection to Petitioner, so the relationship that allegedly disqualifies Dr. Matz does not apply to Dr. Meyer. Dr. Meyer is prepared to provide the same testimony about his public work as Dr. Matz and attests to the accuracy of his declaration under penalty of perjury. To the extent Petitioner disagrees with his opinions, it will have a chance to examine him.

Ultimately, Petitioner's shifting and unsupported theories seek only to deprive the Board of clearly relevant information concerning the publication at the center of the Petition. Tecan, not Petitioner, will be manifestly and irreparably prejudiced by excluding this evidence. Tecan submitted a declaration from Dr. Matz and relied on

it in its response without any knowledge of Dr. Matz's alleged obligations to Petitioner. Any concerns regarding Dr. Matz were raised *after* Tecan relied on Dr. Matz and do not concern Dr. Meyer. Any potential prejudice to Petitioner would be resolved by this substitution, which still includes the submission of a declaration that is based solely on the *public* work described in Meyer.

Excluding evidence is an extreme remedy and has no place here. Tecan has prepared a substitute declaration *at Petitioner's suggestion*. Both the law and fundamental fairness support allowing Tecan to submit a substitute declaration from Dr. Meyer in replacement of the objected-to declaration from Dr. Matz.

## **II. FACTUAL BACKGROUND**

Petitioner contends that various claims of the '108 patent are invalid in view of a 2009 article titled *Sequencing and de novo analysis of a coral larval transcriptome using 454 GSFlx* ("Meyer"). Paper 1 at 28-69. In preparing its response, Tecan retained Dr. Matz, the senior author of Meyer, as a technical expert in connection with this and relating proceedings on May 23, 2025. EX1111. Dr. Matz represented that he had no conflicting obligations in rendering these consulting services and represented he would provide no third-party confidential information to Tecan or Goodwin. *Id.* at 1-2, 3. On July 17, 2025, Dr. Matz submitted a declaration in support of Patent Owner's Response. EX2039.

On July 22, 2025, Petitioner contacted Tecan requesting that it withdraw Dr.

Matz's declaration based on an alleged May 21, 2024 consulting agreement regarding "Patent Litigation Between IDT and Tecan Genomics." EX1090. This was the first time Tecan was notified of such an alleged agreement.

Tecan then sought an explanation of what "confidential information" was allegedly shared by Petitioner with Dr. Matz. EX2103 at 3-4. Petitioner dismissively alleged it concerned "the subject matter of [the current proceeding]" and refused further explanation. *Id.* at 3. Tecan reiterated that this explanation was needed to fairly assess or respond to Petitioner's objection. *Id.* at 1-2. Petitioner flatly refused. *Id.* at 1. With Petitioner's motion to disqualify, Petitioner submitted twelve documents for *in camera* review. Paper 24. These materials were not shared with Tecan to any extent, despite its requests, even though they are extensively cited and relied upon in its motion. Paper 25, 3-4, 7-8.

As Tecan pursued alternative remedies to avoid burdening the Board, Petitioner suggested that Tecan consider an alternate declarant for the Matz testimony. EX2104 at 5. Tecan worked to secure a substitute declaration from Dr. Eli Meyer, the primary author of the Meyer publication. *Id.* at 1. Petitioner then asserted a variety of shifting "concerns" with submitting a substitute declaration, despite having no relationship with Dr. Meyer. EX2105 at 1-2, 4; EX2106 at 7-8.

### III. ARGUMENT

"Disqualification of an expert witness is a drastic measure [the Board]

hesitate[s] to impose except when absolutely necessary.” *FujiFilm Corp. v. Sony Corp.*, IPR2017-01267; IPR2017-01268, Paper 9 at 6 (P.T.A.B. July 10, 2017). To disqualify, the moving party must show that (1) it was “objectively reasonable for [the moving party] to believe that it had a confidential relationship” with expert and (2) that the moving party “disclosed confidential information to [the expert] that is relevant to the current proceeding.” *Galderma*, PGR2019-00062, Paper 56 at 5. Courts further consider “whether disqualification would be fair to the affected party and would promote the integrity of the legal process.” *Packet Intel. LLC v. Juniper Networks Inc.*, 2020 WL 4001460, at \*2 (N.D. Cal. 2020). “To minimize the impact that [granting disqualification] may have on [the nonmoving party],” the Board often allows the nonmoving party to “submit a substitute declaration by a new expert who is willing to adopt wholesale the opinions set forth by [the original expert].” *Galderma*, PGR2019-00062, Paper 56, at 9.

**A. IDT Improperly Seeks to Exclude All Testimony Regarding the Public Disclosure of the Meyer Reference**

**1. Petitioner Fails to Identify Confidential Information Shared with Dr. Matz**

Tecan maintains that Petitioner’s conclusory allegations that Dr. Matz received any confidential information from Petitioner are insufficient to disqualify Dr. Matz. However, in an effort to compromise, Tecan has provided a substitute declaration to fully alleviate any alleged issues with Dr. Matz’s declaration.

That said, Petitioner’s claims regarding “confidential information” are unsupported. There is no presumption that confidential information is exchanged between counsel and experts. *See Hewlett-Packard Co. v. EMC Corp.*, 330 F. Supp. 2d 1087, 1094 (N.D. Cal. Aug. 10, 2004) (“[D]iscussions between parties or counsel and experts do not carry the presumption that confidential information was exchanged.”). Instead, Petitioner must provide specificity as to the ***confidential*** information that ***Petitioner shared with Dr. Matz***. *See id.* (“Because the burden is on the party seeking to disqualify the expert, that party should point to specific and unambiguous disclosures that if revealed would prejudice to the party.”). However, general allegations regarding an engagement letter and vague and conclusory descriptions of the correspondence of what Dr. Matz said are not sufficient.

Rather, the few conclusory allegations in Petitioner’s motion suggest at most that *Dr. Matz* shared *non-confidential* information regarding his publication. Paper 24 at 3-5.<sup>2</sup> For example, Petitioner asserts that Dr. Matz answered “questions” about

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<sup>2</sup> Petitioner’s arguments are predicated on redacted documents that Tecan cannot access, which is manifestly unfair and violates basic due process rights. Tecan concurrently opposes Petitioner’s motion for *in camera* review of these materials. As the Board found in *Agila*, a party cannot be permitted to use confidential or

Meyer and the state of the art (or searching for art) and provided a “diagram” of those same points. *Id.* However, such conclusory allegations are insufficient as a general matter. *See Agila*, IPR2025-00053, Paper 13 at 5 (declining to disqualify an expert based on “conclusory statements” and requiring the moving party to “support its motion with specific evidence and on-point legal authorities.”). Nor are any of these a disclosure of confidential information *by Petitioner*. The alleged discussions concern only “purely technical information” that is not confidential. *Koch Ref. Co. v. Jennifer L. Boudreau M/V*, 85 F.3d 1178, 1182 (5th Cir. 1996); *Cellular Commc’ns. Equip, Inc. v. HTC Corp.*, No. 6:13-cv-507, slip op. at 6–7 (E.D. Tex. Mar. 24, 2016) (denying motion to disqualify expert that was “asked to search for prior invalidating art,” noting such “[p]urely technical information is not confidential.”); *Hewlett-Packard*, 330 F. Supp. 2d at 1097. Lastly, Petitioner’s conclusory allegation that it vaguely shared “litigation strategy” fares no better. Paper 24, 4. They do not meet the specificity sufficient to disqualify (and only reinforce the prejudice of having to defend against information Tecan cannot see). *Agila*, IPR2025-00053, Paper 13.

## **2. Petitioner’s Objection to a Substitute Declaration Is Baseless**

Despite the failures of Petitioner’s motion, Tecan sought alternative remedies

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privileged materials as both a sword and a shield. *Agila Specialties Inc. v. Cephalon, Inc.*, IPR2015-00503, Paper 13 at 5 (P.T.A.B. Aug. 19, 2015).

to address Petitioner's concerns and minimize the prejudice to Tecan. Specifically, *at Petitioner's suggestion*, Tecan sought an alternate declarant to substitute for Dr. Matz's testimony. EX2104 at 5-6. Despite limited notice, Tecan was able to retain Dr. Eli Meyer, the lead co-author of Meyer. *Id.* at 1. Dr. Meyer reviewed the declaration filed with Tecan's Response and agreed to sign a declaration that is substantially similar to Dr. Matz's declaration. *See Galderma*, PGR2019-00062, Paper 56 at 9-10.

Petitioner has now indicated it continues to object. However, the substitute declarant, Dr. Meyer, has no relationship with Petitioner, and there is no basis to disqualify him. Petitioner initially suggested that Dr. Meyer cannot provide the same testimony about *the public disclosure found in the Meyer publication* because of Dr. Matz's initial involvement. *See, e.g.*, EX2105 at 1-2. However, that is the very purpose of a substitute declaration. In any case, like Dr. Matz before him, Dr. Meyer is willing to attest to the accuracy of this declaration under oath. To the extent Petitioner disagrees with his declaration, their obvious recourse is to cross-examine him—not the extreme remedy to exclude all such testimony. Petitioner also contends that contact between Dr. Meyer and Dr. Matz poses a problem. *Id.* at 4-5. Dr. Meyer has not discussed the substance of his declaration with Dr. Matz nor is it relevant in any form to a declaration about his prior work. EX2103 at 3. In essence, Petitioner seeks to undermine the very procedure used in *Galderma* and create new and

baseless hurdles to preclude substitute testimony. There is no legal basis to deprive Tecan and the Board of critical information concerning the flaws in Petitioner's arguments regarding the public disclosures in Meyer.

**B. Prejudice to Tecan Weighs Heavily Against Exclusion of this Evidence**

Tecan will be manifestly prejudiced by the exclusion of testimony regarding Meyer. To fully address Petitioner's claims of invalidity, the Board (and the public) should receive all relevant information related to the allegations. Critically, Dr. Matz and his substitute, Dr. Meyer, are uniquely positioned to discuss their own work. Moreover, Tecan had no role in the supposed conflict. It retained Dr. Matz with written confirmation that he could testify on these issues. EX1111. It would be manifestly unjust for Tecan to bear the sole prejudice from this inadvertent situation. Tecan has attempted to address Petitioner's alleged concerns regarding Dr. Matz, following the procedure Petitioner requested.

In contrast, Petitioner cannot even feign prejudice. Paper 24 at 10. Nor could it. Petitioner's claims of sharing confidential information seem to be based on Dr. Matz's commentary on his own, publicly available research. Dr. Meyer's substitute declaration likewise only concerns public technical information, which courts routinely find as not confidential. *Koch Ref. Co.*, 85 F.3d at 1182; *Cellular Commc'ns. Equip, Inc.*, No. 6:13-cv-507, slip op. at 6–7.

### **C. Petitioner's Efforts to Exclude Clearly Relevant Evidence Should Be Rejected**

At bottom, Petitioner seeks to block relevant testimony on the prior art based on nothing but pretext. Petitioner initially engaged Dr. Matz to speak with them for two hours about his publication and then sought to preclude his testimony from being presented.<sup>3</sup> Petitioner now attempts to prevent having another author testify without any basis for prejudice. Petitioner should not be permitted to specifically tie up the authors of prior art articles or other witnesses for the sole purposes of precluding the Board from gaining a complete understanding of the relevant facts. Ultimately, the issue before the Board concerns Petitioner's allegations of invalidity. Tecan should be permitted to submit all relevant information, which the Board is entitled to see and which sound public policy should demand. To conclude otherwise would be at odds with the law and facts and manifestly unjust.

### **IV. CONCLUSION**

For the foregoing reasons, Tecan respectfully requests that the Board allow Tecan to submit a substitute declaration from Dr. Meyer in replacement of the declaration of Dr. Matz.

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<sup>3</sup> Because of Petitioner's selective redactions, it remains unclear to Tecan whether Petitioner learned that its positions were inaccurate based on discussions with Dr. Matz but continued in his absence, raising concerns with Petitioner's duty of candor.

Dated: August 19, 2025

Respectfully submitted,

By: /Linnea P. Cipriano/  
Linnea P. Cipriano  
(Reg. No. 67,729)  
GOODWIN PROCTER LLP  
620 Eighth Avenue  
New York, NY 10018  
Phone: (212) 813-8800  
Cell: (443) 235-1739  
Fax: (212) 937-2204  
lcipriano@goodwinlaw.com  
*Counsel for Patent Owner Tecan  
Genomics, Inc.*

**CERTIFICATE OF SERVICE**

The undersigned hereby certifies that a copy of the foregoing **PATENT OWNER'S OPPOSITION TO PETITIONER'S MOTION TO DISQUALIFY MIKHAIL V. MATZ AS PATENT OWNER'S EXPERT WITNESS** was served on August 19, 2025 via email to Petitioner by serving the correspondence addresses of record as follows:

|                                                                                                                                                                                                                                                      |                                                                                                                                                                                                                                              |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Lead Counsel:</b><br><b>Thomas S. Fletcher</b><br><b>(Reg. No. 72,383)</b><br>IDT-Tecan-IPRs@wc.com<br>WILLIAMS & CONNOLLY LLP<br>680 Maine Avenue SW<br>Washington, DC 20024<br>Phone: (202) 434-5497<br>Fax: (202) 434-5029                     | <b>Backup Counsel:</b><br><b>Jessamyn S. Berniker</b><br><b>(Reg. No. 72,328)</b><br>IDT-Tecan-IPRs@wc.com<br>WILLIAMS & CONNOLLY LLP<br>680 Maine Avenue SW<br>Washington, DC 20024<br>Phone: (202) 434-5497<br>Fax: (202) 434-5029         |
| <b>Backup Counsel:</b><br><b>Kevin Hoagland-Hanson</b><br><b>(Pro Hac Vice Admission Pending)</b><br>IDT-Tecan-IPRs@wc.com<br>WILLIAMS & CONNOLLY LLP<br>680 Maine Avenue SW<br>Washington, DC 20024<br>Phone: (202) 434-5497<br>Fax: (202) 434-5029 | <b>Backup Counsel:</b><br><b>Patrick Hynds</b><br><b>(Pro Hac Vice Admission Pending)</b><br>IDT-Tecan-IPRs@wc.com<br>WILLIAMS & CONNOLLY LLP<br>680 Maine Avenue SW<br>Washington, DC 20024<br>Phone: (202) 434-5497<br>Fax: (202) 434-5029 |
| <b>Backup Counsel:</b><br><b>Nicholas G. Vincent</b><br><b>(Reg. No. 79,788)</b><br>IDT-Tecan-IPRs@wc.com<br>WILLIAMS & CONNOLLY LLP<br>680 Maine Avenue SW<br>Washington, DC 20024<br>Phone: (202) 434-5497<br>Fax: (202) 434-5029                  | <b>Backup Counsel:</b><br><b>Anna Searle</b><br><b>(Pro Hac Vice Admission Pending)</b><br>IDT-Tecan-IPRs@wc.com<br>WILLIAMS & CONNOLLY LLP<br>680 Maine Avenue SW<br>Washington, DC 20024<br>Phone: (202) 434-5497<br>Fax: (202) 434-5029   |

August 19, 2025

/Linnea P. Cipriano/  
Linnea P. Cipriano  
(Reg. No. 67,729)  
GOODWIN PROCTER LLP  
620 Eighth Avenue  
New York, NY 10018  
Phone: (212) 813-8800  
Fax: (212) 937-2204  
lcipriano@goodwinlaw.com

*Counsel for Patent Owner Tecan  
Genomics, Inc.*