

# low-volume liquid handlers for genomics



 **ttp labtech**

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# low-volume liquid handling with mosquito<sup>®</sup>



## accuracy and precision

with nanolitre to microlitre volumes using rapid true positive-displacement pipetting technology



## reduce sample and reagent consumption

achieve up to 50-fold reduction in reagents



## handles liquids with high viscosity accurately

such as enzymes in glycerol or genomic DNA



## no cross-contamination

no carryover with low-cost disposable pipettes



## future-proof versatile open platform

miniaturise any assay with mosquito by easily creating new protocols

# miniaturise any assay

TTP Labtech's mosquito saves cost and increases throughput for the following applications:

## NGS

### library prep

including quantification, normalisation and magnetic bead-based cleanup

## single cell genomics

## microbial genomics

or any other assay!

## validated protocols include:

- ✓ Nextera XT library prep [1,2]
- ✓ DNA quantification [4]
- ✓ NGS library normalisation [1]
- ✓ CEL-seq cDNA synthesis [3]
- ✓ SMART-seq [5]

## references:

### 1. Miniaturised Nextera XT library preparation and normalisation to study human stem cell differentiation:

Kyle M. Loh\*, Angela Chen\*, Pang Wei Koh, Tianda Z. Deng, Rahul Sinha, Jonathan M. Tsai, Amira A. Barkal, Kimberley Y. Shen, Rajan Jain, Rachel M. Morganti, Ng Shyh-Chang, Nathaniel B. Fernhoff, Benson M. George, Gerlinde Wernig, Rachel E.A. Salomon, Zhenghao Chen, Hannes Vogel, Jonathan A. Epstein, Anshul Kundaje, William S. Talbot, Phillip A. Beachy, Lay Teng Ang<sup>^</sup>, Irving L. Weissman<sup>^</sup>; Mapping the pairwise choices leading from pluripotency to human bone, heart, and other mesoderm cell types; Cell 166.2 (2016), 451-467

Pang Wei Koh\*, Rahul Sinha\*, Amira A. Barkal, Rachel M. Morganti, Angela Chen, Irving L. Weissman<sup>^</sup>, Lay Teng Ang<sup>^</sup>, Anshul Kundaje<sup>^</sup> & Kyle M. Loh<sup>^</sup>, Data Descriptor: An atlas of transcriptional, chromatin accessibility, and surface marker changes in human mesoderm development. Scientific Data 3:160109 (2016)

### 2. Miniaturised Nextera XT library preparation for high-throughput single cell transcriptome sequencing:

Sergio Mora-Castilla, Cuong To, Soheila Vaezeslami, Robert Morey, Srimeenakshi Srinivasan, Jennifer N. Dumdie, Heidi Cook-Andersen, Joby Jenkins, and Louise C. Laurent; Miniaturization Technologies for Efficient Single-Cell Library Preparation for Next-Generation Sequencing, JALA, 2016 Vol 21 (4), 557-567

### 3. Cel-seq2 cDNA synthesis from single macrophages in 5-fold reduced total volume:

Laura Hertrtwich\*, Indrajit Nanda\*, Konstantinos Evangelou\*, Teodora Nikolova\*, Veronika Horn\*, Sagar, Daniel Erny, Jonathan Stefanowski, Leif Fogell, Claudius Klein, Kourosh Gharun, Marie Follo, Maximilian Seidl, Bernhard Kremer, Nikolas Múnke, Julia Senges, Manfred Fliegaufl, Tom Aschman, Dietmar Pfeifer, Sandrine Sarrazin, Michael H. Sieweke, Dirk Wagner, Christine Dierks, Thomas Haaf, Thomas Ness, Mario M. Zaiss, Reinhard E. Voll, Sachin D. Deshmukh, Marco Prinz, Torsten Goldmann, Christoph Hölscher, Anja E. Hauser, Andres J. Lopez-Contreras, Dominic Grün, Vassilis Gorgoulis, Andreas Diefenbach, Philipp Henneke, Antigoni Triantafyllopoulou; DNA Damage Signaling Instructs Polyploid Macrophage Fate in Granulomas, Cell, 2016 Vol 167 (5), 1264-1280.

### 4. Accurate quantitation and normalisation of genomic DNA for high-throughput DNA library construction:

Peter Ellis, Lesley Shirley, Louise Aigrain, Matthew Mayho, Scott Thurston, James Glover, Joby Jenkins, Sara Widaa, Jamieson Lovell, Emma Gray, Tony Cox. Poster session presented at: Advances in Genome Biology and Technology (AGBT) General Meeting, 2017 Feb 13-16; Hollywood Beach, Florida, US

### 5. Miniaturization and automation of CEL-Seq2 and SMARTer-Seq using the mosquito HTS/HV liquid handler:

Josip Herman, Jon Penterman, Sagar, Andreas Diefenbach, Antigoni Triantafyllopoulou, Anne F. Hammerstein, Joby Jenkins, Dominic Grün, Stuart S. Levine and Melanie A. Adams-Cioaba. Poster session presented at: Advances in Genome Biology and Technology (AGBT) General Meeting, 2017 Feb 13-16; Hollywood Beach, Florida, US

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