low-volume liquid handlers for genomics

sptlabtech

low-volume liquid handling with mosquito®

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

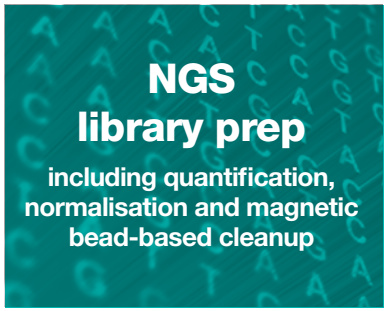
handles liquids with high viscosity accurately
such as enzymes in glycerol or genomic DNA

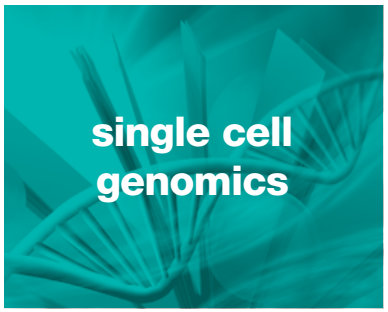
no cross-contamination
no carryover with low-cost disposable pipettes

future-proof versatile open platform
miniaturise any assay with mosquito by easily creating new protocols

miniaturise any assay

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





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]
- ✓ **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, Kimberle 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, Philip A. Beachy, Lay Teng Ang^, Irving L. Weissman^; 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^, Lay Teng Ang^, Anshul Kundaje^ & Kyle M. Loh^, 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:

Nathan J. Gesmundo, Bérengère Sauvagnat, Patrick J. Curran, Matthew P. Richards, Christine L. Andrews, Peter J. Dandliker & Tim Cernak. Nature volume 557, pages 228–232 (2018)

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

Laura Herrtwich*, Indrajit Nanda*, Konstantinos Evangelou*, Teodora Nikolova*, Veronika Horn*, Sagar, Daniel Erny, Jonathan Stefanowski, Leif Rogell, Claudius Klein, Kourosh Gharun, Marie Follo, Maximilian Seidl, Bernhard Kremer, Nikolas Münke, Julia Senges, Manfred Fliegauf, 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. *Co-first author. ^Co-senior autho

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:

Tianyuan Peng Gabe Nagy Dr. Jonathan C. Trinidad Dr. Joy Marie Jackson Prof. Nicola L. B. Pohl Wiley
First published: 27 September 2017 https://doi.org/10.1002/cbic.201700292 Cited by: 1

get in touch

SPT Labtech Ltd

+44 (0) 1223 627 555
discover@sptlabtech.com

SPT Labtech Inc

+1 (855) 601 5867
discover@sptlabtech.com

SPT Labtech India Private Ltd

+91 9968291292
enquiries@sptlabtech.com