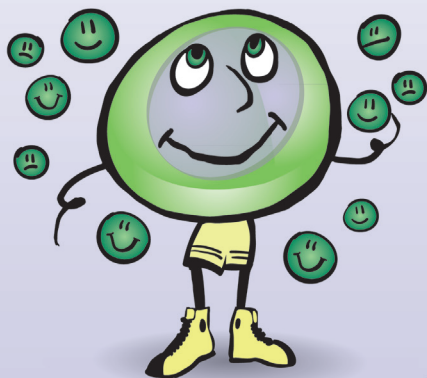
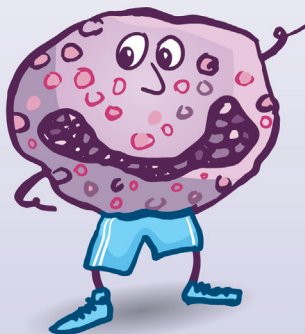


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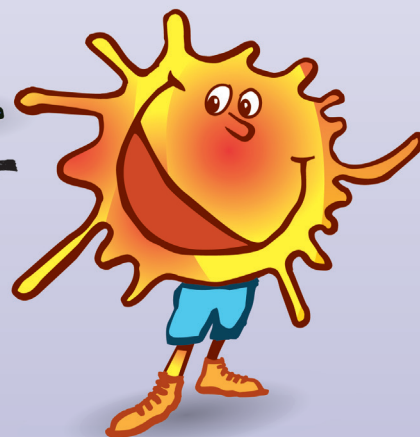
T Helper



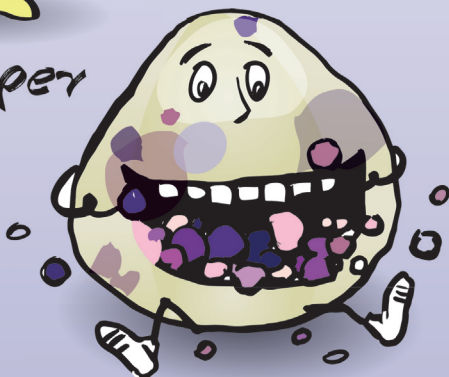
Eosinophil



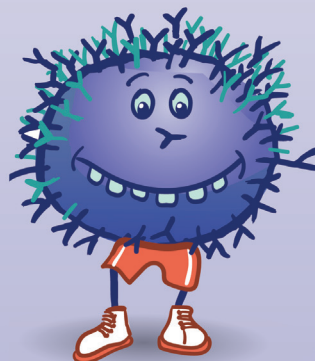
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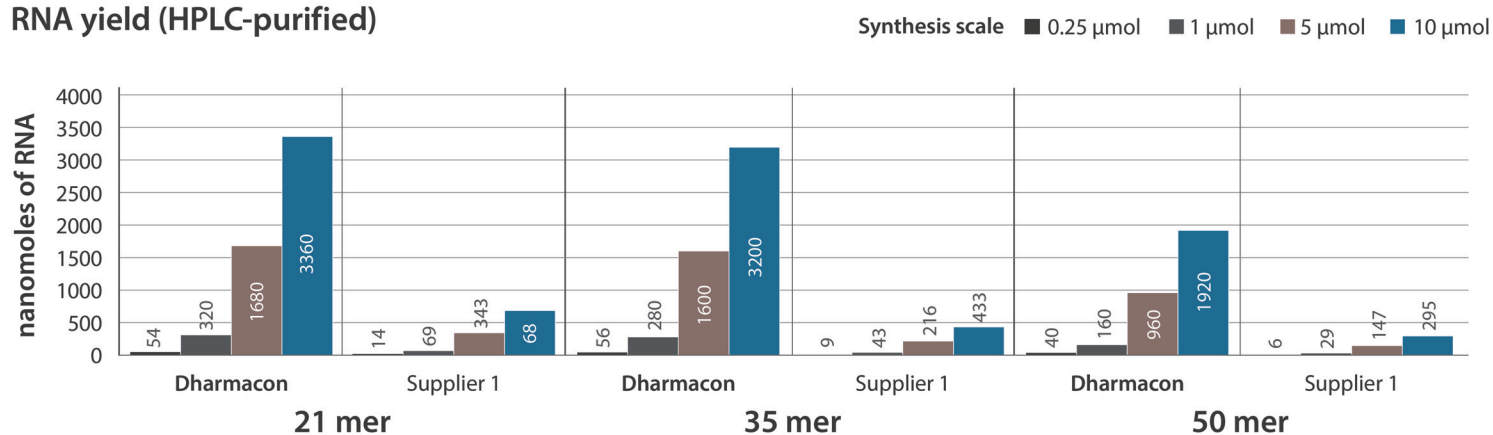
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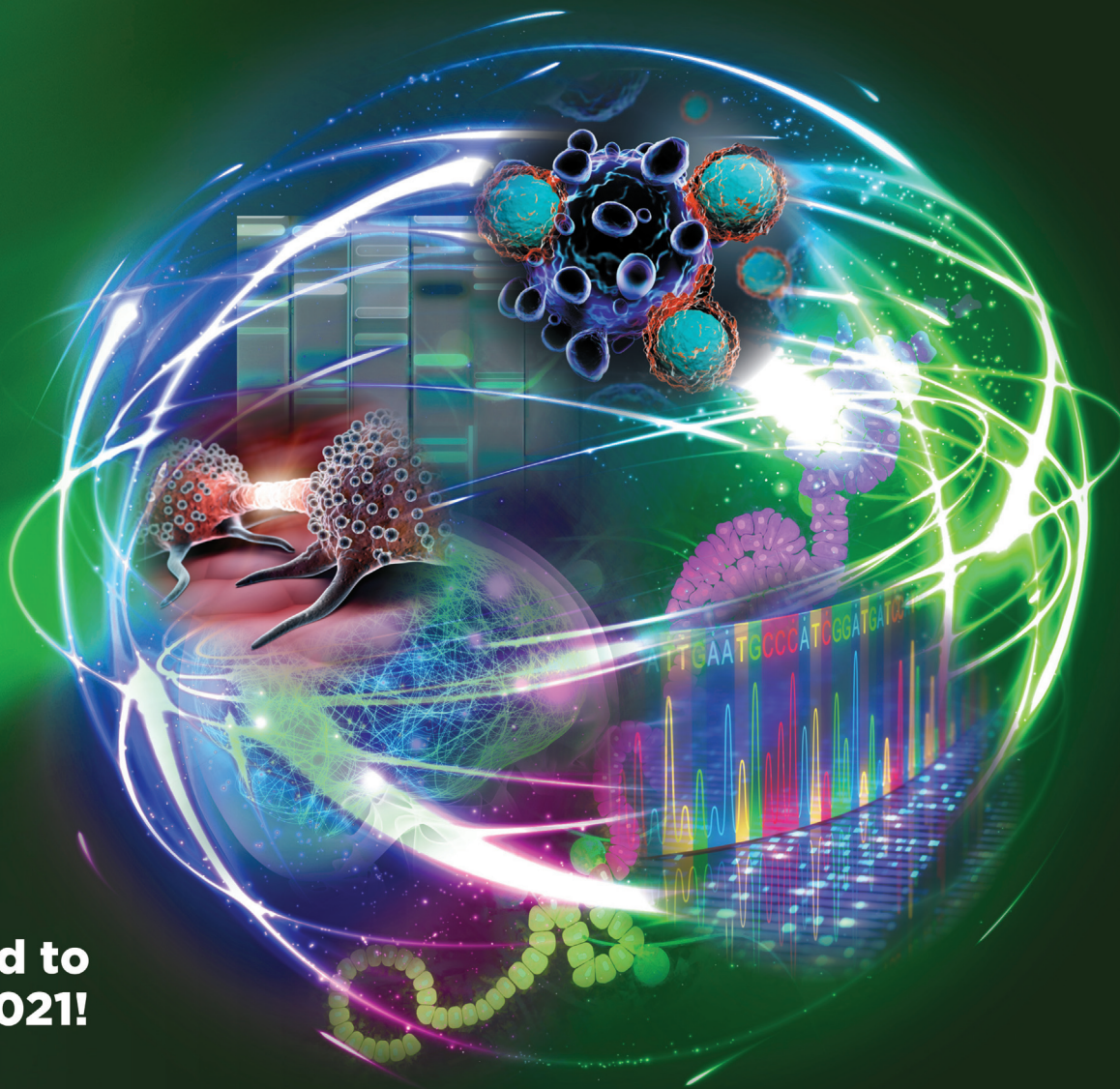
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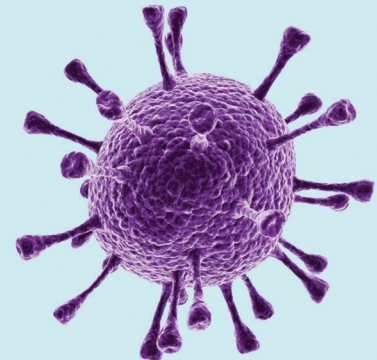
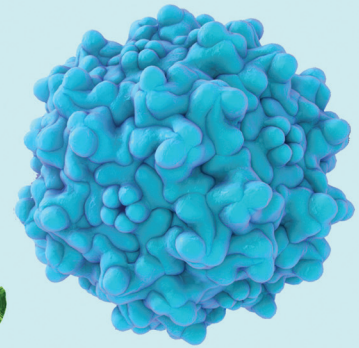
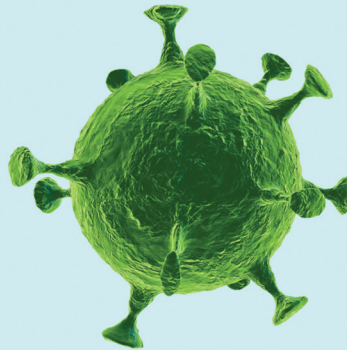


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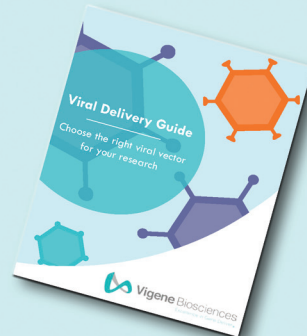
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- **Accurate quantification of gene expression**—PCR-free library preparation process without fragmentation allows for more reliable quantification of gene expression than RNA-seq.
- **Applicable for cryopreserved cells and tissue samples**—The protocol does not contain any incorporation process for labeling.

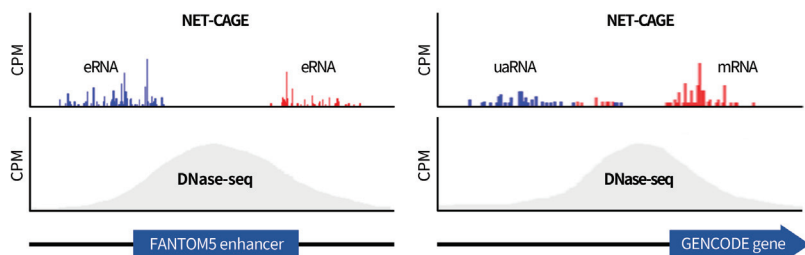


Fig.1. NET-CAGE signals around a region of FANTOM5 enhancer (left) and GENCODE gene (right).

NET-CAGE library preparation /analysis services	
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CAGE library preparation for Illumina sequencers	500 USD/sample
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CAGE bioinformatics analysis	250 USD/sample

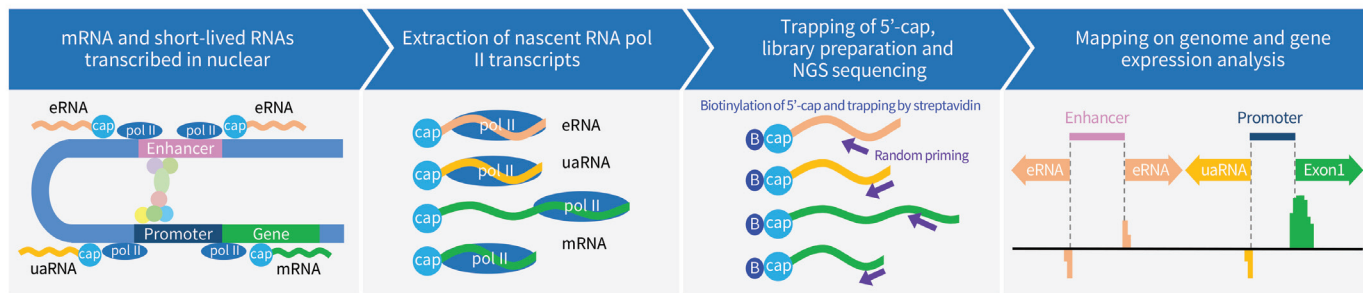


Fig.2. Workflow of the NET-CAGE. NET-CAGE is a unique NGS library preparation method using “cap-trapping” technology.

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