Electronic Supplementary Material (ESI) for Lab on a Chip.

LabDisk for SAXS: A centrifugal microfluidic sample preparation platform for small-angle X-ray scattering

Supplementary information

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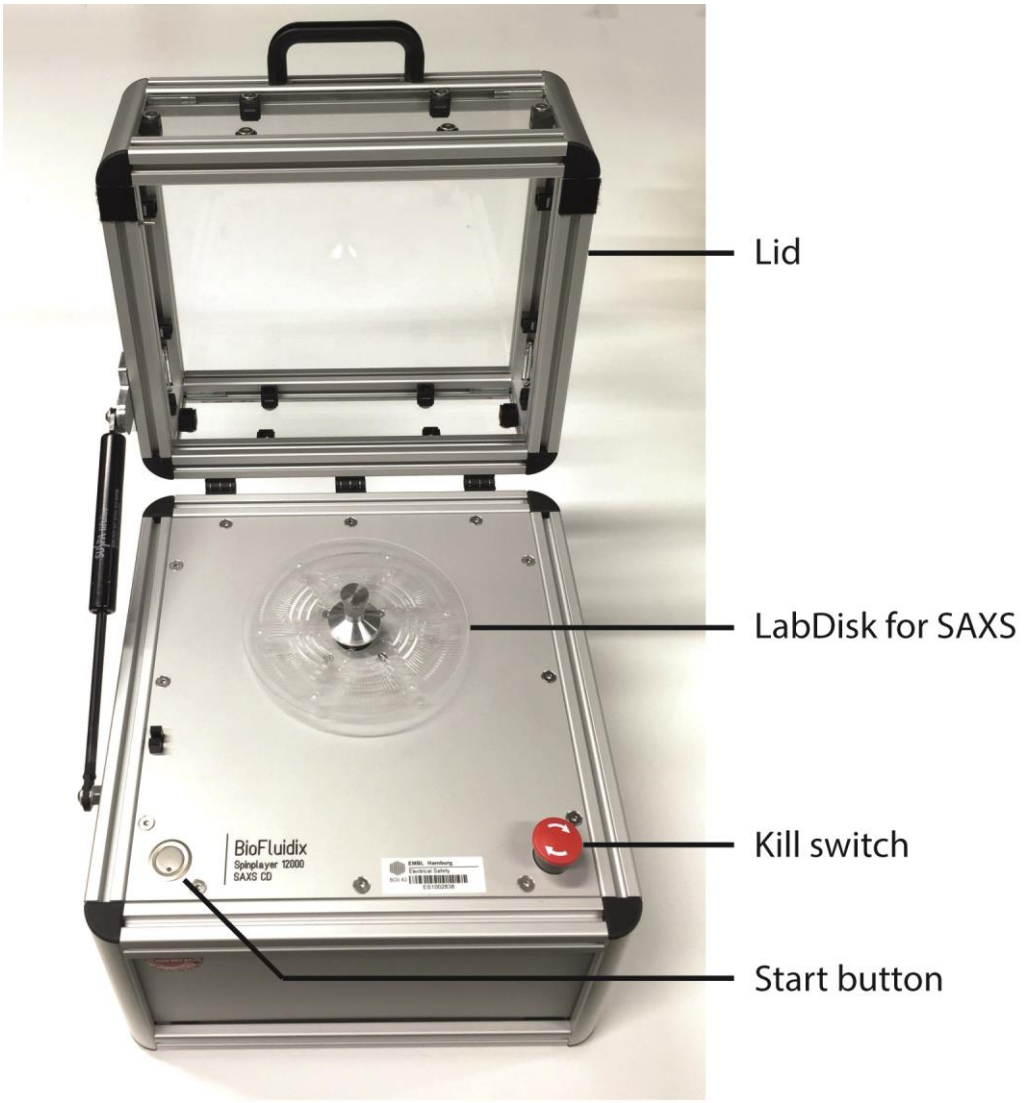
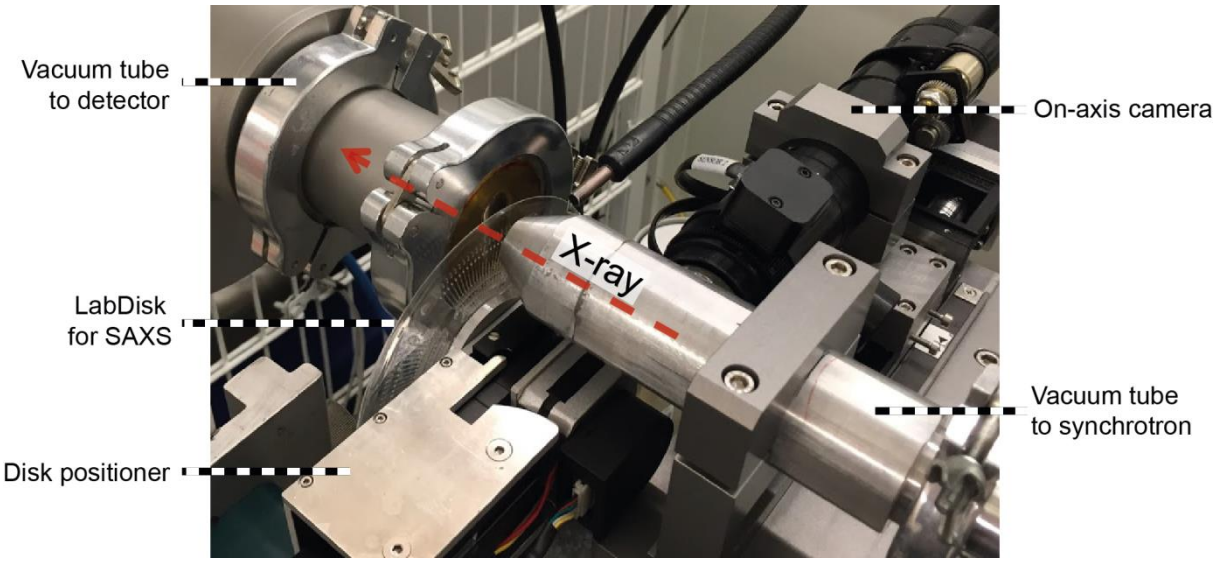
Processing device for the LabDisk for SAXS



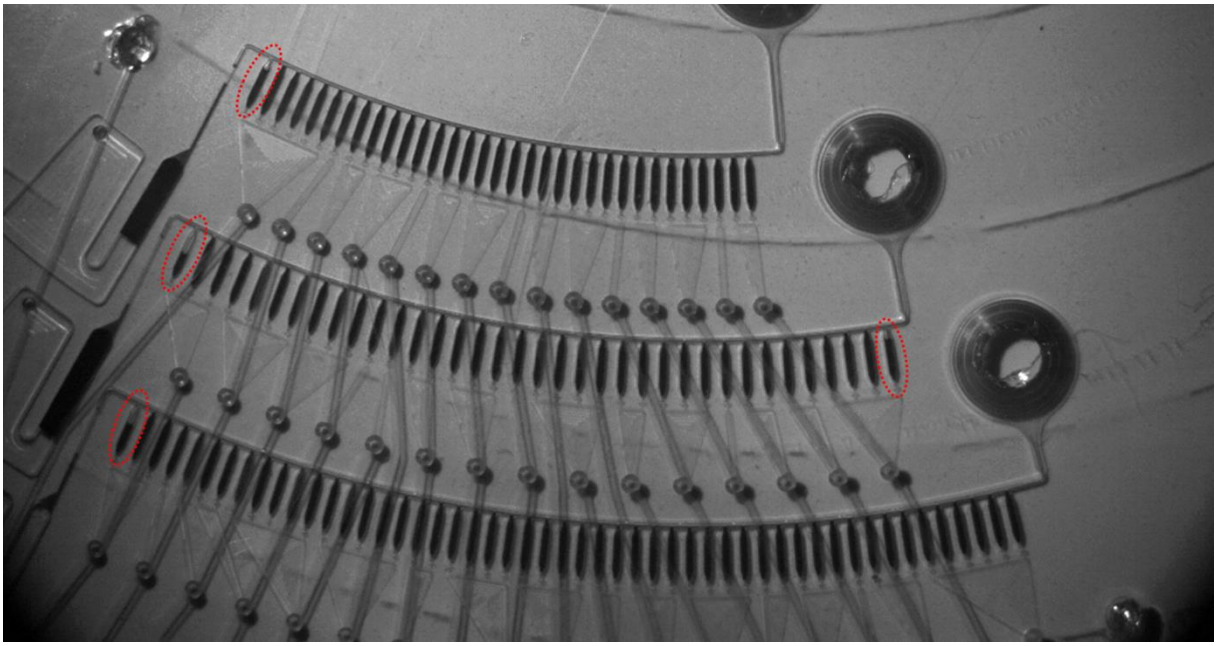
ESI Fig. 1: *The processing device for the LabDisk for SAXS.*

LabDisk for SAXS in P12 beamline



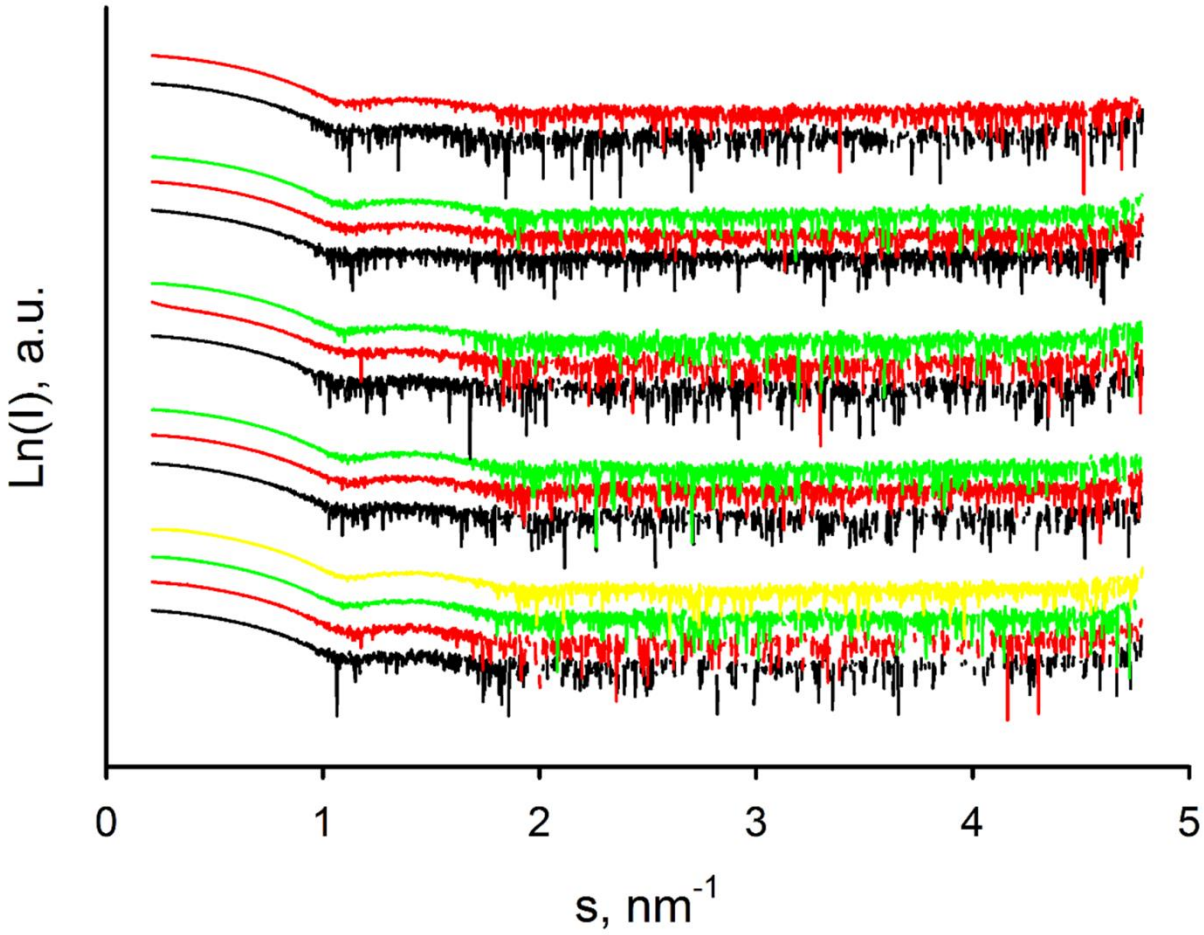
ESI Fig. 2: *LabDisk for SAXS in P12 beamline (PETRA III, DESY) at EMBL Hamburg.*

Liquid loss due to cornerflow



ESI Fig. 3: *Liquid loss due to cornerflow in the first and last aliquoting fingers of the LabDisk for SAXS. Displayed is an older version of the LabDisk for SAXS fabricated as a milled disk in PMMA and sealed with adhesive film. After long holding times liquid loss is clearly visible in the first and last aliquoting finger.*

Buffer subtracted curves collected with the LabDisk for SAXS



ESI Fig. 4: *Buffer subtracted curves collected with the LabDisk for SAXS: the curves are offset for clarity. Protein concentration: 1.8 mg/ml (black), 3.7 mg/ml (red), 5.5 mg/ml (red), 11 mg/ml (yellow). NaCl concentration (from bottom to top): 0 mM, 83 mM, 166 mM, 250 mM, 333 mM.*

Dead volumes

ESI Table 1 shows which amount of protein volume is used for fluidic processing and which amount of protein volume ends up in the actual read-out chambers. Reduction of total sample volume without change to the read-out chambers could be acchieved by reducing the pipetting tolerance, reducing the size of the feeding channel or reducing the excess volume in the read-out chambers.

Another way to reduce total sample volume would be to shrink the size of all volumes. However, this would include reduction of the size of the read-out chambers. In the current design the read-out chamber in the frontside foil has an aspect ratio of 1. Reducing the diameter of the read-out chamber would lead to an aspect ratio larger than 1, which is not recommended for micro-thermoforming. Reducing the depth of the read-out chamber would decrease the height of the measured liquid column, 860 µm in the current design, and consequently reduce the data quality.

ESI Table 1: *Calculation of the protein volume used for SAXS analysis. Out of the total input protein volume of 2.5 µl, 680 nl are used for the actual SAXS analysis. Additional liquid volume is required to tolerate pipetting errors, to ensure proper aliquoting and to ensure complete filling of the read-out chambers.*

Type	Dead volume	Remaining protein volume
Total input protein volume	-	2.5 µl
Extra volume included for pipetting tolerance	500 nl	2.0 µl
Extra volume required to ensure proper aliquoting (limitted by the size of the feeding channel)	~680 nl	1.32 µl
Excess volume included to ensure complete filling of the read-out chambers	49% (123 nl per read-out chamber)	680 nl

Calculation of χ^2

χ^2 can be calculated from eqn (1), where n is the number of data points and σ is the experimental error. [1]

$$\chi^2 = \frac{1}{n-1}\sum_{k=1}^{n}\left[\frac{I_{exp}(q_k) - I_{calc}(q_k)}{\sigma(I_{exp}(q_k))}\right]^2$$

References

1 K. Pearson, *The London, Edinburgh, and Dublin Philosophical Magazine and Journal of Science*, 1900, **50**, 157–175.