

## DNA-PAINT CELLS SLIDE

# MASSIVE-Cells 2-PLEX

Additional information

General information about MASSIVE-Cells 2-PLEX slide found in datasheet.

### EXCHANGING THE IMAGING MIXTURE AND PROPERLY SEALING THE SLIDE

#### Exchanging the imaging mixture

- dilute imagers in Massive Photonics Imaging Buffer to create the imaging mix
- remove both black caps from the Slide
- aspirate the complete volume in the channel and fill the channel with 300  $\mu\text{L}$  imaging mix, repeat this procedure 3 times.

The duration the channel does not contain liquid should be as short as possible.

*Caution: No air bubbles should get stuck in the channel. For optimal filling of the channel lift one side of the slide slightly up and fill the volume in the opposite side (port)*

*Optional: aspirate just the volume of the reservoirs (120  $\mu\text{L}$ ) and perform exchange by pipetting 120-150  $\mu\text{L}$  volume in one side in and in the opposite side out, this procedure must be performed 6 times for optimal exchange.*

Slide can be stored in imaging mix.

Imaging can be performed in a sealed or open channel, but avoid drying out of the channel

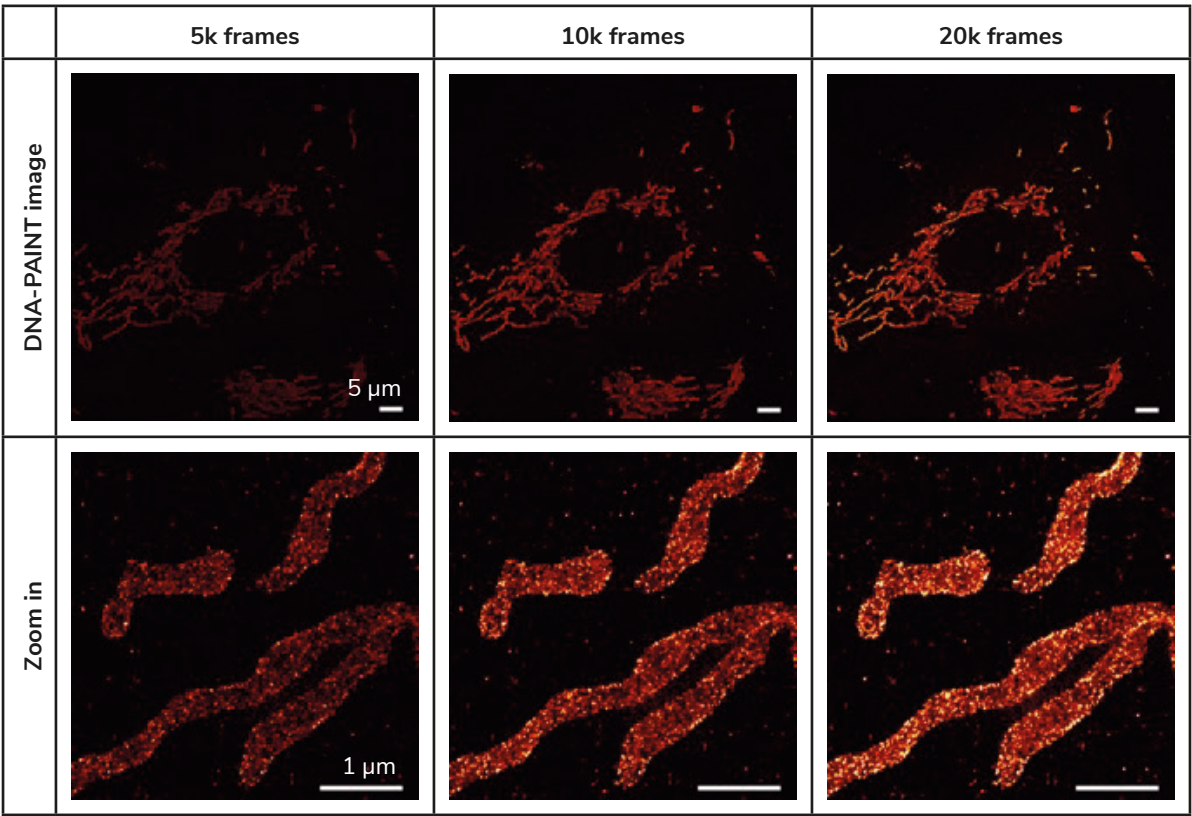
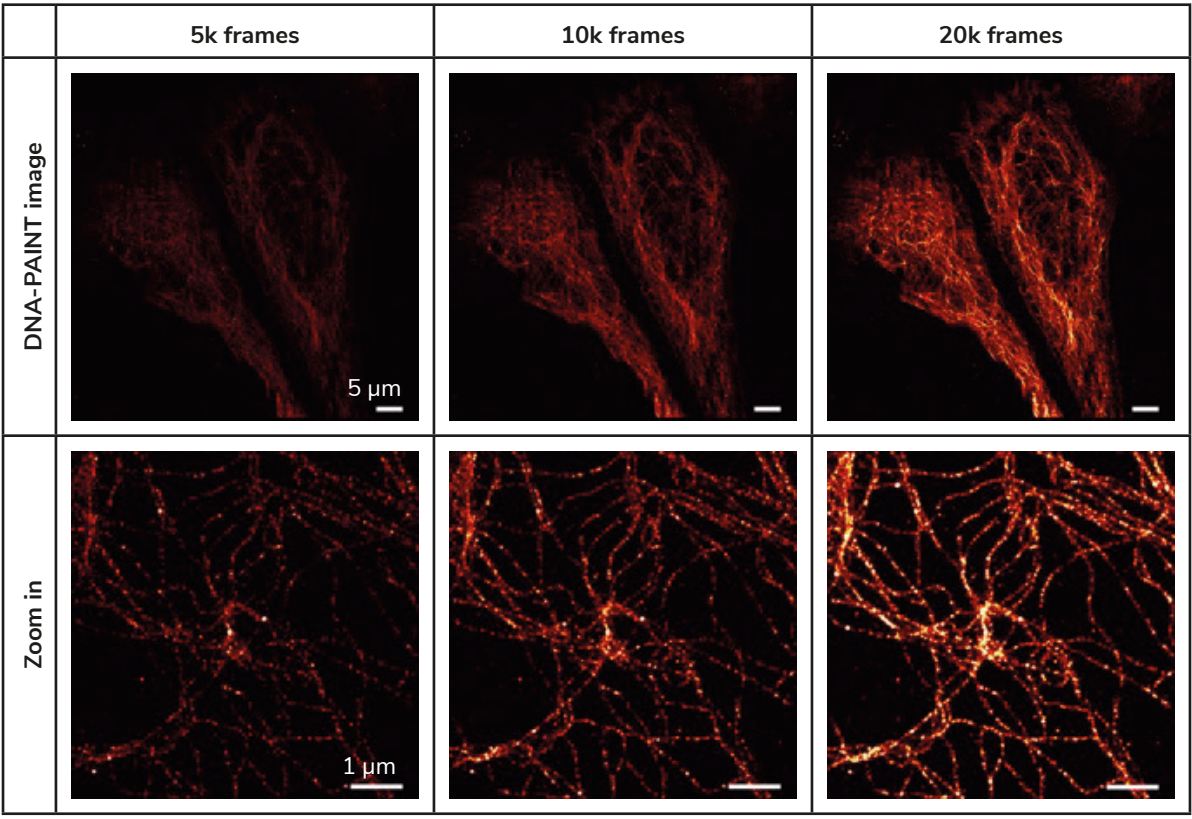
#### Sealing the Slide

- place slide on a flat surface (e.g. paper towel on lab bench)
- fill single-channel-slide completely (total volume about 450  $\mu\text{L}$ , liquid should form a convex meniscus over both ports)
- fill both black caps (about 70  $\mu\text{L}$ )
- connect 1st black cap
- remove spilled liquid
- squeeze second black cap during connection to second port
- remove spilled liquid
- check whether sample contains air bubbles and both caps are properly connected

*Caution: do not push down both sealing caps in parallel, this can cause cracking of the glass slide*

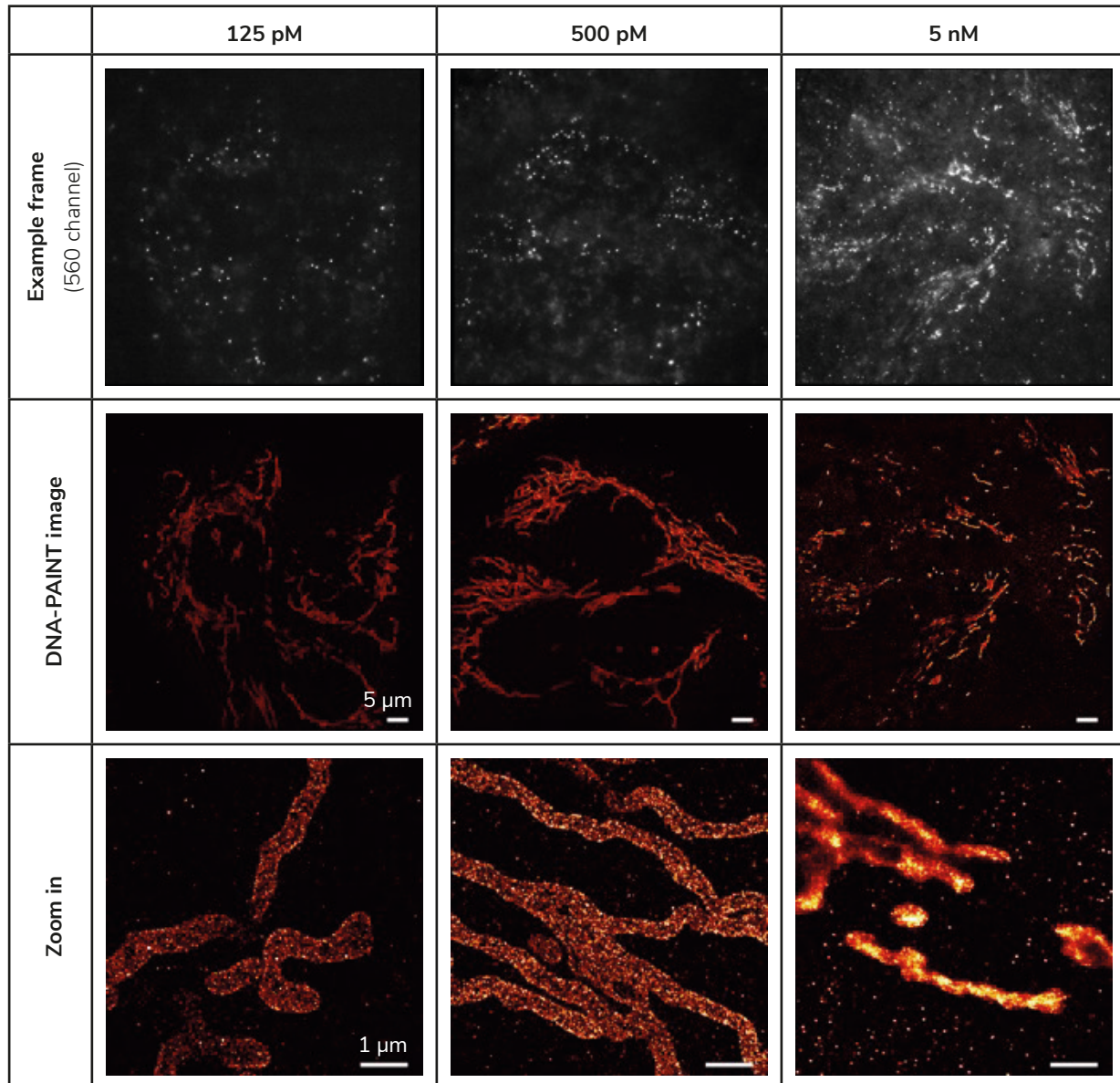
**SETTING THE NUMBER OF IMAGING FRAMES**

Sampling of the target improves with increased number of frames and/or increased imager concentrations. For a good compromise of resolution and imaging duration, a sweet spot between the number of frames and imager concentration needs to be found.



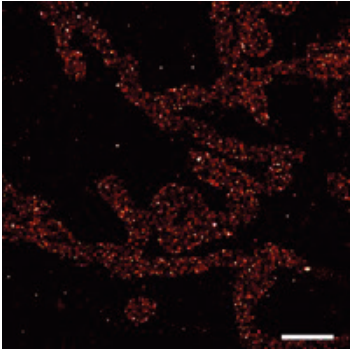
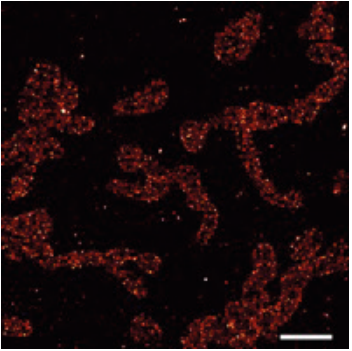
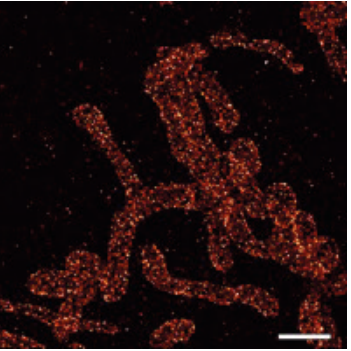
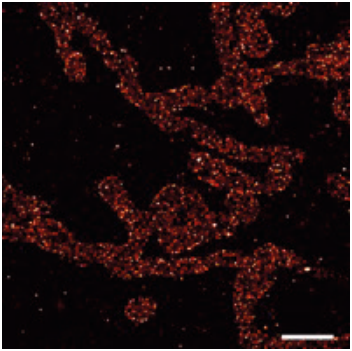
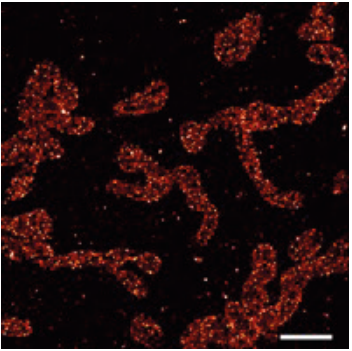
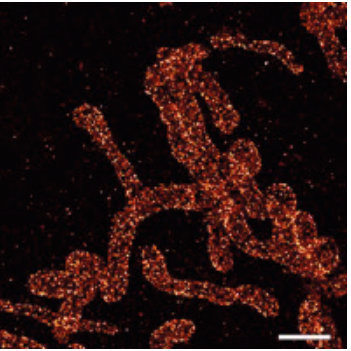
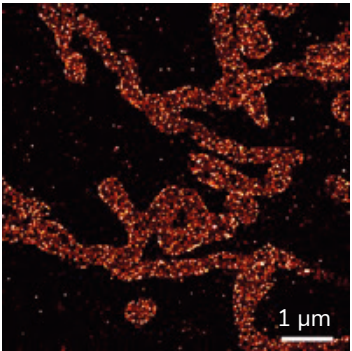
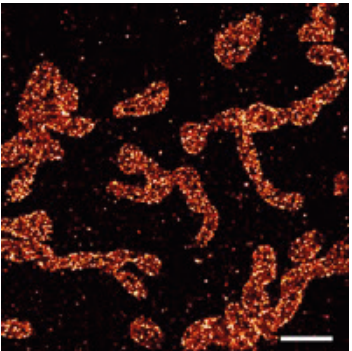
## SETTING THE IMAGER CONCENTRATION

Low imager concentrations result in a high resolutions, but for sufficient sampling a higher number of frames needs to be recorded. Too high imager concentrations result in overlapping point spread functions, ultimately resulting in lower resolution.



## SETTING EXPOSURE TIME

DNA-PAINT imaging can be performed with a range of camera integration times. The highest localization precisions are achieved with integration time is similar to the amount of time the imager is bound to the docking strand. Using the table below as a guide, camera integration time can be adjusted for your experimental needs.

	30 ms, 60 mW	50 ms, 50 mW	75 ms, 30 mW
<b>Example frame</b> (560 channel)	Measurement takes 5 min 	8.33 min 	12.5 min 
<b>DNA-PAINT image</b>	7.5 min 	12.5 min 	18.75 min 
<b>Zoom in</b>	15 min 	25 min 	
<b>Median fit precision</b>	8.5 nm	9.0 nm	6.4 nm
<b>NeNA precision</b>	12.3 nm	11.9 nm	5.5 nm

NeNA precision is a localization precision algorithm cited in Literature 2.

## GOLD NANOPARTICLES AS DRIFT MARKERS

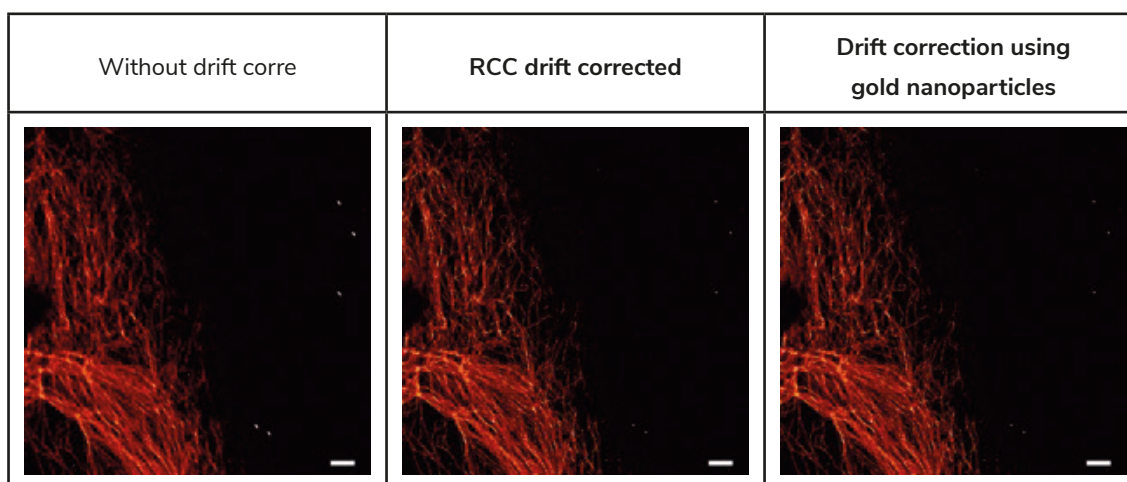
An important post-processing step for DNA-PAINT imaging is to compensate for stage drift that occurred during data acquisition. Drift correction can be performed in Picasso using either the localization events themselves or fiducials (in our case gold nanoparticles).

The drift correction based on localization events utilizes a redundant cross-correlation (RCC) algorithm. In this approach, the recorded movie is divided into several temporal segments, and super-resolution images are generated for each segment. Cross-correlating the resulting super-resolution images allows for determining the spatial shifts between the segments, which are then used to interpolate the drift. Another method for drift compensation in localization-based super-resolution microscopy involves using fiducial markers. These luminescent markers are typically observed in the same emission channel as the fluorescent signal. In Picasso, localizations from these fiducial markers can be selected for drift correction, as they can be assumed to originate from a single, point-like source.

The RCC drift correction can be applied in Picasso (<https://github.com/jungmannlab/picasso>) by navigating to **Render -> Post-processing -> RCC Drift Correction**

For drift correction using gold nanoparticles, follow these steps:

1. Select a few gold nanoparticles using the **Pick** function, which can be accessed in the **Tools** menu (make sure to adjust the pick diameter in **Tools -> Tool Settings** to fully encircle the drifted gold nanoparticle).
2. Use **Tools -> Pick Similar** to automatically identify and select additional gold nanoparticles.
3. Finally, go to **Postprocess -> Undrift from Picked** to perform the drift correction.



## DILUTION FACTORS FOR VARIOUS IMAGER CONCENTRATIONS

<b>Imager concentration</b>	<b>Dilution factor</b> (stock concentration 1 $\mu$ M)
5 nM	200x
1 nM	1,000x
500 pM	2,000x
250 pM	4,000x
100 pM	10,000x

## LITERATURE

1. Schnitzbauer, Joerg, et al. "Super-resolution microscopy with DNA-PAINT." *Nature protocols* 12.6 (2017): 1198-1228.
2. Endesfelder, Ulrike, et al. "A simple method to estimate the average localization precision of a single-molecule localization microscopy experiment." *Histochemistry and cell biology* 141 (2014): 629-638.
3. Steen, Philipp R., et al. "The DNA-PAINT palette: a comprehensive performance analysis of fluorescent dyes." *Nature Methods* (2024): 1-8.

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