**TEM Sample preparation protocol**

* ***Multilayer DNA Origami Packed on Hexagonal and Hybrid Lattices, W.M. Shih, JACS, 2011***

The TEM sample was prepared by dropping 3.5µL of sample solution on a

carbon-coated grid (400 mesh, Ted pella). Before depositing the sample, the grids were

negatively glow discharged for 45 seconds. After 2 minutes, the sample was wicked from

the grid by touching its edge with a piece of filter paper. Then the grid was touched with

a drop of 2 % uranyl formate solution and excess solution was wicked away with a filter

paper. Again the grid was touched with a second drop of uranyl formate solution for 20

seconds, and the excess solution was removed with a filter paper. TEM studies were

conducted using a JEOL JEM-1400 transmission electron microscope, operated at 80 kV

on bright field mode.

* ***DNA Origami Gatekeepers for Solid-State Nanopores, H. Dietz, 2012***

Particles were adsorbed on glow-discharged formvar-supported carbon-coated Cu400 TEM grids and

stained using a 2% aqueous uranyl formate solution containing 25 mM NaOH. Imaging was performed

using a Philipps CM100 electron microscopy operated at 100 kV. Images were acquired using a AMT

4x4 Megapixel CCD camera. Micrograph scale bars were calibrated using 2D catalase crystal lattice

constants as length reference. Imaging was performed at 28500x magnification.

* ***Molecular force spectroscopy with a DNA origami–based nanoscopic force clamp, T. Lidel, Sciece, 2016***

5 μL of purified origami solution was adsorbed onto glow-discharged TEM grids

(formvar/carbon, 300 mesh Cu ; Ted Pella, Redding, CA) at room temperature and then

stained with aqueous uranyl formate solution (2 %) containing sodium hydroxide

(25 mM). Imaging was performed at 25,000 x magnification with a JEM1011

transmission electron microscope (JEOL) operated at 80 kV, equipped with a FastScan-

F114 camera (TVIPS, Gauting, Germany). Generation of aligned and averaged TEM

images was performed by picking particles with the manual boxing routine followed by

iterative 2D alignment and averaging (ml\_align2D) of the Xmipp 3.1 software package

(33).