Electronic Supporting Information:

Chain-like assembly of gold nanoparticles on artificial DNA templates via 'Click Chemistry'

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1 AFM section analysis and TEM derived size distribution of glutathione bisazide modified gold nanoparticles

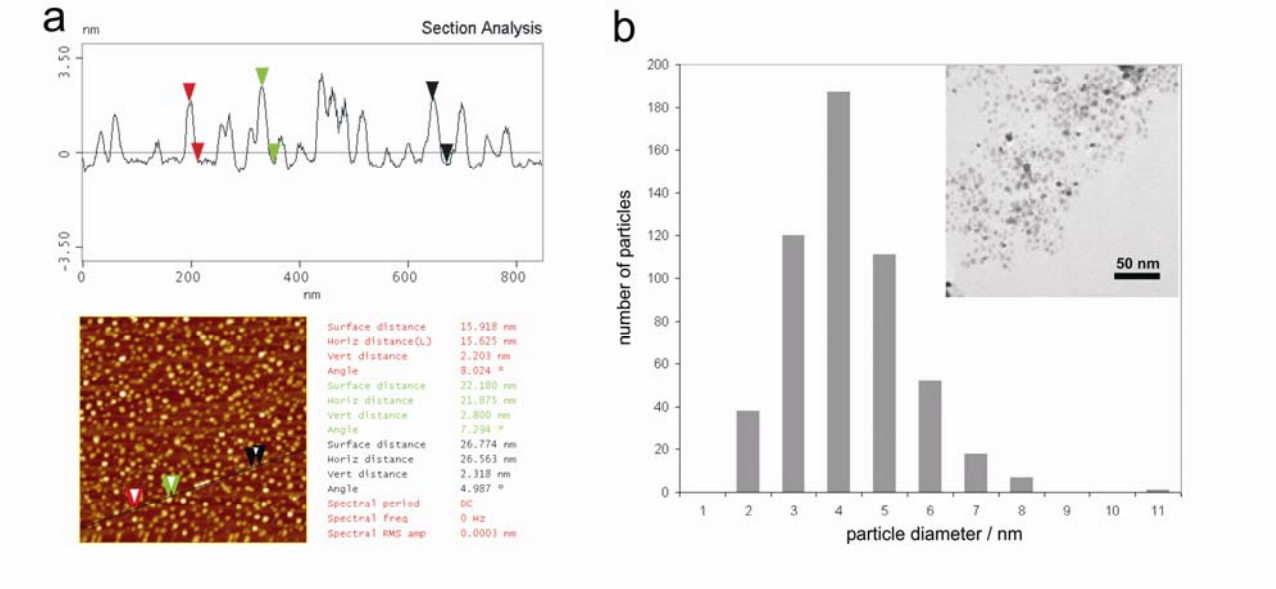

Figure S1 a) section analysis of AFM topography of glutathione bisazide stabilized gold clusters (mean particle size 2-3 nm) and b) TEM derived statistical analysis of the material (mean particle size 4 nm)

2 AFM analysis and additional TEM material of cluster decorated DNA strands

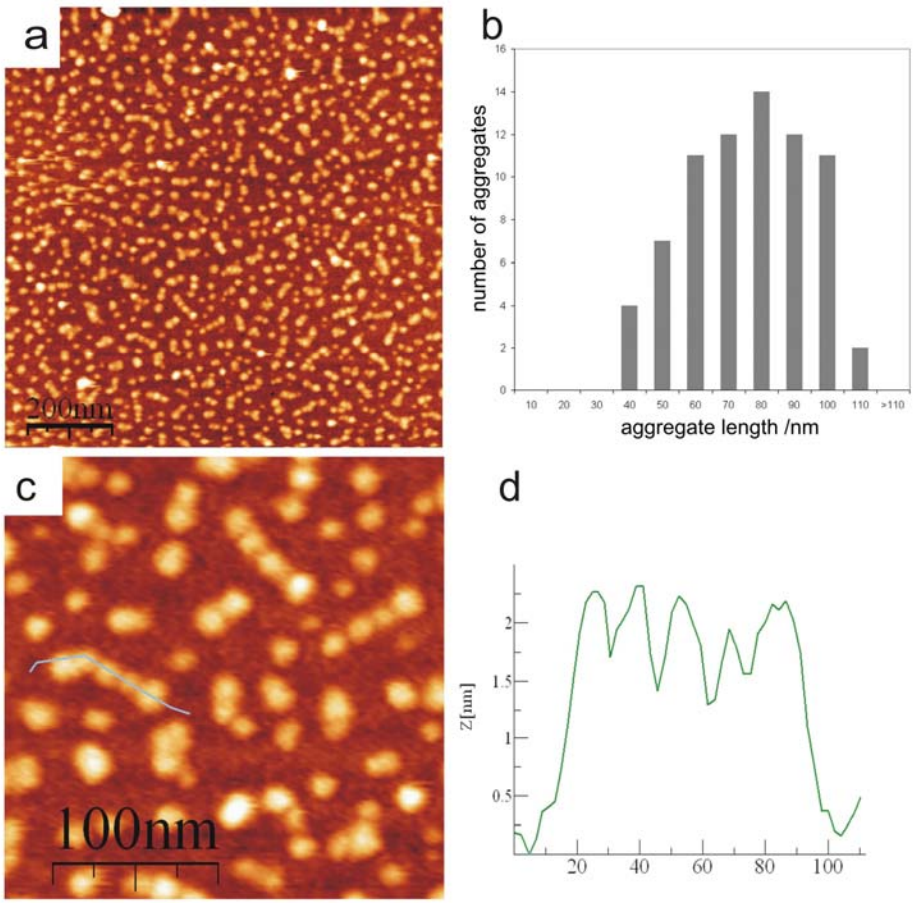

Figure S2 AFM analysis of nanoparticles assembled on 300 meric DNA duplexes. a) depicts an overview of the surface. b) shows the respective analysis of aggregate lengths. c) shows a zoom of a 90 nm long aggregate and d) depicts the height profile of the latter.

The AFM images in Figure S2a) and c) show string-of-pearl-like arrangements of nanoparticles. Figure S2a) represents a characteristic overview of the mica surface after immobilization of the aggregates. A statistic analysis of the aggregate lengths in Figure S2a) is presented in b). All aggregates visible in a) that appear to consist of three or more gold nanoparticles connected to each other are taken into account. We found that almost all aggregates are 100 nm or less in length, which is in accordance to the length of the 300-meric DNA duplexes used in these experiments. Only two aggregates were found to exhibit lengths longer than 100 nm, which might refer to the formation of aggregates consisting of more than

one double strand due to cross-linking. The length found most frequently is 80 nm. This is marginally shorter than the starting material, which can be explained with a certain degree of intra-molecular coiling of the strands and their not fully stretched conformation on the mica substrate.

The magnification in Figure S2c) clearly shows particles assembled linearly along DNA strands. A line scan in Figure S2d) represents a height profile along a 90 nm long strand which appears to be densely covered with particles. It reflects a height of 2.2 nm on top of the particles and 1.2 nm in the deepest point between them. Compared to natural DNA with a diameter of 2 nm, the measured value was lower than expected. This can be explained by the applied conditions of the tapping-mode in the AFM. As the particles presumably are assembled in a very densely packed array the height difference between the strand and the nanoparticles cannot be exactly determined, but was estimated to be in a range of 1-1.5 nm. Due to the radius of the AFM tip the resolution is too low for a more detailed analysis. Thus, further information concerning nanoparticle size and particle distance was gained from TEM investigations.

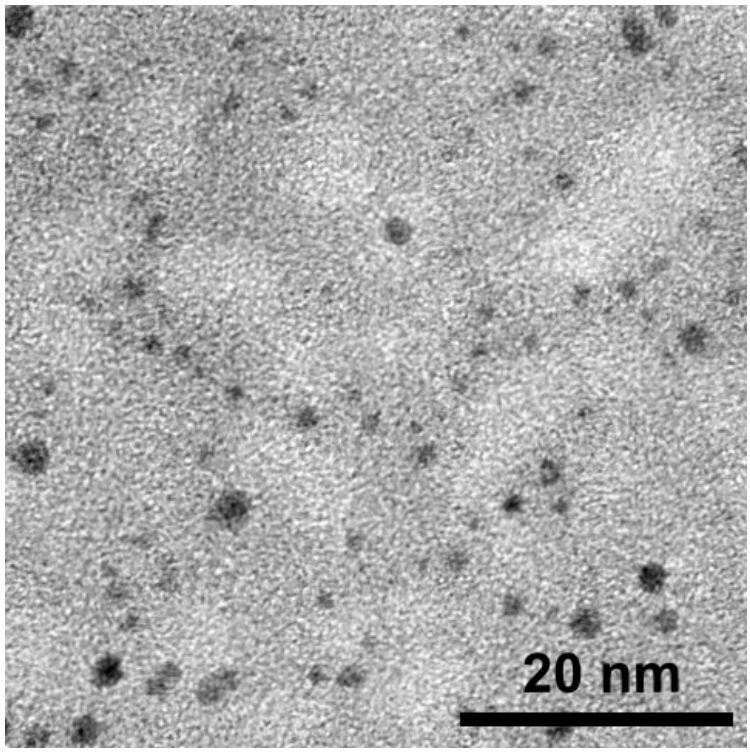

Figure S3 Additional TEM material demonstrating the one-dimensional nanoparticle assembly.

3 Experimental details

3.1 Synthesis of the glutathione bisazide ligand

S-Trt-N-Boc-Protected glutathion-bisazide **4**:[i]

200 mg (0.31 mmol) of the *S*-Trt-*N*-Boc-protected glutathione were dissolved in 5 mL dry THF and 100 mg (0.62 mmol) carbonyldiimidazole were added. After 30 min stirring at room temperature, 62 mg (0.62 mmol) 3-aminopropylazide was added and the mixture was stirred for 14 h. Then, the solvent was removed *in vacuo* and the yellow raw material was subjected to column chromatography (silica gel, $CHCl_3$: MeOH = 10 : 1) which yielded 168 mg (0.21 mmol, 68 %) of the protected bisazide **4** as a yellowish powder.

R_f ($CHCl_3$: MeOH = 9 : 1) = 0.7; **^{1}H-NMR** (400 MHz, D_6-DMSO): δ 1.37 (9 H, s), 1.56–1.74 (5 H, m), 1.74–1.86 (1 H, m), 2.08–2.22 (2 H, m), 2.35-2.42 (2 H, m), 3.04–3.15 (4 H, m), 3.27-3.34 (4 H, m), 3.53 (1 H, dd, *J* = 16.6, 5.4 Hz), 3.67 (1 H, dd, *J* = 16.6, 6.2 Hz), 3.82 (1 H, dd, *J* = 14.4, 8.5 Hz), 4.19 (1 H, dd, *J* = 13.9, 6.7 Hz), 6.88 (1 H, d, *J* = 7.9 Hz), 7.22–7.37 (15 H, m), 7.64 (2 H, t, *J* = 5.9 Hz), 7.87 (1 H, t, *J* = 5.6 Hz), 8.17–8.25 (2 H, m); **^{13}C-NMR** (150 MHz, $CDCL_3$): δ 28.45, 28.72, 28.76, 32.02, 32.05, 32,81, 36.94, 37.11, 43.63, 49.14, 49.21, 53.24, 53.74, 67.59, 127.21, 128.32, 129.64, 144.36, 156.14, 169.14, 170.77, 171.93, 173.04; **IR** (diamond-ATR): ν = 3291, 3060, 2934, 2094, 1646, 1520, 1444, 1366, 1247, 1163, 1083, 1031, 855, 743, 699, 675, 616 cm^{-1}; **EI-HRMS** (pos.): calc. for $C_{40}H_{51}N_{11}O_6SNa$ $[M+Na]^+$: 836.3642; found: 836.3647.

Glutathione bisazide **1**:

100 mg (0.12 mmol) of the protected glutathione-bisazide **4** were dissolved in 10 mL CH_2Cl_2 and 300 µL H_2O, 300 µL triethylsilane and 10 mL trifluoroacetic acid were added. After stirring for 1 h at r.t., all solvents were removed *in vacuo* and the residue was taken up into 5 mL H_2O. The suspension was filtered and the water was removed from the filtrate by lyophilisation to yield 42 mg (0.09 mmol, 80 %) of the free glutathione-bis-azide **1** as a yellowish powder, which could be further purified by reverse phase HPLC (0.1 % TFA in H_2O : MeCN).

^{1}H-NMR (600 MHz, D_2O): δ 1.79-1.90 (4 H, m), 2.19-2.25 (2 H, m), 2.54 (2 H, t, *J* = 7.0 Hz), 3.06 (2 H, dd, *J* = 14.2, 9.0 Hz), 3.30 (1 H, dd, *J* = 14.1, 4.8 Hz, SH), 3.32-3.46 (8 H, m),

3.91-3.99 (2 H, m), 4.03 (1 H, t, *J* = 6.6 Hz), 4.75 (1 H, m), 8.13 (2 H, t, *J* = 6.7 Hz, NH), 8.67 (1 H, t, *J* = 7.6 Hz, NH), 8.83 (2 H, d, *J* = 5.9 Hz, NH). Of the 7 heteroatom-bound hydrogens, only 6 were observed; **^{13}C-NMR** (100 MHz, CD_3OD): δ 26.53, 28.10, 29.62, 29.68, 31.74, 37.78, 38.10, 43.57, 50.01, 50.04, 53.95 ($C_{methine}$), 57.59 ($C_{methine}$), 169.84 (C_{quart}), 171.41 (C_{quart}), 173.03 (C_{quart}), 174.40 (C_{quart}); **MALDI-MS** (pos.): 472.3 $[M+H]^+$, 494.3 $[M+Na]^+$; **ESI-HRMS** (pos.): calc. for $C_{16}H_{30}N_{11}O_4S$ $[M+H]^+$: 472.2197; found: 472.2195.

3.2 Synthesis of the 300 bp artificial DNA duplex

Synthesis of the triphosphate **2**

To a cooled solution (0 °C) of 5-(octa-1,7-diinyle)-2'-desoxyuridine [ii] (0.10 g, 0.3 mmol) and 1,8-bis(dimethylamino)naphthalene (102.8 mg, 0.48 mmol, 1.6 eq) in trimethylphosphate (1mL) $POCl_3$ (41 µL, 0.45mmol, 1.5 eq) was added. The reaction was stirred additional 3 hours at 0 °C. Then a solution of tris-*n*-butylammonium pyrophosphate (188.9 mg, 0.55 mmol, 1.86 eq and tris-*n*-butylamine 0.478 mL in 3 mL DMF) was added. The reaction was quenched with TEAB buffer (triethylammoniumbicarbonate, 1.0 M, 20 mL, pH 8.5) after 20 minutes. After stirring for additional 2 h the reaction mixture was lyophilized. Purification with reversed phase HPLC (C18, 0→50 % 0.1 M triethylammoniumacetate → 20 : 80 H_2O : MeCN with 0.1 M triethylammoniumacetate, gradient in 45 min.) yielded **Y** (30.2 min.) as triethylammonium salt.

^{31}P-NMR (80.9 MHz, D_2O) -22.4 (t, 1 P, J = 20.2 Hz, P-β), -10.5 (d, 1 P, J = 20.4 Hz, P-α), -9.7 (d, 1~P, J = 20.1Hz, P-γ). MALDI-TOF (ATT, M+2H$^+$): 570.6.

For PCR amplification as template the vector *pExp007-pol η* with the polymerase η gene from Rad30 *S. cerevisiae* was used with the primers 5'-TTA ATT GAA TTC GAT TTG GGC CGG ATT TGT TTC-3' and 5'-TTT TAT GCT ATC TCT GAT ACC CTT G-3' which amplify a 294 bp fragment of the pol gene *η*. (Sequence: 5'-TTA ATT GAA TTC GAT TTG GGC CGG ATT TGT TTC AAT ATG CTA ATG TTT GAT AAT GAG TAC GAG CTT ACA GGC GAC TTG AAA CTG AAA GAT GCA TTA AGC AAT ATT CGT GA GGC TTT TAT AGG GGG CAA CTA TGA TAT AAA TTC CCA TCT ACC TCT TAT ACC CGA AAA GAT AAA GTC TCT GAA GTT TGA AGG CGA TGT TTT CAA TCC AGA GGG CAG AGA TCT GAT CAC AGA TTG GGA CGA TGT AAT ACT TGC ACT AGG

ATC TCA GGT ATG CAA GGG TAT CAG AGA TAG CAT AA AA; AT-content: 61 %) The PCR product contains in total 154 alkyne sites.

PCR conditions: The PCR was run with the final concentration of 0.2 mM of each dNTP, 0.3 µM of each primer, 400 ng of template and 2 U Pwo Polymerase (Roche) in the reaction buffer provided by the supplier. Total volume was 50 µL.

Temperature program on a Eppendorf Personal cycler: 95 °C for 2:00 min, then 9 cycles of 95 °C for 0:15 min 58 °C (-1.0 °C each cycle) for 0:30 min, 72 °C for 0:45 min; then 30 cycles of 95 °C for 0:15 min, 57 °C for 0:30 min, 72 °C for 0:45 min.

The PCR product was purified using QIAquick PCR Purification Kit (QIAGEN).

3.3 Synthesis of the azide terminated gold nanoparticles

The reduction solution was prepared using standard Schlenk techniques under nitrogen atmosphere by adding sodium (100 mg, 4.3 mmol) and naphthalene (410 mg, 3.2 mmol) to diglyme (35 mL). The mixture was stirred over night and a dark green solution was obtained. For preparation of diglyme stabilized gold nanoparticles $HAuCl_4 \cdot 3H_2O$ (6 mg, 0.01 mmol) was dissolved in diglyme (5 mL). The reduction solution (0.9 mL) was added under vigorous stirring drop wise via a syringe. The solution turned from a light yellow to a dark, slightly red color. This material was only stable for some minutes as the stabilization in diglyme is very low and particles tend to grow without further addition of a stabilizing ligand.

For the further stabilization an equimolar amount of glutathione azide ligand (1) (referring to $HAuCl_4$) dissolved in water was added after 5 min. The mixture was allowed to stir for one hour and utilized without further purification for AFM and TEM analysis as well as for immobilization experiments on DNA.

3.4 Immobilization of the nanoparticles on the DNA template by copper(I) catalyzed Huisgen “click”- reaction

The catalyst solution for the ‘click’ reaction was prepared by dissolving 1.4 mg CuBr and 11 mg TBTA in 1 mL of a DMSO / *tert*Butanol (3:1) mixture. The catalyst solution was prepared freshly prior to each immobilization experiment.

For the immobilization of the nanoparticles to the DNA templates, 1 µL of the DNA solution (1-10 ng/µL) was incubated with 5 µL of the nanoparticle solution and 1 µL of the catalyst

solution. After addition of 10µL H_2O the mixture was allowed to react at room temperature for 60 min. Subsequently, 21 µL of the reaction mixture and 0.5 µL aqueous $MgCl_2$ solution (0.010 mol/L) were placed on a mica substrate and rinsed with water after 10 min. This substrate was analyzed by means of AFM microscopy. For TEM, a 5 µL drop of the reaction mixture was placed on a carbon coated copper grid, rinsed with H_2O after 2 minutes and dried in a nitrogen stream.

i) M. Gelinsky, R. Vogler, H. Vahrenkamp, *Inorg. Chim. Acta* 2003, **344**, 230;

ii) J. Gierlich, G. A Burley, P. M. E. Gramlich, D. M. Hammond, T. Carell, *Org. Lett.* 2006, **8**, 3639.