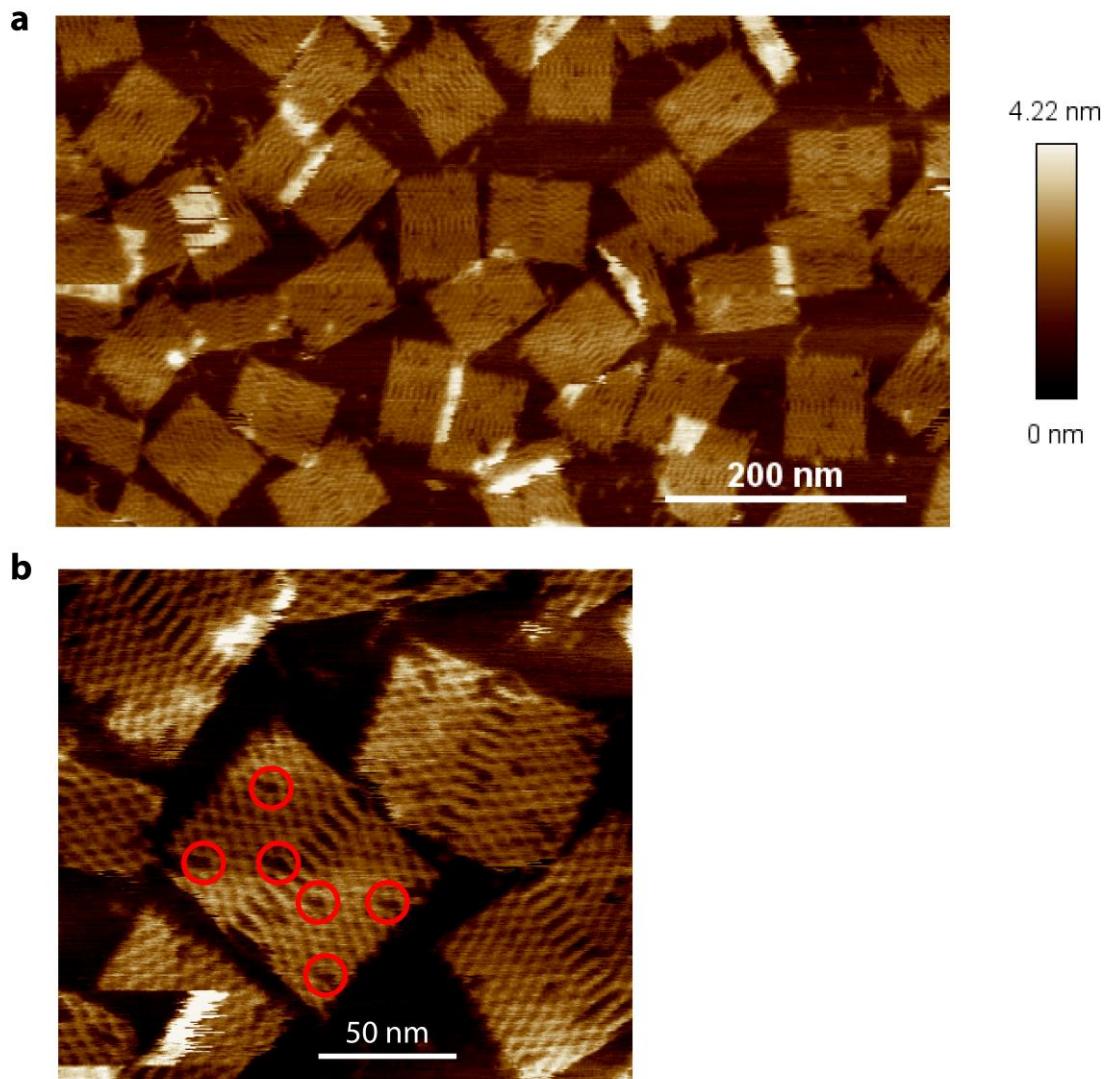
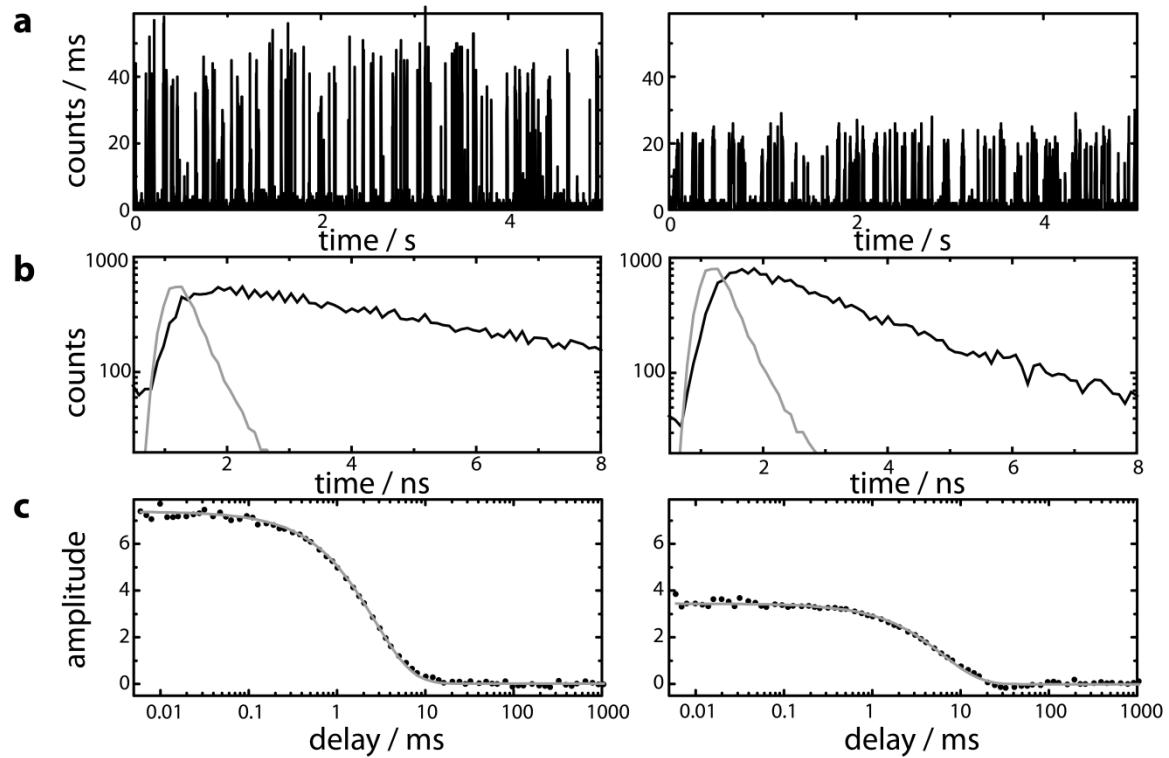


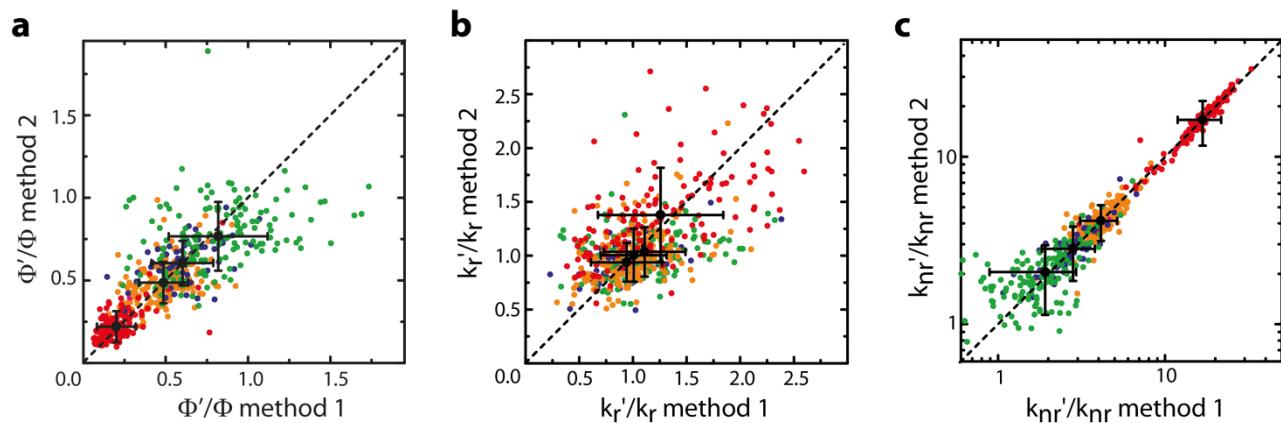
**Supplementary Figure 1 | Detailed design of the rectangular DNA origami.** The scaffold (blue) is crosslinked into the desired shape by staple strands without modification (black) with biotin t the 5' end (green), with a 15A capturing sequence for the NP at the 5' end (magenta) and an ATTO647N dye on one of the red staples. The arrows of the individual staples indicate the 5'-3' direction



**Supplementary Figure 2 | AFM images of rectangular DNA origamis.** **(a)** Overview of area with a multitude of correctly formed rectangular DNA origamis. **(b)** High resolution AFM image of rectangular DNA origamis. The red circles indicate the positions of the six biotin modifications. Since the modified staples are shortened by 5 bases, the positions are visible as gaps in the DNA origami structure.

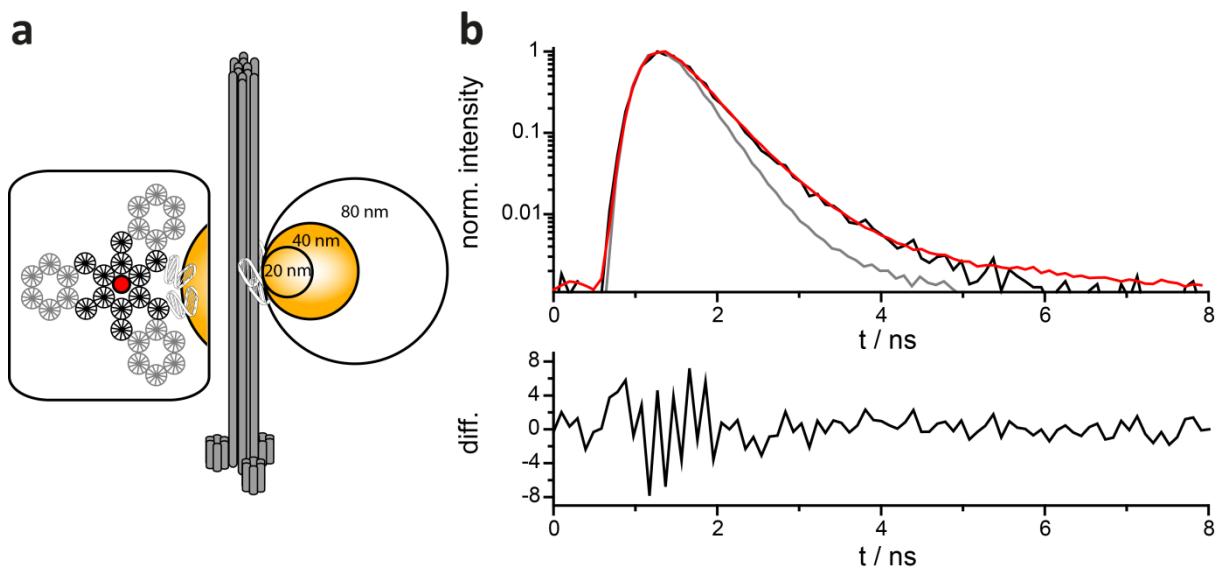


**Supplementary Figure 3 | Exemplary fluorescence transients** (a) with corresponding fluorescence decays (b) and autocorrelation functions (c) for a dye without NP (left) and with a single 20 nm NP at a distance of 8.3 nm (right). This data is used to extract the parameters  $\tau$ ,  $I_{on}$  and  $t_{on}$ .

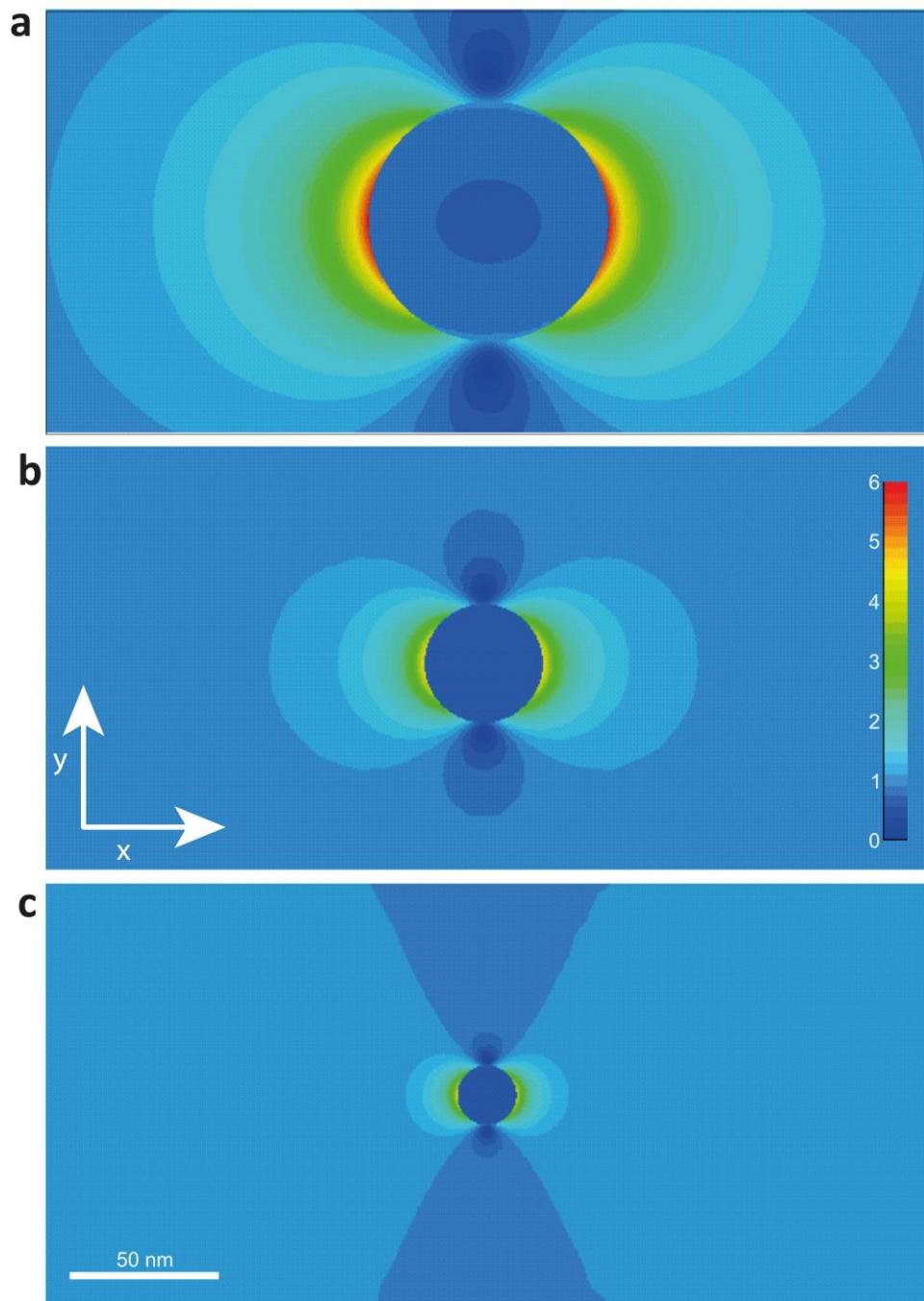


**Supplementary Figure 4 | Comparison between two methods to extract changes of photophysical properties.**

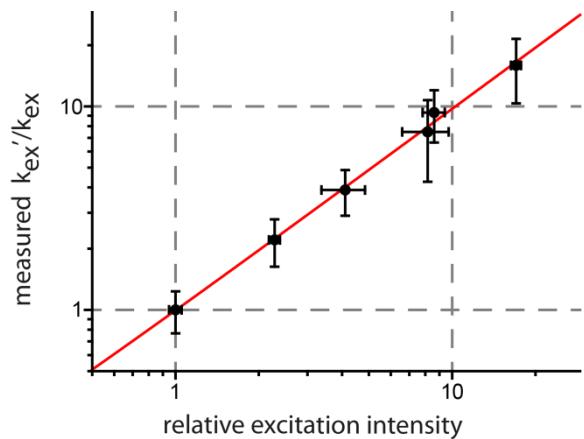
**(a)** Method 1 assumes constant excitation rate and calculates changes of the quantum yield from  $\Phi'/\Phi = I'_{\text{on}}/I_{\text{on}}$ , whereas method 2 uses equation (6) of the main text ( $\Phi'/\Phi = (N'_{\text{on}} \tau')/(N_{\text{on}} \tau)$ ). **(b)** The radiative rate change is calculated with method 1 as  $k'_r/k_r = (I'_{\text{on}} \tau)/(I_{\text{on}} \tau)$  or with method 2 and equation (5) of the main text  $k'_r/k_r = N'_{\text{on}}/N_{\text{on}}$ . **(c)** In both cases nonradiative rate changes are determined with  $k'_{\text{nr}}/k_{\text{nr}} = (\tau'/\tau - \Phi k'_r/k_r)/(1 - \Phi)$  and the intrinsic quantum yield  $\Phi = 0.65$ . Data points represent fluorescent dyes at distances  $d_1 = 6.6$  nm (red,  $n=140$ ),  $d_2 = 8.3$  nm (orange,  $n=181$ ),  $d_3 = 11.2$  nm (blue,  $n=59$ ),  $d_4 = 15.0$  nm (green,  $n=147$ ) to the NP surface (20 nm diameter) and the respective mean values with standard deviation (black). Dashed lines indicate equivalent results for both methods.



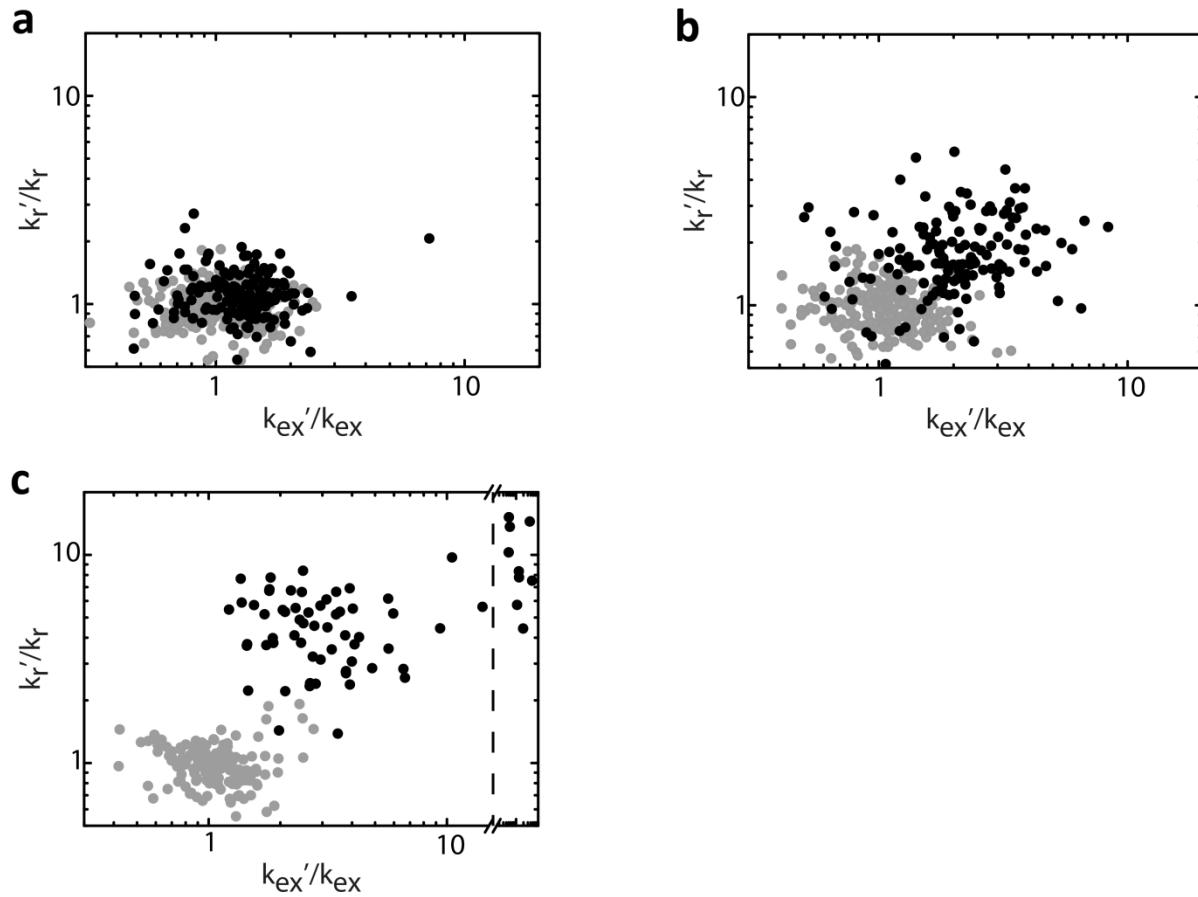
**Supplementary Figure 5 | DNA nanopillar sketch and exemplary fluorescence lifetime decay** **(a)** Sketch of the DNA nanopillar with the fluorescent dye Atto647N in the center of a 12-helix bundle (inset) and a gold NP of 20, 40 or 80 nm diameter attached to the side of the nanopillar. **(b)** Normalized fluorescence lifetime decay (black) with IRF (grey) and reconvoluted fit (red) for a dye close to an 80 nm Au NP with fluorescence lifetime of 0.46 ns. The lower panel shows the difference (not normalized) between the fit and the experimental decay. This decay is close to the lower bound of lifetimes that could be reasonably fitted.



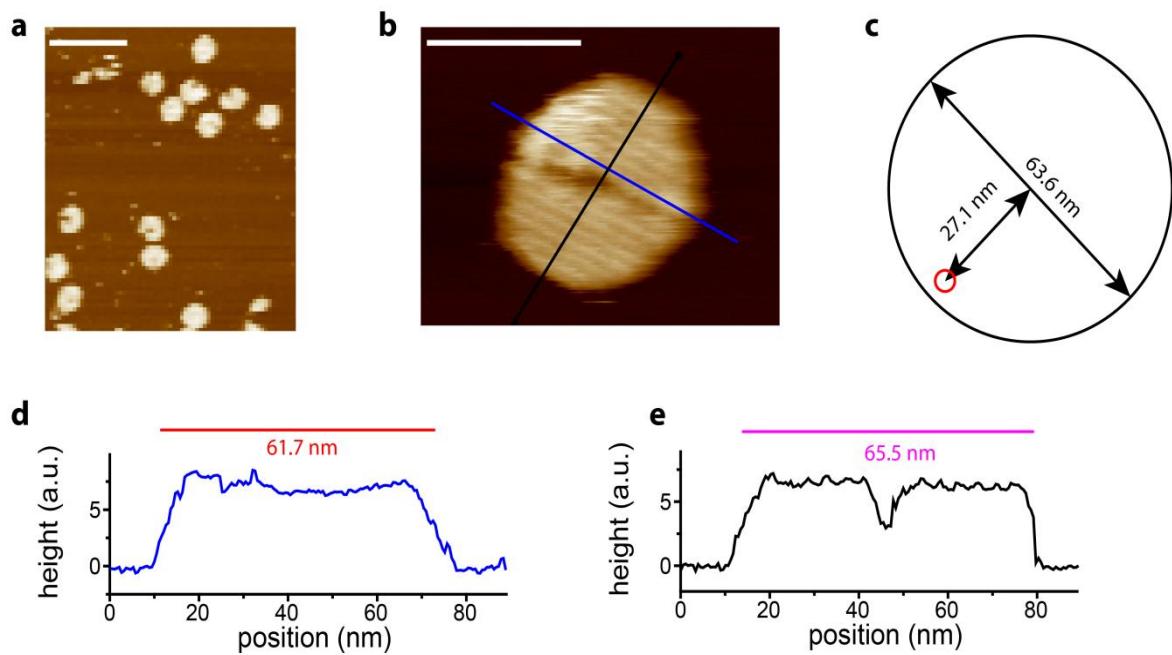
**Supplementary Figure 6 | Electric field distributions in the vicinity of gold NPs.** Electric field amplitude distribution normalized to the incident amplitude at the equatorial plane of gold NPs of different diameters: 80 nm (a), 40 nm (b) and 20 nm (c). The simulations were carried out with light of 640 nm wavelength polarized in x-direction and propagating in z-direction.



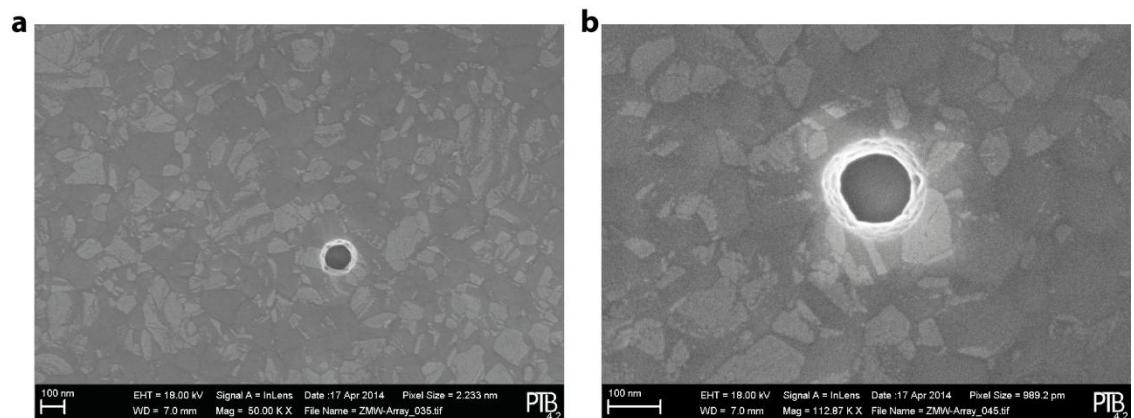
**Supplementary Figure 7 | Excitation rate changes can be quantified over at least one order of magnitude.** Data points represent the measured change of the excitation rate depending on the laser intensity used (0.29 - 4.89  $\mu$ W, n=98, 100, 89, 77, 73, 57 with increasing excitation intensity), normalized to the measurement at the lowest laser intensity. Error bars represent the standard deviation of the calculated rate changes and the laser intensity range measured before and after data collection, respectively. The red line is a linear fit to the data which yields an intercept of 0.024 and a slope of 0.970, which proves that the method can reliably detect changes of the excitation rate.



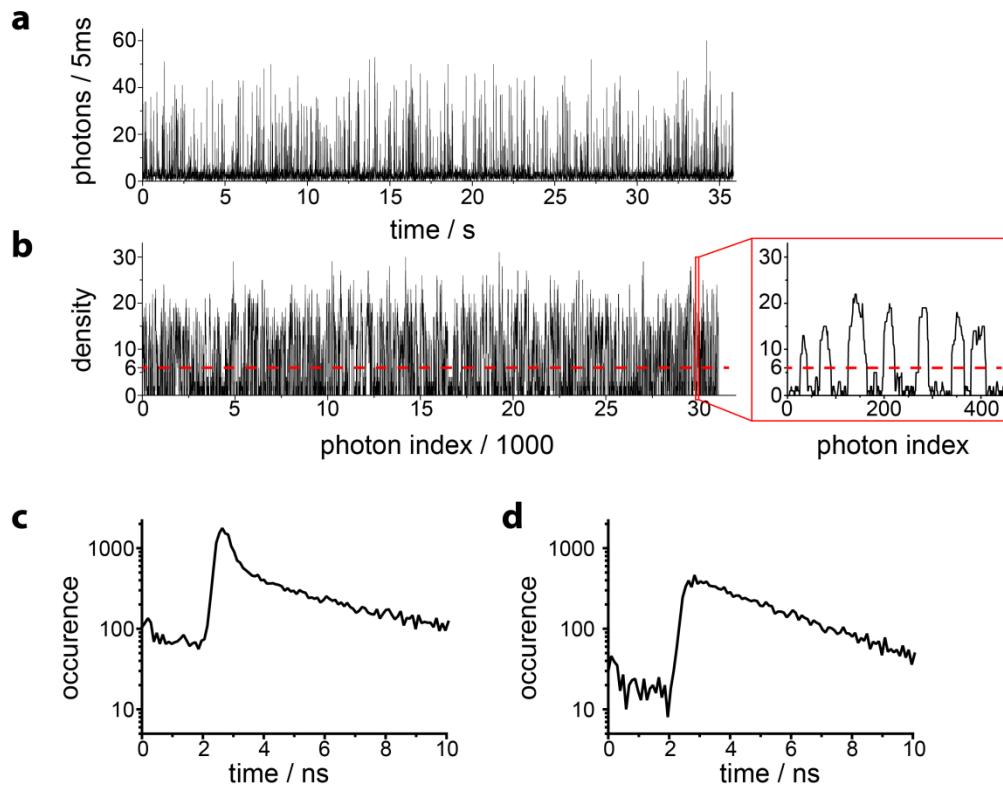
**Supplementary Figure 8 | Correlation of radiative and excitation rate with particle size.** (a-c) Radiative versus excitation rate constants of molecules with (black) and without NP (grey) normalized to the mean value of the molecules without NP for particles sizes of 20 (a), 40 (b) and 80 nm (c). The data points for one particle size do not exhibit a strong correlation between excitation and radiative rate constant. Data points beyond the break in (c) are not considered for the excitation rate because their fluorescence lifetime could not be determined accurately due to the temporal resolution of our experimental setup. According to the simulations in Figure 4 of the main text, the particle size (and also the distance) should affect both excitation and radiative rate in a similar fashion. Since we observe no strong correlation within the individual samples, we conclude that the size distribution of the gold NPs is not the major contribution for heterogeneous excitation rates. This finding is, however, in agreement with the orientational distribution of the DNA nanopillar as measured with superresolution microscopy<sup>1</sup>. Sample size: n=148, 142 and 69 for NPs of 20, 40 and 80 nm diameter; and n=214, 226 and 154 for the reference molecules without NP.



**Supplementary Figure 9 | AFM measurements of the DNA nanodisk.** **(a)** Low resolution AFM image of several self-assembled DNA nanostructures. Scale bar: 200 nm. **(b)** High resolution AFM image of a single DNA nanodisk. The blue and black lines indicate the cross sections presented in panel d and e. Scale bar: 50 nm. **(c)** Dimensions of the nanodisk used for simulation of the position distribution: the diameter of 63.6 nm is the average of the calculated length along the longest helices (61.7 nm, 0.34 nm/bp) and across the helices (65.5 nm, 2.7 nm helix-helix distance, honeycomb lattice). The distance of the dye to the center of the DNA structure is calculated as 27.1 nm. **(d)** Profile of the DNA nanodisk along one double helix together with red bar indicating the calculated length. **(e)** Profile of the DNA nanodisk perpendicular to the helices together with magenta bar indicating the calculated length.



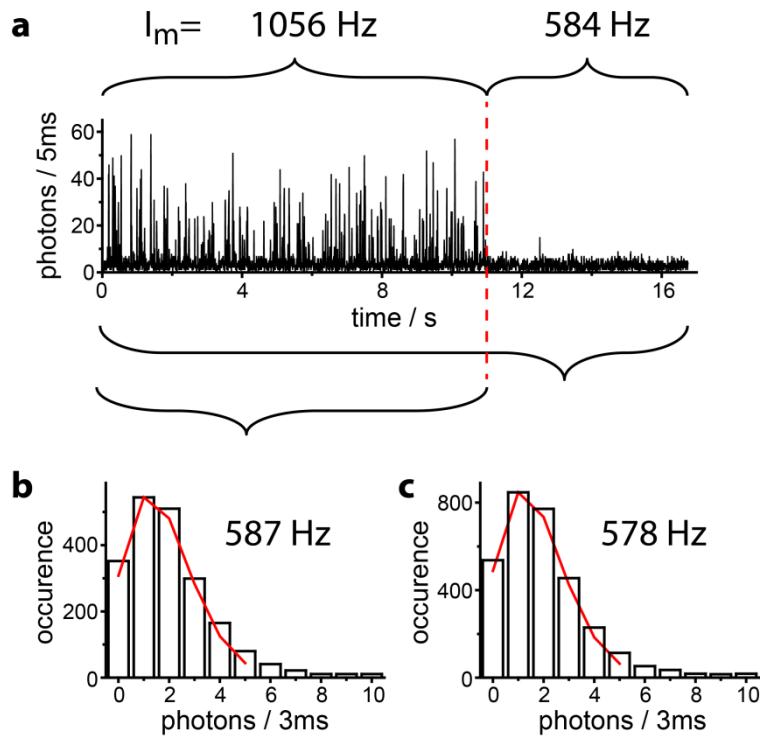
**Supplementary Figure 10 | Exemplary SEM images (a)** Image of 114 nm ZMW with measured width and height of 116.1 nm and 111.7 nm respectively. **(b)** Image of 136 nm sample with measured width and height of 133.5 nm and 135.5 nm respectively.



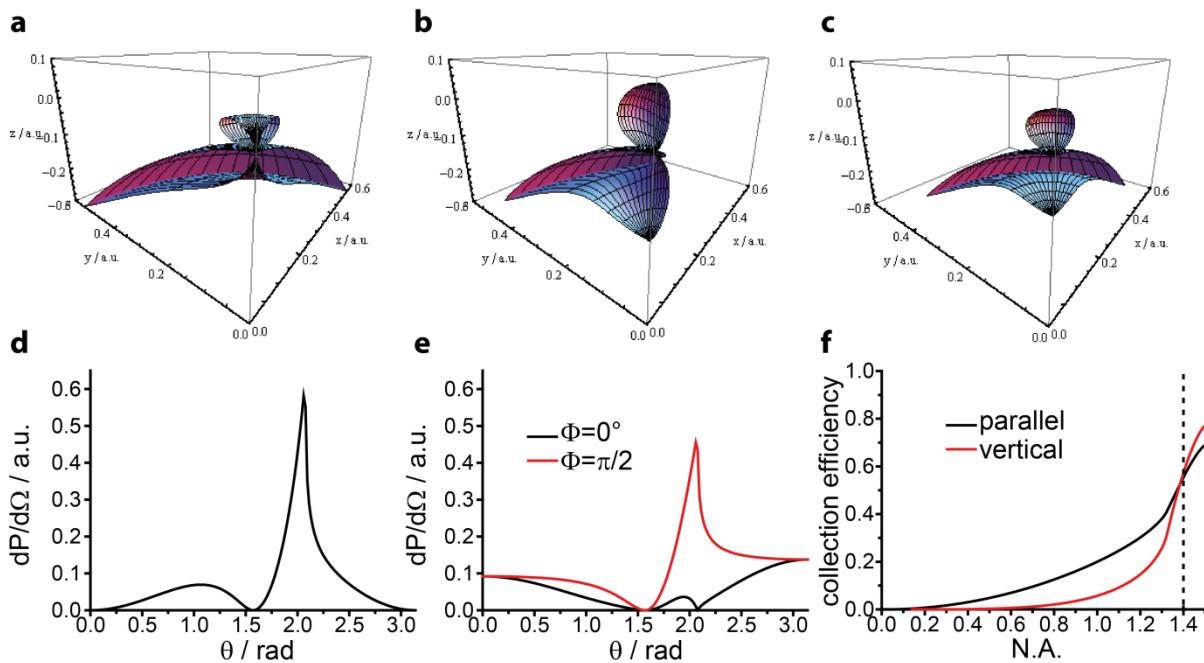
**Supplementary Figure 11 | Fluorescence lifetime analysis in presence of high scattering background.**

**(a)** Fluorescence transient of an Atto647N dye on a DNA nanodisk in a nanopore of 114 nm diameter.

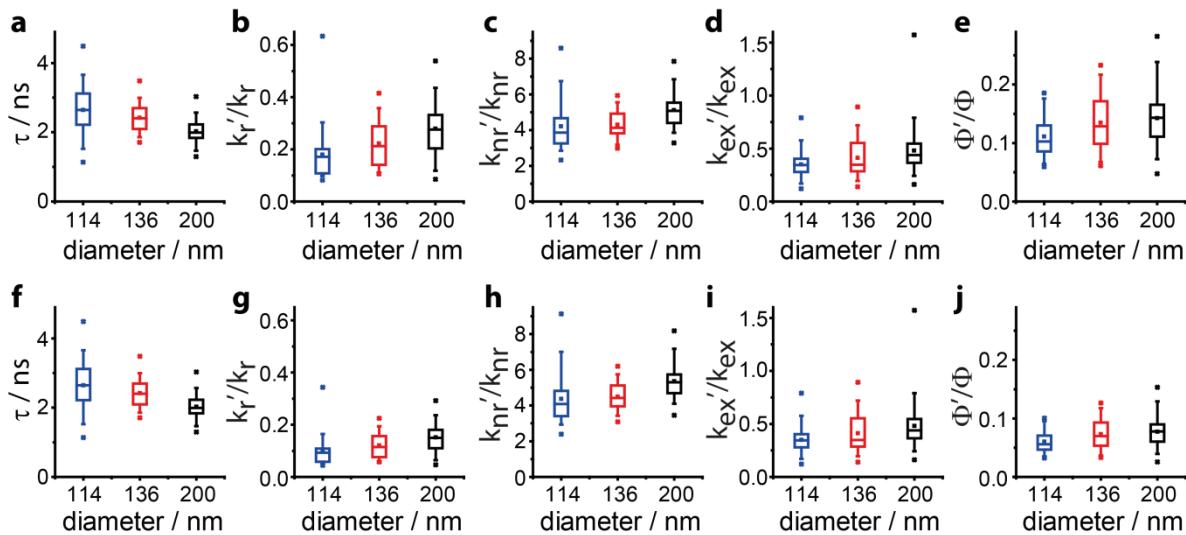
**(b)** In order to remove photons that are clearly associated with scattering, we determine the number of detected photons in a 2 ms window centered around each photon. This photon density can now be used as a threshold to separate on- and off-times. Unlike intensity thresholding, this approach is insensitive to temporal binning of the fluorescence transient. The right plot shows a magnified range of the photon density of the data in panel (a). The mostly used threshold value of 6 photons per 2 ms window is indicated as dashed red line, in some cases the threshold was adjusted as necessary. **(c)** Fluorescence lifetime decay without thresholding exhibits a large portion of scattering. **(d)** Fluorescence lifetime decay after thresholding as indicated in (b). While the majority of scattering is removed, there is still a scattering component present that needs to be considered for analysis. The fluorescence-to-scattering ratio is however clearly improved.



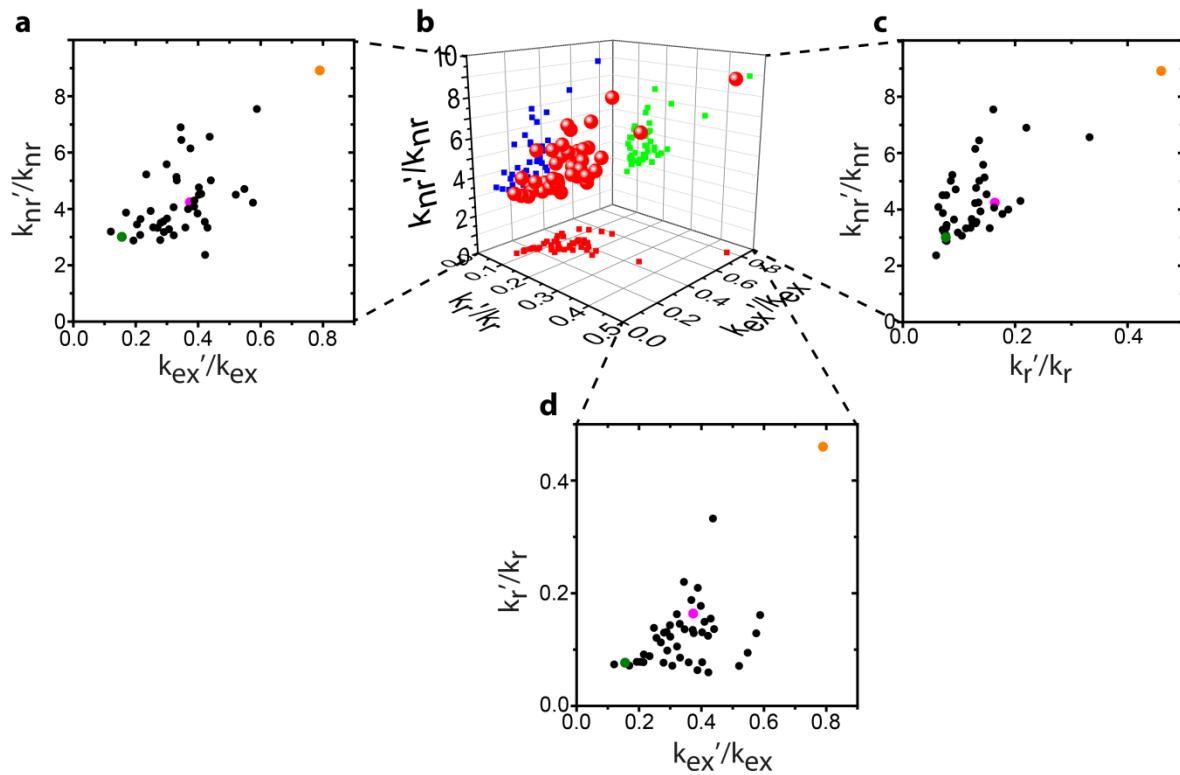
**Supplementary Figure 12 | Background determination with poissonian fitting.** **(a)** Fluorescence transient of an Atto647N dye on a DNA nanodisk in a nanoaperture of 200 nm diameter. The mean intensities  $I_m$  before (1056 Hz) and after bleaching (584 Hz) are indicated. **(b,c)** Intensity histograms of different ranges for 3 ms binning are fitted with a poissonian distribution (red line, numbers indicate mean value of the poissonian). For the fitting procedure both distributions were normalized to their maximum and result in values close to the background intensity after photobleaching. Depending on the background level and intensity of the molecule, the histogram binning and the number of fitted bins were adjusted (1-4 ms and 4-7 bins respectively). The background level for the ZMW measurements was determined by this procedure rather than by measuring the mean intensity after photobleaching, because the lifespan of the dyes in the nanoapertures often exceeded our acquisition time of 30-60 s. The correction of the autocorrelation amplitude for the background intensity is crucial, especially for dim molecules where the average intensity of the transient exceeds the background only slightly.



**Supplementary Figure 13 | Determination of collection efficiency of a fluorophore at the glass/water interface with and without ZMW.** **(a)** Calculated emission pattern for a dipole emitter oriented vertical ( $z$ -direction) at an interface ( $z=0$ ) between glass (below,  $n_g=1.52$ ) and buffer (above,  $n_w=1.33$ ). All calculations follow reference <sup>2</sup>. **(b)** Emission pattern for a dipole oriented in  $x$ -direction (parallel to interface). **(c)** Emission pattern of rotating dye (average of emitters oriented in  $x$ -,  $y$ - and  $z$ -direction). **(d)** Angular power density  $dP/d\Omega (\theta)$  for vertically oriented dipole, with standard spherical coordinates ( $\theta=0$  is the  $z$ -axis). **(e)** Angular power density  $dP/d\Omega (\theta, \Phi)$  for horizontally oriented dipole at selected polar angles. The collection efficiency is calculated by comparing the total emitted power  $P_{\text{all}} = \int_0^{2\pi} d\Phi \int_0^\pi \sin\theta d\theta \frac{dP}{d\Omega}$  with the collected power  $P_{\text{coll}} = \int_0^{2\pi} d\Phi \int_{\theta_m}^\pi \sin\theta d\theta \frac{dP}{d\Omega}$ , where  $\theta_m$  is defined by the numerical aperture (in our case  $NA=1.40$ ). **(f)** Collection efficiency for a horizontal and vertical oriented emitter depending on the NA. For our setup, the collection efficiency of a randomly oriented dipole is  $\eta = 54\%$ . For the ZMW measurements, we make the assumption, that primarily the emission into the upper half space is suppressed, while the emission into the glass remains identical. We therefore only have to relate to the power emitted into the lower half space  $P_{\text{low}} = \int_0^{2\pi} d\Phi \int_{\pi/2}^\pi \sin\theta d\theta \frac{dP}{d\Omega}$ . This gives a collection efficiency of  $\eta' = 75\%$  and therefore the relative collection efficiency  $\alpha = 0.73$ .



**Supplementary Figure 14 | Photophysical rate changes in ZMWs for extreme cases of collection efficiency.** **(a-e)** Results for the case that the collection efficiency with and without ZMW is identical (no change in the emission pattern,  $\alpha = 1$ ). **(f-j)** Results for the extreme case that all emitted fluorescence is collected by the objective ( $\alpha = 0.54$ ). This primarily affects the calculated radiative rate (b, g) and quantum yield (e, j) and has a minor influence on the nonradiative rate (c, h). The trends between ZMW of different diameter remain, however, unchanged as compared to results presented in Figure 7 of the main text (with  $\alpha = 0.73$ ). Sample size: n=45, 45 and 90 for ZMWs of 114, 136 and 200 nm diameter.



**Supplementary Figure 15 | Correlation plots of the photophysical rates for dyes on 114 nm ZMWs. (b)** 3D scatter plot reveals correlation between all three relevant rates ( $n=45$ ). The projections show correlation plots between two respective rates. **(a)** Correlation between the non-radiative and excitation rate. **(c)** Correlation between the non-radiative and radiative rate. **(d)** Correlation between the radiative and excitation rate. The exemplary molecules from Figure 6 (main text) are marked in orange, magenta and olive.

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7[248]	9[255]	GTTTATTTGTCACAATCTTACCGAAGGCCCTTAATATCA	40	
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14[143]	13[159]	CAACCGTTCAAATCACCATCAATTGAGCCA	32	
1[128]	3[127]	TGACAACTCGCTGAGGCTTGCATTATACCA	30	
19[56]	21[63]	TACCGAGCTGAATTGGGAAACCTGTCGTGCAGCTGATT	40	
7[160]	8[144]	TTATTACGAAGAAACTGGCATGATTGCGAGAGG	32	
19[192]	21[191]	ATTATACTAAGAAACCACCAAGAACAGT	32	
23[32]	22[48]	CAAATCAAGTTTTGGGTCGAAACGTGGA	31	
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11[32]	13[31]	AACAGTTTGACCAAAACATTATTTC	30	
1[96]	3[95]	AAACAGCTTTGCAGGATCGTAAACACTAAA	32	
13[224]	15[223]	ACAACATGCCAACGCTAACAGTCTTCTGA	30	
6[175]	4[176]	CAGCAAAAGGAAACGTACCAATGAGCCGC	30	
7[192]	9[199]	ATACATACCGAGGAAACGCAATAAGAAGCGCATTAGACGG	40	
0[271]	1[255]	CCACCCCTCATTTCAGGGATAGCAACCGTACT	32	
4[143]	3[159]	TCATGCCAACAAAGTACAACGGACGCCAGCA	32	
21[96]	23[95]	AGCAAGCGTAGGGTTGAGTGTGAGGGAGCC	32	
7[32]	9[31]	TTTAGGACAAATGCTTAAACAATCAGGTC	30	
11[256]	13[255]	GCCTTAAACCAATCAATAATCGGCACGCCCT	32	
17[224]	19[223]	CATAAATCTTGAATACCAAGTGTAGAAC	30	
15[32]	17[31]	TAATCAGCGGATTGACCGTAATCGTAACCG	30	
18[239]	16[240]	CCTGATTGCAATATATGTGAGTGATCAATAGT	32	
10[207]	8[208]	ATCCAATGAGAATTAACACTGAACAGTTACCAAG	32	
6[143]	5[159]	GATGGTTGAACGAGTAGTAAATTACCATTA	32	
9[224]	11[223]	AAAGTCACAAAATAAACAGCCAGCGTTTA	30	
0[175]	0[144]	TCCACAGACAGCCCTCATAGTTAGCGTAACGA	32	
2[143]	1[159]	ATATTGGAACCATGCCAACGAGAGAAGGA	32	
9[96]	11[95]	CGAAAGACTTGATAAGAGGTATATTGCGCA	32	
13[256]	15[263]	GTTTATCAATATCGTTATACAAACCGACCGTGTGATAAA	40	
14[271]	12[272]	TTAGTATCACAATAGATAAGTCCACGAGCA	30	
7[128]	9[135]	AGACGACAAAGAAGTTGCCATAATTGAGCTCAA	37	
4[47]	2[48]	GACCAACTAATGCCACTACGAAGGGGGTAGCA	32	
12[175]	10[176]	TTTATTAAAGCAAATCAGATATTTTGT	30	
16[239]	14[240]	GAATTATTAAATGGTTGAAATATTCTTACC	32	
4[111]	2[112]	GACCTGCTTTGACCCCCAGCGAGGGAGTTA	32	
10[175]	8[176]	TTAACGTCTAACATAAAAACAGGTAACGGA	30	

17[96]	19[95]	GCTTCCGATTACGCCAGCTGGCGGCTGTTTC	32	
14[207]	12[208]	AATTGAGAATTCTGTCCAGACGACTAAACCAA	32	
2[271]	0[272]	GTTTAACCTAGTACGCCACCCAGAGCCA	30	
3[224]	5[223]	TTAAAGCCAGAGCCGCCACCTCGACAGAA	30	
5[192]	7[191]	CGATAGCATTGAGCCATTGGGAACGTAGAAA	32	
10[79]	8[80]	GATGGCTTATCAAAAAGATTAAGAGCGTCC	30	
13[64]	15[71]	TATATTTGTCATTGCCTGAGAGTGGAAAGATTGTATAAGC	40	
8[111]	6[112]	AATAGTAAACACTATCATAACCCCTATTGTGA	32	
14[111]	12[112]	GAGGGTAGGATTCAAAAGGGTGAGACATCCAA	32	
11[96]	13[95]	AATGGTCAACAGGCAAGGCAAAGAGTAATGTG	32	
17[192]	19[191]	CATTGAAGGCGAATTATTCACTTTGTTGG	32	
<b>magenta</b>				
16[143]		AAAAAAAAAAAAAAAGCCATCAAGCTCATTTAACCAACAAATCCA	47	
15[128]		AAAAAAAAAAAAAAATAATCAAATAATTCGCGTCTCGGAAACC	45	
14[143]		AAAAAAAAAAAAAAACAACCGTTCAAATCACCATCAATTGAGCCA	47	
<b>green</b>				
4[63]	6[56]	ATAAGGGAACCGGATATTCAATTACGTCAAGGACGTTGGAA	40	5' biotin
4[255]	6[248]	AGCCACCACTGTAGCGCGTTCAAGGGAGGGAGGTAAA	40	5' biotin
10[191]	12[184]	GAAACGATAGAAGGCTTATCCGGTCTCATCGAGAACAGC	40	5' biotin
16[63]	18[56]	CGGATTCTGACGACAGTATCGGCCGCAAGGCGATTAAGTT	40	5' biotin
10[127]	12[120]	TAGAGAGTTATTTCAATTGGGGATAGTAGTAGCATTA	38	5' biotin
16[255]	18[248]	GAGAAGAGATAACCTTGCTTCTGTTGGGAGAAACAATAA	40	5' biotin
<b>red</b>				
staples used for individual DNA origamis with dye at five different positions:				
replaces	distance			
7[160]	d1	TTATTACGAAGAACTGGCATGATTGCG	27	3' ATTO647N
9[160]	d2	AGAGAGAAAAATGAAAATAGCAAGC	27	3' ATTO647N
11[160]	d3	CCAATAGCTATCGTAGGAATCATGGC	27	3' ATTO647N
13[160]	d4	GTAATAAGTTAGGCAGAGGGATTATG	27	3' ATTO647N
23[32]	d5	TCAAGTTTTGGGTCGAAACGTGGA	27	5' ATTO647N

**Supplementary Table 1 | Structure details for rectangular DNA origami.** The design is based on the original rectangular structure (7249 nt scaffold derived from M13mp18), but base deletions were included every 48nt along the length of the structure to correct for twist <sup>4,5</sup>.

Start	End	Sequence	Length	Modification
57[98]	59[97]	TAGTAAACGAGAAATAAGAGAGAGTACCTTAATCGA AGAC	42	
50[118]	43[108]	CTGAAAAGGTGGCACAATAATATTCAATT	32	
19[18]	18[18]	GCATAAAGTGCCACACAACA	20	
43[109]	35[111]	TTAGATCTACAGCAAACCTCGCATCAATAGG	31	
18[111]	7[111]	AATCAAATTATCTCACCTGGACGTTAGTATTGCATAAC GCT	42	
41[109]	28[108]	GAGTTATAACCAACGGCAAAGACATGTTTCCTT	35	
34[65]	22[66]	CTCGTGGCGTCAGGGCATTAAAGCGCTGGTTGCCCT TGTC	42	
20[149]	13[156]	ATATTGCTCCCCGTATGGGTCAAATCCTCTGGCCTG AT	41	
10[97]	13[90]	AGAGTGAAATCGAAGCGAAAATACATACAACCGAT	35	
53[77]	50[84]	GAAACAAACCTACCAATATCAAACCTAACGCCAGC	35	
38[34]	45[34]	TCAGTGACGTTGTAAGACAAAAGATTAA	28	
22[34]	29[34]	GCAGGGGATTTCTTCTTCCATCTAAGA	28	
29[35]	30[35]	ACCGGAGGTAGGAATTGTTCCCTCACCCA	28	
60[132]	52[129]	GCAAAGCGACTATTCCCTCAACAATACTGAGA	32	
6[97]	9[90]	TATTATCGGTTTGCAAGAGGAAGGTAATTACCAT	35	
33[56]	34[56]	CAATAATTAAACAACGGCGAACAGTG	28	
1[84]	9[76]	TCCATACTCAATGAGTTAGAGTCTGAGCTCCGGTGTGA AACCCACCACT	49	
53[67]	41[66]	TACAAATCGCTTGAATTGCTTCTATCAAAAAACTATAG TGA	42	
19[112]	23[125]	TTGGTAAGGAGGTTGAACCGCCACCCCTCCATAGTTGAA GACG	42	
9[77]	6[83]	AGCACCAATATTGAAGTCTAATGAAGTCTGCAGAC	36	
32[128]	25[129]	CGTAAACAGCAAAAAAGCTGTATGCAGCCCTAGAG	35	
46[62]	53[55]	CCCTTCTGACCTGATAGCCCTCGAATTATACAGTA	35	
50[128]	42[126]	GGGCAAAGAATACTTTGTAATGTAGAGGGT	31	
59[60]	51[66]	AGTATTAGACATAATACTATTTTGGCAACTTG	35	
53[140]	56[133]	AGCAACAAAAACCAAGATAACAGTAGCTAACATGTATT GCTGTGAATCC	49	
18[97]	21[90]	GAGCAGCGACGCAGTCACATAAAAACAATAGCTA	35	
30[139]	37[139]	CTGGCGATTCCGGTTTGCAGACTTT	28	
8[107]	3[122]	CCAATCACCGCGTTGCGTAGCGCGTTTCATCGG	35	
23[126]	14[126]	CCTGGTCACTGCGTGATTGTGGTGTGAGTATTGCTTAT CAA	42	
34[55]	41[55]	TAGCGGTCTCGTTATGCGTTAGAAATAC	28	
1[60]	0[60]	GTTGTGCAGAAAAAGATTG	20	
61[119]	59[132]	TTACCCCTGGATTGCCGAGCTCAAAGCG	28	
9[91]	10[98]	TAGCAATAATCAAACCAGAACTAAAAGATCAAAGG	35	
34[97]	37[90]	TTTGAGGGCTCATTAACGGAATCATAATAAGTAC	35	

25[35]	26[35]	AATAAGACGAGCGTTCACCACTGTTG	28	
17[119]	18[112]	CAGGAGTTATTCGAGTAAGCGCTGAAACAGCAA	35	
50[139]	57[141]	TATTTCGACCATTAAATAGCGCGGAATCG	30	
51[67]	46[63]	CTGAGGTGAGGCCATTGATAGAA	24	
34[139]	41[139]	ACGTTGGCGTCTGGTAAAACAATTGTGT	28	
53[34]	52[31]	AACGTCAGGAAATTGCGTA	19	
10[118]	17[118]	CGCTGGCAACTATCCTGAATTGATGATA	28	
29[161]	30[161]	TCAGCGGGCGAATATTAACCAGGTGCGG	28	
		AGGGATTAAGGTTGTAACCAGGCTCCGATAGGCAATG		
31[109]	19[111]	CCATGAA	45	
34[76]	41[76]	GCGCTAGGCTAACAAAAGCCATAAGGC	28	
21[77]	18[84]	AATAGCAGGGAAAGCCGCTCACTGCCCTGTCTGA	35	
34[183]	41[177]	TCTCCGTGGGAGCGAGACGAAGGAAC	26	
		CTTGCCGGCCGGAAAATCGGTTGACCGCCTCAGACGG		
44[166]	53[156]	AACAAAC	44	
25[140]	26[140]	CATTTCTAGCATTTGTCGCGCAACA	28	
54[83]	61[76]	CAATATCTGGTCAGAGGAGCATATCATCCATTATC	35	
28[107]	21[108]	AATAGACGTTCGATCTAACCTCATAGTACCGAGG	35	
		GCATACAGAATTATGGTTACCGCGCCAGAACGTTG		
7[49]	14[56]	CCCTCACTCGC	49	
0[97]	3[90]	ATGAGTATGTTCTTCAGGCCGAAACGTTGCC	35	
26[160]	33[160]	TAGAAGAACATGCGTAATAATTACAATGA	28	
		TCAATCCCATCGCGCCCCCGGTATGAGCCTATTTATCCA		
32[23]	20[22]	TTGAG	44	
3[63]	1[83]	AATCAGTAGCGACAGAACATCAATACCAATCTTGT	35	
49[119]	50[119]	TAAGAACAGTTGAGGGCAAGGGCGCGAG	28	
53[119]	54[119]	GGAATTATTTGCAAGTAGATATGCAAC	28	
21[46]	8[42]	TAACAGAACGGAAAAGAACCAACCGGTTCATATCACC	38	
37[13]	38[15]	AATGCCAGCTAACATGGTGGAGTAA	28	
30[160]	37[160]	GCCTCTCGGAAACTGCGAGGCCATT	28	
54[118]	61[118]	TAAAGTATTGCGGAAAACAGTCAGGTCT	28	
58[82]	60[65]	GAGCCGTCAATAGTTACAACGAACGTTATT	32	
48[107]	41[108]	CCAACCTTATATTCAAAGAGTAACGCATAGAACG	35	
		GCAGCAAATGAAAACACCGCCGAAC		
51[35]	42[45]	TGAAAGCGTAATT	46	
29[140]	30[140]	GCTAAACTGAAAATCGCATTACGCCAG	28	
33[140]	34[140]	CGATAGTAGGCCGACCGCTTATAGGTC	28	
3[91]	6[98]	TTTAGCGTCAGACTCATTTTACATAGGTTGAG	35	
25[56]	26[56]	TAACGTCCTGAATAGCTGATTGCC	28	
28[44]	21[45]	ATCGCGTTTACGCTAAACGATTCTGAACGAGT	35	
53[91]	54[98]	TTCGCAATGCAGATAGAGGGGTGATTCTGGAAAGT	35	
41[35]	42[35]	AAATTAAATCGCAGCAACTGCAACA	28	
26[55]	33[55]	AGCAGGCAACAAGATTTATAACCAAT	28	
52[128]	45[129]	GGCGGAGGCAATTCATCTGGCTCAAATTGGGGAT	35	

37[56]	38[56]	CATTTCTATCATAGAACATCAGGCCAGAA	28	
31[130]	26[119]	GCTAAGGGGGCCAAGCTAAAATGCGCCGCC	31	
21[140]	22[140]	GC GG GTGCCGGATGCTGGAATTAACT	28	
13[91]	14[98]	TGAGGCCACCAGAGCCAGTAACAAGACCAGAGTTT	35	
17[31]	18[35]	AACGGAATACCAAACCGAGGAGATGATCCGCT	32	
31[46]	22[45]	CGGTGAACCAAGTTGGAAATCGTGAGACGAAT	35	
29[119]	30[119]	GAATTTGCTCCAAGCCAGTGATGTGCT	28	
34[34]	41[34]	CCACCACGAGCACGAGTATAACTGACCT	28	
25[161]	26[161]	CAATAGGCAGTACAGCCAGGATCAGAAA	28	
6[118]	0[98]	GTACTCAAACATCGAACATTGCAAGGAGTTTATAA	35	
21[56]	22[56]	AATAAGAAATTAACTAACTCACCAGCTG	28	
30[118]	37[118]	GCAAGGCAAGATCGAGCAGCGTACAGAG	28	
42[125]	49[118]	AGCTATTTT GAGAAATGCAATGGTTAGCGATT	35	
30[23]	22[18]	TTGGATAGGGTTCCGAAGGGTGGTGAGGCAGTTT	34	
45[91]	46[98]	TTTTCCCTCATCACTTAATCCTCATAACGCAAG	35	
30[149]	19[150]	ATTCAACCCTCATTACAGGACTTGTGAGCGAATGAA	35	
22[139]	29[139]	CTCAGGCAGTCAGGCCACAGAGGATTT	28	
46[34]	44[23]	GTGGCACAGTCTTCTGAGCAAAAGAAGAAACATCTCC TT	40	
6[143]	13[139]	GAGTCTGTAGTGT CGTCTGCCACCGCAGGTC	32	
22[118]	29[118]	CAGAGCAGATGAACACCGTAAAGTAAT	28	
29[12]	30[9]	AAGGCTTATAATAGCAAGCCCAGGGTCGAGGTGC	35	
46[118]	53[118]	AAGCCTTCATACAATTAGGGCCAAAA	28	
21[109]	8[108]	CTGTTATTCTGGCTTTTACCGTTCCGCCGCCG	35	
37[35]	38[35]	AA CATGTTTACCTATAACGTTATAA	28	
17[67]	2[63]	CCTATATAAAAAAGACATATTGCAAAATATCGATA	38	
45[140]	46[140]	CAAATCACAGAACGAAAGATTCTTATGAC	28	
49[35]	50[32]	CAAAATTCAATTACAATGCGCTGCAACAGTG	31	
41[91]	42[98]	AAACACACAAAGTACGCTGGCTAGTCTGGAAAGGCT	35	
11[126]	6[119]	TTACGCACATATGAATT CGCGTCAGATGATGACC	35	
39[25]	30[24]	AACGCCACCC TGTACACCCGCCAGGGAGCTTT	35	
50[151]	39[150]	CCTGTCAATAAAAAAAACAAAAGGGTAGCTGATGTC	37	
33[14]	34[10]	AAATAATACAATAGACCTAAGCGCTTAATGC	32	
18[34]	25[34]	CACAATTAAAGCCGAGGGTACAATCCA	28	
17[77]	14[84]	CAGTATGTTAAGAACCGGGTACCGAGGAAGAACCC	35	
41[161]	42[161]	TGTTACTAGGGAACACCCCGGATATTCA	28	
29[67]	17[66]	CGGATTTATAAAATGACGGGAGGCAAGAACAGATA GGACT	42	
26[184]	33[177]	ACATCATTGAAGGGATTCAACTAACAC	27	
37[91]	38[98]	CGACACGAGGGTAGAACGCGTTAACTAAATT	35	
35[112]	39[125]	AACGCCACCA CGCAATT GTATCATCGCGTGTACATCGA TGA	42	
38[160]	45[166]	GATTGTACATATGTCGA ACTGAAAGCTGCTCATT	34	

14[83]	21[76]	AATATTACATAACATGGATCCAAGTAAGACAATGA	35	
14[162]	21[166]	TTGTTGTTCCCGTGAACAGTGAGTACCAAGCGGA	36	
60[97]	60[98]	CCCGATATTAAATCGGAACAAAGAAAACCATAATGAG GAAG	42	
14[139]	21[139]	ACTCCTGTAAACTGTAATGCCAGGATTA	28	
59[98]	51[111]	TTCAAATATCGCGTGGATTAGGTCACTTCGGTGTCCAAT TCT	42	
41[67]	29[66]	TAATGTTAGGAGCCAGACGACAACGGCTGTGAACAAG CTTG	42	
38[118]	45[118]	GTTAAAAAAGAGAAGACCAGGTCTTGAC	28	
42[83]	49[76]	GGCCTTGCTGGTAAACACGACATAACCTACCTTT	35	
50[97]	53[90]	TACTAATTAAACAGTGTGGAAGGGTAGATAACGGA	35	
12[128]	9[144]	AGCGGTTGAGCTCAGAGACCGGAACCGCCTCCCTCA	36	
29[56]	30[56]	CTCCCGACAAGCCGGTCCACTGATGCC	28	
49[91]	50[98]	ACATATTGTGAATTCAATAACATCTCAATT	35	
29[91]	30[98]	AAGATCGTCTTCCTGTATCGTACGACTGGGTA	35	
38[55]	43[62]	TCCTGAGATTAGTAGCTGATGTCAATAGTGAATTGTAA ATCCAGATT	49	
57[77]	54[84]	GATTATAGCGGAATCTAACAACTAATCTCATCAAT	35	
38[97]	41[90]	TTGTTAAGCCTGAGGAAACCTCCGGCTTAAGAATA	35	
42[139]	49[139]	ATGCCGGGTAGGTAAGTAGTATTATACC	28	
18[139]	25[139]	AAACTGCCTGGAACATAGGTGCCACCC	28	
30[55]	37[55]	CACTACGGGAAAGCCATGTTCGCAGAGG	28	
10[83]	17[76]	TCCCCATTCTGCAACAAAACATGGCAACTATTACG	35	
49[140]	50[140]	AGTCAGGTTACAGGAATTAAAGTAGCTA	28	
19[151]	11[151]	CGGCGCTAACACGAAGTGCCATCCTGGAA	29	
43[168]	34[171]	GACAGTCCAATATGTTGATAACCCAAAATAATGTGAA C	39	
14[97]	17[90]	CTGCGCGTATTACGACCGAAGCCCTTTAGCAA	35	
25[91]	26[98]	AGAATAGAACCGCCAAGTTGTGGCGAATATCTG	35	
45[130]	32[129]	ATTATGAACGCTGATAACTCATCTGGACTAAGGAT	35	
30[34]	37[34]	AATCAAGCCCCGATGCGCTGCAACGCC	28	
2[123]	10[119]	CCCCCTTATTAGGAACCAGAGCCACCCACCATGCTG ATGTCTGA	47	
46[97]	49[90]	GATAAAAGTAGCATCTGATTGCTTGAACAGT	35	
43[63]	34[66]	ACCAAGTCTATCCAGCACTGCACGGTACAGCGGGAGGC G	39	
29[77]	26[77]	TGAAGCCACCGCACACTCCAACGTCACTTGAGCAGC AAG	42	
58[132]	50[129]	GAAGCAAGAGCTATTAAATTAGTTATT	32	
30[97]	33[90]	ACGCCAGGACGACAAAAAAGGTAAAGTACCAAGAA	35	
37[161]	38[161]	AACGGGTCTAAACTAACATACAGGAA	28	
17[56]	18[56]	TGATTAACCGAACAGAGTCAGTCTGTTCC	28	
42[97]	45[90]	ATCAGGTTAGAACCAAATCAATATATGGACTACC	35	

42[44]	31[45]	CATTCTTGAAAGTGTGCTTCCACGCTGTTGA	35	
21[119]	22[119]	TCAAGAGGTACTCACACCATCGAAGCGG	28	
32[170]	25[177]	TCGCATGCCAGGAATTAGTGAGATCGTCACAACCATGTA	41	
17[91]	18[98]	ACGTAGTCATACATGAAACATGAAGGTGACTAAC	35	
6[82]	13[76]	ATCACGAAGGTGTGTTATACGGAAATAAGGGC	34	
22[55]	29[55]	CATTAATGGGCAACCTTACCAAGCGAAC	28	
22[97]	25[90]	ACTGGGGTGTGAGTGTAGTTGCTATTTACAGAG	35	
38[76]	45[76]	GACAGGACTGAGTAGTTATTCATAGG	28	
52[48]	45[45]	AAATAAAATGAATATTCAATTACATTAATTAAAGAA	39	
33[35]	34[35]	TACGAGCGCAGAACTTAGAGCCCGTAA	28	
61[65]	53[66]	AGTAAATATTCCATCCTGAAATTATTCTTT	30	
8[144]	17[139]	AGAACTCACAGCCAGGTGAGTATCTGTCGCTATCCAGAATTAATAAG	47	
55[123]	60[112]	TTAACTCCAACAGGTCAATTAAATTATCAAAA	31	
13[140]	14[140]	AGACGATATTAAAGTACGGGGTGGGAAG	28	
25[77]	22[84]	CAGCCTTGCACCTGGCCCTGAGAGGTATGCTTT	35	
46[139]	53[139]	CCTGTAATTAGCAATAGAAAGTAGTAAG	28	
42[55]	49[55]	TTACCGCACATTGGGTCGCTATTAAACA	28	
15[161]	25[160]	GACGGAAGAACGAGGATATTGGAAAGAATTGATATGCAAGCC	42	
41[13]	42[19]	AGTTAATTAGAAAACACGCAGG	24	
30[76]	37[76]	CCGTCTAACGAAAGGCCAGACGTAATAAG	28	
18[55]	25[55]	TGTGTGAAAGTGAGCTGAAACACTTTGTT	28	
26[118]	33[118]	TGAACCAAACGACGAAGGAGCGAGGTGA	28	
33[91]	34[98]	CGGGTTTATCAGCTGCATGGGTATGGCTGCCAG	35	
15[28]	22[35]	GTTTATGAAACGAACCCACAAGAATTAAAGTCATGGGGTGCACACGC	49	
25[130]	12[129]	CCATATACCAAGGATTCCCTGCCGTACTGGGAA	35	
57[53]	58[60]	CATCAATATATGATTATTCTAAAAATT	27	
41[56]	42[56]	CGACCGTTGAAATATAACATAACAATA	28	
10[62]	17[55]	GAAATGACTGATACACGATACCAAAAGACACTGGCA	35	
26[97]	29[90]	CCACTCATTCCCAGGTATTAAACCAAGTTAAATC	35	
46[82]	53[76]	TCTGGCCAACAGAAAAATAAGTTACAATCGGGA	34	
7[112]	11[125]	TGTGAAACCTCAGACAGCATTGACAGGAGCAGTCTGACATCA	42	
37[140]	38[140]	TTCATGAAATACACCCCTCCTATATTAA	28	
22[65]	10[63]	GTGCATTAATTCAAGCAGGAGAAATCCTCGCTCTGTATGTGCGA	45	
61[77]	58[83]	ATTTTGCCTTGCACAAATCGACAACTTGAGATTA	36	
34[160]	41[160]	TTGACCGGCTTCAGAAAGAGTGCTCCA	28	
53[56]	54[52]	ACAGTACTGCACGTGCATCACATCAACAGTTG	32	
0[121]	1[120]	ACATACATTGCTGATACCG	19	
14[125]	21[118]	GCACTGCACTGGTGGATGGGAAACCTAACAGACTCC	35	

49[77]	46[83]	TTAATGGAATACCACCGAACGAACCATAATGGACAT	36	
39[151]	30[150]	AATTAAGCAAGTAGCCATAATGGGCTGGTGCCGCT	35	
21[91]	22[98]	TCTTAAAGTATTAAGCCACCCACCTTTCATGACG	35	
33[151]	20[150]	CCGTTCACGAACCTTCACGCCTGAGGGATAAAGT	35	
20[166]	29[160]	AGAGGGACCAGCAGAGAGGTTCGAAGTGCAAGTTAAC TACAAACAGTT	48	
9[42]	7[62]	GCCATTGGGAATTAGAGCCATAAAGGTAAATTTC	35	
54[97]	57[97]	TTCATTCCCTTTGTGCCACCAGAAGGACTTCTGAATAA TAA	42	
7[63]	6[49]	CATGAAGTTATGTAGATGAAGGTATAGA	28	
30[184]	37[178]	TGTTGGGAAGTTGCCAGATATATGTAA	28	
33[161]	34[161]	CAACAACCTGAGGCCAGGCAACGGCGGA	28	
51[112]	55[122]	GCGAACGAAAGAAGGACTGGATAGCGTCATGCTTTGG C	39	
60[111]	48[108]	AGATTAACAAAAATTCAAGAAAATGTTATTTGCCACAT AACATA	46	
45[46]	28[45]	GAGCAAATCCATGGTTTACAAATAATTAGAGCTAATA TGTAGATTTC	49	
13[77]	10[84]	GACATTCATAAAGGTATAGATGATTATTGAACAAA	35	
42[160]	49[164]	ACCGTTCTGAGAAACTGACGAGAAGAAAAATC	32	
52[155]	40[150]	ACGACGATACTATCATAACATTAACGTTGGAAACACA CGTAACACCA	48	
49[56]	52[49]	ATTCATGCAGAGGAAACATGCGGTCACTTAAATC TAAAAAAACAG	49	
41[77]	38[77]	GTAAATAGGTTGGGAAGAACTCAAATTATAAGGGAT TTTA	42	
26[76]	33[76]	CGGTCCAACGTGGTCATCGACTTCCT	28	
42[34]	49[34]	GGAAAAAAATCGTCTCTAGAAAAGAAAA	28	
45[77]	42[84]	TCTGAGATGAGTGACAGTAATAAAAGTTCACTATC	35	
40[177]	32[171]	GTCAATCATATAGCCGGCACCAACAAAATACTCGG	35	
41[140]	42[140]	CGAAATCTGAAAGACTAGCATAAATTA	28	
18[83]	25[76]	ATTCGTAATCATGGTGCCTGGCATTAGAAAATAG	35	
25[11]	26[9]	AGCCATATTAATTGCCGGCGCCAATCGGCAAATC	36	
40[149]	33[150]	ACTCGCGACCGCAAAAGGGAAAGTTGAGTTAATGCG	35	
26[139]	33[139]	CAGCAATTATTATTCTCCAATTGATAC	28	
14[55]	21[55]	GGGGATTCACTTCAAGTTACGCCAAT	28	
22[44]	10[38]	CGGCCTAATGAATTGTTATAATGTATTTAGGTGGAAC GTGCAAATT	49	
17[140]	18[140]	TTTTAACAAACAGTGAAAGCAAGTAGGG	28	
50[83]	57[76]	AGAAGATAAAACAGAACCTCAATATCAATTGTTG	35	
34[170]	23[173]	AAAAGCGCCAGGCAGTACAGTTCTCAGCAGGATCT	37	
45[35]	46[35]	GACGCTGATTTCCGAAATGGAGAAC	28	
39[126]	31[129]	ACGGTAAAACGTTATAATTCTGTAGATGCCA	32	
13[31]	14[28]	TCAATAGAAAAATAAGTCGAGTACTCTGAACCTCGCTA C	39	

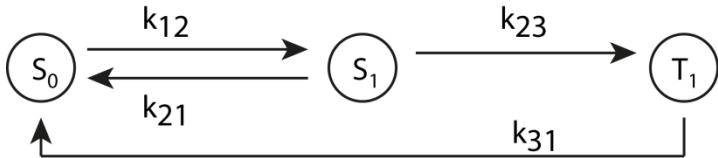
26[34]	33[34]	ATGGTGGTTGAGTGTCAATTACCTAATT	28	
45[119]	46[119]	AAGAACCCCTTGAGATGCCTGAGCGGGAG	28	
22[83]	29[76]	CCAGTCGGAAACCCACCGCCAGCTACAGAGGTTT	35	
45[23]	32[24]	AGCTTGAACCGTCACTTAGCCAACATTAAATTAA	37	
38[139]	45[139]	AATTGTATCGTAAAAGGACAGCATTACC	28	
33[77]	30[77]	TATCATTATTCTGTAAGGGAAAGAAAGACGGAAGGGCG AAAAAA	42	5'-biotin
33[119]	31[108]	ATTTCTTCACCCCTCCACTCCAGGGCGCATCGTAACCGTG CATCCTC	46	5'-biotin
37[119]	38[119]	GCTTGATTGACCCTCAAAAAATATTTT	28	5'-biotin
37[77]	34[77]	AGAATATTACTAGAAGGAGGCCGATTCAAGGCAGAAAGG AGCGG	42	5'-biotin
47[22]	39[24]	GCTATTAGACAATACGCTCACGCTCATAATT	31	3'-Atto647N

**Supplementary Table 2 | DNA origami structure details for DNA nanodisk.** The DNA nanodisk is designed from an 8634 nt long M13mp18 derived scaffold and generally consists of four layers in a honeycomb lattice. The table presents the full list of staple strands, modified staple strands are grouped at the end.

<u>Thermocycler Program</u>
80°C for 4 minutes
80°C for 24 sec -0.1°C per cycle 200 times
60°C for 12 minutes -0.1°C per cycle 400 times
5°C for ever
End

**Supplementary Table 3.** Detailed folding program for the DNA origami nanodisk

## Supplementary Note 1 - Autocorrelation analysis with derivation



We consider a three level system with rate constants  $k_{mn}$  for transition from state m to state n. The three states are the singlet ground state  $S_0(t)$ , the first excited singlet state  $S_1(t)$  and the triplet state  $T_1(t)$ . The system is fully described by the following set of homogeneous first order differential equations:

$$\frac{d}{dt} \vec{X}(t) = \frac{d}{dt} \begin{pmatrix} S_0(t) \\ S_1(t) \\ T_1(t) \end{pmatrix} = \begin{pmatrix} -k_{12} & k_{21} & k_{31} \\ k_{12} & -k_{21} - k_{23} & 0 \\ 0 & k_{23} & -k_{31} \end{pmatrix} \begin{pmatrix} S_0(t) \\ S_1(t) \\ T_1(t) \end{pmatrix}$$

Considering that radiative and non-radiative processes occur on a significantly faster timescale than the intersystem crossing, one can assume  $k_{21} \gg (k_{23} + k_{31})$ . With this, the solution to this set of equations with the molecule initially in its ground state  $\vec{X}(0) = (1, 0, 0)$  can be simplified to:

$$S_0(t) = \frac{k_{21} k_{31}}{k_{21} k_{31} + k_{12}(k_{23} + k_{31})} + \frac{k_{12}}{(k_{12} + k_{21})} \exp[-(k_{12} + k_{21})t] + \frac{k_{12} k_{23} k_{21}}{(k_{12} + k_{21})(k_{21} k_{31} + k_{12}(k_{23} + k_{31}))} \exp[-\left(\frac{k_{12} k_{23}}{k_{12} + k_{21}} + k_{31}\right)t]$$

$$S_1(t) = \frac{k_{12} k_{31}}{k_{21} k_{31} + k_{12}(k_{23} + k_{31})} - \frac{k_{12}}{(k_{12} + k_{21})} \exp[-(k_{12} + k_{21})t] + \frac{(k_{12})^2 k_{23}}{(k_{12} + k_{21})(k_{21} k_{31} + k_{12}(k_{23} + k_{31}))} \exp[-\left(\frac{k_{12} k_{23}}{k_{12} + k_{21}} + k_{31}\right)t]$$

$$T_1(t) = \frac{k_{12} k_{23}}{k_{21} k_{31} + k_{12}(k_{23} + k_{31})} - \frac{k_{12} k_{23}}{(k_{21} k_{31} + k_{12}(k_{23} + k_{31}))} \exp[-\left(\frac{k_{12} k_{23}}{k_{12} + k_{21}} + k_{31}\right)t]$$

and describes the probability that an individual molecule resides in the  $S_0$ ,  $S_1$  or the  $T_1$  state at a certain time t after it is reset to its ground state at  $t=0$ <sup>6</sup>. The constant term is the steady state probability, while the terms with decay constants  $\tau_2 = (k_{12}+k_{21})^{-1}$  and  $\tau_3 = (k_{12} k_{23}/(k_{12}+k_{21}) + k_{31})^{-1}$  represent the antibunching and triplet dynamics, respectively.

Following ref.<sup>7</sup>, the normalized autocorrelation function (AC) for three states can be defined as

$$G'(\tau) = \frac{\langle I(t)I(t+\tau) \rangle}{\langle I(t) \rangle^2} = \frac{\sum_{m=1}^3 \sum_{n=1}^3 I_m I_n P(m)P(m,t|n,t+\tau)}{\left(\sum_{m=1}^3 I_m P(m)\right)^2}$$

where  $P(m)$  is the probability of detecting a molecule in state  $m$  and  $P(m,t|n,t+\tau)$  the probability of subsequently detecting it in state  $m$  at time  $t$  and in state  $n$  at time  $t+\tau$ . The formula greatly simplifies, since in our case only state 2 (the excited singlet state  $S_1$ ), is fluorescent ( $|I_m| = |I_2|^2 \delta_{m2} \delta_{n2}$ , with Kronecker delta  $\delta$ ).  $P(2)$  is the steady state probability of the  $S_1$  population  $S_1(\infty)$  and because after each detected photon the system is reset to its groundstate,  $P(m,t|n,t+\tau)$  can simply be expressed as  $S_1(\tau)$  presented above. This can be summarized to

$$\begin{aligned} G'(\tau) &= \frac{S_1(\tau)}{S_1(\infty)} = 1 - \frac{k_{12}}{(k_{12} + k_{21})} \frac{k_{21} k_{31} + k_{12}(k_{23} + k_{31})}{k_{12} k_{31}} \text{Exp}[-(k_{12} + k_{21})\tau] \\ &\quad + \frac{(k_{12})^2 k_{23}}{(k_{12} + k_{21})} \frac{1}{k_{12} k_{31}} \text{Exp}\left[-\left(\frac{k_{12} k_{23}}{k_{12} + k_{21}} + k_{31}\right)\tau\right] \\ &= 1 - 0 + \frac{k_{12} k_{23}}{(k_{12} + k_{21})} \frac{1}{k_{31}} \text{Exp}\left[-\left(\frac{k_{12} k_{23}}{k_{12} + k_{21}} + k_{31}\right)\tau\right] \\ &= 1 + A_3 \text{Exp}\left[-\frac{\tau}{\tau_3}\right] \end{aligned}$$

We ignore the second term, since these antibunching dynamics occur on shorter timescales than observed in our autocorrelation analysis and therefore  $\text{Exp}[-(k_{12} + k_{21})\tau] = 0$ . Because we only measure monoexponential autocorrelation functions, we now omit the index “3” of the amplitude and decay time in the following for simplicity. The parameters of the autocorrelation function generally relate to the macroscopic on- and off-times as follows:

$$\tau = (k_{\text{off}} + k_{\text{on}})^{-1}$$

$$A = \frac{k_{\text{off}}}{k_{\text{on}}}$$

$$t_{\text{off}} = k_{\text{on}}^{-1} = \tau(1 + A)$$

$$t_{\text{on}} = k_{\text{off}}^{-1} = \tau(1 + \frac{1}{A})$$

The experimental observables relate to the rate constants from Figure 1 of the main text as

$$k_{\text{off}} = \frac{k_{12} k_{23}}{k_{12} + k_{21}} = \frac{k_{\text{ex}} k_{\text{ISC}}}{k_{\text{ex}} + (k_r + k_{nr})} = k_{\text{ex}} k_{\text{ISC}} \tau_{\text{fl}} = t_{\text{on}}^{-1}$$

$$k_{\text{on}} = k_{31} = k_t$$

Here  $\tau_{\text{fl}}$  is the fluorescence lifetime of the excited state and we employ the low excitation regime approximation ( $k_{\text{ex}} \ll \tau_{\text{fl}}^{-1}$ ). The expression for the off-rate equals equation (1) of the main text.

Experimentally, the correlations  $G(\tau)$  are calculated from the fluorescence transients  $I(t)$  as

$$G(\tau) = G'(\tau) - 1 = \frac{\langle I(t)I(t + \tau) \rangle}{\langle I(t) \rangle^2} - 1 = \frac{\langle \delta I(t)\delta I(t + \tau) \rangle}{\langle I(t) \rangle^2}$$

where  $\langle \cdot \rangle$  denotes temporal averaging and  $\delta I(t) = I(t) - \langle I(t) \rangle$ . Compared to the conventional AC definition, we subtract the constant offset of value 1. The AC is fitted with the monoexponential decay model presented above. We multiply the background correction factor  $C$  to the amplitude of the decay to account for the influence of uncorrelated background signal<sup>8</sup>. The time-averaged background signal  $B$  is determined for each molecule after the fluorophore bleached (NP measurements) or from a poissonian fit to an intensity histogram (ZMW measurements, see Supplementary Figure 10).

$$C = \frac{\langle I(t) \rangle^2}{(\langle I(t) \rangle - B)^2}$$

Together with the mean intensity  $I_m = \langle I(t) \rangle$  we extract the number of detected photons before blinking occurs  $N_{\text{on}}$ . The intensity  $I_{\text{on}}$  during  $t_{\text{on}}$  represents the intensity in the fluorescence transient if no blinking was present.

$$I_m = B + I_{\text{on}} \cdot \frac{t_{\text{on}}}{t_{\text{on}} + t_{\text{off}}}$$

$$N_{\text{on}} = I_{\text{on}} t_{\text{on}} = (I_m - B) \cdot (t_{\text{on}} + t_{\text{off}})$$

$$I_{\text{on}} = (I_m - B) \cdot \frac{(t_{\text{on}} + t_{\text{off}})}{t_{\text{on}}}$$

While this derivation describes triplet blinking as employed for the ZMW measurements, it is also valid for monoexponential radical blinking used for the NP measurements. When the triplet state is 100% reduced to a radical state (i.e. only single component in AC function), the definitions of the on-time and on-counts do not change. Only the off-time is changed since radical states have a generally longer off-time compared to triplet states, but the off-states are irrelevant for the analysis presented here.

## Supplementary References

- 1 Schmied, J. J. *et al.* DNA Origami Nanopillars as Standards for Three-dimensional Superresolution Microscopy. *Nano Lett.* **13**, 781-785 (2013).
- 2 Enderlein, J., Ruckstuhl, T. & Seeger, S. Highly Efficient Optical Detection of Surface-Generated Fluorescence. *Appl. Opt.* **38**, 724-732 (1999).
- 3 Acuna, G. P. *et al.* Fluorescence enhancement at docking sites of DNA-directed self-assembled nanoantennas. *Science* **338**, 506-510 (2012).
- 4 Rothemund, P. W. Folding DNA to create nanoscale shapes and patterns. *Nature* **440**, 297-302 (2006).
- 5 Woo, S. & Rothemund, P. W. K. Programmable molecular recognition based on the geometry of DNA nanostructures. *Nat. Chem.* **3**, 620-627 (2011).
- 6 Widengren, J., Mets, U. & Rigler, R. Fluorescence correlation spectroscopy of triplet states in solution: a theoretical and experimental study. *J. Phys. Chem.* **99**, 13368-13379 (1995).
- 7 Kim, H. D. *et al.* Mg<sup>2+</sup>-dependent conformational change of RNA studied by fluorescence correlation and FRET on immobilized single molecules. *Proc. Natl. Acad. Sci. U.S.A.* **99**, 4284-4289 (2002).
- 8 Bernard, J., Fleury, L., Talon, H. & Orrit, M. Photon bunching in the fluorescence from single molecules: A probe for intersystem crossing. *J. Chem. Phys.* **98**, 850-859 (1993).