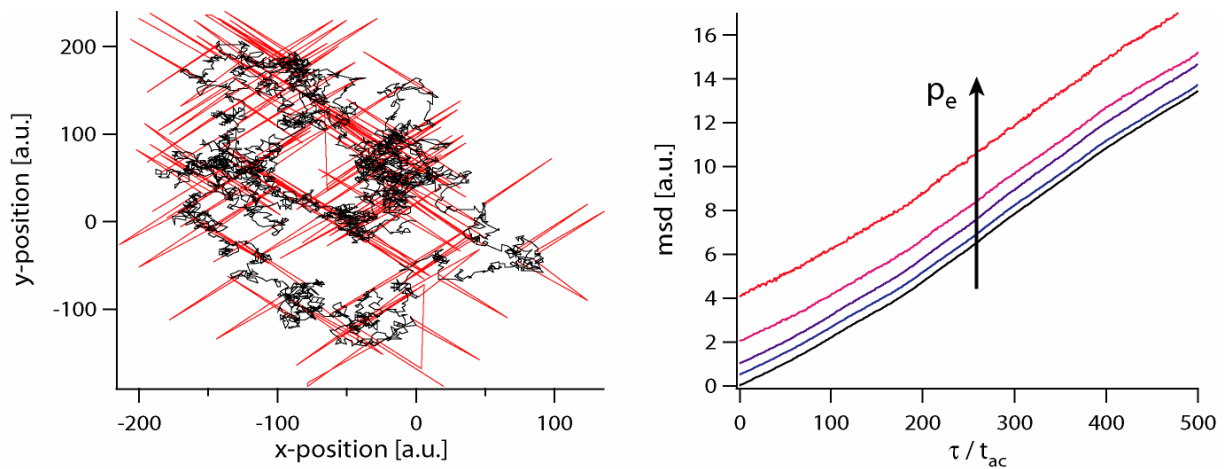
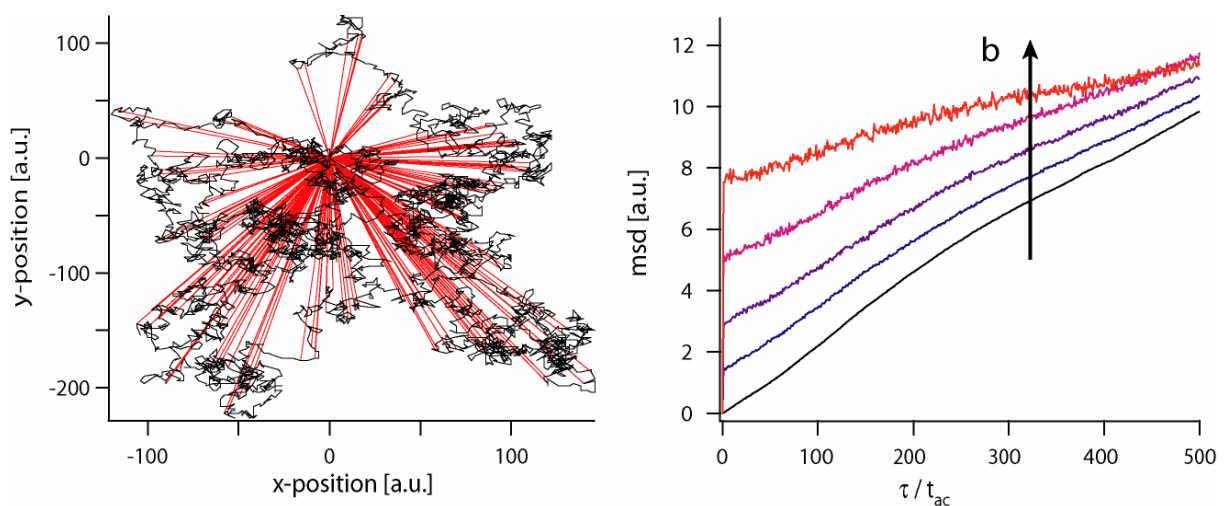


Supplementary Information

Influence of tracking errors:



Supplementary figure 1. Two-dimensional simulation of a random walk in arbitrary units (5.000 data points) mimicking the occurrence of tracking errors. The black trajectory shows the original data, the red trajectory was created by introducing a tracking error probability of $p_e = 40\%$. The corresponding *msds* with increasing error probability p_e , from $p_e = 0\%$ (black) to $p_e = 40\%$ (red), exhibit an growing offset but are still parallel. Again, only the first 10 % of the calculated *msds* are shown. The time axis is given in units of the image acquisition time t_{ac} .



Supplementary figure 2. In this simulation the fixed particle position (0 | 0) was assigned to each dark state of the particle. The black trajectory shows the original data, the red trajectory was created by introducing a blinking probability of $b = 2.5\%$. The corresponding *msds* with increasing b from $b = 0\%$ (black) to $b = 40\%$ (red) exhibit an growing offset, again. Moreover, the slope of the *msd* is continuously decreased down to 50 % of its original value.

Peptides:

Mass spectra (ESI) were performed on a Finnigan LCQ instrument. For the constructs used in this study the following values were obtained (molecular masses in Da):

cyclo(-RGDfK[biotinyl]-):	ESI-MS (m/z): 416.3 [(M+2H)/2] ⁺ , 830.6 [M+H] ⁺ .
cyclo(-RβADfK[biotinyl]-):	ESI-MS (m/z): 844.7 [M+H] ⁺ .
cyclo(-RGDfK[Ahx-Ahx-biotinyl]-):	ESI-MS (m/z): 529.2 [(M+2H)/2] ⁺ , 1056.8 [M+H] ⁺ .
cyclo(-RβADfK[Ahx-Ahx-biotinyl]-):	ESI-MS (m/z): 1070.8 [M+H] ⁺ .
cyclo(-RGDfK[Hegas-Hegas-biotinyl]-):	ESI-MS (m/z): 737.5 [(M+2H)/2] ⁺ , 1473.0 [M+H] ⁺ .
cyclo(-RDGfK[Hegas-Hegas-biotinyl]-):	ESI-MS (m/z): 737.5 [(M+2H)/2] ⁺ , 1473.0 [M+H] ⁺ .