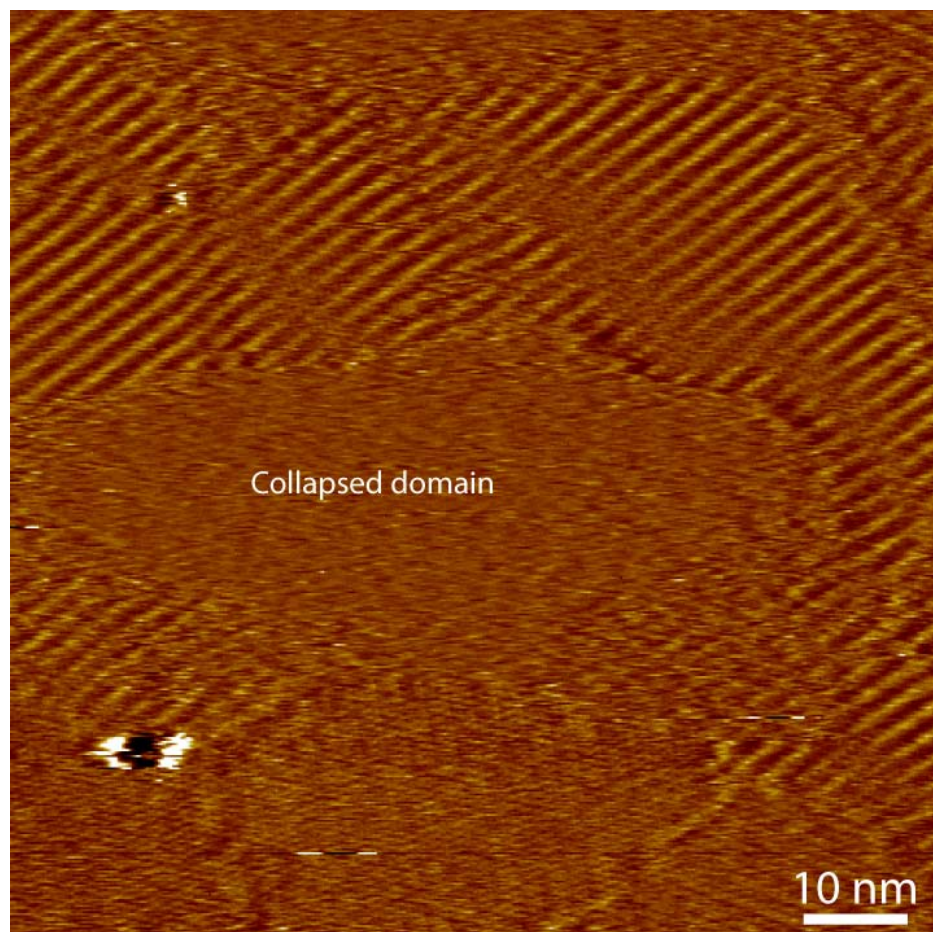# Two-dimensional network stability of nucleobases and amino acids on graphite under ambient conditions: adenine, L-serine and L-tyrosine

**Supporting information:**

Figure S1: Current STM image (I=200pA, V=0.8V). The image shows the surroundings of a previously scanned area (10 x 10 nm^2), which had collapsed due to tip interactions. As seen, the collapse affects not only the scanned area, but a complete domain.
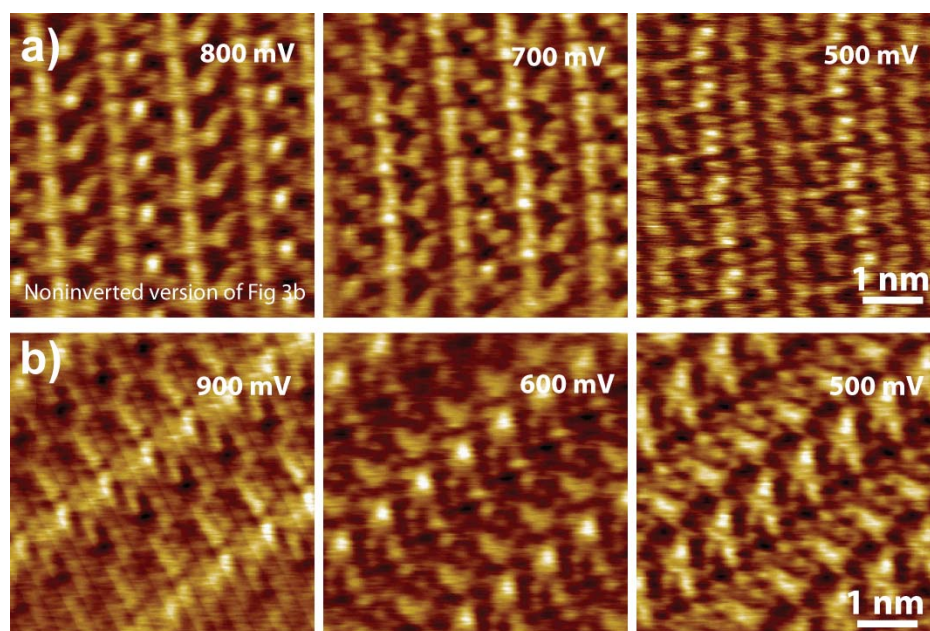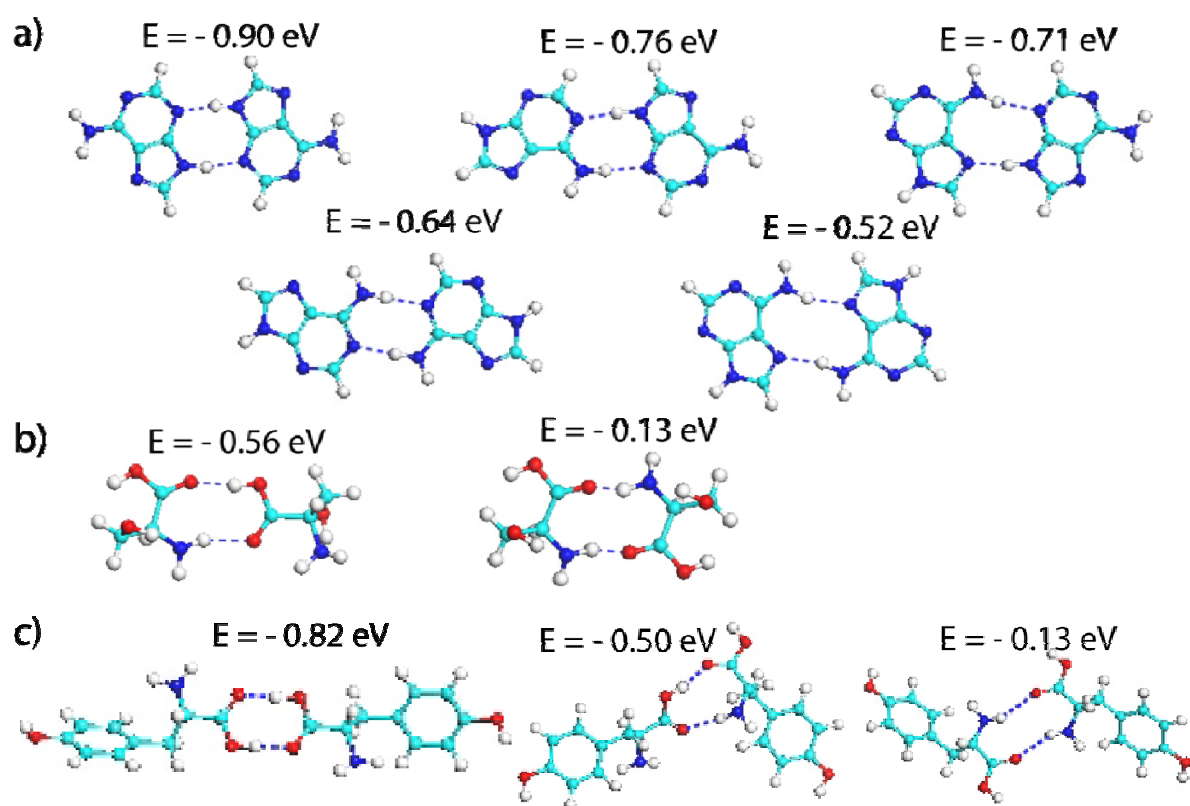
Figure S2: Bias-dependent sequences of STM images (I=200 pA in all cases) obtained after deposition from the adenine/L-serine solution. (a) Image sequence of a homoochiral A domain obtained after contrast inversion had occurred. The last image in (a) is the originally recorded version of the image displayed in Fig. 3b. The latter had been inverted by means of the image processing software for better illustration. (b) Image sequence of a hetorochiral B domain.
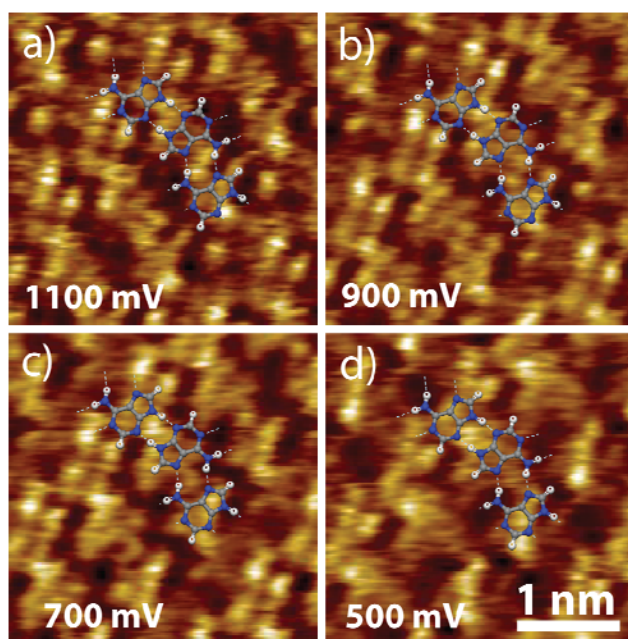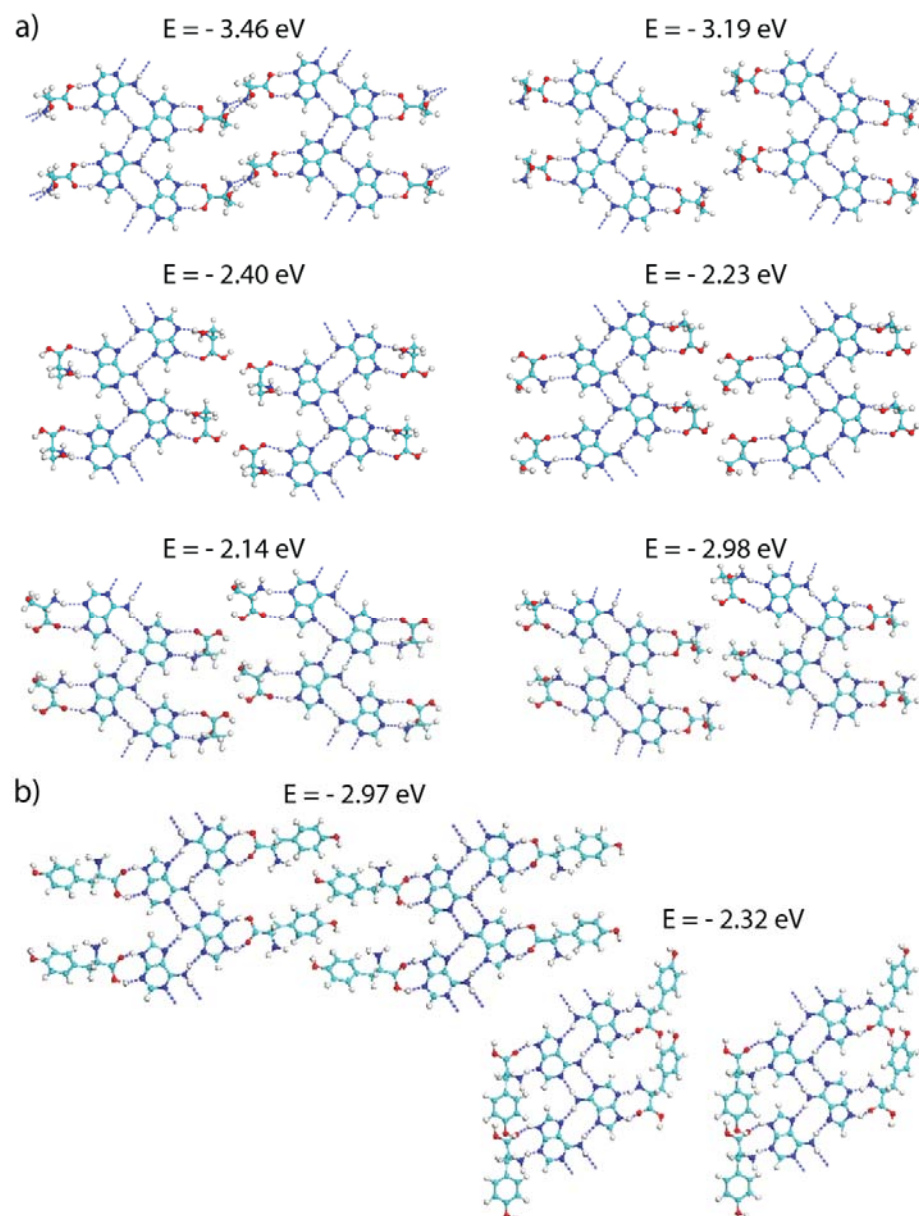

Figure S3: Bias-dependent sequence of STM images of a hetorochiral adenine domain (I=200 pA).

Homodimers

a)

E = - 0.90 eV   E = - 0.76 eV   E = - 0.71 eV

E = - 0.64 eV   E = - 0.52 eV

b)

E = - 0.56 eV   E = - 0.13 eV

c)

E = - 0.82 eV   E = - 0.50 eV   E = - 0.13 eV

Figure S4: Stabilization energies and structures of molecular dimer arrangements calculated by DFT: (a) Adenine-adenine, (b) L-serine/L-serine, (c) L-tyrosine/L-tyrosine.

a)
E = - 3.46 eV   E = - 3.19 eV

E = - 2.40 eV   E = - 2.23 eV

E = - 2.14 eV   E = - 2.98 eV

b)
E = - 2.97 eV

E = - 2.32 eV

Figure S5: Calculated stabilization energies and structures of intermixed molecular networks: (a) Adenine/L-serine, (b) Adenine/ L-tyrosine.