Supporting Information

Synthetic approaches to nucleopeptides containing all the four nucleobases and nucleic acid-binding studies on a mixed-sequence nucleo-oligolysine

Giovanni N. Roviello1* and Domenica Musumeci1,2*

¹CNR, Istituto di Biostrutture e Bioimmagini – Via Mezzocannone 16, 80134 Napoli, Italy; Tel: +39-(0)81-2534585. Fax: +39-(0)81-2534574;

E-mail: giovanni.roviello@cnr.it

²Università di Napoli "Federico II", Dipartimento di Scienze Chimiche, 80126 Napoli,

Italy; Tel: +39-(0)81-674143;

E-mail: domenica.musumeci@unina.it

* Corresponding authors. These authors contributed equally to this work



Figure S1: Structures of the protected nucleolysine monomers and calculated molecular weights



Fig. S2: LC-ESIMS (positive ions) of the four the nucleolysine monomers (RP C18 column, HPLC method: 15 to 70 % of B in A over10 minutes)



Fig. S3: Structural representation of the nucleopeptides 1 and 2 object of this work.



Fig. S4: (A) CD profiles relative to **2** and complementary DNA solutions before (black line) and after (red) mixing, both at a 10 μ M concentration in 10 mM phosphate buffer, pH 7.5, at 5 °C (total volume after mixing= 2 mL). (B) UV thermal denaturation curve relative to the above-described nucleopeptide **2**/DNA complex.



Fig. S5: UV thermal denaturation curve relative to PNA (NH_2 -gcattt-CONH₂)/RNA complex (6.7 / 1.5 μ M respectively, in 10 mM phosphate buffer-pH 7.5; V=3mL).



Fig. S6: CD profiles relative to 2 (C=4 μ M) and double stranded DNA (C=2 μ M) solutions before (black line) and after (red) mixing, in 10 mM phosphate buffer, pH 7.5, at 5 °C (total volume after mixing= 2 mL).