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Supporting Information

Access to a stabilized *i*-motif DNA structure through four successive ligation reactions on a cyclopeptide scaffold

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Table of contents

Abbreviations:	S2
General details:	S2
Peptides Synthesis:	. S 3
Oligonucleotides synthesis:	S8
Conjugates synthesis:	S12
Circular Dichroism studies:	S25

1. Abbreviations

Alloc: Allyloxycarbonyl; Boc: tert-butoxycarbonyl; CD: Circular Dichroism; CPG: Controlled Pore Glass; CuAAC: Copper Catalyzed Alkyne-Azide Cycloaddition; DCM: dichloromethane; Dde: bis-N-[1-(4,4-dimethyl-2,6-dioxocyclohexylidene)ethyl]; DIEA: diisopropylamine; DMF: dimethylformamide; DTT: dithiothreitol; EDTA: Ethylenediaminetetraacetic acid; Eei: *N&*-ethoxyethylidene; ESI-MS: Electrospray Ionization Mass Spectrometry; ISAHC: imidazole-1-sulfonylazide hydrochloride MALDI-Tof-MS: Matrix Assisted Laser Desorption Ionization - Time of Flight Mass Spectrometry; OL: oxime ligation; PBS: phosphate buffer saline; RP-HPLC: Reverse-Phase High Performance Liquid Chromatography; Rt: Retention time; SEC: Size Exclusion Chromatography; SPOS: solid-phase oligonucleotide syntheses; SPPS: solid-phase peptide synthesis; TC: thiol-iodoacetamide SN2 reaction; TCEP: tris(2-carboxyethyl)phosphine, TFA: trifluoroacetic acid; THPTA: Tris-(hydroxypropyltriazolylmethyl)amine; TIS: triisopropylsilane; Tm: melting temperature; TRIS: 2amino-2-hydroxymethyl-propane-1,3-diol; UPLC: Ultra Performance Liquid Chromatography; UV: Ultraviolet.

2. General details

ESI mass spectra were performed on an Esquire 3000 spectrometer from Bruker or on an Acquity UPLC/MS system from Waters equipped with a SQ Detector 2 within a column heater set at 60°C. MALDI-Tof mass spectra were performed on an Autoflex Bruker using hydropiccolinic acid (HPA, 45 mg; ammonium citrate 4 mg in 500 μ L H₂O/CH₃CN) as matrix. Peptides were analyzed in positive mode and oligonucleotides and conjugates in negative mode. The mass spectra display either the relative abundance of ion signals (total ion counts) against the *m/z* ratios or the total ion counts against the *m/z* ratios. All solvents and reagents used were of highest purity commercially available.

3. Peptide synthesis

General details

The synthesis was performed on a Syro II synthesizer using Fmoc/tBu strategy on a 2-Chlorotrityl resin.

The courses of the reactions were monitored by using UPLC system Waters, it includes reverse phase chromatography using Nucleosil C18 column (130 Å, 2.1 x 50 mm, 1.7 μ m) and detection by UV at 214 nm and 250 nm. A 0.6 mL/min flow linear gradient from 95% solvent A (0.1% formic acid in water) and 5% solvent B (0.1% formic acid in acetonitrile) to 100% B for 3 minutes was applied. The purified products were analyzed by the same UPLC system and the chromatograms display the UV absorbance at 214 nm against time.

RP-HPLC purifications were performed on a Gilson system with Nucleosil C18 column (100 Å, 250 x 21 mm, 7 μ m) with UV monitoring at 214 nm and 250 nm. A 22 mL/min flow linear gradient was applied from 95% solvent A (0.1% formic acid in water) and 5% solvent B (0.1% formic acid in acetonitrile) to 100% B for 15 minutes.



Scheme S1. Synthesis of peptide 4a.



Figure S1. ESI mass spectrum of intermediate peptide β : ESI-MS (+): m/z calcd for $C_{70}H_{116}N_{20}O_{18}SCI$: 1591.8, m/z found: 1613.9 [M+Na]⁺.



Figure S2. HR-ESI mass spectrum of intermediate peptide β : ESI-MS (+): m/z calcd for $C_{70}H_{116}N_{20}O_{18}$ SCI: 1591.8186, m/z found: 1591.8196.



Figure S3. ESI mass spectrum of peptide 4a ESI-MS (+): m/z calcd for $C_{61}H_{102}N_{20}O_{15}SCI$: 1421.7, m/z found: 1421.9 [M+H]⁺.



Scheme S2. Synthesis of peptide 4b.



Figure S4. ESI mass spectrum of intermediate α : ESI-MS (+): m/z calcd for C₈₂H₁₂₈N₁₈O₂₀S: 1716.92, m/z found: 1716.97 [M+H]⁺.



Figure S5. ESI mass spectrum of intermediate β : ESI-MS (+): m/z calcd for C₇₄H₁₁₈N₁₈O₁₉SCI: 1629.34, m/z found: 1629.95 [M+H]⁺.



Figure S6. ESI mass spectrum of peptide **4b:** ESI-MS (+): *m/z* calcd for C₇₀H₁₁₅N₁₈O₁₇SCI: 1546.27, *m/z* found: 1546.93 [M+H]⁺.



Figure S7. ESI mass spectrum of peptide **4b:** ESI-HRMS (+): *m/z* calcd for C₇₀H₁₁₄N₁₈O₁₇SCI: 1545.8018, *m/z* found: 1545.8003 [M]⁺.

4. Oligonucleotide synthesis

General details

Oligonucleotides were prepared using β -cyanoethylphosphoramidite chemistry on a 3400 DNA synthesizer at 1 μ mol scale.

RP-HPLC analyses were performed on a Waters HPLC system using C18 Nucleosil column (Macherey-Nagel, 100 Å, 250 x 4.6 mm, 5 μ m) with UV-monitoring at 260 nm and 280 nm. A 1 mL/min flow linear gradient was applied. Solvent A (50 mM triethylammonium acetate buffer with 5% acetonitrile) and solvent B (acetonitrile with 5% water) were used. A stepwise gradient of 0-30% B in 20 min then from 30 to 100% B in 10 min was applied for the gradient. The RP-HPLC purifications of oligonucleotides were performed on a Gilson system with Nucleosil C-18 colunm (Macherey-Nagel, 100 Å, 250 x 10 mm, 7 μ m) with UV-monitoring at 260 nm and 280 nm using 4 mL/min flow linear gradient. A stepwise gradient of 0-30% B in 20 min then from 30 to 100% B in 10 min was applied.

Desalting of oligonucleotides was performed by SEC on NAP 25 cartridge using manufacturer's protocol.

Quantification of oligonucleotides was performed at 260 nm using Nanodrop apparatus (molar extinction \mathcal{E}_{260nm} was estimated according to the nearest neighbor model).

a) Synthesis of oligonucleotide 2



Scheme S3. Synthesis of oligonucleotide 2.



Figure S8. RP-HPLC chromatogram of pure oligonucleotide 2.



Figure S9. ESI mass spectrum of oligonucleotide **2.** ESI-MS (-): m/z calcd for C₁₁₂H₁₄₈N₃₇O₇₀P₁₂: 3502.60, m/z found: 3502.68 [M-H]⁻.

b) Synthesis of oligonucleotide 3



Scheme S4. Synthesis of oligonucleotide 3.



Figure S10. RP-HPLC chromatogram of pure oligonucleotide 3.



Figure S11. ESI mass spectrum of oligonucleotide **3.** ESI-MS (-): m/z calcd for $C_{113}H_{151}N_{37}O_{69}P_{12}S$: 3534.4, m/z found: 3534.9 [M-H]⁻.

c) Synthesis of oligonucleotide 10







Figure S12. RP-HPLC chromatogram of oligonucleotide 10.



Figure S13. ESI mass spectrum of oligonucleotide **10.** ESI-MS (-): m/z calcd for C₁₁₃H₁₅₅N₄₀O₆₉P₁₂S: 3579.63, m/z found: 3579.58 [M-H]⁻.

5. Conjugates synthesis

General details

RP-HPLC analyses were performed on a Waters HPLC system using C18 Nucleosil column (Macherey-Nagel, 100 Å, 250 x 4.6 mm, 5 μ m) with UV-monitoring at 260 nm and 280 nm. A 1 mL/min flow linear gradient was applied. Solvent A (50 mM triethylammonium acetate buffer with 5% acetonitrile) and solvent B (acetonitrile with 5% water) were used. Two gradients have been used: gradient I (0-30% B in 30 minutes) and gradient II (0-50% B in 30 minutes).

The course of reactions were monitored by using UPLC-MS system Waters, it includes reverse phase chromatography using Nucleosil C18 column (130 Å, 2.1 x 50 mm, 1.7 μ m) equipped with a column heater set at 60°C and detection by UV at 260 nm and 280 nm and by electron spray ionization mass spectrometry. A 0.3 mL/min flow linear gradient with solvent C (triethylamine (15mM) and hexafluoro-2-propanol (50mM) in water) and solvent D (triethylamine (15mM) and hexafluoro-2-propanol (50mM) in wethanol) was used.

The RP-HPLC purifications of conjugates were performed on a Gilson system with Nucleosil C-18 column (Macherey-Nagel, 100 Å, 250 x 10 mm, 7 μ m) with UV-monitoring at 260 nm and 280 nm using 4 mL/min flow linear gradient. Solvent A (50 mM triethylammonium acetate buffer with 5% acetonitrile) and solvent B (acetonitrile with 5% water) were used.

a) Synthesis of conjugate 5



Figure S14. RP-HPLC chromatogram of conjugate 5 (oxime ligation).



Figure S15. MALDI-Tof-MS mass spectrum of oligonucleotide 5. MALDI-MS (-): m/z calcd for $C_{173}H_{245}N_{57}O_{84}P_{12}SCI$: 4906.3, m/z found: 4906.9 [M-H]⁻.

b) Synthesis of conjugate 6



Figure S16. RP-HPLC chromatogram of conjugate 6 (CuAAC reaction).



Figure S17. ESI mass spectrum of oligonucleotide **6.** ESI-MS (-): *m/z* calcd for C₁₇₃H₂₄₅N₅₇O₈₄P₁₂SCI: 4906.3, *m/z* found: 4907.2 [M-H]⁻.

c) Synthesis of conjugate 7



Figure S18. RP-HPLC chromatogram of conjugate 7 (TC reaction).



Figure S19. ESI mass spectrum of oligonucleotide **7.** ESI-MS (-): *m/z* calcd for C₂₈₆H₃₉₅N₉₄O₁₅₃P₂₄S₂: 8405.2, *m/z* found: 8403.5 [M-H]⁻.

d) Synthesis of conjugate 8



Figure S20. RP-HPLC chromatogram of conjugate 8.



Figure S21. ESI mass spectrum of oligonucleotide **8.** ESI-MS (-): *m/z* calcd for C₂₈₆H₃₉₃N₉₆O₁₅₃P₂₄S₂: 8430.8, *m/z* found: 8433.8 [M-H]⁻.

e) Synthesis of conjugate 9



Figure S22. RP-HPLC chromatogram of conjugate 9 (diazo transfer reaction).



Figure S23. ESI mass spectrum of oligonucleotide **9.** ESI-MS (-): *m/z* calcd for C₁₇₃H₂₄₃N₅₉O₈₄P₁₂SCI: 4932.3, *m/z* found: 4934.4 [M-H]⁻.

f) Synthesis of conjugate 11



Figure S24. Reaction monitoring (UPLC-MS, negative mode) of the formation of conjugate 11 from oligonucleotide 10 (*TC reaction*).



Figure S25. RP-HPLC chromatogram of pure conjugate 11.



Figure S26. ESI mass spectrum of conjugate **11:** ESI-MS (-): *m/z* calcd C₁₈₃H₂₆₈N₅₈O₈₆P₁₂S₂: 5089.46, *m/z* found: 5089.68 [M-H]⁻.

g) Synthesis of conjugate 12



Figure S27. Reaction monitoring (UPLC-MS, negative mode) of the formation of conjugate **12** from **11** (*CuAAC reaction*).



Figure S28. RP-HPLC chromatogram of pure conjugate 12.



Figure S29. ESI mass spectrum of conjugate **12:** ESI-MS (-): *m/z* calcd C₁₈₃H₂₆₈N₅₈O₈₆P₁₂S₂: 5089.46, *m/z* found: 5089.62 [M-H]⁻.

h) Synthesis of conjugate 13



Figure S30. Reaction monitoring (UPLC-MS, negative mode) of the formation of conjugate **13** from **12** (*diazo transfer reaction*).



Figure S31. ESI mass spectrum of conjugate **13:** ESI-MS (-): *m/z* calcd C₁₈₃H₂₆₇N₆₀O₈₆P₁₂S₂: 5116.45, *m/z* found: 5116.21 [M-H]⁻.

i) Synthesis of conjugate 14



Figure S32. Reaction monitoring (UPLC-MS, negative mode) of the formation of conjugate **14** from **13** (*CuAAC reaction*).



Figure S33. RP-HPLC chromatogram of pure conjugate 14.



Figure S34. MALDI-Tof mass spectrum of conjugate 14. MALDI-Tof-MS (-): m/z calcd $C_{295}H_{413}N_{97}O_{156}P_{24}S_2$: 8617.05, m/z found: 8613.61 [M-H]⁻.

j) Synthesis of conjugate 1b



Figure S35. Reaction monitoring (UPLC-MS, negative mode, 60°C) of the formation of conjugate 1b from 14 (oxime ligation). The top chromatogram is the crude reaction. The bottom chromatogram is the pure conjugate 1b after Size Exclusion filtration (NAP 25 cartridge) and freeze-drying to remove volatile TFA reagent and the water byproduct and solvent. The UPLC was performed at 60°C in conditions where 1b do not form the i-motif topology.



Figure S36. RP-HPLC chromatogram of conjugate **1b** at room temperature. This chromatogram shows two peaks which corresponds to a mixture of conformers, one peak corresponding to the folded i-motif structure and the other to one or more unfolded forms of the conjugate **1b**.



Figure S37. MALDI-Tof mass spectrum of conjugate **1b:** MALDI-Tof-MS (-): *m/z* calcd C₂₉₁H₄₀₅N₉₇O₁₅₄P₂₄S₂: 8528.99, *m/z* found: 8526.68 [M-H]⁻.



Figure S38. mass spectrum of conjugate 1b from LC-MS analysis: m/z calcd $C_{291}H_{405}N_{97}O_{154}P_{24}S_2$: 8528.99, m/z found: 8528.00 [M-H]⁻.

6. Circular Dichroism studies



Figure S39. CD spectra of conjugate 8 at different pH (PBS buffer) at room temperature.



Figure S40. A/ Raw CD traces for conjugate 1b (2 μ M) in 10 mM PBS buffer at pH 6, Temperature varied from 5°C to 90°C, B/ CD signal intensities at λ_{max} versus temperature.



Figure S41. A/ Conjugate 1b (2 μ M) in 10 mM PBS buffer at pH 7, Temperature varied from 5°C to 60°C. B/ CD signal intensities at λ_{max} versus temperature.