Supporting Information

N10-C11 Imine is essential for Gram-negative antibacterial activity of broad spectrum pyrrolobenzodiazepines

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Purity determination of synthesized final compounds

The level of purity of the compounds for biological testing has been evaluated through LC-MS analysis, using two different gradient methods, reported hereafter. LC-MS analyses were performed on a Waters Alliance 2695 system (from Waters), with elution in gradient. HPLC grade solvents were used as mobile phase while a Monolithic C18 50 X 4.60 mm column (from Phenomenex) was used as stationary phase. UV detection was performed using a Waters 2996 photo array detector (from Waters). Injection volume has been set to 10 µL. The compounds have been dissolved in a mixture of H₂O/ACN (50/50, v/v) or DMSO/ACN (50/50, v/v) accordingly to the solubility. The area of the peak corresponding to the compound has been automatically determined by the software included in the LC-MS system. The eventual presence of solvent UV trace has been subtracted to the total in order to determine the percentage of purity.

LC-MS methods:

Method A: flow 0.5 mL/min

A) water +0.1 % formic acid

B) acetonitrile + 0.1% formic acid

| Time (min) | 0 | 3 | 3.5 | 4.5 | 5 |
|------------|----|----|-----|-----|----|
| A (%) | 95 | 10 | 5 | 5 | 95 |
| B (%) | 5 | 90 | 95 | 95 | 5 |

Method B: flow 1 mL/min

A) water +0.1 % formic acid

B) acetonitrile + 0.1% formic acid

| Time (min) | 0 | 2 | 5 | 6 | 7.5 | 9 | 10 |
|------------|----|----|----|----|-----|----|----|
| A (%) | 95 | 95 | 50 | 50 | 5 | 95 | 95 |
| B (%) | 5 | 5 | 50 | 50 | 95 | 5 | 5 |

| Compound | 5 minutes method | 10 minutes method |
|----------|------------------|-------------------|
| | | |

| | Retention time (min.) | Purity | Retention time (min.) | Purity |
|----|-----------------------|--------|-----------------------|--------|
| 7a | 3.12 | ≥98% | 5.95 | ≥98% |
| 8a | 3.30 | ≥98% | 6.40 | ≥98% |

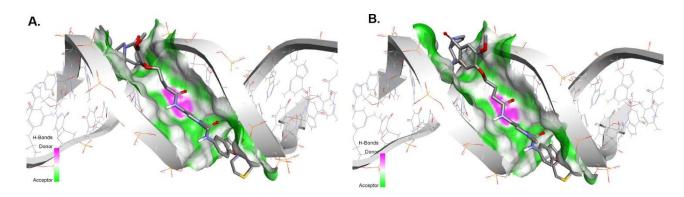


Figure S1: DNA binding of compounds 7 (A) and 7a (B) within the DNA minor groove of Sequence-2.