

# Corrigendum

## Different duplex/quadruplex junctions determine the properties of anti-thrombin aptamers with mixed folding

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The authors wish to make the following corrections to their article:

Table 2 was calculated on an initial model of the complex in which the nucleotide sequence was not correct. Tables 1 and 3 were based on the correct model deposited into PDB and are therefore correct. A new Table 2 based on the PDB model is provided below and supersedes the published Table.

**Table 2.** Stacking interactions as calculated by 3DNA-DSSR (41) among residues belonging to the duplex, the junction and the quadruplex of RE31

| Nucleotide 1 | Nucleotide 2 | Structural motif | Base stacking (Å <sup>2</sup> )* |
|--------------|--------------|------------------|----------------------------------|
| Thy2         | Gua3         | Duplex           | 4.5                              |
| Gua3         | Ade4         | Duplex           | 3.7                              |
| Ade4         | Cyt5         | Duplex           | 3.4                              |
| Cyt5         | Gua6         | Duplex           | 1.4                              |
| Gua6         | Thy7         | Junction         | 7.0                              |
| Thy7         | Thy17        | Junction         | 7.4                              |
| Thy17        | Gua16        | Junction         | 8.0                              |
| Gua16        | Gua14        | Junction         | 3.2                              |
| Gua14        | Gua13        | Quadruplex       | 4.4                              |
| Ade30        | Cyt29        | Duplex           | 1.3                              |
| Cyt29        | Thy28        | Duplex           | 7.1                              |
| Thy28        | Gua27        | Duplex           | 7.0                              |
| Gua27        | Cyt26        | Duplex           | 1.3                              |
| Cyt26        | Gua25        | Junction         | 4.6                              |
| Gua25        | Ade8         | Junction         | 2.2                              |
| Ade8         | Gua24        | Junction         | 4.6                              |
| Gua24        | Gua23        | Junction         | 2.5                              |
| Gua23        | Gua22        | Quadruplex       | 4.3                              |

\*Base-stacking is quantified as the area of the overlapped polygon defined by the two bases of the interacting nucleotides, where the base atoms are projected onto the mean base plane.

### REFERENCE

- Lu, X.J. and Olson, W.K. (2008) 3DNA: a versatile, integrated software system for the analysis, rebuilding and visualization of three-dimensional nucleic-acid structures. *Nat. Protoc.*, 3, 1213–1227.

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