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CORRECTION

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Correction: Aptamer-based strategies for recognizing adenine, adenosine, ATP and related compounds

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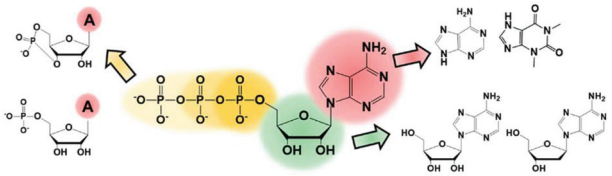
Correction for 'Aptamer-based strategies for recognizing adenine, adenosine, ATP and related compounds' by Yuqing Li *et al.*, *Analyst*, 2020, **145**, 6753–6768, DOI: 10.1039/D0AN00886A.

The authors regret unfortunate errors in their paper on pages 6754 and 6760. The nucleoside structures are missing the oxygen in their sugar rings in Fig. 1, 2A, 8B and the graphical abstract. In addition, the L-enantiomer should be the D-enantiomer in Fig. 2A. The seven bases in the 3′-end of Fig. 2D are missing. The corrected Fig. 1, 2, 8B and graphical abstract figure are given below.



Graphical abstract figure

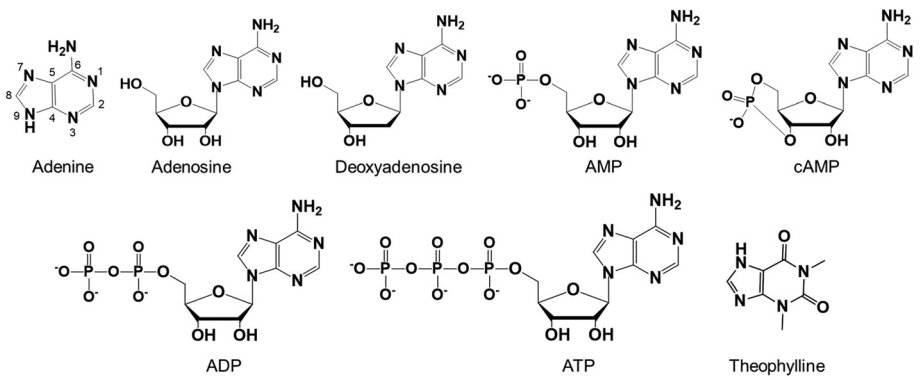


Fig. 1 Chemical structures of adenine and its derivatives reviewed including adenosine, deoxyadenosine, AMP, cAMP, ADP, ATP and theophylline.

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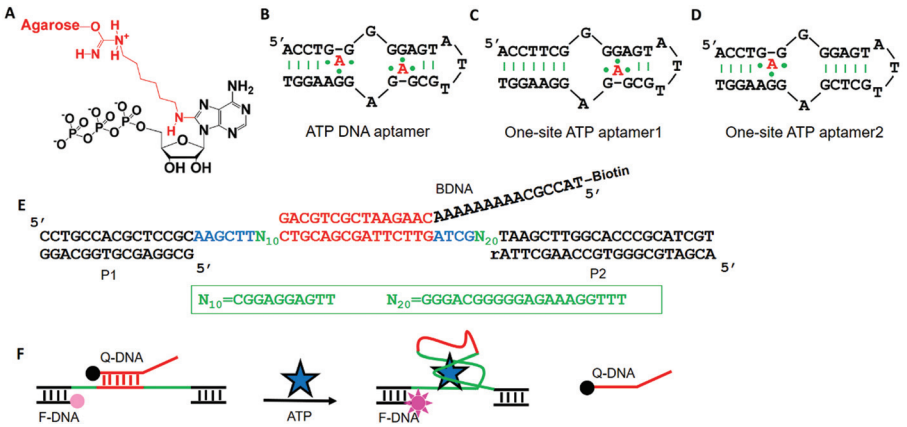

Fig. 2 (A) Immobilization of ATP on agarose through a 9-atom spacer on its C8 position. The secondary structures of (B) the ATP binding DNA aptamer (the red A symbols denote for target molecules),[29] (C) the engineered one-site aptamer1,[31] and (D) one-site aptamer2.[31] (E) The library design for selecting signaling ATP aptamers.[35] (F) A scheme describing the structural switching process induced by ATP.[35]

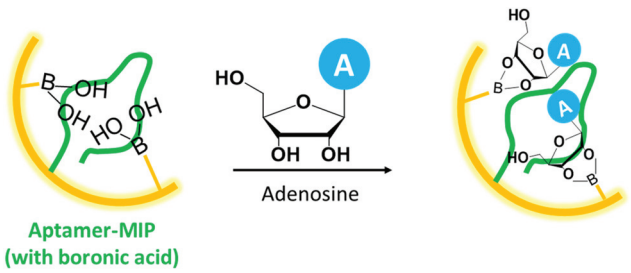

Fig. 8 (B) Boronic acid improves binding specificity of the adenosine aptamer in MIPs (only adenosine can bind).

The Royal Society of Chemistry apologises for these errors and any consequent inconvenience to authors and readers.