CORRIGENDUM

Natural and engineered nicking endonucleases—
from cleavage mechanism to engineering of strand-specificity

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In the last paragraph of page 3, it is mentioned that BsmAI, BsmBI and BsaI are proposed to have two catalytic sites. Jakubauskas et al. [J. Mol. Biol. (2007) 370, 157–169], however, shows that the BsaI isoschizomer Eco31I (GGTCTC 1/5), which shares high amino acid sequence homology to the aforementioned enzymes and recognizes a common core GTCTC recognition sequence, contains a HNH catalytic motif through sequence analysis and mutagenesis. The HNH catalytic motif is conserved in BsmAI, BsmBI and BsaI. Although mutation equivalent to R236D of BsaI (Eco31I R264D) also results in a top-strand nicking variant, mutation of Arg475 to Ala does not affect the cleavage activity of Eco31I (Mutation R442G, the equivalent Arg in BsaI, results in a bottom-strand nicking phenotype). It suggests that Arg442 and the equivalent Arg in this family of enzyme are not the catalytic residues, and the Arg to Gly mutation at this position that lead to the nicking phenotype in BsmBI and BsaI might act through mechanisms yet to be understood.