Supplementary Material for:

One recognition sequence, seven restriction enzymes, five reaction mechanisms

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FIGURE S1 (top)

1 column width

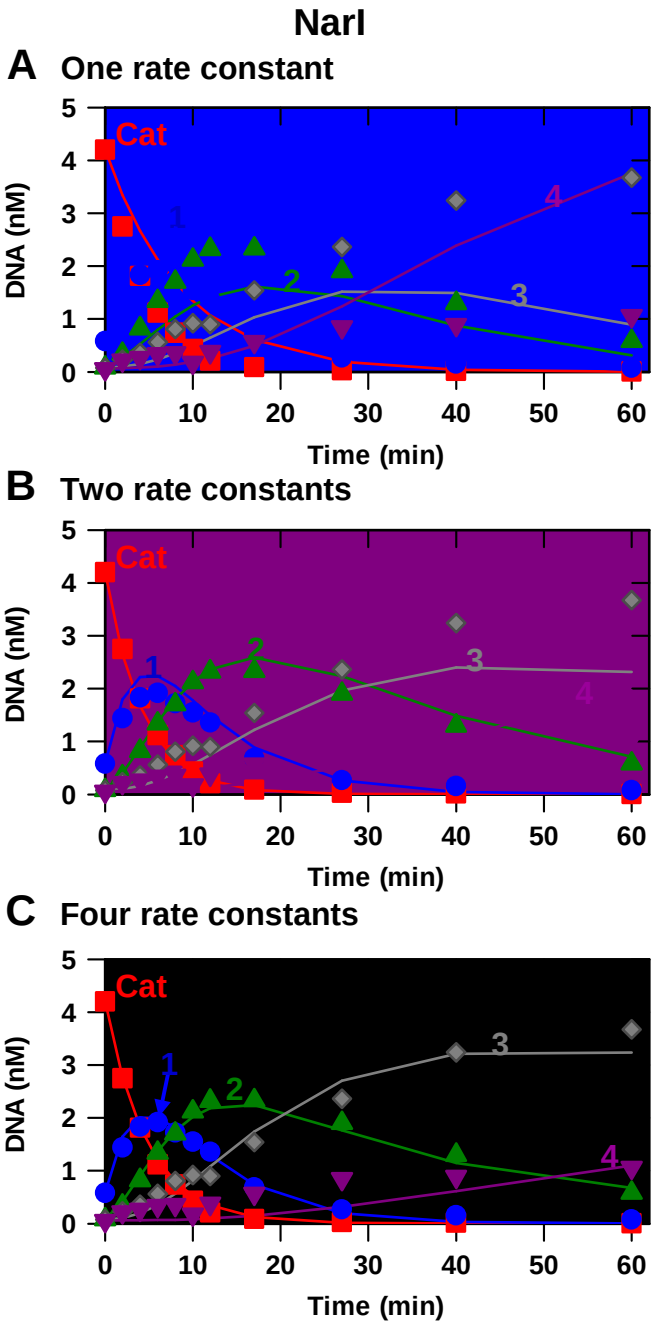

Figure S1. Kinetic models for NarI. In all three panels, the data points are the values from Fig. 3B, the NarI reaction on the catenane with one site in each ring. They note the concentrations of the following forms of the DNA during this reaction: intact catenane, red squares; the sums of the products cleaved in one phosphodiester bond, blue circles; products cleaved in two bonds, green triangles; products cleaved in three bonds, grey diamonds; product cleaved in four bonds, purple inverted triangles. The lines drawn are the theoretical lines for the following forms of the DNA, calculated from the scheme in Fig. 3A with the values of the rate constant(s) that gave the minimal sum-of-squares deviation from the experimental data: red line, intact catenane; blue line, sum of the products cleaved in one phosphodiester bond; green line, products cleaved in two bonds, triangles; grey line, products cleaved in three bonds, diamonds; purple line, product cleaved in four bonds. For (A), the calculation employed one rate constant for all of the steps in the reaction scheme: the minimal deviation was obtained with a value of 0.057 s^{-1}. For (B), the calculation employed two rate constants, one for all reactions at an intact NarI site and another for all reactions at a nicked site; the minimal deviation was obtained with values of 0.12 and 0.019 s^{-1}, respectively. For (C), the calculation employed four rate constants, for reactions *in cis* at intact sites, *in cis* at nicked sites, *in trans* at intact sites and *in trans* at nicked sites: the minimal deviation was obtained with values of 0.10, 0.052, 0.019 and 0.007 s^{-1}, respectively.