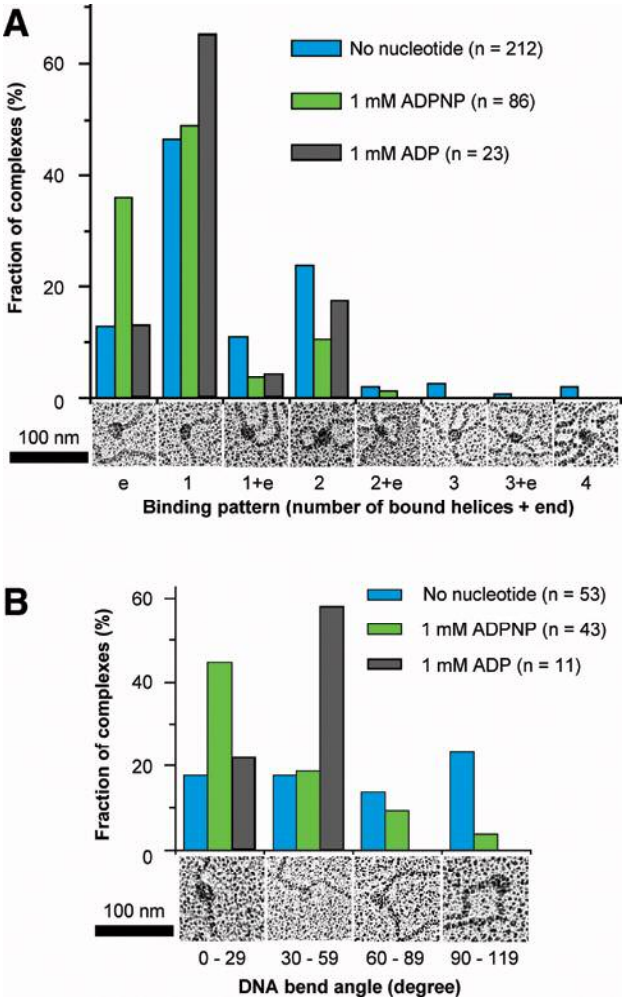

Fig. S1. Structural features of reverse gyrase–DNA complexes. Reverse gyrase was incubated with linearised pBR322 DNA in the absence of nucleotide (blue bars), in the presence of ADPNP (green bars), or in the presence of ADP (grey bars). Complexes were imaged by EM after rotary shadowing. Electron micrographs below the graphs illustrate the typical appearance of a complex in the specified class. (**A**) The number of DNA helices and DNA ends (e) bound to one protein molecule was counted for n bound proteins, and the distribution of binding patterns is shown. (**B**) DNA bend angles were measured for n complexes consisting of a protein molecule bound to a single DNA helix, and the distribution of angles is shown. Bend angles greater than 119° were possibly present in a small number of complexes (6 complexes in the absence of nucleotide and 2 complexes in the presence of ADPNP), data not shown.

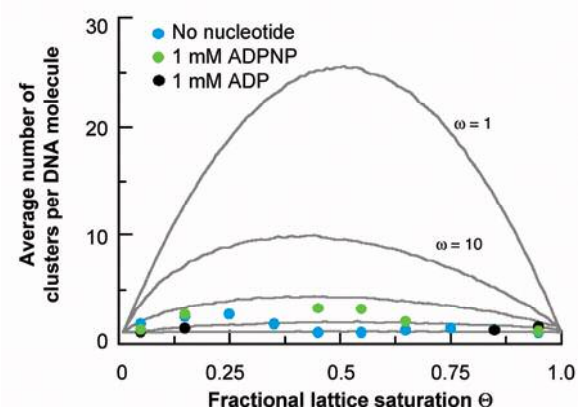

Fig. S2. Reverse gyrase binding to DNA is cooperative. The number of protein clusters per linear DNA molecule was measured, values for molecules within the same θ range (bin width 0.1) were averaged and are plotted as circles. Grey lines are computer-generated by a program which simulates cluster formation for noncooperative binding (binding cooperativity parameter ω = 1) and for binding with increasing cooperativity. The maximum of the curve decreases with increasing ω; the ω-values used were 1, 10, 100, 1000, 10000.