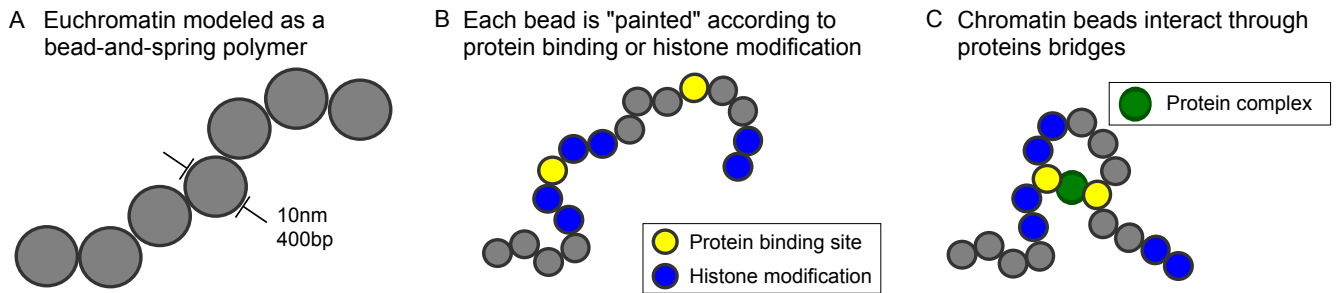


# Additional Files



**Additional file 1: Figure S1: Chromatin is modelled as a bead-and-spring polymer.** (A) Beads represent a region of chromatin containing 400 bp of DNA, approximately two nucleosomes. This coarse graining sets the resolution of our simulations, but does not specify a particular structure for the chromatin fibre; the physical size of the bead is not specified, but fitting results to FISH measurements (see Methods and Additional file 7: Figure S5) suggests a bead diameter of 16 nm. We set the persistence length (i.e. length over which the polymer behaves like a stiff rod, and a measure of the stiffness of the polymer) to 4 bead diameters (64 nm), a reasonable choice for euchromatin (1,55). Changing this parameter does not significantly affect our results (see Additional file 8: Figure S6). (B) and (C) Experimental data such as ChIP-seq or DNase-seq is used to specify which beads can be bound by the protein complexes in our simulations.