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High throughput mapping of nucleosome DNA sequences has shown that special motifs are conserved but weakly at certain positions of nucleosomal region. However such nucleosome core sequences come as truncated or with some extra linker DNAs attached to the core in either end due to imperfect digestion. Aligning the nucleosome sequences is exceedingly challenging. We propose a maximum entropy alignment approach, which operates on the elongated nucleosomal sequences and progressively maximizes the total entropy of the alignment. We show that this method is effective in improving the intensity of conserved signal over the center alignment. (Received September 04, 2007)