**Fig1: Base composition readers may shape the epigenome**

DNA associates with nucleosomes to form chromatin, which is available to conventional transcription factors (TFs) but also to proteins that bind to short sequence motifs. The significance of CpG binders (shown as small yellow circles in the figure) at CpG island promoters has recently emerged, but other such proteins (for example, AT‑run binders; shown as blue and green pentagons in the figure) are relatively unstudied. Our hypothesis is that these proteins recruit chromatin or DNA-modifying complexes (modifiers; shown as larger circles in the figure) on the basis of features of the DNA sequence. In particular, we suggest that proteins of this kind may amplify and interpret subtle fluctuations in DNA base composition to mould epigenetic landscapes.