



## Editor's Introduction to This Issue (G&I 15:4, 2017)

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Spatial folding of the DNA double helix into a chromatin structure and their dynamic interactions within the nucleus are important for regulating gene transcription and controlling the fate of cells during development. Regarding this issue, Dr. Tae-You Kim's group (Seoul National University Hospital, Korea) has comprehensively reviewed recent knowledge about the roles of CCCTC-binding factor and cohesion in genome folding, their biological implications for gene expression, and their association with human diseases. This information could be very useful for CRISPR/Cas9-based epigenome editing technology, which is another attractive option for future epigenome-based anticancer therapy.

There is another interesting review in this issue. Syno-

nymous sites are generally considered to be functionally neutral. However, a number of contradictory findings have been reported recently. For example, some synonymous single nucleotide polymorphisms (SNPs) have a similar effect size in disease association as nonsynonymous SNPs. Dr. Sun Shim Choi's group (Kangwon National University, Korea) reviewed this story. They introduced evidence that highly expressed genes tend to have a greater preference toward so-called optimal codons than lowly expressed genes. There are seven original articles regarding diverse genomics and bioinformatics research and one application note in this issue.

For further details, please visit the G&I homepage (<https://genominfo.org/>).

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