Professor Pan and his colleagues have revolutionised the way in which we view tRNA from a genomic perspective. In order to achieve these goals, Professor Pan and his team have developed high throughput sequencing methods that quantify the abundance, modification and charging of tRNA. Furthermore, the team are also exploring how mistranslation can be adaptive under stressful environmental conditions.

Sequencing the human genome was one of the most revolutionary biological studies conducted in the twenty-first century. The first draft human genome sequence, published in 2001, revealed areas where our knowledge was limited, for example in the field of ribonucleic acid (RNA). This inspired Professor Pan to focus on the field of RNA biology and in particular transfer RNA (tRNA). By developing new methods to examine many aspects of tRNA, the team was able to conduct in-depth studies which investigate the diversity and function of tRNA from a genomic perspective.

THE ROLE OF tRNA IN GENE EXPRESSION
Gene expression, whereby information provided by the genetic code is used to synthesise proteins, is the foundation of life. Messenger RNA (mRNA) replicates a specific DNA segment which encodes a protein. However, RNA and proteins, which consist of amino acids, have different chemical structures. Therefore, an adaptor molecule is required to interpret the genetic information encoded by the mRNA. These translational tools, cloverleaf in secondary structure consisting of three hairpin loops, and L-shaped in three-dimensional structure, are called transfer RNA (tRNA). One of the hairpin loops contains an ‘anticodon’, a specific three-nucleotide sequence that binds to a complementary mRNA ‘codon’. The codon-anticodon pair encodes a particular amino acid which is covalently attached to the tRNA. Eventually an amino acid chain is formed which is then further processed to form functional proteins.

ABUNDANCE, MODIFICATION AND CHARGING
Professor Pan and his colleagues performed functional genomic studies on tRNA. Functional genomics is a field of molecular biology that explores all molecules of the same type (i.e. tRNA) in cells simultaneously. The team explored the three processes that occur during mRNA decoding: abundance, modification and charging. ‘Abundance’ refers to the quantity of each tRNA type per cell. The human genome has around 600 tRNA genes distributed among around 300 different species. Interestingly, Professor Pan and his team discovered that humans have a high level of tRNA genetic diversity termed ‘isodecoders’ – tRNAs which have the same anticodon, but have different body sequences. Preventive and identity elements, found in the body sequence, ensure that the correct amino acid is covalently attached to the tRNA. However, altering the body sequence to produce a new isodecoder may remove the vital preventive element, meaning that an incorrect amino acid could be attached to the tRNA, increasing the risk of mistranslation. Outwardly, it appears that isodecoders are harmful. However, studies have shown that isodecoders can actually
Transfer RNA interacts with a variety of proteins involved in processes that are not directly related to protein synthesis.