Novel coding elements have been shown to arise from existing genomic information through gene duplication, transposable elements, lateral gene transfer, exon shuffling, gene fusion/fission and by *de-novo* origination. The aim of this project is to investigate the evolution of novel protein coding regions by the process of both exon shuffling and chimerism (fusion of existing coding elements) in amniote species. Exon shuffling is typified by a gene duplication event followed by a loss/gain of an exon within the duplicated copy. Using sequence similarity network methods we will identify promiscuous exons and we will assess their functions. Of particular interest to us are coding changes related to biomedicine/disease across the amniota, for example changes correlated with longevity and cancer resistance in the naked mole rat and certain bat lineages. The second genomic rearrangement mechanism we will explore are gene fusion events. Chimeric or fusion genes are defined as the juxtaposition of two or more genes to produce an open reading frame containing a concatenated gene. Chimeric genes are generally formed by chromosomal inversion, deletion, or translocation. If we consider the estimates for the frequency of these chromosomal perturbations, there are ample opportunities for chimeric genes to emerge, even at shallow levels of divergence. Therefore we will initially focus this part of the analysis on the great apes, and will later expand to all amniotes. The level of protein-coding similarity between the great apes, the quality of their genomes, their shallow divergence times and uncontroversial phylogeny, provides us with a good system to estimate the amount of chimeric genes that have evolved, and to identify and time the origins of these chimeras. These analyses represent the first large-scale genome wide analysis of chimeric gene formation in great apes and more broadly in amniotes, and will provide important insights into the multi-domain structure of the amniote proteins.