Kinases are among the most studied proteins, as they are important in many cellular processes. Today's research shows that their activity is not only dependent on the composition of the domains, but on the non-domain regions as well. This thesis tried to comprehend the influence of the linkers' composition on the function of multi-domain protein kinases in general. This was done by clustering human two-domain protein kinases with one protein kinase domain by the averaged physicochemical attributes of their inter-domain regions. The uniqueness of Gene Ontology terms and Enzyme Commission numbers within these clusters of proteins with different architectures was then investigated. However, due to multiple missteps, no such influence has been witnessed.