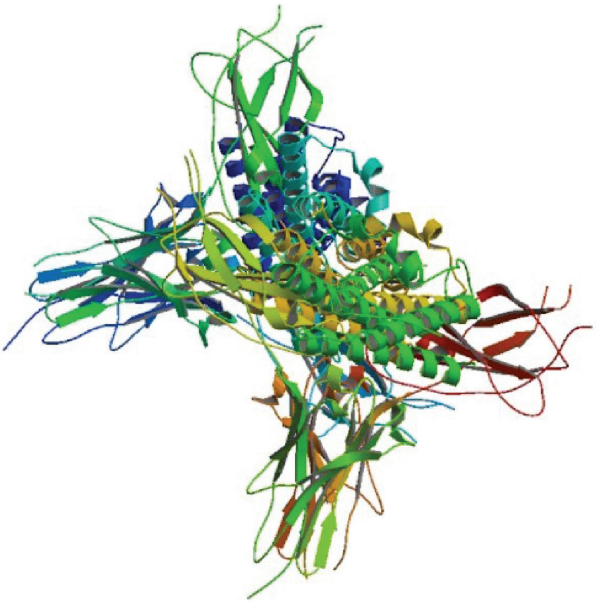

Figure 1.7 The 3D structure of filgrastim.

1.3 Motifs and domains

The primary and secondary structures are involved in a single polypeptide chain, the rest of the interaction of two or more identical or different polypeptide chains. The secondary structure leads to the formation of α-helices and β-sheets (Figure 1.6), which give rise to 3D structures, which are referred to as tertiary structures that provide the unique physicochemical and biological properties to proteins. The tertiary structures may acquire one or more peculiar folding patterns called *motifs* or supersecondary structure or complex folds, which are essentially "local tertiary structures" and should not be confused with the final or the global tertiary structure. The same applies to groups of motifs that are called domains, which are one or more independent compact regions of a protein. While motifs are structural elements, domains are functional elements, regardless of their size (Figure 1.8).

Proteins containing two or more domains are called multidomain proteins, wherein the domains may be covalently linked by highly flexible bonds called linkers. Despite the complexity of various HOSs, small changes in the amino acid sequence may not necessarily affect the HOS, a protein demonstrating the same activity. There can be more than one polypeptide chain, in which case, more than one tertiary structure is bonded to produce quaternary structures. Proteins can aggregate to form dimers, trimers, and tetramers; there is some confusion regarding the label used to describe these; a tetramer can be four polypeptide chains bonded through sulfur bonds, but that does not make a new monomer.