



A large photo-montage created from a Haemoglobin image using the Metapixel software. The source input images (17560) were taken from a 90% non-redundant selection of the PDBWiki images.

On the 8th of April 2008, the number of macromolecular structures released into the PDB reached 50,000. This milestone in structural biology represents over half a century of technological, scientific and cultural progress. The very first protein structures were solved in 1960 showing for the first time the atomic coordinates of horse hemoglobin and sperm whale myoglobin (Perutz 1960, Kendrew 1960). These initial structures provided a wealth of data for the analysis of proteins and generated tens of scientific publications. These early structures served both as a means of validating previous theoretical models (Pauling 1951a, Pauling 1951b, Kauzmann 1959) and as a basis for developing new theories of protein structure, function and evolution (Perutz 1962, Monod 1965, Perutz 1965). For example, the structure of myoglobin confirmed the model of alpha-helix proposed by Pauling. Despite the different amino acid composition of hemoglobin, the structure of its subunits showed essentially the same tertiary structure as myoglobin. At the time this observation lead Kendrew to comment that "myoglobin possesses a structure the significance of which extends beyond a particular species and even beyond a particular protein". Today these facts are taken for granted.