The beta adrenoceptor (β-AR) structures that have been elucidated by x-ray crystallography provide an enormously valuable, but static, picture of these important therapeutic targets. In addition the GPCR subtypes for which structural data exists have all been extensively engineered to aid crystallization: each has been truncated, mutated for thermostabilisation, or had additional proteins added; inevitably this has produced molecules that, though they signal fully, do so with altered pharmacology compared to their natural counterparts. In the case of the now numerous β1-AR structures available, the receptor species is turkey, not human. All these issues raise the question as to whether these crystals act as suitable templates for drug design - despite the conventional binding pocket being conserved. This work presents the results of homology modelling the human β-ARs, with an emphasis on whether the template used plays a significant part in the structure and predicted properties of the modelled protein. Additionally, the flexibility and deformability of the β-AR binding pockets have been assessed using the novel modelling technique of Active Site Pressurization (ASP). A comparison of the human β-ARs on the basis of structural and dynamic metrics has been produced and correlations of these with previously published pharmacological data investigated.