Proteins diverge during biological evolution. At the level of sequences, different aminoacids evolve at different rates, which is a clear evidence of natural selection. We recently found that the rate of evolution of a site depends on the stress of the protein´s active structure generated when it mutates, which is linked to its packing density. At the level of structure, even though preliminary studies have been made, the role of natural selection has not been elucidated yet. To study this, we analyzed protein families with a distinct approach. For each family we compared a set of experimental structures with two equivalent sets of simulated structures generated according to different models: purely mutational or mutational restricted by natural selection. To simulate these mutants we chose a reference protein and we generated successive random mutations by perturbing the oscillators coupled to the site. Only for the set restricted by natural selection, we selected each mutation according to its fixation probability, which we predicted based on the packing density of the site. The profiles we analyzed were both in Cartesian coordinates and projected on the normal modes of proteins. We found that the agreement between experimental and simulated profiles is high either considering or not natural selection in the simulations. Moreover, there are no clear differences between simulated profiles. These results suggest there is no evidence of natural selection on the structural evolution of proteins and go against the common belief that natural selection governs molecular evolution.