The immune system has developed a number of distinct complex mechanisms to shape and control the antibody repertoire. One of these mechanisms, the affinity maturation process, works in an evolutionary-like fashion: after binding to a foreign molecule, the antibody-producing B-cells exhibit a high-frequency mutation rate in the genome region that codes for the antibody active site. Eventually, cells that produce antibodies with higher affinity for their cognate antigen are selected and clonally expanded. Here, we propose a new statistical approach based on maximum entropy modeling in which a scoring function related to the binding affinity of antibodies against a specific antigen is inferred from a sample of sequences of the immune repertoire of an individual. We use our inference strategy to infer a statistical model on a data set obtained by sequencing a fairly large portion of the immune repertoire of an HIV-1 infected patient. The Pearson correlation coefficient between our scoring function and the IC\textsubscript{50} neutralization titer measured on 30 different antibodies of known sequence is as high as 0.77 (p-value $10^{-6}$), outperforming other sequence- and structure-based models.