



Figure S2: (A) Categories into which each of the 20 amino acid is placed for analyzing site-specific amino acid diversity. (B) Entropy-based analysis of ABE7.10 mutations. (C) Binned-entropy based analysis of ABE7.10 mutations. (D) Difference in the binned and regular entropy values to highlight the increase in entropy of site 108 and decrease in the entropy of site 84.