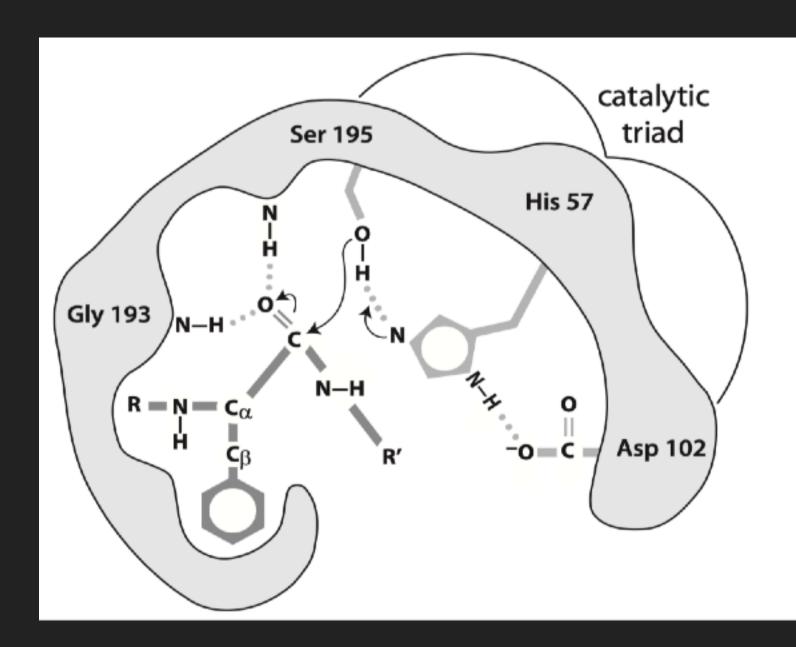
POST-ACTIVITY

- N-Acetyletyrosine Ethyl Ester has the Higher Affinity for the Enzyme
 - ▶ It has the lowest K_M value

- Why does the shape of the substrates affect the affinity?
 - Tyrosine resembles the phenyl group from the phenyl alanine, so it fits in the substrate pocket.

- ightharpoonup Just by looking at the structure , we cannot determine V_{max}
 - We need the rate constants, k_{cat} in order to calculate V_{max}



A diagram of the enzyme active site for chymotrypsin is shown. The amino acids Gly 193, Ser 195, His 57 and Asp 102 form part of the active site. The amino acids Ser 195, His 57 and Asp 102 comprise what is known as the catalytic triad. A portion of a natural peptide substrate from R to R' is depicted with the residue phenylalanine occupying the hydrophobic pocket of the enzyme.

- The K_M for the reaction of chymotrypsin with N-Acytlvaline Ethyl Ester = $8.8 * 10^{-2}$ M
- ► The K_M for the reaction of chymotrypsin with N-Acytltyrosine Ethyl Ester = 6.6 * 10-4 M

TESTING THE MODEL

- Various reactions are performed at known Enzyme and Substrate concentrations.
- The initial rates of the reactions are plotted against the substrate concentrations
- If the graph is hyperbolic, then it can be assumed the enzyme obeys the Michaelis-Menten model.
 - \blacktriangleright We can calculate K_M and V_{max}

