Types of catalysis

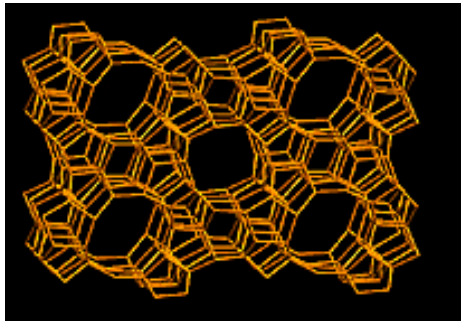
Homogeneous catalysis - the catalyst is in the same phase as the reactants.
Example: acid or base catalysis

Heterogeneous catalysis - the catalyst is in a different phase from the reactants.
Example: metal complexes, surfaces, zeolites

Enzymatic catalysis - the catalyst is a protein that has a substrate binding site and controlled reaction path

Zeolites:
an important class of catalysts

Database of zeolite structures:
http://www.iza-structure.org/databases/

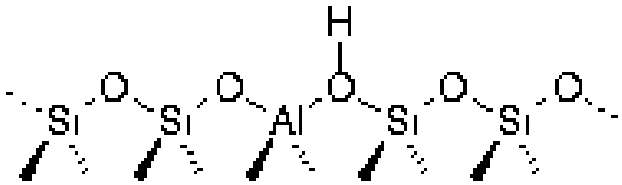


Example: search for ZSM-5

Unit cell parameters:
a = 20.090Å b = 19.738Å c = 13.142 Å
alpha = 90.0° beta = 90.0° gamma = 90.0°
volume = 5211.28 $Å^3$

Basis for heterogeneous catalysis in zeolites

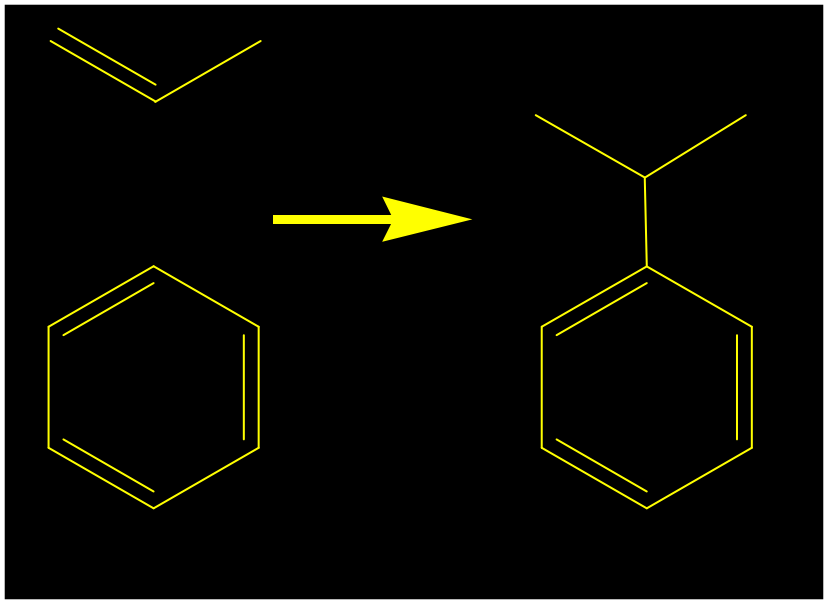
Zeolites are crystalline solids made up of SiO_4 building blocks. These tetrahedral units join together to form several different ring and cage structures. The characteristic that separates zeolites from all-silica minerals is the substitution of aluminum into the crystalline framework. The substitution of aluminum generates a charge imbalance, which is compensated by a proton. The acid site formed behaves as a classic Brønsted acid or proton donating acid site. The highly acidic sites combined with the high selectivity arising from shape selectivity and large internal surface area makes the zeolite an ideal industrial catalyst.



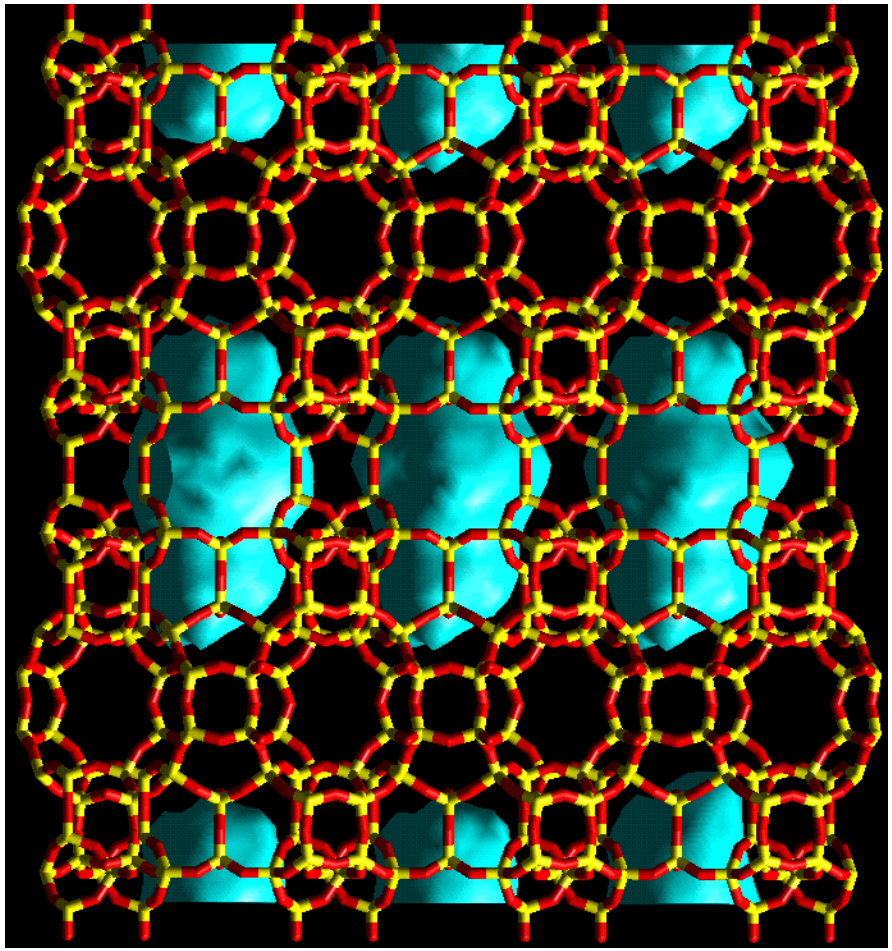
Zeolites: shape selective catalysis

The alkylation of benzene with propylene is an important petrochemical process because the product (cumene) is a chemical intermediate used to synthesize phenol and acetone.

Classical industrial processes are based on "olid phosphoric acid" catalysts, with problems of handling, safety, corrosion and waste disposal. These can be avoided by using zeolite catalysts.

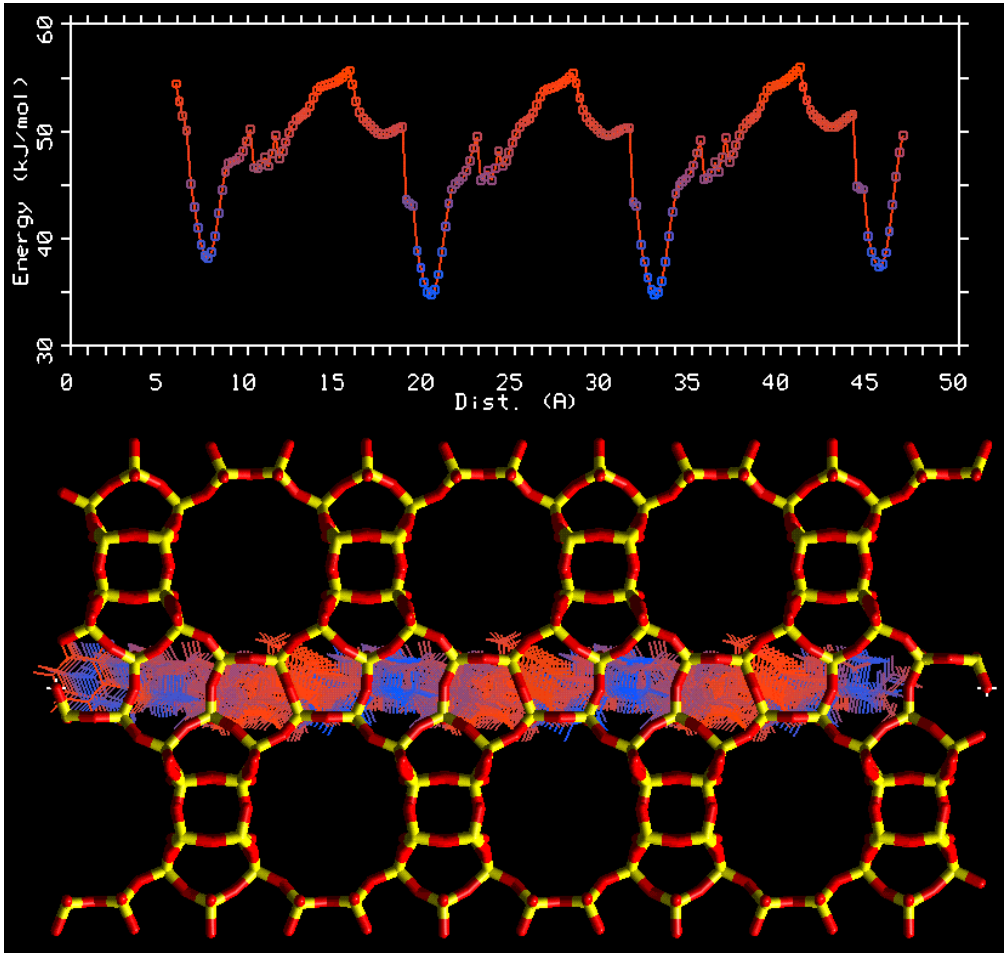


Zeolites: shape selective catalysis



The medium pore size zeolite ERB-1 has greater reactivity for cumene formation than larger pore size catalysts.

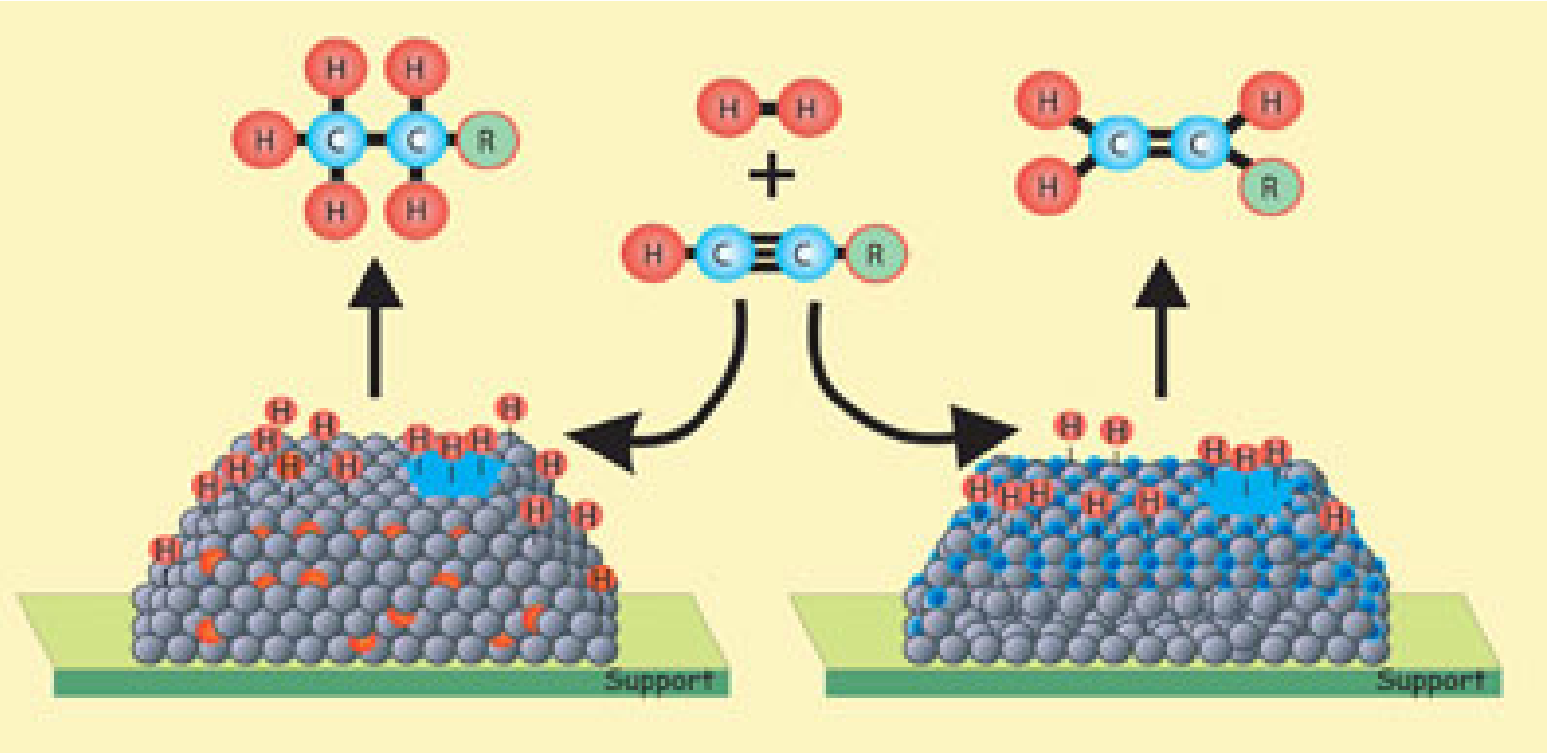
Zeolites: shape selective catalysis



Calculated energy surface for cumene in BEA.

Diffusion of cumene in zeolite BEA.

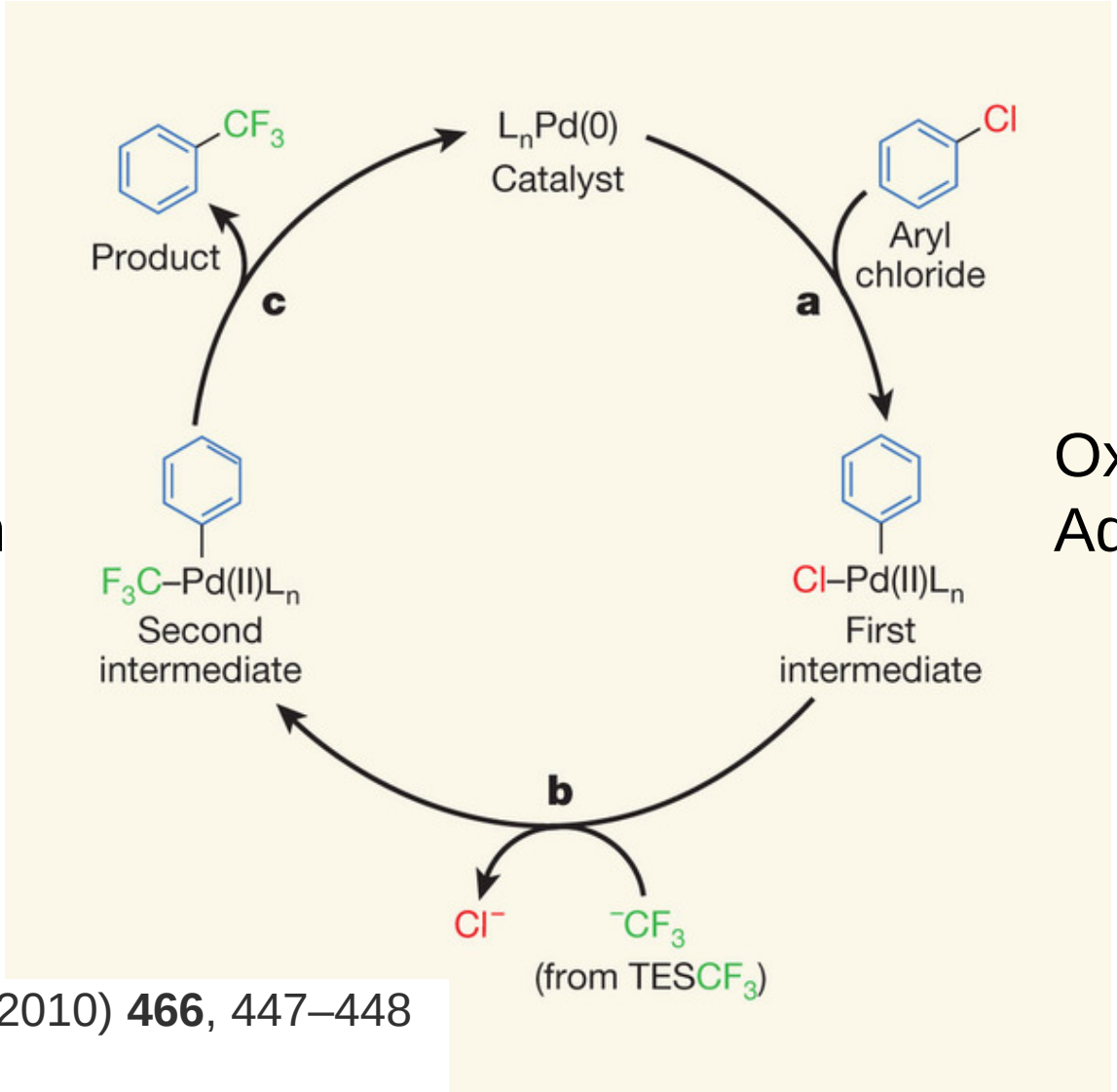
Heterogeneous Pd hydrogenation



D Teschner *et al, Science*, 2008, DOI: 10.1126/science.1155200

Palladium fluorination catalyst

Reductive Elimination



Oxidative Addition

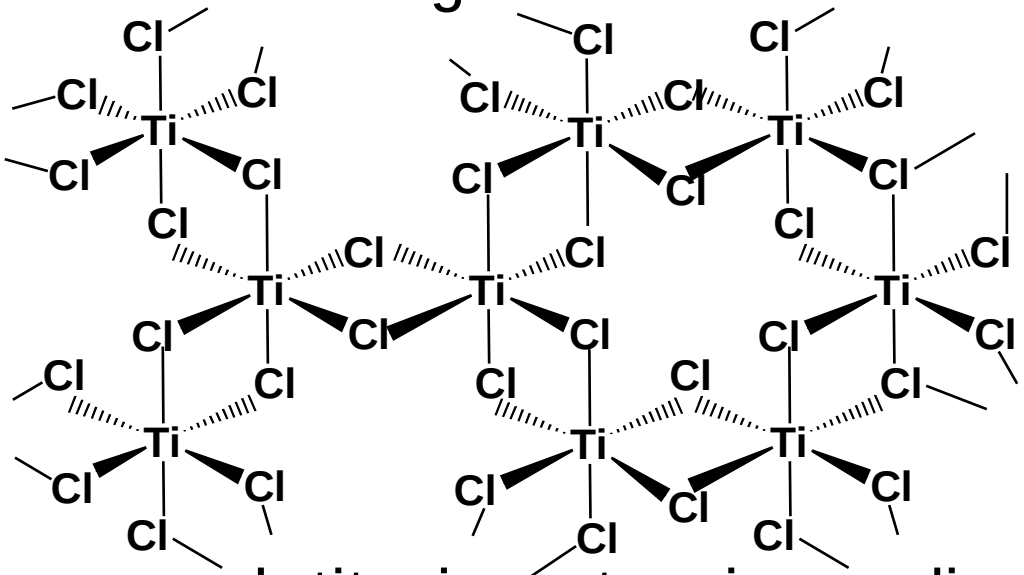
Ritter Nature (2010) **466**, 447–448

Ziegler-Natta catalyst for polymerization of ethylene

Ziegler-Natta catalysts are an important class of mixtures of chemical compounds remarkable for their ability to effect the polymerization of olefins (hydrocarbons containing a double carbon-carbon bond) to polymers of high molecular weights and highly ordered (stereoregular) structures. These catalysts were originated in the 1950s by the German chemist Karl Ziegler for the polymerization of ethylene at atmospheric pressure. Ziegler employed a catalyst consisting of a mixture of titanium tetrachloride and an alkyl derivative of aluminum. Giulio Natta, an Italian chemist, extended the method to other olefins and developed further variations of the Ziegler catalyst based on his findings on the mechanism of the polymerization reaction.

Ziegler-Natta catalyst for polymerization of ethylene

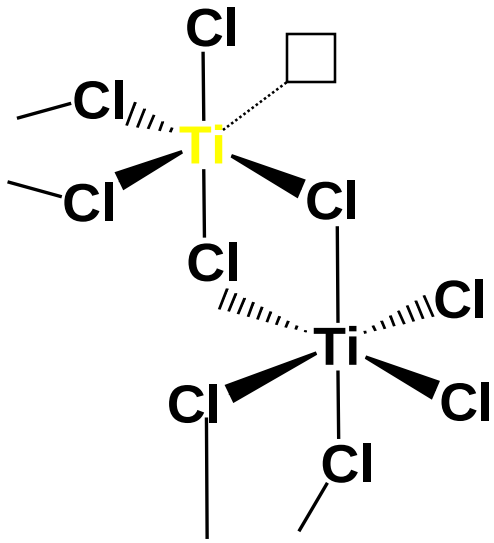
$TiCl_3$ can arrange itself into a number of crystal structures. The one that we're interested in is called α-$TiCl_3$. It looks something like this:



As we can see, each titanium atom is coordinated to six chlorine atoms, with octahedral geometry.

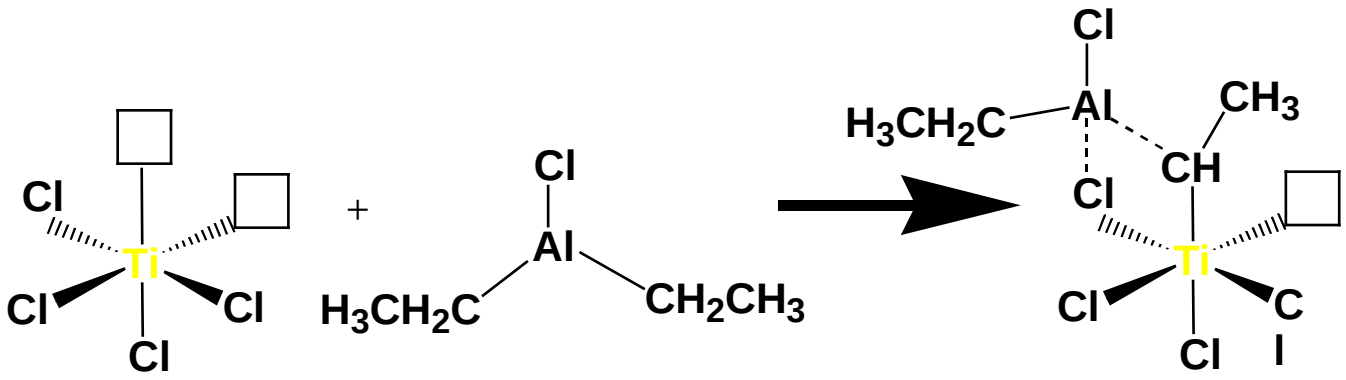
Ziegler-Natta catalyst for polymerization of ethylene

At the surface of the crystal a titanium atom is surrounded on one side by five chlorine atoms, but on the other side by empty space. This leaves titanium a chlorine short. Titanium, as one of the transition metals, has six empty orbitals (resulting from one 4s and five 3d-orbitals) in the outermost electron shells. The surface Ti atom has an empty orbital, shown as an empty square in the picture.



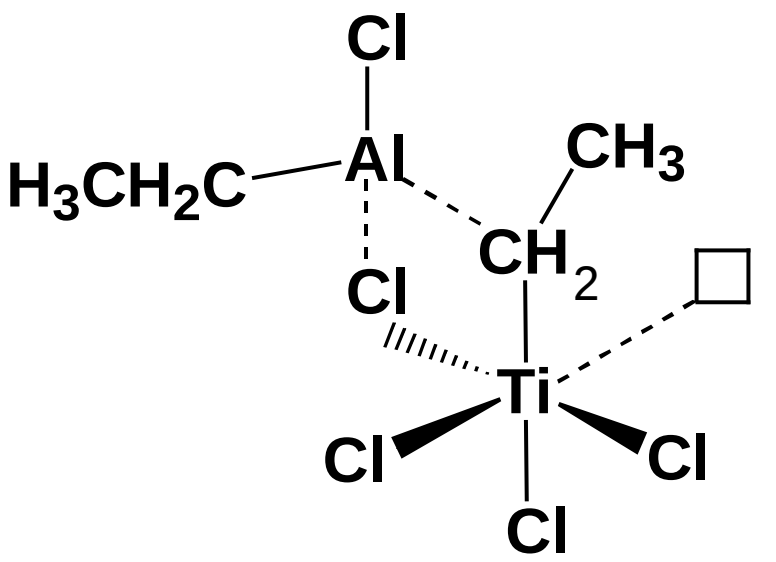
Ziegler-Natta catalyst for polymerization of ethylene

Titanium wants to fill its orbitals. But first, $Al(C_2H_5)_2Cl$ enters the picture. It donates one of its ethyl groups to the impoverished titanium, but kicks out one of the chlorines in the process. We still have an empty orbital.



Ziegler-Natta catalyst for polymerization of ethylene

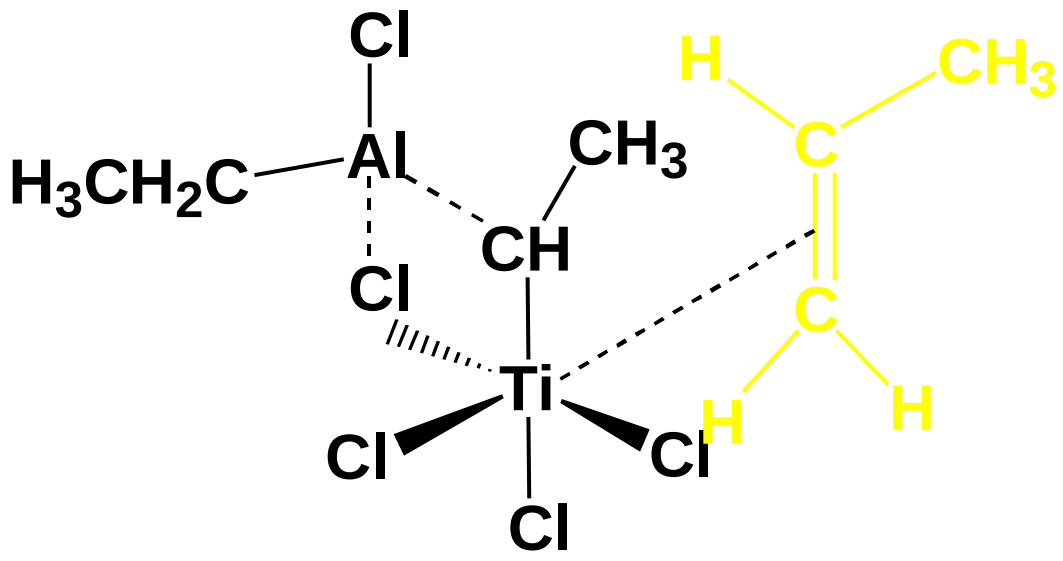
The aluminum is coordinated, though not covalently bonded, to the CH_2 carbon atom of the ethyl group it donated to the titanium and to one of the chlorine atoms adjacent to the titanium.



There is still a vacant site where polymerization can occur.

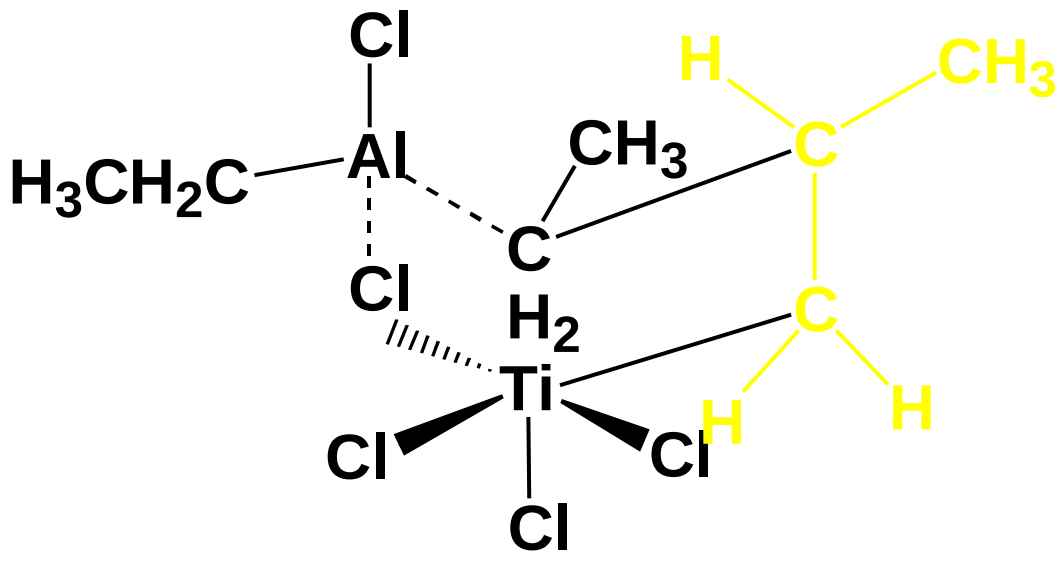
Ziegler-Natta catalyst for polymerization of ethylene

This process forms the active polymerization catalyst, which happens to be insoluble (unlike the 2 components that make up the complex), so we have what is commonly termed a heterogeneous catalyst (also known as a solid solution).



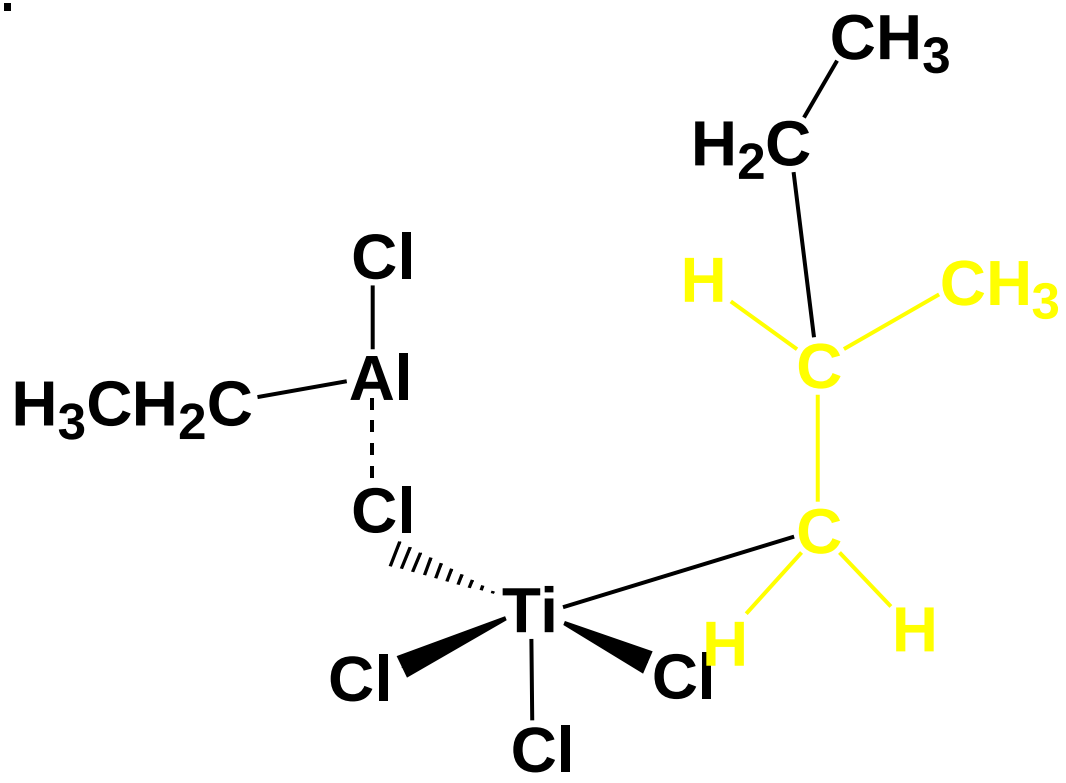
Ziegler-Natta catalyst for polymerization of ethylene

Upon binding ethylene forms bonds with the Ti atom and the carbon of the ethylene ligand.



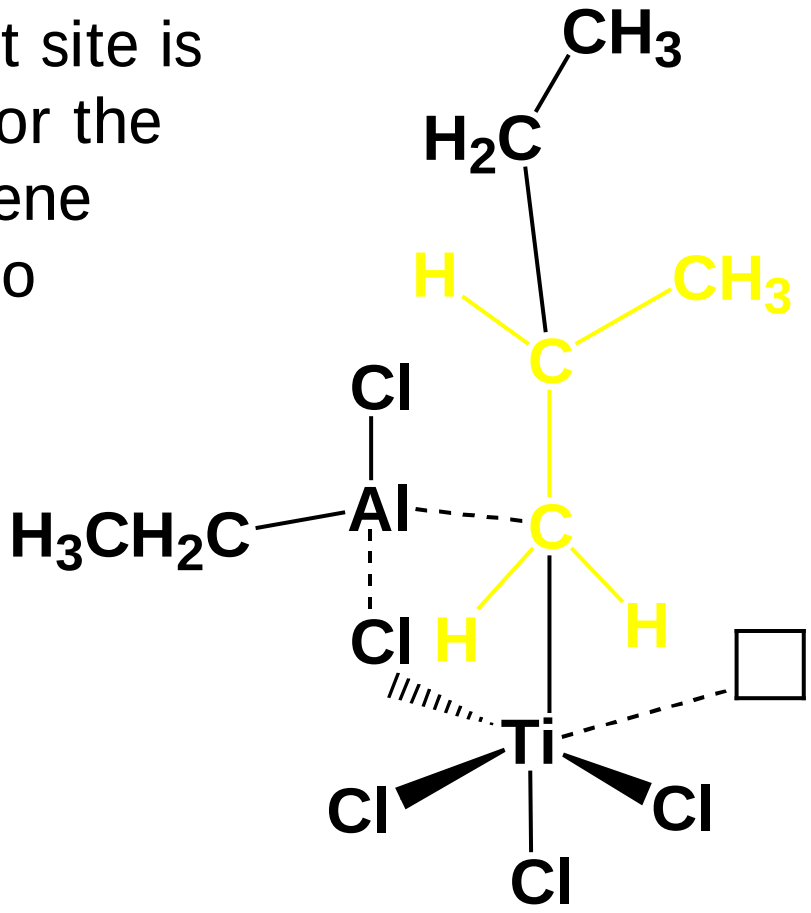
Ziegler-Natta catalyst for polymerization of ethylene

The growing polymer chain is initiated.



Ziegler-Natta catalyst for polymerization of ethylene

The vacant site is available for the next ethylene molecule to bind.



Serine Proteases

Trypsin is one of the three principal digestive proteinases, the other two being pepsin and chymotrypsin. Trypsin and chymotrypsin are both serine proteases that are quite similar. They have a catalytic triad of

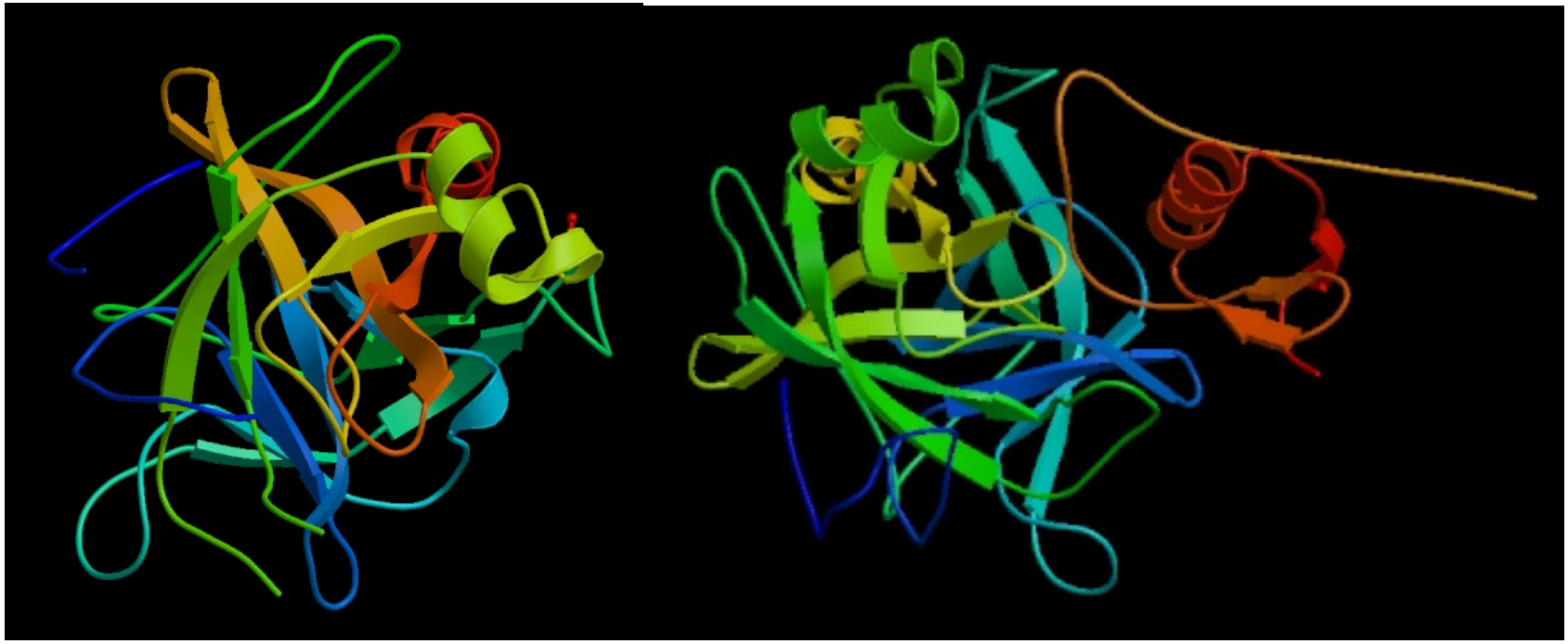
Asp-His-Ser.

Trypsin continues the process of digestion (begun in the stomach) in the small intestine where a slightly alkaline environment (about pH 8) promotes its maximal enzymatic activity.

Trypsin hydrolyzes peptides containing arginine and lysine. Chymotrypsin hydrolyzes peptides containing tyrosine, phenylalanine, tryptophan, methionine, and leucine. Trypsin is the most discriminating of all the proteolytic enzymes in terms of the restricted number of chemical bonds that it will attack. Chemists use trypsin widely as a reagent for the orderly and unambiguous cleavage of such molecules.

Zymogens: protease precursors

Most proteases are synthesized in an inactive form. This form is known as the zymogen. A protein cleaveage step is required to active the protease. This type of control is important for the transport of enzymes capable of protein degradation.



Chymotrypsin

Chymotrypsinogen with inhibitor

Prokaryotic structural examples

Trypsin from Streptomyces griseus

Mechanistic overview

1. Substrate binding

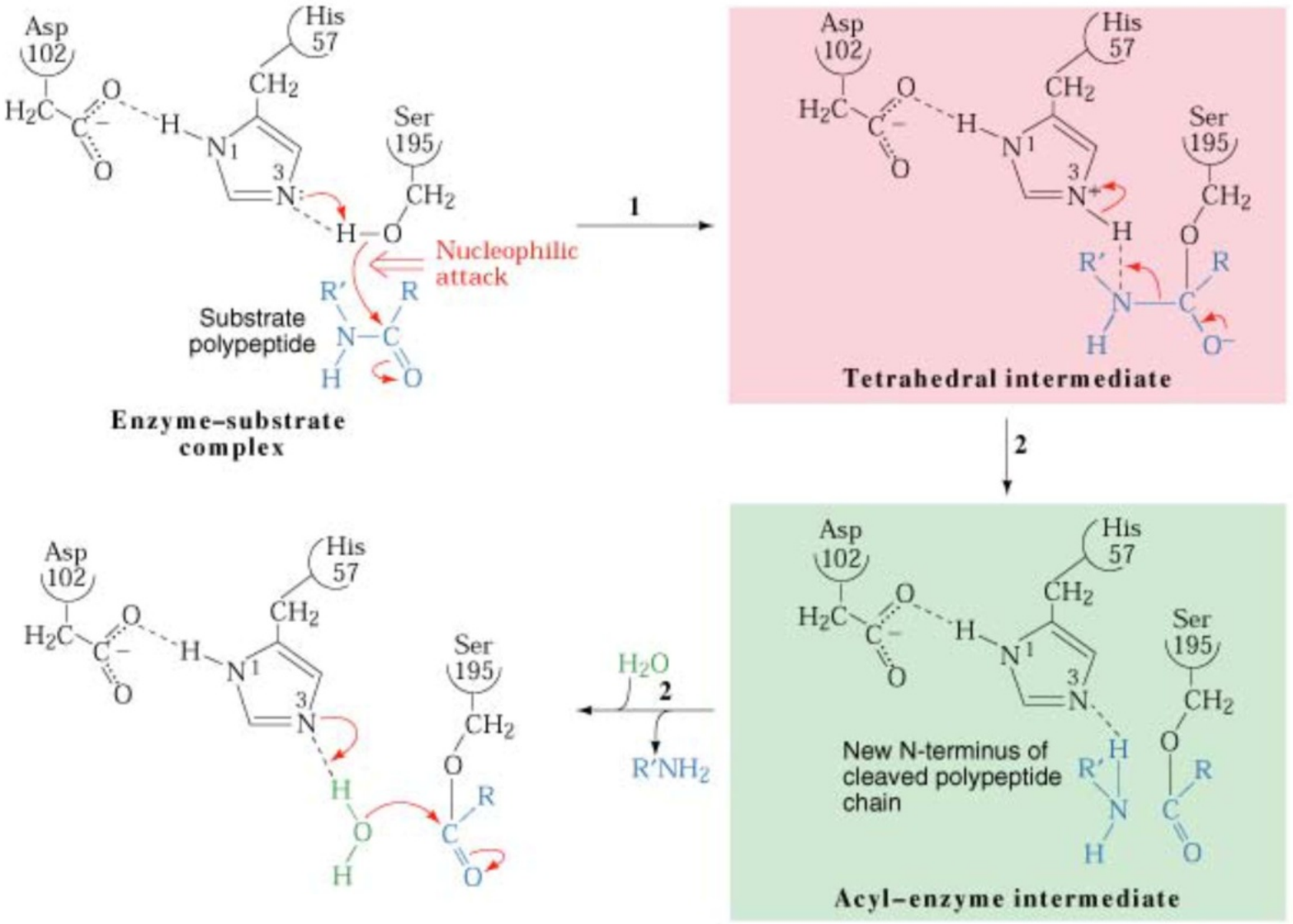
2. General base catalysis by imidazole to activate the Ser-OH

3. Nucleophilic catalysis by Ser-OH to form a tetrahedral adduct

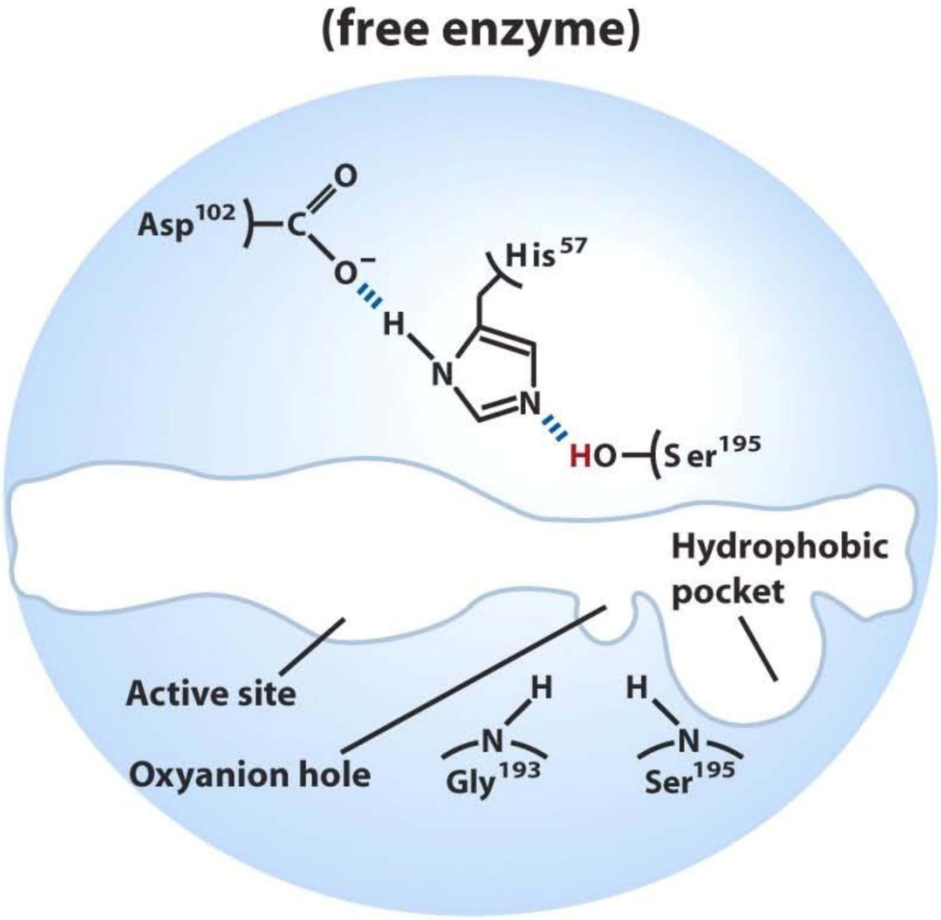
4. Stabilization of the tetrahedral transition state by hydrogen bonding to the "oxyanion hole"

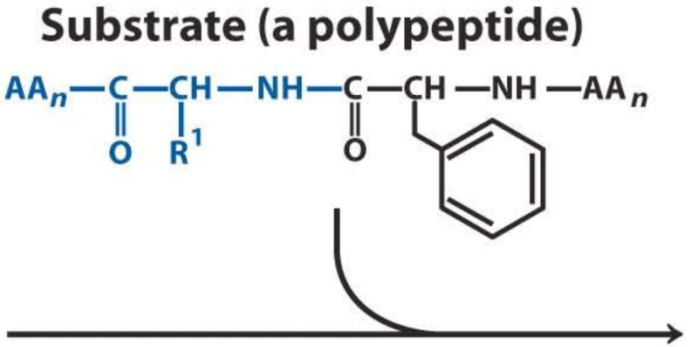
5. General acid catalysis of the departure of the leaving group to form the acyl-enzyme (covalent) intermediate and departure of the leaving groups

Serine protease mechanism



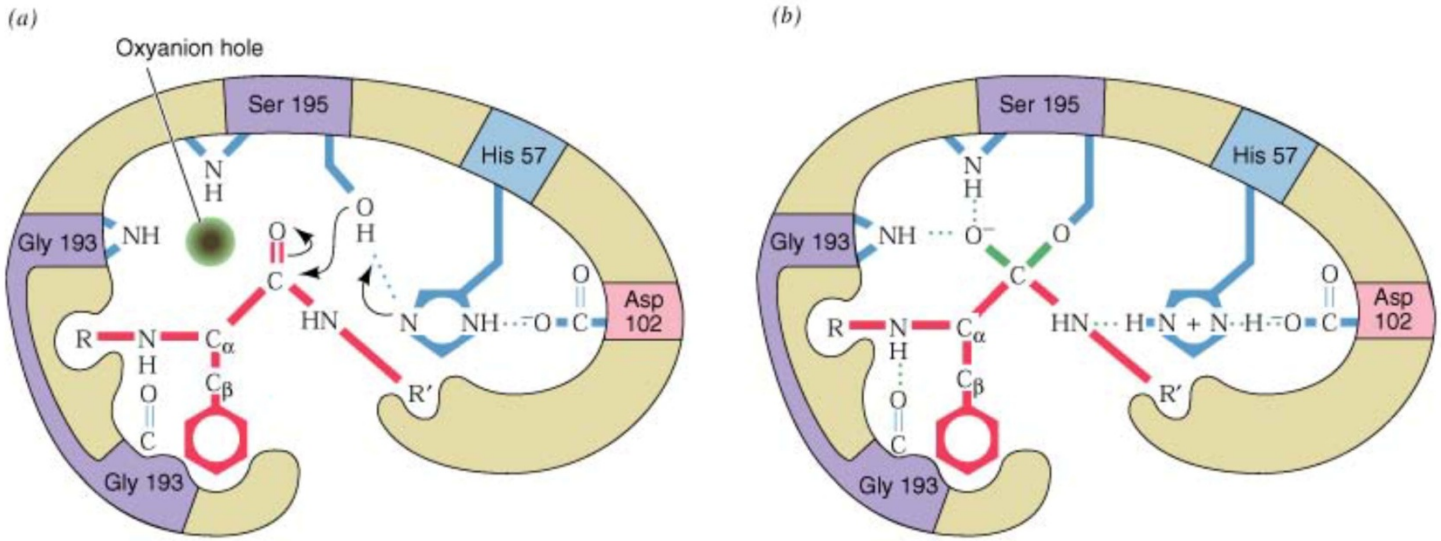
Substrate binding to chymotrypsin





When substrate binds, the side chain of the residue adjacent to the peptide bond to be cleaved nestles in a hydrophobic pocket on the enzyme, positioning the peptide bond for attack.

The oxyanion hole in serine proteases



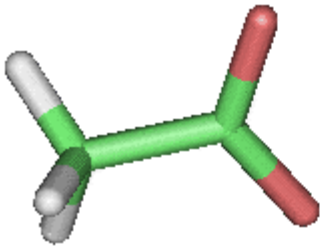
After Robertus, J.D., Kraut, J., Alden, R.A., and Birktoft, J.J., *Biochemistry* 11, 4302 (1972).

Role of oxyanion hole in serine protease mechanism:

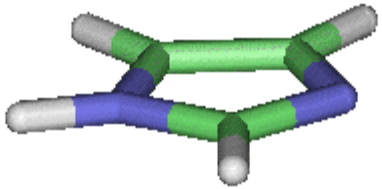
- Electrostatic catalysis
- Preferential binding of transition state

The catalytic triad

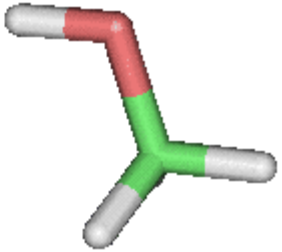
The key experiment that elucidates the role of aspartate in the Asp-His-Ser catalytic triad is the mutation of aspartate 102 to asparagine. Since the aspartate residue is essential there has been a great deal of interest in understanding the charge relay hypothesis.



Acetic Acid
(Asp)



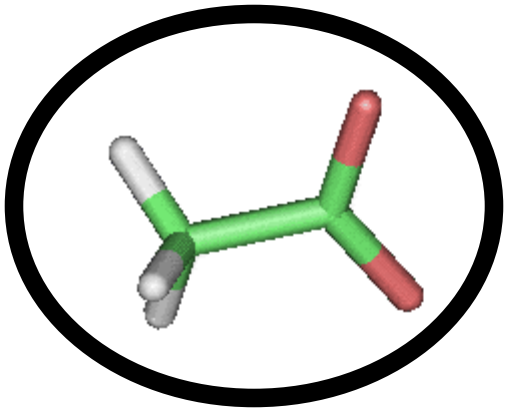
Imidazole
(His)



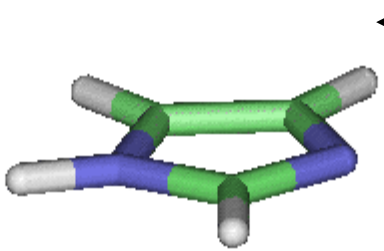
Methanol
(Ser)

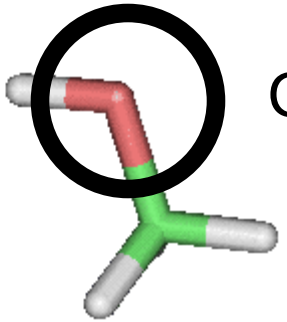
Using Density Functional Theory to model the catalytic triad

The role of the aspartate can be modeled by determining the charge on oxygen and the potential energy for removal of hydrogen in from the serine oxygen by calculation.



PES = Potential Energy Surface

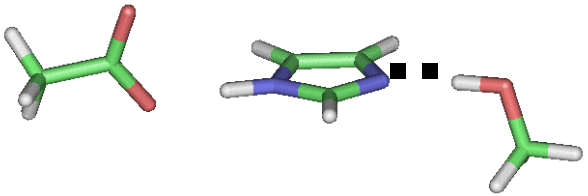


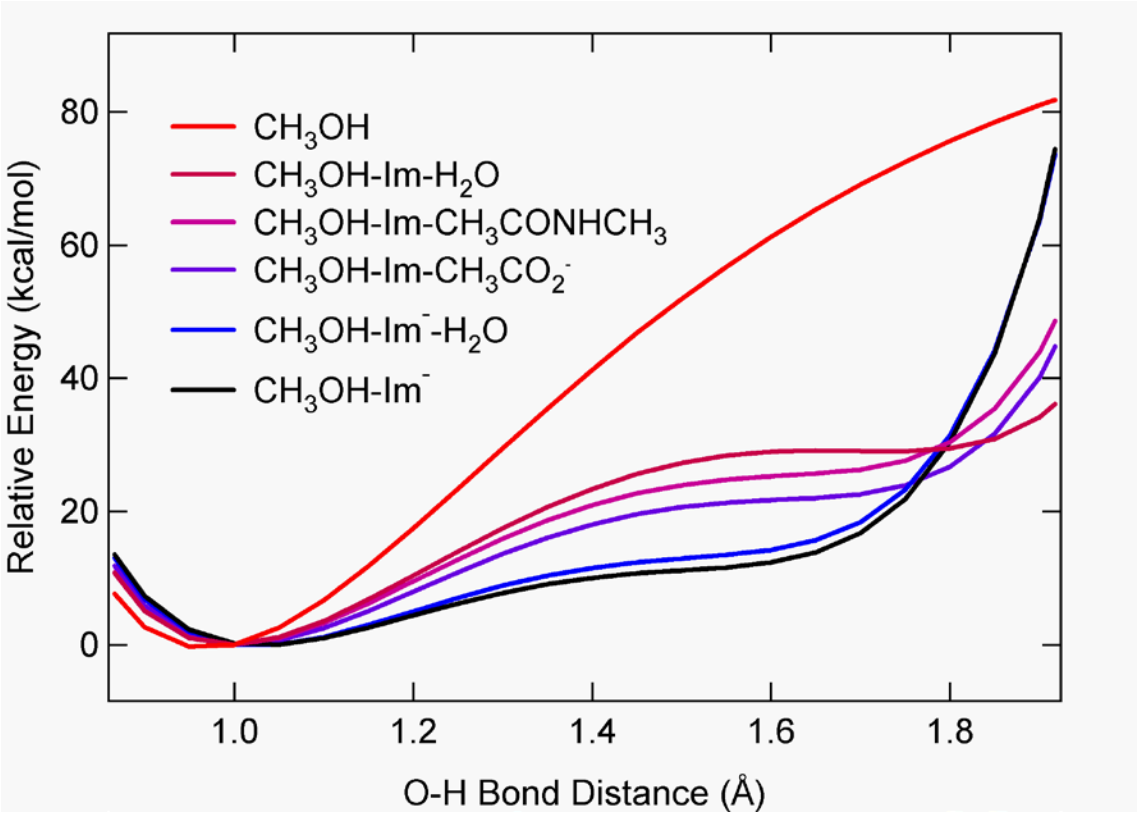


Charge on O

Systematically change this group to H_2O, ^{-}OH, etc.

Calculated potential energy surfaces for deprotonation of the serine hydroxyl





Modified Michaelis-Menten scheme for serine proteases

The appropriate reaction scheme for a serine protease involves the release of two intermediates (i.e. the N- and C-terminus of the cleaved peptide).

$$E + S \underset{k_{-1}}{\overset{k_1}{\Leftrightarrow}} ES \xrightarrow{k_2} EA \xrightarrow{k_3} E + P$$

$$\downarrow$$

$$P_1$$

To distinguish between rates k_2 and k_3 one uses esters that form a stable 4-coordinate intermediate. For these $k_3 < k_2$.

See Ferscht “Enzyme Kinetics” Chapter 5