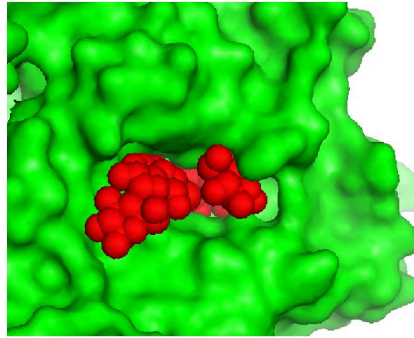
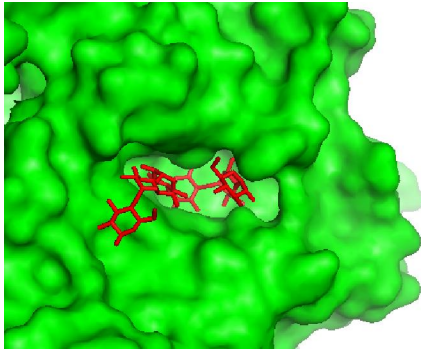


TB3-Lock and Key vs Induced Fit

Each **enzyme** acts by utilising its **active site**. The active site is the part of the protein which binds to the ligand. Once the ligand is bound in the active site, the enzyme gets to work and performs its function, **catalysing** the desired reaction. There are two main models which can be used to represent the relationship between the enzyme and the substrate – the **Lock and Key**, and the **Induced Fit** models.

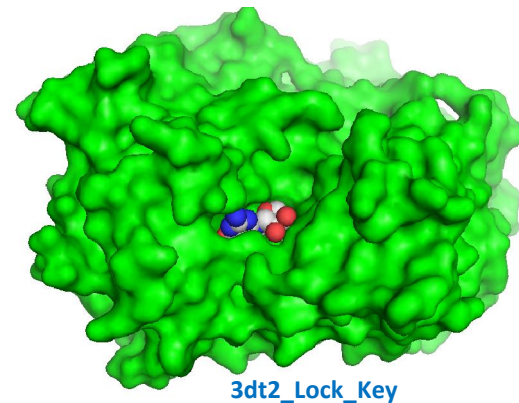


1qho_Amylase_Active_Site
showing the substrate in
both a stick representation
and a sphere model.

THE LOCK AND KEY MODEL

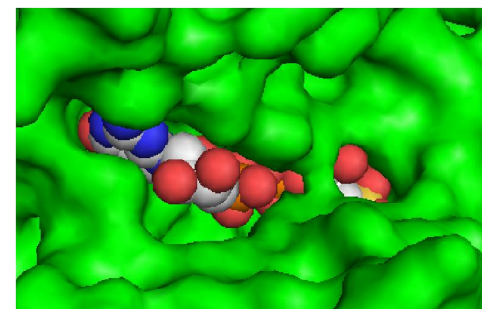
This model represents the enzyme as a lock, and the substrate as a key. It assumes that the substrate binds into the active site, where it is a **perfect complementary fit**, and then the enzyme can catalyse its reaction. In this model, there is **only one substrate which fits into the active site, just as only one key will work inside a lock**.

In the protein shown, the substrate appears to be an almost perfect fit to the active site. The lock and key hypothesis assumes that the substrate can just slide right into the active site.



THE INDUCED FIT MODEL

This model is more **accurate** than the classical lock and key one. It doesn't assume that the substrate is a perfect fit for the active site. Instead it takes advantage of the **flexibility** of the **polypeptide chains** which make up the enzyme. As a substrate enters the active site, it begins to **interact** with the amino acids which constitute the active site. This causes the active site to change shape very slightly, and **moulds the active site around the substrate**, to give a good, complementary fit. It is worth remembering though, that the induced fit is only a very **slight** change, and it is not always easy to detect!



3dt7_Induced_Fit

In the protein shown, the substrate appears to be enveloped inside the active site. It is difficult to imagine that the substrate bound to the active site without the protein having to undergo a conformational change of some sort, encasing the substrate in the active site. This is the principle of the induced fit model – that there is some flexibility in the structures.