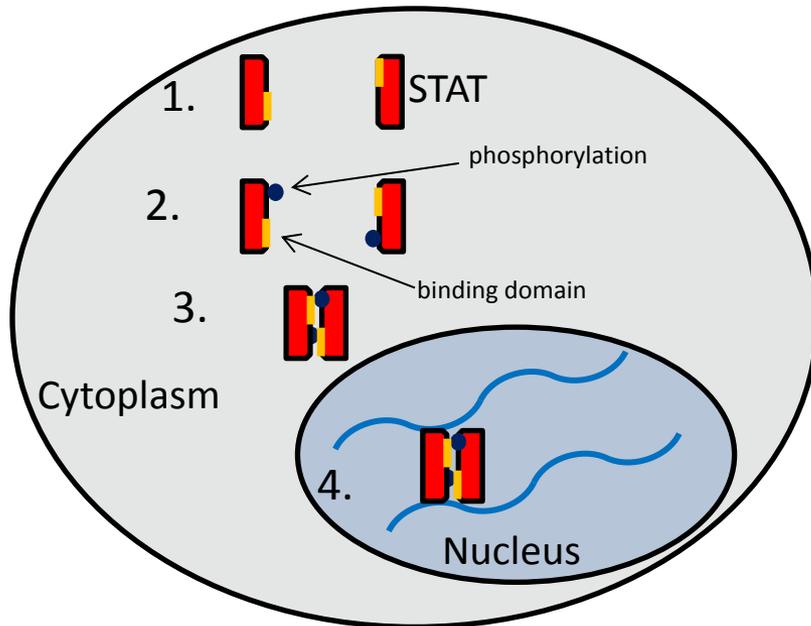


How do STAT proteins work?

Overview:

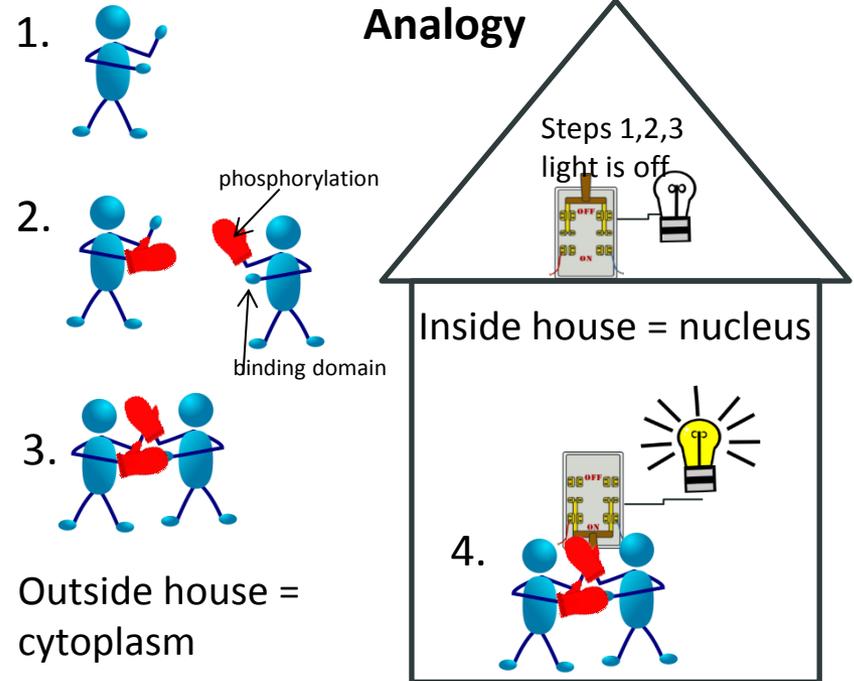
For 2 STATs to bind together, each one must be activated. This activation, called phosphorylation, is a modification to the STAT protein. This means a phosphoryl group is added to the STAT protein. There are other modifications that can occur to proteins, and usually these modification(s) will result in the protein having a different function. In our case, the phosphorylation of STAT causes it to be activated, allowing it to bind to another phosphorylated STAT protein.

In the cell



1. Each red rectangle is one STAT protein (monomer). The monomers generally reside in the cytoplasm of the cell.
2. The monomer can be activated by another protein which adds a phosphoryl group to it (dark blue circle). This phosphorylation site allows the STAT to bind to the binding domain (orange area) of another STAT.
3. The binding of one activated STAT monomer to another forms a dimer (2 STATs bound together). This is because the phosphorylation site fits into the binding domain/pocket (orange area) on the opposite STAT. The dimer is transported into the nucleus.
4. This STAT dimer can then go from the cytoplasm to the nucleus and cause transcription of certain genes.

Analogy



1. Each person is one STAT protein (monomer). The people are outside of a house in cold weather.
2. Each person now has one hand modified with a mitten (mitten = phosphorylation). Each person has cold hands and didn't want to hold hands previously because of this. We can equate each person's cold bare hand as the binding domain.
3. Now that each person is wearing a mitten, a mitten hand holds a bare hand; this is an activated STAT dimer. For simplicity sake, we can say the door is already open so they walk into the house (nucleus).
4. From our previous transcription analogy, only 2 tall people can turn on the light switch, so working together, their height and joining of hands allows them to turn on the light switch. The light produced is the gene product.