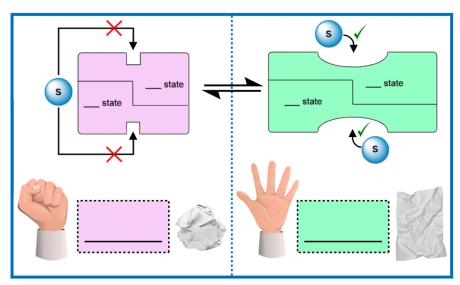
### **CONCEPT:** ALLOSTERIC ENZYME CONFORMATIONS

- Protein \_\_\_\_\_: alternative 3-dimensional *states* that a protein can achieve.
  - □ Recall: proteins are not completely rigid structures; protein structures can be induced to changes.
  - □ Different protein *conformations* can have different abilities and/or \_\_\_\_\_.

### T State & R State

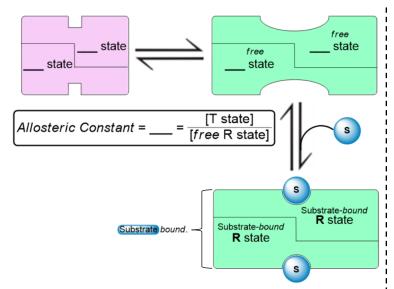
- Allosteric enzymes can exist in one of two states: 1) \_\_\_\_ State (Tense State) 2) \_\_\_\_ State (Relaxed State)
  - □ T state: catalytically \_\_\_\_\_\_ & has a \_\_\_\_\_ affinity for substrates (binds substrates inefficiently).
  - □ R state: catalytically \_\_\_\_\_ & has a \_\_\_\_ affinity for substrates (binds substrates efficiently).

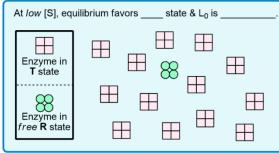
#### **EXAMPLE:**



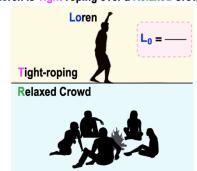
### Allosteric Constant (L<sub>0</sub>)

- •\_\_\_\_\_ Constant (L<sub>0</sub>): \_\_\_\_\_ of T States over *free* R States (T/R) when *no substrate* is present.
  - ☐ T State is more \_\_\_\_\_ than free R State, so at low [S], equilibrium favors \_\_\_\_ State.





Loren is Tight-roping over a Relaxed Crowd.



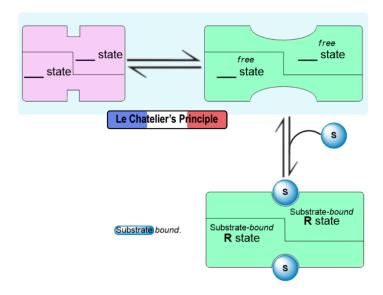
### **CONCEPT: ALLOSTERIC ENZYME CONFORMATIONS**

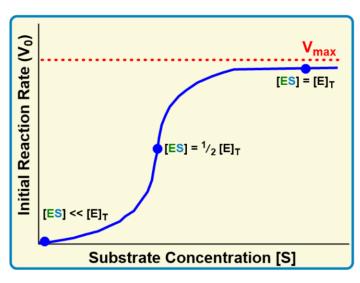
**PRACTICE:** Which of the following is true about allosteric enzyme conformational states?

- a) The T state is more stable than the R state of the enzyme when no substrate is present.
- b) Rearrangement of the protein's secondary structure dictates T vs. R states.
- c) The R state of the enzyme has a higher affinity for substrate molecules than the T state.
- d) When a substrate is released from the R state, the enzyme remains in that state indefinitely.
- e) All of the above are correct.
- f) Only A and D are correct.
- g) Only A and C are correct.

# T/R Conformations Allow for Cooperative Kinetics

- Sigmoidal kinetics ("S"-shaped curve) displayed by allosteric enzymes suggests that **S** binding is \_\_\_\_\_\_\_.
  - □ Positive Cooperativity: binding of one **S** molecule makes it \_\_\_\_\_\_ for other **S** molecules to bind enzymes.
  - □ Question: How does cooperative **S**-binding work?
- Recall: at low [S], equilibrium favors \_\_\_\_ State; HOWEVER, increasing [S] disrupts this equilibrium.
- •S binding to free R state produces **S**-bound-R-state, but consequently \_\_\_\_\_ [free R state].
  - □ By Le Chatelier's Principle, lowering [free R state] causes reaction to shift towards the free \_\_\_\_\_ state.

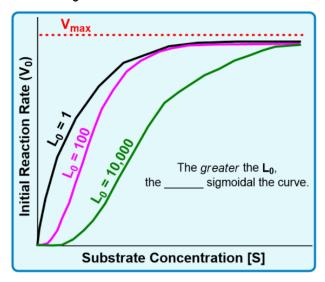




### **CONCEPT: ALLOSTERIC ENZYME CONFORMATIONS**

# **L<sub>0</sub> Dictates Curve in Kinetics Plots**

- •The allosteric constant (\_\_\_\_\_), dictates the extent of an allosteric enzyme's sigmoidal curve.
  - $\Box$  The *greater* the L<sub>0</sub>, the \_\_\_\_\_ sigmoidal the curve will be in a kinetics plot (V<sub>0</sub> vs [S]).
  - □ The smaller the L<sub>0</sub>, the \_\_\_\_\_ sigmoidal and the more the curve resembles Michaelis-Menten kinetics.



•	models	explain	the sia	moidal	kinetics	of a	allosteric	enzv	mes:
			0					- ,	

- 1) \_\_\_\_\_ (or \_\_\_\_\_) Model. 2) \_\_\_\_\_ (or \_\_\_\_\_) Model.
- □ In *both* models, allosteric enzyme reaction activity can be affected by allosteric \_\_\_\_\_.

**PRACTICE:** An allosteric enzyme that follows the concerted model mechanism has a  $L_0$  = 10,000 in the absence of substrate. A mutation in this enzyme caused the  $L_0$  to now be 1/10,000 (reciprocal to its original value). What affect does this mutation have on the reaction rate of the enzymatic reaction?

- a) The enzyme will retain the T state and the reaction will not occur.
- b) Reaction rate remains independent of the substrate concentration.
- c) The association constant (K<sub>a</sub>) for formation of the enzyme-substrate complex will not change with the mutation.
- d) Kinetics will appear to be similar to Michaelis-Menten kinetics, since the enzyme is nearly always in its R state.