CHEM523 Homework 4 Key

14) Mutual attraction. What is meant by the term binding energy?
Binding energy refers to the numerous IMFs made between the enzyme and the substrate as the two form the enzyme-substrate complex (ES complex). Each IMF knocks the activation energy down a bit by warping the substrate conformation(s) towards the transition state.

19) Free energy! Assume that you have a solution of 0.1 M glucose 6-phosphate. To this solution, you add the enzyme phosphoglucomutase, which catalyzes the following reaction:

Glucose6-phosphate⇌glucose1-phosphate

The $\Delta G^{\circ\prime}$ for the reaction is +7.5 kJ mol^{-1}

a) Does the reaction proceed as written? If so, what are the final concentrations of glucose 6-phosphate and glucose 1-phosphate?

Use $\Delta G^{\circ\prime} = -RT \ln K'_{eq}$, with
$R = 8.315 * 10^{-3}$ kJ mol^{-1} K^{-1} 1 and
$T = 298$ K.

Plug everything in and you should have:
+ 7.5 kJ mol^{-1}=–(8.315×10^{-3} kJ^{-1} mol^{-1} K^{-1})(298 K)(ln [G1P]/[G6P])

Solve for ln [G1P]/[G6P]:
ln [G1P]/[G6P]=-3.03
[G1P]/[G6P]=$e^{-3.03}$
[G1P]/[G6P]= 0.0485

Now we need to do a bit of algebra to solve for [G1P]. We know that everything in the reaction is either G1P or G6P and we started with G6P at 0.1M. If some amount, x, gets converted to G1P, then [G6P]=0.1M – x. We can plug those relationships into the ratio:
[G1P]/[G6P]=x/(0.1 M−x)=0.0485
Solve for x and you get 0.0046 M which is the [G1P].
That means that the [G6P]=0.1M-00046M= 0.0954M.

This shows us that the reaction doesn't proceed very much at all.

b) Under what cellular conditions could you produce glucose 1-phosphate at a high rate?
Supply G6P at a high rate and remove G1P at a high rate by other reactions. In other words, make sure that the [G6P]/[G1P] is high. If there is no product (G1P) present, then the reaction will move forward incrementally, so constantly siphoning off G1P at a high G6P concentration will produce G1P.

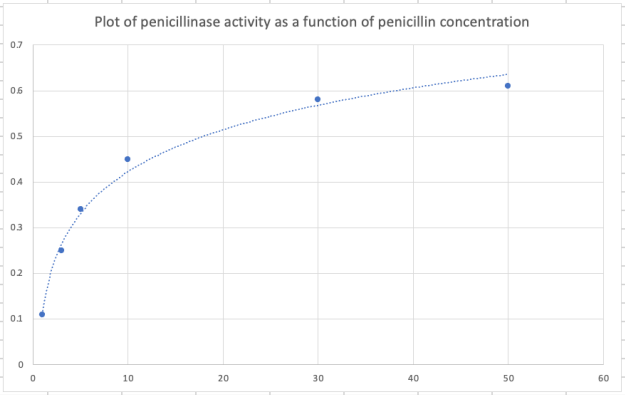
21) The three-dimensional structure of an enzyme is stabilized by interactions with bound substrates, reaction intermediates, or products. This stabilization due to a bound ligand minimizes the thermal denaturation.

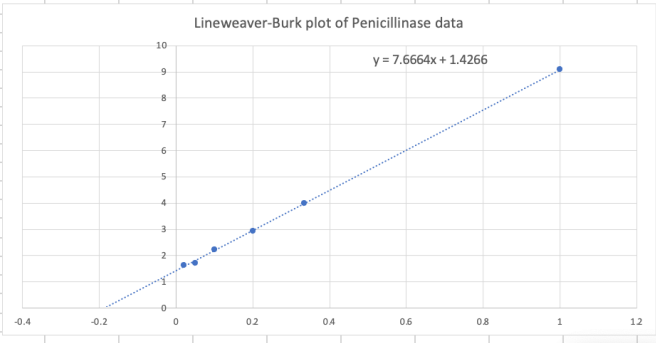
22) When the substrate concentration is close to the value of K_M, the enzyme displays significant catalytic activity yet also remains sensitive to changes in the substrate concentration.

24)
a, 7
b,4
c,5
d,1
e,8
f,2
g,9
h,6
i,10
j,3

28)

	A	B	C
1	[penicillin] (uM)	amount hydrolyzed (nmol) per minute	
2	1	0.11	
3	3	0.25	
4	5	0.34	
5	10	0.45	
6	30	0.58	
7	50	0.61	
26	1/[penicillin]	1/amount hydrolyzed per minute	
27	0.02	1.63934426	
28	0.05	1.72413793	
29	0.1	2.22222222	
30	0.2	2.94117647	
31	0.333333333	4	
32	1	9.09090909	
36	From the trendline		
37	Km/Vm=	7.6664	
38	1/Vm=	1.4266	
40	Vm=	0.70096733	nmol/min
41	which is 7.009x10^-10 mol/min		
43	Km=	5.37 uM	



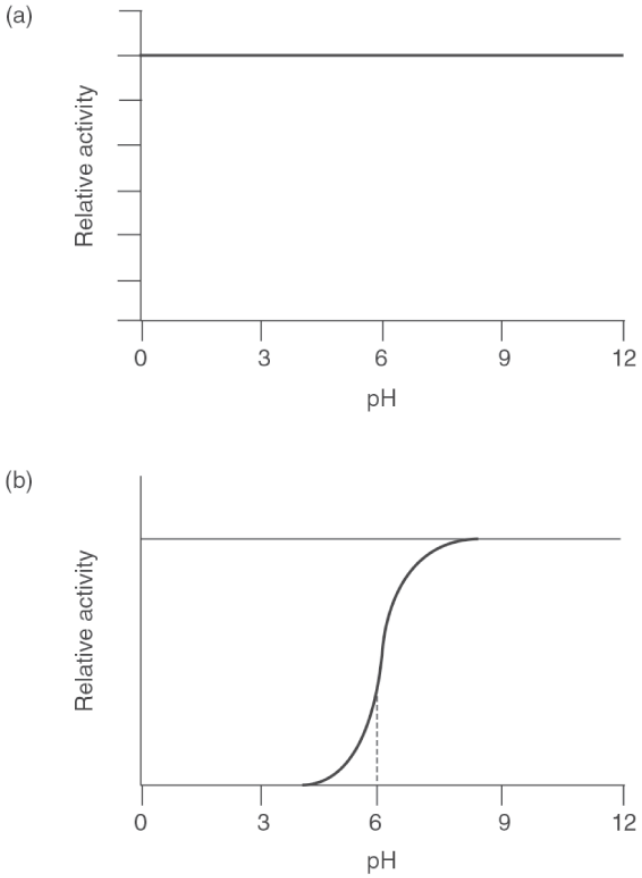


a) Km appears to be 5uM in the Michaelis-Menton plot, but using the double reciprocal plot, we can see that the Km=5.37 uM
b) Vm = 7.009x10^-10 mol/min
c) Turnover=mol S s^{-1}/mol E=$(6.84\times10^{-10})/[(60\times10^{-9})/29{,}600]$=337 min^{-1}

39) The concentration of asparagine in the environment is relatively low. In spite of its lower Vmax, Asparaginase 2 is more active against the low concentration of asparagine found in the environment. Therefore, Asparaginase 2 is expected to be the more effective chemotherapeutic agent.

46) The mechanism suggests that H+ is behaving like a competitive inhibitor since it is binding to the free enzyme. This means that we can remove the effect of pH by saturating the system with substrate.

a) If [S] is much higher than Km, than Vo will = Vm at all pH values.
b) At a low [S], the ionizable residue plays an important role and the curve will look like a titration curve, with Vo dependent on the ionization state of the catalytic residue.



c) At pH 6 (the pKa of the ionizable residue), Vo would equal 0.5Vm.

49) Only a few amino acid residues are actually involved in catalysis in enzymes, yet enzymes are constructed of at least 100 amino acids, and often many more. Suggest some functions for the noncatalytic amino acids.

Amino acids that form an active site are likely to be distant from each other in the primary sequence of the protein.
The noncatalytic amino acids are important for the overall protein folding into a framework that brings together a few specific amino acids to form a specific active site that is complementary to a substrate.
The geometry of this active site and its flexibility for adapting to a particular transition state during a reaction require a larger framework of noncatalytic amino acids, far beyond just the few chemical groups that form the active site.

In other words, the non-catalytic residues are responsible for determining the:

a) Tertiary structure of the enzyme
b) The geometry of the binding site
c) Placing catalytic residues near substrate when bound