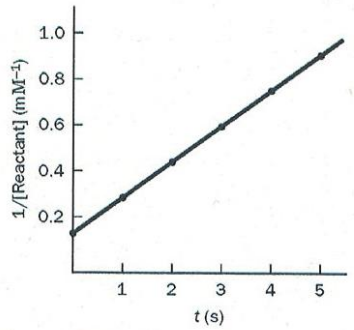
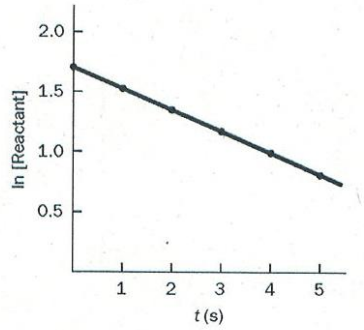
5. Only a plot of 1/[reactant] versus t gives a straight line, so the reaction is second order. The slope, k, is 0.15 $mM^{-1} \cdot s^{-1}$.

Time (s)	1/[reactant] (mM^{-1})
0	0.16
1	0.32
2	0.48
3	0.62
4	0.78
5	0.91

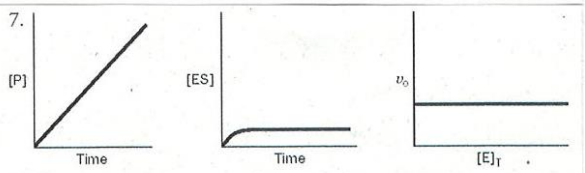


6. Only a plot of ln[reactant] versus t gives a straight line, so the reaction is first order. The negative of the slope, k, is 0.17 s^{-1}.

Time (s)	ln[Reactant]
0	1.69
1	1.53
2	1.36
3	1.16
4	0.99
5	0.83

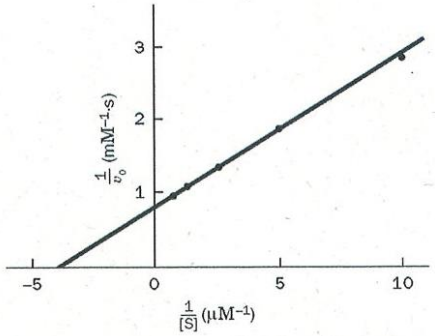


7.



8. Enzyme activity is measured as an initial reaction velocity, the velocity before much substrate has been depleted and before much product has been generated. It is easier to measure the appearance of a small amount of product from a baseline of zero product than to measure the disappearance of a small amount of substrate against a background of a high concentration of substrate.

9. Construct a Lineweaver–Burk plot.

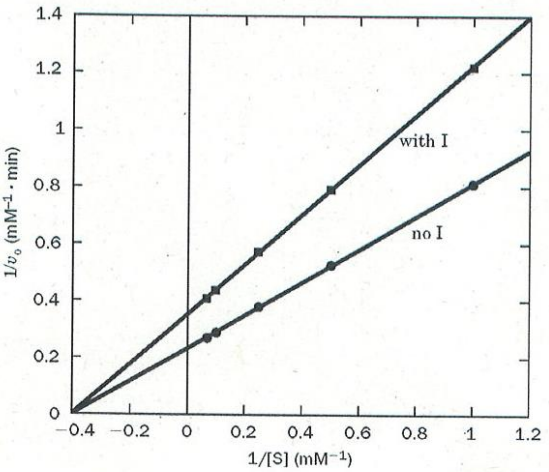


$K_M = -1/x\text{-intercept} = -1/(-4\ \mu M^{-1}) = 0.25\ \mu M$

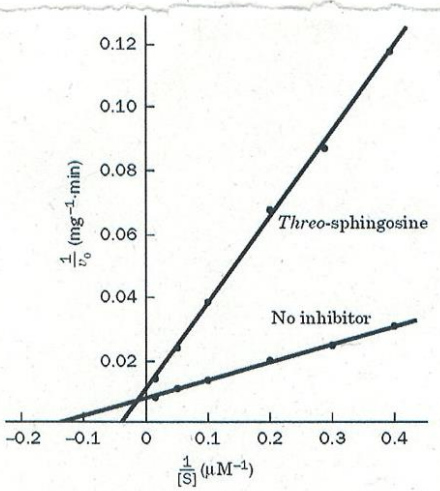
$V_{max} = 1/y\text{-intercept} = 1/(0.8\ mM^{-1} \cdot s) = 1.25\ mM \cdot s^{-1}$

27. The lines of the double-reciprocal plots intersect to the left of the $1/v_o$ axis (on the 1/[S] axis). Hence, inhibition is mixed (with $\alpha = \alpha'$).

[S]	1/[S]	$1/v_o$	$1/v_o$ with I
1	1.00	0.7692	1.2500
2	0.50	0.5000	0.8333
4	0.25	0.3571	0.5882
8	0.125	0.2778	0.4545
12	0.083	0.2500	0.4167



30.



(a) K_M is determined from the x-intercept ($= -1/K_M$). In the absence of inhibitor, $K_M = 1/0.14\ \mu M^{-1} = 7\ \mu M$. In the presence of inhibitor, $K_M^{app} = 1/0.04\ \mu M^{-1} = 25\ \mu M$. V_{max} is determined from the y-intercept ($= 1/V_{max}$). In the absence of inhibitor, $V_{max} = 1/0.008\ mg^{-1} \cdot min = 125\ mg \cdot min^{-1}$. In the presence of inhibitor, $V_{max}^{app} = 1/0.01\ mg^{-1} \cdot min = 100\ mg \cdot min^{-1}$.

(b) The lines in the double-reciprocal plots intersect very close to the $1/v_o$ axis. Hence, *threo*-sphingosine is most likely a competitive inhibitor. Competitive inhibition is likely also because of the structural similarity between the inhibitor and the substrate, which allows them to compete for binding to the enzyme active site.

22. (a) 31.1 μmol; (b) 0.05 μmol; (c) 622 s^{-1}, a midrange value for enzymes (Table 8.5).

23. (a) Yes, $K_M = 5.2 \times 10^{-6}$ M; (b) $V_{max} = 6.8 \times 10^{-10}$ mol $minute^{-1}$; (c) 337 s^{-1}.