

**LOSCHMIDT  
LABORATORIES**



# **Enzyme Kinetics**

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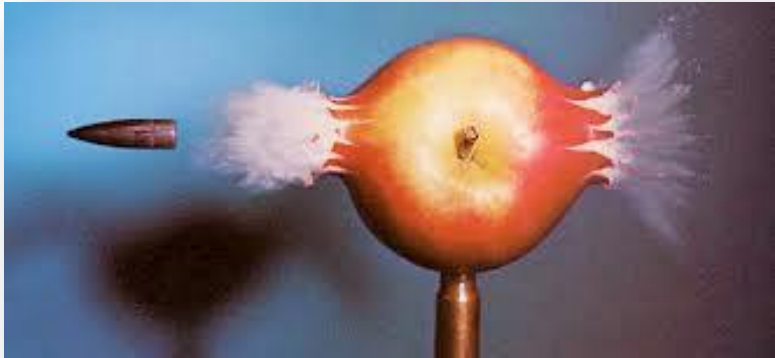
# OUTLINE



- ❑ ENZYME KINETICS
- ❑ STEADY-STATE vs. TRANSIENT KINETICS
- ❑ MATHEMATICS AND SOFTWARES
- ❑ RAPID MIXING TECHNIQUES
- ❑ KINETIC MECHANISMS
- ❑ KINETICS IN PROTEIN ENGINEERING

# ENZYME KINETICS

- **KINETICS** - study of motion and its causes



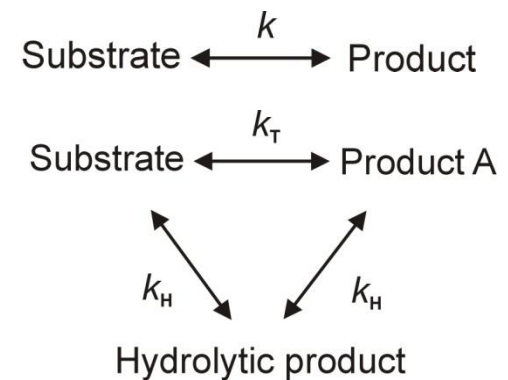
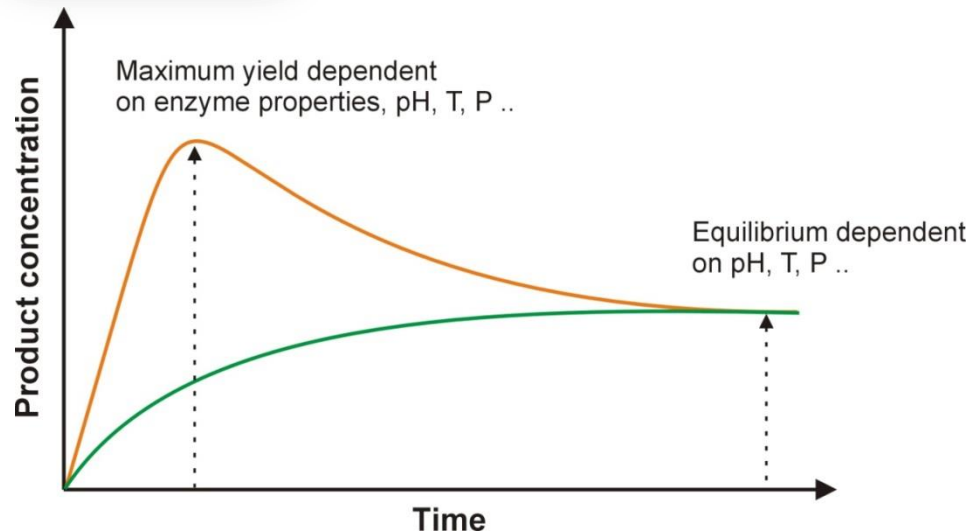
# ENZYME KINETICS

□ **KINETICS** - study of motion and its causes

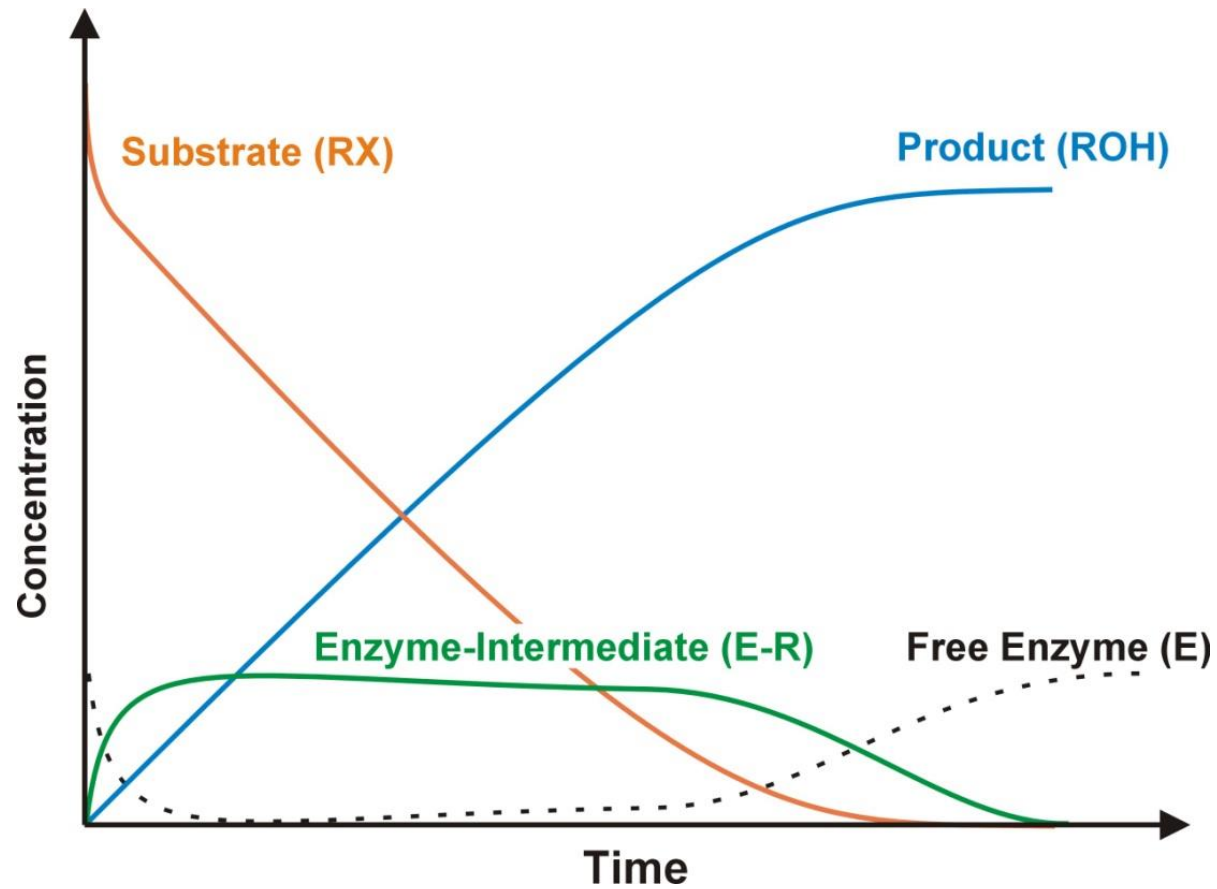
□ **(BIO)CHEMICAL KINETICS** - rate of reactions/interactions



- chemical kinetics
- enzyme kinetics
- binding kinetics
- (un)folding kinetics
- pharmacokinetics

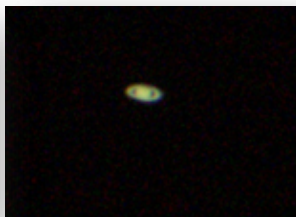
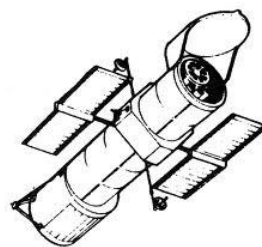
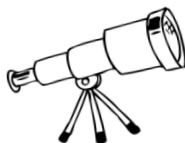
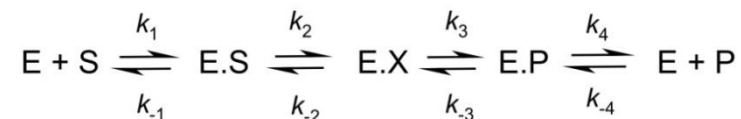
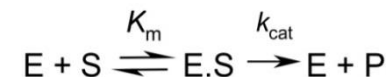
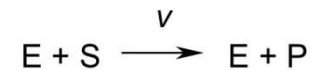


# ENZYME REACTION



# STEADY-STATE vs. TRANSIENT

- ❑ ACTIVITY ANALYSIS
- ❑ STEADY-STATE KINETICS
- ❑ TRANSIENT KINETICS

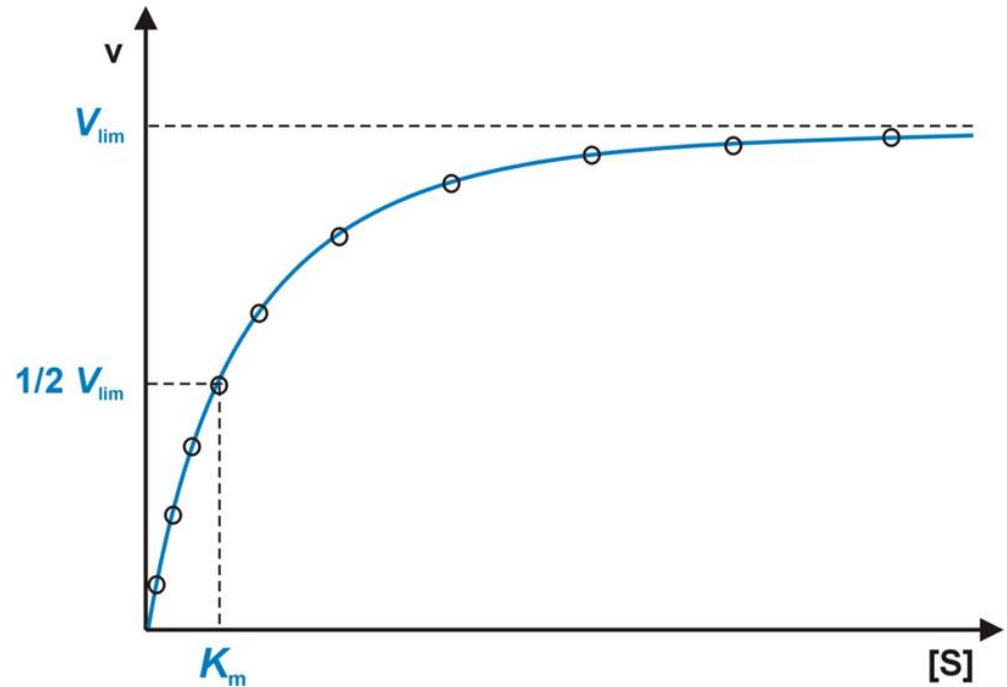
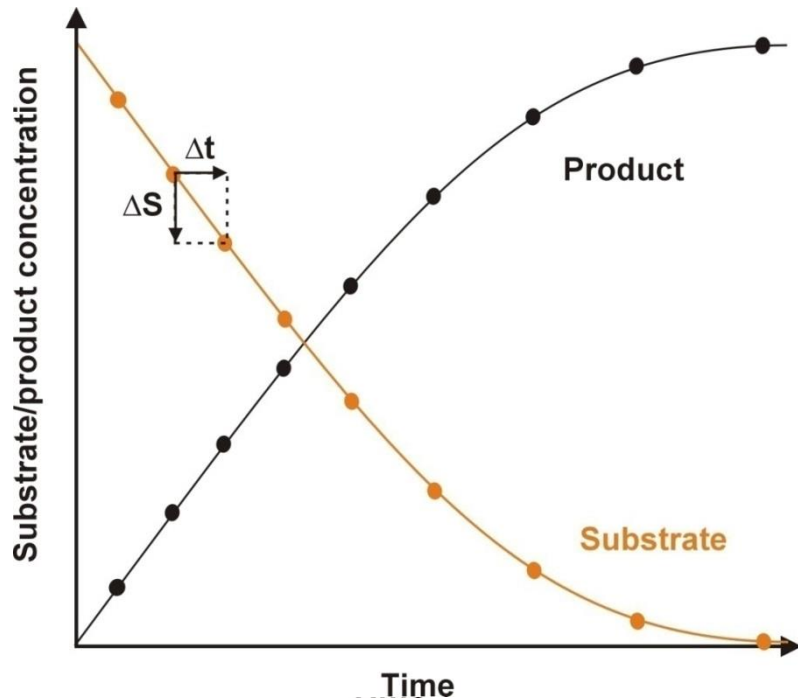


$$K_m = \frac{k_{-1} \cdot (k_{-2} \cdot (k_{-3} + k_{-4}) + k_{-3} \cdot k_{-4}) + k_{-2} \cdot k_{-3} \cdot k_{-4}}{k_1 \cdot ((k_2 + k_{-2}) \cdot (k_{-3} + k_{-4}) + k_{-2} \cdot k_{-3} + k_{-3} \cdot k_{-4})}$$

$$k_{cat} = \frac{k_2 \cdot k_3 \cdot k_4}{(k_2 + k_{-2}) \cdot (k_{-3} + k_{-4}) + k_{-2} \cdot k_{-3} + k_{-3} \cdot k_{-4}}$$

# STEADY-STATE KINETICS

- ❑ ACTIVITY ANALYSIS
- ❑ MICHAELIS-MENTEN KINETICS



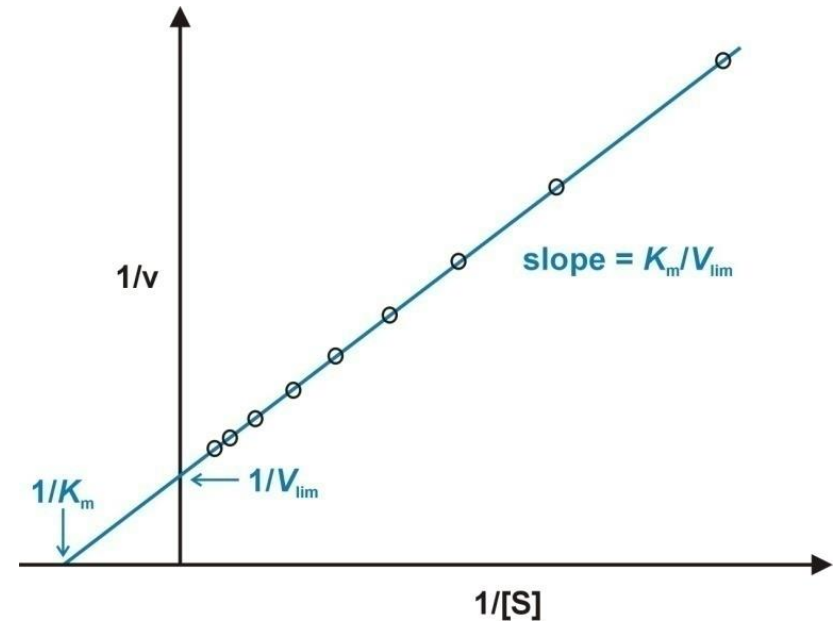
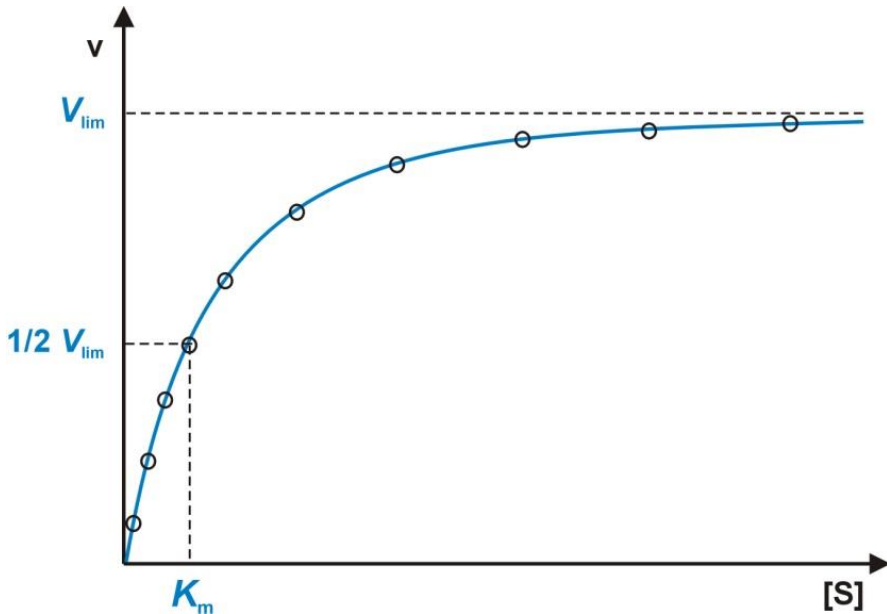
# STEADY-STATE KINETICS

## □ linearization

$$v = \frac{k_{\text{cat}} \cdot [\text{S}]}{K_m + [\text{S}]}$$



$$\frac{1}{v} = \frac{1}{V_{\text{lim}}} + \frac{K_m}{V_{\text{lim}}} \cdot \frac{1}{[\text{S}]}$$





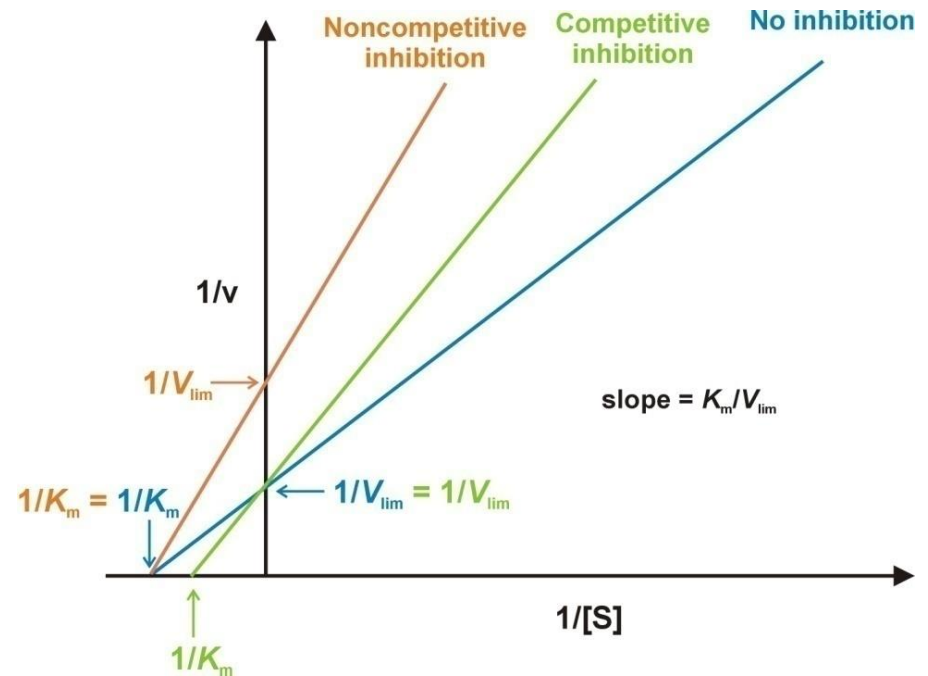
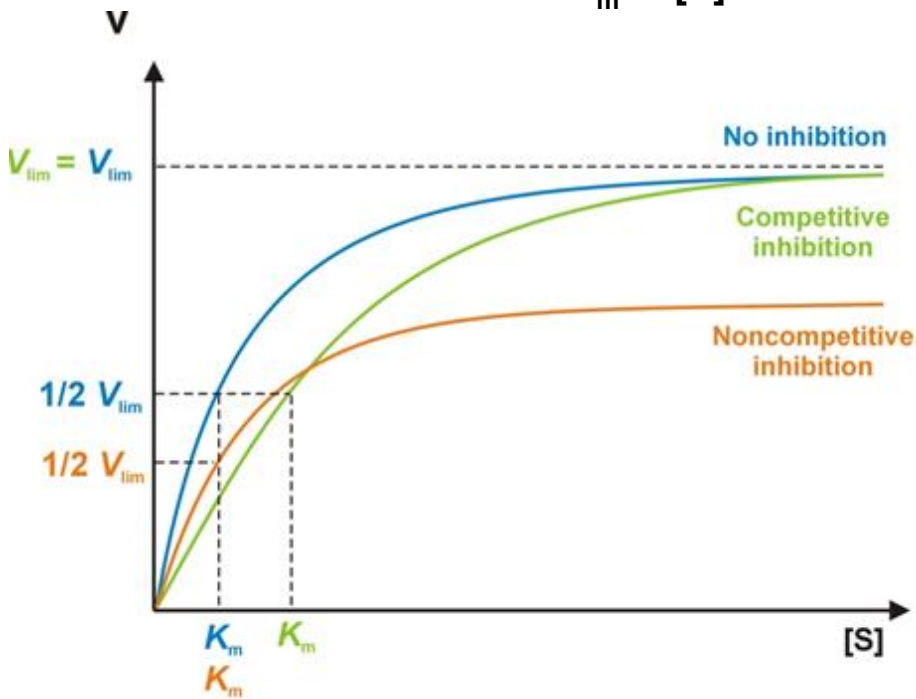
# STEADY-STATE KINETICS

## □ linearization

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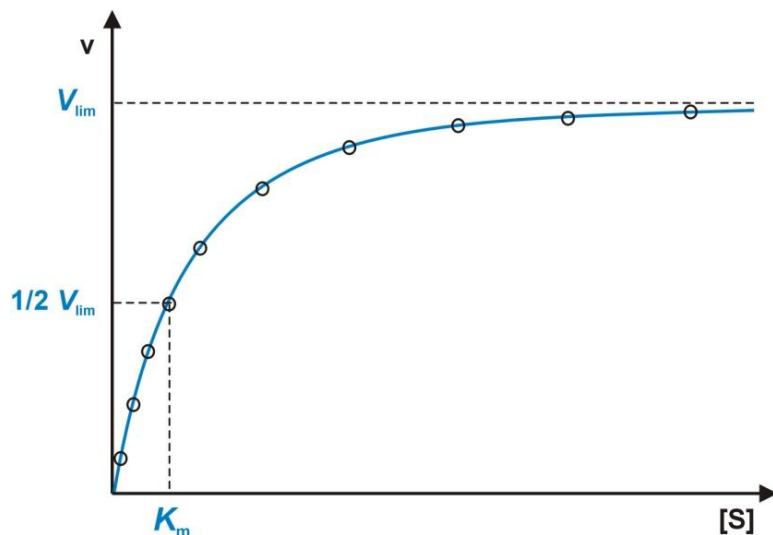


# STEADY-STATE KINETICS

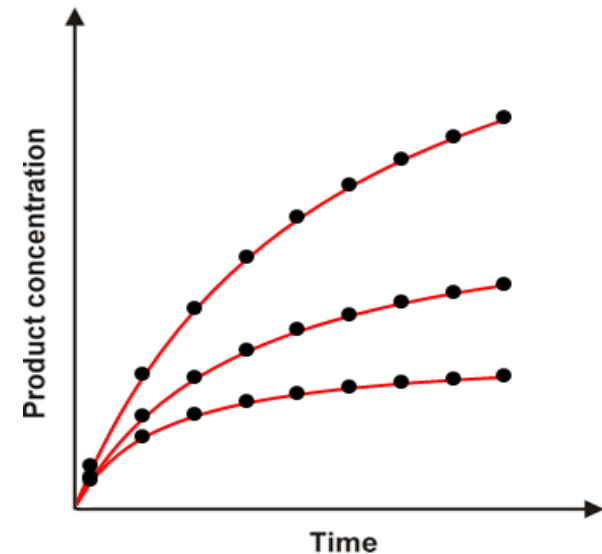
- linearization
- nonlinear regression (e.g., SigmaPlot, Origin, Enzfiter)
- numerical simulation (e.g., Gepasy, DynaFit, Kintek Explorer)



$$v = \frac{k_{cat} \cdot [S]}{K_m + [S]}$$



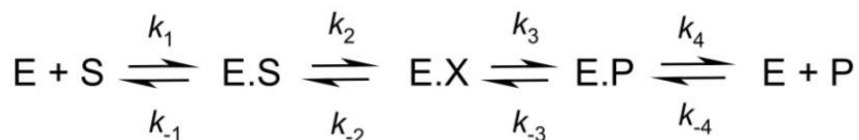
$$\frac{d[S]}{dt} = -k_1 \cdot [E] \cdot [S] + k_{-1} \cdot [ES]$$
$$\frac{d[ES]}{dt} = k_1 \cdot [E] \cdot [S] - k_{-1} \cdot [ES]$$
$$\frac{d[P]}{dt} = k_2 \cdot [ES]$$



# STEADY-STATE KINETICS



$$K_m = \frac{k_{-1} \cdot (k_{-2} \cdot (k_{-3} + k_4) + k_3 \cdot k_4) + k_2 \cdot k_3 \cdot k_4}{k_1 \cdot ((k_2 + k_{-2}) \cdot (k_{-3} + k_4) + k_2 \cdot k_3 + k_3 \cdot k_4)}$$



$$k_{cat} = \frac{k_2 \cdot k_3 \cdot k_4}{(k_2 + k_{-2}) \cdot (k_{-3} + k_4) + k_2 \cdot k_3 + k_3 \cdot k_4}$$

## □ Michaelis-Menten constant, $K_m$ ( $\text{mol.l}^{-1}$ )

- apparent equilibrium constant
- determined by true binding constant and rates of catalytic steps

## □ Turnover number, $k_{cat}$ ( $\text{s}^{-1}$ )

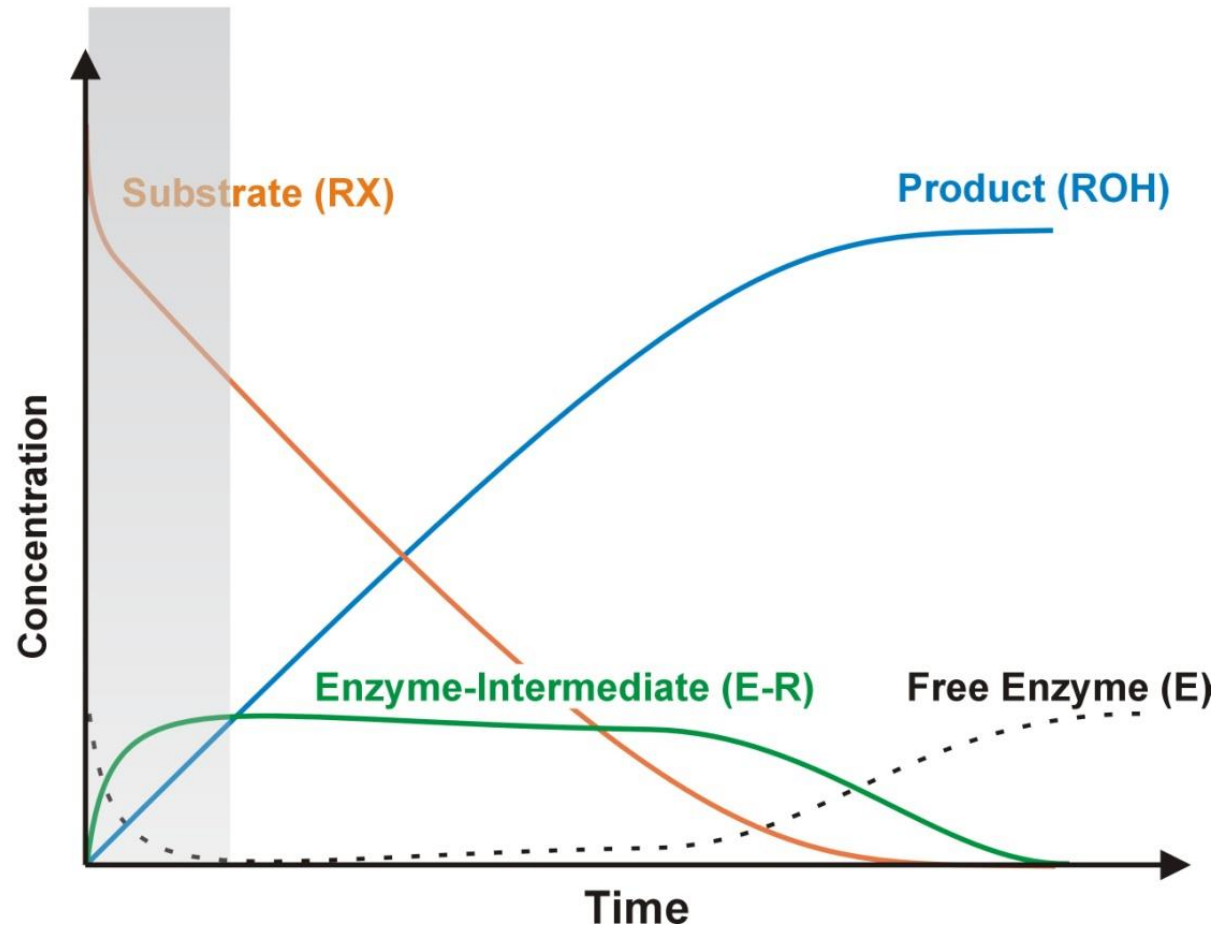
- number of molecules converted per second by one enzyme molecule under saturation
- influenced only by rates of catalytic steps (limiting step)

## □ Specificity constant, $k_{cat}/K_m$ ( $\text{mol.l}^{-1} \cdot \text{s}^{-1}$ )

- apparent second order rate constant

# TRANSIENT KINETICS

TRANSITION STATE



# RAPID MIXING TECHNIQUES

## STOPPED-FLOW

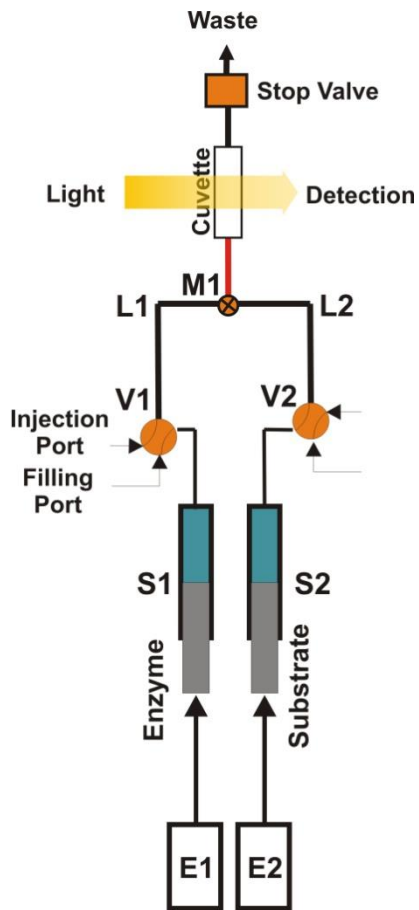


## RAPID QUENCH-FLOW

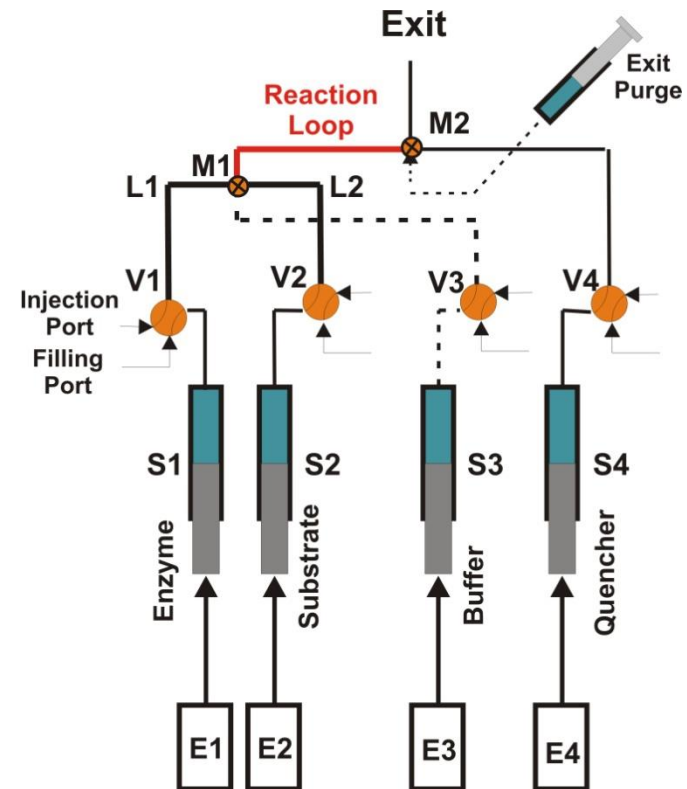


# RAPID MIXING TECHNIQUES

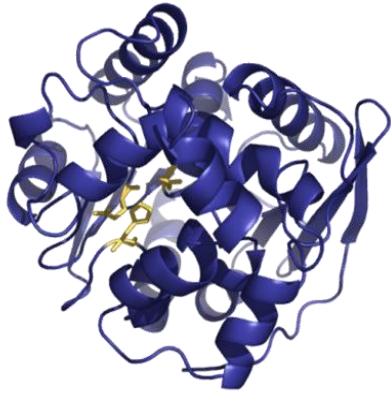
## STOPPED-FLOW



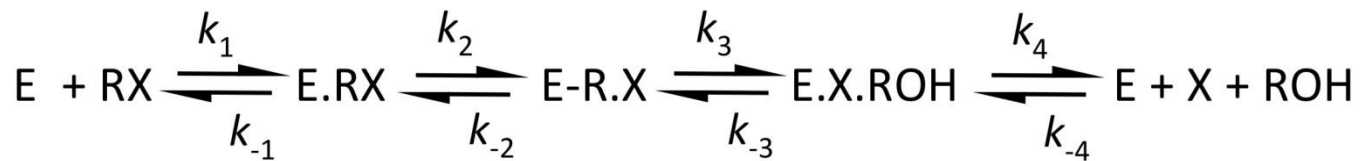
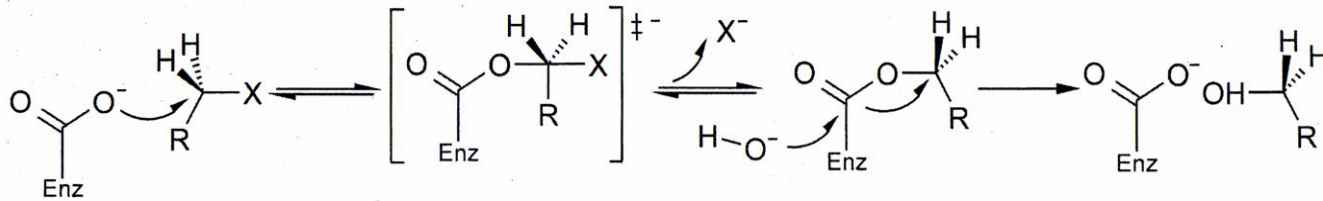
## RAPID QUENCH-FLOW



# KINETIC MECHANISMS



- ❑ **dehalogenase** (EC 3.8.1.5)
- ❑ **globular** proteins
- ❑ **monomeric/oligomeric**
- ❑ **no cofactor** requirement
- ❑ cleavage **carbon-halogen** bond

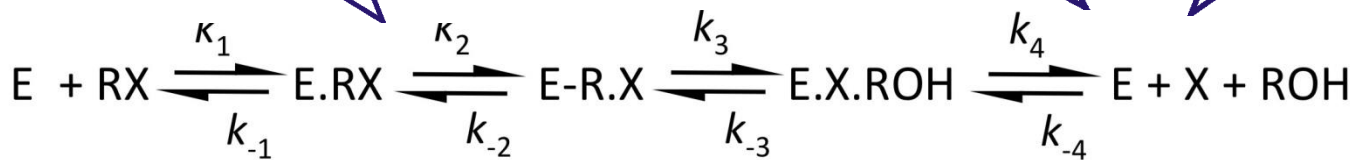
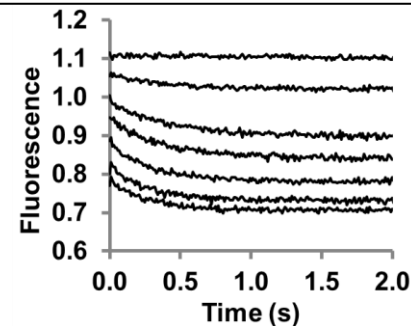
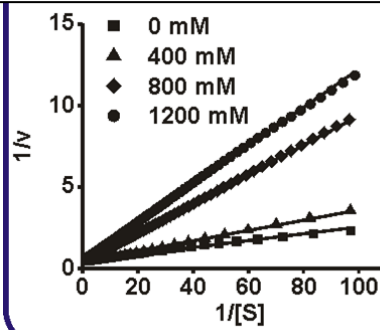
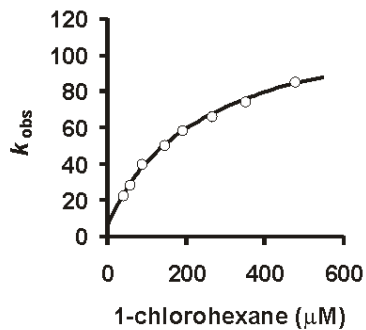
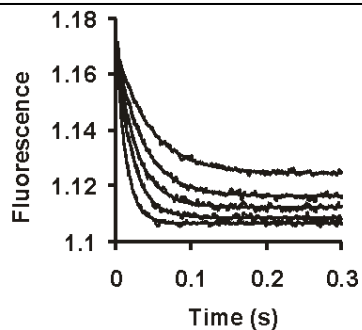


# KINETIC MECHANISMS

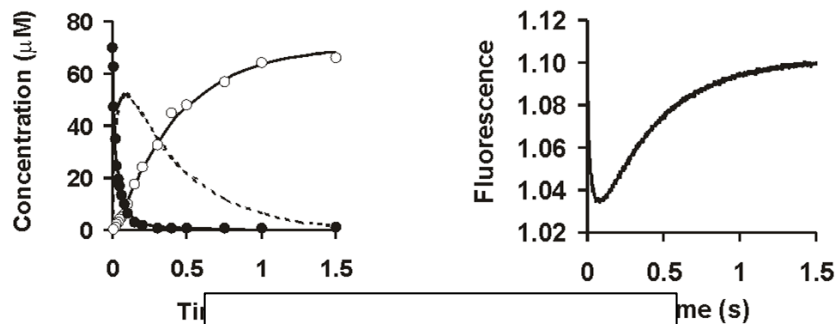
$$k_{\text{obs}} = \frac{k_2 \cdot [S]}{[S] + K_s} + k_{-2} + k_3$$

$$v = \frac{[S] \cdot k_{\text{cat}}}{K_m \cdot (1 + [P]/K_{p1}) + [S] \cdot (1 + [P]/K_{p2})}$$

$$k_{\text{obs}} = \frac{[P] \cdot k_{4b}}{K_{4a} + [P]} + k_{-4b}$$

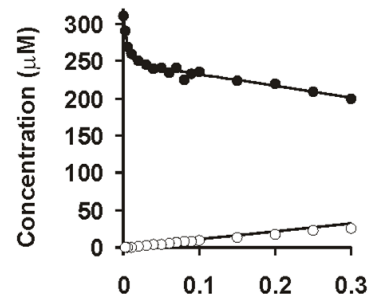


## SINGLE TURNOVER KINETICS



$$A = A_1 \cdot e^{-k_1 \cdot t} + A_2 \cdot e^{-k_2 \cdot t}$$

## REACTION BURST



$$A = A_0 \cdot e^{-k \cdot t} + k_2 \cdot t$$



# KINETIC MECHANISMS

	Substrat	$K_s$ ( $\mu\text{M}$ )	$k_2$ ( $\text{s}^{-1}$ )	$k_{-2}$ ( $\text{s}^{-1}$ )	$k_3$ ( $\text{s}^{-1}$ )	$k_4$ ( $\text{s}^{-1}$ )	$K_m$ ( $\mu\text{M}$ )	$k_{\text{cat}}$ ( $\text{s}^{-1}$ )
LinB	1-chlorohexane	240	117	0.4	3.2	-	16	2.6
	bromocyclohexane	> 450	> 200	1.1	2.5	-	23	1.8
	chlorocyclohexane	> 500	> 40	12.5	0.075	-	221	0.1
DhIA	1,2-dibromeethane <sup>1</sup>	> 27	> 130	-	10	4	10	3
	1,2-dichloroethane <sup>1</sup>	2 200	50	-	14	8	530	3.3
DhaA	1,3-dibromopropane <sup>2</sup>	60 - 300	300	-	14.8	3.9	5	2.7

**distinct rate-limiting steps  
for relative enzymes**

# PROTEIN ENGINEERING

## RATIONAL DESIGN

### 1. Computer aided design



### 2. Site-directed mutagenesis



Individual mutated gene

### 3. Transformation

### 4. Protein expression

### 5. Protein purification

6. *not applied*

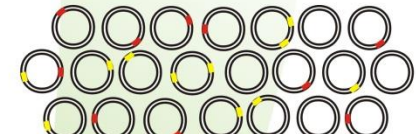


Constructed mutant enzyme

## DIRECTED EVOLUTION

1. *not applied*

### 2. Random mutagenesis



Library of mutated genes  
( >10,000 clones )

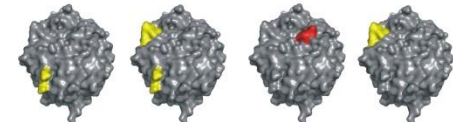
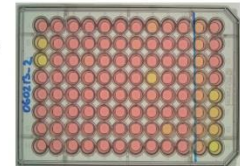
### 3. Transformation

### 4. Protein expression

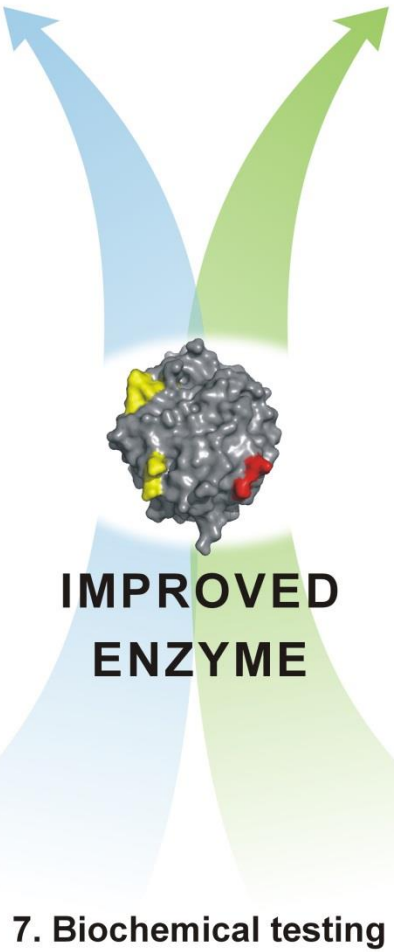
5. *not applied*

### 6. Screening and selection

- stability
- selectivity
- affinity
- activity



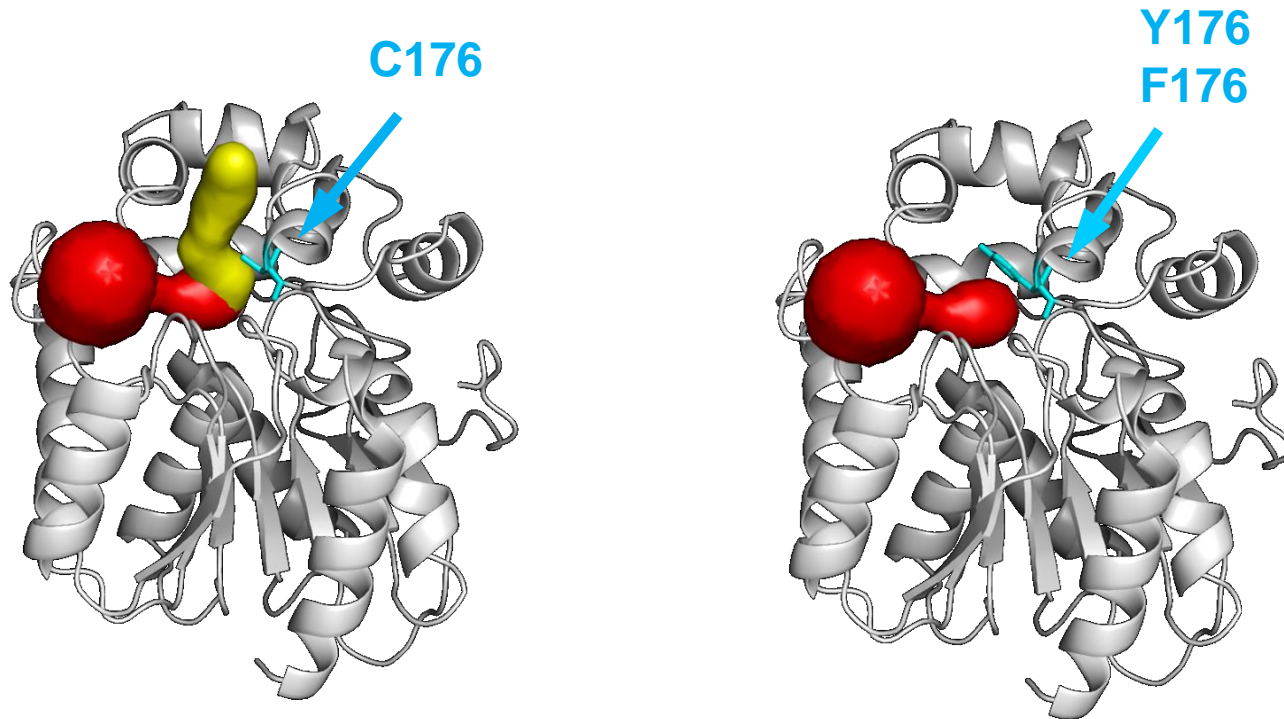
Selected mutant enzymes



### 7. Biochemical testing

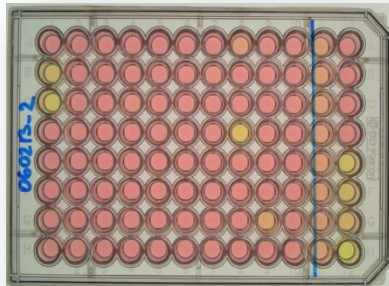
# PROTEIN ENGINEERING

- ❑ **conversion of 1,2,3-trichloropropane**  
by dehalogenase from *Rhodococcus sp.*
- ❑ importance of access pathways

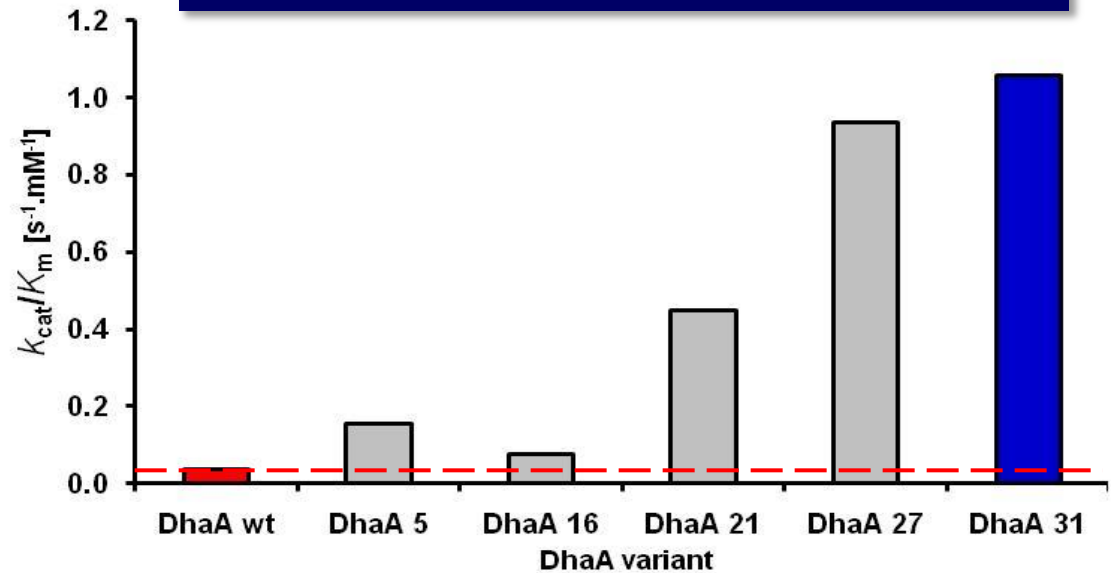


# PROTEIN ENGINEERING

- ❑ library of 5,300 clones
- ❑ **steady-state kinetics**

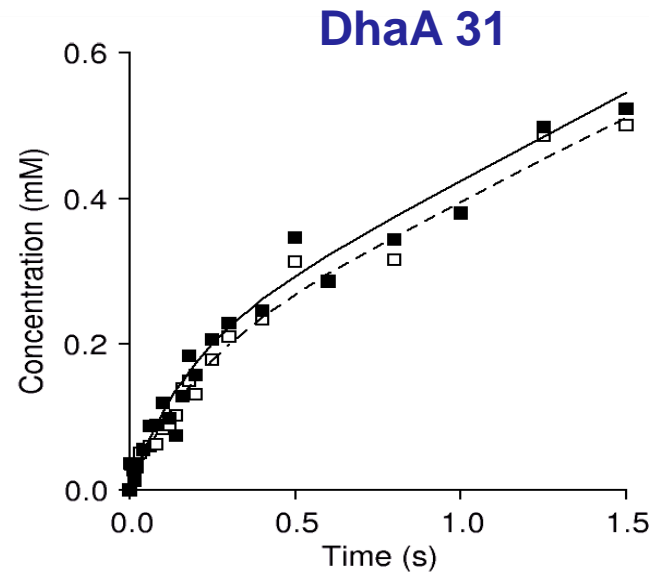
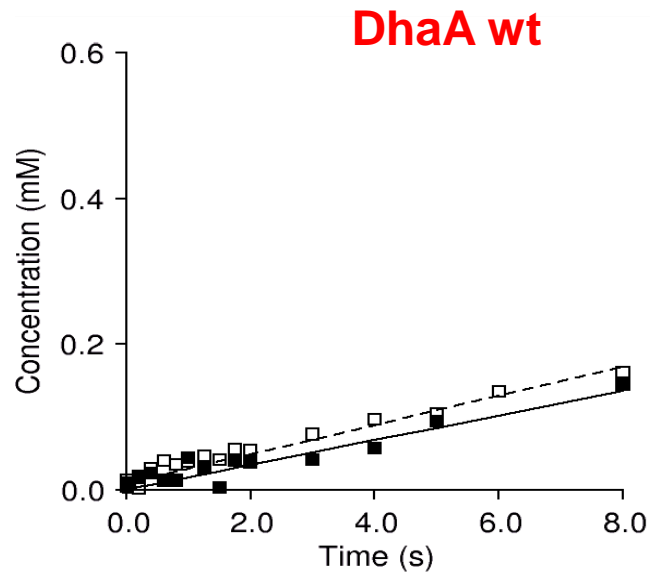


**steady-state catalysis  
improved 26x**

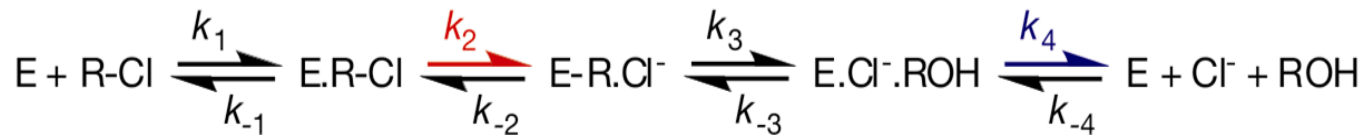


	$K_m$ (mM)	$k_{cat}$ ( $s^{-1}$ )	$k_{cat}/K_m$
<b>DhaA wt</b>	<b><math>0.98 \pm 0.17</math></b>	<b><math>0.035 \pm 0.002</math></b>	<b>0.04</b>
<b>DhaA 31</b>	<b><math>1.19 \pm 0.15</math></b>	<b><math>1.26 \pm 0.05</math></b>	<b>1.06</b>

## □ transient kinetics



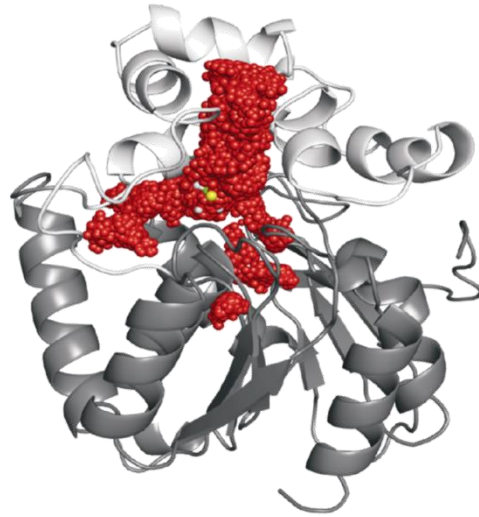
**Chemical reaction**



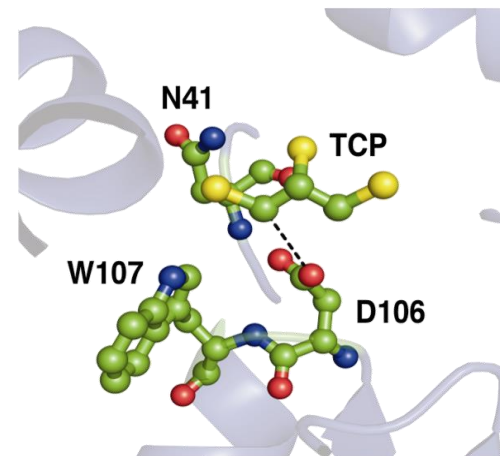
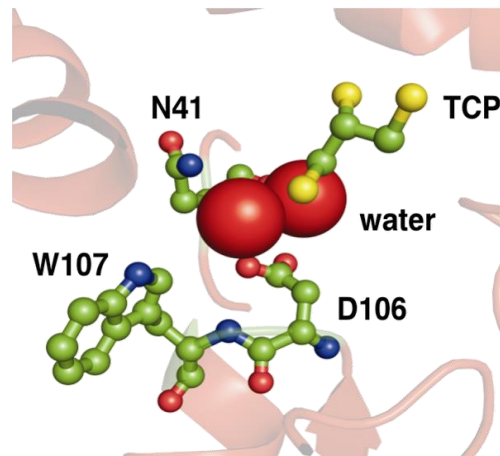
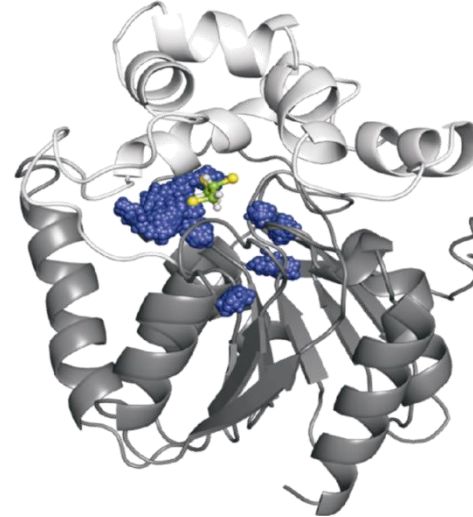
**Product release**

# PROTEIN ENGINEERING

**DhaA wt**

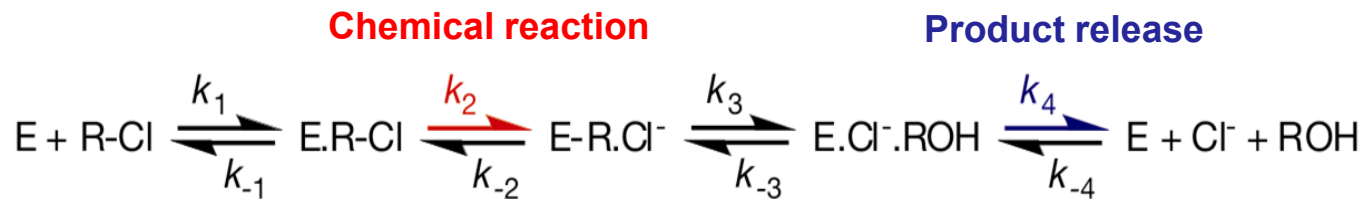
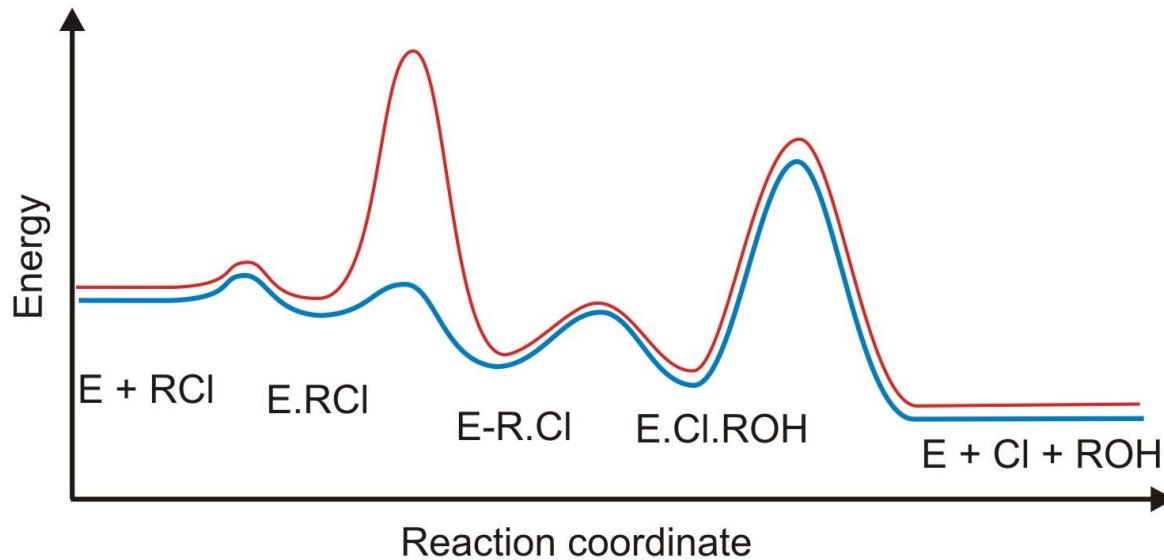


**DhaA 31**





## □ transient kinetics



**chemical step improved 450x**