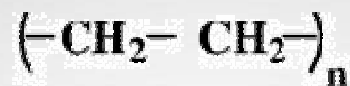


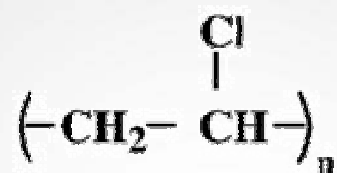
# **INVESTIGATION OF NOVEL CUTINASES FOR BIOTRANSFORMATIONS**

Peter James Baker & Jin Kim Montclare  
Department of Chemical & Biological Sciences  
Polytechnic Institute of New York University  
August 19<sup>th</sup> 2009

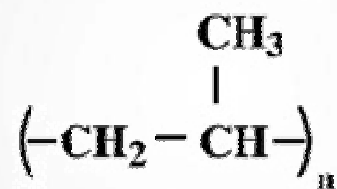
# Conventional Petrochemical Thermo Plastics



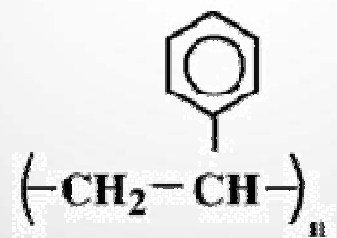
Polyethylene (PE)



Polyvinyl Chloride (PVC)



Polypropylene (PP)

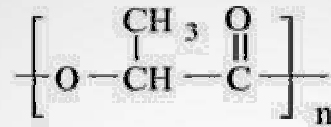


Polystyrene (PS)

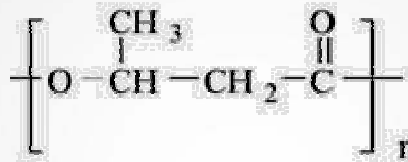
Pavia DL., et. al., *Introduction to Organic Labrotory Techniques*. 3<sup>rd</sup> Ed. 1988

Shah AA., et. al. *Biotechnology Advances*. 2008, 246-65

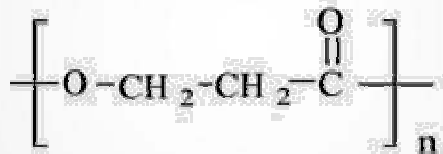
# Biodegradable Plastics



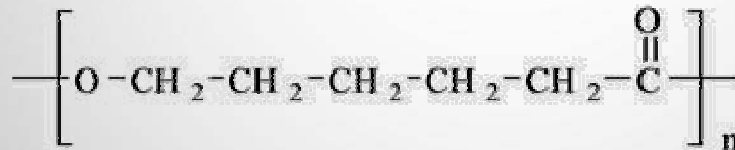
Poly(lactide) (PLA)



Poly(3-hydroxybutyrate) (PHB)



Poly(propiolactone) (PPL)



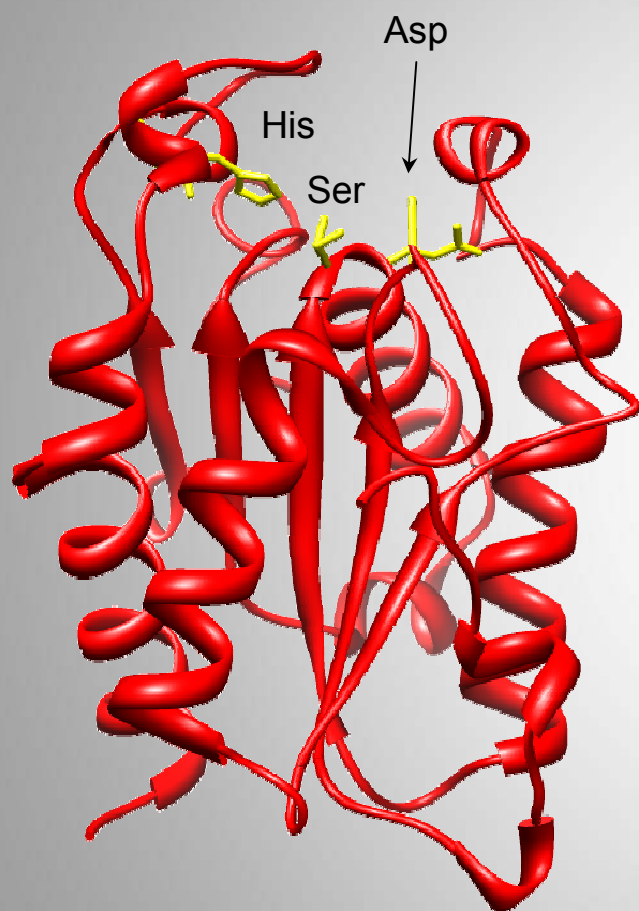
Poly( $\epsilon$ -caprolactone) (PCL)

Shah AA., et. al. *Biotechnology Advances*. **2008**, 246-65

Tokiwa Y., et. al. *Biotechnol. Lett.* **2004**, 1181-9

Azios, T., *The Christian Science Monitor*. **2007**.

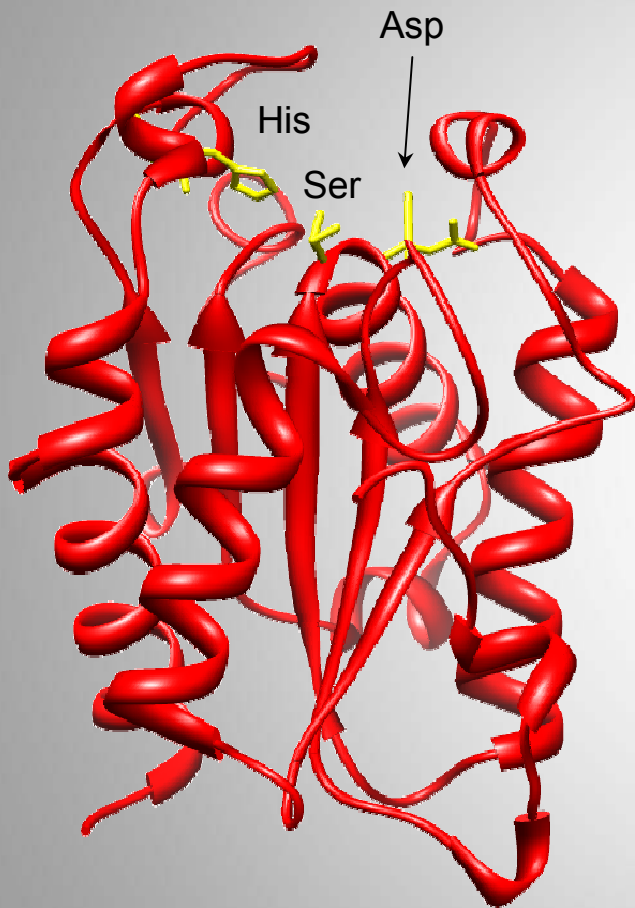
# Hydrolytic Enzymes Employed in Organic Chemistry



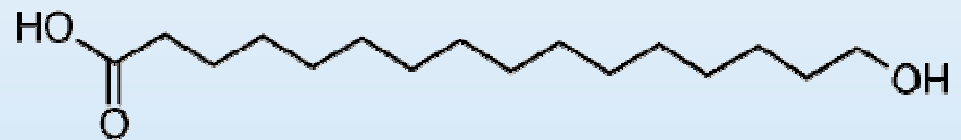
- Proteases, cellulases, lipases, amylases, and **cutinases**
- Cutinases member of serine hydrolase family
- Cutinases have a more exposed active site opening up different potential applications
- Catalytic triad composed of Ser, His and a carboxyl group
- Oxyanion hole Ser, Gln; which stabilize the transition state

Purdy RE., *et al.*, *Biochemistry*, **1975**, 2832-40  
Longhi, S., *et al.*, *J.Mol. Biol.*, **1997**, 779-99  
Nicholas, A., *et al.*, *Biochemistry*, **1996**, 398-410  
Pdb code: 1cex

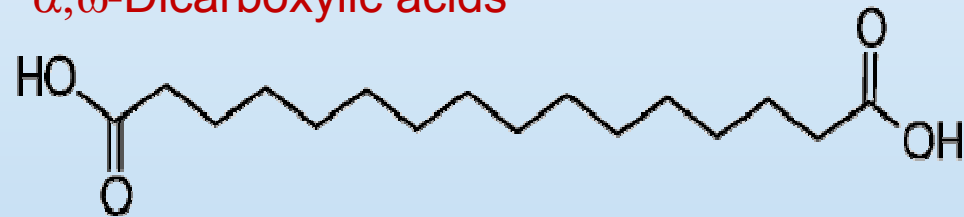
# *Fusarium solani* Cutinase (FsC)



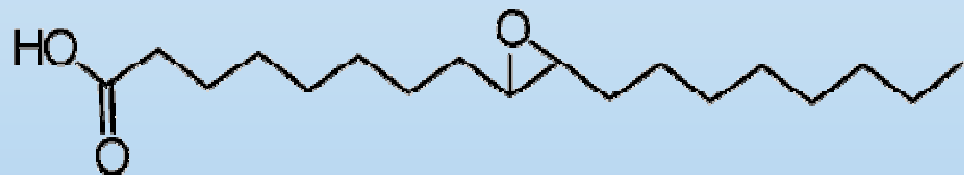
## $\omega$ -Hydroxy fatty acids



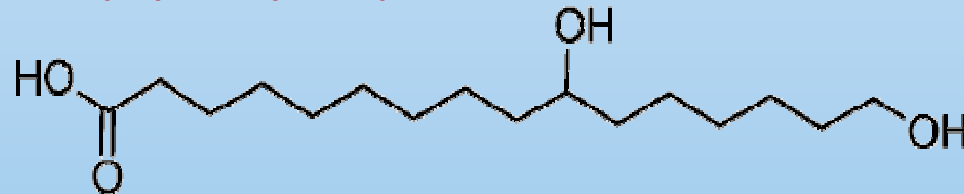
## $\alpha,\omega$ -Dicarboxylic acids



## Epoxy-fatty acids



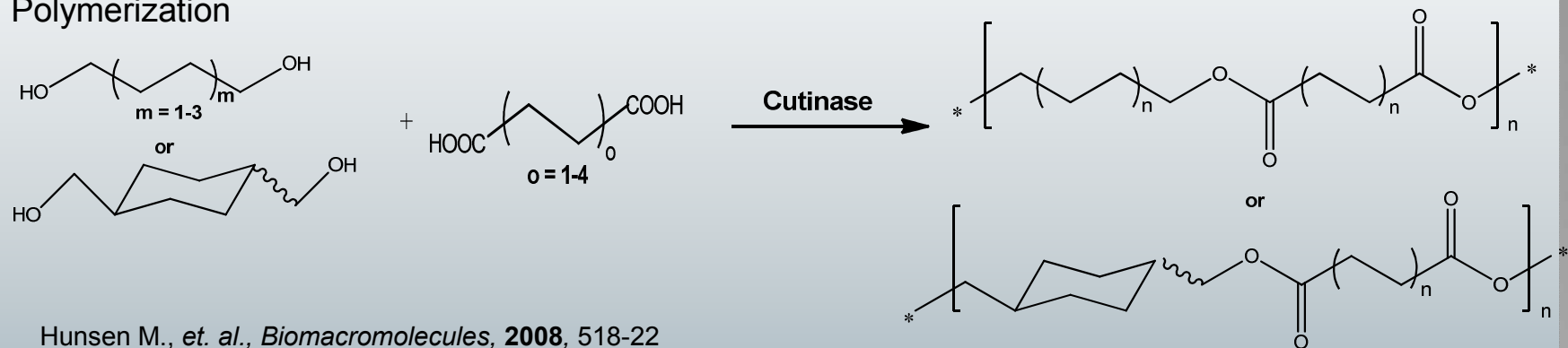
## Polyhydroxy-fatty acids



Purdy RE., *et al.*, *Biochemistry*, **1975**, 2832-40  
Longhi, S., *et al.* *J.Mol. Biol.*, **1997**, 779-99  
Pollard M., *et al.* *Trends in Plant Science*, **2008**, 1360-85  
Pdb code: 1cex

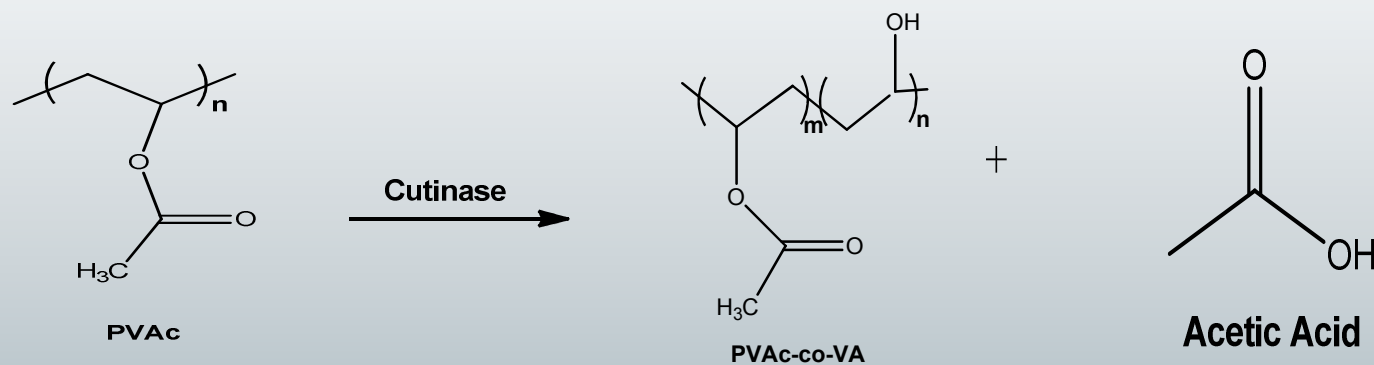
# Examples of Biotransformations using Cutinase

## I. Polymerization



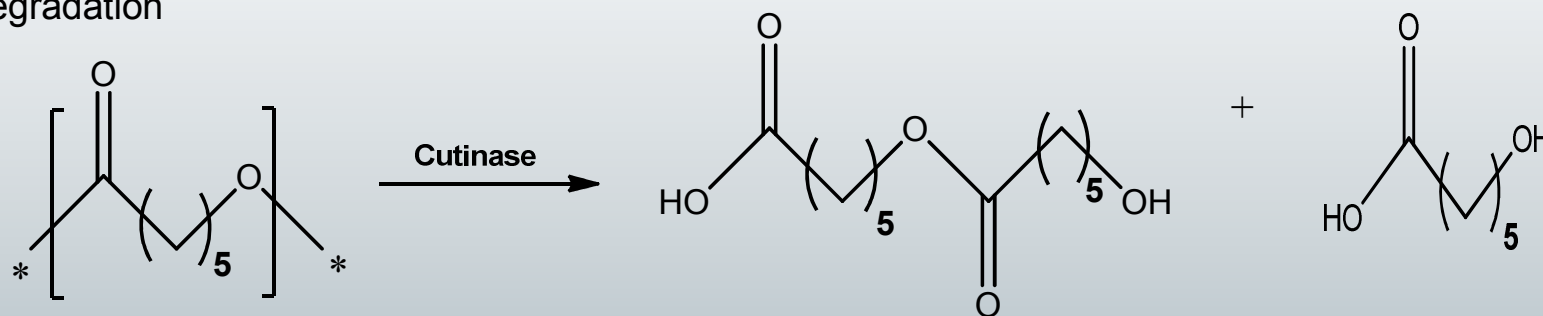
Hunsen M., et. al., *Biomacromolecules*, **2008**, 518-22

## II. Modification



Ronkvist, A., PhD. Dissertation NYU:POLY

## III. Degradation



Liu Z., et. al., *JACS*, **2009**, under revision

# Searching the Natural Diversity

```

AbC  --MMNLNLLLSKPC-----QA-STTRNELETGSSDACPRTFIFARGSTE
AfC  --MKFALLS LAAMAVASPV----AIDVRQT-AITGDELRTG---PCEPITFFIFARGSTE
AoC  MHLRNIVIALAATAVASPV----DLQDRQL--TGGDELRDG---PCKPITFFIFARASTE
HiC  -----GAIENGLES GSANACPDAILIFARGSTE
FsC  MKFFALTTLLAATASALP TSNPAQLEARQLGRTRRDDL LINGNSASC RDVIFIYARGSTE
      : * * . * :*:**.***
    
```

```

AbC  AGNMGALVGPFTANALE SAYGASN VVWVQGVG GPYTAGLVENALPAGTSQA AIREAQR LFN
AfC  PGLLGITTPGVCNALKLS-RPGQVACQGVGPAYIADLASNFLPQGTSQVA IDEAAAGLFK
AoC  PGLLGISTGPAVCNRLKLA-RSGDVACQGVGPRYTADLPSNALPEGTSQA AIAEAQGLFE
HiC  PGNMGITVGPALANGLES--HIRNIWIQGVG GPYDAALATNFLPRGTSQA NIDEGKR LFA
FsC  TGNLG-TLGP SIANLES AFGKDG VWIQVGGAYRATLGDNALPRGTSQA AIREMLGLFQ
      . * : * ** .. * : : **** * * * * * ** * * **
    
```

```

AbC  LAASKCPNTPITAGGYSQGA AVMSNAIPGLSAAVQDQIKGVVLF GYTKNLQNGGRIPNFP
AfC  LAASKCPDTKIVAGGYSQGA AVMHGAIRNLP SNVQNMKGVVLF GDRNKQDGGRIIPNFP
AoC  QAVSKCPDTQIVAGGYSQGTAVMNGAIKRLSADVQDKIKGVVLF GYTRNAQERQIANFP
HiC  LANQKCPNTPVAVAGGYSQGAALIAAAVSELSGAVKEQVKGVALFGYTQNLQNRGGIPNYP
FsC  QANTKCPDATLIAGGYSQGAALAAASIEDLSAIRDKIAGTVLFGYTKNLQNRGRIIPNYP
      * ***: : : ******: : : * . : : : *..*** *:* * : * *.*:*
    
```

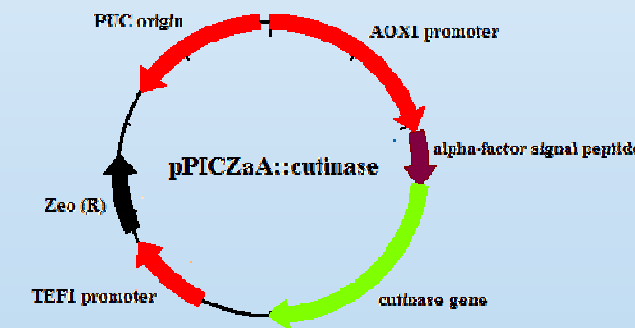
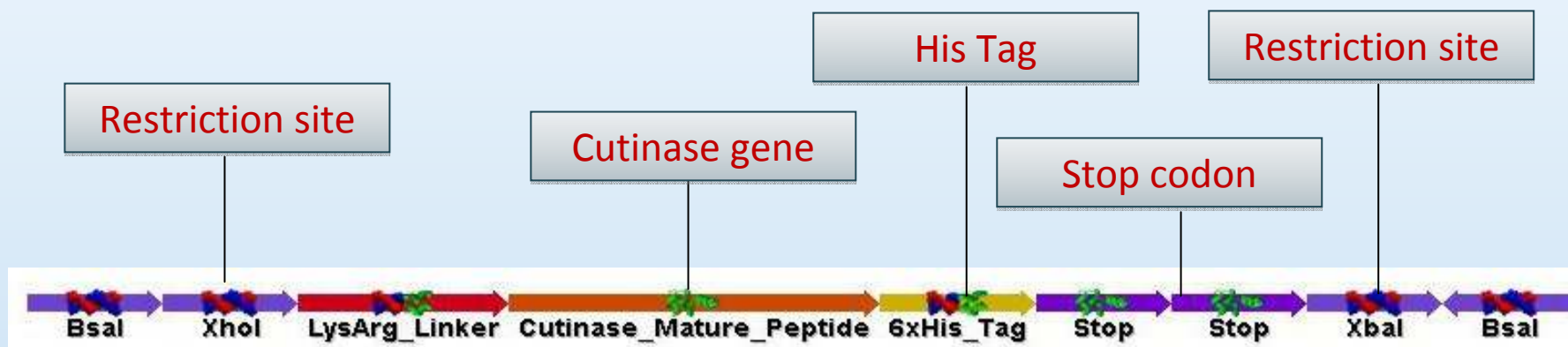
```

AbC  TSKTTIYCETGDLVCGT LIITPAHLLYSDEAAVQA PTF LRAQID----SA
AfC  TDRTKIYCAFGDLVCDGT LIITPAHLSYGDDVP-SATSFLLSKV-----
AoC  KDKVKVYCAVGDLVCLGT LIVAPP HFSYLSDT-GDASDFLLS QL G-----
HiC  RERTKVECNVGDVCTGT LIITPAHLSYTI EARGEAARFLRDRIR-----
FsC  ADRTKVECNTGDLVCTGSLIVAAPHLAYGPDARGPAPEFLIEKVRVARGSA
      . . . : * ** * * * : * : * : * . * * : :
    
```

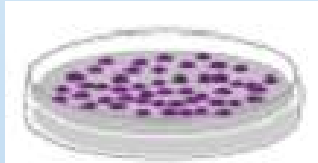
## FsC as parental sequence

- 116 potential sequence were identified
- Sequences were eliminated if they were mutants or previously studied
- 4 sequences were selected which showed conservation of catalytic residues

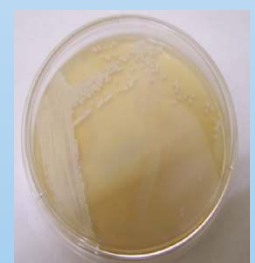
# Expression and Cloning of Cutinase



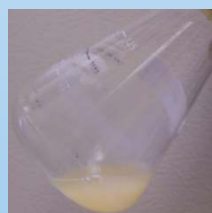
Transform into *Pichia pastoris*



Agar Plate



Pre culture



Fermentor

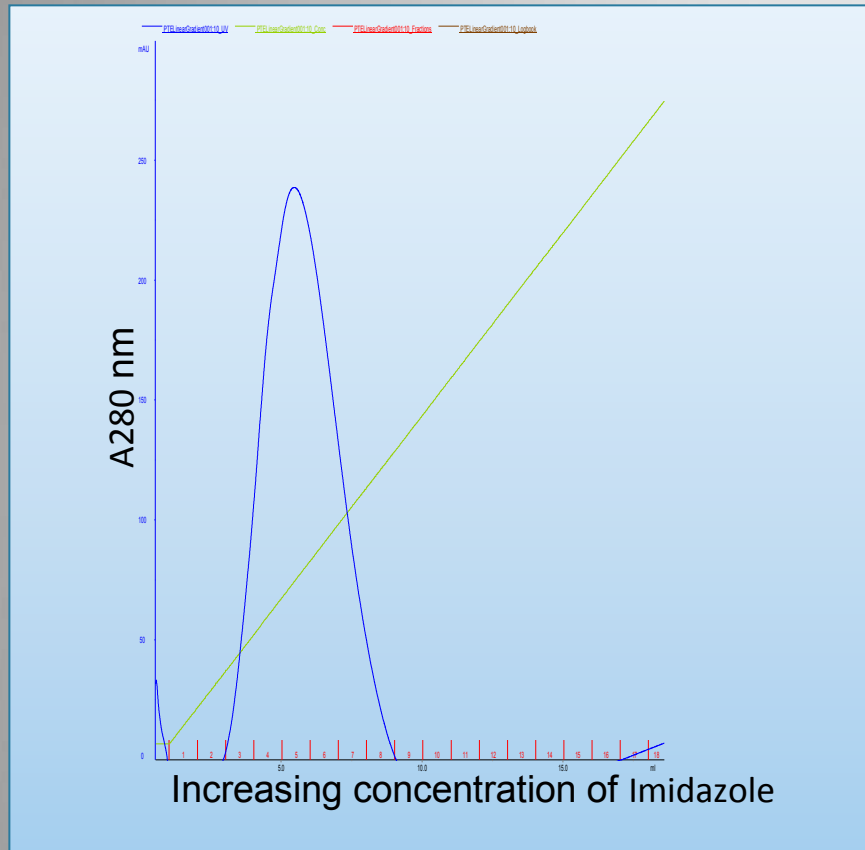


Concentrator





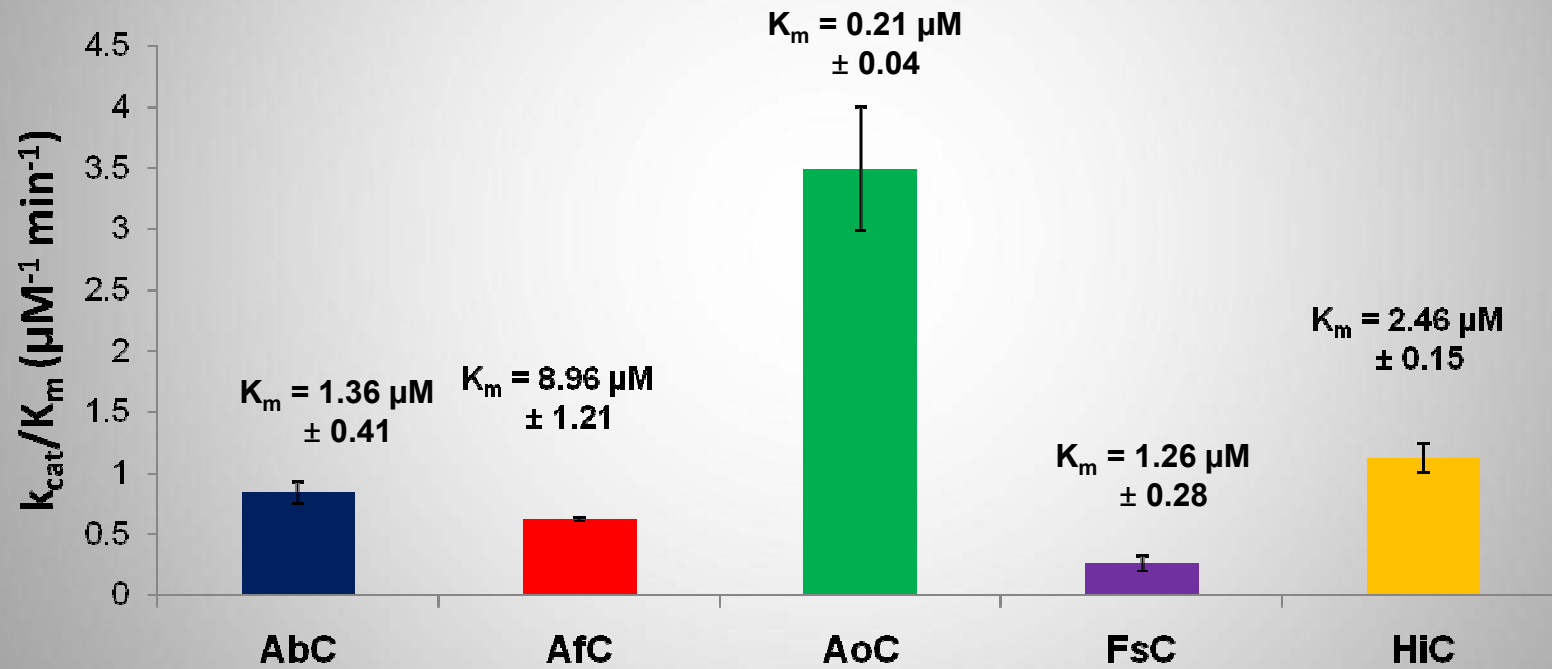
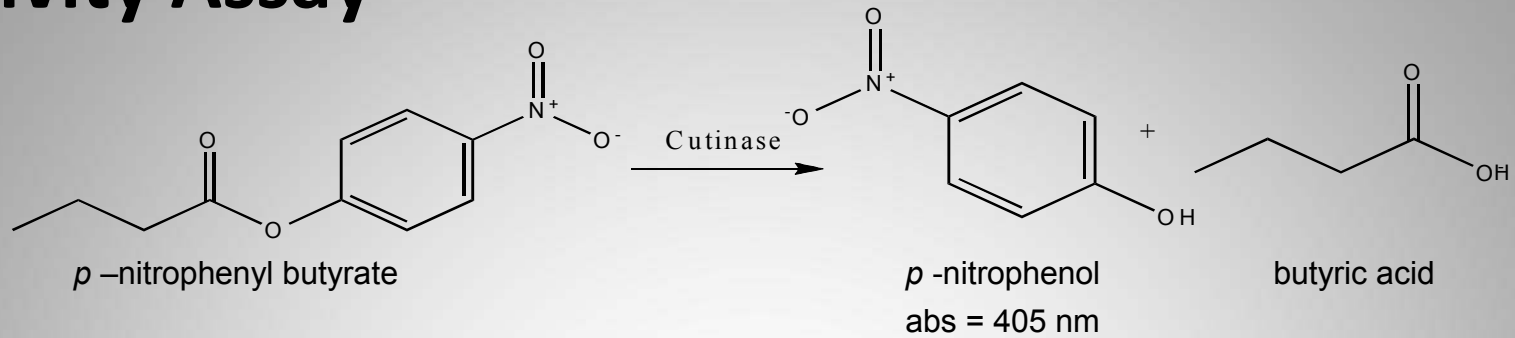
# Purification of Cutinase



Estimated yield for a 3L expression ~600mg

Column: GE His Trap FF Column  
Elution Buffer: 50 mM Na Phosphate  
500 mM Imidazole, pH 8.0

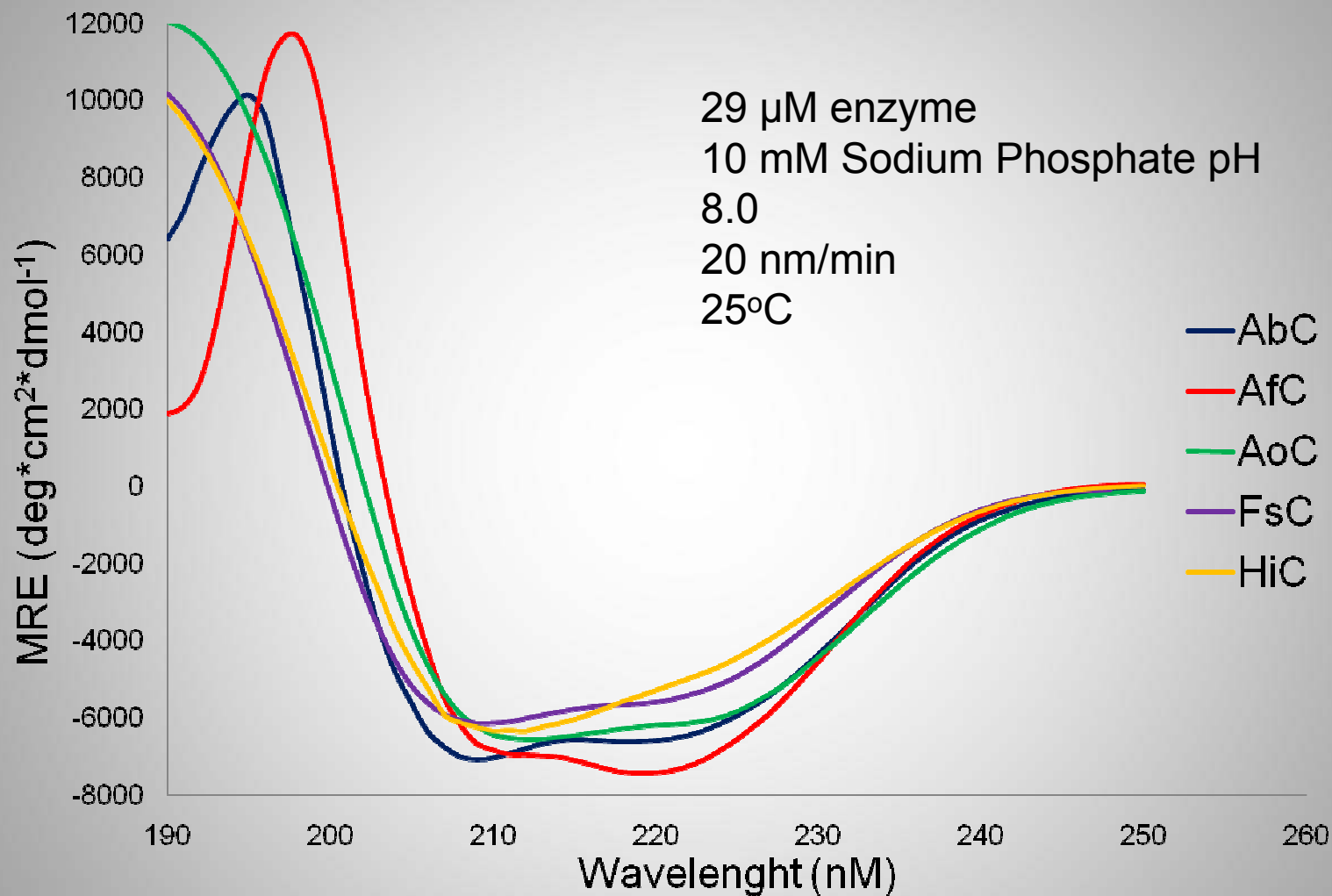
# Activity Assay



$K_m$ : AoC > FsC > AbC > HiC > AfC  
 $k_{\text{cat}}/K_m$ : AoC > HiC > AbC > AfC > FsC

Reaction Conditions  
 14.5 mM Tris, pH 7.5  
 0.75% Glycerol  
 25°C

# Secondary Structural Analysis

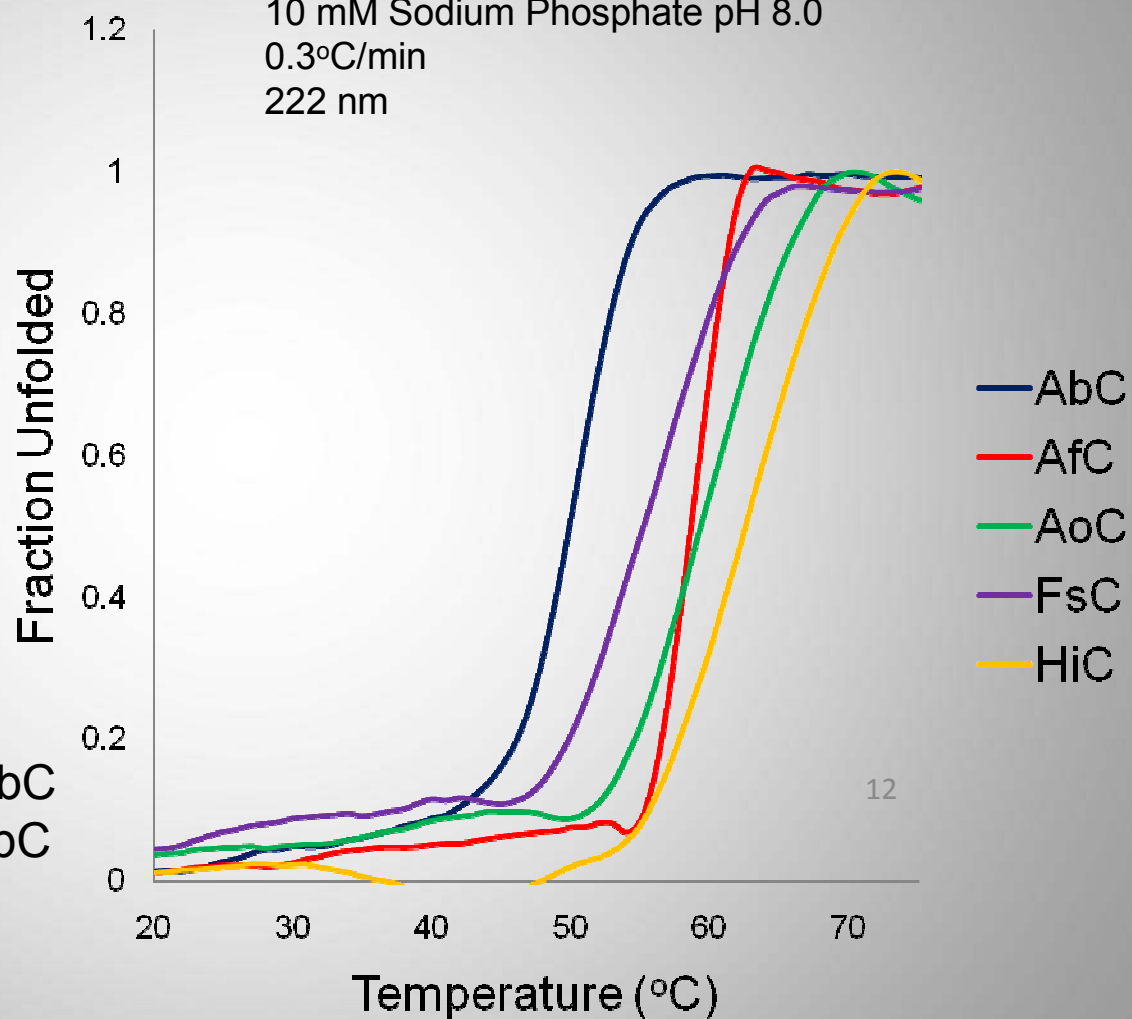


All proteins exhibit similar  $\alpha/\beta$  secondary structure characteristics, hallmarked by a double minima at 208nm and 222nm

# Biophysical Properties at pH 8.0

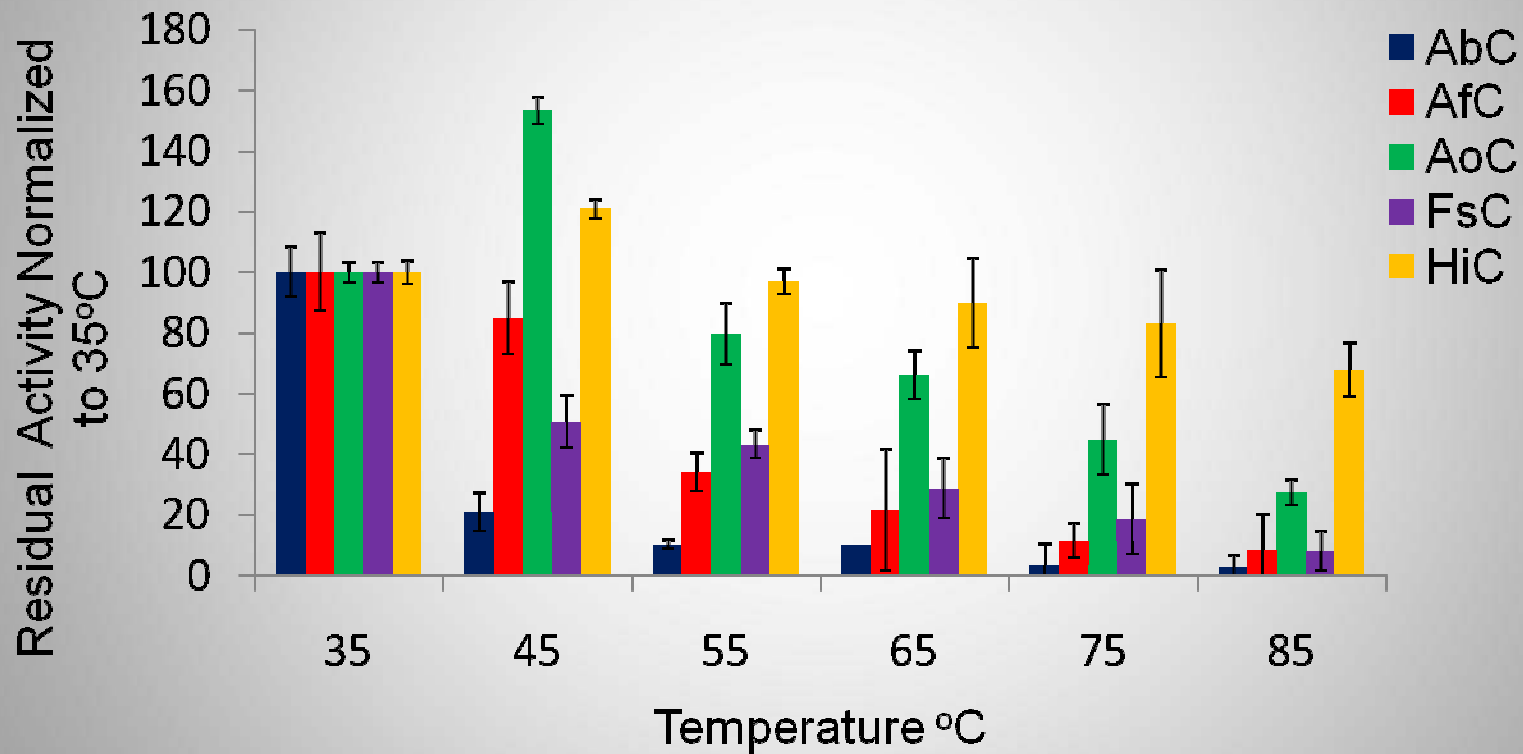
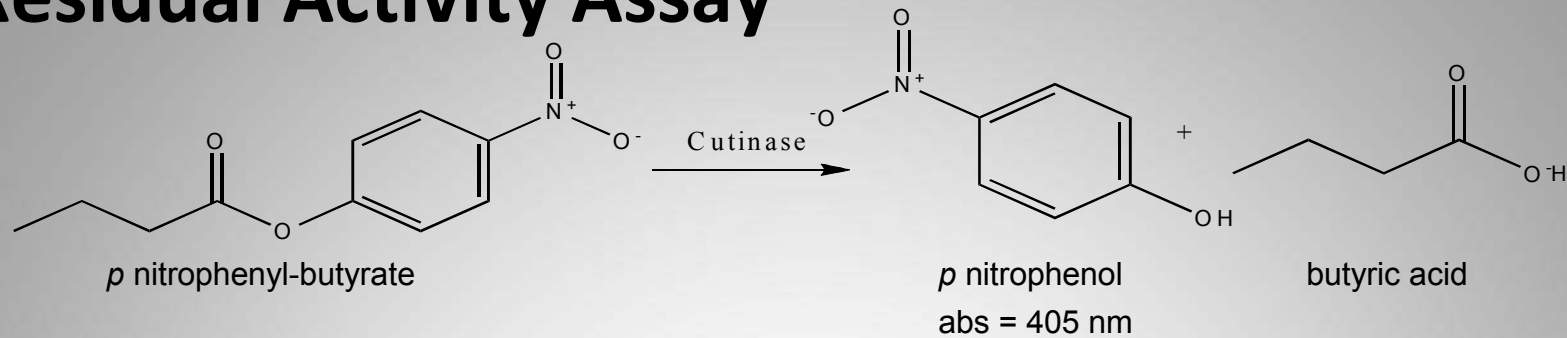
29  $\mu$ M enzyme  
 10 mM Sodium Phosphate pH 8.0  
 0.3°C/min  
 222 nm

	$T_m$ (°C)	$\Delta H$ (kJ/mol)
AbC	50	517.13
AfC	59	601.53
AoC	58	622.61
FsC	56	562.21
HiC	62	541.42



$T_m$ : HiC > AfC > AoC > FsC > AbC  
 $\Delta H$ : AoC > AfC > HiC > FsC > AbC

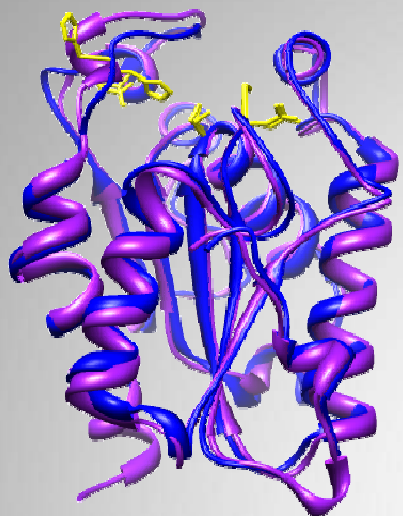
# Residual Activity Assay



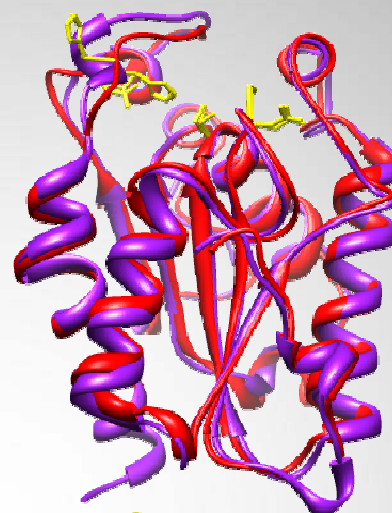
Reaction Conditions  
 14.5 mM Tris, pH 7.5  
 0.75% Glycerol

# Backbone Homology at pH 8.0

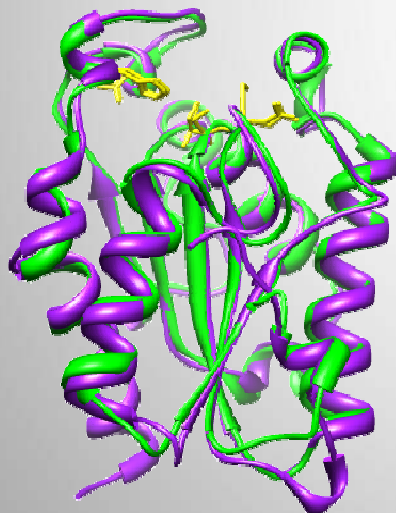
AbC  
pI = 6.06



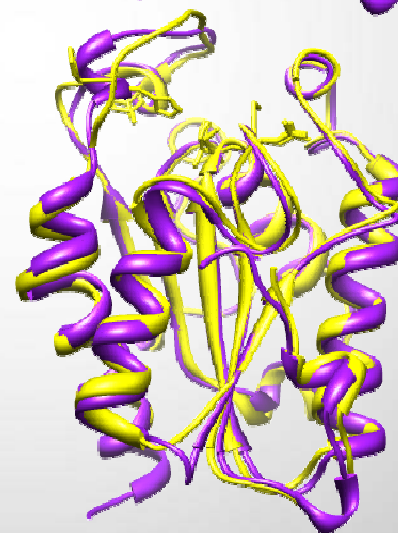
AfC  
pI = 7.66



AoC  
pI = 5.79



HiC  
pI = 8.17

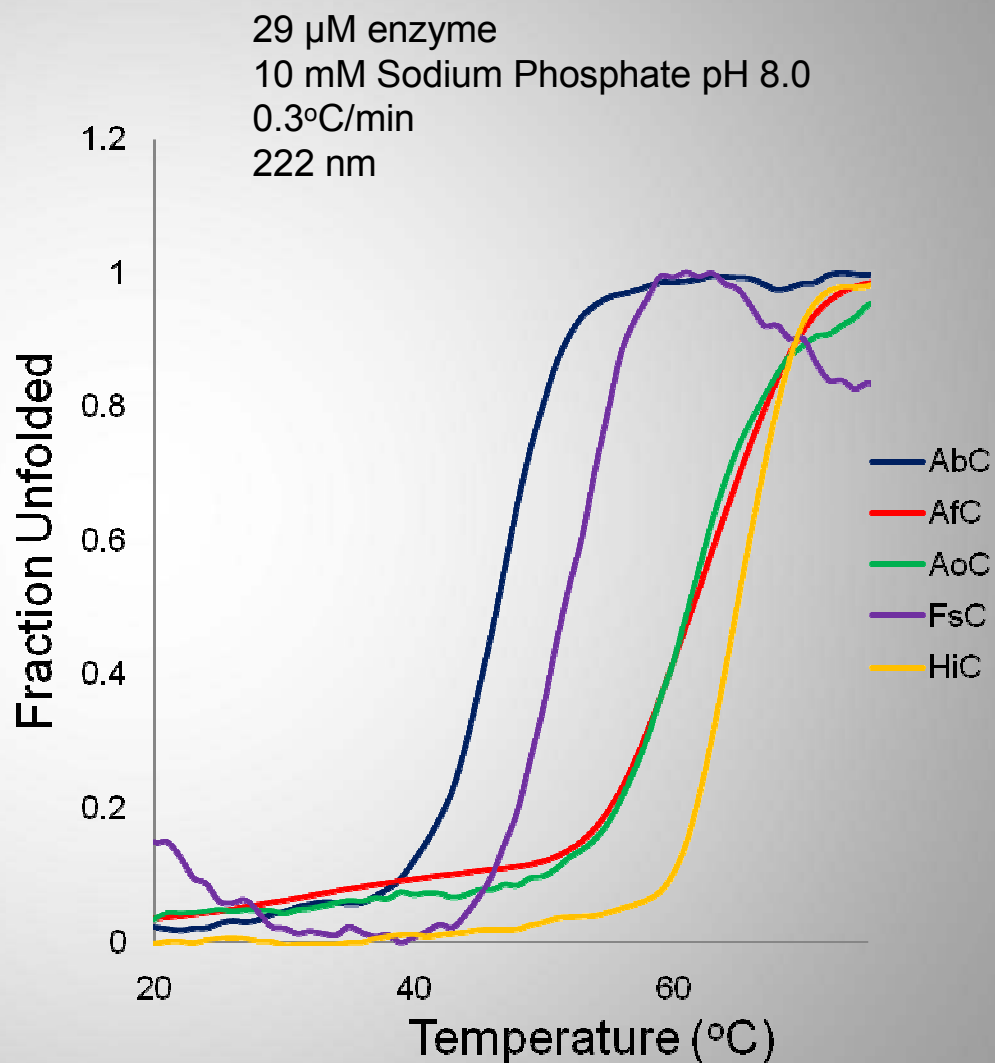


# Biophysical Properties at pH 5.0

	$T_m$ (°C)	$\Delta H$ (kJ/mol)
AbC	50	445.69
AfC	64	675.00
AoC	61	612.34
FsC	53	536.77
HiC	63	563.06

$T_m$ : HiC > AfC > AoC > FsC > AbC

$\Delta H$ : AfC > AoC > HiC > FsC > AbC

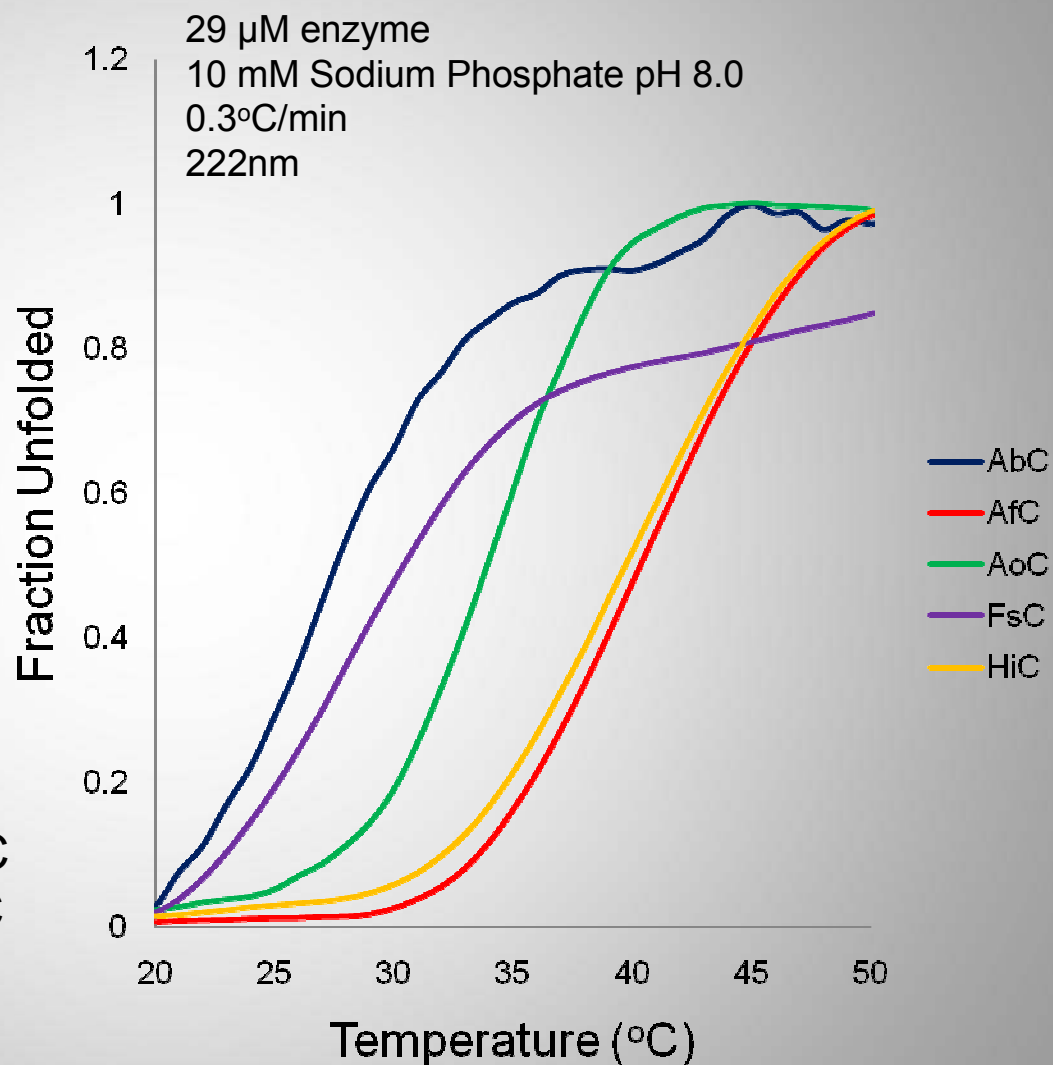


# Biophysical Properties at pH 3.0

	$T_m$ (°C)	$\Delta H$ (kJ/mol)
AbC	26	425.31
AfC	39	604.42
AoC	35	593.72
FsC	27	314.13
HiC	38	328.50

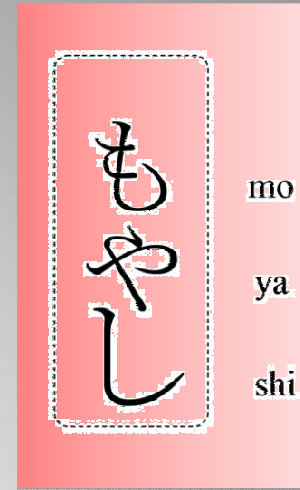
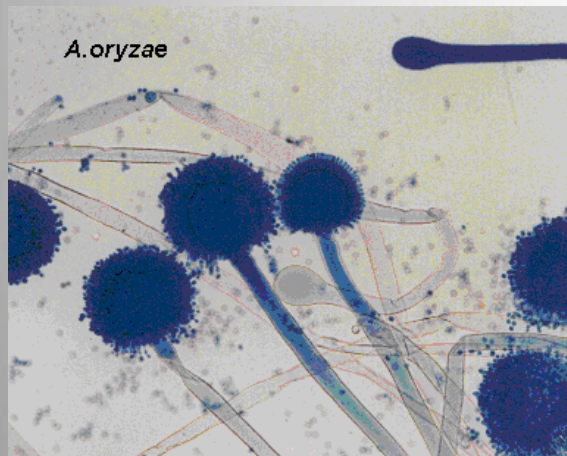
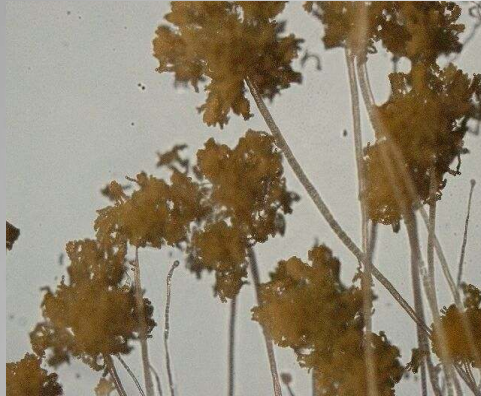
$T_m$ : AfC > HiC > AoC > FsC > AbC

$\Delta H$ : AfC > AoC > AbC > HiC > FsC





# Exploration of *Aspergillus oryzae*



## *Aspergillus oryzae* (koji mold)

- Filamentous fungus in the Japanese fermentation industry for the production sake, soy sauce, and miso
- *A. oryzae* is capable of living in broad range of pH and temperatures
- Fungi is capable of using biodegradable polymers as sole carbon source

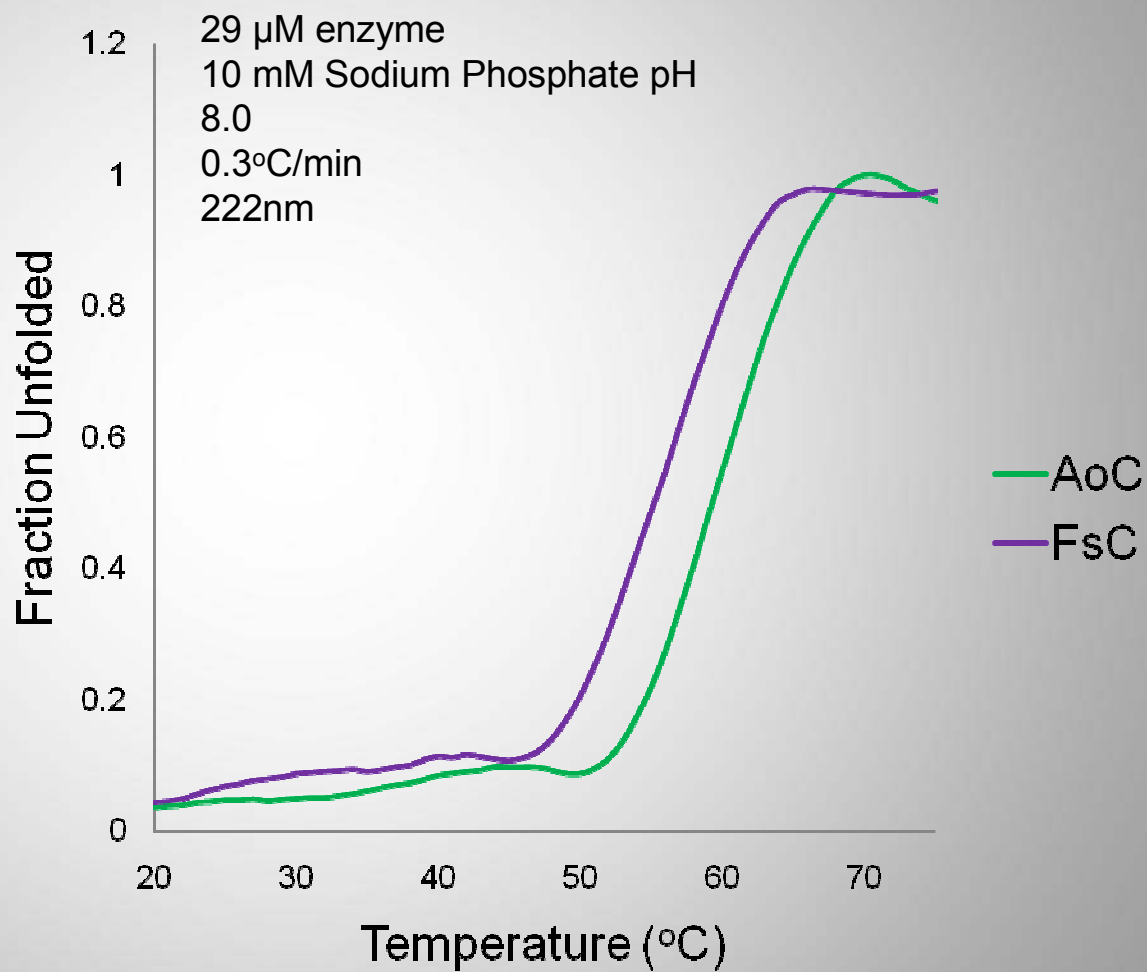
Maeda H., et. al., *Appl. Microbiol Biotechnol.*, **2005**, 778-788

Machida M., et. al., *Nature*, **2005**, 1157-61

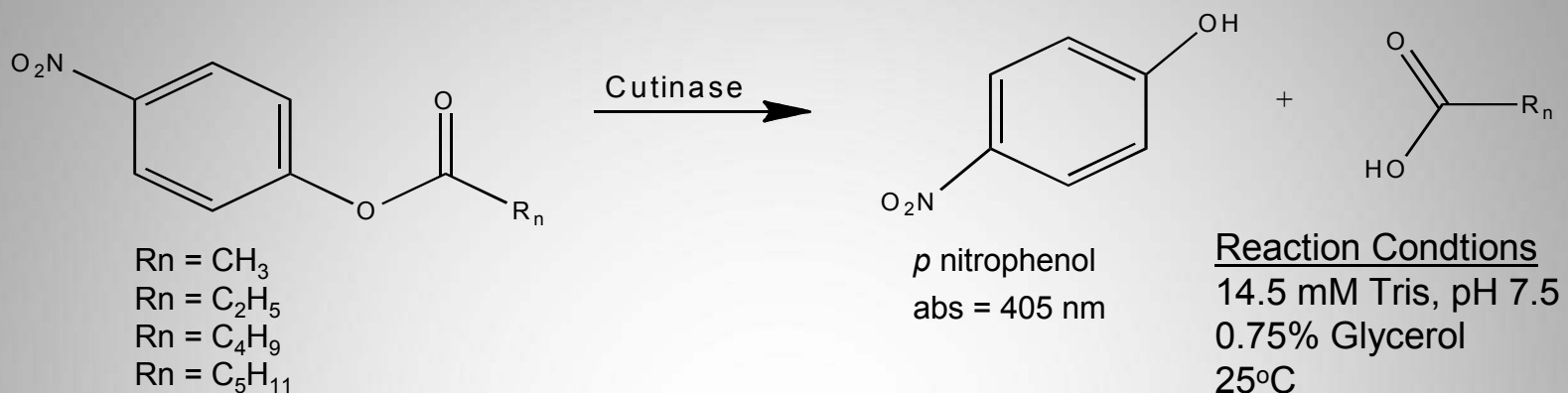
Machida M., et. al., *DNA Research*, **2008**, 173-83

# Comparison of FsC and AoC

	$T_m$ (°C)
AoC	58
FsC	56



# Kinetic Comparison of FsC & AoC

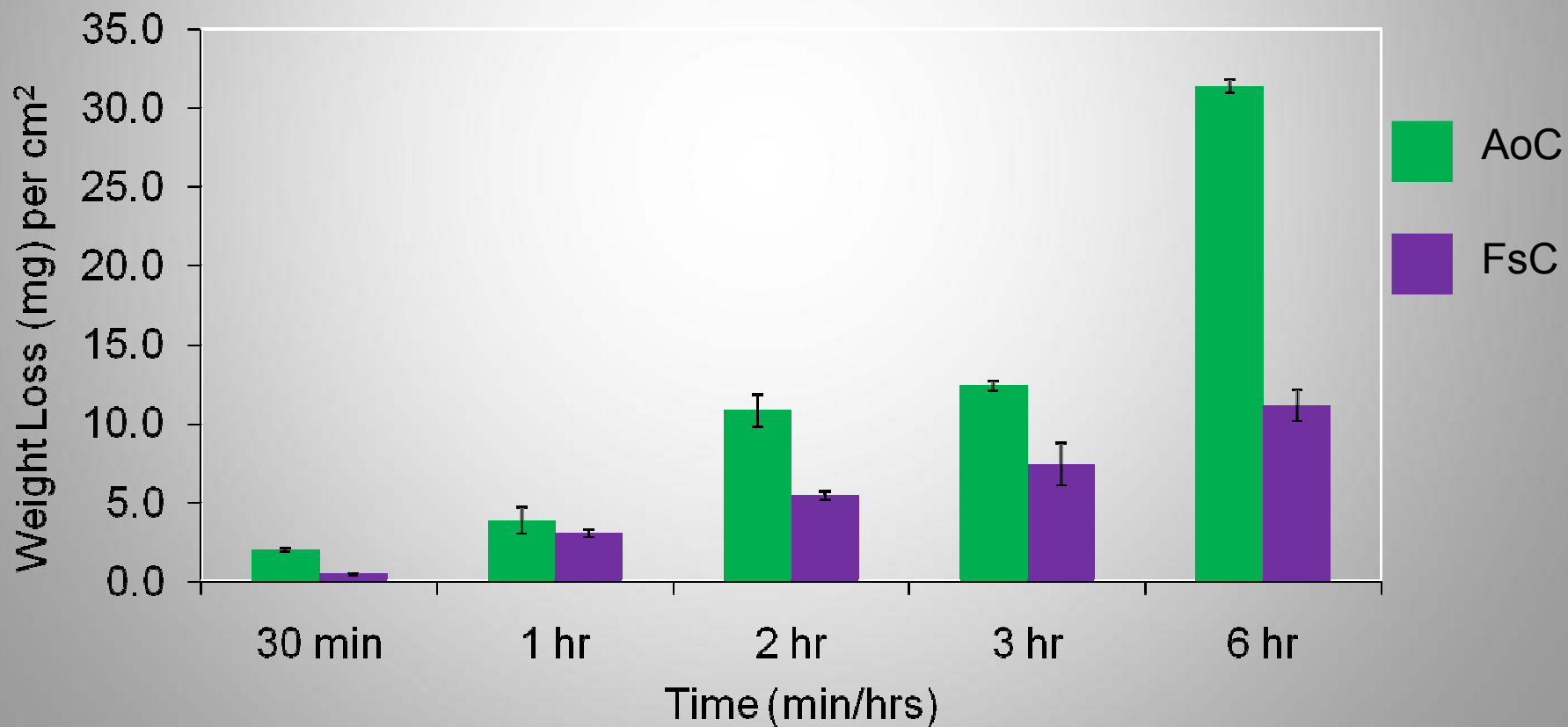
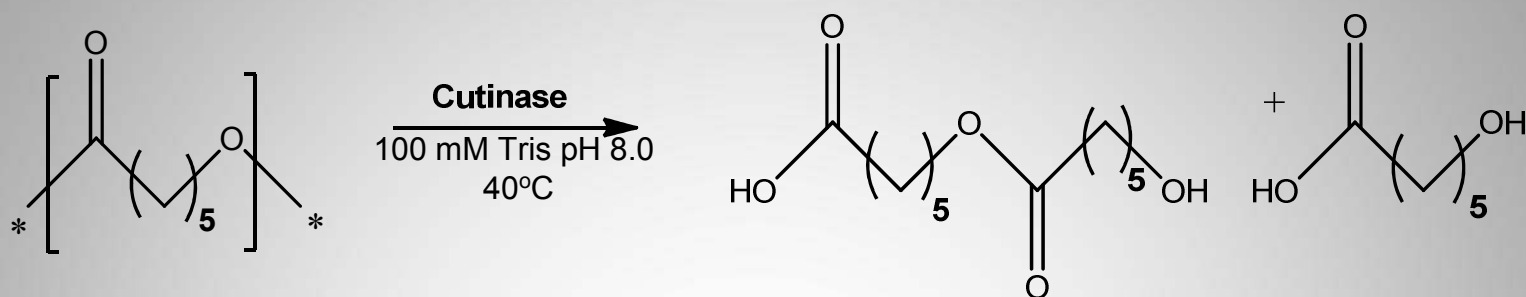


$K_m$ ( $\mu\text{M}$ )	pNPA	pNPB	pNPV	pNPH
FsC	$0.67 \pm 0.23$	$1.26 \pm 0.28$	$1.48 \pm 0.56$	$1.50 \pm 0.19$
AoC	$4.96 \pm 0.11$	$0.21 \pm 0.04$	$0.04 \pm 0.01$	$0.29 \pm 0.09$

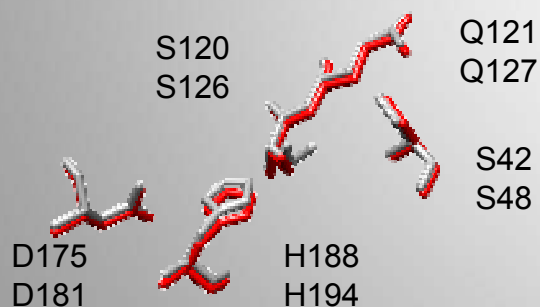
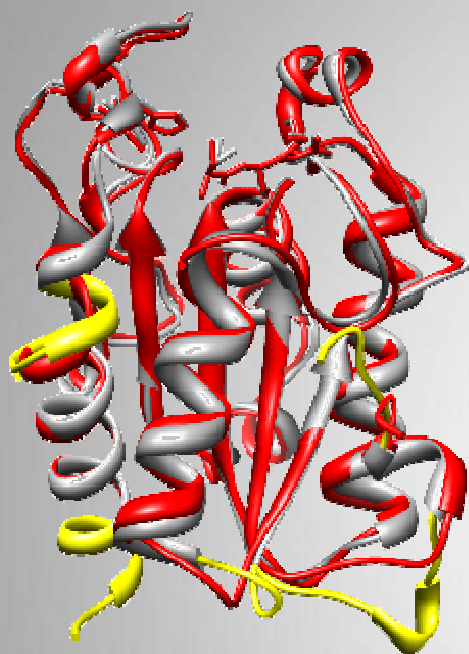
$k_{\text{cat}}/K_m$	pNPA	pNPB	pNPV	pNPH
FsC	$2.53 \pm 1.11$	$0.26 \pm 0.06$	$0.61 \pm 0.40$	$0.14 \pm 0.02$
AoC	$0.07 \pm 0.01$	$3.49 \pm 0.51$	$3.32 \pm 0.74$	$1.34 \pm 0.48$

AoC has a higher affinity towards the more hydrophobic substrates  
 AoC is more active towards the more hydrophobic substrates

# Poly( $\epsilon$ -caprolactone) degradation



# Backbone Comparison of FsC & AoC



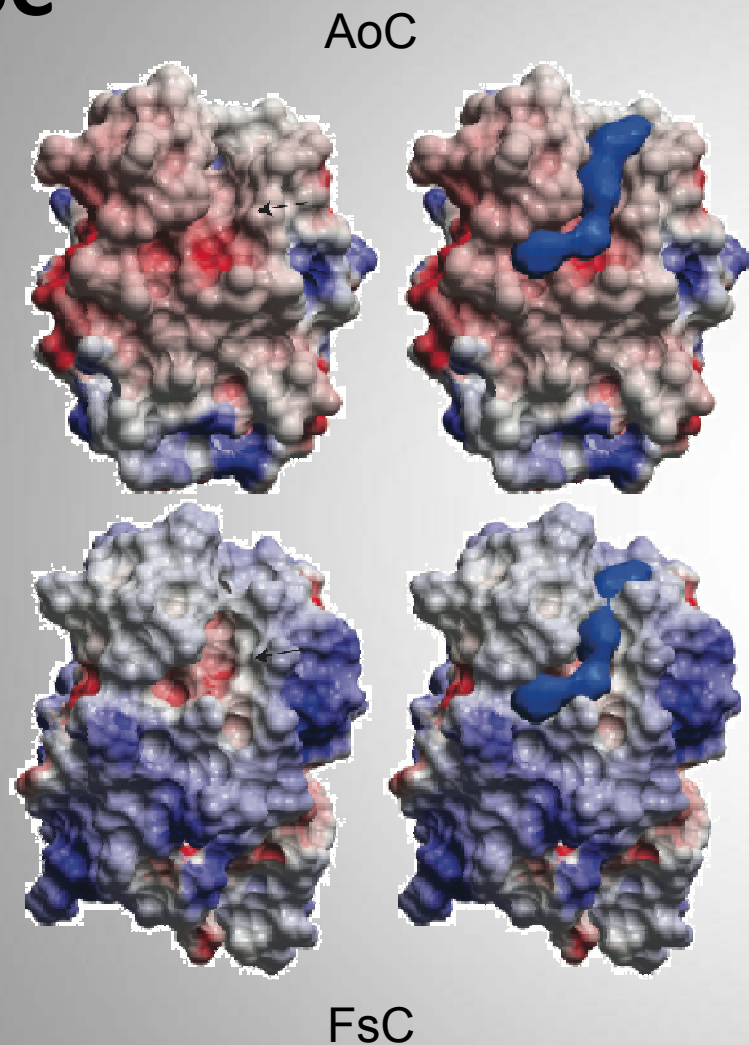
Overlay of active site

## Superposition of AoC (red) and FsC (grey)

- Crystal structure was determined at 1.75 Å
- Overall rms deviation 1.02Å
- Main chain deviation 0.87Å
- AoC shorter in sequence than FsC
- AoC has one less  $\beta$ -strand than FsC
- An extra disulfide bond between Cys63-Cys76

- Backbone orientation and distances between the catalytic residues is similar

# Comparison of Groove by Active site for FsC and AoC



- Distinguishable long and deep groove in AoC active site relative to FsC
- Although the sequence of catalytic site is conserved, the geometric arrangements of the hydrophobic regions are different

# Conclusion

- Identified, expressed and characterized genetically distinct cutinase species
- Although these species exhibit similar structural similarities, they present different activities, thermostability and thermodynamics as a function of pH
- Cutinase from *Aspergillus oryzae* demonstrates a higher affinity towards more hydrophobic substrates, this increased affinity is correlated to the protein surface of the enzyme
- Cutinase from *Aspergillus oryzae* is capable of degrading bioplastics

# Acknowledgements

## Montclare Lab

- Jin K. Montclare
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- Susheel Kumar
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- Yogesh Tengarai Ganesan
- Carlo Yuvienko

\*Zhejiang University of Technology

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- Jeremy Minshull

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- Wenhua Lv
- David Feder

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- Grium Alemu
- Ziyang Lu

## NYU

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- Huiguang Li
- Glenn Butterfoss

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