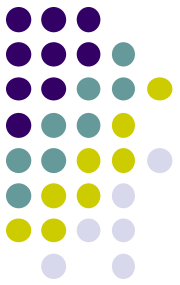


Basic characteristics of the most important enzymes for technological applications

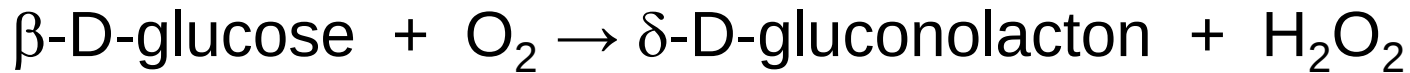
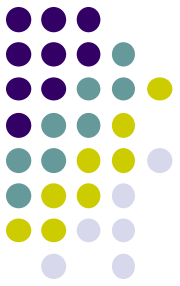


Oxidoreductases

- catabolism, respiration, bioenergetics
- Mostly intracellular, bound to the structures

Glucose oxidase, peroxidase, catalase, lipoxygenase, polyphenol oxidase, lactoperoxidase, xanthin oxidase, ascorbate oxidase etc.

Glukose oxidase, β -D-glucose: O_2 1-oxidoreductase,
EC 1.1.3.4 (notatin)



Present in fungi *Aspergillus*, *Penicillium*, insects etc.

Properties: Mw 130 -175 kDa, 2 identical subunits,

Cofactor FAD (prosthetic group), Fe

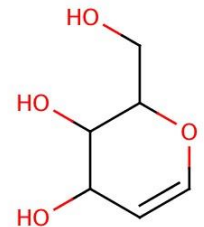
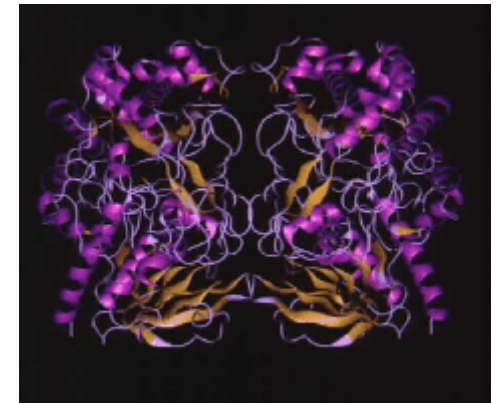
Glycoprotein: 11-13 % of neutral saccharides (mannose),

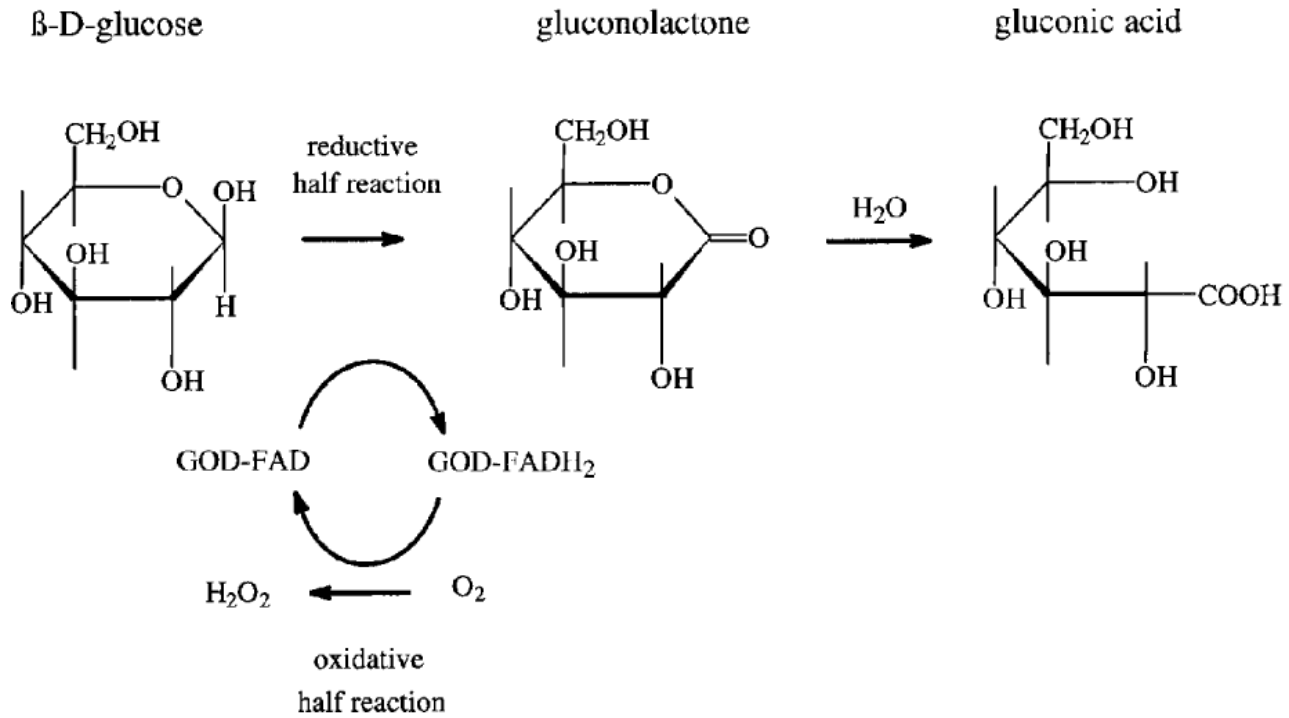
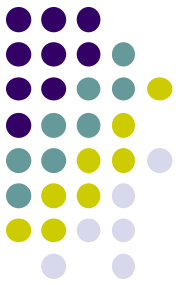
2% aminosaccharides

pH optimum: 5,5 – 5,8, pI = 4,2

Inhibitors: Ag^{2+} , Hg^{2+} , Cu^{2+} , D-glucal, H_2O_2 (E-FADH₂ 100x higher)

Physiological function: production of H_2O_2 - antibacterial and antifungicide effect





Specificity

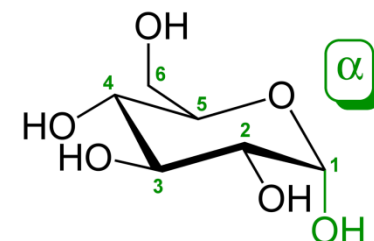
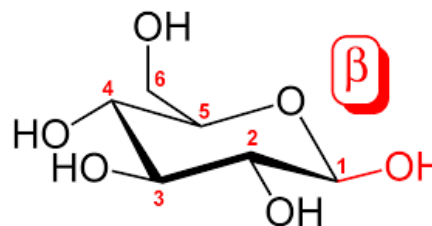


Substrate	Relative rate of oxidation (%)
β -D-glucose	100
α -D-glucose	0,64
L-glucose	0
D-mannose	1,0
D-xylose	1,0
D-galactose	0,5
maltose	0,2
melibiose	0,1
cellobiose	0,09

2-deoxy-D-glucose (20–30%), 4-O-methyl-D-glucose (15%), 6-deoxy-D-glucose (10%)

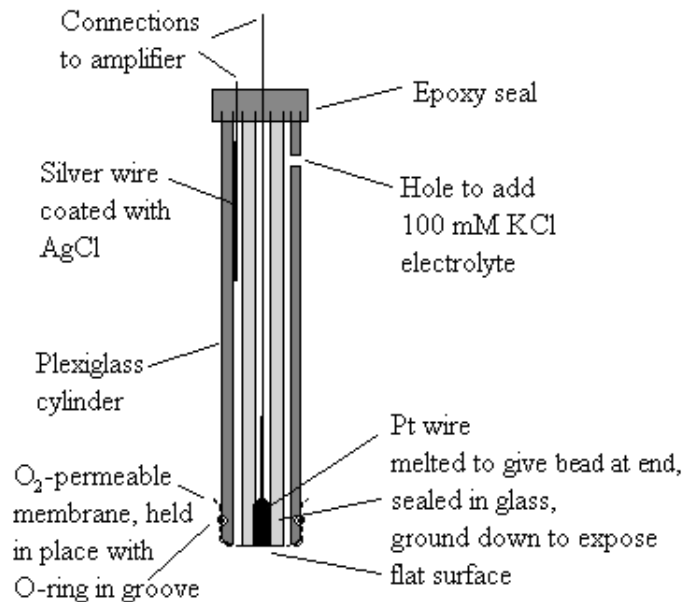
Structural characteristics of the substrate:

- pyranose ring in chair conformation
- equatorial –OH on C3 atom



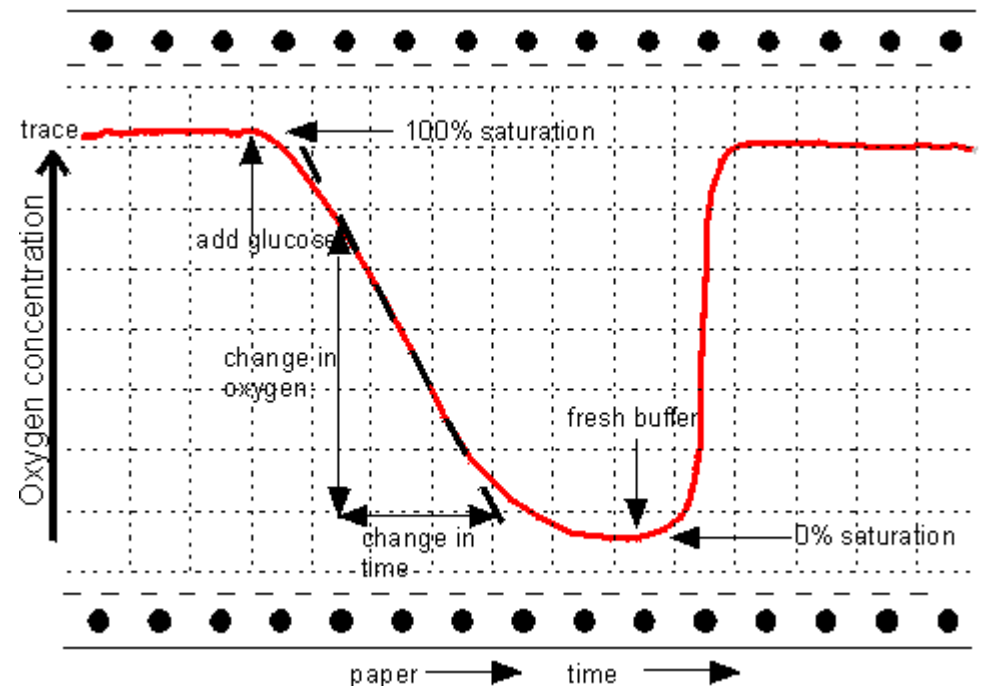
Determination of GOD activity

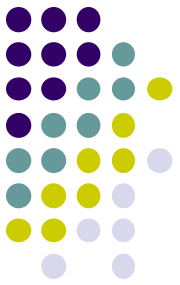
1. Consumption of oxygen (Clark oxygen electrode)
2. Determination of hydrogen peroxide
3. Titration of gluconic acid



Ag anode: $4\text{Ag} + 4\text{Cl}^- \rightarrow 4\text{AgCl} + 4\text{e}^-$

Pt cathode: $\text{O}_2 + 4\text{H}^+ + 4\text{e}^- \rightarrow 2\text{H}_2\text{O}$





1. Consumption of oxygen (Clark oxygen electrode)

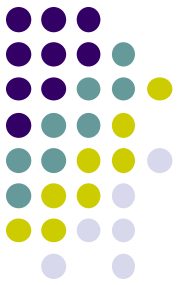
2. Determination of hydrogen peroxide

3. Titration of gluconic acid

Classical methods: oxidation of I^- , ferrocyanide

Enzymatic – POD + chromogenic acceptor – spectrometry VIS

(o-dianisidine, 2, 2'-Azino-di-[3-ethylbenzthiazolin-sulfonate] - ABTS etc.)



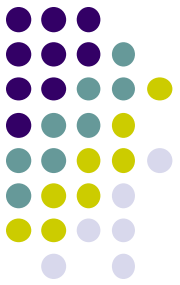
Applications of glucose oxidase

- Removal of glucose (Maillard's reactions)
- Removal of oxygen (from packed foods or beverages)
- Preparation of gluconic acid (food, concrete)
- Production of hydrogen peroxide
- Quantitative determination of glucose or other compounds which can be converted to glucose (saccharose, starch ...)
- Activity determination of enzymes producing glucose (invertase, amylase etc.)

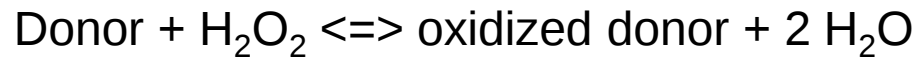
Oxidoreductases catalyzing decomposition of hydrogen peroxide

catalase

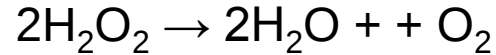
peroxidase

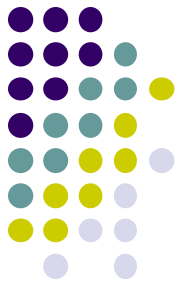


Peroxidase:



Catalase





Peroxidases EC 1.1.11.1 - 21 (mostly heme enzymes)

1. **Animal** - lactoperoxidase, myeloperoxidase – antimicrobial activity

2. **Plant and microbial**

Group I: intracellular (yeast cyt c POD, chloroplastic, cytosolic ascorbate POD and bacterial POD)

Group II: extracellular fungal (Fungi) LiP, MnP, LiP/MnP : ligniperoxidous fungi

Group III: extracellular plant (horse radish – HRP , ascorbate peroxidase - APX)
+ haloperoxidases (CPO) – formation of halogenderivatives of org. compounds - antimicrobial effect

Application of peroxidases:

1. Analytics
2. label in immunochemistry
3. Biotransformations - hydroxylations
4. Biodegradation of polyphenols (dyes, PCB)
5. Biochemical changes in food raw materials

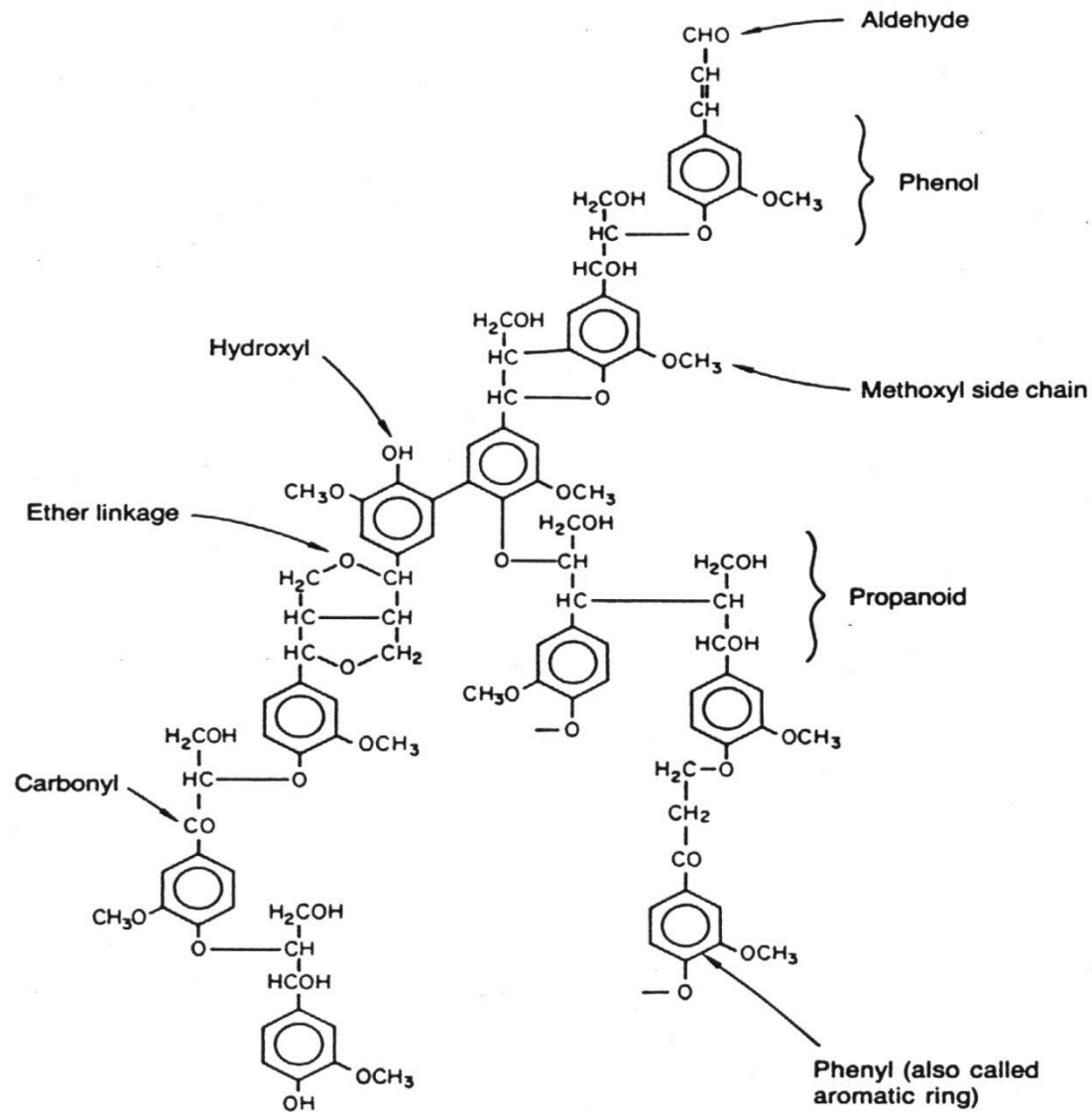
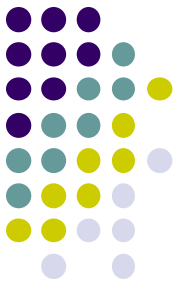


Serpula lacrymans-the dry rot fungus

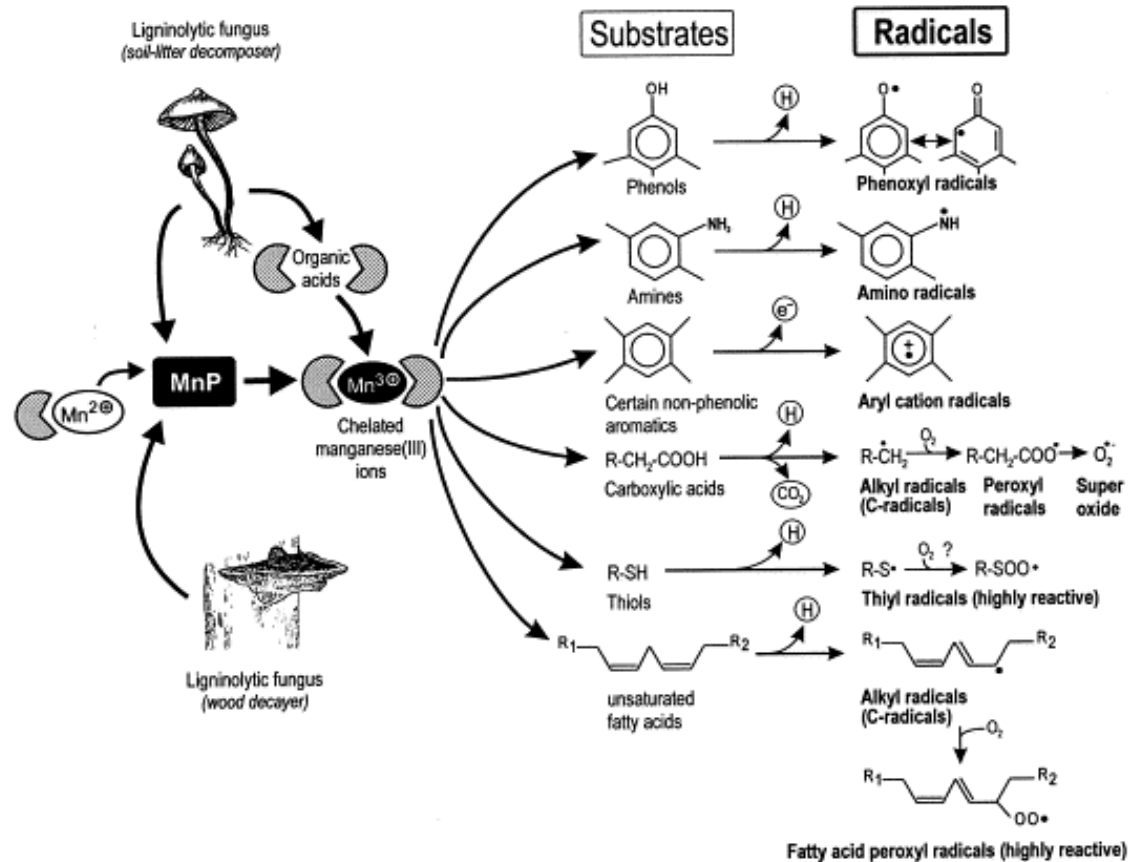


Gloeophyllum trabeum

Lignine structure – substrate for fungal peroxidases



Lignin and mangan peroxidases:



Low stability- heme oxidation by the reaction products - radicals
 Low production – response to the low content of nutrients

Lipoxygenase, EC 1.13.11.12

Linoleate:O₂ oxidoreductase,
(Lipoxidase, caroten oxidase)

Specific for **pentadiene** conformation

In all eukaryots

Isoenzymes

Classified according to the site of
oxidation

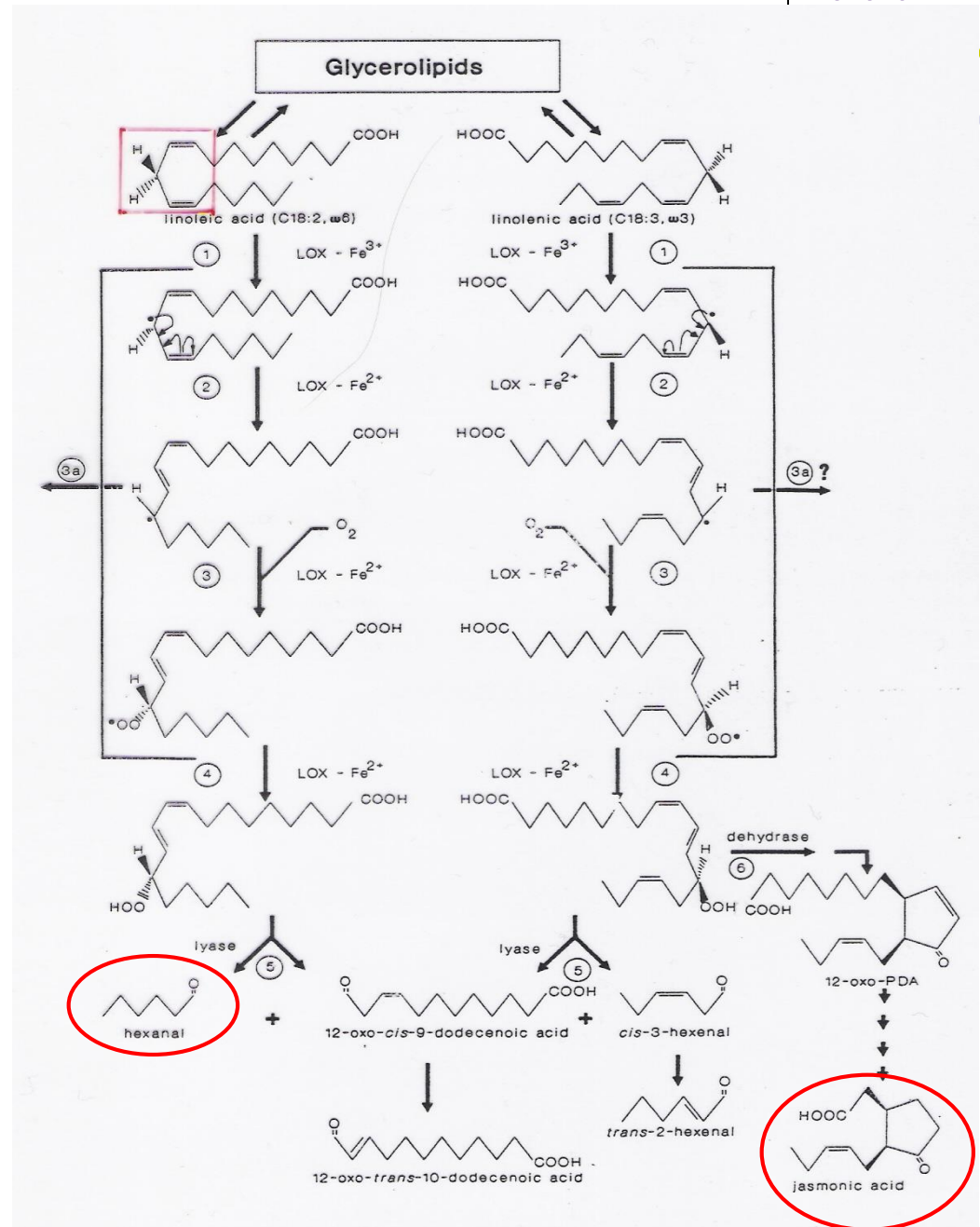
9-LOX, 13-LOX

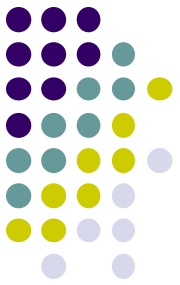
Substrate: linoleic, linolenic,
arachidonic acid

Co-oxidation reaction

Activity determination:

1. Consumption of O₂
2. UV absorbancy of dienoic structure
formed (234 nm)





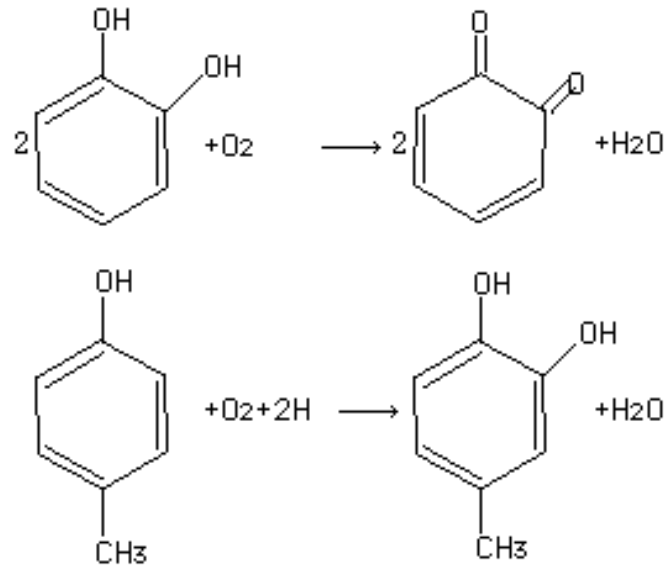
Other oxidoreductases:

Polyphenol oxidase, EC 1.10.3.1, o-diphenol: O_2 oxidoreductase

Tetramer containing 4 atoms of Cu^{2+}

Catalyzes 2 types of reactions:

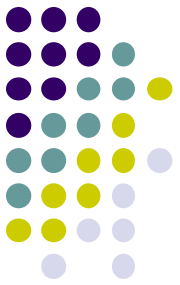
1. Formation of o-quinones
2. Formation of polyphenols



Tyrosinase, phenol oxidase EC 1.14.18.1

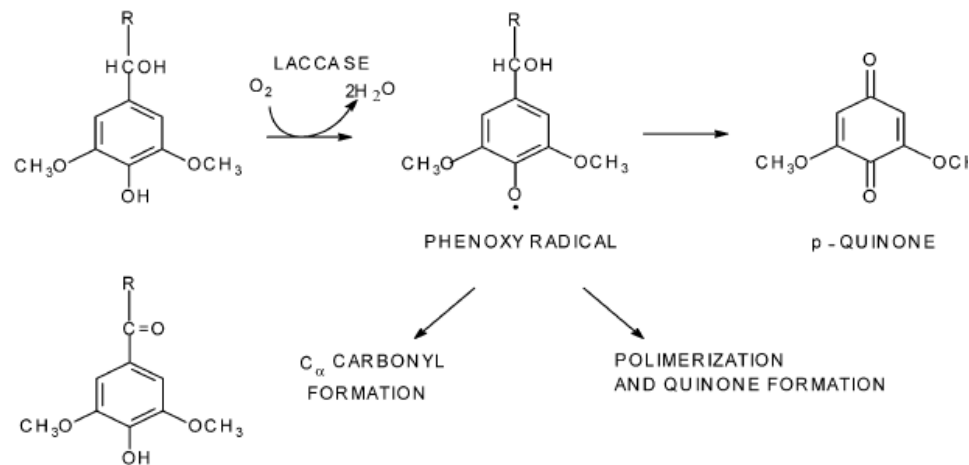
Catechol oxidase, cresolase ...





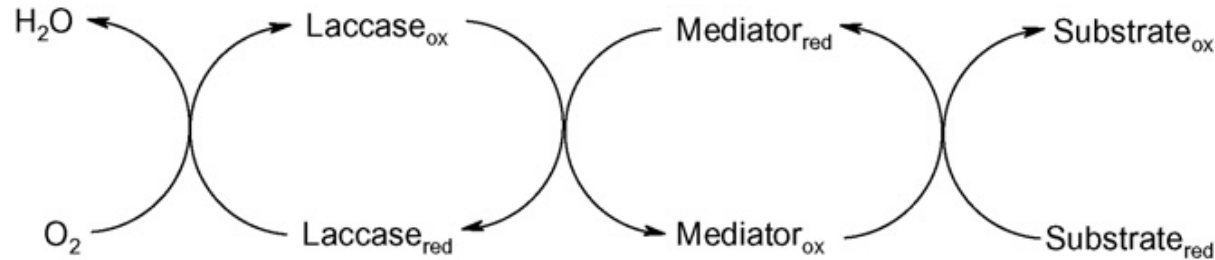
Laccase EC 1.10.3.2 – bacteria, fungi, plants

Substrates: 4-benzene diol , wide specificity, polyphenols, substituted polyphenols, diamines and many other **but not tyrosine**

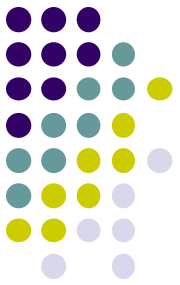


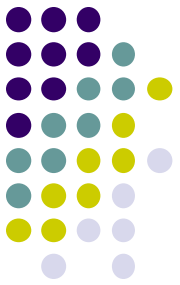
Application: textile, paper, wood industry, bioremediations, wine production, canning and sugar industry

Lignine degradation by laccase:



- Laccase (70 kDa) cannot penetrate into wood
- Not able to oxidize (low redox potential ~0.5 -0.8V) non-phenolic lignin units (redox potential >1.5V)
- Oxidizes only phenolic units – less than 20% in wood
- Applied together with **oxidation mediator** – small molecules (LMS) capable to oxidize non-phenolic components of lignin and overcome the accessibility problem

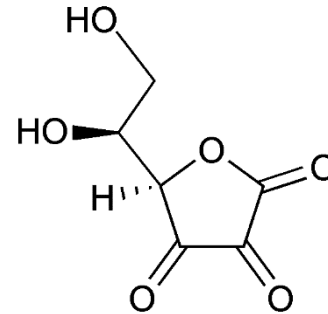
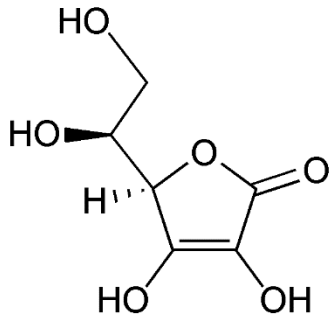




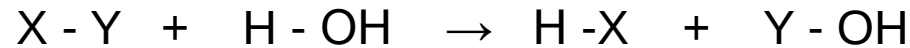
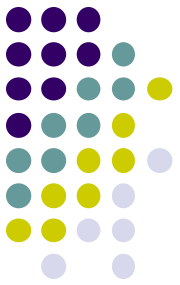
Ascorbate oxidase, EC 1.10.3.3, ascorbate:O₂ oxidoreductase

8 Cu²⁺, plants

Ascorbic acid + O₂ ----->. Dehydroascorbic acid + H₂O



Hydrolases

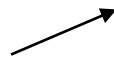


Nomenclature: classification according to the type of splitted bond

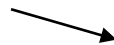
In technology according to the type of the substrate:

Proteases

Glycosidases



Glucopolysaccharides
(starch degrading enzymes)

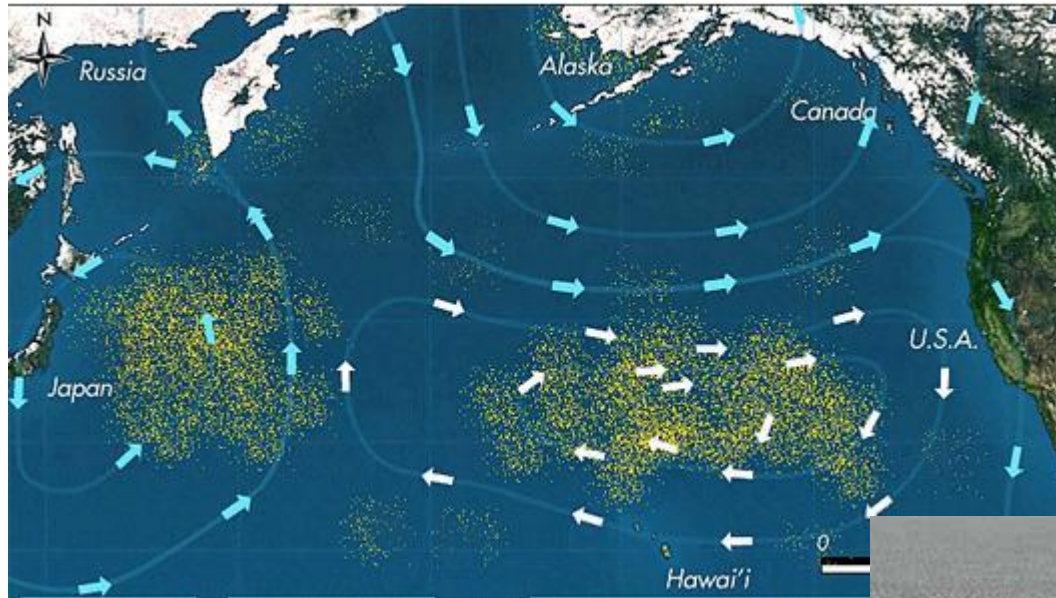
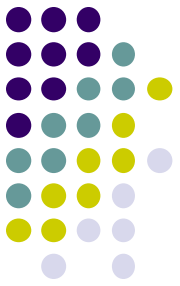


Pectic compounds,
hemicelluloses, cellulose

Lipases,
Phospholipases

Others - ie. esterases, aminoacylases

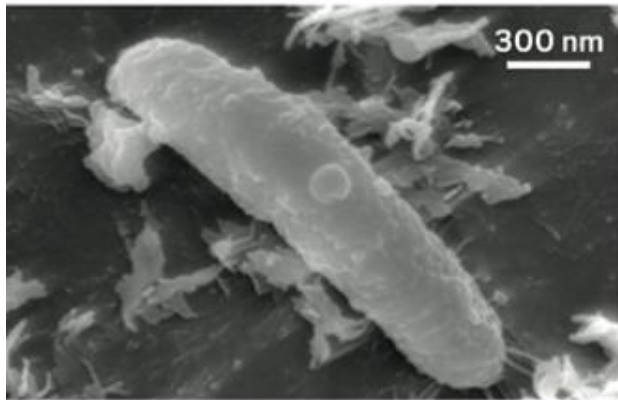
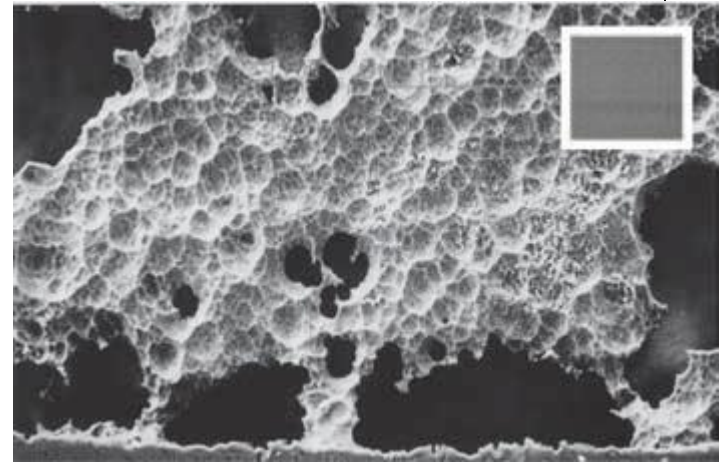
Discovery of new enzyme in 2016!!



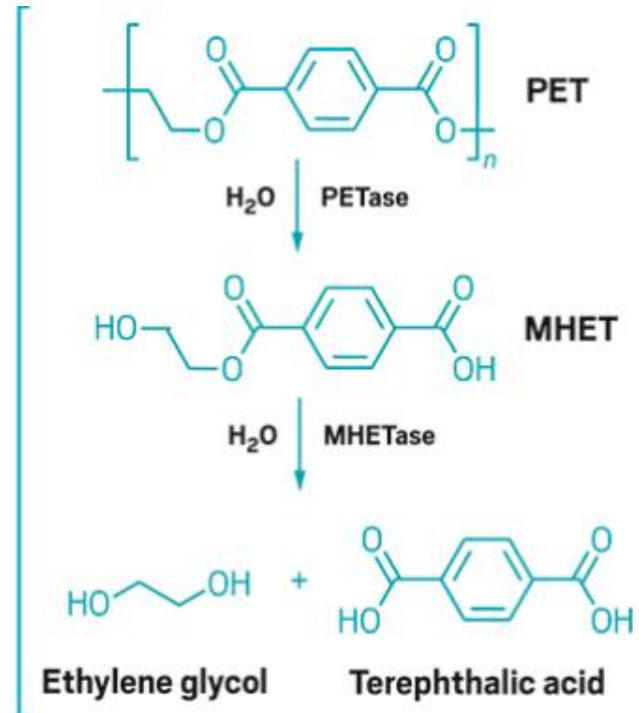
PETase EC 3.1.1.101

Bacteria *Ideonella sakaiensis*

Genetically engineered mutant enzyme



Ideonella sakaiensis



polyethylene furanoate - PEF

Proteases

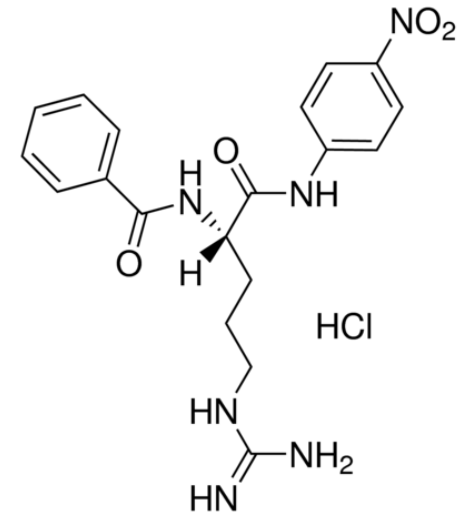


Classified according to different aspects:

1. Origin
2. localisation in organisms, inactive forms
3. pH optimum
4. Specificity (endo, exo)
5. Mechanism of catalysis -

Activity determination:

- Natural substrates (hemoglobin, casein), UV determination
- Natural substrates with adsorbed dyes, VIS
- Synthetic substrates – BAPA, VIS
- Others – washing tests

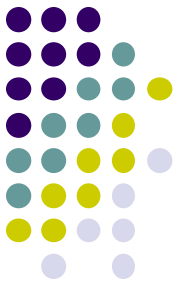


*N*_α-Benzoyl-L-arginine 4-nitroanilide hydrochloride

Animal proteases

Serine - trypsin, chymotrypsin

Aspartate - pepsin, chymosin



Chymotrypsin

pH optimum: ~ 8,0

Specificity: preferentially peptide bond behind aromatic AA

Trypsin

pH optimum: ~ 8,0

Specificity: Arg, Lys

Pepsin

pH optimum 1,0 - 2,0

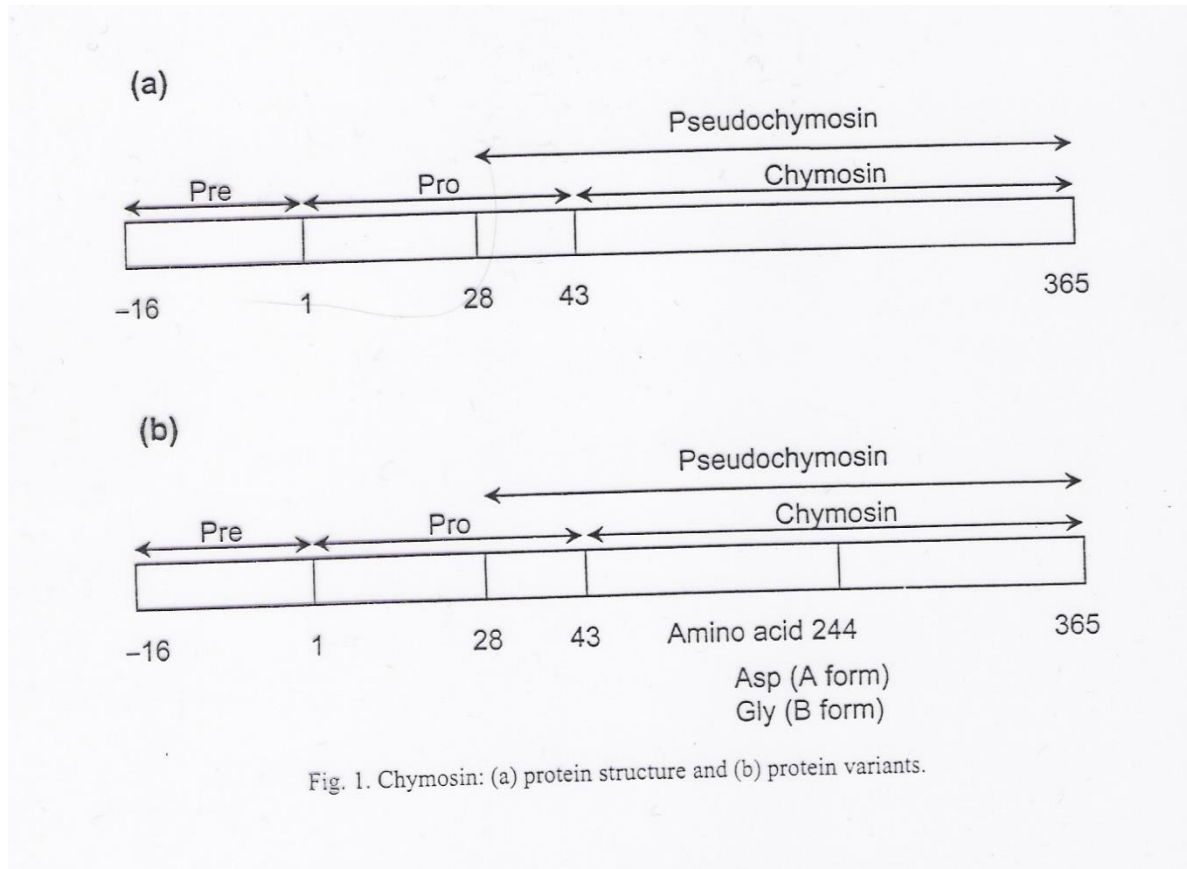
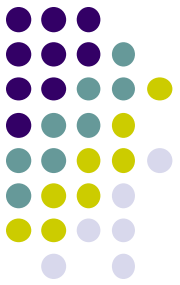
hydrophobic, preferably aromatic AA residues

Application: pharmaceuticals (digestives, treatment of injuries, post operational treatment etc, Wobenzym)

Chymosin (rennin), EC 3.4.23.4

Autocatalytic activation - pH 5 $\rightarrow$ chymosin

pH 2 $\rightarrow$ pseudochymosin

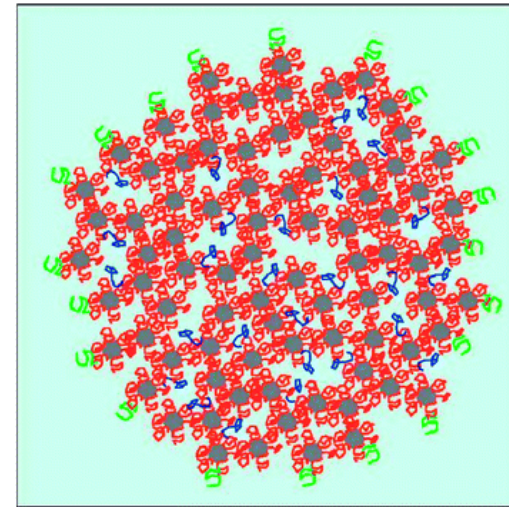


Chymosin

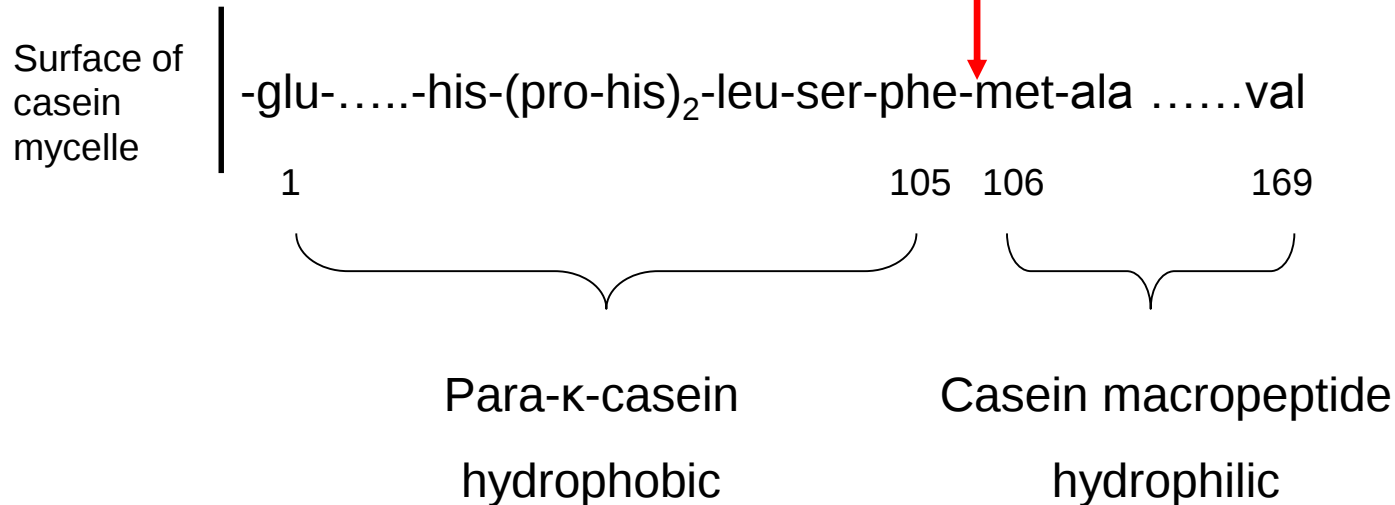
Aspartate protease,
pH optimum 3,5 - 6,5

Specificity: κ -casein

Casein mycelles



K-casein
 β -casein
 α -S1, S2



Recombinant: mRNA from calf abomasum - production MO - E.coli, B. subtilis, S.cerevisiae, K. lactis, A. niger

Plant proteases

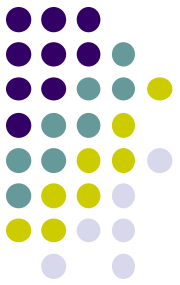


Papain	}	latex from <i>C. papaya</i> , 5-8%, zymogen
Bromelain		SH-proteases, wide specificity,
Ficin - preferentially		-Tyr , Phe
Actinidin		
Cardosin (cynarase)		aspartate protease



Cardoon –
***Cynara cardunculus* L**

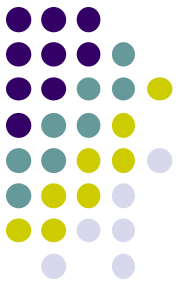
Microbial proteases



MIKROBIÁLNÍ PROTEASY

Mikroorganismus		serinové	SH-	aspartátové	metalo
Bacillus	alcalophilus	+			
	amyloliquefaciens	+			
	amyloliquefaciens	+			
	licheniformis	+		+	
	lentus				+
	polymixa				+
	subtilis				+
	thermoproteolyticus				+
	thermoproteolyticus				+
Aspergillus	flavus	+			
	melleus	+			
	oryzae	+		+	+
	niger			+	
	saitoi			+	
	sojae			+	
Endothia parasitica				+	
Mucor miehei				+	
Mucor pusillus				+	
Penicillium sp.				+	
Rhizopus delemar				+	
Clostridium sp.					+
Streptomyces griseus					+

Microbial proteases - characteristics



■ Bacterial (Bacillus)

Neutral - metalloproteases, serine proteases

pH 5 – 8, low thermotolerance (advantageous for protein hydrolysates)

not inhibited by plant proteinase inhibitors (STI - antinutritional)

specificity – hydrophobic AA

Thermolysine - Zn^{2+} metalloprotease from *B. thermoproteolyticus*, stabilised by Ca^{2+} at higher temperature (1h, 80 °C, 50% of activity) – production of Aspartam

Alkaline - pH optimum ≈ 10 , temp. optimum ≈ 60 °C (suitable for biodetergents)

wide specificity (from alkaliphilic or alkalitolerant MO)

Subtilisin – alkalic serine protease from *B. amyloliquefaciens*, 27.5 kDa, type Carlsberg and BPN

cat. triade Asp32,His61,Ser221

Protein engineering: mutation of 50% of AA from 275

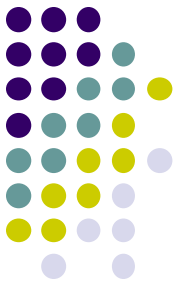
↑activity, – SDM Met222xSer, Ala

changing specificity by mutations in the binding site

↑thermostability – introduction of S-S bridges

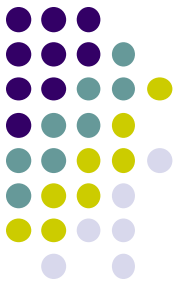
↑stability in alkalic solutions

↓autoproteolytic activity



- **Fungal** – acidic, neutral, alkalic, metallo,
extracellular
wide range of pH optima 4 – 11
wide specificity, lower thermotolerance

Aspergillus, Penicillium, Cephalosporium, Trychoderma...



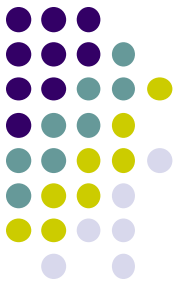
Glycosidases

Hydrolyse glycosidic bonds in homo- and heteroglycosides

Factors affecting the specificity of glycosidases

- configuration of the saccharide (D-, L-, α -, β -)
- character of the cyclic form (furanose, pyranose)
- character of aglycone, character of the atom in glycosidic bond
- size of the saccharide molecule

Determination of the glycosidase activity



- Increase of the reduction potential of the products
- Changes of the physical properties of the substrates (viscosity)
- Change of the optical rotation (polarimetry)
- Colorimetry or fluorometry using dyed polysaccharides
- Special methods (enzymatic)

Glycosidases



➤ Starch degrading enzymes

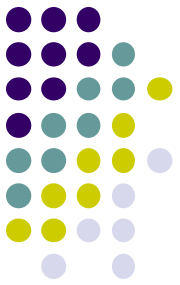
Endoamylases	α -amylase (α -1 $\rightarrow$ 4) GH13	}	Specific cleavage from non-reducing end of oligo- or polysaccharide
Exoamylases	β -amylase (α -1 $\rightarrow$ 4) GH14		
	Glucoamylases (α -1 $\rightarrow$ 4 and α -1 $\rightarrow$ 6)		
	α -glucosidases (α -1 $\rightarrow$ 4 and α -1 $\rightarrow$ 6)		
Debranching enzymes	pullulanases (α -1 $\rightarrow$ 6)		
	Isoamylases (α -1 $\rightarrow$ 6)		
Transferases	Cyclodextrin glycosyltransferase (α -1 $\rightarrow$ 4)		
	Branching enzyme (α -1 $\rightarrow$ 6)		

➤ Celulolytic enzymes

➤ Pectolytic enzymes

➤ Invertase, β -galactosidase

Glycosidases are classified according to structural similarities



B.Henrissat: Glycosidase families
Biochem Soc Trans. (1998) 26,153-6



Carbohydrate-Active enZymes Database
<http://www.cazy.org>

CAZY - GH13

www.cazy.org/GH13.html

CAZY CARBOHYDRATE-ACTIVE ENZYMES

HOME ENZYME CLASSES ASSOCIATED MODULES GENOMES

Glycoside Hydrolases Glycosyltransferases Polysaccharide Lyases Carbohydrate Esterases Auxiliary Activities

Glycoside Hydrolase Family 13

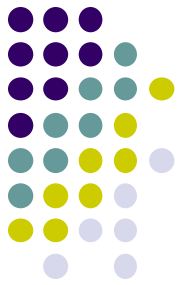
GH13 Go GH13_1 Go

Activities in Family	α-amylase (EC 3.2.1.1) ; pullulanase (EC 3.2.1.41) ; cyclomaltodextrin glucanotransferase (EC 2.4.1.19) ; cyclomaltodextrinase (EC 3.2.1.54) ; trehalose-6-phosphate hydrolase (EC 3.2.1.93) ; oligo-α-glucosidase (EC 3.2.1.10) ; maltogenic amylase (EC 3.2.1.133) ; neopullulanase (EC 3.2.1.135) ; α-glucosidase (EC 3.2.1.20) ; maltotetraose-forming α-amylase (EC 3.2.1.60) ; isoamylase (EC 3.2.1.68) ; glucodextranase (EC 3.2.1.70) ; maltotriose-forming α-amylase (EC 3.2.1.98) ; maltotriose-forming α-amylase (EC 3.2.1.116) ; branching enzyme (EC 2.4.1.18) ; trehalase synthase (EC 5.4.99.16) ; 4-α-glucanotransferase (EC 2.4.1.25) ; maltopentaose-forming α-amylase (EC 3.2.1.1) ; amylomannanase (EC 3.2.1.4) ; sucrose phosphorylase (EC 2.4.1.7) ; maltotetraose-forming α-amylase (EC 3.2.1.141) ; isomaltulose synthase (EC 5.4.99.11) ; maltotetraose-forming α-amylase (EC 5.4.99.15) ; amylase (EC 3.2.1.33) ; α-1,4-glucan: phosphate α-maltosyltransferase (EC 2.4.99.16) ; 6'-P-sucrose phosphorylase (EC 2.4.1.1) ; amino acid transporter
Mechanism	Retaining
Clan	GH-H
3D Structure Status	(β / α) ₈
Catalytic Nucleophile/Base	Asp (experimental)
Catalytic Proton Donor	Glu (experimental)
Note	New: many members have been assigned to subfamilies as described by Stam et al. (2006) Protein Eng Des Sel. 19, 555-562 (PMID: 17085431)
External resources	CAZypedia ; EBI Protein of the Month ; HOMSTRAD ; PDB Molecule of the Month ; PRINTS
Commercial Enzyme Provider(s)	MEGAZYME; PROZOMIX
Statistics	GenBank accession (59277); Uniprot accession (7858); PDB accession (476); 3D entries (112); cryst (2)

Summary

All (54480) Archaea (381) Bacteria (50875) Eukaryota (3094) unclassified (130) Structure (112 - 2 cryst) Characterized (812)

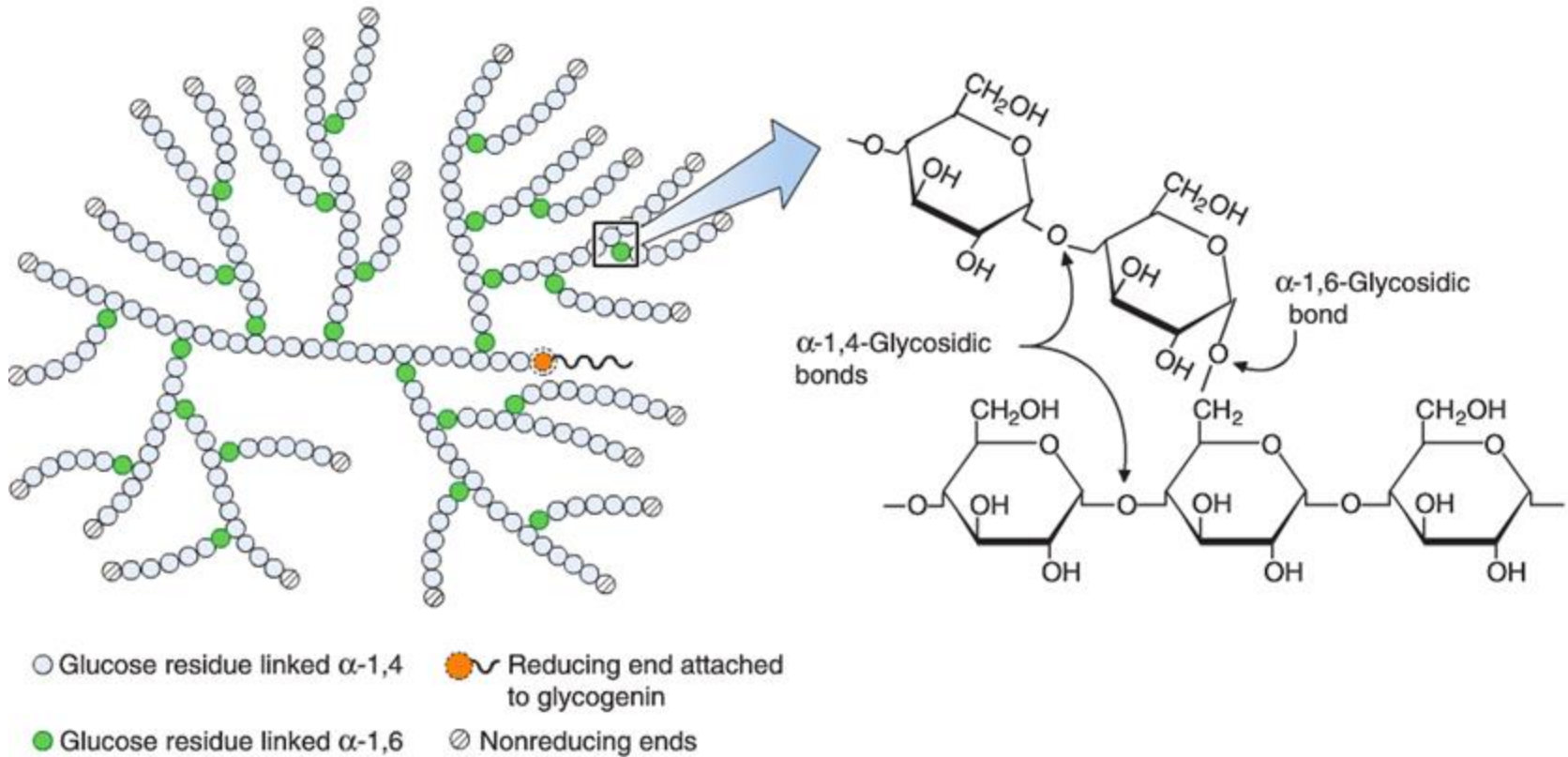
Last update: 2018-03-13 © Copyright 1998-2018
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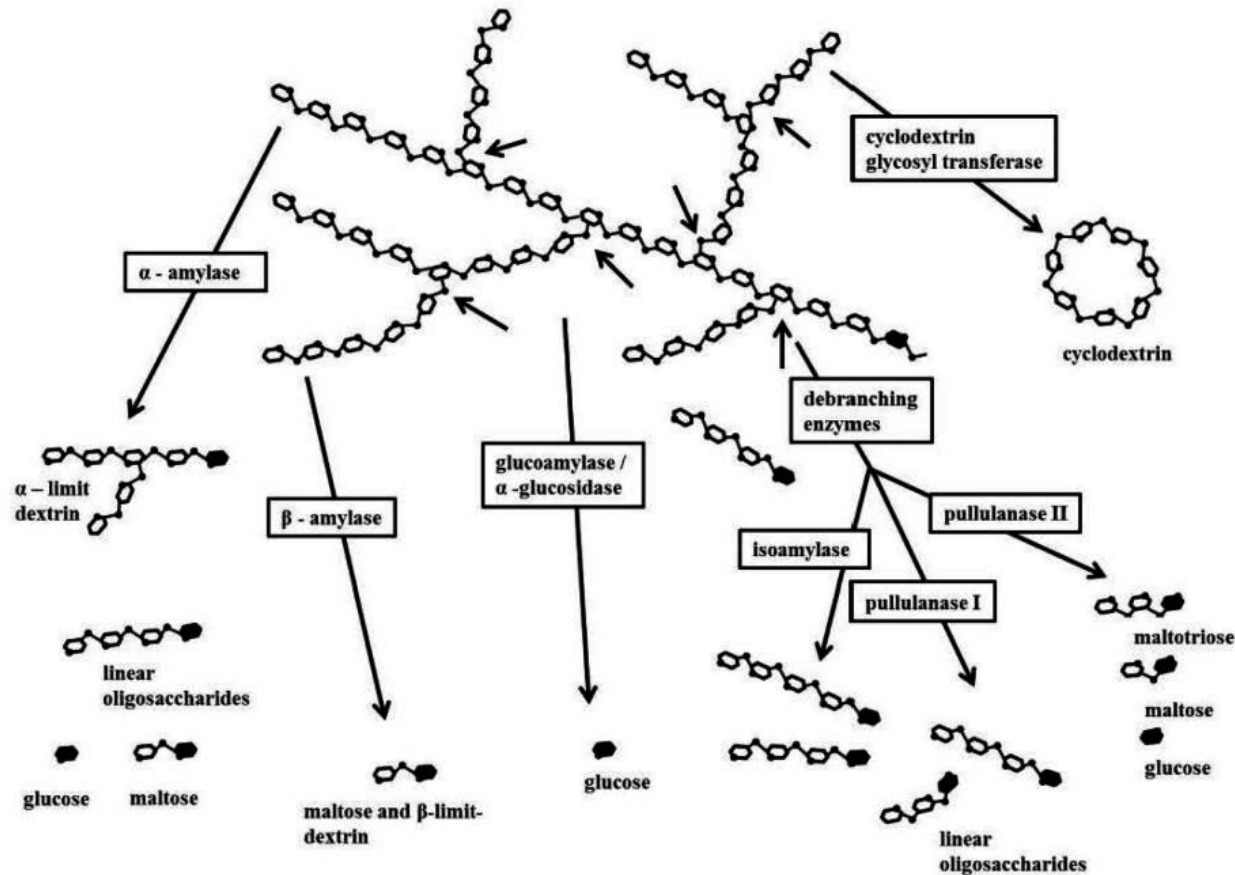
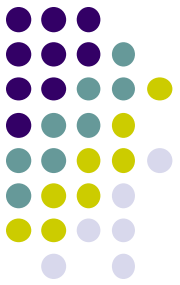
Starch degrading enzymes

Amylose – linear

Amylopectin branched

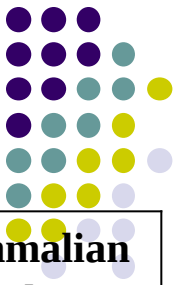


Starch degrading enzymes



Alpha- and beta – limit dextrans

Sources and properties of amylases



Plant α -amylase	Plant β -amylase	Bacterial α -amylase	Fungal α -amylase	Glucos- amylase	Mammalian α -amylase
Barley and malted barley	Barley and malted barley	<i>Bacillus amyloliquefaciens</i>	<i>Aspergillus oryzae</i>	<i>Aspergillus niger</i>	Saliva
Wheat and malted wheat	Soybean sweet potato	<i>Bacillus subtilis</i>	<i>Aspergillus candidus</i>	<i>Rhizopus delemar</i>	Pancreas
Malted sorghum	Wheat	<i>Bacillus licheniformis</i>		<i>Rhizopus niveus</i>	
		<i>Pseudomonas stutzeri</i> (G4 amylase)			

Bacterial - thermostable (110 °C), pH - neutral, Ca^{2+} stabilised by substrate

Fungal - lower temperature stability, specificity of β -amylase



Debranching enzymes

R-enzymes (plant, animal)

Pullulanases (microbial)

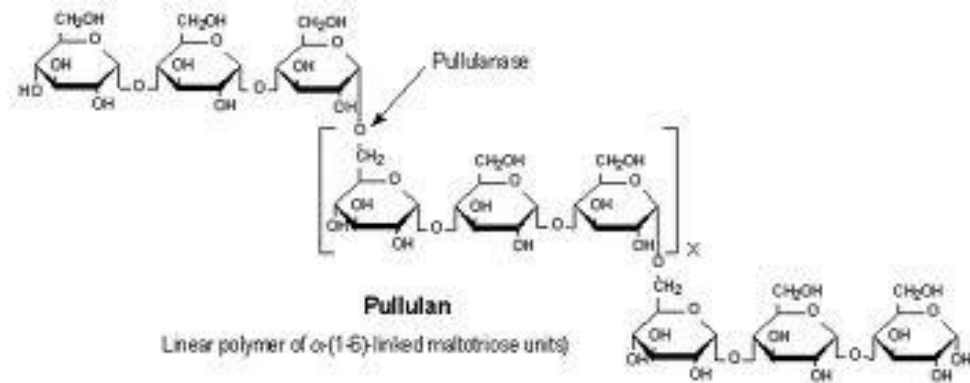
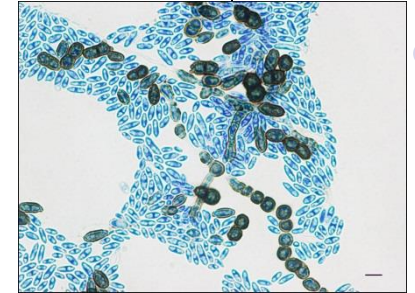
Type I specific for

α -1,6 glycosidic bonds

Type II specific for α -1,6 and α -1,4 glycosidic bonds

Aureobasidium pullulans

Yeast like fungus



Transferase activity

1. Glycosidases in general
2. Amylomaltase (EC 2.4.1.25, forming α -1,4 bonds)
3. Branching enzyme (EC 2.4.1.18, forming α -1,6 bonds)
4. Cyclodextrin glycosyltransferase, (EC 2.4.1.19) *B.macerans*



Cyclodextrins:

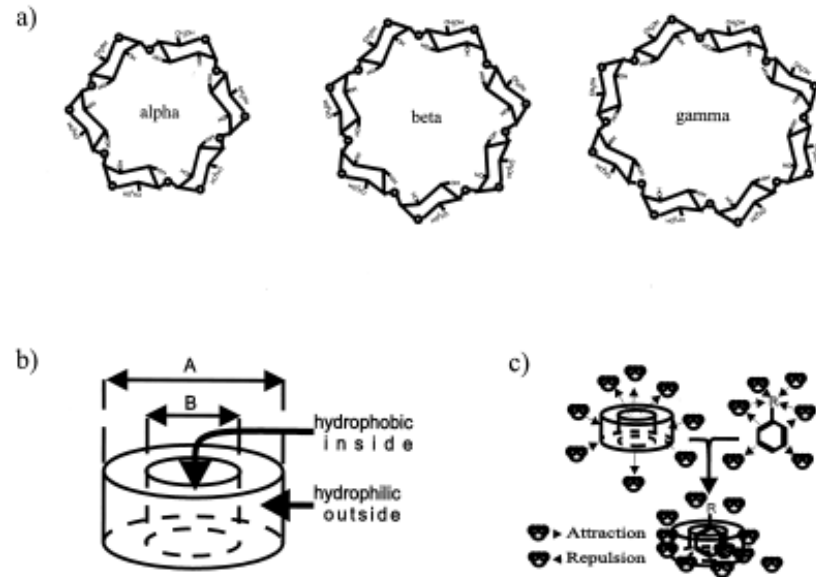


Fig. 1. Structure and properties of cyclodextrins. (a) α -, β -, and γ -cyclodextrins; (b) three-dimensional form and properties of cyclodextrins (for sizes of A and B, see Table I); (c) formation of inclusion complex of a cyclodextrin with a hydrophobic molecule. (Reproduced from Pennings [139].)

Effect of cyclodextrins on the incorporated molecules:

Stabilisation

Lower volatility

Change of chemical reactivity

Increased solubility

Change of sensoric properties

Application:

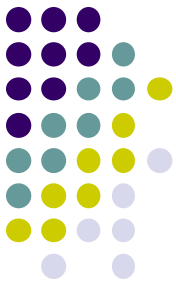
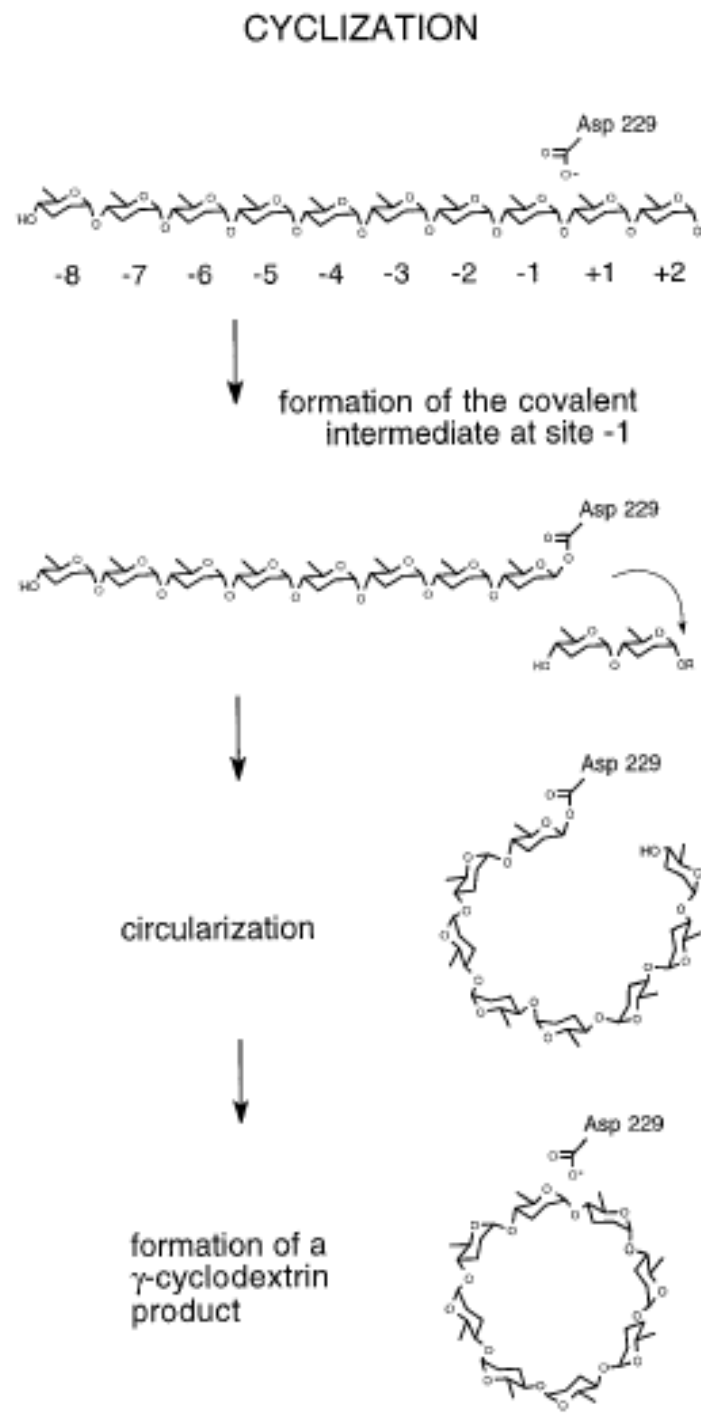
Analytical chemistry

Production of pharmaceuticals (prolonged effect)

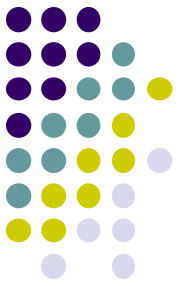
Food industry (additives, aromas etc..)

Cosmetics

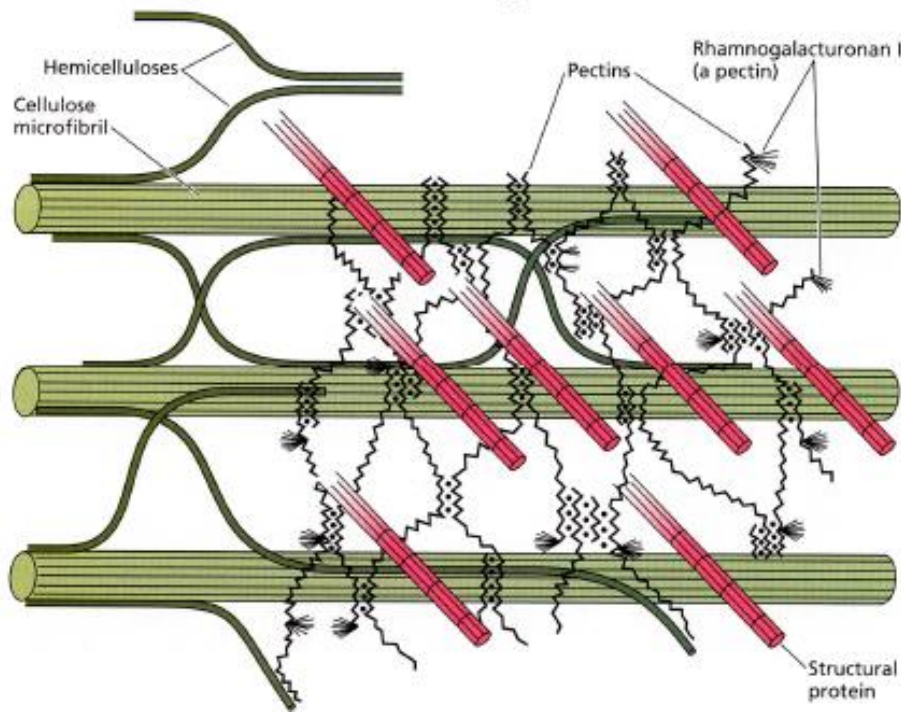
Reaction
catalyzed by
CGTase



Enzymes degrading polysaccharides of the plant cell walls



Components of the plant cell walls:

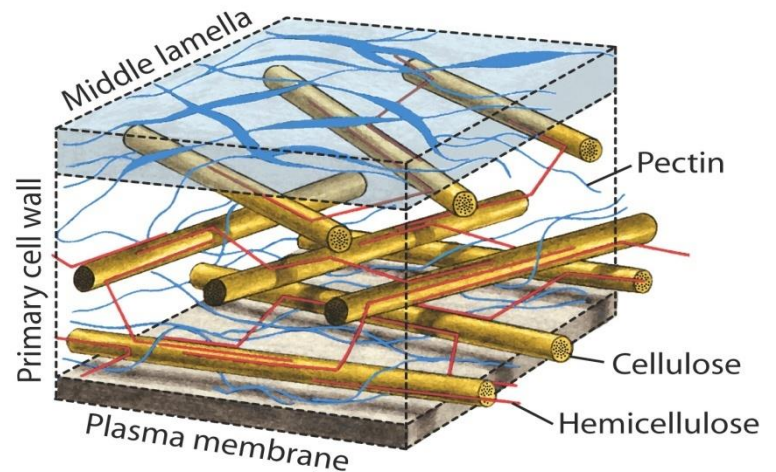


Cellulose

Hemicelluloses

Pectin

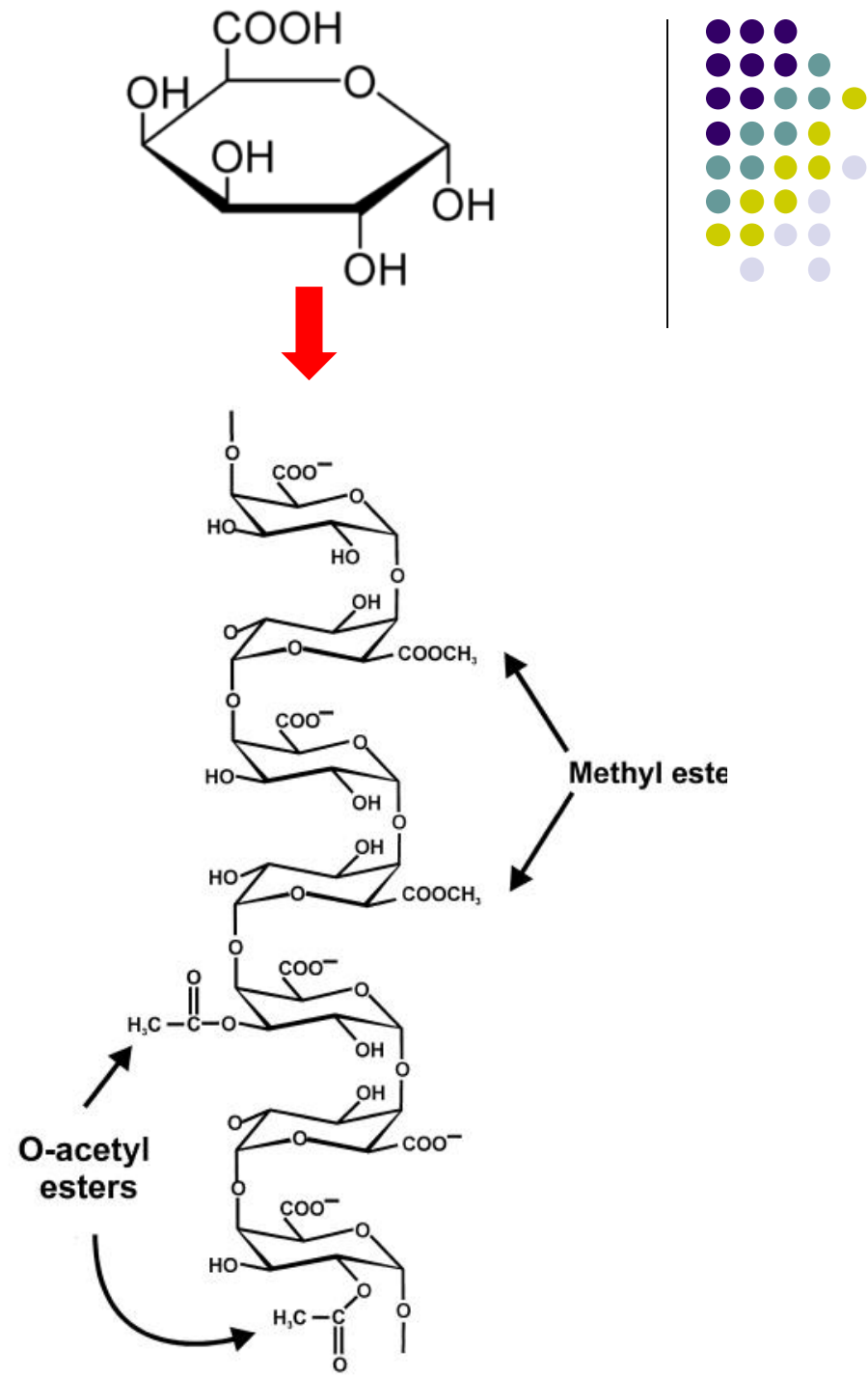
Structural protein - extensin



Pectic compounds – structure:

1. Homopolygalacturonan
2. Rhamnogalacturonan I
3. Rhamnogalacturonan II

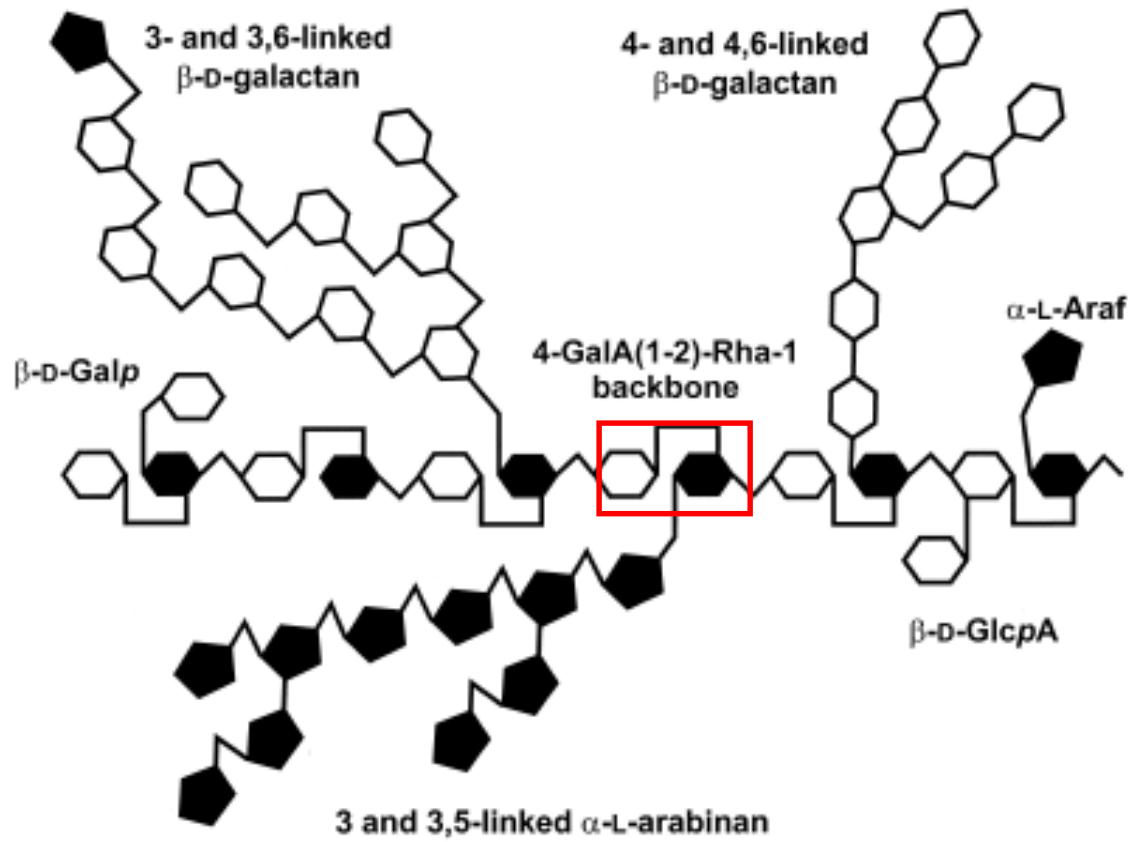
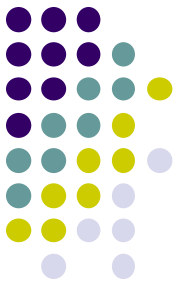
Homogalacturonan (HG) - linear
galacturonic acids,
 α -1,4- bonds
~ 200 monosacch.units
Partially esterified

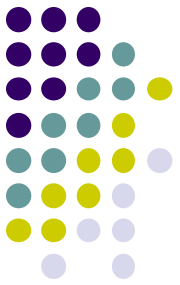


Rhamnogalacturonan I - branched,

backbone $[\rightarrow 4)\text{-}\alpha\text{-D-GalpA-(1}\rightarrow 2)\text{-}\alpha\text{-L-Rhap-(1}\rightarrow]$

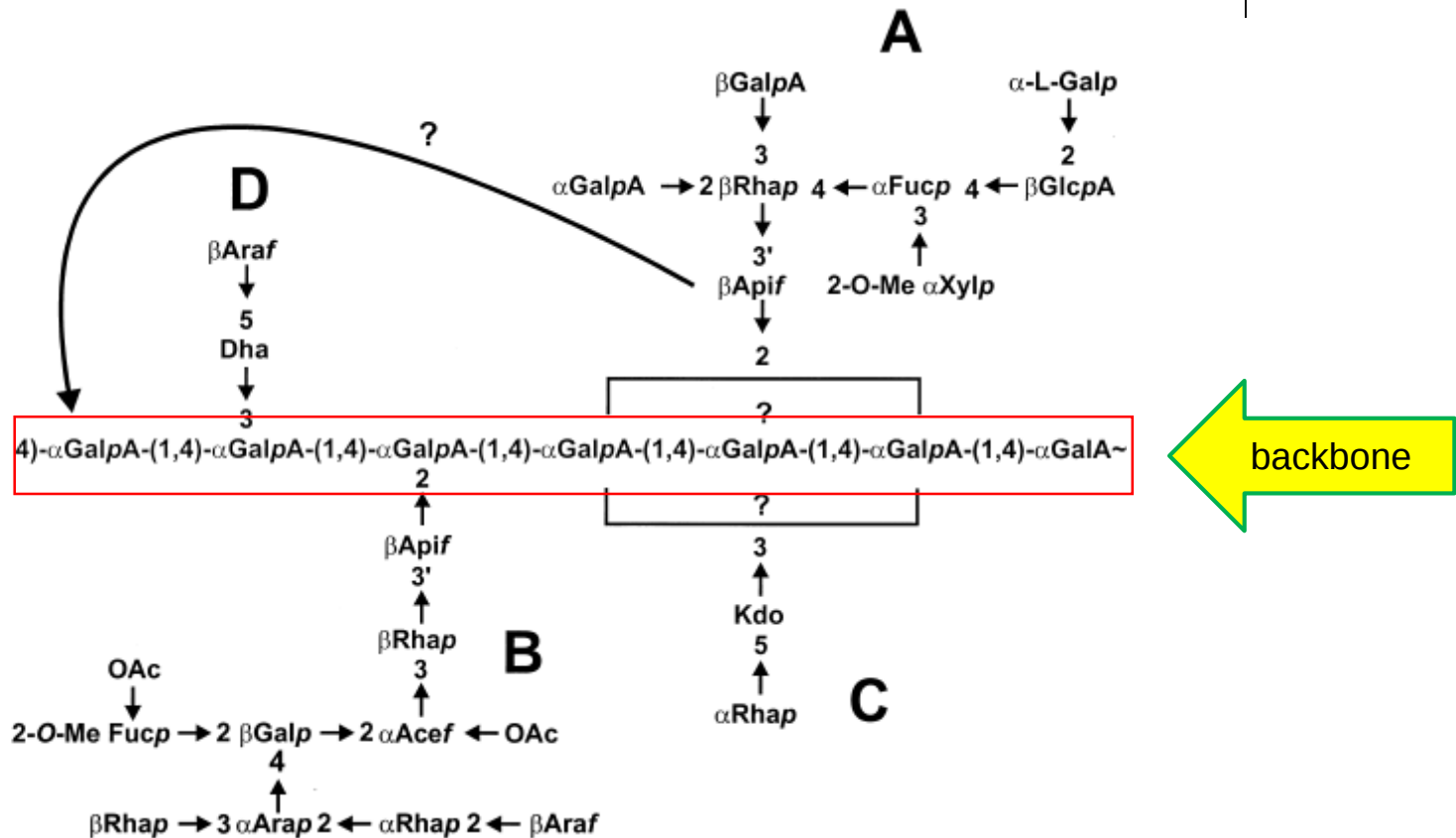
Branching on C4 Rha





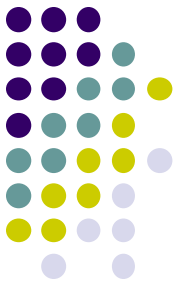
Rhamnogalacturonan II, branched

Backbone: polygalA, 4 types of side chains



Kdo = 3-deoxy-D-manno-octulosonic acid

Pectine structure



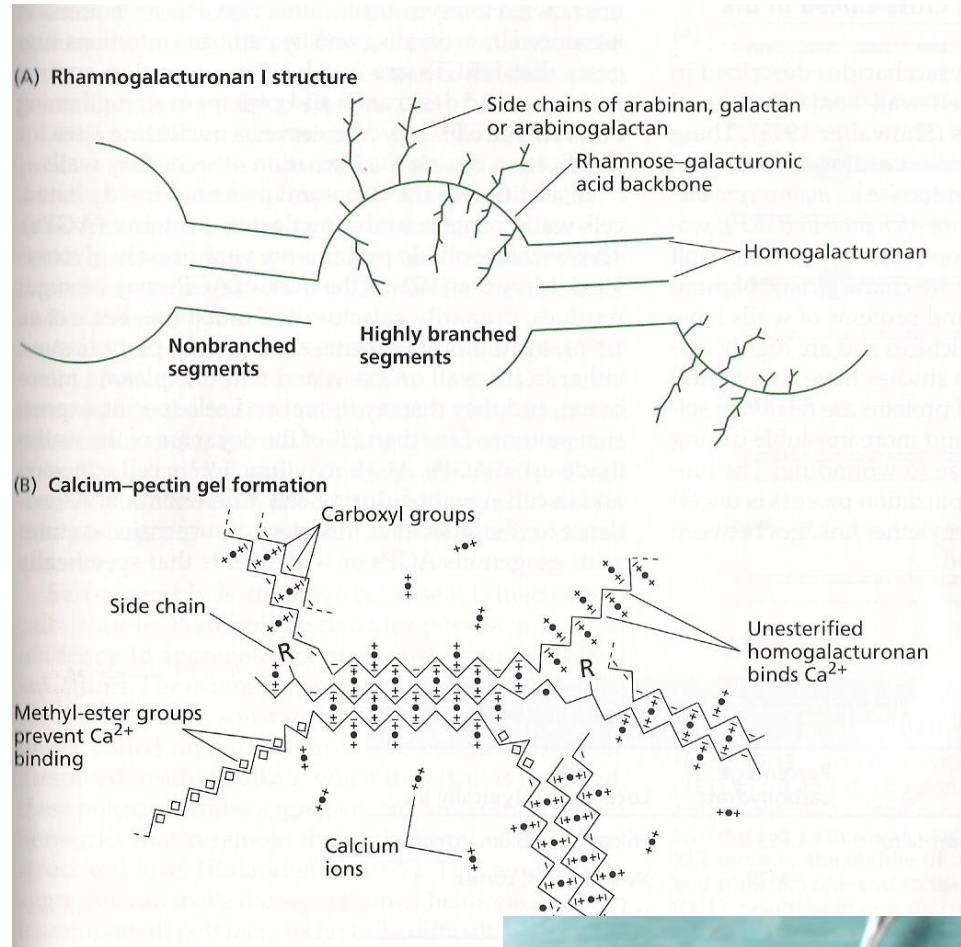
Mh:

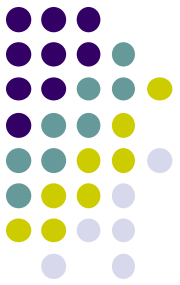
Apples, lemon: 200 - 300 kDa

Pears, plums: 25 - 35 kDa

Oranges: 40 - 50 kDa

Sugar beet: 40 - 50 kDa





Pectic compounds – classification (in food industry)

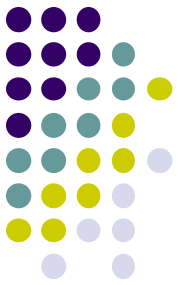
1. **Protopectin** – insoluble in water, present in the intact tissue (non-ripened fruit), limit hydrolysis leads to pectin and pectic acid
2. **Pectinic acid** – polygalacturonan with the degree of esterification less than 75%
3. **Pectin** – polymethylgalacturonan, at least 75% of carboxylic groups are esterified
4. **Pectic acid** – soluble homopolygalacturonan, practically non esterified

Fruit ripening

Immature (firm texture)

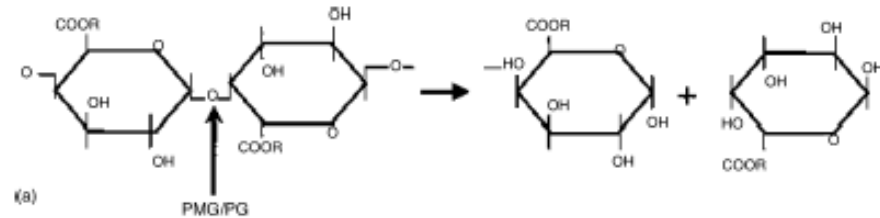


Mature (mashy)

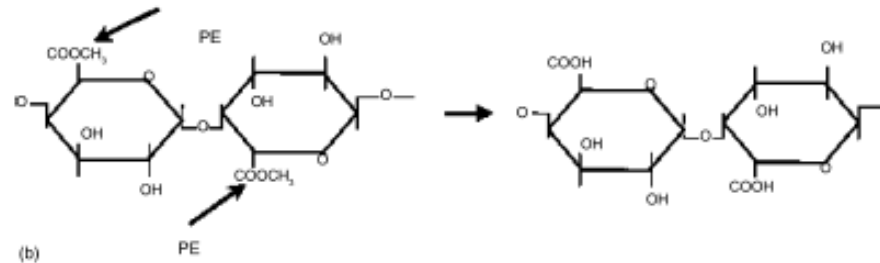


Reactions catalyzed by pectolytic enzymes

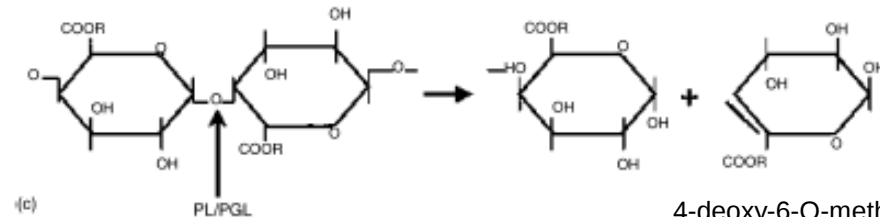
Polygalacturonases
– depolymerizing e.



Pectin esterases

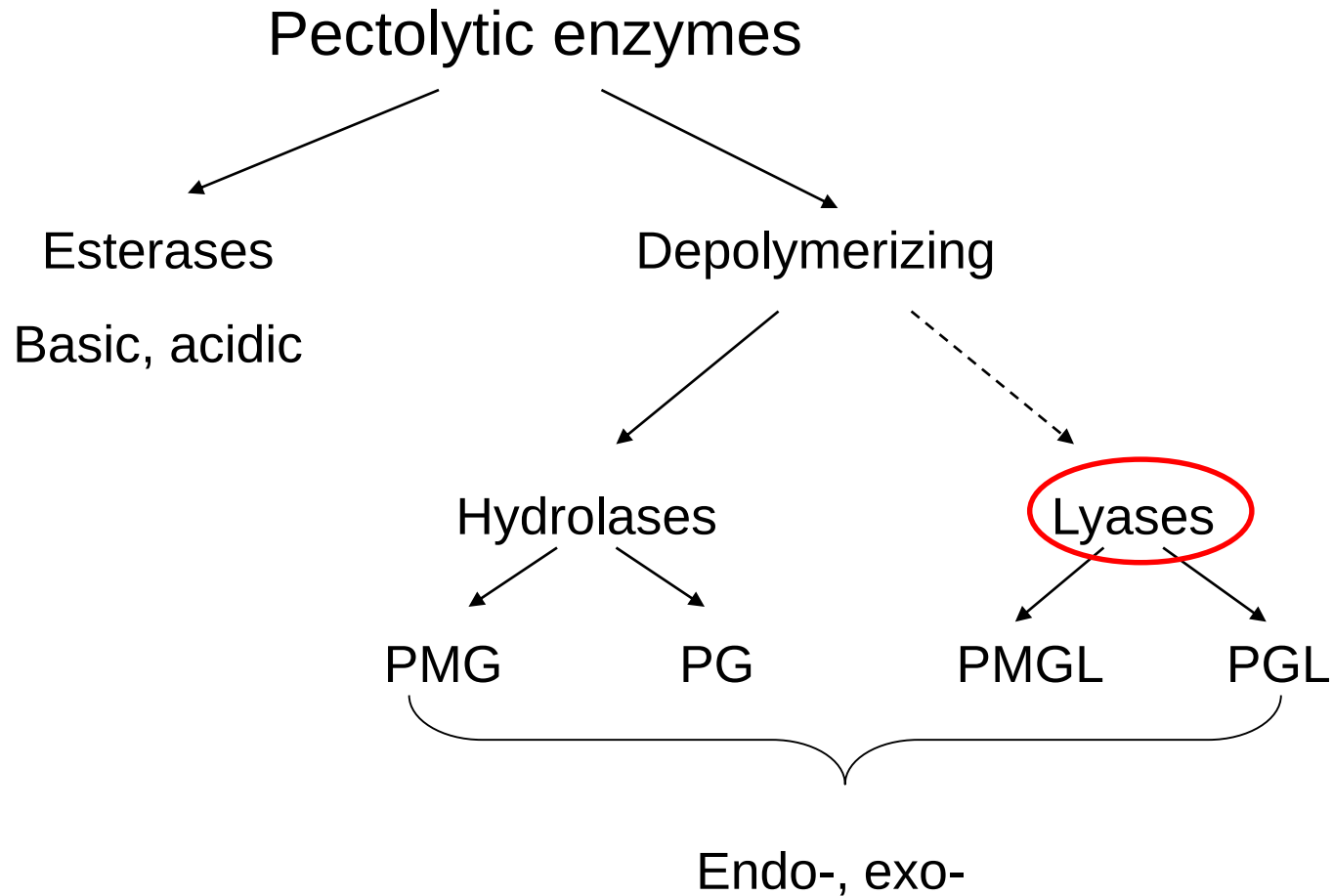
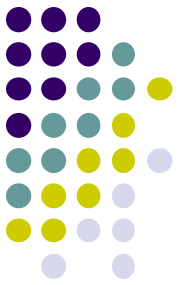


Pectin lyases -
depolymerizing

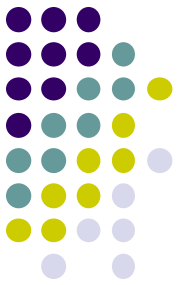


4-deoxy-6-O-methyl-alpha-D-galact-4-enuronosyl

Degradation of pectic compounds is functional in physiological processes – most important is fruit ripening



favoured substrates: PMG- Polymethylgalacturonan, PG -polygalacturonan –



Depolymerazing enzymes

1. Polygalacturonases (according to preferred substrate – pectin resp. pectic acid)

pH-optimum 4 -5

Endopolygalacturonases	x	exopolygalacturonases
Decrease of viscosity		digalacturonic acid (bacterial)
higher oligogalacturonides		galacturonic acid (fungal)
		able to cleave digalacturonans

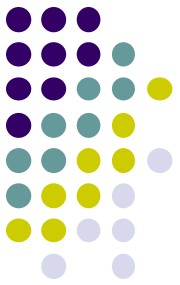
2. Lyases

pH optimum 8 - 9

fungal, bacterial, plant

Activity determination: ΔA_{235}

Substrate – highly esterified pectin



Pectin esterases

Specificity: D-methylgalacturonans, free carboxyl in the vicinity

Basic (pH optimum 7 - 8)

- plant
- microbial
- fungal

Acidic (pH optimum 4 - 6)

- fungal



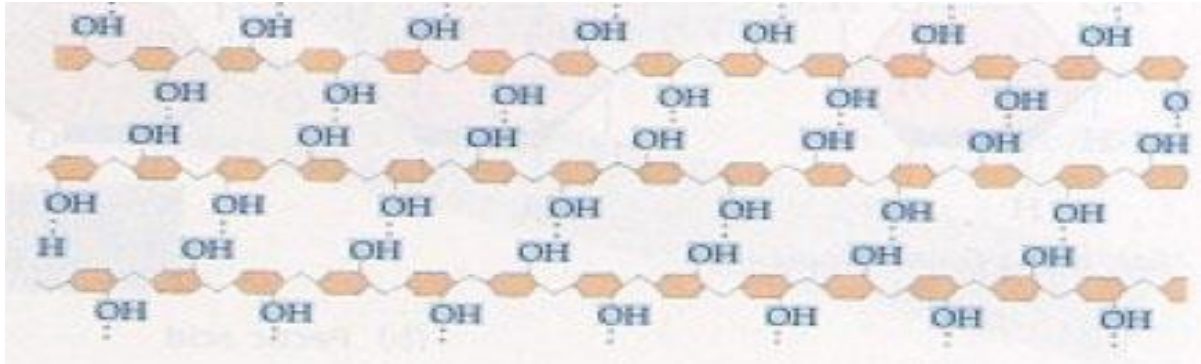
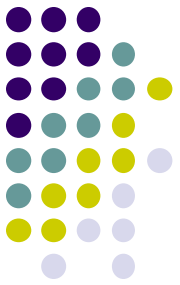
deesterification in blocs

Inhibited by reaction
product (pectic acid)

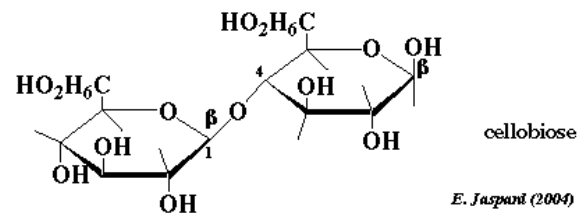
deesterification proceeds
statistically

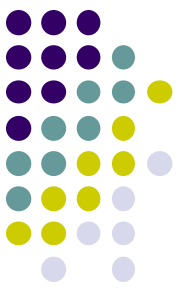
Esterases don't decrease the viscosity of pectins in solution, on the contrary increase of viscosity in the presence of Ca^{2+} occurs

Cellulose structure

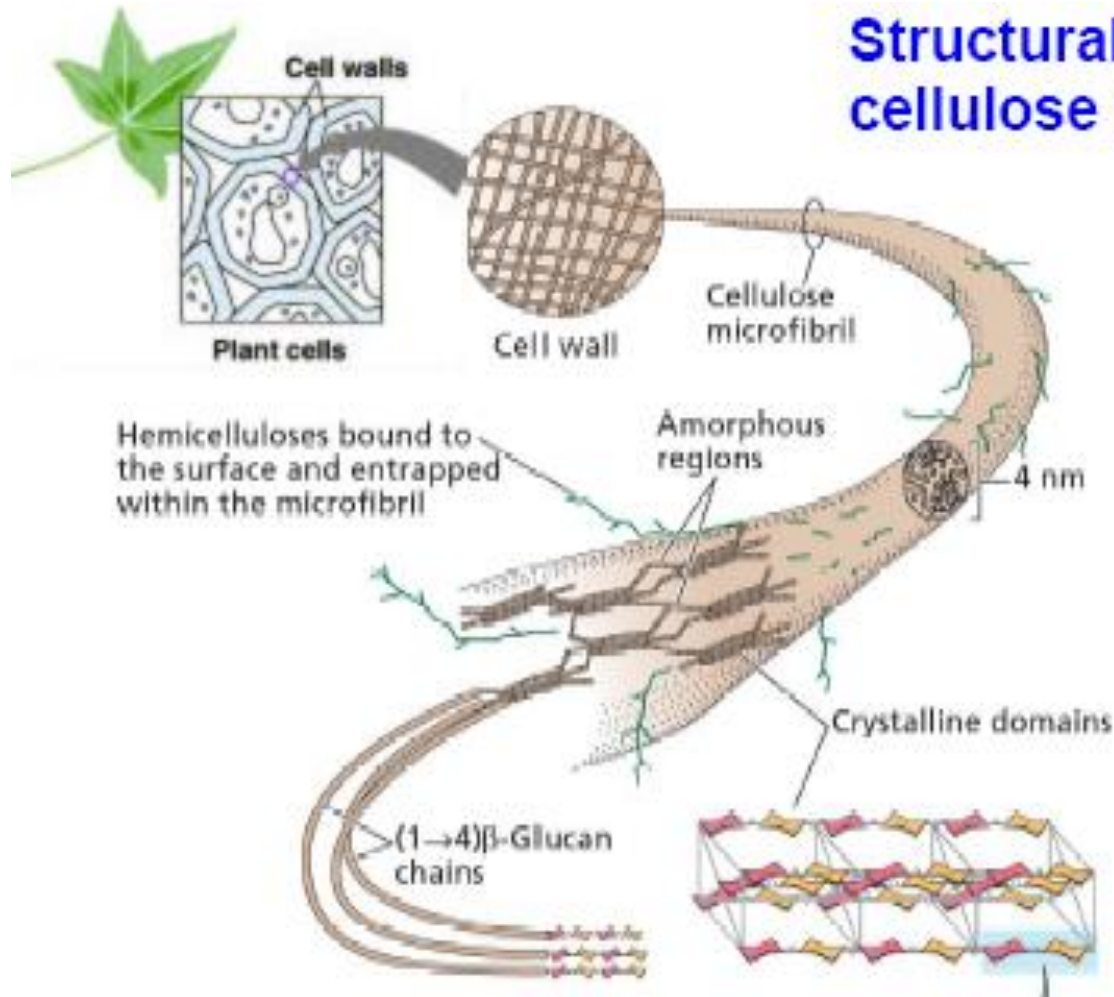


Cellobiose – structural unit

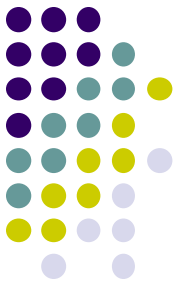




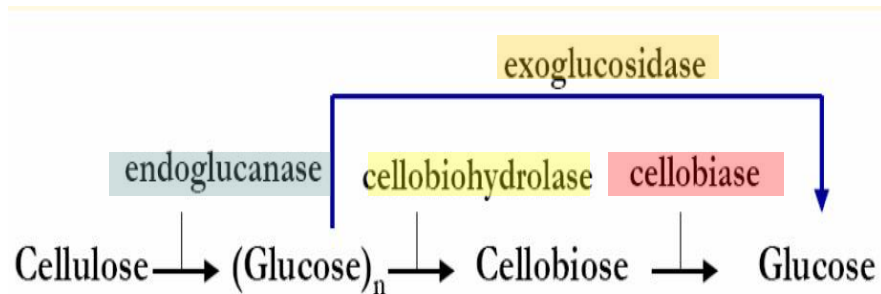
Structural model of a cellulose microfibril



Celulolytic enzymes



multicomponent enzyme system:

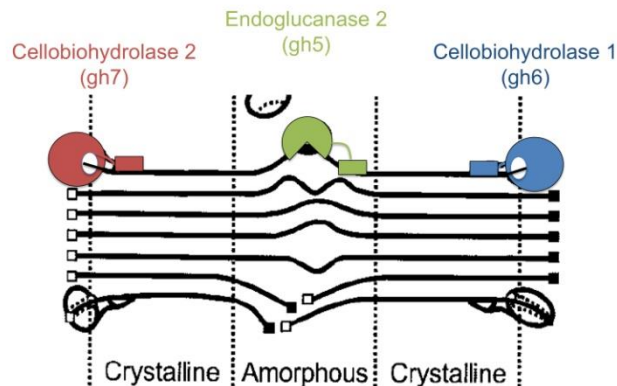


Main producer : *Trichoderma reesei*

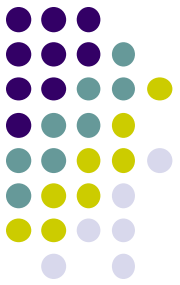
Problem: glucose and cellobiose are inhibitors of cellulase system

glycoprotein

2 domains: catalytic + binding



Current model for enzymatic degradation of cellulose



Hemicelluloses

(soluble in diluted alkali)

(A) Xyloglucan

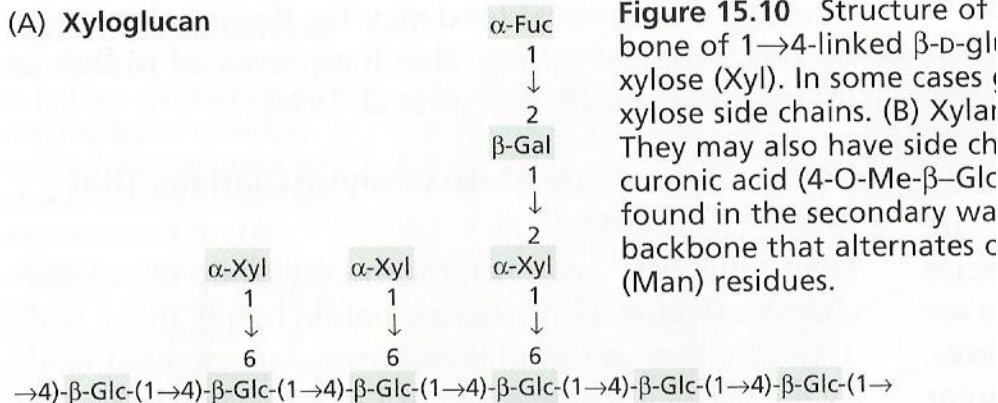
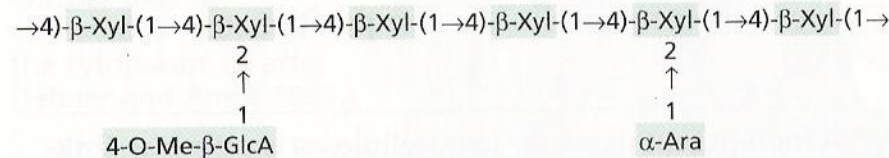
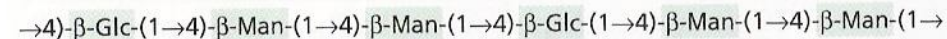


Figure 15.10 Structure of the backbone of 1→4-linked β-D-glucopyranose (Glc) units with xylose (Xyl) side chains. (B) Xylans. They may also have side chains of galactose (Gal) or glucuronic acid (4-O-Me-β-GlcA) found in the secondary wall. The backbone that alternates with (Man) residues.

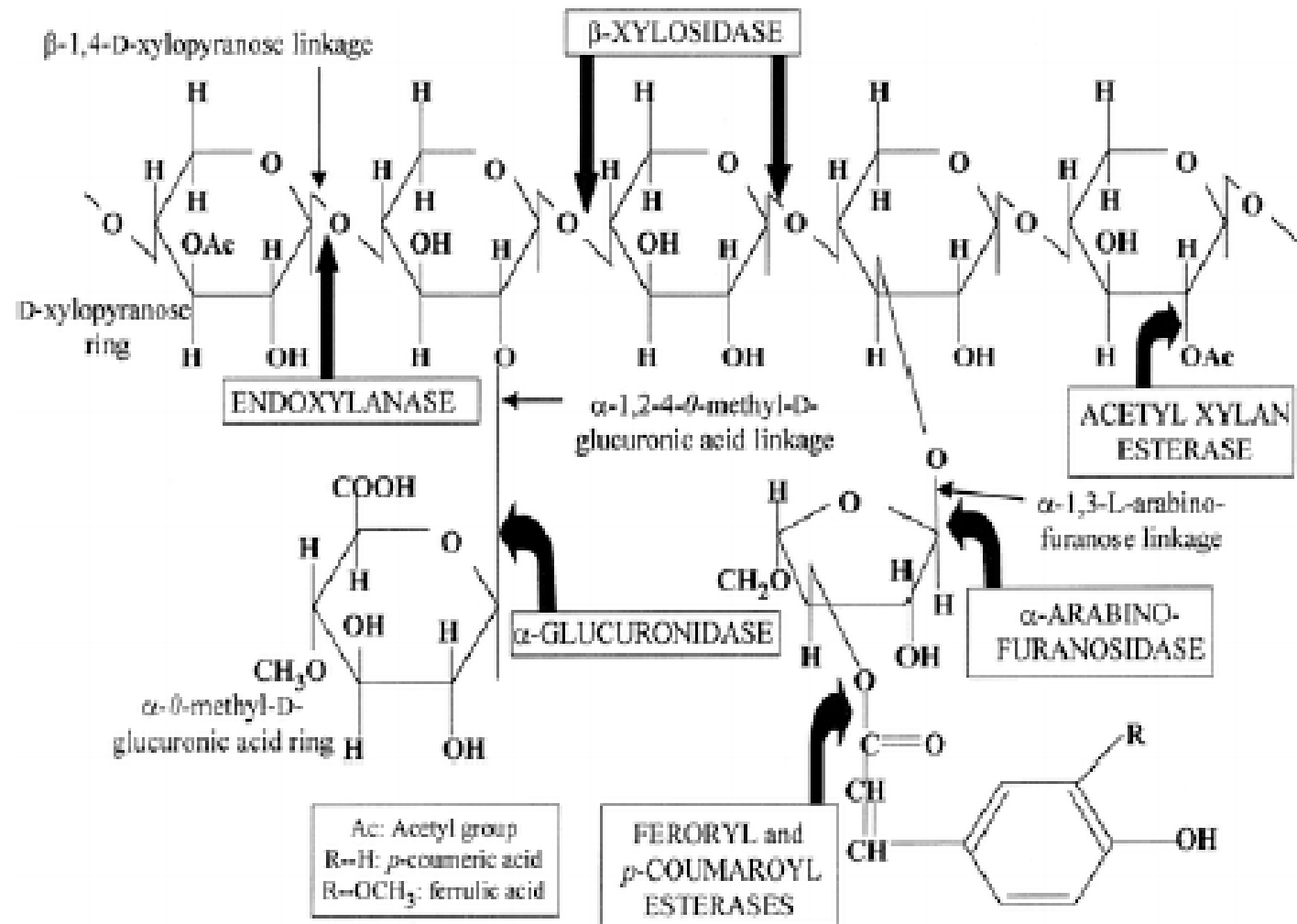
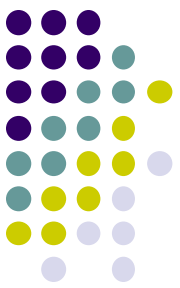
(B) Xylans

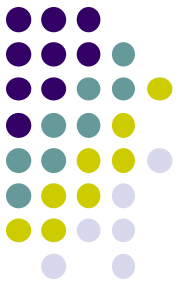


(C) Glucomannans



Hemicellulases





β -galactosidase - (EC 3.2.1.23)



Sources: bacteria, fungi, yeasts

Fungal: - acid pH 2,4 - 5,4, 50°C

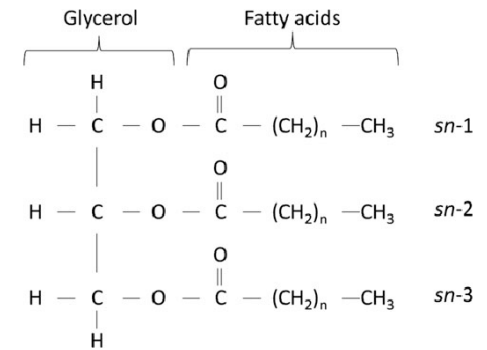
Psychrophilic microorganisms

Degradation of lactose in milk products

Transglycosylation reaction - biotransformations

Lipases

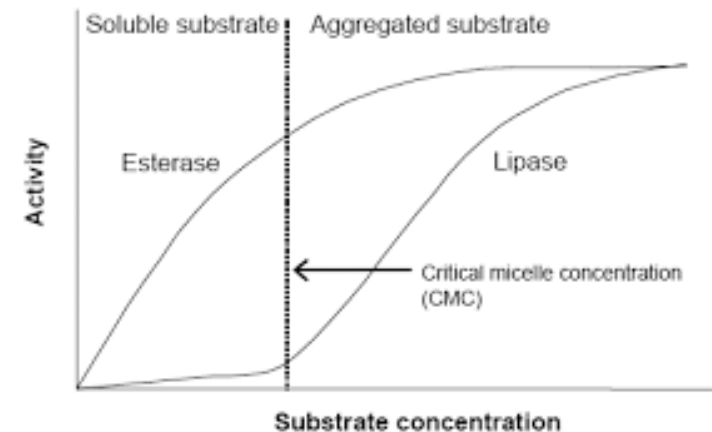
TAG $\rightarrow$ DAG (1,2 or 1,3) $\rightarrow$ MAG $\rightarrow$ FA + glycerol



Animal, plant, microbial

Active on the oil-water interface (CMC – critical micelle concentration)

mechanism - catalytic triad similar to the serin proteases



Highly stereospecific (biotransformations)

Very low specificity to FA and position of ester bond in triacyl glycerol

Some bacterial lipases specific for position 2

Reactions catalysed by lipases



Hydrolysis :



Ester synthesis :



Acidolysis :



Interesterification :



Alcoholysis :

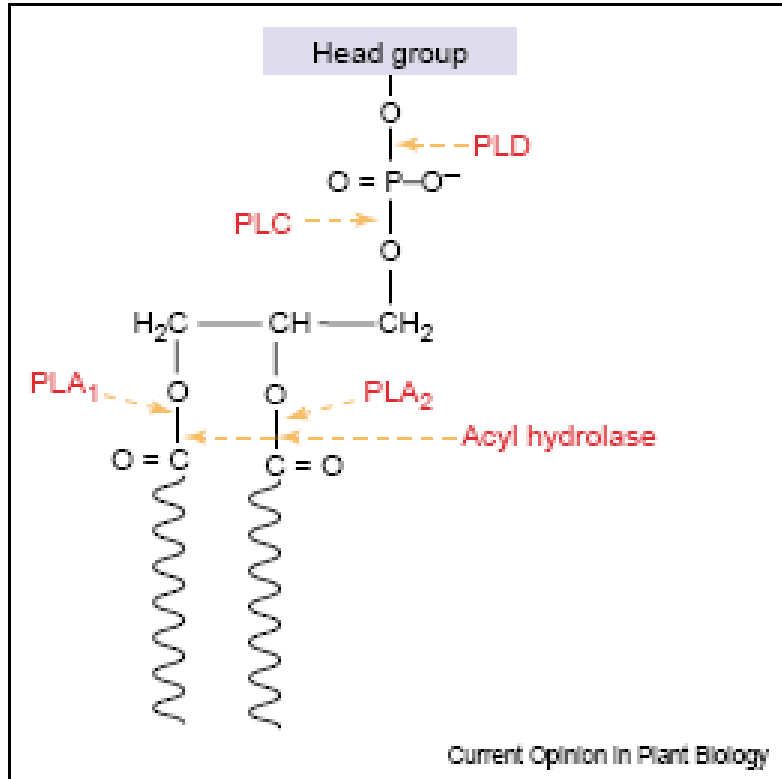
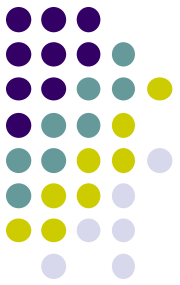


Aminolysis :



Phospholipases

Animal, plant, microbial



Reaction products:

PLD: **PA** + polar head

PI-PLC: DAG + IP₃

PC-PLC: DAG + P-Chol

PLA: FA + **lysoPL**

PA – low solubility, oil spoilage

lysoPL - surfactants

Transphosphatidylation reaction of PLD

