

A few words about plant pathogens



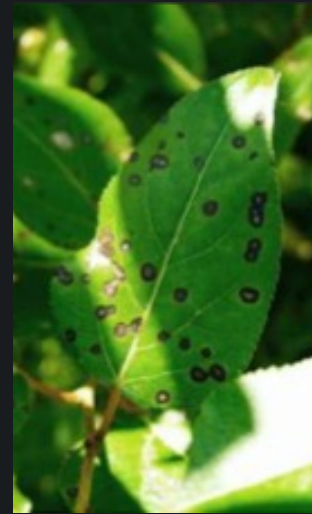
Zymoseptoria
tritici
(Mycgr)



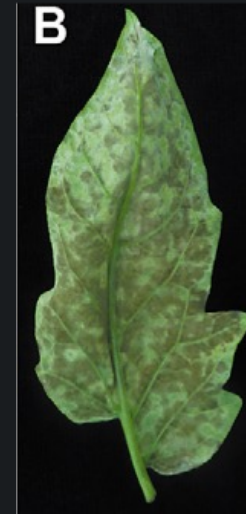
Pseudocercospora
fijiensis
(Mycfi)



Mycosphaerella
populorum
(Sepmu)



Mycosphaerella
populicola
(Seppo)



Cladosporium
fulvum
(Clafu)



Dothistroma
septosporum
(Dotse)

Molecular determinants of fungal pathogenicity

Sensing the host, growth

Differentiation of specialized cells

Manipulation of the host

- secreted-small proteins (SSPs)

- secreted proteases

- secondary metabolites (SMs)

Degradation, toxins

- secreted carbohydrate-active enzymes (CAZymes)

- secondary metabolites

- secreted toxic peptides

Nutrient uptake

Secreted-small proteins = protein effectors

Signal peptide

No transmembrane domain (TM)

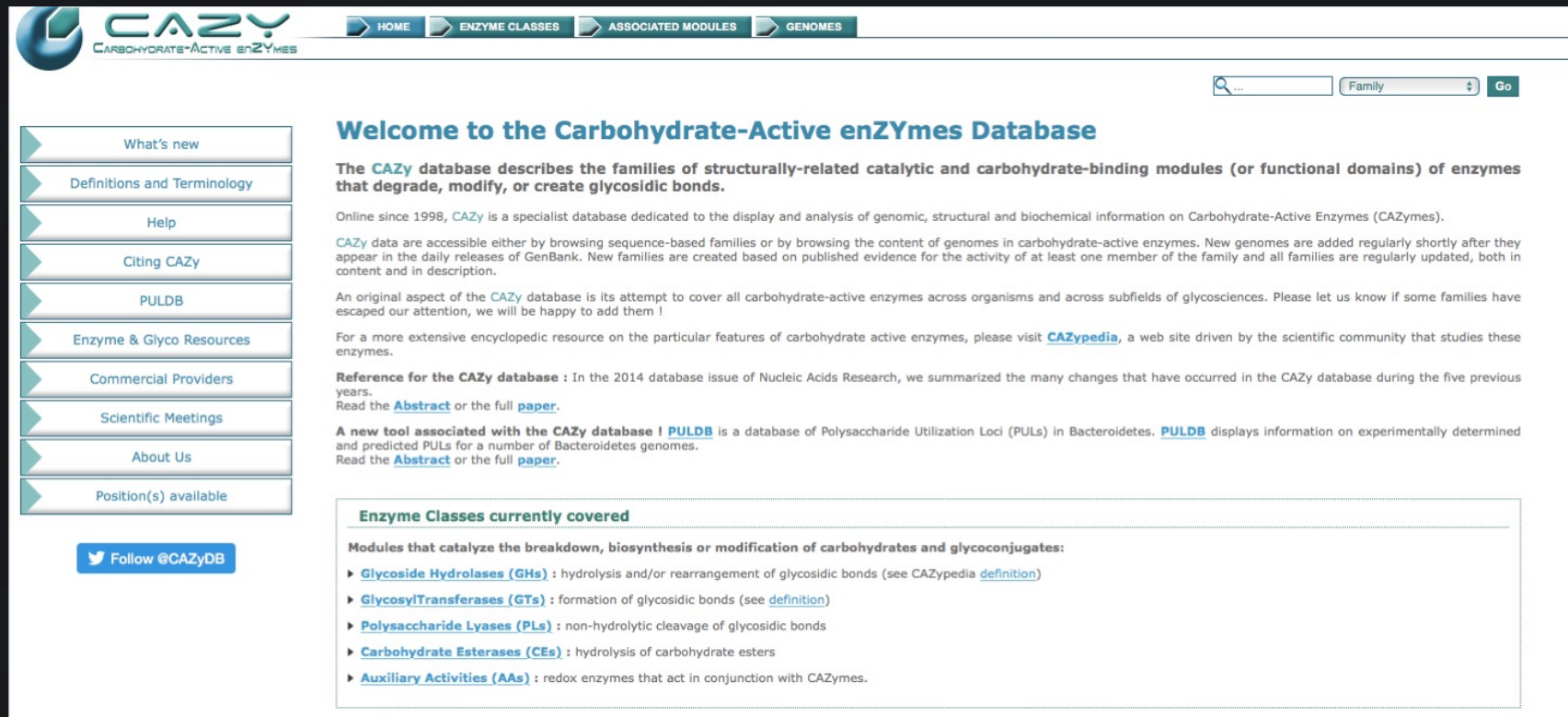
No GPI-anchor signal

<300 amino acids

≥ 4 cysteines

Can be apoplastic or cytoplasmic

CAZymes



The screenshot shows the CAZy database homepage. At the top, there is a navigation bar with links to HOME, ENZYME CLASSES, ASSOCIATED MODULES, and GENOMES. The CAZy logo is on the left. A search bar and a family dropdown menu are on the right. A left sidebar contains links to What's new, Definitions and Terminology, Help, Citing CAZy, PULDB, Enzyme & Glyco Resources, Commercial Providers, Scientific Meetings, About Us, and Position(s) available. The main content area has a welcome message, a description of the database, and a list of enzyme classes currently covered.

CAZY
CARBOHYDRATE-ACTIVE ENZYMES

HOME ENZYME CLASSES ASSOCIATED MODULES GENOMES

What's new
Definitions and Terminology
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Follow @CAZyDB

Welcome to the Carbohydrate-Active enZymes Database

The **CAZy** database describes the families of structurally-related catalytic and carbohydrate-binding modules (or functional domains) of enzymes that degrade, modify, or create glycosidic bonds.

Online since 1998, CAZy is a specialist database dedicated to the display and analysis of genomic, structural and biochemical information on Carbohydrate-Active Enzymes (CAZymes).

CAZy data are accessible either by browsing sequence-based families or by browsing the content of genomes in carbohydrate-active enzymes. New genomes are added regularly shortly after they appear in the daily releases of GenBank. New families are created based on published evidence for the activity of at least one member of the family and all families are regularly updated, both in content and in description.

An original aspect of the CAZy database is its attempt to cover all carbohydrate-active enzymes across organisms and across subfields of glycosciences. Please let us know if some families have escaped our attention, we will be happy to add them !

For a more extensive encyclopedic resource on the particular features of carbohydrate active enzymes, please visit [CAZypedia](#), a web site driven by the scientific community that studies these enzymes.

Reference for the CAZy database : In the 2014 database issue of Nucleic Acids Research, we summarized the many changes that have occurred in the CAZy database during the five previous years.
Read the [Abstract](#) or the full [paper](#).

A new tool associated with the CAZy database ! [PULDB](#) is a database of Polysaccharide Utilization Loci (PULs) in Bacteroidetes. [PULDB](#) displays information on experimentally determined and predicted PULs for a number of Bacteroidetes genomes.
Read the [Abstract](#) or the full [paper](#).

Enzyme Classes currently covered

Modules that catalyze the breakdown, biosynthesis or modification of carbohydrates and glycoconjugates:

- ▶ [Glycoside Hydrolases \(GHs\)](#) : hydrolysis and/or rearrangement of glycosidic bonds (see CAZypedia [definition](#))
- ▶ [GlycosylTransferases \(GTs\)](#) : formation of glycosidic bonds (see [definition](#))
- ▶ [Polysaccharide Lyases \(PLs\)](#) : non-hydrolytic cleavage of glycosidic bonds
- ▶ [Carbohydrate Esterases \(CEs\)](#) : hydrolysis of carbohydrate esters
- ▶ [Auxiliary Activities \(AAs\)](#) : redox enzymes that act in conjunction with CAZymes.

Enzyme classes: GH / GT / PL / CE / AA / CBM

Proteases/Peptidases

MEROPS
[Switch to Inhibitors](#)
Peptidase
Name
Identifier
Gene name
Organism
Substrates
Family
Clan
SEARCHES
BLAST MEROPS
SUBMISSIONS
Other Information
What's New
About
Images
EST cell lines
Unsequenced
Genomes
Statistics

Families of Proteolytic Enzymes

A family is a set of homologous proteolytic enzymes. The homology is shown by a significant similarity in amino acid sequence either to the type enzyme of the family, or to another protein that has already been shown to be homologous to the type enzyme, and thus a member of the family. The relationship must exist in the peptidase unit at least. A family can contain a single enzyme if no homologues are known, and a single gene product such as a virus polyprotein can contain more than one proteolytic enzyme each assigned to a different family. Each family is identified by a letter representing the catalytic type of the proteolytic enzymes it contains together with a unique number. Some families are divided into subfamilies because there is evidence of a very ancient divergence within the family, e.g. S1A, S1B.

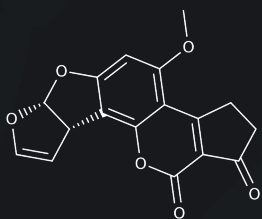
[Aspartic \(A\)](#), [Cysteine \(C\)](#), [Glutamic \(G\)](#), [Metallo \(M\)](#), [Asparagine \(N\)](#), [Mixed \(P\)](#), [Serine \(S\)](#), [Threonine \(T\)](#), [Unknown \(U\)](#)

Aspartic (A) Peptidases		
FAMILY	SUBFAMILY	TYPE ENZYME
A1	A1A	pepsin A (<i>Homo sapiens</i>)
	A1B	nepenthesin (<i>Nepenthes gracilis</i>)
A2	A2A	HIV-1 retropepsin (human immunodeficiency virus 1)
	A2B	Ty3 transposon peptidase (<i>Saccharomyces cerevisiae</i>)
	A2C	Gypsy transposon peptidase (<i>Drosophila melanogaster</i>)
	A2D	Osvaldo retrotransposon peptidase (<i>Drosophila buzzatii</i>)
A3	A3A	cauliflower mosaic virus-type peptidase (cauliflower mosaic virus)
	A3B	bacilliform virus peptidase (rice tungro bacilliform virus)
A5		thermopsin (<i>Sulfolobus acidocaldarius</i>)
A8		signal peptidase II (<i>Escherichia coli</i>)
A9		spumapepsin (human spumaretrovirus)
A11	A11A	Copia transposon peptidase (<i>Drosophila melanogaster</i>)
	A11B	Ty1 transposon peptidase (<i>Saccharomyces cerevisiae</i>)
A22	A22A	presenilin 1 (<i>Homo sapiens</i>)
	A22B	impas 1 peptidase (<i>Homo sapiens</i>)
A24	A24A	type 4 prepilin peptidase 1 (<i>Pseudomonas aeruginosa</i>)

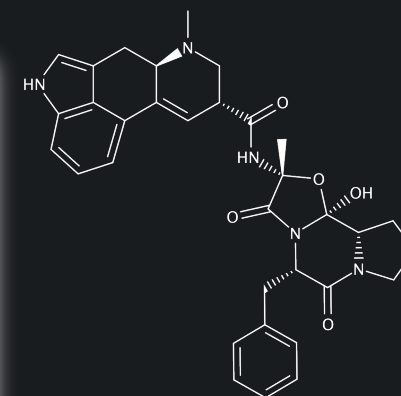
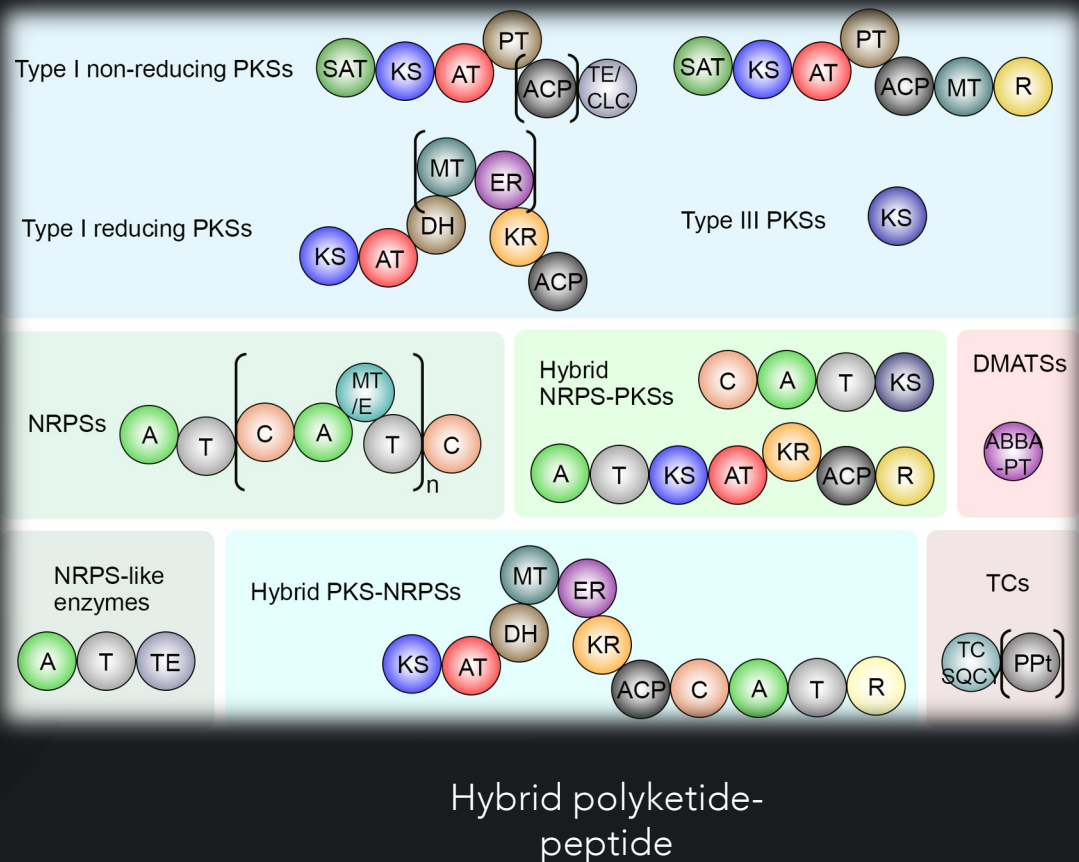
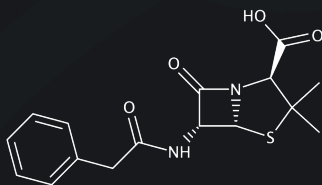
Enzyme families according to catalytic mechanism

Secondary metabolites: biosynthetic core enzymes

Polyketides



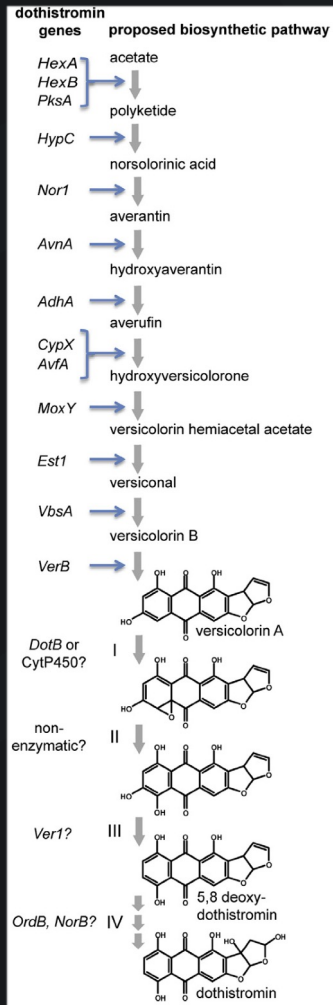
Non-ribosomal peptides



Indole alkaloids

Terpenes

Fungal biosynthetic gene clusters



Precursors

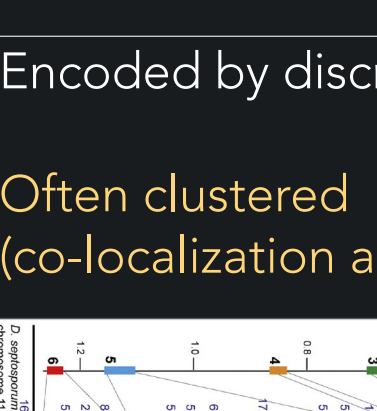
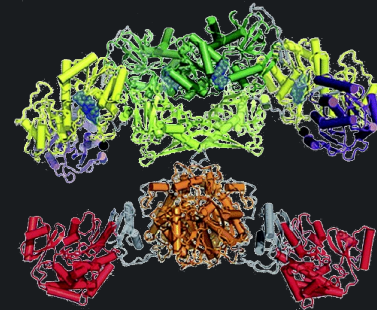
Core enzyme

Raw intermediate

Decorating/tailoring enzymes

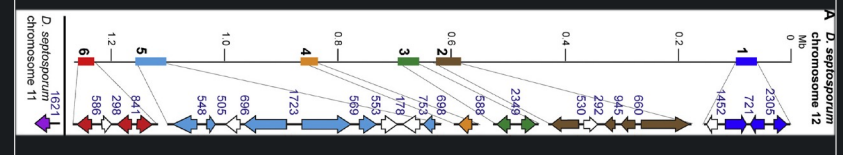
Intermediates

Final compound(s)



Encoded by discrete genes

Often clustered
(co-localization and co-regulation)



Chettri *et al.*, 2013

Functional annotation – Day 2

Part 1

1. Exercise 1: orthologous protein families
2. Exercise 2: compare the gene content between different species

Part 2

3. Exercise 3: case study with expression data
4. Exercise 4: case study with secondary metabolite gene clusters



SUCCESS!