

The background of the slide is a grayscale micrograph showing a dense network of thin, branching, filamentous structures, characteristic of Oomycetes. The filaments vary in thickness and some show small, rounded or bulbous protrusions. The overall appearance is that of a complex, interconnected web of biological material.

# Projet 4

**Caractérisation du domaine CBM1 des Oomycètes**

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# Objectif

fCBD (Fungal-type cellulose-binding domain)

CBM1 (carbohydrate-binding module)

Origine: Champignon/fungi

Oomycètes: Ni champignons, ni végétaux, se développent essentiellement en milieu liquide

*Phytophthora parasitica* N° O42830

## CBEL protein, formerly GP34 precursor

UniProtKB/Swiss-Prot: O42830

[Identical Proteins](#) [FASTA](#) [Graphics](#)Go to: 

LOCUS O42830\_PHYPR 268 aa linear PLN 28-NOV-2006  
 DEFINITION CBEL protein, formerly GP34 precursor.  
 ACCESSION O42830  
 VERSION O42830  
 DBSOURCE UniProtKB: locus O42830\_PHYPR, accession [O42830](#);  
 class: preliminary.  
 created: Jun 1, 1998.  
 sequence updated: Jun 1, 1998.  
 annotation updated: Nov 28, 2006.  
 xrefs: X97205.1, CAA65843.1  
 xrefs (non-sequence databases): GO:0005576, GO:0030248, GO:0004553,  
 GO:0004252, GO:0007596, GO:0005975, GO:0006508, InterPro:IPR000177,  
 InterPro:IPR000254, InterPro:IPR003014, InterPro:IPR003609,  
 Pfam:PF00024, SMART:SM00223, SMART:SM00236, PROSITE:PS50948

KEYWORDS Signal.  
 SOURCE *Phytophthora parasitica*  
 ORGANISM [Phytophthora parasitica](#)  
 Eukaryota; Stramenopiles; Oomycetes; Peronosporales; Phytophthora.

REFERENCE 1 (residues 1 to 268)  
 AUTHORS Mateos,F.V., Rickauer,M. and Esquerre-Tugaye,M.T.  
 TITLE Cloning and characterization of a cDNA encoding an elicitor of  
*Phytophthora parasitica* var. *nicotianae* that shows

Change region shown ▾

Customize view ▾

### Analyze this sequence

Run BLAST

Identify Conserved Domains

Highlight Sequence Features

Find in this Sequence

### Recent activity

[Turn Off](#) [Clear](#)

- CBEL protein, formerly GP34 precursor Protein
- RecName: Full=Melanoma-associated antigen E1; AltName: Full=Alpha- Protein
- RecName: Full=Melanoma-associated antigen D1; AltName: Full=MAGE-D1 Protein
- mf92a11.r1 Soares mouse embryo NbME13.5 14.5 *Mus musculus* cDN; Nucleotide
- Rattus norvegicus ROR-B mRNA for opioid receptor B, complete cds Nucleotide

— **Analyze this sequence**



Run BLAST

Identify Conserved Domains



Highlight Sequence Features

Find in this Sequence

# Conserved domains on [gi|75219384|sp|O42830|O42830\_PHYPR]

View

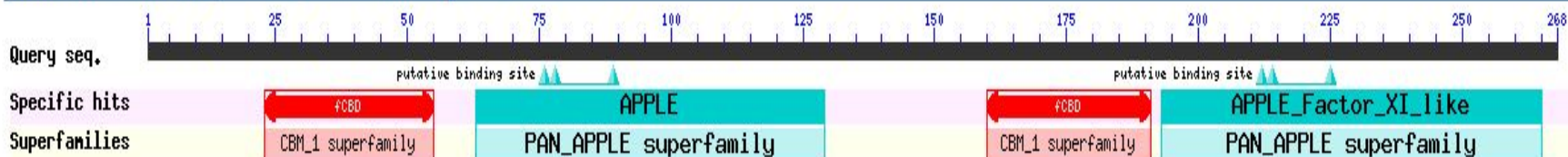
CBEL protein, formerly GP34 precursor.

## Protein Classification

**APPLE\_Factor\_XI\_like and fCBD domain-containing protein** (domain architecture ID 11261017)

APPLE\_Factor\_XI\_like and fCBD domain-containing protein

## Graphical summary Zoom to residue level



## List of domain hits

<input type="checkbox"/>	Name	Accession	Description	Interval	E-value
<input type="checkbox"/>	APPLE	smart00223	APPLE domain; Four-fold repeat in plasma kallikrein and coagulation factor XI. Factor XI apple ...	63-129	2.74e-19
<input type="checkbox"/>	APPLE_Factor_XI_like	cd01100	Subfamily of PAN/APPLE-like domains; present in plasma prekallikrein/coagulation factor XI, ...	193-265	1.95e-17
<input type="checkbox"/>	fCBD	smart00236	Fungal-type cellulose-binding domain; Small four-cysteine cellulose-binding domain of fungi	160-191	2.49e-06
<input type="checkbox"/>	fCBD	smart00236	Fungal-type cellulose-binding domain; Small four-cysteine cellulose-binding domain of fungi	23-55	3.74e-05

smart00236: **fcBD**

Download alignment ?

### Fungal-type cellulose-binding domain

Small four-cysteine cellulose-binding domain of fungi

#### Links ?

**Source:** smart

**Taxonomy:** Eukaryota

**PubMed:** 1 link

**Protein:** [Representatives](#)  
[Specific Protein](#)  
[Related Protein](#)  
[Related Structure](#)  
[Architectures](#)

**Superfamily:** [cl02521](#)

#### PubMed References ?

▸ Domains in microbial beta-1, 4-glycanases: sequence conservation, function, and enzyme families. Microbiol Rev 1991 Jun ; 55(2):303-15

**smart00236** is classified as a model that may span more than one domain.

**smart00236** is a member of the superfamily [cl02521](#).



There are **5841** fCBD domains in 5233 proteins in SMART's nrdb database.

Click on the following links for more information.

▼ **Evolution** (species in which this domain is found)

**Taxonomic distribution of proteins containing fCBD domain.**

This tree includes only several representative species. The complete taxonomic breakdown of all proteins with fCBD domain is also [available](#). ←

Expand all nodes search for a taxonomic node...

#### Bacteria

└─ undefined kingdom

#### Eukaryota

+ Fungi

└─ Metazoa

└─ Viridiplantae

└─ undefined kingdom

Click on the protein counts, or double click on taxonomic names to display all proteins containing fCBD domain in the selected taxonomic class.

▶ **Cellular role** (predicted cellular role)

▶ **Metabolism** (metabolic pathways involving proteins which contain this domain)

▶ **Structure** (3D structures containing this domain)

▶ **Links** (links to other resources describing this domain)

## Taxonomic distribution of proteins with fCBD domain.

Expand all nodes

	Proteins	%	Domains	%
<b>Bacteria</b>				
undefined kingdom	1	0.02	1	0.02
Bacteroidetes	1	0.02	1	0.02
<b>Eukaryota</b>	<b>5232</b>	<b>99.98</b>	<b>5840</b>	<b>99.98</b>
Fungi	4967	94.92	5271	90.24
Metazoa	2	0.04	5	0.09
Viridiplantae	8	0.15	25	0.43
undefined kingdom	255	4.87	539	9.23
Chromerida	2	0.04	4	0.07
Phaeophyceae	12	0.23	23	0.39
undefined class	12	0.23	23	0.39
undefined phylum	241	4.61	512	8.77
Bangiophyceae	4	0.08	13	0.22
Dinophyceae	16	0.31	27	0.46
Oomycetes	207	3.96	450	7.70
Lagenidiales	1	0.02	2	0.03
Peronosporales	42	0.80	99	1.69
Pythiales	10	0.19	26	0.45
Saprolegniales	154	2.94	323	5.53
undefined class	14	0.27	22	0.38



# Échantillonnage

BLASTp O42830

Organism : oomycetes

xp nr

# **Alignement multiple**

Clustal w

Visualisation sur Jalview

# Recherche de motif (MEME)



Version 5.5.4

MEME discovers novel, **ungapped** motifs (recurring, fixed-length patterns) in your sequences (sample output from sequences). MEME splits variable-length patterns into two or more separate motifs. See this Manual for more information.

## MEME Suite 5.5.4

Jobs running: 3  
Jobs waiting to run: 0

► Motif Discovery

► Motif Enrichment

► Motif Scanning

► Motif Comparison

► Gene Regulation

► Utilities

► Manual

► Guides & Tutorials

► Sample Outputs

► File Format Reference

► Databases

► Download & Install

► Help

► Alternate Servers

► Authors & Citing

► Recent Jobs

↔ Previous version 5.5.3

### Data Submission Form

Perform motif discovery on DNA, RNA, protein or custom alphabet datasets.

#### Select the motif discovery mode [?](#)

Classic mode  Discriminative mode  Differential Enrichment mode

#### Select the sequence alphabet

Use sequences with a standard alphabet or specify a custom alphabet. [?](#)

DNA, RNA or Protein  Custom

#### Input the primary sequences

Enter sequences in which you want to find motifs. [?](#)

[?](#)

#### Select the site distribution

How do you expect motif sites to be distributed in sequences? [?](#)

#### Select the number of motifs

How many motifs should MEME find? [?](#)

#### Input job details

(Optional) Enter your email address. [?](#)

### Select the sequence alphabet

Use sequences with a standard alphabet or specify a custom alphabet. [?](#)

DNA, RNA or Protein  Custom

Choisir un fichier

Aucun fichier choisi

### Input the primary sequences

Enter sequences in which you want to find motifs. [?](#)

Type in sequences

PROTEIN [?](#)

```
MVASPLRLAAVL SAAA VVVVTDATSIAGNTVTPVELNSPLNNDHPAFGGPAS,  
APNTSAPTWT PQPTTTPSPTAVNSTEHTRRLEATSADVQRLESHFGQWMERN:  
DSIN YRWSGEASPAEKYARAFGRNPTDFMNDVSAKLGVDSLNWMRSCSSDAEC:  
WAPAAIQEPEPRCAVNKNGVQFYVQDLKALMTAMYAGAGVPVFTGARYDGGNI  
NIMGRFGKAFIVDVSPGAEVWNQPVRYGVREV KYMSIDQAAQQYFSVARYPFI  
STGKVDGVTHNQEFYLLLEDDNDNIIGGEWLYDSQRYHPDFLWFTTANPSND,  
NPGTCGSDATGATSCPSGQYCPWNPFSFYQCRSIDAKCGQQETGVDFYGDIA:  
YNADGKAYCYLKKGSGQRQSKTGAVSAVIQSGGDS CAPRGGSCGNQWSGPQCC  
VNVDYYGDDISTHQLTLPEQCCDKCAQTAGCKAYTFINYNADGKAYCYLKKGT  
WGSCGNAAGASCCPDNQYCPWDAGNYQCIYTPSKCSRQQTNVDFYGD DLAQ  
NQPQPACYLKKGTGEQRYHPTAVSAQLN  
>POM76297.1 Cellulose binding elicitor lectin (CBEL)  
MTKIAFIVALSVVLSVAAGDTC SNGNGASCGDSTTAYCCQDNLYCMPWSSNYV  
GLQPGDCCAACLTTDGC LAYTFVNNFSGTTACYLKAGMGSPRVTPGIISAVID:  
FDIMMRTLVAATVAVIAGFADAACPNTNLGKCGDASNPECCPDGDYCMPWAPI  
TVYGLQPGDCCATCLSTSGCLAYTFINNNSGTTACYLKAGMGQPRKVVGAISA  
GLPQTLDKLKLN
```

### Select the site distribution

How do you expect motif sites to be distributed in sequences? [?](#)

Zero or One Occurrence Per Sequence (zoops)

### Select the number of motifs

How many motifs should MEME find? [?](#)

3

## DISCOVERED MOTIFS

	Logo <a href="#">?</a>	E-value <a href="#">?</a>	Sites <a href="#">?</a>
1.	<p>Sequence logo for motif 1 showing amino acid conservation across 30 positions. The sequence is FPNYDFYGNDI...T...YGIQPG...CCTR...CSE...T...GCKAYTFVNSNPGQPACYLK.</p>	2.6e-1120	31
2.	<p>Sequence logo for motif 2 showing amino acid conservation across 17 positions. The sequence is AAYG...CGSS...GATCCPSGY...YQC...QPPAKCSKQ.</p>	6.8e-788	31
3.	<p>Sequence logo for motif 3 showing amino acid conservation across 20 positions. The sequence is KYDYYGNDIKTVYVSLPSLCCDACA...ST...GCKAYTYINNNPGQ.</p>	2.2e-643	26

Stopped because requested number of motifs (3) found.

2.





# Création du profil HMM

Utilisation de MobaXterm

Recherche par correspondance des positions du domaine dans le blast

Alignement des domaines

```

NSEQ 94
EFFN 2.435486
CKSUM 2335925816
STATS LOCAL MSV -7.3691 0.71998
STATS LOCAL VITERBI -7.7928 0.71998
STATS LOCAL FORWARD -4.1317 0.71998
HMM
K A C D E F G H I
L M N P Q R S T
V W Y
m->m m->i m->d i->m i->i d->m d->d
COMPO 2.91107 1.91345 2.94296 3.18260 3.57047 2.47630 4.08557 3.83979
3.26848 3.38215 4.38241 3.04158 2.81227 2.67394 3.50192 2.63507 3.1539
9 3.51747 3.29085 2.51895
2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518 4.58477 3.61503
0.01271 4.76772 5.49007 0.61958 0.77255 0.00000 *
1 4.00131 0.13835 5.52877 5.50065 5.45656 4.35788 5.98736 4.89507 5.40173 4.88857 5.85664 5.32580 5.10447 5.70482 5.34122 4.26626 4.53504 4.54100 6.54541 5.71177 1 C - - -
2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518 4.58477 3.61503
0.01271 4.76772 5.49007 0.61958 0.77255 0.48576 0.95510
2 4.09548 5.69806 4.92695 4.95613 5.92984 0.11442 5.92442 5.83079 5.23988 5.31955 6.35909 5.09511 5.09658 5.49650 5.29936 4.30280 4.63267 5.19457 6.71209 6.08720 2 G - - -
2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518 4.58477 3.61503
--More-- (13%)
Most commands optionally preceded by integer argument k. Defaults in brackets.
Star (*) indicates argument becomes new default.
-----
<space> Display next k lines of text [current screen size]
z Display next k lines of text [current screen size]*
<return> Display next k lines of text [1]*
d or ctrl-D Scroll k lines [current scroll size, initially 11]*
q or Q or <interrupt> Exit from more
s Skip forward k lines of text [1]
f Skip forward k screenfuls of text [1]
b or ctrl-B Skip backwards k screenfuls of text [1]
^ Go to place where previous search started
= Display current line number
/<regular expression> Search for kth occurrence of regular expression [1]
n Search for kth occurrence of last r.e [1]
!<cmd> or :!<cmd> Execute <cmd> in a subshell
v Start up /usr/bin/vi at current line
ctrl-L Redraw screen
:n Go to kth next file [1]
:p Go to kth previous file [1]
:f Display current file name and line number
. Repeat previous command
-----
0.01271 4.76772 5.49007 0.61958 0.77255 0.48576 0.95510
3 3.17086 5.54307 2.17431 2.64327 5.12304 3.60272 4.22448 4.64700 3.20096 4.16396 4.98317 2.47589 4.23025 3.38912 3.75495 0.82586 3.50608 4.16351 6.31708 4.86111 3 s - - -
2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518 4.58477 3.61503
0.01271 4.76772 5.49007 0.61958 0.77255 0.48576 0.95510
4 2.94943 5.85819 0.85452 2.51483 5.19089 3.63392 4.13357 4.71478 3.10346 4.18957 5.00579 2.43881 4.22723 2.83861 3.68856 2.56296 3.55796 4.26366 6.33975 4.83874 4 d - - -
2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518 4.58477 3.61503
0.33653 4.76772 1.28280 0.61958 0.77255 0.48576 0.95510
5 1.76747 4.86637 3.16491 2.59759 4.10228 3.55487 3.42311 3.50929 2.30580 3.11954 3.94576 3.10133 3.94247 2.90188 2.26094 2.52295 2.95233 3.20059 3.91613 4.05343 5 a - - -
2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518 4.58477 3.61503
0.01752 4.44871 5.17106 0.61958 0.77255 0.27300 1.43166
6 1.77495 5.31021 2.15978 2.32059 4.63834 3.57328 3.48364 4.11616 2.54673 3.60931 4.35994 2.84874 3.98515 2.74233 3.04249 2.20054 2.67869 3.69265 5.75363 4.34599 6 a - - -
2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518 4.58477 3.61503
0.01271 4.76772 5.49007 0.61958 0.77255 0.48576 0.95510
7 2.85076 4.78828 4.20592 4.14311 5.28533 0.43344 5.20940 4.74485 4.32905 4.45846 5.28801 4.10488 4.33943 4.55871 4.52471 3.04715 2.48041 4.02003 6.56996 5.47106 7 G - - -
2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518 4.58477 3.61503

```

# Pattern/Signature

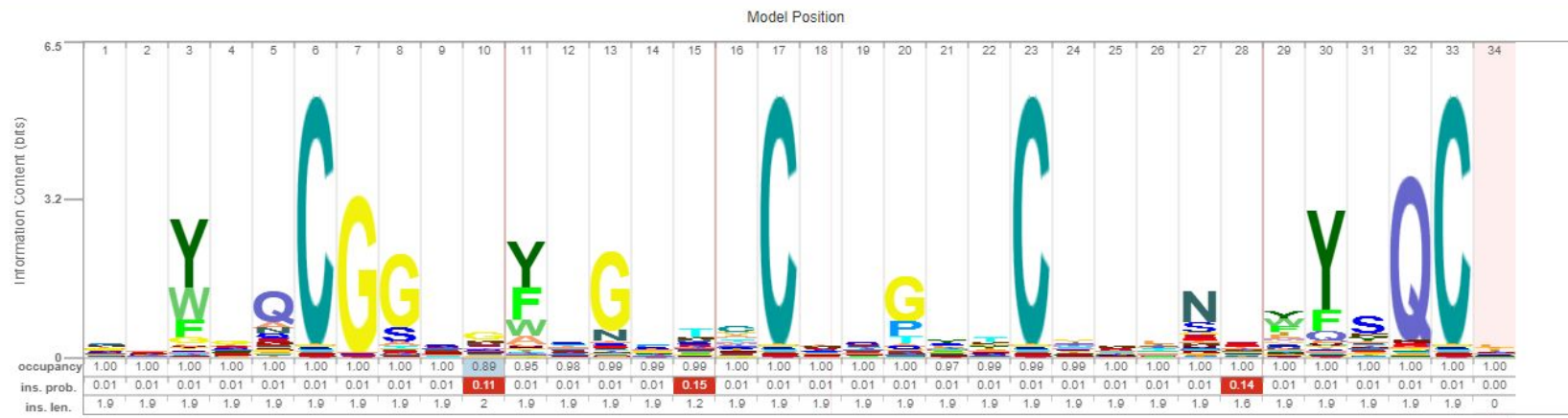
Alignement multiple

Création d'une signature du domaine

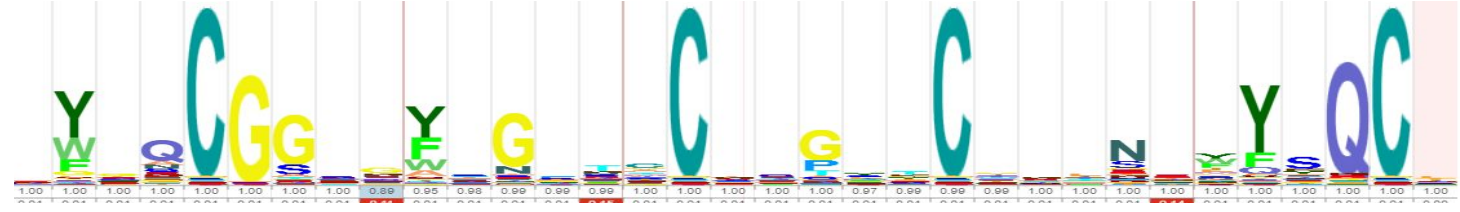
<input checked="" type="checkbox"/>	<a href="#">CBEL protein [Phytophthora nicotianae]</a>	<a href="#">Phytophthora nicotianae</a>	530	530	100%	0.0	99.63%	268	<a href="#">KUF64868.1</a>
<input type="checkbox"/>	<a href="#">PAN domain [Phytophthora infestans]</a>	<a href="#">Phytophthora infestans</a>	454	454	100%	2e-161	90.30%	303	<a href="#">KAF4140643.1</a>
<input checked="" type="checkbox"/>	<a href="#">PAN/Apple domain [Phytophthora cactorum]</a>	<a href="#">Phytophthora cactorum</a>	449	449	100%	3e-160	91.79%	268	<a href="#">KAF1795259.1</a>
<input type="checkbox"/>	<a href="#">PAN domain [Phytophthora infestans]</a>	<a href="#">Phytophthora infestans</a>	449	449	100%	4e-160	90.30%	264	<a href="#">KAF4149176.1</a>
<input type="checkbox"/>	<a href="#">PAN domain [Phytophthora infestans]</a>	<a href="#">Phytophthora infestans</a>	449	449	100%	1e-159	89.93%	305	<a href="#">KAF4043783.1</a>
<input checked="" type="checkbox"/>	<a href="#">cellulose binding elicitor lectin (CBEL), putative [Phytophthora infestans T30-4]</a>	<a href="#">Phytophthora infestans T30-4</a>	446	446	100%	9e-159	89.93%	262	<a href="#">EEY66097.1</a>
<input checked="" type="checkbox"/>	<a href="#">hypothetical protein Pcac1_g16529 [Phytophthora cactorum]</a>	<a href="#">Phytophthora cactorum</a>	445	445	100%	1e-158	89.55%	262	<a href="#">KAG2772549.1</a>
<input type="checkbox"/>	<a href="#">small cellulose-binding protein [Phytophthora infestans]</a>	<a href="#">Phytophthora infestans</a>	444	444	100%	3e-158	88.81%	264	<a href="#">ACM68430.1</a>
<input checked="" type="checkbox"/>	<a href="#">hypothetical protein JG688_00003535 [Phytophthora aleatoria]</a>	<a href="#">Phytophthora aleatoria</a>	438	438	100%	1e-155	90.30%	262	<a href="#">KAG6973435.1</a>
<input type="checkbox"/>	<a href="#">hypothetical protein DVH05_011987 [Phytophthora capsici]</a>	<a href="#">Phytophthora capsici</a>	435	435	100%	1e-154	83.21%	265	<a href="#">KAG1700180.1</a>
<input type="checkbox"/>	<a href="#">PAN domain [Phytophthora infestans]</a>	<a href="#">Phytophthora infestans</a>	436	436	100%	2e-154	89.93%	303	<a href="#">KAF4136065.1</a>
<input checked="" type="checkbox"/>	<a href="#">putative CBEL-like protein [Phytophthora sojae]</a>	<a href="#">Phytophthora sojae</a>	427	427	100%	2e-151	83.96%	261	<a href="#">EGZ28485.1</a>
<input checked="" type="checkbox"/>	<a href="#">unnamed protein product [Phytophthora fragariaefolia]</a>	<a href="#">Phytophthora fragariaefolia</a>	427	427	100%	1e-150	81.55%	308	<a href="#">GMF17913.1</a>
<input type="checkbox"/>	<a href="#">hypothetical protein PHYPSEUDO_000732 [Phytophthora pseudosyringae]</a>	<a href="#">Phytophthora pseudosyringae</a>	426	426	100%	3e-150	86.19%	307	<a href="#">KAG7375531.1</a>
<input type="checkbox"/>	<a href="#">cellulose binding elicitor lectin [Phytophthora cinnamomi]</a>	<a href="#">Phytophthora cinnamomi</a>	420	420	100%	1e-148	82.46%	267	<a href="#">KAG6609279.1</a>
<input checked="" type="checkbox"/>	<a href="#">hypothetical protein PR002_g6863 [Phytophthora rubi]</a>	<a href="#">Phytophthora rubi</a>	420	420	100%	2e-148	81.72%	267	<a href="#">KAE9036882.1</a>
<input type="checkbox"/>	<a href="#">hypothetical protein ON010_g3852 [Phytophthora cinnamomi]</a>	<a href="#">Phytophthora cinnamomi</a>	418	418	100%	1e-147	82.09%	267	<a href="#">KAJ8575361.1</a>
<input checked="" type="checkbox"/>	<a href="#">hypothetical protein PF003_g5771 [Phytophthora fragariae]</a>	<a href="#">Phytophthora fragariae</a>	418	418	100%	1e-147	79.93%	269	<a href="#">KAE8910526.1</a>

**Comparaison au domaine général:**

## Family alignment for the fCBD domain, HMM/Weblogo format









Letunic et al. (2017) *Nucleic Acids Res* doi: 10.1093/nar/gkx922  
Letunic et al. (2020) *Nucleic Acids Res* doi: 10.1093/nar/gkaa937

SMART MODE:

NORMAL  
GENOMIC

Simple  
Modular  
Architecture  
Research  
Tool

[HOME](#) [SETUP](#) [FAQ](#) [ABOUT](#) [GLOSSARY](#) [WHAT'S NEW](#) [FEEDBACK](#)

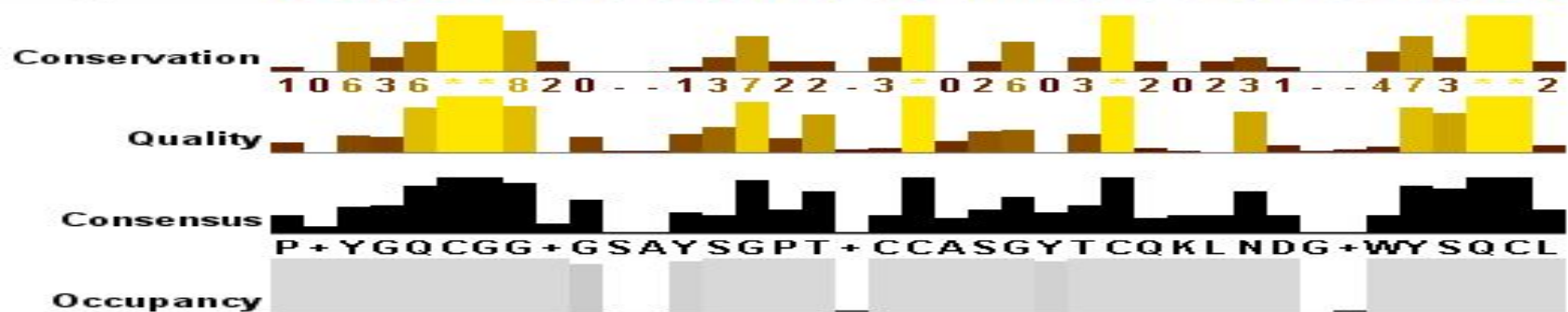
## Family alignment for the fCBD domain, CLUSTAL format

CLUSTAL W(1.60) multiple sequence alignment

```
PPGP34DEF_1/1- PSFGNCGSD---AAGVS-CCQSTQYCQPWNA--NYYQCL
PPGP34DEF_1/2- APYGSCGSS----NGAT-CCPSGYCQPWND--SFYQCI
S71569_1/1-34 AKWQCGGNG--FNGPT-CCQNGSRCQFVNE--WYSQCL
FOKCH_1/1-37 PAYYQCGGSKSAYPNGNLACATGSKCKVKQNE--YYSQCV
AF074951_1/1-3 PKYGQCGGRE--WSGSF-VCADGSTCQMONE--WYSQCL
GUX1_HUMGR/1-3 GRWQCGGIG--FTGPT-QCEEPYICTKLND--WYSQCL
NCCBH1_1/1-34 AHWAQCGGIG--FSGPT-TCPEPYTCAKDHD--IYSQCV
HGC_1/1-34 GAWQCGGVG--FSGST-SCVSGYTCVYLND--WYSQCQ
AB015511_1/1-3 SAYAQCGGNG--WTGAT-VCFTGYTCTYSNA--FYSQCV
403431/1-34 PVWGQCGGNG--WTGPT-TCASGSTCVKQND--FYSQCL
TRAXE1_1/1-34 THWGQCGGQG--WTGPT-QCESGTTCCQVISQ--WYSQCL
TRBEMA_1/1-33 PLYGQCGGSG--YTGPT-CCAQG-TCIYSNY--WYSQCL
2315274/1-34 TLYGQCGGSG--YSGPT-RCAPPATCSTLNP--YYAQCL
B48939/1-35 PFGSQCGGLG--YAGPTGVCPSPYTCQALNI--YYSQCI
PCCBH_1/1-34 PQWGQCGGIG--YTGST-TCASPYTCHVLNP--YYSQCY
GUXC_FUSOX/1-3 DQWGQCGGQN--YSGPT-TCKSPFTCKKIND--FYSQCQ
FOBCH_1/1-34 GVWAQCGGQN--WSGTP-CCTSGNKCVKLND--FYSQCQ
PP08843_1/2-0 KPYGQCGGMN--YSGKT-MCSPGFKCVELNE--FFSQCD
PP08843_1/4-0 GRYAQCGGMG--YMGST-MCVGGYKCMATSEGSMYKQCL
PP08843_1/1-34 VLYEQCGGIG--FDGVT-CCSEGLMCMKMGP--YYSQCR
PP08843_1/3-0 KEYAACGGEM--FMGAK-CCKFLVCYETSG-KWQSQCR
```

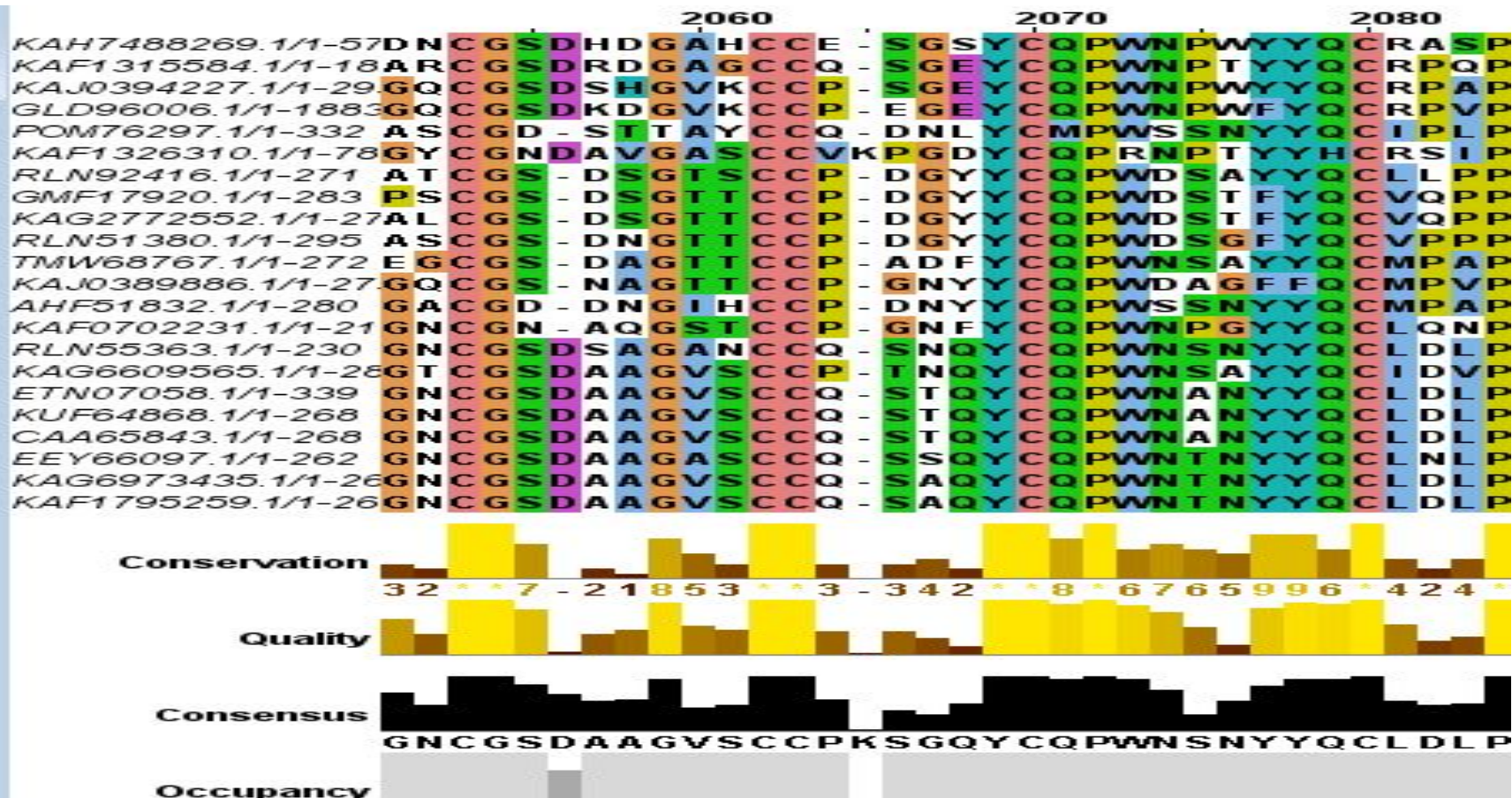
# Domaine fCBD général

	10										20										30																		
PPGP34DEF_1/1-1	P	S	F	G	N	C	G	S	D	-	-	-	A	A	G	V	S	-	C	Q	S	T	Q	Y	C	Q	P	W	N	A	-	-	N	Y	Y	Q	C	L	
PPGP34DEF_1/2-1	A	P	Y	G	S	C	G	S	S	-	-	-	-	N	G	A	T	-	C	C	P	S	G	Y	C	Q	P	W	N	D	-	-	S	F	Y	Q	C	I	
S71569_1/1-34	A	K	W	G	Q	C	G	G	N	G	-	-	F	N	G	P	T	-	C	C	Q	N	G	S	R	C	Q	F	V	N	E	-	-	W	Y	S	Q	C	L
FOKCH_1/1-37	P	A	Y	Y	Q	C	G	G	S	K	S	A	Y	P	N	G	N	L	A	C	A	T	G	S	K	C	V	K	Q	N	E	-	-	Y	Y	S	Q	C	V
AF074951_1/1-34	P	K	Y	G	Q	C	G	G	R	E	-	-	W	S	G	S	F	-	V	C	A	D	G	S	T	C	Q	M	Q	N	E	-	-	W	Y	S	Q	C	L
GUX1_HUMGR/1-3	G	R	W	Q	Q	C	G	G	I	G	-	-	F	T	G	P	T	-	Q	C	E	E	P	Y	I	C	T	K	L	N	D	-	-	W	Y	S	Q	C	L
NCCBH1_1/1-34	A	H	W	A	Q	C	G	G	I	G	-	-	F	S	G	P	T	-	T	C	P	E	P	Y	T	C	A	K	D	H	D	-	-	I	Y	S	Q	C	V
HGC_1/1-34	G	A	W	Q	Q	C	G	G	V	G	-	-	F	S	G	S	T	-	S	C	V	S	G	Y	T	C	V	Y	L	N	D	-	-	W	Y	S	Q	C	Q
AB015511_1/1-34	S	A	Y	A	Q	C	G	G	N	G	-	-	W	T	G	A	T	-	V	C	F	T	G	Y	T	C	T	Y	S	N	A	-	-	F	Y	S	Q	C	V
403431/1-34	P	V	W	G	Q	C	G	G	N	G	-	-	W	T	G	P	T	-	T	C	A	S	G	S	T	C	V	K	Q	N	D	-	-	F	Y	S	Q	C	L
TRAXE1_1/1-34	T	H	W	G	Q	C	G	G	Q	G	-	-	W	T	G	P	T	-	Q	C	E	S	G	T	T	C	Q	V	I	S	Q	-	-	W	Y	S	Q	C	L
TRBEMA_1/1-33	P	L	Y	G	Q	C	G	G	S	G	-	-	Y	T	G	P	T	-	C	C	A	Q	G	-	T	C	I	Y	S	N	Y	-	-	W	Y	S	Q	C	L
2315274/1-34	T	L	Y	G	Q	C	G	G	S	G	-	-	Y	S	G	P	T	-	R	C	A	P	P	A	T	C	S	T	L	N	P	-	-	Y	Y	A	Q	C	L
B48939/1-35	P	F	G	S	Q	C	G	G	L	G	-	-	Y	A	G	P	T	G	V	C	A	S	P	Y	T	C	Q	A	L	N	I	-	-	Y	Y	S	Q	C	I
PCCBH_1/1-34	P	Q	W	G	Q	C	G	G	I	G	-	-	Y	T	G	S	T	-	T	C	A	S	P	Y	T	C	H	V	L	N	D	-	-	Y	Y	S	Q	C	Y
GUXC_FUSOX/1-3	D	Q	W	G	Q	C	G	G	Q	N	-	-	Y	S	G	P	T	-	T	C	K	S	P	F	T	C	K	K	I	N	D	-	-	F	Y	S	Q	C	Q
FOBCH_1/1-34	G	V	W	A	Q	C	G	G	Q	N	-	-	W	S	G	T	P	-	C	C	T	S	G	N	K	C	V	K	L	N	D	-	-	F	Y	S	Q	C	Q
PP08843_1/2-0/1-3	K	P	Y	G	Q	C	G	G	M	N	-	-	Y	S	G	K	T	-	M	C	S	P	G	F	K	C	V	E	L	N	E	-	-	F	F	S	Q	C	D
PP08843_1/4-0/1-3	G	R	Y	A	Q	C	G	G	M	G	-	-	Y	M	G	S	T	-	M	C	V	G	G	Y	K	C	M	A	I	S	E	G	S	M	Y	K	Q	C	L





# Domaine CBM1 chez les Oomycètes



# **Comparaison des modèles aux banques protéiques et résultats:**

[include splice variants \(UniProtKB/Swiss-Prot\)](#)

## Hits for USERPAT1 "C-G-x(4)-[GT]-x(2)-C-C-x(4)-[YH](0,1)-C-[QM]-P-W-x(4)-Y-Q-C-x" on UniProtKB/Swiss-Prot and UniProtKB/TrEMBL reference

UniProtKB/Swiss-Prot (Release 2023\_04 of 13-Sep-23) contains 570157 entries.

UniProtKB/TrEMBL (Release 2023\_04 of 13-Sep-23) contains 0 entries.

found: 60 hits in 58 sequences

### Legend:



Please note that the graphical representations of domains displayed hereafter are for illustrative purposes only, and that their colors and shapes are not intended to indicate homology or shared function.

For more information about how these graphical representations are constructed, go to <https://prosite.expasy.org/mydomains/>.

hits by patterns: [60 hits (by 1 pattern) on 58 sequences]



```
# hmmsearch :: search profile(s) against a sequence database
# HMMER 3.2.1 (June 2018); http://hmmer.org/
# Copyright (C) 2018 Howard Hughes Medical Institute.
# Freely distributed under the BSD open source license.
#
# query HMM file:                profiloom.hmm
# target sequence database:      /bank/ebi/uniprot/current/fasta/uniprot_trembl.fasta
# output directed to file:      requetetrembl.search
#
```

Query: domaineoom [M=28]

Scores for complete sequences (score includes all domains):

--- full sequence ---			--- best 1 domain ---			-#dom-		Sequence	Description
E-value	score	bias	E-value	score	bias	exp	N		
9.8e-32	121.9	59.6	1.1e-10	54.6	13.6	5.3	3	tr A0A8K1C7V2 A0A8K1C7V2_PYTOL	Apple domain-containing protein
4.5e-31	119.8	57.3	2.1e-11	56.9	13.9	5.6	4	tr K3WRY9 K3WRY9_GLOUD	Apple domain-containing protein
4.2e-28	110.3	59.1	2.9e-08	46.9	13.0	5.0	3	tr K3WPX2 K3WPX2_GLOUD	Apple domain-containing protein
2.9e-24	98.0	66.5	1.5e-08	47.8	12.4	4.7	3	tr A0A662X6K5 A0A662X6K5_9STRA	Apple domain-containing protein
1.3e-23	95.9	64.5	5.7e-09	49.1	13.5	4.6	3	tr A0A8T1WUT2 A0A8T1WUT2_9STRA	Apple domain-containing protein
4.5e-23	94.2	53.2	5.2e-09	49.2	14.0	4.6	3	tr A0A3F2RJX1 A0A3F2RJX1_9STRA	Apple domain-containing protein
6.4e-23	93.7	46.2	2.1e-11	56.9	14.4	3.2	2	tr A0A8T1V3K1 A0A8T1V3K1_9STRA	Apple domain-containing protein
8.6e-23	93.3	37.5	3.9e-12	59.2	14.2	3.1	2	tr A0A8G1EIF6 A0A8G1EIF6_PHYRM	Cellulose binding elicitor lecti
8.6e-23	93.3	46.4	1.9e-11	57.0	14.4	3.2	2	tr A0A8T1VML4 A0A8T1VML4_9STRA	Apple domain-containing protein
9.3e-23	93.2	45.1	3.8e-12	59.3	14.5	3.0	2	tr A0A2P4YER5 A0A2P4YER5_9STRA	Cellulose binding elicitor lecti
1.1e-22	92.9	52.5	5.2e-09	49.2	14.0	4.6	3	tr A0A3R7JT10 A0A3R7JT10_9STRA	Apple domain-containing protein
1.1e-22	92.9	52.5	5.2e-09	49.2	14.0	4.6	3	tr A0A8J4W6Q6 A0A8J4W6Q6_9STRA	Apple domain-containing protein
1.2e-22	92.9	37.5	4.3e-12	59.1	14.2	3.1	2	tr A1EA00 A1EA00_PHYRM	Cellulose binding elicitor lecti
1.2e-22	92.8	37.5	4.4e-12	59.1	14.2	3.1	2	tr B2ZU37 B2ZU37_PHYRM	Cellulose binding elicitor lecti
1.3e-22	92.8	37.5	4.5e-12	59.0	14.2	3.1	2	tr B2ZU72 B2ZU72_PHYRM	Cellulose binding elicitor lecti
1.3e-22	92.7	37.5	4.5e-12	59.0	14.2	3.1	2	tr B2ZU45 B2ZU45_PHYRM	Cellulose binding elicitor lecti
1.3e-22	92.7	37.5	4.5e-12	59.0	14.2	3.1	2	tr B2ZU70 B2ZU70_PHYRM	Cellulose binding elicitor lecti
1.4e-22	92.6	37.5	4.6e-12	59.0	14.2	3.1	2	tr A0A8G1A8S0 A0A8G1A8S0_PHYRM	Cellulose binding elicitor lecti
1.4e-22	92.6	37.5	4.7e-12	59.0	14.2	3.1	2	tr A0A650FQH8 A0A650FQH8_PHYRM	Cellulose binding elicitor lecti
1.4e-22	92.6	37.5	4.7e-12	59.0	14.2	3.1	2	tr B2ZU32 B2ZU32_PHYRM	Cellulose binding elicitor lecti
1.5e-22	92.6	37.5	4.8e-12	58.9	14.2	3.1	2	tr B2ZU31 B2ZU31_PHYRM	Cellulose binding elicitor lecti
1.5e-22	92.5	44.7	7.1e-12	58.4	14.4	3.2	2	tr A0A081A0S9 A0A081A0S9_PHYPR	Apple domain-containing protein
1.5e-22	92.5	44.7	7.1e-12	58.4	14.4	3.2	2	tr W2L0R5 W2L0R5_PHYPR	Apple domain-containing protein
1.5e-22	92.5	44.7	7.1e-12	58.4	14.4	3.2	2	tr W2Z356 W2Z356_PHYPR	Apple domain-containing protein
1.5e-22	92.5	44.7	7.1e-12	58.4	14.4	3.2	2	tr V9EX27 V9EX27_PHYPR	Apple domain-containing protein
1.5e-22	92.5	44.7	7.1e-12	58.4	14.4	3.2	2	tr W2N786 W2N786_PHYPR	Apple domain-containing protein
1.5e-22	92.5	44.7	7.1e-12	58.4	14.4	3.2	2	tr W2GNC4 W2GNC4_PHYPR	Apple domain-containing protein
1.5e-22	92.5	44.7	7.1e-12	58.4	14.4	3.2	2	tr W2WSU4 W2WSU4_PHYPR	Apple domain-containing protein
1.7e-22	92.4	37.5	5e-12	58.9	14.2	3.1	2	tr A0A088CB98 A0A088CB98_PHYRM	Cellulose binding elicitor lecti
1.7e-22	92.4	37.5	5e-12	58.9	14.2	3.1	2	tr B2ZU23 B2ZU23_PHYRM	Cellulose binding elicitor lecti
1.7e-22	92.4	37.5	5e-12	58.9	14.2	3.1	2	tr B2ZU49 B2ZU49_PHYRM	Cellulose binding elicitor lecti
1.7e-22	92.4	37.5	5e-12	58.9	14.2	3.1	2	tr B2ZU62 B2ZU62_PHYRM	Cellulose binding elicitor lecti
1.8e-22	92.3	37.5	5.1e-12	58.8	14.2	3.1	2	tr A0A650F0U8 A0A650F0U8_PHYRM	Cellulose binding elicitor lecti
2.1e-22	92.1	38.3	9.6e-12	58.0	14.4	3.3	2	tr A0A329S4Z6 A0A329S4Z6_9STRA	Apple domain-containing protein
2.2e-22	92.0	36.2	1.9e-11	57.0	13.7	3.4	2	tr A0A8E5JRZ0 A0A8E5JRZ0_PHYCP	CBEL_0S=Phytophthora capsici_0X=
2.3e-22	92.0	38.2	3.8e-12	59.3	14.5	3.0	2	tr A0A2P4XL73 A0A2P4XL73_9STRA	Cellulose binding elicitor lecti
2.3e-22	91.9	68.8	9.3e-06	38.8	15.0	4.4	3	tr K3WI68 K3WI68_GLOUD	Apple domain-containing protein
2.6e-22	91.8	45.6	3e-11	56.4	15.7	3.2	2	tr A0A8S9UJC7 A0A8S9UJC7_PHYIN	PAN domain_0S=Phytophthora infes
2.6e-22	91.8	45.6	3e-11	56.4	15.7	3.2	2	tr A0A8S9U4S3 A0A8S9U4S3_PHYIN	PAN domain_0S=Phytophthora infes
2.7e-22	91.7	37.9	1e-11	57.9	14.9	3.4	2	tr A0A8T1WVR7 A0A8T1WVR7_9STRA	Apple domain-containing protein
2.9e-22	91.6	38.2	6.9e-12	58.4	14.7	3.1	2	tr A0A225V861 A0A225V861_9STRA	A cellulose-binding elicitor and
3.7e-22	91.3	45.6	8.1e-12	58.2	14.4	3.2	2	tr W2Q1I5 W2Q1I5_PHYPN	Apple domain-containing protein
4.5e-22	91.0	72.3	2e-08	47.4	14.0	5.0	3	tr A0A833SME1 A0A833SME1_PHYIN	PAN domain_0S=Phytophthora infes

--More-- (1%)



# IPR000254 Cellulose-binding domain, fungal ★

[InterPro entry](#) ⓘ


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- AlphaFold 12k
- Pathways 34

ACCESSION	NAME	SPECIES	MATCHES
A0A024TMX1	CBM1 domain-containing protein	Aphanomyces invadans	
A0A024TS35	CBM1 domain-containing protein	Aphanomyces invadans	
A0A024U9A9	CBM1 domain-containing protein	Aphanomyces invadans	
A0A024U4A0	CBM1 domain-containing protein	Aphanomyces invadans	

Output format: Graphical view - this view shows ScanProsite results together with ProRule-based predicted intra-domain features [\[help\]](#).

Hits for USERPAT1 "C-G-x(4)-[GT]-x(2)-C-C-x(4)-[YH](0,1)-C-[QM]-P-W-x(4)-Y-Q-C-x" on sequences A0A397CN61-unreviewed-CBM1, A0A397CV34-u

**no hit!**

# Bibliographie

[https://web2.mendelu.cz/af\\_291\\_projekty2/vseo/print.php?page=151&typ=html](https://web2.mendelu.cz/af_291_projekty2/vseo/print.php?page=151&typ=html)

<https://fr.wikipedia.org/wiki/Oomycota>

<http://snp.toulouse.inra.fr/~mathe/BIS/projets.html>