

Index of keywords

Keyword	Abstract Ref
a1 pheromone	PR1.32
ABC transporter	PR1.14, PR1.28, PR1.56, PR4.57
abfA	PR9.6
abiotic stresses	PS6.4
<i>Absidia</i>	PR3.12
accessory chromosomes	PS3.3
AcdX	PR7.20
acetate repression	PR7.20
acriflavin	PR7.27
actin	PR1.17, PR1.44
actin cytoskeleton	PR1.32
Acyl-CoA-binding protein	PR4.65
Adaptation	PR3.36, PR3.42
Adhesion	PR4.34, PR7.37
Aegerolysin	PR2.11
<i>Agaricomycete</i>	PR1.30
<i>Agaricus bisporu</i>	PR3.6, PR4.51
Ageing	PS5.3, PS6.5
alb1	PR8.15
alc regulon	PR7.20
aldehyde dehydrogenase	PR4.49
alfa-L-arabinofuranosidase	PR9.6
alfa-tubulin	PR1.34
alkaline protease	PR9.2
alkaliphilic fungi	PR10.8
<i>Alternaria</i>	PR3.14
<i>Alternaria brassicicola</i>	PR8.54
alternative splicing	PR1.5
ambruticin	PR7.26
ammonium sulphate	R4.35
ammonium transport	PR4.7, PR4.36
Amphotericin B	PR1.64
Amyloid	PS8.7
anastomosis group	PR10.18
anthracnose	PR4.2, PR4.26, PR4.74
anthranilate synthase component II	PR1.9
antifungal compounds	PR4.39, PR4.48, PR4.51, PR8.59, PR8.77, PR9.5, PR9.9
antifungal protein	PAF, PR1.53
antimicrobial effect	PR10.10
antimicrobial peptides	PR8.13, PR9.5
apical dominance	PR4.29
apocarotenoid	PR2.14
apomixis	PR3.19
apoptosis	PR10.10
appressoria	PR7.36, PR4.74
ApsB	PR1.43
APSES proteins	PR1.57
aquaglyceroporin	PR7.21
aquaporin	PR7.21
<i>Arabidopsis</i> pathogen	PS3.1
<i>Arabidopsis thaliana</i>	PR4.15
arbuscular mycorrhiza symbiosis	PR4.7, PS5.6
AREA	PR1.52
AREB	PR1.52
Arf proteins	PR1.77
arginine	PR1.25
argonaute protein	PR3.23
<i>Arnium arizonense</i>	PR3.19
<i>Ascochyta rabiei</i>	PR7.15
ascomycetes evolution	PR3.2
ascospore development	PR2.4
ascospore germination	PR1.9

asexual development	PR7.2, PR7.19, PR7.32
<i>Ashbya gossypii</i>	PR1.75, PR4.64
<i>Aspergillus</i>	PR1.17, PR1.40, PR3.10, PR3.15, PR3.18, PR3.30, PR3.34, PR4.1, PR7.12, PR8.4, PR8.29, PR8.35, PR8.50, PR8.66, PR10.12
<i>Aspergillus aculeatus</i>	PR7.30
<i>Aspergillus clavatus</i>	PR8.26
<i>Aspergillus flavus</i>	PR8.39
<i>Aspergillus fumigatus</i>	PR1.28, PR1.36, PR4.46, PR6.5, PR7.24, PR9.8, PR10.16
<i>Aspergillus nidulans</i>	PR1.29, PR1.44, PR1.61, PR4.38, PR7.2, PR7.19, PR7.21, PR7.32, PR8.60
<i>Aspergillus niger</i>	PR3.32, PR3.38, PR8.5, PR8.11, PR8.12, PR8.15, PR8.19, PR9.3, PR9.12, PR10.17
<i>Aspergillus oryzae</i>	PR1.11, PR1.38, PR1.46, PR1.56, PR1.68, PR8.20, PR8.40, PR8.42, PR10.9, PR10.15
<i>Aspergillus terreus</i>	PR8.19, PR10.7
aspyridone	PR8.20
asteromella	PR2.8
asymmetry	PS1.7
aurofusarin	PR1.67
autolysis	PR9.12
autonomously replicating plasmid	PR8.41
autophagy	PR4.54, PS6.5
autoregulators	PR7.2, PR7.32
auxin	PR4.31
avirulence genes	PR4.6
b mating type	PR2.9
b -tubulin	PR10.6
bafilomycin B1	PR9.3
barley	PR4.31
basic helix-loop-helix	PR10.9
basidia	PR2.6
basidiomycete telomeres	PS3.6
Basidiomycota	PR3.1, PR2.11, PR3.35, PS5.7, PR8.55, PR8.59, PR8.63
Bax Inhibitor-1	PR4.45
Bayesian analysis	PR10.14
Bem46	PR1.9
benzimidazole	PR8.77
beta oxidation	PR3.21
beta-galactofuranosidase activity	PR9.6
beta-glucan	PR4.27, PS9.7
beta-glucosidase	PR8.67
Bikaverin	PR1.67, PR7.9, PR7.14
Bikisocoumarin	PR1.67
biocontrol	PR1.3, PR3.5, PR4.34, PR4.53, PR8.36
bioengineering	PR8.34
bioethanol production	PR8.24
biofilm	PR1.64, PR7.37, PR8.15, PR8.22
biofuels	PS8.1
bioinformatics	PR3.33, PR3.35, PR8.5, PR8.63
biological control	PR4.23, PR8.57, PR9.2
biomass	PS5.6
biosynthesis	PR8.34, PR8.59
Biotechnology	PR3.30, PS8.5
biotin	PR1.11
biotrophy	PR4.2, PR4.31, PR4.76
<i>bipolaris</i>	PR10.14
b-lactam biosynthetic pathway	PR8.33
<i>Blakeslea trispora</i>	PR2.14
blue mold	PR10.6
<i>Blumeria graminis</i>	PS4.6
BNI-1	PS1.3
Boletales	PR8.25
Botrytis	PR7.3
<i>Botrytis cinerea</i>	PR7.3
branching	PR1.21, PR1.59
Brassicaceae	PR4.10
BUD-6	PS1.3
button mushroom	PR3.20
CadA	PR8.19

Calcineurin	PR1.10, PR1.63, PR7.3
Calcipressin	PR7.3
Calcium	PR7.3
Calcium signalling	PR1.31
Callose	PR4.60
Calmodulin	PR1.31
Calnexin	PS4.5
<i>Candida albicans</i>	PS1.1, PR1.64, PR3.22, PS9.7
<i>Candida</i> spp.	PR1.65, PR3.15, PR8.77
Canola	PR4.18
Carboamyl-Aspartate, Dihydroorotate	PR1.23
carbohydrate-active enzymes	PR8.18
carbon catabolite repression	PR1.68
carbon metabolism	PR3.6
carbon repression	PR1.52
carotenoid biosynthesis	PR1.55
carrier protein	PR8.65
catalase-peroxidase	PR3.17
catheters	PR1.65, PR1.64, PR8.22
CAZy	PR8.37, PR8.66
CBM	PR9.7
Cdc42	PR1.59, PR1.60, PR2.6
cell development	PR1.26
cell fusion	PR1.31
cell penetration	PR9.9
Cell polarity	PR1.1
cell signaling pathway	PR1.22, PR1.23
cell wall	PR9.3, PS9.4, PR9.4, PS9.5, PS9.7, PR9.12
cell wall degrading enzymes	PR3.42
cell wall integrity	PR1.47, PS9.6, PR9.8
cell wall polymer	PR4.27
cell wall proteins	PR8.43
cell wall stress	PR9.5
cellobiohydrolase	PR8.56
cellobiose induction	PR7.30
cellobiose response regulator ClbR	PR7.22
cellodextrin transporter	PR8.67
cellulase	PS8.1, PR8.47, PR8.60, PR8.62, PR8.67
cellulose	PR7.22, PR8.53
centromere	PL2.1, PR3.22
Cephalosporins	PR8.32
cerato-platanin	PS9.5
<i>Cercospora zeina</i>	PR8.27
cereal	PR4.49, PR10.2
CgEP1	PR4.26
<i>Chaetomium globosum</i>	PR8.50
characterization	PR8.56
cheating	PR4.33
chemical genetic profiling	PR10.3
ChemiGenomics	PR8.17
chemotropism	PR1.18
chemotype	PR4.49
ChIP-sequencing	PL2.1
chitin	PR9.4, PS9.5
chitin synthases	PS9.4, PR9.4
chitinase	PR1.19, PR3.43, PR9.2, PR9.12
chitosan	PR4.39
<i>Chlamydomonas reinhardtii</i>	PR7.15
chromosome	PR1.50, PR1.73
cis-prenyltransferase	PR10.11
citreoisocoumarin	PR1.67
citrus fruit	PR9.4
Clip1	PR8.1
cloning and expression	PR8.26
ClpXP Complex	PS5.5
<i>Cochliobolus</i>	PS3.7

co-evolution	PR3.42
<i>Colletotrichum</i>	PR1.50, PR4.74, PR7.35
<i>Colletotrichum acutatum</i>	PR3.41
<i>Colletotrichum graminicola</i>	PR4.25, PR4.26
<i>Colletotrichum higginsianum</i>	PR4.47
Color mutants	PR10.17
Comparative Genomics	PS3.7, PR3.15, PR3.29, PR3.30, PR8.66
Compartmentalization	PR1.4, PR8.32
conditional mutant	PR9.3
confocal microscopy	PR4.15
confrontation	PR4.53
conidia	PR1.71
Conidial pigmentation	PR10.17
conidiation	PR1.35, PR7.6, PR7.14, PR8.23, PR10.9
<i>Conidiobolus</i>	PR3.12
conidiophore	PR7.2, PR7.19, PR7.32
contaminations types	PR1.65
COP9 signalosome	PS8.3
<i>Coprinopsis cinerea</i>	PS2.1, PR2.11, PR4.59, PR8.44, PR8.50
CreA	PR1.68, PR8.12
crown and foot rot	PR8.48
cryptic speciation	PR10.13
cryptic splicing	PR10.15
cryptochrome photoreceptor	PR7.14
cryptochrome/photolyase	PR7.10
<i>Cryptococcus adeliensis</i>	PR4.3
<i>Cryptococcus neoformans</i>	PR1.22, PR1.23, PR1.70
CSP typing	PR10.16
cuticle degrading serine proteases	PR4.41
cutinase	PR8.35
cycloheximide	PR8.11
CYP53A15	PR4.48
cysteine proteases	PR4.50, PR4.54
cytochrome	P450, PR4.48, PR8.6
cytokinesis	PR1.42, PR1.44, PR1.74
cytoskeleton	PR2.10
data mining	PR3.40
de novo assembly	PR8.45
deep sequencing of sRNA	PR1.20
defense signaling	PR4.55
Defensin-like protein	PR10.10
Dehydrins	PR8.54
deoxyhypusine hydroxylase (DOHH)	PR4.52
deoxyhypusine synthase (DHS)	PR4.52
deoxynivalenol	PR1.57
dermatophytes	PR7.27
detoxification	PR1.41, PR3.9
development	PR1.35, PR2.2
developmental genetics	PR8.63
dicer	PR1.12
<i>Dichomitus squalens</i>	PR8.46, PR8.56
differential gene expression	PR4.43
differential regulation	PR2.12
differentiation	PS8.7
Dihydroorotase	PR1.23
dikaryosis	PS2.4
dikaryotic state	PS2.2
dimorphism	PR2.1, PR4.9
diseases resistance	PR3.20
disruptants	PR3.21
divergence	PR2.3
diversity	PR3.26, PR10.18
DMI	PR8.51
DNA barcode	PR3.1
DNA recombination	PS5.7
DNA repair	PR7.14

DON induction	PR4.35
<i>Dothidiomycete</i>	PS3.7, PR3.14, PR4.48
drug discovery	PR10.3
drug resistance	PR1.36, PR1.56
drug resistant fungi	PR9.5
drug response	PR7.26
drug target	PR4.48, PR10.3
D-xylose	PR8.12
dynammin-like GTPase	PS3.8
Dynein	PR8.1
Dysdercus peruvianus	PR8.57
E3 ubiquitin ligase	PR4.66
Ectomycorrhiza	PR4.22, PR4.43, PR4.49, PR4.64, PR4.78
ecto-phosphatase	PR4.34
effector	PR3.11, PR3.36, PR4.37, PR4.2, PS4.4, PS4.6, PR4.6, PR4.7, PS4.7, PR4.16, PR4.30, PR4.62, PR4.76
effector genes	PR3.8, PS4.8
effector protein	PS3.1, PR4.26, PR4.75
Efg1	PS9.7
eisosome	PR1.9
endocytosis	PR1.32, PR1.38, PR8.13
endogenous sRNA	PR1.12, PR1.20
endophyte	PR4.31, PR4.36, PS8.5, PR9.7
Endoplasmic reticulum (ER)	PR1.72
endosomes	PS1.4
ENGase	PR1.3, PR1.19
ensembl	PR3.29
entomophthorales	PR4.41
environmental adaptation	PR3.9
enzymatic hydrolysis	PR8.53
enzyme	PR8.62
enzyme discovery	PR8.4
<i>Epichloe</i>	PR1.16, PL6.2, PR1.63
ergosterol	PS7.5
ER-targeting	PR8.9
esterase	PR8.35, PR8.55
ethanol detoxification	PR4.43
eukaryotic translation initiation factor 5A (eIF5A)	PR4.52
evolution	PR2.6, PS2.6, PR2.8, PR3.23, PR3.41, PR10.13
evolutionary Genomics	PS3.3, PR3.36
exonic-siRNAs	PR1.12
experimental evolution	PS7.6
expressed sequence tags	PR3.28
expression	PR1.34, PR8.6
extracellular enzymes	PR3.10
fatty acids	PR3.21
Fgap1	PR7.5
fiber degrading enzymes	PS8.5
filamentous fungi	PR1.51, PR8.1, PR8.33, PR8.45, PR8.61, PR10.10
filamentous growth	PR1.1, PR1.2, PS1.7, PR1.77
Fish	PS4.4
fission	PS5.3
fitness	PS7.6
flocculation	PS3.2
flow cytometry	PR4.1
FLP/FRT recombination system	PR8.10
fludioxonil	PR7.26
fluorescence	PR2.13
fluorescence spectroscopy	PS1.8
fluorescent microscopy	PR4.1
fluorescent probes	PR8.8
forkhead	PR7.2
FPP synthase	PR10.11
frequency of mutation	PR3.22
Fruit rot	PR8.58
fruiting body	PS2.2, PR3.6
fum gene cluster	PR3.38

FUM1, FUM21	PR8.49
fumonisin	PR10.2
fumonisin B1	PR1.15
fumonisin B2	PR3.38
fumonisin biosynthesis	PR8.49
functional analysis	PR4.8
fungal cell factory	PR8.29
fungal cell wall biosynthesis	PR9.5
fungal cells	PR8.8
fungal defense	PR4.59
fungal development	PR7.7
fungal diversity	PR1.16
fungal effectors	PR4.44, PR4.78
fungal genomes	PR3.29
fungal growth	PR3.40
fungal hybrid	PR3.17
fungal pathogen	PS3.5
fungal regulators	PR8.32
fungal RNAi	PR3.23
fungal transformation	PR1.36
fungal-insect interactions	PR4.63
fungicide resistance	PR3.3, PR8.6, PR10.6
fungicide sensing	PS7.6
fungicides	PR8.17, PR10.1
fungivorous nematodes	PR4.64
fungus-plant interaction	PR4.43, PR4.49, PR4.70
Fus3	PR7.7
fusarin	PR3.13, PR8.14, PR8.31
<i>Fusarium</i>	PR1.73, PS3.5, PR3.11, PR3.13, PR4.9, PR4.49, PR4.58, PR4.66, PS6.3, PS7.2, PR8.14, PR8.17, PR8.31, PR10.1, PR10.2
<i>Fusarium fujikuroi</i>	PR7.9, PR7.10, PR8.2, PR8.16
<i>Fusarium graminearum</i>	PR1.7, PR1.35, PR4.4, PR4.5, PR4.29, PR4.35, PS7.4, PR7.5, PR9.11
<i>Fusarium</i> head blight	PR4.49
<i>Fusarium oxysporum</i>	PR1.66, PR3.8, PS4.8, PR4.23
<i>Fusarium verticillioides</i>	PR1.15, PR8.49
fusarubin	PR8.16
fusion	PS7.3, PS5.3, PS7.5
fusion PCR	PR1.36
fusion protein	PR8.54
G protein signaling	PR4.66
G protein-coupled receptors	PS7.4, PR7.17
G proteins	PR1.1, PR7.31
GABA	PR1.10
galactofuranose (Galf)	PR9.10
galactofuranose transporter	PR9.10
galectins	PR2.11
Ganoderma sp.	PR4.39
gasteroid	PR2.6
GATA factors	PR1.52
GC kinase	PR1.33
gene cluster	PR3.13, PR8.49
gene Disruption	PR1.3
gene expression	PR1.29, PR1.35, PR2.12, PS3.6, PS4.8, PR4.22, PR4.59, PR7.26, PR8.64
gene knock out	PR1.57
gene prediction	PR3.18
gene regulation	PR1.51, PR7.8
gene regulatory network	PR7.1
gene replacement	PR7.17
gene silence	PR8.60
genetic engineering	PS8.6, PR8.41
genetic variability	PR10.13
genetically modified	PS8.5
genetics	PR1.73
genome	PR1.50, PS2.4, PR2.10, PR3.2, PR3.3, PS3.4, PS3.6, PR3.15, PR3.25, PR3.26, PR3.27, PR3.29, PR3.33, PR3.34, PR3.37, PR3.41
genomics	PR1.27, PR3.5, PR3.16, PR3.18, PR3.31, PR8.47

genotypic analysis	PR3.11
germination	PR1.71
GH18	PR9.12
<i>Gibberella</i> ear rot	PR4.49
<i>Gibberella zeae</i>	PR4.27
gibberellin biosynthesis	PR8.2
gibberellins	PR7.9
gliotoxin	PR1.6
<i>Glomus intraradices</i>	PR4.7
glucanase	PR9.2
glucanosyltransferase	PR4.56
glucose analog	PR1.38
glucose oxidase	PR4.14
glucose repression	PR1.68
glutamate decarboxylase	PR1.10
glutamine synthetase	PR7.9
glutathione	PR1.14
glutathione transferase	PR3.9
glycerol	PR7.18
glycoconjugates	PR9.10
glycolysis	PR1.4
glycoside hydrolases	PR1.51, PR7.31
glycosyl hydrolase	PR9.6
glycosylation	PR8.36
Golgi	PR1.72, PR1.77
GPCR-PIPK	PL1.2
grapes	PR3.38
grey leaf spot	PR8.27
Grey mold	PR4.71, PR8.6
growth and development	PR4.10
Growth profile	PR8.24, PR8.66
GTPase-activating protein	PR1.60
GTPases	PR1.59
H ₂ O ₂	PR4.60
haloacid dehalogenase family	PR7.18
HAMP domain	PS7.6
Haploinsufficiency	PR10.3
haustorial interface	PS3.1
HD1 and HD2 gene pairs	PS2.1
Hemibiotrophic Development	PR4.25
hemicellulose	PR8.24, PR8.26
heterokaryon incompatibility	PR4.33
heterologous expression	PS8.6, PR8.20, PR8.41, PR8.60, PR8.65
heterologous transposition	PR8.48
heterothallism	PR2.3
HFBI	PR8.61
high thermotolerance	PR1.70, PR3.39
histidine kinase	PR7.12
histidine-alanine rich proteins	PR4.30
histone modification	PL2.1
Hog1-like	PR6.2
homeobox genes	PS2.2
homeodomain transcription factors	PS2.1
homing endonuclease	PS5.7
homothallism	PR3.19
horizontal chromosome transfer	PR1.66, PS4.8
Horizontal gene transfer	PR2.15, PS3.5
Hormones	PR4.64
Host response	PR4.71
Host specific toxin	PR3.14, PS4.7
Host Specificity	PR3.3, PR3.36, PR4.28
host-induced gene silencing	PS4.6, PR4.56
host-interaction	PR3.23, PR3.33, PR4.4, PR4.5, PR4.6, PR4.25, PR4.34, PR4.41, PR6.2
Hsp70	PR1.56
HSP90	PS3.1
Hu1A	PR1.68

hydrolases	PR8.4, PR8.12
hydrophobin	PR4.70, PR8.9, PR8.35
Hydroxy-methyl-glutaryl CoA reductase	PR8.2
Hyphal modification	PS1.1, PR1.21, PR1.63, PR2.11, PR6.3
<i>Hyphodermella</i>	PR8.58
<i>Hypocrea jecorina</i>	PS2.7
hypoxia	PR8.40, PR10.12
Hypusine	PR4.52
i-AAA Protease	PS5.5
ICU	PR1.65
IGS	PR3.1
immunity	PR9.1, PS9.7
incompatibility	PR2.3
Indole-3-acetic acid (IAA)	PR4.77
insertional mutagenesis	PR4.15, PR4.21
interspecies fusion	PR1.16, PR2.15
intron retention	PR1.5
Invasive Growth	PS3.2
iron	PR1.25, PR1.28, PR1.41, PR1.62
isoelectric focusing	PR4.55
Itaconic acid	PR8.19
ITS	PR3.1, PR4.18, PR4.19, PR8.58
karyotype	PR1.50
kinesin	PS1.4
kinetochore	PL2.1
kinome	PR1.2
laccase	PR2.12, PS3.4, PR8.7, PR8.64
<i>Lactuca sativa</i> (lettuce)	PR4.23
leaf extract	PR1.37
Lectins	PR9.7
<i>Leptosphaeria</i>	PL3.3
<i>Lichtheimia</i>	PR3.12
light	PS2.7, PR4.21, PR7.6, PR7.31, PR7.34
lignin	PR4.39, PR8.38
lignocellulose	PR8.37, PR8.53, PR8.55
lipid	PS1.7
lipidomic	PR1.15
Lis1	PR8.1
litter-decomposing fungi	PR8.38
Live-cell imaging	PR1.1, PR1.66, PR8.13
<i>Longibrachiatum</i>	PR10.20
LysM	PR4.73, PR9.7
<i>Magnaporthe oryzae</i>	PR3.10, PR9.1
Maize	PR1.15, PR4.7, PR4.44, PR4.66
MAK-2	PS7.3
maltose permease	PR1.38
MAMPs	PR9.1
manganese peroxidase	PR8.38
mannitol	PR2.4
MAPK	PR1.18, PR1.33, PR1.47, PR1.75, PR4.4, PR4.5, PR6.2, PS7.3, PS7.5, PR7.7, PS7.7, PR7.23, PR7.29, PR7.33
MATE transporter	PR4.49
mating	PR1.59, PR2.1, PS2.1, PR2.5, PS2.5, PS2.6, PR3.19, PR3.27
MDR	PR8.51
Melanin	PR8.15, PR10.17
melanised rock-inhabiting fungi	PR3.2
Membrane Proteins	PR8.33
Membrane trafficking	PR1.70
membrane transport	PR5.1
Mesosyteny	PS2.4
metabolic engineering	PS8.6
metabolism	PS1.8, PR3.21, PS4.7, PR8.6, PR8.30
<i>Metarhizium anisopliae</i>	PR4.34, PR8.57
MFS transporters	PR8.32
MIC	PR10.12
micafungin	PR1.47

microarray	PR1.35, PR4.8, PR7.34, PR7.36
microbial communication	PR4.46
microbial volatile organic compounds (MVOCs)	PR4.23
Microtubules	PS1.4, PR1.17, PR1.32, PR1.43
miRNA	PR8.28
mitochondria	PR1.11, PR1.25, PR1.62, PR3.1, PR5.1, PS5.3, PS5.6, PS5.7, PR8.19
mitogen-activated protein kinase	PS7.2, PR7.25
Mitosis	PR8.1
molecular identification	PR10.14
molecular taxonomy	PR10.8
morphogenesis	PS1.1, PR1.37
mRNA	PR1.20, PR1.74, PR7.19
mucin	PR7.23
<i>Mucor</i>	PR1.55
MudPIT	PR7.29
multidrug resistance	PR3.3
mushroom development	PR2.9, PR4.51, PR8.63
Mushroom genomics analysis platform	PS3.4
mutational analysis	PR1.61
<i>Myceliophthora heterothallica</i>	PR8.18
<i>Myceliophthora thermophila</i>	PR8.65
mycoparasitism	PR3.16, PR3.43, PR4.53, PR4.57, PR7.11
Mycorrhiza	PR4.42, PR4.70, PR4.77
<i>Mycosphaerella graminicola</i>	PS3.3, PR4.68, PR8.30, PR8.51
mycotoxin	PR4.9, PR8.14
Mycovirus	PR10.16
myosin	PR1.17, PR1.44
NADPH oxidase	PS6.2, PL6.2, PS6.3
natural products	PR8.25, PR8.39, PR8.59
Natural Selection	PS3.2
NDR kinase	PR1.21, PR1.33, PR1.42
Necrotrophic effectors	PR10.13
Necrotrophic fungi	PR4.15, PR4.71, PR4.72
Nematotoxic proteins	PR4.59
<i>Neosartorya fischeri</i>	PR2.4, PR10.10
<i>Neurospora crassa</i>	PS1.3, PR1.9, PR1.19, PR1.21, PR1.27, PR1.31, PR1.42, PR1.47, PS3.8, PS7.3, PS7.5, PR8.13, PR8.67
next generation sequencing	PR4.28, PR8.45
N-glycosylation	PS4.5, PR8.1
Nitrogen	PR1.52, PR4.7, PR4.36, PR7.8, PR7.9, PR8.31, PR8.42
NMR	PR1.53
non ribosomal peptide	PR8.34, PR9.11
non-host resistance	PR4.45
nosocomial infections	PR1.64, PR1.65
NPR1	PR4.20
Nrg1	PS1.1
NRPS	PR9.11
nutrient acquisition and signaling	PR4.69, PR7.31
Obestatin	PR8.61
Obligate Biotrophy	PS3.1
<i>Oomycete</i>	PS4.4
Organ Specificity	PR4.62
Organismic Interaction	PR4.64
Ornithine	PR1.25, PR1.62
Osmotic Stress	PR7.18, PR7.21
Oxalate Decarboxylase	PR8.46
Oxalic Acid	PR8.46
Oxidative Burst	PR4.44
Oxidative Stress	PR6.4, PR7.5, PR8.54
Oxylipins	PR1.15
oxysporum	PR1.73
P450	PR8.30
PAL	PR4.17, PR4.20
parasexual development	PR2.15
Pathogen	PR3.26, PR3.27, PR3.31, PR4.46, PR4.58, PS6.2, PR10.14
Pathogen emergence	PR3.37
Pathogenesis	PR3.27, PR4.52, PR4.72

Pathogenicity	PR1.18, PR1.57, PR1.74, PR2.2, PR4.10, PR4.32, PR7.37, PR4.40, PR4.74
pathogenicity chromosome(s)	PS4.8
Pathogenicity Factor	PR4.26, PR4.65
Pathogenicity Genes	PR4.41
Pathogenicity Screen	PR4.47
P-body	PR1.46
Pectin	PR1.27
Pectinases	PR4.40
Penicillin	PR2.5, PR8.21, PR8.23, PR8.28, PR10.5
<i>Penicillium</i>	PR1.51, PR3.30
<i>Penicillium chrysogenum</i>	PR2.5, PR4.14, PR8.10, PR8.21, PR8.23, PR8.28, PR10.5
<i>Penicillium digitatum</i>	PR4.40, PR9.4
<i>Penicillium expansum</i>	PR4.14, PR10.6
Peptide expression	PR8.61
Peptide synthetase	PR8.25, PR8.39
Perithecia	PR1.37, PS7.4, PR8.16
Peroxidase	PR4.44
Peroxisomes	PR1.4, PR1.11, PR1.40, PR1.43
pH sensing	PR7.35
Phaeosphaeria	PS3.5, PR10.13
Phagocytosis	PR7.1
<i>Phanerochaete chrysosporium</i>	PR3.9
Phenotypic plasticity	PR7.28
Pheromone	PR1.18, PR1.75, PS2.6, PS2.7, PR7.7
<i>Phlebia radiata</i>	PR3.28
Phosphatidylinositolphosphate	PS1.7, PR1.53, PR1.77
phosphoinositide	PS1.7
phospholipase D	PL1.2
phospho-proteomics	PR7.25
Phosphorylation	PS1.1, PR2.13
Photobiology	PR7.14
Photodynamic toxin	PS6.4
phylogenomic analysis	PR3.12
Phylogeny	PR1.50, PR2.3, PR3.14, PR3.26, PR3.27, PR10.14, PR10.20
Phytoalexins	PR4.60
phytohormones and IAA-biosynthesis	PR4.43
Phytophthora	PL1.2
Phytotoxicity	PR7.15
Phytotoxin	PR10.7
<i>Pichia pastoris</i> expression system	PR9.6
<i>Piriformospora indica</i>	PR4.31
planktonic	PR8.22
plant cell wall degradation	PR1.27, PR8.67
plant microbe interaction	PR4.7
Plant Pathogen	PR1.45, PR3.17, PR3.29, PR3.33, PR4.21, PR4.28, PR4.32, PR4.56, PR4.60, PR4.69, PR7.35, PR9.1
plasma membrane	PR1.53, PR1.77, PR7.23
<i>Plectosphaerella cucumerina</i>	PR4.15
Pleurotus	PR3.7, PR8.3, PR8.7
Podospora	PS2.2, PS5.5, PS6.5, PR8.24
polarisome	PS1.3
polarity	PR1.13, PS1.4
polyamines	PR1.62
Polyketide	PL3.3, PR3.13, PR8.34
Polyketide Synthase	PR1.67, PR7.15, PS8.3, PR8.14, PR8.16, PR8.20, PR10.7
Polysaccharide Degradation	PR3.10, PR8.18, PR8.66
Population genetics	PS3.3
Postharvest	PR4.14
Post-transcriptional suppression	PR10.15
potato	PR4.58, PR10.18
PR genes	PR4.17, PR4.20
premature polyadenylation	PR10.15
premeiotic recombination	PS3.8
prf1	PR2.1
programmed cell death	PR4.45
promoter study	PS8.6
Proteases	PR3.16, PR3.35, PR4.22, PR8.60

protein body formation	PR8.9
protein evolution	PR3.43
protein expression platform	PR8.1
Protein Glycosylation	PR9.9
protein interaction	PR8.35
Protein Kinase	PR1.2, PR7.24, PR9.8
protein phosphatases	PR1.2
Protein production	PR4.1, PR8.52
protein secretion	PR8.29
protein-protein interaction	PR5.1
Proteome	PR1.30, PR1.45, PR8.40, PR8.43, PR8.52
Proteomics	PR1.27, PR4.10, PS6.3
<i>Prunus</i>	PR8.58
<i>Pseudomonas fluorescens</i>	PR8.57
qRT-PCR	PR2.12
QST/GST comparisons	PR7.28
QTL	PR3.20
quantitative proteomics	PR8.11
Quantitative Real-Time PCR	PS5.6
Rac	PR1.59
Rad52	PR3.22
<i>Ramularia collo-cygni</i>	PR2.8, PS6.4
Ras protein	PR2.10
reactive nitrogen intermediates	PR6.5
Reactive Oxygen Species	PR4.4, PR4.5, PR6.6, PR7.10
real-time PCR	PR1.55, PR10.1, PR10.2
receptor	PR1.18
recombinant protein production	PR8.29
redox homeostasis	PR1.4, PR6.6
Redox-enzymes	PR8.43
Regulation and Development	PL6.1
Regulatory Variation	PS3.2
repeated DNA	PL2.1
repeat-induced point mutation	PS3.8
repetitive elements	PS5.7
retrotransposon	PR4.42
RGS protein	PR7.33
<i>Rhizoctonia solani</i>	PR4.17, PR4.18, PR4.19, PR10.18
Rho1	PR1.1
RHO-GTPases	PR1.42
<i>Rhynchosporium commune</i>	PR7.28
Rice blast	PR4.2
RIP	PS3.8
RNA interference	PR4.68
RNA silencing	PR1.12, PR1.20, PR1.55, PR4.56, PR4.70, PR8.28
RNA transport	PR1.13
RNA-binding protein	PR1.74
RNA-dependent RNA Polymerases	PR1.12, PR1.20
RNA-Seq	PR1.45, PS2.4, PR3.7, PR3.18, PR4.29, PR4.32, PR7.27, PR8.51
Root endophyte	PR4.30
Root hairs	PR4.64
ROS	PS6.2, PL6.2, PS6.3, PR6.3, PR6.4
RT-qPCR	PR4.55, PR8.46
Rubellin	PS6.4
RXLR effector target	PL1.2
RX-RGS domains	PR7.33
saccharification	PR8.18
<i>Saccharomyces cerevisiae</i>	PS5.3, PR6.4, PR8.17
Safflower	PR4.19
SAGA complex	PR7.20
SAGA/ADA complex	PR4.38
Salicylate hydroxylases	PR4.61
Salicylic acid	PR4.37
<i>Saprolegnia parasitica</i>	PS4.4
scaffold protein	PR1.33
scanning electron microscopy	PR10.8

Schizophyllum sclerotium	PR1.30, PR2.6, PR2.9, PR2.10, PR2.12
SDF-2 peptide	PR4.65
Sec7	PR1.70
Secondary Metabolism	PR1.29, PL3.1, PS3.7, PR3.13, PR4.35, PR4.63, PR4.66, PR7.24, PR7.10, PS8.3, PR8.23, PR8.25, PR8.31, PR8.50, PR8.59
Secondary Metabolite	PL3.3, PR4.46, PR8.5, PR8.16, PR8.34
Second-generation ethanol	PR8.26
secreted effector	PR4.50, PR7.23
Secreted enzymes	PR4.37, PR4.41
Secretion	PR1.51, PR1.72, PR2.2
Secretome	PR8.3, PR8.11, PR8.43
sensing	PS7.4, PS7.7, PR7.17
sensitivity to high temperature	PR1.22, PR1.23
Septation	PR1.42, PR1.44
Septin	PR1.60
<i>Septoria</i>	PR8.30
<i>Septoria tritici</i>	PR4.16
Sequencing	PR3.25
sexM	PS2.5
sexP	PS2.5
Sexual Development	PR1.33, PS2.1, PS2.7, PR3.19, PR6.3, PR7.2, PR7.36
sexual recombination	PR2.5
sexual reproductive system	PR2.3
Shiitake	PS3.4
Siderophores	PR1.25, PR1.28, PR1.40, PR1.41, PR1.62
Signal transduction	PR2.10, PR7.11, PR7.3
Signalling	PR4.76, PS7.3, PS7.5, PS9.6
silenced gene clusters	PS8.3
silent gene cluster	PR4.46
simple sequence repeat	PR8.27
Single Nucleotide Polymorphism	PR3.5
siRNA	PR8.28
sMTOC	PR1.43
Smut Fungi	PR3.36, PR4.75
SOD	PS6.5
Sodiumnitrate	PR4.35
Soil fungi	PR4.64
Solanapyrone	PR7.15
SOLiD	PR4.59
Solid-state fermentation	PR8.40
<i>Sordaria macrospora</i>	PR1.26, PR2.13, PR6.3, PR7.29
South Africa	PR8.27
SPA-2	PS1.3
Speciation	PR3.37
Spermagonia	PR2.8
splinkerette-PCR	PR8.48
Spores	PR8.8
<i>Sporisorium reilianum</i>	PR4.28, PR4.60
SptC	PR7.20
<i>Stagonospora</i>	PS3.5, PS4.7
Staurosporine	PR1.14
Ste11	PR7.7
Ste12	PR1.75
Ste7DD	PR1.75
stone fruits	PR4.3
<i>Streptomyces</i>	PS8.7
Stress	PR1.41, PR1.46, PR2.4, PR4.4, PR4.5, PR6.2, PR6.4, PR7.1, PS7.4
STRIPAK	PR1.26, PR2.13
structure modelling	PS7.6
subcellular localization	PR7.8
submerged fermentations	PR8.53
Sugar uptake	PR4.69
sulfate transport	PR4.58
superSAGE	PR8.63
Surface hydrophobicity	PR9.11

susceptibility testing	PR10.12
Symbiosis	PR1.63, PR4.23, PR4.78, PS5.6, PL6.2
Synteny	PS3.6
Tandem-affinity purification	PR2.13, PR4.38, PR7.29
<i>Taphrina</i>	PR3.31
taxonomy	PR3.27
Temperature adaptation	PR7.28
tenellin	PR8.20
terrein	PR10.7
thallic complexity	PR1.5
thermophilic fungi	PR8.18
Thiabendazole resistance	PR10.6
thiamine biosynthesis	PR6.4
thioredoxin system	PR6.6
Tip growth	PR1.17
Tomato	PR3.8, PR4.71
transcription factor	PR1.29, PR1.36, PR1.56, PR1.57, PR3.21, PR4.29, PR4.72, PR4.76, PR7.2, PR7.6, PR7.8, PR7.19, PR7.24, PR7.34, PR7.36, PS8.1, PR8.7, PR8.49, PR8.50, PR10.5, PR10.9
transcriptome analysis	PR1.5, PR1.45, PR1.71, PS2.4, PR2.9, PR3.6, PR3.16, PR3.28, PR4.25, PR4.71, PR7.1, PS7.7, PR7.24, PR8.5, PR8.37, PR8.40, PR8.42, PR8.52
transformation	PR1.55, PR2.8, PR8.44
Transition bias	PR3.22
Translocation	PS4.4
transmembrane receptor	PR7.11
transport	PR1.14, PR1.61, PR4.58, PR5.1, PR8.51
Transposon	PR3.8, PR3.32, PR8.48, PR10.15
Tri genes	PR7.5
<i>Trichoderma</i>	PR1.3, PR1.10, PR1.48, PR1.59, PR1.72, PR1.78, PS2.7, PR3.5, PR3.16, PR3.43, PR4.53, PR4.57, PR7.11, PR7.31, PR8.9, PR8.36, PR8.37, PR8.47, PR8.61, PR8.64, PS9.5, PR10.11, PR10.20
<i>Trichoderma reesei</i>	PR8.53
<i>Tricholoma</i>	PR4.42, PR4.64, PR4.70
<i>Trichophyton rubrum</i>	PR7.26, PR7.27
Trichothecene	PR1.7, PR4.9, PR7.5
Trisporic acids	PS2.5, PR2.14
<i>Triticum aestivum</i>	PR4.27
<i>Triticum durum</i>	PR8.48
TUP1	PR2.1
two dimensional gel electrophoresis	PR1.30
UPR	PR2.2
<i>Ustilago</i>	PR1.74, PR2.2, PS2.6, PR7.33, PR7.36
<i>Ustilago hordei</i>	PR4.45
<i>Ustilago maydis</i>	PR1.13, PR1.60, PR2.1, PS4.5, PR4.7, PR4.44, PR4.45, PR4.54, PR4.61, PR4.65, PR4.69, PR4.73, PR4.75, PR4.76, PR7.25, PR8.1, PS9.4
Vacuolar H ⁺ -ATPase	PR9.3
vacuole	PR1.38, PR1.41
Vector	PR8.44
vegetative hyphal fusion	PR1.16
velvet complex	PR8.21, PR8.23
<i>Venturia inaequalis</i>	PR4.6
<i>Verticillium</i>	PR1.45, PR3.17, PR4.10, PR7.37
vesicle transport	PR1.39
virulence	PS7.2, PR4.21, PR4.47, PR6.5, PR7.17, PR7.23
Wheat	PS4.7, PR10.1
White-Collar	PR7.6, PR7.10
white-rot fungi	PR3.28, PR8.3, PR8.46, PR8.56
whole genome	PR3.11, PR3.39
wood decay	PR3.28, PR8.43
Woronin body	PR1.11
Xenobiotic	PR8.30
XlnR	PR3.10, PR7.22, PR7.30, PR8.12
yeast	PR4.3, PR5.1, PR3.31, PR7.37, PR9.2
yeast deletion library	PR8.17
<i>Zea mays</i>	PR10.2
<i>Zygomycetes</i>	PS2.5, PR2.15