Supplementary material

Characterization of a yellow laccase from *Botrytis cinerea* 241

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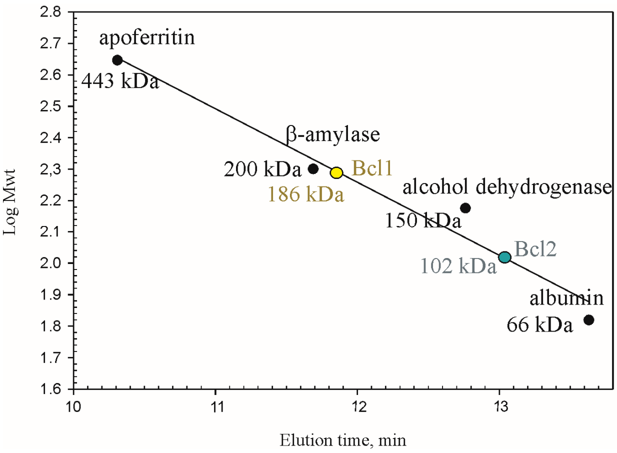

Figure S1. Analytical gel filtration chromatography of Bcl1 and Bcl2. The calibration curve used to estimate the native molecular mass based on the elution position during analytical gel filtration is indicated.

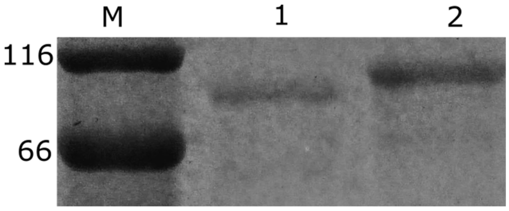

Figure S2. Deglycosylation of Bcl1. SDS-PAGE analysis of proteins after (1) and before (2) deglycosylation.

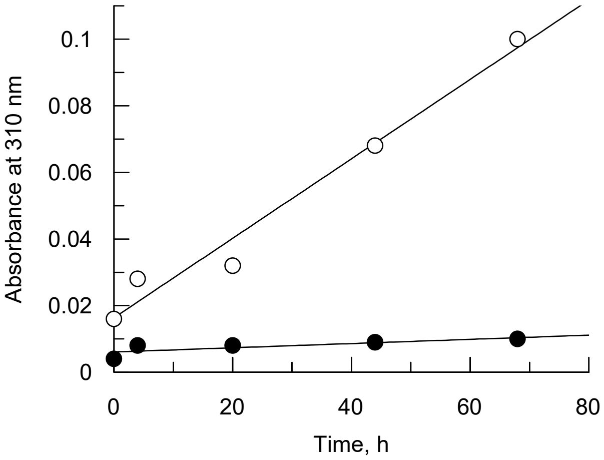

Figure S3. Oxidation of veratryl alcohol by the Bcl1 (empty circle, ○) and Bcl2 (full circle, ●) laccase.

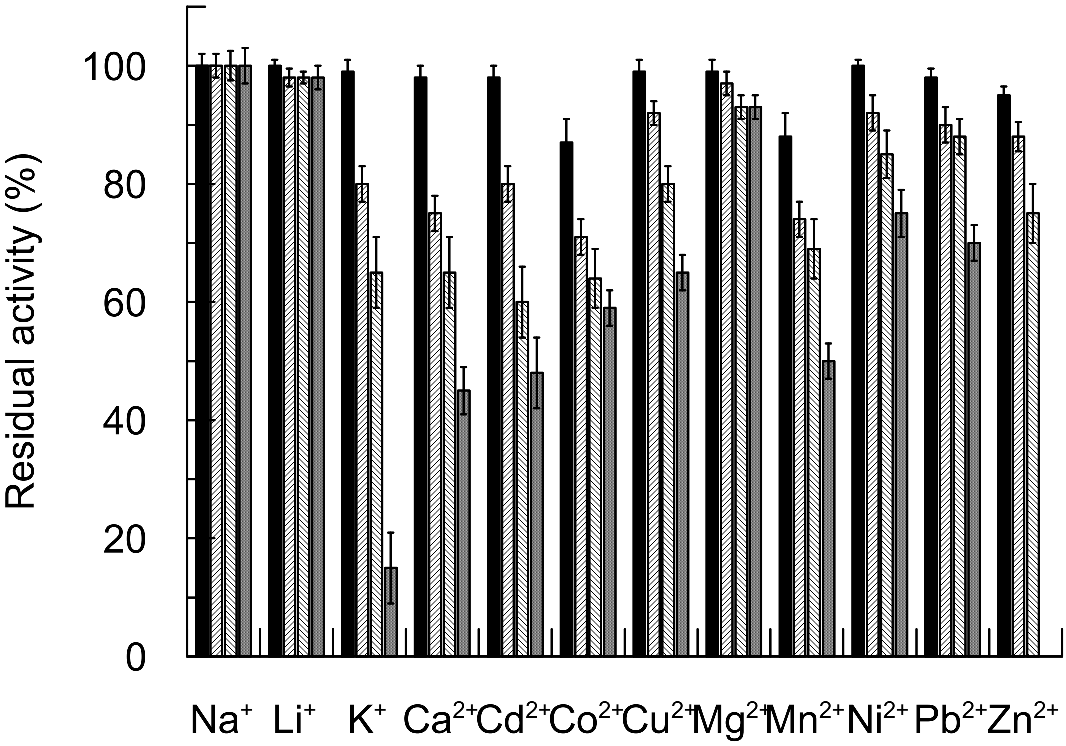

Figure S4. Effect of metal ions on the Bcl1 activity. Four different concentrations of metal ions were tested – in each set from left to right: 1, 5, 10 and 25 mM. N=3.

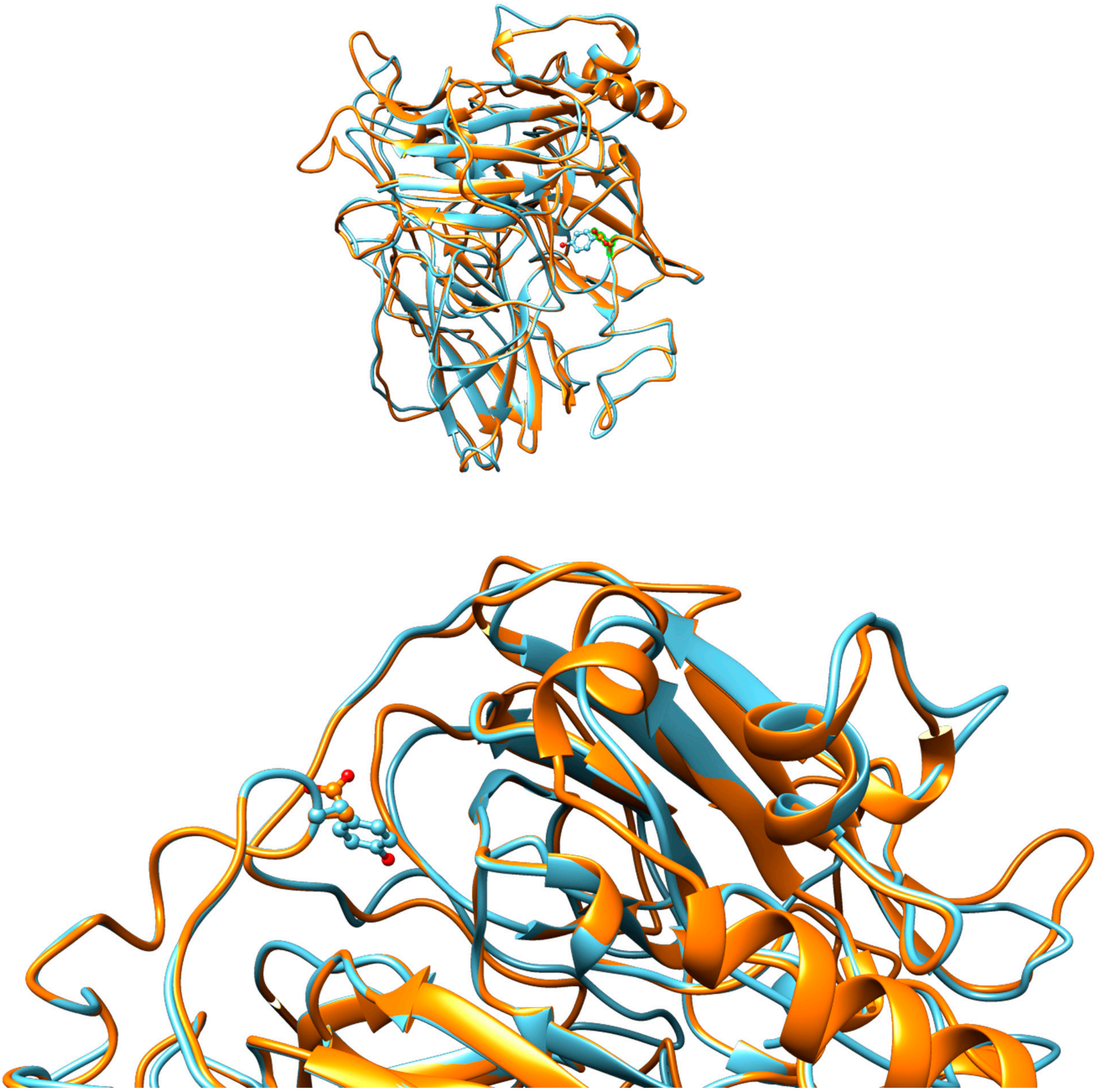

Figure S5. Comparison of 3D models of the laccases from *Botrytis cinerea* 241 (Bcl1, orange) and *Sclerotinia sclerotiorum* (blue). Y65, which is involved in binding of phenolic compounds, in a flexible loop of the laccase from *Sclerotinia sclerotiorum* and D132 in Bcl1 are shown.

Table 1. Purification of laccases Bcl1 and Bcl2 from a 3 L of culture.

Purification step	**Protein, mg**	**Total activity, U**	**Specific activity, U/mg**	**Yield, %**	**Purification (fold)**
Bcl1					
Culture liquid	6800	506	0.074	100	1
CM Toyopearl 650 M chromatography	29	292	10	57.7	135
Source PHE 15 chromatography	2.17	165	76	32.6	1027
Bcl2					
Culture liquid	3900	12621	3.2	100	1
Clarification with DEAE	3400	12600	3.7	100	1.1
Ultrafiltration	785	10200	12.9	81	3.9
PHE FF Sepharose chromatography	130	7658	59	60.7	18.2
Super Q Toyopearl 650M chromatography	33	4208	127	33	39.2
Source PHE 15 chromatography	26.3	3876	147	30.7	45.4

Table 2. The list of amino acid sequences used for the phylogenetic analysis.

> MT707622 Botrytis cinerea 241
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ATQFGTSWYHSHYSSQYGEGMLGGIVINGPATSNYDVDLGVYTITDWYYTPVFALGERIAHSQAGPPSGDNGLINGSMVA
PAGQSGGKYTTNTITAGKKYRLRLINTSVDNHFMVSLDNHAFTVITSDFVPIVPYTTNWIFIGIGQRYDVIITANQTVGS
YWFRAEVQNGCGTNNNNGNIKSIFTYSGAASTTPSSSATPYTGRCTDETGIIPFWDSFVPSGPLSGNVDQLDVAVNIGVD
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FFLLGTGIGTYNNTLDSPNLDYDNPTRRDVAMLPAGGWMVLAFQTDNPGAWLMHCHIAWHVSEGLAVQFLETKNQINAVN
PISPALTNTCNKWNAWYPSQAPYIKTDSGL
>TGO72679.1 hypothetical protein BELL_0429g00110 [Botrytis elliptica]
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PAGQSGGKYTTNTITAGKKYRLRLINTSVDNHFMVSLDNHAFTVITSDFVPIVPYTTNWIFIGIGQRYDVIITANQTVGS
YWFRAEVQNGCGTNNNNGNIKSIFTYSGAASTTPSSSATPYTGRCTDETGIIPFWDSFVPSGPLSGNVDQLDVAVNIGVD
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FFLLGTGIGTYNNTLDSPNLDYDNPTRRDVAMLPAGGWMVLAFQTDNPGAWLMHCHIAWHVSEGLAVQFLETKNQINAVN
PISPALTNTCNKWNAWYPSQAPYIKTDSGL
>KAF7911640.1 hypothetical protein EAE98_011905 [Botrytis deweyae]
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PAGQSGGKYTTNTITAGKKYRLRLINTSVDNHFMVSLDNHAFTVITSDFVPIVPYTTNWIFIGIGQRYDVIITANQTVGS
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FFLLGTGIGTYNNTLDSPNLDYDNPTRRDVAMLPAGGWMVLAFQTDNPGAWLMHCHIAWHVSEGLAVQFLETKNQINAVN
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>XP_037195563.1 putative laccase protein [Botrytis fragariae]
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PAGQTGGKYTTNTITAGKKYRLRLINTSVDNHFMVSLDNHAFTVITSDFVPIVPYTTNWIFIGIGQRYDVIITANQTVGS
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>KAF7912300.1 hypothetical protein EAF01_001321 [Botrytis porri]
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PAGATGGKYTTNTITSGKKYRLRLINTSVDNHFMVSLDNHAFTVITSDFVPIVPYTTNWIFIGIGQRYDVIITANQTVGS
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FFLLGTGVGTYNNTINAPNLDYDNPTRRDVAMLPAGGWMVLAFQTDNPGAWLMHCHIAWHVSEGLAVQFLETKNQINAVN
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>TGO84187.1 hypothetical protein BPOR_0537g00020 [Botrytis porri]
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ATQFGTSWYHSHYSAQYGEGMLGGIVINGPATSNYDVDLGVYTISDWYYTPVFALGERIAHSQAGPPSGDNGLINGSMVA
PAGATGGKYTTNTITSGKKYRLRLINTSVDNHFMVSLDNHAFTVITSDFVPIVPYTTNWIFIGIGQRYDVIITANQTVGS
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ASGPIVTWGINLSAIDVDWKKPILQYVLDGNNSWPASENLIELPNAAQWYYWIIQEVPGNVNGNPVSINVPHPMHLHGHD
FFLLGTGVGTYNNTINAPNLDYDNPTRRDVAMLPAGGWMVLAFQTDNPGAWLMHCHIAWHVSEGLAVQFLETKNQINAVN
PISQALTNTCNKWNAWYPSQAPYLKTDSGL
>Q96UM2.1 RecName: Full=Laccase-3; AltName: Full=Benzenediol:oxygen oxidoreductase 3; AltName: Full=Diphenol oxidase 3; AltName: Full=Urishiol oxidase 3 [Botrytis cinerea]
PGPTLYADWGDMIQVTLKNSMPDNGTGIHWHGLRQYHTCTEDGVPGITECPLAPGDTKTYTFQATQFGTSWYHSHYSSQY
GEGMLGGIVINGPATSNYDVDLGVYTISDWYYTPVFALGERIAHSQAGPPSGDNGLINGSMVAPAGQTGGKYTTNTITAG
KKYRLRLINTSVDNHFMVSLDNHAFTVITSDFVPIVPYTANWIFIGIGQRYDVIITANQTVGSYWFRAEVQNGCGTNNNN
GNIKSIFTYSGAASTTPSSSATPYTGRCTDETGIIPFWDSFVPSGPLSGNVEQLNVAINIGVDASGPIVTWGINLSAIDV
DWKKPILQYVLDGNNSWPASENLIELPNAAQWYYWVIQEVPGNVNGNPVSINVPHPMHLHGHDFFLLGTGVGTYNNTING
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>KAF7916227.1 hypothetical protein EAE98_010812 [Botrytis deweyae]
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AGVYNQVSGLVPGAKYRLRIINMSIDNHFQVTLDSHSFQVIQTDFVPIQPYTTNTIFIAIGQRYDVIITADQTPSNYWFR
AIVPKPPTQKGFGCGQNANNGSINAIFSYQGVELSEPNSKSFLIPQSCEDETQLVSWNEKSVPENEFVWPTAQELIVTGP
GSNSLPKAPAPYVWSINDTYMEIEWDKPTLQYVAQGNKNYNVHQSIIELPDANVWTFWIIKNAAAIPHPIHLHGHDFYIL
GQENGVNFTDKSSLNFANPARRDVAMLPALGYLVIAFVTDNPGAWLLHCHIAFHVGEGLALQFLERELEIAQRVDLSTVD
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>THV54741.1 hypothetical protein BGAL_0021g00440 [Botrytis galanthina]
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PDGTPRWMLVVNGTYPGPTITANWGDTLEITVVNQIITDGVSIHWHGVVQKNTNTMDGVNGITECPIPPGSSKVYKFLAT
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AGVYNRVSGLVPGAKYRLRIINTSIDNHFQVTLDSHFFQVIQTDFVPIQPYTTNTIFIAIGQRYDVIITANQTPSNYWFR
AIVPKPPTQKGFGCGQNANNGSINAIFSYQGIELSKPTSKSFLIPQSCEDETQLVSWHEKAVPETEFVWPTAQELIVTGP
GSNSLPKAPAPYVWSINDTYMEIEWDNPTLQYVAQGNKNYNVHQSIIELPDANVWTFWIIKNAAAIPHPIHLHGHDFYIL
GQENGANFTDKSSLNFANPARRDVAMLPALGYLVIAFVTDNPGAWLLHCHIAFHVGEGLALQFLERESEIAQRVDLSTVD
AGCKRWDTWYNTERVDNAWNTEFDSGI
>KAF7891547.1 hypothetical protein EAF02_001872 [Botrytis sinoallii]
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PDGTPRWMLVVNGTYPGPTITANWGDTLEITVINQIITDGVSIHWHGIVQKNTNTMDGVNGITECPIPPGSSKVYKFLAT
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AGVYNQISGLVPGAKYRLRIINTSIDNHFQVTLDSHSFQVIQTDFVPIQPYTTNNIFIATGQRYDVIITADQTPSNYWFR
AIVPKPPAQKGFGCGQNANNGSINAIFSYQGVELSEPNSKSFLIPQSCEDETQLVSWNEKSVPENEFVWPTAQELIVTGP
GSNSLPKAPAPYVWSINDTYMEIEWDKPTLQYVAQGNKNYNVHRSIIELPDANVWTFWIIKNAAAIPHPIHLHGHDFYIL
GQENGVNFTDKTSLNFANPARRDVAMLPALGYLVIAFVTDNPGAWLLHCHIAFHVGEGLALQFLERESEITQRVDLSTVD
AGCKRWDTWYNTERVDNAWNTEFDSGI
>XP_024552410.1 Bclcc12 [Botrytis cinerea B05.10]
MFFTVMLSIAILIRTCLPSAIPSQALSNNKRTSASTCLNAASSRNCWNGNYSINTDTEEAWPDTGVVVAYTLVITNQTMS
PDGTPRWMLVVNGTYPGPTITASESAPMWPPSSSAMSAYLFIDWGDTLEITVVNQIITDGVSMHWHGIVQKNTNTMDGVN
GITECPIPPGSSKLYKFLATQHGTSWYHSHHAAQYGDGVLGSIVVNGPASLNYDHDLGPLPITDFYYNSTYEEGLLSVSR
GPPKADNGLINGTNRNPQKTAGVYNQVSGLVPGAKYRLRIINTSIDNHFQVTLDSHYFQVIQTDFVPIQPYTTKTIFIAI
GQRYDVIITADQTPSNYWFRAIVPNPPTQKGFGCGQNANNGSINAIFSYQGVESSEPTSKSFLMPQSCEDETQLVSWHEK
AVPEDEFVWPTSQELIVTGPGSNSLSKAPAPYIWSINDTYMKIEWDKPTLQYVIQGNKSYNVHQSIIELPDANVWTFWII
KNAAAIPHPIHLHGHDFYILGQENGINFTDKSSLNFANPARRDVAMLPALGYLVIAFVTDNPGAWLLHCHIAFHVGEGLA
LQFLERESEIAQRVDLSTVDTGCKMWNAWYNTERVDNAWNTEFDSGI
>XP_037188192.1 putative laccase precursor protein [Botrytis fragariae]
MSGALSLLAELDKETNKAPSRKNSQAKPRTSRSTANSRSSSVQSRGPSQTQRPTSAPGPSPVIPPQNITPRRTTQSTNVT
PRTSFELGTERSRSQGPDSRRVSFAEAPRPQTRTLMIPSKENMPSSGFPYNIKLNKYGVSEHEWSQFTKEIIETLPPSKS
FSWLWKRGKITAIIKRDLQYESELKSALRQWNKGFRRRGFQVYLEIPVEKDLTDDEVSGDTKEEKKQAKKDAKKFRFIIG
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VDHAPGSTQGIGPTERRDLYTEICILDENLTITSGGFMGLLLLWPLIPRIALPTFVMELALSNIKRTSTSNCLNTASSRN
CWNGNYSIDTDSEEAWPDTGVVVAYTLTITNQTMSPDGTPRWMLVVNGTYPGPTITANWGDTLEITVANQIITDGVSIHW
HGIVQKNTNTMDGVNGITECPIPPGSSKIYKFLATQHGTSWYHSHHAAQYGDGVLGSIVINGPASLNYDHDLGPLPITDF
YYKSTYEEGLLSVSKGPPKADNGLINGTNRNPHKTAGVYNQASGLVPGAKYRLRIINTSIDNHFQVTLDSHSFQVIQTDF
VPIQPYTTNTVFIAIGQRYDVIITADQTPSNYWFRAIVPKPPTQKGFGCGQNANNGSINAIFSYQGVELSEPTSNSFLIP
QSCEDETQLVSWHEKAVPENEFVWPTAQELVVTGPGSSSLPKAPAPYIWSINDTYMEIEWDKPTLQYVTQGNKNYNVHQS
IIELPDANVWTFWIIKNAAAVPHPIHLHGHDFYILGQENSVNFTDKSTLNFANPARRDVAMLPALGYLVIAFVTDNPGAW
LLHCHIAFHVGEGLALQFLERESEIAQRVDLSAVDAECKTWDAWYNTERVDNAWNTEFDSGV
>KAF7941588.1 hypothetical protein EAE97_006425 [Botrytis byssoidea]

MYFTLLLCIAILIPSCLPSAIPSQVLSNNKRASASTCLNSASSRNCWNGKYSIDTDSEEAWPNTGVVVAYTLIIKNQTMS
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GITECPIPPGSSKVYKFLATQHGTSWYHSHHAAQYGDGVLGSIVINGPASLNYDYDLGPLPITDFYYKSTYEEGLLSVSK
GPPKADNGLINGTNRNPHKTAGAYNQVSGLVPGAKYRLRIINTSIDNHFQVTLDSHSFQVIQTDFVPIQPYTTNTIFIAI
GQRYDVIITADQTPSNYWFRAIVPKPPIQKGFGCGQNANNGSIKAIFSYQGVESSEPDSKSFLIPQSCEDETHLVSWHEK
SVPENEFLWPTAQELIVTGPGSNSVPKVPAPYVWSINDTYMEIEWDKPTLQYVAQGNKNYNVHQSIIELPDANVWTFWII
KNAAAIPHPIHLHGHDFYILGQENGVNFTDKSSLNFAKPARRDVAMLPALGYLVIAFVTDNPGAWLLHCHIAFHVGEGLA
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>TGO16908.1 hypothetical protein BTUL_0022g00090 [Botrytis tulipae]
MYFTLLLCIAILVPSCLPSAIPSQVLTNNKRTSTSTCLKAASSRNCWNGNYSIDTDSEEAWLNTGVVVAYTLTITNQTMS
PDGTPRWMLVANGTYPGPTITSSEFFPMWPPFPSAMLAHLFTDWGDTLEITVVNQIITDGVSIHWHGIVQKNTNTMDGVN
GITEYPIPPGSSKVYKFLATQHGTSWYHSHHAAQYGDGVLGSIVINGPASLNYDYDLGPLPITDCYYKSTYDEGLLSVSK
GPPKADNGLINGTNRNPHKTAGVYNQVSGLVPGAKYRLRIINTSMDNHFQVTLDSHSFQVIQTDFVPIQPYTTNTIFIAI
GQRYNVIITADQTPSNYWFRAIVPKPPTQKGFGCGQNANNGSINAIFSYQGVESSEPDSKSFLIPQSCEDETQLVSWHEK
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>TGO29266.1 hypothetical protein BPAE_0017g00740 [Botrytis paeoniae]
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PDGTPRWMLVVNGTYPGPTITASEFFPMWPPFPSATLAHLFIDWGDTLEITVVNQIITDGVSMHWHGIVQNNTNTMDGVN
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GQRYDVIITTDQTPSNYWFRAIIPKPPTQKGFGCGQNANNGSINAIFSYQGVGLLEPTSKSFVIPQNCEDETQLVSWHEK
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KNAAAIPHPIHLHGHDFYILGQENSVNFTDKSTLNFANPARRDVAMLLALGYLVIAFVTDNPGAWLLHCHIAFHVGDGLA
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>EMR90689.1 putative laccase precursor protein [Botrytis cinerea BcDW1]
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SRGPPKADNGLINGTNRNPQKTAGVYNQVSGLVPGAKYRLRIINTSIDSHFQVTLDSHYFQVIQTDFVPIQPYTTKTIFI
AIGQRYDVIITADQTPSNYWFRAIVPNPPTQKGFGCGQNANNGSINAIFSYQGVESSEPTSKSFLMPQSCEDETQLVSWH
EKAVPEDEFVWPTSQELIVTGPGSNSLSKAPAPYIWSINDTYMKIEWDKPTLQYVIQGNKSYNVHQSIIELPDANVWTFW
IIKNAAAIPHPIHLHGHDFYILGQENGINFTDKSSLNFANPARRDVAMLPALGYLVIAFVTDNPGAWLLHCHIAFHVGEG
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>TGO27265.1 hypothetical protein BPAE_0045g00640 [Botrytis paeoniae]
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ILSVNGSVPGPTIIADWGDTIVIHVKNSMPDYGTGIHFHGIRQNYTNQMDGVPSITQCPIAPETSFTYTWKATQYGSSWY
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TIFKSGTRYRIRLVNTAADTHFKFSIDNHTMEVIAADFVPIVPYTSDAIAISMGQRYDIIVTANAAVDNYWMRAVAQTVC
SKNVNADNIYGIIRYDSTSINDPTSVRWANASTDELCEDELMSSLIPYVPIVASDSPAEEDEFSVIINKTNGVIWQMGTH
SFLNQWDYPTLLQAYEGNDTWAPEQEVYQLPEANVWVYWIIETTNAQSHPMHLHGHDFWVLGQGTGTYDSTTANLTLVNA
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SGI
>THV56020.1 hypothetical protein BGAL_0001g00820 [Botrytis galanthina]
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YGSSWYHSHFILQYGDGLFGPLVINGPATANYDVDLGMLFLNDWNHVPVQSLWDKAKTGAPPTLLTGLMNGTNTYNGAGK
KFQTTFTPGKKYRIRVVNTAVDGHFQFSIDGHSFQVIAMDFVPIVPYNATSILVSIAQRYDIIVTANAAVGNYWIRAGWQ
TACSGNTNAANITGILRYTGSSSTADPTTTSTVTASTSCLDEPLASLVPFVPINPVASSIMKTTLTTGGGQWLFNGSSLL
LNWTDPTLLTVLNSGNIWPTEYNVIPVESTTANKGWAVLAISGPNGPNHPIHLHGHDFWTLSQGTGAYTATTALNLVNPP
RRDVMTLPSGGHLVIAFQIDNPGSWLMHCHIAWHASEGLALQFVESESKILPTIGTADVSTFQDTCAAWNAWTPTEPFPQ
DDSGI
>KAF7949645.1 hypothetical protein EAE97_003154 [Botrytis byssoidea]
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DGVSRPTLNFNGTIPGPQITADWGDNVIVHVTNKLTNNGTSIHWHGIRQLNNAQYDGVPGITQCPIAPGDTLTYKFHADN
YGSSWYHSHFILQYGDGLFGPLVINGPATANYDVDLGMLFLNDWNHVPVQLFWDKAKTGAPPTLLTGLMNGTNTYNGAGK
KFQKTFTPGKKYRIRVINTAVDGHFQFSIDGHSFQVIAMDFVPIVPYNATSILVSIAQRYDIIVTANAAVGNYWIRAGWQ
TACSGNTNAANITGILRYTGSSSTADPTTTSTVTASTSCLDEPLTSLVPFVPINPVASSIMKTTLTTGGGQWLFNGSSLL
LNWTDPTLLTVLNSGNIWPTEYNVIPVESTTANQGWAVLAISGPNGPNHPIHLHGHDFWTLSQGTGAYTATTALNLVNPP
RRDVMTLPSGGHLVIAFQIDNPGSWLMHCHIAWHASEGLALQFVESESKILPTIGTADVSTFQDTCAAWNAWTPTEPFPQ
DDSGI

>KAF7938180.1 hypothetical protein EAE99_001852 [Botrytis elliptica]
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YGSSWYHSHFILQYGDGLFGPLVINGPATANYDVDLGMLFLNDWNHVPVQSLWDKAKTGAPPTLLTGLMNGTNTYNGAGK
KFQTTFTPGLKYRIRVVNTAVDGHFQFSIDGHSFQVIAMDFVPIVPYNATSILVSIAQRYDIIVTANAAVGNYWIRAGWQ
TACSGNTNAANITGILRYTGSSSTADPTTTSTVTASTSCLDEPLTSLVPFVPINPVASSIMKTTLTTAGGQWLFNGSSLL
LNWTDPTLLTVLNSGNIWPTEYNVIPVESTTANKGWAVLAISGPNGPNHPIHLHGHDFWTLSQGTGAYTATTALNLVNPP
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DDSGI
>TGO31276.1 hypothetical protein BPAE_0001g01740 [Botrytis paeoniae]
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DGVSRPTLNFNGTIPGPQITADWGDDVIVHVTNKLTNNGTSIHWHGIRQLNNAQYDGVPGITQCPIAPGDTFTYKFHADN
YGSSWYHSHFILQYGDGLFGPLVINGPATANYDVDLGMLFLNDWNHVPVQSLWDKAKTGAPPTLLTGLMNGTNTYNGAGK
KFQTTFTPGLKYRIRVVNTAVDGHFQFSIDGHSFQVIAMDFVPIVPYNATSILVSIAQRYDIIVTANAAVGNYWIRAGWQ
TACSGNTNAANITGILRYTGSSSTADPTTTSTITASTSCLDEPLTSLVPFVPINPVASSIMKTTLTTGGGQWLFNGSSLL
LNWTDPTLLTVLNSGNIWPTEYNVIPVESTTANNGWAVLAISGPNGPNHPIHLHGHDFWTLSQGTGAYTATTALNLVNPP
RRDVMTLPSGGHLVIAFQIDNPGSWLMHCHIAWHASEGLALQFVESESNILPTIGTADVSAFQDTCAAWNAWTPTEPFPQ
DDSGI
>XP_037197222.1 putative laccase 2 protein [Botrytis fragariae]
MHTSSLLTALLKIPPTEYYSVLAQWSSGKGLLCVRGGERPHVRFRDATFSLRSADMETKDEDIVVVSEVQLIFTRKEKDI
GCVIGDISADNSLAKFASLSLALALPTAEVIPSALEERQSCANTATTRSCWGQYSASTNSYTTVPQTGVTREYWLVVQNT
TLSADGVSRPTLNFNGTIPGPQITADWGDDVIVHVTNKLTNNGTSIHWHGIRQLNNAQYDGVPGITQCPIAPGDTLTYKF
HADNYGSSWYHSHFILQYGDGLFGPLVINGPATANYDVDLGMLFLNDWNHVPVQSLWDKAKTGAPPTLLTGLMNGTNTYN
GAGKKFQTTFTPGLKYRIRVVNTAVDGHFQFSIDGHSFQVIAMDFVPIVPYNATSILVSIAQRYDIIVTANAAVGNYWIR
AGWQTTCSGNTNAANITGILRYTGSSSTADPTTISTITASTSCLDEPLTNLVPFVPINPVASSIMKTTLTTAGGQWLFNG
SSLLLNWTDPTLLTVLNSGNIWPTDYNVIPVESTTANKGWAVLAISGPTGPNHPIHLHGHDFWTLSQGTGAYTATTALNL
VNPPRRDVMTLPSGGHLVIAFQIDNPGSWLMHCHIAWHASEGLALQFVESESKILPTIGTADVSTFQDTCAAWNAWTPTE
PFPQDDSGI
>TGO18838.1 hypothetical protein BTUL_0007g00560 [Botrytis tulipae]
MKNSFFSSLAKFASLSLALALPTAEVIPFALEERQSCANTATTRSCWGQYSASTNSYTTVPQTGVTREYWLVVQNTTLSA
DGVSRPTLNFNGTIPGPQITADWGDDIIVHVTNKLTNNGTSVHWHGIRQLNNAQYDGVPGITQCPIAPGDTLTYKFHADN
YGSSWYHSHFILQYGDGLFGPLVINGPTTANYDVDLGMLFLNDWNHVPVQSLWDKAKTGAPPTLLTGLMNGTNTYNGAGK
KFQTTFTPGKKYRIRVVNTAVDGHFQFSIDGHSFQVIAMDFVPIVPYNATSILVSIAQRYDIIVTANAAVGNYWIRAGWQ
TACSGNTNAANITGILRYTGSSSTADPTTTSTVTASTSCLDEPLTSLVPFVPINPVASSIMKTTLTTGGGQWLFNGSSLL
LNWTDPTLLTVLNSGNIWPTEYNVIPVESTTANQGWAVLAISGPNGPNHPIHLHGHDFWTLSQGTGAYTATTALNLVNPP
RRDVMTLPSGGHLVITFQIDNPGSWLMHCHIAWHASEGLALQFVESESKILPTIGTTDVSTFQDTCAAWNAWTPTEPFPQ
DDSGI
>KAF7928481.1 hypothetical protein EAE98_005537 [Botrytis deweyae]
MKNPFFSSLAKFASLSLALALPTAEVVPSALEERQSCANTATTRSCWGQYSASTNSYTTVPQTGVTREYWLVVQNTTLSA
DGVSRPTLNFNGTIPGPQITADWGDDVIVHVTNKLTNNGTSIHWHGIRQLNNAQYDGVPGITQCPIAPGDTLTYKFHADN
YGSSWYHSHFILQYGDGLFGPLVINGPATANYDVDLGMLFLNDWNHVTVQSLWDKAKTGAPPTLLTGLMNGTNTYNGAGK
KFQTTFTPGLKYRIRVVNTAVDGHFQFSIDGHSFQVIAMDFVPIVPYNATSILVSIAQRYDIIVTANAAVGNYWIRAGWQ
TACSGNTNAANITGILRYTGSSSTADPTTTSTVTASTSCLDEPLTSLVPFVPINPVASSIMKTTLTTAGGQWLFNGSSLL
LNWTDPTLLTVLNSGNIWPTEYNVIPVESTTANKGWAVLAISGPNGPNHPIHLHGHDFWTLSQGTGAYTATTALNLVNPP
RRDVMTLPSGGHLVIAFQIDNPGSWLMHCHIAWHASEGLALQFVESESKILPTIGTADVSTFQDTCAAWNAWTPTEPFPQ
DDSGI
>XP_024546494.1 Bclcc1 [Botrytis cinerea B05.10]
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DGVSRPTLNFNGTIPGPQITADWGDDVIVHVTNKLTSNGTSIHWHGIRQLNNAQYDGVPGITQCPIAPGGTLTYKFHADN
YGSSWYHSHFILQYGDGLFGPLVINGPATANYDVDLGMLFLNDWNHVPVQSLWDKAKTGAPPTLLTGLMNGTNTYNGAGK
KFQTTFTPGLKYRIRVVNTAVDGHFQFSIDGHSFQVIAMDFVPIVPYNATSILVSIAQRYDIIVTANAAVGNYWIRAGWQ
TACSGNTNAANITGILRYTGSSSTADPTTTSTVTASTSCLDEPLASLVPFVPINPVASSIMKTTLTTGGGQWLFNGSSLL
LNWTDPTLLTVLNSGNIWPTEYNVIPIESTTANKGWAVLAISGPNGPNHPIHLHGHDFWTLSQGTGAYTATTALNLVNPP
RRDVMTLPTGGHLVIAFQIDNPGSWLMHCHIAWHASEGLALQFVESESSILPTIGTADVSTFQNTCAAWKAWTPTEPFPQ
DDSGI
>TGO33572.1 hypothetical protein BHYA_0239g00120 [Botrytis hyacinthi]
MKNSFFSSLAKFASLSLALALPTAEVIPSALEERQSCANTATTRSCWGQYSASTNSYTTVPQTGVTREYWLVVQNTTLSA
DGVSRPTLNFNGTIPGPQITADWGDNVIVHVTNKLTNNGTSIHWHGIRQLNNAQYDGVPGITQCPIAPGDTLTYKFHADN
YGSSWYHSHFILQYGDGLFGPLVINGPATANYDVDLGMLFLNDWNHVPVQSLWDKAKTGAPPTLLTGLMNGTNTYNGAGK
KFQTTFTPGKKYRIRVVNTAVDGHFQFSIDGHNFQVIAMDFVPIIPYNATSILVSIAQRYDIIVTANAAVGNYWIRAGWQ
TACSGNTNAANITGILRYTGSSSTADPTTTSTVTASTSCMDEPLTSLVPFVPINPVASSIMKTKLTTGGGQWLFNGSSLL

LNWTDPTLLTVLNSGNIWPTEYNVIPVESTTANKGWAALAISGPNGPNHPIHLHGHDFWTLSQGTGTYTATTALNLVNPP
RRDVMTLPSGGHLVIAFQIDNPGSWLMHCHIAWHASEGLALQFVESESKILPTIGTADVSTFQDTCAAWNAWTPTEPFPQ
DDSGI
>XP_037194516.1 putative multicopper oxidase protein [Botrytis fragariae]
MHLPVLLRVLILVPFVLAAPKYGESSLTKRCVNSADDRSCWGDYDISTNYYNDGPDTGVVREYWWDIVNTTAAPDGIERV
ILSVNGSVPGPTIIADWGDTIVIHVKNSMPNYGTGIHFHGIRQNYTNQMDGVPSITQCPIAPGTSFTYTWKATQYGSSWY
HSHFYVQAWDGIFGGIQINGPATANYDEDLGTLTLSDWSHVTAEVEAVAALAAPPTLDNGLINGTNTYNNSGTIVGSRFE
TTFKSGTRYRIRLVNTAADTHFKFSIDNHTMEVIAADFVPIVPYTSDTIAISMGQRYDIIVTANAAVDNYWMRAVAQTVC
SKNVNADNIYGIVRYDSTSTDDPTSVRWANASTDELCEDELMTSLVPYVPIVASDSPAEEDEFSVIINKTNGVIWQMGTH
SFLNQWDYPTLLQSYEGNDTWAPEQEVYQLPVANVWVYWIIETTNAQSHPMHLHGHDFWVLGQGTGTYDSTTANLTLVNA
PRRDVVLLPGSGWVVMAFYTDNPGAWIMHCHIAWHTSEGLAVQILERESELVDLLDGDLLNSTCAAWNSYASADNVIQPD
SDAIPGKGESNLTFGLELEYIFATVDADKPDPHPEDPREVDGKKFPDKEAINRDILKKLTGVGIPAVITSSDMTDEESIT
CWILKEDTTVGDNTLRPAENKSKIYHRNGMEMTSPPYYYTEPARNAIRKVLKTVRENYRVCVDETAGLHVHVGNSFNGFH
FLILQHILAIAYTYERQTELIFSSDRVSGEWCPPFSKGRFGMANPDLTRVEVVEKILGYTDNESLIEDFGESLTAGRLAF
NLEGLKTPYQDGIRTIEFRHHQGSLDPGAILNWIHVCVKLVEKACFAKHDELLAQLRQDIAKPIGFGEGDLSTIDFLMWL
GCPAQAYYYCANMVIDKNTFEQRIKDDTARQEKSLKWARARLIRLAKDAEEHEARVAARLGKDGSKESEPTTSNSESADE
NEADQDEGGNDGSGDSGNTPSNPNEDES
>KAF7893007.1 hypothetical protein EAF02_000545 [Botrytis sinoallii]
MENSFFSSFAKFASLSLALALPTAEVVPSALEERQSCANTATTRSCWGQYSASTNSYTTVPQTGVTREYWLVVQNTTLSA
DGVSRPTLNFNGTIPGPQITADWGDDVIVHVTNKLTNNGTSIHWHGIRQLNNAQYDGVPGITQCPIAPGDTLTYKFHADN
YGSSWYHSHFILQYGDGLFGPLVINGPATANYDVDLGMLFLNDWNHDKAKTGAPPTLLTDLMNGTNTYNGAGKKFQTTFT
PGSKYRIRVVNTAVDGHFQFSIDGHSFQVIAMDFVPIVPYNATSILVSIAQRYDIIVTANAAVGNYWIRAGWQTACSGNT
NAANITGILRYTGSSSTADPTTTSTVTASTSCLDEPLTSLVSFVPINPVASSIMKTTLTTAGGQWLFNGSSLLLNWTDPT
LLTVLNSGNIWPTEYNVIPVESTTANKGWAVLAISRPNGPNHPIHLHGHDFWTISQGTGAYTATTALNLVNPPRRDVMTL
PSGGHLVIAFQIDNPGSWLMHCHIAWHASEGLALQFVESESKILPTIGTADVSTFQDTCAAWNAWTPTEPFPQDDSGI
>Q12570.3 RecName: Full=Laccase-1; AltName: Full=Benzenediol:oxygen oxidoreductase 1; AltName: Full=Diphenol oxidase 1; AltName: Full=Urishiol oxidase 1; Flags: Precursor [Botrytis cinerea]
MKNSFFSSLAKFASLSLAFALPTAEVIPSALEERQSCANTATTRSCWGQYSASTNSYTTVPKTGYWLVVQNTTLSADGVS
RPTLNFNGTIPGPQITADWGDDVIVHVTNKLTSNGTSIHWHGIRQLNNAQYDGVPGITQCPIAPGGTLTYKFHADNYGSS
WYHSHFILQYGDGLFGPLVINGPATANYDVDLGMLFLNDWNHVPVQSLWDKAKTGAPPTLLTGLMNGTNTYNGAGKKFQT
TFTPGLKYRIRVVNTAVDGHFQFSIDGHSFQVIAMDFVPIVPYNATSILVSIAQRYDIIVTANAAVGNYWIRAGWQTACS
GNTNAANITGILRYTGSSSTADPTTTSTVTASTSCLDEPLASLVPFVPINPVASSIMKTTLTTGGGQWLFNGSSLLLNWT
DPTLLTVLNSGNIWPTEYNVIPIESTTANKGWAVLAISGPNGPNHPIHLHGHDFWTLSQGTGAYTATTALNLVNPPRRDV
MTLPTGGHLVIAFQIDNPGSWLMHCHIAWHASEGLALQFVESESSILPTIGTADVSTFQNTCAAWKAWTPTEPFPQDDSG
I
>TGO29104.1 hypothetical protein BPAE_0019g00800 [Botrytis paeoniae]
MRLHILLALCLSFCQIQASPLFGWSFNPIATLQTDLLKIINQVECLVSTKVSIIPSILTTGNTNAVTSNKCSTTSGKTTS
AAAVQTSLSSLQSVASSKWSSLQSLLSTTTSLPPILTTSLTVTTAKPTSTSSVKSTSTTANTVSSTTKSSSITSTTSLVS
SSTASSTSKTSSSAVASGTPCAGNTAADRSKWCDYSTSTDYYNEVPNTGVTREYWFNVQDGVASPDGFSRYVQAINGSIP
GPTIIADWGDNIVVHVTNSLSTNGSSIHFHGIHQKNTNQNDGVPSVTQCPIAYGDTYTYRWRATQYGSSWYHSHVGLQAW
EGVAGGIIINGPATANYDEDKGTLMLSDWGHETVDELYEKVQTTGPQSMTTGLINGTNVFGADGASNQTGSRFSTSVESG
KSYRFRLVNSAIDTHFKFSVDSHTMTVMAMDFVPIVPYQTEILNIAIGQRYDVVITANQASVASDFFIRAIPQSSCSEND
NSDNIRGVLHYGSSTGLPTTTGYTFTDECVDEPVSSLVPYLPKTVSAASKSPEEAVTVAQNSQNLFKWYLNNSTFLSEWE
EPTLLMVQNNITTFGTPDNLVAVPNANEWIYLVIHSALPVPHPIHLHGHDFFVVSQQATTFDTTTAISTYNLNNPPRRDV
ATLPGGGYLVLAFETDNPGAWLMHCHIGWHTSMGFAMQFLERASEIPKLLDTTQLQDTCTAWNGHAVIQEDSGV
>TGO32268.1 hypothetical protein BHYA_0333g00040 [Botrytis hyacinthi]
MRLHILLALCLSFCQIQASPLFGWSFNPIATLQADLLKIINQVECLASTKVSYIPSLLTFGNTNAVTSNKCSTTSGKTTS
AAAVQTSLSSLQSVASSKWSSLQSLLSTTTSLPPIFTSSLAVTTAKPTSTSSATSTSTTANTVSSTAKSSTITGTTSPAS
SSTASSTSKTSSSAVASGTPCAGNTAADRSKWCDYSTSTDYYNEVPNTGVTREYWFNVQDGVASPDGVSRYVQTINGSIP
GPTIIADWGDNVVVHVTNSLSTNGSTIHFHGIHQKNTNQNDGVPSVTQCPIAYGNTYTYRWRATQYGSSWYHSHVGLQAW
EGVAGGIIINGPATANYDEDKGTLMLSDWGHQTVDELYEKVQTVGPQSMTTGLINGTNVFGADGASNQTGSRFSTSVESG
KSYRFRLVNSAIDSQFKFSVDSHTMTVMAMDFVPIVPYQTNILNIAIGQRYDVVITANQASVASDFFIRAIPQSSCSEND
NSDNIRGVLHYGSSTGLPTTTGYTFTDECVDEPVSSLVPYLPKTVSAASKSPEEAVTVAQNSQKLFKWYLNNSTFLSEWK
DPTLLMVQNNITAFGTPDNLVEVPNANEWIYLVIHSALPVPHPIHLHGHDFFVVSQQATAFDATTAVSTYNLNNPPRRDV
ATLPGGGYLVLAFETDNPGAWLMHCHIGWHTSMGFAMQFLERASEIPKLLDTTQLQDTCTAWTGHAVIQEDSGV
>XP_001547254.1 Bclcc8 [Botrytis cinerea B05.10]
MRLHILLALCLSFCQIHASPLFGWSFNPIATLQADLLKIINQAECLVATKVSIIPSILTFGNSNPVTSNKCSTTSGKTTS
SAAIQTSLSSLQSVASSKWSSLQSLLSTTTSLPPILTTSFTATTAKPTTTSSVKSTSTTANTVSSTAKPSSITSTASSTA
SSTSKTSSSAVASGTPCAGNTAADRSKWCNYSTSTDYYNEVPDTGVTREYWFNVQDGVASPDGISRYVQTINGSIPGPTI
IADWGDNVVVHVTNSLTTNGSSIHFHGIHQKNTNQNDGVPSVTQCPIAYGDTYTYRWRATQYGSSWYHSHVGLQAWEGVT
GGIIINGPATANYDEDKGTLMLSDWGHETVDELYQKVQTVGPQSMTTGLINGTNVFGADGASNQTGSRFSTSVQSGKSYR

FRLVNSAIDSQFKFSVDSHTMTVMAMDFVPIVPYQTEILNIAIGQRYDVVITANQASVASDFFIRAIPQSSCSENDNSDN
IRGVLHYGSSTGLPTTTGYTFTDECVDEPVASLVPYLPKTVSSASKSPEEAVTVAQNSQKLFKWYLNNSTFLSEWEDPTL
LMVQNNVTAFGTPDNLVEVPNANEWIYLVIHSALPVPHPIHLHGHDFFVVSQQSTTFDATTAVSTYNLNNPPRRDVATLP
GGGYLVLAFETDNPGAWLMHCHIGWHTSMGFAMQFLERASEIPKLLDTTQMLDTCTAWNGHAIIQEDSGV
>KAF7892221.1 hypothetical protein EAF01_010301 [Botrytis porri]
MKYFTVFTALTVFFAQASASAIPAVRSPLTPRQNTTASCANSATSRSCWGEYSIDTNWYDVTPTGVTREYWLSVENSTIK
PDGYTRSAMTFNGTVPGPAIIADWGDNLIIHVTNNLEYNGTSIHWHGIRQLGSLEYDGVPGVTQCPIAPGDTLTYKFQVT
QYGTTWYHSHFSLQYGDGLFGPLIINGPATADYDEDAGVIFLQDWAHESVFEIWDSARIGAPPALENTLMNGTNTFDCSA
STDPNCVGGGKKFELTFVEGTKYRLRLINVGIDSHFEFAIDGHTLTVIATDLVPIVPYTTETLLIGIGQRYDVIVEANAA
AGNYWIRGNWGNACSANNEAANATGILRYDSSSTADPTSVGTTPRGTCEDEPVASLVPHLALNVGDYSLVDEQVSFAFTN
YFTWTINSSSLLLDWSSPTTLKIFNNETIFPTDYNVVPLEQTNNEEWVVYVIEDLTGFGIWHPIHLHGHDFFIVAQEADV
FNADKSPAKFNLVNPPRRDVAALPGNGYLAIAFKLDNPGSWLLHCHIAWHASEGFAMQFVESQSSIAVGMTDTAIFENTC
ANWNAYTPTQLFAEDDSGI
>XP_001553186.1 Bclcc2 [Botrytis cinerea B05.10]
MKYSTVFTALTALFAQASATAIPAVRSPLAPRQSTTASCANSATSRSCWGEYSIDTNWYDVTPNTGVTREYWLSVENSTI
TPDGYTRSAMTFNGTVPGPAITADWGDNLIIHVTNNLQHNGTSIHWHGIRQLGSLEYDGVPGVTQCPIAPGDTLTYKFQA
TQYGTTWYHSHFSLQYADGLFGPLIINGPATADYDEDVGAIFLQDWAHKSVFEIWDSARQGAPPALENTLMNGTNIYDCS
ASTDANCVGGGKKFELTFVEGTKYRLRLINVGIDSHFEFAIDNHTLTVIANDLVPIVPYTTDTLLIGIGQRYDVIVEANA
AADNYWIRGNWGTTCSSNSEAANATGILRYDSSSTVDPTSVGVTPRGTCADEPVASLVPHLALDVGGYSLVDEQVSFAFT
NYFTWTINSSSLLLDWSSPTTLKIFNNETIFPTDYNVVALNQTDANEEWVVYVIEDLTGFGIWHPIHLHGHDFYVVAQET
DVFSATKSPANFNLVNPPRRDVAALPGNGYLAIAFKLDNPGSWLLHCHIAWHASEGLAMQFVESQSSIAIGMSDTDIFED
TCANWNAYTPTELFAEDDSGI
>TGO86421.1 hypothetical protein BPOR_0305g00070 [Botrytis porri]
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PDGYTRSAMTFNGTVPGPAIIADWGDNLIIHVTNNLEYNGTSIHWHGIRQLGSIEYDGVPGVTQCPIAPGDTLTYKFQVT
QYGTTWYHSHFSLQYGDGLFGPLIINGPATADYDEDAGVIFLQDWAHESVFEIWDSARIGAPPALENTLMNGTNTFDCSA
STDPNCVGGGKKFELTFVEGTKYRLRLINVGIDSHFEFAIDGHTLTVIATDLVPIVPYTTETLLIGIGQRYDVIVEANAA
AGNYWIRGNWGNACSANNEAANATGILRYDSSSTADPTSVGTTPRGTCEDEPVASLVPHLALNVGDYSLVDEQVSFAFTN
YFTWTINSSSLLLDWSSPTTLKIFNNETIFPTDYNVVPLEQTNNEEWVVYVIEDLTGFGIWHPIHLHGHDFFIVAQEADV
FNADKSPAKFNLVNPPRRDVAALPGNGYLAIAFKLDNPGSWLLHCHIAWHASEGFAMQFVESQSSIAVGMTDTAIFENTC
ANWNAYTPTQLFAEDDSGI
>AFC76164.1 laccase [Botrytis aclada]
MKYFTVFTALTALFAQASASAIPAVRSTLTPRQNTTASCANSATSRSCWGEYSIDTNWYDVTPTGVTREYWLSVENSTIT
PDGYTRSAMTFNGTVPGPAIIADWGDNLIIHVTNNLEHNGTSIHWHGIRQLGSLEYDGVPGVTQCPIAPGDTLTYKFQVT
QYGTTWYHSHFSLQYGDGLFGPLIINGPATADYDEDVGVIFLQDWAHESVFEIWDTARLGAPPALENTLMNGTNTFDCSA
STDPNCVGGGKKFELTFVEGTKYRLRLINVGIDSHFEFAIDNHTLTVIANDLVPIVPYTTDTLLIGIGQRYDVIVEANAA
ADNYWIRGNWGTTCSTNNEAANATGILRYDSSSIANPTSVGTTPRGTCEDEPVASLVPHLALDVGGYSLVDEQVSSAFTN
YFTWTINSSSLLLDWSSPTTLKIFNNETIFPTEYNVVALEQTNANEEWVVYVIEDLTGFGIWHPIHLHGHDFFIVAQETD
VFNSDESPAKFNLVNPPRRDVAALPGNGYLAIAFKLDNPGSWLLHCHIAWHASEGLAMQFVESQSSIAVKMTDTAIFEDT
CANWNAYTPTQLFAEDDSGI
>KAF7924682.1 hypothetical protein EAE97_010633 [Botrytis byssoidea]
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AAAVQTSLSSLQSVASSKWSSLQSLLSTTTSLPPIFTSSITVTTANPTSISSATSTSTTANTVSSTAKSSSITSTTSPVS
SSTASSTSKTSSSAVASGTPCAGNTAADRSKWCDYSTSTDYYNEVPNTGVTREYWFNVQDGVASPDGVSRYVQTINGSIP
GPTIIADWGDNVVVHVTNSLATNGSTIHFHGIHQKNTNQNDGVPSVTQCPIAYGDTYTYRWRATQYGSSWYHSHVGLQAW
EGVAGGIIINGPATANYDEDKGTLMLSDWGHVTVDELYQKIQTIGPQSMATGLINGTNVFGADGASNQTGSRFSTSVESG
KSYRFRLVNSAIDSQFKFSVDSHTMTVMAMDFVPIVPYQTEILNIAIGQRYDVVITANQASVASDFFIRAIPQSSCSEND
NSDNIRGVLHYGSSTGLPTTTGYTFTDECVDEPVSSLIPYLPKTVSAASKSPEEAVTIAQNSQKLFKWYLNNSTFLSEWE
DPTLLMVQNNITAFGTPDNLVEVPNANEWIYLVIHSALPVPHPIHLHGHDFFVVSQQATTFDAATAVSTYNLNNPPRRDV
ATLPGGGYLVLAFETDNPGAWLMHCHIGWHTSMGFAMQFLERASEIPKLLDTKQLQDTCTAWTGHAVIQEDSGV
>3V9E_A Structure of the L499M mutant of the laccase from B.aclada [Botrytis aclada]
MKYFTVFTALTALFAQASASAIPAVRSTLTPRQNTTASCANSATSRSCWGEYSIDTNWYDVTPTGVTREYWLSVENSTIT
PDGYTRSAMTFNGTVPGPAIIADWGDNLIIHVTNNLEHNGTSIHWHGIRQLGSLEYDGVPGVTQCPIAPGDTLTYKFQVT
QYGTTWYHSHFSLQYGDGLFGPLIINGPATADYDEDVGVIFLQDWAHESVFEIWDTARLGAPPALENTLMNGTNTFDCSA
STDPNCVGGGKKFELTFVEGTKYRLRLINVGIDSHFEFAIDNHTLTVIANDLVPIVPYTTDTLLIGIGQRYDVIVEANAA
ADNYWIRGNWGTTCSTNNEAANATGILRYDSSSIANPTSVGTTPRGTCEDEPVASLVPHLALDVGGYSLVDEQVSSAFTN
YFTWTINSSSLLLDWSSPTTLKIFNNETIFPTEYNVVALEQTNANEEWVVYVIEDLTGFGIWHPIHLHGHDFFIVAQETD
VFNSDESPAKFNLVNPPRRDVAALPGNGYLAIAFKLDNPGSWLLHCHIAWHASEGMAMQFVESQSSIAVKMTDTAIFEDT
CANWNAYTPTQLFAEDDSGI
>THV50112.1 hypothetical protein BGAL_0164g00030 [Botrytis galanthina]
MRLHILLALCLSFCQIQASPLFGWSFNPIATLQADLLKIINQVECLASTKVSYIPSLLTFGNTNAVTSNKCSTTSGKTTS

AAAVQTSLSSLQSVASSKWSSLQSLLSTTTSLPPIFTSSLTVTTAKPTSTSSVASTSTTANTMSPTAKSSSITSTTSPVS
SSTASSTSKTSSSAVASGTPCAGNTAADRSKWCDYSTSTDYYNEVPNTGVTREYWFNVQDGVASPDGVSRYVQTINGSIP
GPTIIADWGDNVVVHVTNSLATNGSTIHFHGIHQKNTNQNDGVPSVTQCPIAYGDTYTYRWRATQYGSSWYHSHVGLQAW
EGVAGGIIINGPATANYDEDKGTLMLSDWGHVTVDELYQKIQTIGPQSMATGLINGTNVFGADGASNQTGSRFSTSVESG
KSYRFRLVNSAIDSQFKFSVDSHTMTVMAMDFVPIVPYQTEILNIAIGQRYDVVITANQASVASDFFIRAIPQSSCSEND
NSDNIRGVLHYGSSTGLPTTTGYTFTDECVDEPVSSLVPYLPKTVSAASKSPEEAVTIAQNSQKLFKWYLNNSTFLSEWE
DPTLLMVQNNITAFGTPDNLVEVPNANEWIYLVIHSALPVPHPIHLHGHDFFVVSQQATTFDAATAVSTYNLNNPPRRDV
ATLPGGGYLVLAFETDNPGAWLMHCHIGWHTSMGFAMQFLERASEIPKLLDTTQLQDTCTAWTGHAVIQEDSGV
>XP_037193984.1 putative extracellular dihydrogeodin oxidase protein [Botrytis fragariae]
MKYSTLFTALTAFFAQASASAIPAVRSPLTPRQNTTASCANSATSRSCWGEYSIDTNWYDVTPTGVTREYWLSVENSTIA
PDGYTRSAMTFNGTVPGPAIIADWGDNLVIHVTNNLEYNGTSIHWHGIRQLGSLEYDGVPGVTQCPIAPGDTLTYKFQVT
QYGTTWYHSHFSLQYGDGLFGPLIINGPATADYDEDVGAIFLQDWAHESVFEIWDSAKLGGPPALENNLMNGTNIFDCSA
STDPNCVGGGKKFELTFVEGTKYRLRLINVGIDSHFEFAIDGHTLTVIANDLVPIVPYTTDTLLIGIGQRYDVIVEANAA
ADNYWIRGNWGTACSANNEAANATGILRYDSSSTADPTSVGTTPRGTCEDEPVASLVPHLALDVGGYSLVDEQLSFAFTN
YFTWTINSSSLLLDWSSPTTLKIFNNETIFPTDYNVVPLEQTSANEEWVVYVIEDLTGFGIWHPIHLHGHDFYIVAQEAD
VFDPDTSPAEFNLVNPPRRDVAALPGNGYLAIAFKLDNPGSWLLHCHIAWHASEGLAMQFVESQSSIAVGMSDTAIFEDT
CANWNAYTPTQLFAEDDSGI
>KAF7947057.1 hypothetical protein EAE97_004306 [Botrytis byssoidea]
MKCSTIFTALTAFFAQASASAIPAVRSPLTPRQNTTTSCANSATSRSCWGEYSIDTNWYDVTPTGVTREYWLSVENSTIT
PDGYTRSAMTFNGTVPGPAIIADWGDNLIIHVTNNLEHNGTSIHWHGIRQLGSLEYDGVPGVTQCPIAPGDTLTYKFQAT
QYGTTWYHSHFSLQYGDGLFGPLIINGPATADYDEDVGVIFLQDWAHESVFEIWDSARLGAPPALENTLMNGTNTFDCSA
STDPNCVGGGKKFELTFVEGTKYRLRLINVGIDSHFEFAIDGHTLTVIANDLVPIVPYTTDTILIGIGQRYDVIVEANAA
ADNYWIRGNWGTTCSGNMEAANATGILRYDSSSTADPTSVETTPRGTCEDEPVASLVPHLALDVGGYSLVDEQMSFAFTN
YFTWTINSSSLLLDWSSPTTLKIFNNETIFPTEYNVVPLEQTNANEEWVVYVIEDLTGFGIWHPIHLHGHDFFIVAQEAD
VFNPDKSPAKFNLVNPPRRDVAALPGNGYLAIAFKLDNPGSWLLHCHIAWHASEGLAMQFVESQSSIAVGMSDTAIFENT
CANWNAYTPTQLFAEDDSGI
>KAF7914060.1 hypothetical protein EAF01_000466 [Botrytis porri]
MRLHILLALCLSLCQIQASPLFGWSFNPIATLQADLLKIINQVECLVSTKVSIIPSILTSGNTNAVTSNKCSTTSGKTTS
AAAIQTSLSSLQSVASSKWSSLQSLLSTTTSLPPILTTSLVTSTAKPTITSSVQSTSTTANTVSSTAKSSSITSTTSPVS
SSTSPSTSKTSSSAVASGTPCAGNTAADRSKWCDYSTSTDYYNEVPNTGVTREYWFNVQDGVASPDGFSRYVQTINGSIP
GPTIIADWGDNVVVHVTNSLSANGSSIHFHGIHQKNTNQNDGVPSVTQCPIAYGTTYTYRWRATQYGSSWYHSHVGLQAW
EGVTGGIIINGPATANYDEDKGILMLSDWGHQTVDELYEKVQTIGPQSMTTGLINGTNVFGEDGASNQTGSRFATSVESG
KSYRFRLVNSAIDTQFKFSVDSHTMTVMAMDFVPIVPYQTEILNIAIGQRYDVVITANQASVASDFFIRAIPQSSCSEND
NSNNIRGVLHYGSSTGLPTTTGYTFTDECVDEPVSSLVPYLPKTVSAASQSPEEAVTVAQNSQKLFKWYLNNSTFLSEWN
DPTLLMVENNITAFGTPDNLVAIPNANEWIYIVIHSALPVPHPIHLHGHDFFVVSQQATTFDAATAVSTYNLNNPPRRDV
ATLPGGGYLVLAFETDNPGAWLMHCHIGWHTSMGFAMQFLERASEIPKLLDTTQLQDTCAAWTGHAVIQEDSGV
>TGO30877.1 hypothetical protein BPAE_0003g01630 [Botrytis paeoniae]
MKYSTVFTVLTAFFAQASASAIPAVRSPLTPRQNTTASCANSATSRSCWGEYSIDTNWYDVTPTGVTREYWLSVENSTIT
PDGYTRSAMTFNGTVPGPAIIADWGDNLIIHVTNNLENNGTSIHWHGIRQLGSLEYDGVPGVTQCPIAPGDTLTYKFQVT
QYGTTWYHSHFSLQYGDGLFGPLIINGPATADYDEDVGVIFLQDWAHESVFEIWDSARLGAPPALENTLMNGTNTFDCSA
STDPNCVGGGKKFELTFVEGTKYRLRLINVGIDSHFEFAIDGHTLTVIANDLVPIVPYTTDTLLIGIGQRYDVIVEANAA
ADNYWIRGNWGTACSGNTEAANATGILRYDSSSTVDPTSVGTTPRGTCEDEPVASLVPHLALDVGGYSLVDEQMSFAFTN
YFTWTINSSSLLLDWSSPTTLKIFNNEKIFPTEYNVVPLEQTNANEEWVVYVIEDLTGFGIWHPIHLHGHDFFIVAQEAD
VFNPEKSPAKFNLVNPPRRDVAALPGNGYLAIAFKLDNPGSWLLHCHIAWHASEGLAMQFVESQSSIAVGMSDTAIFEDT
CANWNAYTPTQLFAEDDSGI
>TGO11347.1 hypothetical protein BTUL_0112g00370 [Botrytis tulipae]
MRLHILLALCLSFCQIQASPLFGWSFNPIATLQADLLEIVNQVECLASTKISYIPSLLTFGNTNTVTPNKCSPTSGKTTS
AAAVQTSLSSLQSVASSKWSSLQSLLSTTTSLPPILTSSLTVTTAKPTSTSSATSTSTTANTVSSTAKSSSITSTTSPVS
SSTASSTSKTSSSAVASGTPCAGNTAADRSKWCDYSTSTDYYNEVPNTGVTREYWFNVQDGVASPDGVSRYVQTINGSIP
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KSYRFRLVNSAIDSQFKFSVDSHTMTVMAMDFVPIVPYQTEILNIAIGQRYDVVITANQASVASDFFIRAIPQSSCSEND
NSDNIRGVLHYGSSIGLPKTTGYTFIDECVDEPVSSLVPYLPKTVSAASKSPEEAVTVAQNSQKLFKWYLNNSTFLSEWK
DPTLLMVQNNITAFGTPDNLVVLPNANEWIYLVIHSALPVPHPIHLHGHDFFVVSQQATAFDAATAVSTYNLNNPPRRDV
ATLPGGGYLVLAFETDNPGAWLMHCHIGWHTSMGFAMQFLERASEIPKLLDTKQLQDTCTAWTGHTVIQEDSGV
>KAF7857155.1 hypothetical protein EAF02_011388 [Botrytis sinoallii]
MRLHILLALCLSFCQIQASPLFGWFFNPIATLQADLLNIINQAECLVSTKVSYIPSILTSGNTNAVTSNKCSTTSGKTTS
AAAVQSSLSSLQSVASSKWSSLQSLLSTTTSLPPILTTSLTTSTAKPTSTSSVTSTSTTANTVSSTAKPSSITSTTSPVS
SSTASSTSKTSSSAVASGTPCAGNTAADRSKWCDYSTSTDYYNEVPDTGVTREYWFNVQDGVASPDGFSRYVQTINGSIP
GPTIIADWGDDVVVHVTNSLATNGSTIHFHGIHQKNTNQNDGVPSVTQCPIAYGNTYTYRWRATQYGSSWYHSHVGLQAW
EGVAGGIIINGPATANYDEDKGTLMLSDWGHETVDELYQKVQTVGPQSMTTGLINGTNVFGADGASNQTGSRFSTSVESG

KSYRFRLVNSAIDSQFKFSVDSHTMTVMAMDFVPIVPYQTDILNIAIGQRYDVVITANQASVASDFFIRAIPQSSCSEND
NSDNIRGVLHYGSSTGLPTTTGYTFTDECVDEPVSSLVPYLPKTVSAASKSPEEAVTVAQNSQQLFKWYLNNSTFLSEWE
DPTLLMVQNNITAFGTPDNLVEVPNANEWIYLVIHSALPVPHPIHLHGHDFFVVSQQATTFDATTAISTYNLNNPPRRDV
ATLPGGGYLVLAFETDNPGAWLMHCHIGWHTSMGFAMQFLERASEIPKLLDTTQLQDTCAAWTGHAVIQEDSGV
>KAF7883499.1 hypothetical protein EAF02_005419 [Botrytis sinoallii]
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PDGYTRSAMTFNGTVPGPAIIADWGDNLIIHVTNNLEYNGTSIHWHGIRQLGSLEYDGVPGVTQCPIAPGDTLTYKFQAT
QYGTTWYHSHFSLQYGDGLFGPLIINGPATADYDEDVGAIFLQDWAHESVFEIWDSARLGAPPALENTLMNGTNIFDCSA
STDPNCVGGGKKFELTFVEGTKYRLRLINVGIDSHFEFAIDGHTLTVIANDLVPIVPYTTDTLLIGIGQRYDVIVEANAA
ADNYWIRGNWGTTCSANMEAANATGILRYDSSSTADPTSVGTTPRGTCEDEPVASLVPHLALDVGAYSLVDEEVSFAFTN
YFTWTINSSSLLLDWSSPTTLKIFNNETIFPTEYNVVPLEQTNNEEWVVYVIEDLTGFGIWHPIHLHGHDFYIVAQEADV
FNPKTSPAKFNLVNPPRRDVAALPGNGYLAIAFKLDNPGSWLLHCHIAWHASEGLAMQFVESQSSIAVGMSDTAIFEDTC
ANWNAYTPTQLFAEDDSGI
>KAF7918470.1 hypothetical protein EAE98_009713 [Botrytis deweyae]
MRLHILLALCLSFCQIQASPLFGWFFNPIATLQADLLNIINQAECLVSTKVSYIPSILTSGNTNAVTSNKCSTTSGKTTS
AAAVQSSLSSLQSVASSKWSSLQSLLSTTTSLPPILTTSLTTSTAKPTSTSSVTSTSTTANTVSSTAKPSSITSTTSPVS
SSTASSTSKTSSSAVASGTPCAGNTAADRSKWCDYSTSTDYYNEVPDTGVTREYWFNVQDGVASPDGFSRYVQTINGSIP
GPTIIADWGDNIVVHVTNSLATNGSTIHFHGIHQKNTNQNDGVPSVTQCPIAYGNTYTYRWRATQYGSSWYHSHVGLQAW
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KSYRFRLVNSAIDSQFKFSVDSHTMTVMAMDFVPIVPYQTDILNIAIGQRYDVVITANQASVASDFFIRAIPQSSCSEND
NSDNIRGVLHYGSSTGLPTTTGYTFTDECVDEPVSSLVPYLPKTVSAASKSPEEAVTVAQNSQKLFKWYLNNSTFLSEWE
DPTLLMVQNNITAFGTPDNLVEVPNANEWIYLVIHSALPVPHPIHLHGHDFFVVSQQATTFDASTAISTYNLNNPPRRDV
ATLPGGGYLVLAFETDNPGAWLMHCHIGWHTSMGFAMQFLERASEIPKLLDTTQLQDTCAAWTGHAVIQEDSGV
>KAF7926490.1 hypothetical protein EAE99_005685 [Botrytis elliptica]
MRLHILLALCLSFCQIQASPLFGWFFNPIATLQADLLNIINQAECLVSTKVSYIPSILTSGNTNAVTSNKCSTTSGKTTS
AAAVQSSLSSLQSVASSKWSSLQSLLSTTTSLPPILTTSLTTSTAKPTSTSSVTSTSTTANTVSSTAKPSSITSTTSPVS
SSTASSTSKTSSSAVASGTPCAGNTAADRSKWCDYSTSTDYYNEVPDTGVTREYWFNVQDGVASPDGFSRYVQTINGSIP
GPTIIADWGDNVVVHVTNSLATNGSTIHFHGIHQKNTNQNDGVPAVTQCPIAYGNTYTYRWRATQYGSSWYHSHVGLQAW
EGVAGGIIINGPATANYDEDKGTLMLSDWGHQTVDELYQKVQTVGPQSMTTGLINGTNVFGADGASNQTGSRFSTSVESG
KSYRFRLVNSAIDSQFKFSVDSHTMTVMAMDFVPIVPYQTDILNIAIGQRYDVVITANQASVASDFFIRAIPQSSCSEND
NSDNIRGVLHYGSSTGLPTTTGYTFTDECVDEPVSSLVPYLPKTVSAASKSPEEAVTVAQNSQKLFKWYLNNSTFLSEWE
DPTLLMVQNNITAFGTPDNLVEVPNANEWIYLVIHSALPVPHPIHLHGHDFFVVSQQATTFDASTAISTYNLNNPPRRDV
ATLPGGGYLVLAFETDNPGAWLMHCHIGWHTSMGFAMQFLERASEIPKLLDTTQLQDTCAAWTGHAVIQEDSGV
>KAF7960387.1 hypothetical protein EAE96_000070 [Botrytis aclada]
MRLHILLALCLSICQIQATPLFGWSFNPIATLQADLLKIINQVECLASTKLSVIPSILTFGNTNAVTSNKCSTTAGKTTS
AAAVQTSLSSLQSVASSKWSSLQSLLSTTTSLPPILTSSLTVTTTKPTTTSSVQSTSITASTVSSTAKSSSITGTTSPVS
SSTASSTSKTSSSAVASGIPCAGNTAADRSKWCDYSTSTDYYNEVPDTGVTREYWFNVEDGVASPDGFSRYVQTINGSIP
GPTIIADWGDNIVVHVTNSLATNGSTIHFHGIHQKNTNQNDGVPSVTQCPIAYGSTYTYRWRATQYGSSWYHSHVGLQAW
EGVAGGIIINGPATANYDEDKGTLMLSDWGHETVDALYQKVQTVGSQSMTTGLINGTNVFGADGASNQTGSRFSTSVEAG
KSYRFRLVNSAIDSQFKFSVDSHTMTVMAIDFVPIVPYQTEILNIAIGQRYDVVITANKASVASDFFIRAMPQSSCSEND
NSDNIRGVLHYGSSIGLPTTTAYTFTDECVDEPASSLVPYLPKTVSAASKSPEEAVTIAQNSQKLFKWYLNNSTFLSEWE
DPTLLMVQNNITTFGTPDNLVAVPNANEWIYLVIHSALPVPHPIHLHGHDFFVVSQQTTTFDAATAVSTYNLNNPPRRDV
ATLPGGGYLVLAFETDNPGAWLMHCHIGWHSSMGFAMQFLERASEIPKLLDTTQLQDTCAAWNGHAVIQEDSGV
>TGO42259.1 hypothetical protein BHYA_0010g00190 [Botrytis hyacinthi]
MKYSTVFTALTALFAQASASAIPAARSPLTPRSPLTPRSPLTPRSPLTTRQNTTASCANSATSRSCWGEYSIDTNWYDVT
PTGVTREYWLSVENSTITPDGYTRSAMTFNGTVPGPAIIADWGDNLIIHVTNNLENNGTSIHWHGIRQLGSLEYDGVPGV
TQCPIAPGDTLTYKFQVTQYGTTWYHSHFSLQYGDGLFGPLIINGPATADYDEDVGAIFLQDWAHESVFEIWDSARLGAP
PALENTLMNGTNIFDCSASTDPNCVGGGKKFELTFVEGTKYRLRLINVGIDSHFEFAIDGHTLTVIANDLVPIVPYTTDT
LLIGIGQRYDVIVEANAAADNYWIRGNWGTACSGNLEAANATGILRYDSSSTADPTSVGTTPRGTCEDEPVASLVPHLAL
DVGGYSLVDEEVSFAFTNYFTWTINSSSLLLDWSSPTTLKIFNNETIFPTEYNVVPLEQTNANEEWVVYVIEDLTGFGIW
HPIHLHGHDFFVVAQESDVFNPDKSPAKFNLINPPRRDVAALPGNGYLAIAFKLDNPGSWLLHCHIAWHASEGLAMQFVE
SQSSIAVGMSDTAIFEDTCANWNAYTPTQLFAEDDSGI
>KAF7925358.1 hypothetical protein EAE99_006222 [Botrytis elliptica]
MKYSTVFTALTAFFAQASASAIPAVRSPLTPRQNTTASCANSATSRSCWGEYSIDTNWYDVTPTGVTREYWLSVENSTIT
PDGYTRSAMTFNGTVPGPAIIADWGDNLIIHVTNNLEYNGTSIHWHGIRQLGSLEYDGVPGVTQCPIAPGDTLTYKFQAT
QYGTTWYHSHFSLQYGDGLFGPLIINGPATADYDEDVGAIFLQDWAHESVFEIWDSARVGAPPALENTLMNGTNIFDCSA
STDPNCVGGGKKFELTFVEGTKYRLRLINVGIDSHFEFAIDGHTLTVIANDLVPIVPYTTDTLLIGIGQRYDVIVEANAA
ADNYWIRGNWGTTCSANMEAANATGILRYDSSSTADPTSVGTTPRGTCEDEPVASLVPHLALDVGAYSLVDEEVSFAFTN
YFTWTINSSSLLLDWSSPTTLKIFNNETIFPTEYNVVPLEQTNNEEWVVYVIEDLTGFGIWHPIHLHGHDFYIVAQEADV
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ANWNAYTPTQLFAEDDSGI

>KAF7922626.1 hypothetical protein EAE98_008152 [Botrytis deweyae]
MKYSTVFTALTAFFAQASASAIPAVRSPLTPRQNTTASCANSATSRSCWGEYSIDTNWYDVTPTGVTREYWLSVENSTIT
PDGYTRSAMTFNGTVPGPAIIADWGDNLIIHVTNNLEYNGTSIHWHGIRQLGSLEYDGVPGVTQCPIAPGDTLTYKFQAT
QYGTTWYHSHFSLQYGDGLFGPLIINGPATADYDEDVGAIFLQDWAHESVFEIWDSARVGAPPALENTLMNGTNIFDCSA
STDPNCVGGGKKFELTFVEGTKYRLRLINVGIDSHFEFAIDGHTLTVIANDLVPIVPYTTDTLLIGIGQRYDVIVEANAA
ADNYWIRGNWGTTCSANMEAANATGILRYDSSSTADPTSVGTTPRGTCEDEPVASLVPHLALDVGAYSLVDEEVSFAFTN
YFTWTINSSSLLLDWSSPTTLKIFNNETIFPTEYNVVPLEQTNNDEWVVYVIEDLTGFGIWHPIHLHGHDFYIVAQEADV
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ANWNAYTPTQLFAEDDSGI
>THV49336.1 hypothetical protein BGAL_0200g00140 [Botrytis galanthina]
MKYSTVFTALTAFFAQASASAIPAVRSLLTPRQNTTASCANSATSRSCWGEYSIDTNWYDVTPTGVTREYWLSVENSTIT
PDGYTRSAMTFNGTVPGPAIIADWGDNLIIHVTNNLEYNGTSIHWHGIRQLGSLEYDGVPGVTQCPIAPGDTLTYKFQAT
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STDPNCVGGGKKFELTFVEGTKYRLRLINVGIDSHFEFAIDGHTLTVIANDLVPIVPYTTDTLLIGIGQRYDVIVEANAA
ADNYWIRGNWGTTCSGNLEAANATGILRYDSSSTADPTSVGTTPRGTCGDEPVASLVPHLALDVGGYSLVDEEVSFAFTN
YFTWTINSSSLLLDWSSPTTLKIFNNETIFPTEYNVVPLEQTNANEEWVVYVIEDLTGFGIWHPIHLHGHDFFVVAQESD
VFNPEKSPAKFNLINPPRRDVAALPGNGYLAIAFKLDNPGSWLLHCHIAWHASEGLAMQFVESQSSIAVGMSDTAIFENT
CANWNAYTPTQLFAEDDSGI
>AYM55298.1 laccase2, partial [Botrytis cinerea]
AIPAVRSPLAPRQSTTASCANSATSRSCWGEYSIDTNWYDVTPNTGVTREYWLSVENSTITPDGYTRSAMTFNGTVPGPA
ITADWGDNLIIHVTNNLQHNGTSIHWHGIRQLGSLEYDGVPGVTQCPIAPGDTLTYKFQATQYGTTWYHSHFSLQYADGL
FGPLIINGPATADYDEDVGAIFLQDWAHKSVFEIWDSARQGAPPALENTLMNGTNIYDCSASTDANCVGGGKKFELTFVE
GTKYRLRLINVGIDSHFEFAIDNHTLTVIANDLVPIVPYTTDTLLIGIGQRYDVIVEANAAADNYWIRGNWGTTCSSNSE
AANATGILRYDSSSTVDPTSVGVTPRGTCADEPVASLVPHLALDVGGYSLVDEQVSFAFTNYFTWTINSSSLLLDWSSPT
TLKIFNNETIFPTDYNVVALNQTDANEEWVVYVIEDLTGFGIWHPIHLHGHDFYVVAQETDVFSATKSPANFNLVNPPRR
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>TGO17305.1 hypothetical protein BTUL_0019g00960 [Botrytis tulipae]
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PDGYTRSAMTFNGTVPGPAIIADWGDNLIIHVTNNLEYNGTSIHWHGIRQLGSLEYDGVPGVTQCPIAPGDTLTYKFQAT
QYGTTWYHSHFSLQYGDGLFGPLIINGPATADYDEDAGVIFLQDWAHESVFEIWDTARLGAAPALENTLMNGTNTFDCSA
STDSNCVGGGKKFELTFVEGTKYRLRLINVGIEGHFEFAIDGHTLTVIANDLVPIVPYTTETLLIGIGQRYDVIVEANAA
ADNYWIRGNWGVTCSSNPEAANATGILRYDSSSTADPTSVGTTPRGTCEDEPVASLVPHLALDVGGYSLVDEQLSFAFTN
YFKWTINSSSLLLDWSSPTTLKIFNNETIFPTEYNVVPLEQTNANEEWVVYVIEDLTSLGVWHPIHLHGHDFFIVAQEAD
MFDPDESPAKFNLVNPPRRDVAALPANGYLAIAFKLDNPGSWLLHCHIAWHASEGLALQFVESQSSIAVGMSDTAIFENT
CANWNAYTPTQLFAEDDSGI
>KAF7909066.1 hypothetical protein EAE99_011547 [Botrytis elliptica]
MSFTLLLCIAILIPACLPSALPSKVSSNNKRISTPTCLNAASSRNCWNGNYSIDTNSEEAWPNTGVVVAYTLTITNQTMS
PDGTPRWMLVVNGTYPGPTITANWGDTLEITVVNQIITDGVSIHWHGIVQKNTNTMDGVNGITECPIPPGSSKVYKFLAT
QHGTSWYHSHHAAQYGDGVLVLGSIVINGPASLNYDYDLGPLPITDFYYKSTYEEGLLSVSKGPPKADNGLINGTNRNPH
KTAGVYNQVSGLVPGAKYRLRIINTSIDNHFQVTLDSHSFQVIQTDFVPIQPYTTNTIFIAIGQRYDVIITADQTPSNYW
FRAIVPKPPTQKGFGCGQNANNGSINAIFSYQGVELSEPNSKSFLIPQSCEDETQLVSWNEKSVPENEFVWPTAQELIVT
GPGSNSLPKAPAPYVWSINDTYMETEWDKPTLQYVAQGNKNYNVHQSIIELPDANVWTFWIIKNAAAIPHPIHLHGHDF
>XP_037197881.1 putative multicopper oxidase protein [Botrytis fragariae]
MRLHILLALCLSFCQIQAIPLFGWSFNPIATLQADLLKIINQVECLASTKVSIIPSILTSGNTNAVTSNKCSTTSGKTTS
AAAVQTSLSSLQSVASSKWSSLQSLLSTTTSLPPILTSSLTVTTAKPTSTSSAKSTSTTANTVSSTAQSSSITSKTSPVS
SSTASLTSKTSSSAVASGTPCAGNTAADRSKWCNYSTSTDYYNEVPNTGVTREYWFNVQDGVASPDGFSRYVQTINGSIP
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KSYRFRLVNSAIDTQFKFSVDSHTMTVMAMDFVPIVPYQTEILNIAIGQRYDVVITANQASVASDFFIRAIPQSSCSEND
NSDNIRGVLHYGSSTGLPTTTGYTFTDECVDEPVSSLVPYLPKTVSAASKSPEEAVTVAQNSQKLFKWYLNNSTFLSEWE
DPTLLMVQNNITTFGTPDNLVAVPNANEWIYLVIHSALPVPHPIHLHGHDFFVVSQQATTFDATTAISTYNLNNPHEETW
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>TGO35656.1 hypothetical protein BHYA_0151g00280 [Botrytis hyacinthi]
MYFTLLLCVAILIPSCLPSAIPSQVLSNNKRTSTSTCLNAASSRNCWNGNYSIDTDPEEAWPNTGVVVAYTLTITNQTMS
PDGTPRWMLVVNGTYPGPTITASELFPMWPPFPSAKLAHLFTDWGDTVQITVVNQIITDGVSIHWHGIVQKDTNTMDGVN
GITECPIPPGSSKVYKFLATQHATSWYHSHHAAQYGDGVLGSIVINGPASLNYDYDLGPLPITDFYYKSAYEEGLLSVSK
GPPKADNGLINGTNQNPHKIAGVYNQVSGLVPGAKYRLRIINTSIDNHFQVTLDSHSFQVIQTDFVPIQPYTTNTIFMAI
GQRYDIIITADQTPSNYWFRAIVPKPPTQKGFSCGQNANNGSINAIFSYQGVESSEPNSKSFLIPQSCEDETQQVSWHEK
SVPENEFVWPTAQELIVTGPGSNSLPKSPAPYVWSINDTYMEMEWDKPTLQYVAQGNKNYNVHQSIIELPDANVWDILDH
QKCCRDTTPYSSSWSRLLHFRTGEWCQFHRQI
>KAF7933110.1 hypothetical protein EAE97_008877 [Botrytis byssoidea]

MLFADFITQATTLLVASLSQLQTNGLSLWGTLDVPQLPLYNSTNAPQTSLQNTYGVIPNTGRTVYYDWTITRGYIAPDGV
NKSVILINGQFPGPLLDANWGDMIQVTVRNHIKDEGTTIHWHGLLQKGTPWMDGVPGISQCPISPGSQFTYRFRADQYGT
SWYHSHYSGQYGAGLFGPLVIYGPQNVHYDIDIGPVMLHDWYHADYYQVVERLFSVPANPLAANNNLINGKMDFNCSAIT
VNASCTANAGLSKFHFHPGKTHRLRLINPGTEGNQKFSIDGHLLTVIAVDFVPVVPYDTNVVTVGVGQRTDVIVKAVGKV
GSSYWMRSNFSQLCASSPSLQPNALAVVLYDGADPNSRPKSTAFPYNETNCLNDPLNTTTPYIKSTPPVTPQVTQTIDIN
YLINGSGMFLFTFGGSSFRADYNQPVLLTAATATTSTSNSGIYTNSTSLYPTTMNVHDFGTPATVRLIITNSVPVSHPMH
LHGHNFWILAEGVGTWDGTITNPSNPIRRDTFMMAAALRSGPKAYTVIEYVADNPGVWPFHCHVAGHVSTGLLINVLEQP
DVLANNSQALNSISPTCESWQKWTKSHLVDEIDSGE
>XP_024550974.1 Bclcc3 [Botrytis cinerea B05.10]
MVSHVFGRILCLVGSYLRFIDLSDYCFSEQSSIPADNTPTSRDCWGAYDIHTDYSNEWPTTNVVREYDLTASNMWIAPDG
VEVLGMVFNSQFPAPTIEADWGDTLRITVHNNLMNLNGTAVHWHGLRQLNSNWQDGVPGVSQCPITPFQSYTYEFQVTQY
GVSWYHSHFALQYPAGLYGPLKINGPTSQNYDIDIGPLLISDWFHQSPFSLFYEELCCNTPIPNSHLLQGQGVYYDETTG
LRSGSFYSLGVARGKKYKISLVNAGTSTQFTFWIDGHTFTVVGTDFVPIEGYETDTLNIAVGQRYDIIIKANAGCSHGTN
FWIHARDCNSPTQISTLGILRYDPTSTELPPDSHDNQLNFGCLEPPAKFLVPVVSKKVGKPINGLTPNQYLNVSLQPYPK
LDPDTHLLKWSLKNYPMYLNWSVPSLKLIQDNSDTTGVAFPQDYVPIFLDYPDNDWLYFLIEGMFNTTDPTIEVSNSSHP
IHLHGHDFSILAQSHTPFDISTFSPNLDNPPRRDTAMLPQNGYLVIGFEMNNPGAWLLHCHIAWHASSGMAVQFVESSGQ
LQSMIRKAGIMSSLEDQCDAWTSWYYDYNVPAEHTQDAESGV
>TGO22870.1 hypothetical protein BPAE_0152g00250 [Botrytis paeoniae]
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NKSVILINGQFPGPLLDANWGDMIQVTVRNYIKDEGTTIHWHGLLQSGTPWMDGVPGISQCPISPGSQFTYRFRADQYGT
SWYHSHYSGQYGAGLFGPLVIYGPQNVHYDVDIGPVMLHDWYHADYYQVVERLFSVPANPLAANNNLINGKMDFNCSAIT
VNASCTANAGLSKFQFYPGKTHRLRLINPGTEGNQKFSIDGHVLTVIAVDFVPVVPYDTNVVTIGVGQRTDVIVKAIGKV
GSSYWMRSNFSQLCASSPSLQPNALAVVLYDGANPNSRPNSTPFPYNETNCLNDPLNTTTPYVKSSPPVTPQVTQTIDIN
YVINGSGMFLFTFGGSSFRADYNQPVLLTAATATTSTSNSSIYTNSTSLYPTTMNVHDFGTPASVRLIITNSVPVSHPMH
LHGHNFWILAEGVGTWDGTITNPSNPIRRDTFMMAAALRTGSKAYTVIEYVADNPGVWPFHCHVSGHVSTGLLINVLEQP
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>THV45850.1 hypothetical protein BGAL_0444g00080 [Botrytis galanthina]
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GSSYWMRSNFSQLCASSASLQPNALAVVLYEGADPNSRPKSTPFPYNETNCLNDPLNTTTPYVKSTPPVKPQVTQTIDIN
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LHGHNFWILAEGVGTWDGTITNPSNPIRRDTFMMAAALRTGSKAYTVIEYVADNPGVWPFHCHVAGHVSTGLLINVLEQP
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>KAF7935780.1 hypothetical protein EAE99_002760 [Botrytis elliptica]
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GSSYWMRSNFSQLCASSPSLQPNALAVVLYDGANPNSRPKSTPFPYNETNCLNDPLNTTTPYVKSTPPVTPQVTQTIDIN
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LHGHNFWILAEGVGTWDGTITNPSNPIRRDTFMMAAALRTGPKAYTVIEYVADNPGVWPFHCHVAGHVSTGLLINVLEQP
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>KAF7930322.1 hypothetical protein EAE98_004723 [Botrytis deweyae]
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GSSYWMRSNFSQLCASSPSLQPNALAVVLYDGANPNSRPKSTPFPYNETNCLNDPLNTTTPYVKSTPPVTPQVTQTIDIN
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>KAF7881612.1 hypothetical protein EAF02_006300 [Botrytis sinoallii]
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VNASCTANAGLSKFHFHPGKTHRLRLINPGTEGNQKFSIDGHVLTVIAIDFVPVVPYDTNVVTVGVGQRTDVIVKAIGKV
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LHGHNFWILAEGVGTWDGTITNPSNPIRRDTFMMAAALRTGSKAYTVIEYVADNPGVWPFHCHVAGHVSTGLLINVLEQP

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>KAF7955862.1 hypothetical protein EAE96_004784 [Botrytis aclada]
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VNASCTANAGLSKFHFHPGKTHRLRLINPGTEGNQKFSIDGHVLTVIAVDFVPVVPYDTNVVTVGVGQRTDVVVKATGKV
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>TGO73487.1 hypothetical protein BELL_0357g00060 [Botrytis elliptica]
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LHGHNFWILAEGVGTWDGTITNPSNPIRRDTFMMAAALRTGPKAYTVIEYVADNPGVWPFHCHVAGHVSTGLLINVLEQP
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>KAF7929387.1 hypothetical protein EAE98_005305 [Botrytis deweyae]
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SLAAETSSTTQNLDIGSYVNDTGSFLWTLGGTSFRANYNNPILSLANQGNFTYPDEWNVRNFGSNTTIRVVVNNPTPASH
PMHLHGHNMQILHEGDGDWDGVTITRQANPQRRDVQLVRANGHLVWQITTDNPGVWPFHCHIAWHVSGGLYANILERPDD
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>XP_037196983.1 putative extracellular dihydrogeodin oxidase laccase protein [Botrytis fragariae]
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>TGO17900.1 hypothetical protein BTUL_0014g00230 [Botrytis tulipae]
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VNASCTANAGLSKFHFHPGKTHRLRLINPGTEGNQKFSIDGHVLTVIAVDFVPVVPYDTKVVTVGVGQRTDVIVKAIGKV
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>THV54155.1 hypothetical protein BGAL_0033g00270 [Botrytis galanthina]
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>KAF7922903.1 hypothetical protein EAE99_007095 [Botrytis elliptica]
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SLAAETSSTTQNLDIGSYVNDTGSFLWTLGGTSFRANYNNPILSLANQGNFTYPDEWNVRNFGSNTTIRVVVNNPTPASH
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>KAF7893241.1 hypothetical protein EAF02_000779 [Botrytis sinoallii]
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>TGO25281.1 hypothetical protein BPAE_0083g00130 [Botrytis paeoniae]
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>TGO13734.1 hypothetical protein BTUL_0064g00350 [Botrytis tulipae]
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TLAAETPSTTQNLDIGSYVNDTGTFLWTLGGTSFRANYNNPILSLANEGNFTYPDEWNVRNFGSNTTIRIVVNNPTPASH
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>TGO33302.1 hypothetical protein BHYA_0254g00180 [Botrytis hyacinthi]
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>KAF7894537.1 hypothetical protein EAF01_009988 [Botrytis porri]
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>XP_024546439.1 Bclcc5 [Botrytis cinerea B05.10]
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SLSAETPSTTQNLDINSYVNETGTFLWTLGGTSFRANYNSPVLSLANQGNFTYPDEWNVRNFGSNTTIRIVVNNPTPASH
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>KAF7959086.1 hypothetical protein EAE96_002603 [Botrytis aclada]
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SLAAETPSTTQNLDINFYVNDTENFLWTLGGTSFRANYNNPILSLANQGNFTYPDEWNVRNFGSNTTIRVIVNNPTPASH
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>KAF7949419.1 hypothetical protein EAE97_002928 [Botrytis byssoidea]
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>QFF92556.1 extracellular dihydrogeodin oxidase/laccase-like protein isoform 2 [Botrytis fabae]
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>QFF92555.1 extracellular dihydrogeodin oxidase/laccase-like protein isoform 1 [Botrytis fabae]
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>XP_001549796.1 Bclcc9 [Botrytis cinerea B05.10]
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DCSTKAAGDNATCNDENYMPPTFKFTAGLKHRLRLINAGTEGMQKFAIDGHNMTVIANDFVPIIPYTTQVVTLGVGQRTD
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>KAF7936664.1 hypothetical protein EAE97_008030 [Botrytis byssoidea]
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>KAF7884133.1 hypothetical protein EAF01_011556 [Botrytis porri]
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VIVEGLPTETSGSYWMRSTIAGCSLFKNPEAKALVYYGLEPNVNSTTTASTIFTDSVANVCANDPLNETTPWYPITPDPN
PPTTEQIDIGFGKNASGNWLWSMNNSSFHANYNEPILLLSNQGNNSYPDSPEWNVYNFGDNSSIRIYITNPTTVSHPMHL
HGHNMFVLNEGVGAWDGQTVVRPSNPQRRDVQTLQAGGYMVLQITADNPGVWPLHCHIAFHVGSGLYVSVLERPADIAKL
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>TGO35326.1 hypothetical protein BHYA_0162g00140 [Botrytis hyacinthi]
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VIVEGLPTETTGSYWMRSTIAGCSLFKNPEAKALVYYGLEPNVNSTTTASTIFIDSVANVCANDPLNETIPWYPITPDPN
PPTMEQIDIGFGQNASGNWLWSMNNSSFRANYNEPILLLSNQGNNSYPDSPEWNVYNFGDNSSIRIYITNPTTVSHPMHL
HGHNMFVLNEGVGLWDGQTVVRPSNPQRRDVQTLQAGGYMVLQITADNPGVWPLHCHIAFHVGSGLYVSVLERPADIAKL
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>KAF7879922.1 hypothetical protein EAF02_007559 [Botrytis sinoallii]
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VIVEGIPTETTGSYWMRSTIAGCSLFKNPEAKALVYYGLEPNVNSTTTASTIFNDSVANVCANDPLSETTPWYPITPDPN
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